Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AAAAAAAAAAAAAAAGAGAGAK	1597.8	2	4.4626	0.1607
AAAAAAAAAPAAAATAATTAATTAATAAQ	2343.5	3	6.4211	0.6104
AAAAAAAAVPSAGPAGPAPTSAAGR	2033.2	3	3.9727	0.2052
AAAAAAALQAK	957.1	2	4.5182	0.1574
AAAAAASAGSSASSGNQPPQELGLGELLEEFSR	3175.4	3	4.2192	0.361
AAAAMAPIKVGDAIPAVEVFEGEPGNKVNLAELFK	3569.1	3	4.5655	0.2735
AAAARLVGAAASRGPTAAR	1739.0	2	2.4034	0.161
AAAASAAEAGIATTGTEDSDDALLK	2321.4	2	4.9462	0.4043
AAAAVVAAAAR	942.1	2	3.2658	0.2436
AAADFATHGK	989.1	2	2.6591	0.2291
AAADLMAYCEAHAKEDPLLTPVPASENPFR	3229.6	3	3.9506	0.3231
AAAEDVNVTFEDQQK	1665.7	2	3.4392	0.3163
AAAEEGHIIPR	1164.3	2	2.6917	0.2919
AAAEVNQDYGLDPK	1491.6	2	4.5187	0.3826
AAAFEEQENETVVVK	1664.8	2	2.7826	0.2462
AAAFEQLQK	1006.1	2	2.708	0.2175
AAAFVTSPPLSPDPTTPDFLNSLLSCGDLQVTGSAHCTFNTAQK	4523.0	3	4.1208	0.3308
AAAGLGGGDSGDGTAR	1333.3	2	4.0286	0.4745
AAAGLLPGGK	855.0	2	2.6562	0.1021
AAAHIHSSPGR	1104.2	2	3.1979	0.3498
AAALAHLDR	938.1	2	2.9462	0.3167
AAALEAMKDYTK	1312.5	2	3.4032	0.3004
AAALEFLNRFEEAKR	1766.0	3	3.7671	0.3074
AAANEQLTR	974.1	2	3.0768	0.2306
AAAPQAWAGPMEEPPQAQAPPR	2272.5	2	3.4175	0.2612
AAAQLLQSQAQQSGAQQTK	1958.1	3	4.0766	0.1488
AAASTDYYKR	1146.2	2	2.4162	0.2259
AAATAEEPDPK	1100.2	2	3.0728	0.2412
AAATKKPAPEK	1112.3	2	2.7523	0.176
AAATPESQEPQAK	1328.4	2	3.2025	0.1008
AAATQPDAKDTPDEPWAFPAR	2256.4	3	3.6119	0.1413
AAATQPDAKDTPDEPWAFPAREFLR	2802.1	3	4.5161	0.2604
AAAVLAAESMVVTLAK	1545.9	2	4.1261	0.381
AAAVLPVLDLAQR	1337.6	2	3.5689	0.3874
AAAVPVEFQEHHLSEVQNMASEEKLEQVLSSMK	3698.1	3	5.0332	0.36
AAAVPVEFQEHHLSEVQNMASEEKLEQVLSSMKENK	4069.5	3	6.2007	0.4203

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AAAVSEAEADFYEQNSR	1858.9	2	2.9136	0.2662
AAAYSAQVQPVDGATR	1605.7	2	4.1852	0.3411
AADALEEQQR	1131.2	2	2.9883	0.1632
AADAVEDLRWFR	1449.6	2	2.4542	0.1516
AADDTWEPFASGK	1395.5	2	4.7341	0.4758
AADEVAEGK	889.9	2	2.8842	0.3146
AADEVAEGKLNDHFPLVVWQTGSGTQTNMNVNEVISNR	4143.5	3	7.0249	0.4894
AADEVLAEAKKPR	1398.6	2	2.7889	0.1917
AADFQLHTHVNDGTEFGGSIYQK	2536.7	3	5.0949	0.4309
AADGNYYNAR	1115.1	2	2.6809	0.2129
AADIDQEVKER	1274.4	2	3.0473	0.2503
AADISLDNLVEGKR	1501.7	2	3.6619	0.268
AADKGVYIIGSSGFDSIPADLGVIYTR	2787.1	3	4.9586	0.2437
AADKLIQNLDANHDGR	1751.9	3	4.0237	0.332
AADLNGDLTATR	1218.3	2	3.6695	0.2994
AADLQLEMTQKPHKKPGPGEPLVFGK	2818.3	3	6.5341	0.4212
AADMGNPVGQSGLGMAYLYGR	2129.4	2	5.8488	0.6132
AADPGPGAELDPAAPPPAR	1770.9	2	3.3488	0.4416
AADPLVGVFLWGVAHSINELSQVPPPVMLLPDDFK	3774.4	3	3.8761	0.1642
AADPPAENSSAPEAEQGGAE	1898.9	2	4.4129	0.3779
AADPTAPGSDSAVTLRGTSVER	2159.3	2	2.6602	0.1894
AADPVSPLLHELTFQAMAYDLLDIEQDTYRYETTGLSEAR	4546.0	3	3.2786	0.1184
AADRLPNLSSPSAEGPPGPPSGPAPR	2496.7	3	5.288	0.3626
AADVLVYLADDTVVPLAVENLPSLSAHELHR	3329.7	3	4.595	0.3282
AAEAAINILK	1014.2	2	3.347	0.2321
AAEAAPPTQEAQGETEPTEQAPDALEQAADTSR	3382.5	3	5.0162	0.4124
AAEAAPPTQEAQGETEPTEQAPDALEQAADTSRR	3538.6	3	4.6774	0.4522
AAEAGGAEEQYGFLTTPTK	1942.1	2	3.3333	0.2946
AAEAHVDAHYYEQNEQPTGTCAACITGDNR	3237.4	3	6.4609	0.2388
AAEALHGEADSSGVLAAVDATVNK	2297.5	3	5.0434	0.3649
AAEAVAAAVGTGATTAAVMAAAGIAAIGPAK	2626.0	3	5.0909	0.475
AAEDDEDDDVDTKKQK	1822.8	2	5.1059	0.2429
AAEDDEDDDVDTKKQKTDEDD	2398.3	3	4.9538	0.2649
AAEEAFVNDIDESSPGTEWER	2353.4	2	5.4415	0.4331
AAEEEDEADPKR	1360.4	2	3.7358	0.3007
AAEEPSKVEEK	1217.3	2	2.8178	0.1592

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AAEEVEAK	846.9	2	2.4123	0.1444
AAEFGEPTSEQTGTAAGK	1752.8	2	3.9223	0.3105
AAEKEAALVQQEEEKAEQR	2158.3	3	4.6505	0.3168
AAEKLYLADPMKAR	1577.9	2	3.7139	0.2523
AAEKRPAEDYVPR	1502.7	3	3.523	0.382
AAEKRPAEDYVPRK	1630.8	3	3.3862	0.2357
AAEKVSEAR	961.1	1	2.354	0.1516
AAELEMELNEHSLVIDTLKEVDETR	2886.2	3	3.6077	0.2141
AAELEMELNEHSLVIDTLKEVDETRK	3014.4	3	5.4961	0.368
AAELFHQLSQALEVLTDAAAR	2255.5	3	3.6655	0.2594
AAELIANSLATAGDGLIELR	1999.3	2	6.0425	0.4578
AAEMMASLLKDLAEIGIAVGNNDVKQPEGTGMIDEEFTVAR	4336.9	3	5.6732	0.4809
AAESETPGKSPEK	1331.4	2	2.7274	0.1225
AAESETPGKSPEKKPK	1684.9	2	3.8267	0.2452
AAESLADPTEYENLFPGLK	2066.3	2	5.0896	0.379
AAETDPGMVHLALGSDLTTLGLNLNSPENLYPK	3453.9	3	5.3907	0.4003
AAETHFGFETVSEEEKGGK	2054.2	3	4.0192	0.3535
AAFALGGLGSGFASNREELSALVAPAFAHTSQVLVDK	3704.1	3	3.9016	0.1955
AAFDDAIAELDTLSEESYK	2089.2	2	5.9763	0.5203
AAFDDAIAELDTLSEESYKDSTLIMQLLR	3260.6	3	6.1606	0.5514
AAFERESDVPLKTEEFEVTK	2326.5	2	5.1461	0.4399
AAFGEEVDAVDTGISR	1637.7	2	3.252	0.2978
AAFGLSEAGFNTACVTK	1687.9	2	3.4878	0.227
AAFGQGSGPIMLDEVQCTGTEASLADCK	2801.1	3	3.9809	0.1486
AAFIKAEKENPGLTQDIIMK	2218.6	3	4.0982	0.3695
AAFKELQSTFK	1270.5	2	2.4205	0.2351
AAFNSGK	694.8	1	1.822	0.185
AAFNSGKVDIVAINDPFIDLNYMVYMFQYDSTHGK	3986.5	3	6.1484	0.4791
AAFNSGKVDIVAINDPFIDLNYMVYMFQYDSTHGKFHGTVK	4656.3	3	5.8955	0.4419
AAFQLGSPWR	1133.3	2	3.5662	0.2741
AAFQPEANPSHLTLNTALVESEDL	2568.8	2	4.0096	0.2448
AAFSKDESKEPIVEVR	1806.0	2	4.4406	0.3905
AAFTAFEEAQLPR	1451.6	2	2.8828	0.1713
AAGEVLEPANLLAEEKDEDLLFE	2516.7	2	3.1643	0.2165
AAGGDGDDSLYPIAVLIDELR	2161.4	3	5.116	0.3488
AAGGGAGSSEDDAQSR	1436.4	2	3.6851	0.3492

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AAGGGSYKGHVDILAPTVQELAALEK	2596.9	3	5.3815	0.2912
AAGGGSYKGHVDILAPTVQELAALEKEAQTSFLHLGYLPNQLFR	4713.3	3	6.5398	0.5327
AAGHLLKPR	963.2	2	3.2177	0.2038
AAGHPGDPESQQR	1350.4	2	2.8924	0.2304
AAGIDEQENWHEGKENIR	2097.2	2	4.6415	0.3691
AAGKGPLATGGIKK	1269.5	2	3.477	0.3323
AAGKLKAEGSEIR	1330.5	2	3.0599	0.2065
AAGPSLSHTSGGTQSK	1486.6	2	4.1125	0.4649
AAGSGELGVTMK	1121.3	2	3.291	0.4317
AAGSGELGVTMKGPK	1403.6	2	3.4845	0.3842
AAGTDGSDFQHR	1262.3	2	2.5558	0.139
AAGVNVEPFWPGLFAK	1704.0	2	4.3197	0.4713
AAGVVLEMIR	1059.3	2	3.3014	0.2573
AAHFGNPEAAHPAPLYSPTRPVSR	2544.8	3	4.1413	0.3716
AAHGVLLQALDEMR	1524.8	2	4.4919	0.3647
AAHIFNEALVCHQIR	1723.0	2	4.4623	0.3383
AAHSEGNTTAGLDMR	1531.6	2	4.1549	0.5143
AAHVAPAAPDAGAPTAPAASATR	2043.2	2	4.7651	0.4646
AAHVLMPHESTVEHTHVDINEMESPLATR	3253.6	3	4.8683	0.4363
AAIAQLNGKEVK	1242.5	2	3.0342	0.1978
AAIDWFDGKEFHGNIIK	1962.2	3	4.8125	0.4488
AAIDWFDGKEFSGNPIK	1896.1	3	4.5176	0.3835
AAIISAEGDSK	1062.2	1	2.8662	0.3828
AAIISAEGDSKAAELIANSLATAGDGLIELR	3042.4	3	6.2618	0.4397
AAILETAPK	914.1	2	2.7485	0.1236
AAILETAPKEVPMVVVPPVGAK	2217.7	3	4.6042	0.3794
AAILQTEVDALR	1300.5	2	3.3219	0.3288
AAIVHNVDSDDLISMGSNDIEVLK	2556.8	2	5.7551	0.4875
AAIYDKYKEFAIPEEEAEWVGLTLEEAIEK	3486.9	3	3.5134	0.1824
AAIYDKYKEFAIPEEEAEWVGLTLEEAIEKQR	3771.2	3	3.8814	0.1275
AAKADEEPTPADGR	1428.5	2	3.269	0.1859
AAKLEILQQQLQVANEAR	2024.3	2	5.4595	0.3548
AAKPLPFKDPNFVHSGHGGAVAGK	2403.7	3	3.4715	0.2272
AAKQPHVGDYR	1242.4	2	2.533	0.2799
AAKVLEQLTGQTPVFSK	1818.1	2	5.2664	0.4284
AALAGGTTMIIDHVVPEPGTSLLAAFDQWR	3139.6	3	3.9033	0.1935

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AALAHPFFQDVTKPVPHLRL	2258.7	3	3.8923	0.2158
AALAHSEEVTASQVAATK	1784.9	2	5.7291	0.5776
AALAPAKESPR	1111.3	2	2.6646	0.2721
AALDGTPGMIGYGMAK	1553.8	2	4.3352	0.4196
AALDIVHPVRVDAGGSFLSYELWPRALRKR	3394.9	3	3.4516	0.1135
AALDKATVLLSMSK	1448.8	2	4.1121	0.355
AALEDTLAETEAR	1390.5	2	4.7816	0.4341
AALEYLEDIDLK	1393.6	2	2.8707	0.2459
AALEYLEDIDLKTLEKEPR	2247.5	3	4.2629	0.3643
AALGESGEQADGPK	1330.4	2	2.9407	0.279
AALHLYSNTLNFQISEVEPK	2275.5	3	4.1951	0.1083
AALHPPALAVLSHTPDGATQTIAWVGK	2724.1	3	4.2372	0.2856
AALLDQALSNAR	1243.4	2	3.0838	0.2627
AALLHGETR	968.1	2	2.6925	0.3023
AALLNQHYQVNFK	1546.8	2	4.0594	0.16
AALLWALAAALER	1369.6	2	3.1852	0.3263
AALMESQGQQQEER	1605.7	2	4.7375	0.2931
AALNTVHEANGTEDERAVSK	2113.2	3	3.2534	0.2151
AALPSHVVTMLDNFPTNLHPMSQLSAAVTALNSESNFAR	4154.7	3	7.087	0.5765
AALQELLSK	973.1	2	3.2952	0.1964
AALQELLSKGLIK	1384.7	2	4.0148	0.211
AALQELLSKGLIKLVSK	1812.2	3	4.1485	0.3604
AALQHAHAHSSGYFITQDSAFGNLILPVLPR	3333.7	3	3.4452	0.1932
AALQLVVDPGDPR	1351.5	2	2.5448	0.2482
AALRDYETVVK	1265.4	2	3.0392	0.1526
AALSAGKVSPETVDSVIMGNVLQSSSDAIYLAR	3351.8	3	4.8302	0.2707
AALSASEGEEVPQDKAPSHVPFLLIGGGTAAFAAAR	3537.9	3	5.6177	0.4828
AALSEEELEKK	1247.4	2	3.1104	0.1679
AALSSQQQQQLALLLQQFQTLK	2486.9	3	4.3333	0.3033
AALTGLLHR	952.1	2	3.105	0.3445
AALTVHQAR	967.1	2	2.7278	0.293
AALVAQNYINYQQGTPHR	2045.2	2	4.6681	0.43
AALVDLEPGTMDSVR	1574.8	2	4.0368	0.2911
AAMAAAQSGTPGPVFVELPVDVLYPYFMVQK	3298.9	3	4.4377	0.2869
AAMALEK	733.9	1	1.7569	0.1239
AAMDNSEIAGEK	1236.3	2	2.8013	0.1893

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AAMDNSEIAGEKK	1364.5	2	3.4219	0.2393
AAMDNSEIAGEKKSAQWRTVEGALKERR	3133.5	3	3.6049	0.1239
AAMEALVVEVTKQPAIISQLDPVNER	2823.3	3	5.6825	0.4278
AAMFPETLDEGMQIPSTQFDAAHPTNVQR	3204.5	3	4.7544	0.4336
AAMQRGSLPANVPTPRGLLGDAPNDPR	2773.1	3	3.2943	0.1906
AANDAGYFNDEMAPIEVK	1956.1	2	5.5418	0.4588
AANEVSSADVK	1091.2	2	3.6605	0.2477
AANEVSSADVKQVK	1446.6	2	3.6935	0.2683
AANGVVLATEKK	1201.4	2	2.9704	0.2321
AANMLQQSGSK	1135.3	2	3.2196	0.3538
AANNGALPPDLSYIVR	1671.9	2	3.1832	0.3056
AANQLDKDHAK	1211.3	2	2.5838	0.1779
AANSLEAFIFETQDK	1684.8	2	4.8969	0.4104
AANVLLSEHGEVK	1367.5	2	3.4448	0.2507
AAPASSAGASDAR	1132.2	2	3.5503	0.4199
AAPAVQTK	785.9	1	1.7551	0.2073
AAPFNNWMESAMEDLQDMFIVHTIEEIEGLISAHDQFK	4409.9	3	5.044	0.4423
AAPFSLEYR	1054.2	1	2.537	0.1533
AAPGAEFAPNKR	1229.4	2	2.5385	0.3785
AAPLAGFGYGLPISR	1490.7	2	4.945	0.5398
AAPLIVEVFNKVLHSSNPVPLYAPNLSPPADSR	3515.0	3	3.307	0.1737
AAPLQGMLPGLLAPLR	1619.0	2	4.2206	0.3976
AAPPPGQSQAQSQGQPVPTAPAR	2242.4	3	4.1478	0.2512
AAPRPAPVAQPPAAAPPSAVGSSAAAPR	2534.9	3	5.5501	0.4757
AAPSTAPAEATPPKPGEAEAPPKHPGVLK	2818.2	3	3.6028	0.2728
AAPTAASDQPDSAATTEK	1732.8	2	5.7203	0.5149
AAPTASGKAEPLAVGKEDPVSK	2124.4	3	3.4511	0.3443
AAQASDLEK	933.0	2	2.9636	0.2949
AAQASDLEKIHLDEK	1668.8	3	3.4147	0.3746
AAQASDLEKIHLDEKSFR	2059.3	3	4.945	0.4405
AAQEEYVK	938.0	2	2.4841	0.2292
AAQEEYVKR	1094.2	2	3.1026	0.1871
AAQELQEGQR	1130.2	2	3.6059	0.2101
AAQIFITELTLR	1376.6	2	2.8579	0.1503
AAQKADVLTTGAGNPVGDKLNVITVGPR	2764.1	3	6.8956	0.4647
AAQLQHSEK	1012.1	2	2.6632	0.2948

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AAQLVDKDSTFLSTLEHHLSR	2369.6	3	7.0794	0.5263
AAQMHSGYQR	1149.3	2	2.8545	0.2769
AAQNISK	731.8	1	1.6001	0.1624
AAQQQEEQEEKEEEDDEQTLHR	2700.7	3	5.2651	0.2537
AAQSTAMNR	950.1	2	3.005	0.2257
AASAAGAAGSAGGSSGAAGAAGGGAGAGTRPGDGGTASAGAAGPGAATK	3671.8	3	7.5985	0.5051
AASAATAAPTATPAAQESGTIPK	2084.3	3	4.5814	0.278
AASADSTTEGTPADGFTVLSTK	2128.2	2	5.9902	0.5258
AASAGQEPLHNEELAGAGR	1879.0	2	5.4733	0.3624
AASAGVPYHGEVPVSLAR	1782.0	2	3.2107	0.3141
AASAHAIGTVK	1026.2	2	2.7997	0.3291
AASDIAMTELPPTHPIR	1821.1	2	4.7114	0.4312
AASGEAKPK	859.0	2	2.6009	0.2117
AASGEAKPKVK	1086.3	2	2.7404	0.2044
AASGFNAMEDAQTLR	1582.7	2	4.9455	0.4624
AASGFNAMEDAQTLRK	1710.9	2	5.1237	0.4558
AASGYPVKVPLEVQEADEAKLQQTEAELR	3171.5	3	7.7458	0.4728
AASIFGGAKPVDTAAR	1532.7	2	3.6244	0.3745
AASNIIFSNGNLDPWAGGGIR	2131.3	2	4.1139	0.2802
AASQGYTVAR	1024.1	2	2.5546	0.2971
AASQPGELKDWFVGR	1661.8	2	4.4308	0.4932
AASQPTSLAPEKLREE	1727.9	2	2.9742	0.2622
AASQQEIEQSIETLNMLMLDLEPASAAAPLHK	3451.9	3	3.446	0.2512
AASSAAQGAFQGN	1180.2	2	3.1456	0.3946
AASSPGGSAPR	958.0	2	2.5539	0.1514
AATALKDVVK	1016.2	1	3.4365	0.2166
AATAPLLEAVDNLSAFASNPEFSSIPAQISPEGR	3472.8	3	4.1946	0.321
AATFGLILDDVSLTHLTFGK	2120.4	2	5.3533	0.4436
AATFGLILDDVSLTHLTFGKEFTEAVEAK	3125.5	3	4.0782	0.2556
AATHGLMLGALQGDGPLPAELEELR	2560.9	3	5.9384	0.401
AATHGLMLGALQGDGPLPAELEELRNR	2831.2	3	4.8217	0.3679
AATLAQELEKFNR	1491.7	2	2.4614	0.1753
AATSDLEHYDKTR	1507.6	2	4.2557	0.3568
AATSEGVQVK	990.1	2	3.0441	0.2558
AATSPALFNR	1048.2	2	2.6851	0.2052
AATSVKDLAQR	1160.3	2	2.7289	0.1426

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AAVAGEDGR	845.9	2	2.4563	0.1347
AAVAGEDGRMIAGQVLDINLAAEPK	2510.9	3	6.2204	0.2144
AAVAGKKPVVGK	1125.4	2	2.9772	0.1543
AAVAGKKPVVGKK	1253.6	2	3.3176	0.3092
AAVAIQSQFR	1091.2	2	3.6139	0.2719
AAVATFLQSVQVPEFTPK	1934.2	2	5.2914	0.4484
AAVAWEAGKPLSIEEIEVAPPK	2306.6	2	3.6028	0.3206
AAVAWEAGKPLSIEEIEVAPPKAHEVR	2899.3	3	5.8336	0.4358
AAVDAGFVPNDMQVGQTGK	1906.1	2	5.0358	0.4762
AAVEALQSQALHATSQQPLRK	2248.5	3	4.3657	0.3102
AAVEDPRVLLLDL	1424.7	2	3.8933	0.2644
AAVENHVR	896.0	2	2.5567	0.2003
AAVENLPTFLVELSR	1659.9	2	5.1725	0.3863
AAVEWFDGKDFQGSK	1685.8	2	4.0216	0.4255
AAVFDLDGVLALPAVFGVLGR	2101.5	3	4.0911	0.3284
AAVFHEK	801.9	2	2.4727	0.1538
AAVFHEKDYDSLAQPGFFDR	2314.5	3	4.6265	0.4295
AAVFHEKDYDSLAQPGFFDRFIR	2731.0	3	3.2728	0.2224
AAVGQESPGGLEAGNAK	1556.7	2	3.1851	0.2919
AAVGRPLDKHEGALETLLR	2047.3	2	3.9585	0.3358
AAVGVKKQKKPLVGKKAAATKKPAPEKKPAEKK	3455.2	3	3.2004	0.117
AAVHYDR	831.9	2	2.4106	0.2749
AAVKGYLGPEQLPDCLKGCDVVVIPAGVPR	3066.6	3	5.9043	0.3896
AAVLEYLTAEILELAGNAAR	2089.4	3	5.0919	0.3269
AAVMVHQLSK	1084.3	2	2.9044	0.3135
AAVPDAVGK	827.9	1	1.9278	0.1785
AAVPIVNLKDELLFPSWEALFSGSEGPLKPGAR	3511.0	3	4.4995	0.4081
AAVPPGTVVPTEAAAPTEVTEGPGVAAPTK	2787.1	3	3.3711	0.3493
AAVPSGASTGIYEALELR	1806.0	2	5.3262	0.4268
AAVQVLDDIEK	1201.4	2	2.7839	0.1276
AAVSHWQQQSYLDSGIHSGATTTAPSLSGK	3087.3	3	5.7504	0.4468
AAVTALASLYGTK	1266.5	2	2.89	0.3109
AAVVESHK	840.9	2	2.4151	0.145
AAVVESHKLGGTCVNVGCVPK	2069.4	3	3.6502	0.1943
AAVVHHFESFPAGSTLIFYK	2222.5	3	4.6706	0.3801
AAVVTSPPPTTAPHKER	1760.0	2	2.9232	0.3326

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AAVYHHFISDGVR	1472.6	2	3.6519	0.3831
AAWEAGKFGNEVIPVTVTVK	2117.4	3	4.6123	0.2183
AAWIPHVENR	1193.3	1	2.9404	0.2592
AAYEAELGDAR	1166.2	2	4.0189	0.3832
AAYEAELGDARK	1294.4	2	3.4529	0.2563
AAYEAELGDARKTLDSVAKER	2294.5	3	3.7957	0.3744
AAYFGIYDTAK	1220.4	2	2.8262	0.3506
AAYKEYISNK	1187.3	2	2.6984	0.2825
AAYLQETGKPLDETLKK	1906.2	2	4.6151	0.4507
AAYPDLENPPLLVTPSQQAK	2153.4	3	5.5948	0.3751
AAYSFYNVHTQTPLLDLMSDALVLAK	2883.3	3	5.4851	0.4152
ACALSIEESCRPGDKVPPIKPNAGEESVMNLDK	3500.0	3	5.2215	0.2519
ACALSIEESCRPGDKVPPIKPNAGEESVMNLDKLR	3769.3	3	4.8567	0.2382
ACANPAAGSVILLENLR	1713.0	2	4.4497	0.4463
ACEFAGFQCQIQFGPHNEQK	2283.5	3	3.988	0.1258
ACHILECPEGLAQDVISTIGQAFELR	2815.2	3	3.9739	0.2937
ACKTEADGRVVEGNHMVYR	2136.4	2	2.4237	0.3552
ADAAPDEKVLDSGFREIENK	2205.4	2	5.2951	0.3725
ADAASSLTVDVTPPTAK	1644.8	2	3.9342	0.3968
ADAEEEAATR	1063.1	2	3.6499	0.2487
ADAEGESDLENSR	1393.4	2	3.4408	0.3726
ADAEKAQEQQQMAELHSK	2171.3	3	6.6752	0.3831
ADAETLRK	904.0	2	2.5337	0.1213
ADAGKEGNNPAENGDAK	1658.7	2	3.813	0.3596
ADAGKEGNNPAENGDAKTDQAQK	2330.4	3	4.907	0.3113
ADAGKEGNNPAENGDAKTDQAQKAEGAGDA	2901.9	3	4.7737	0.399
ADAGKEGNNPAENGDAKTDQAQKAEGAGDAK	3030.1	3	4.8995	0.3563
ADAGPSGQGDSVSIGK	1446.5	2	3.3602	0.2673
ADALQAGASQFETSAAK	1666.8	2	4.8902	0.4263
ADASEAHESSSRGEAGAPGEEDIQGPTK	2784.8	3	5.0773	0.2026
ADAVQDSEMVELVELEIR	2047.3	2	3.1068	0.1858
ADAVWNKIQEENVIPR	1883.1	3	3.6852	0.28
ADDKETCFAEEGKK	1571.7	3	5.0126	0.3079
ADDLGKGGNEESTK	1421.4	2	3.7185	0.3755
ADDLGKGGNEESTKTGNAGSR	2065.1	3	5.2062	0.5441
ADDNATIR	875.9	2	2.5813	0.1252

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ADDPSSYMEVVQAANTSGNWEELVK	2741.9	3	5.8265	0.502
ADDTSAATIEK	1122.2	2	2.6321	0.1242
ADDTSAATIEKK	1250.3	2	3.0748	0.235
ADDYEQVKNVADYYPEYK	2211.3	2	4.3406	0.4265
ADEARPNTIDFGKDDQHFTVTGLHK	2814.0	3	4.488	0.2454
ADEGISFR	895.0	2	2.6669	0.2686
ADELQKQKEELQR	1615.8	3	4.0989	0.2899
ADEPQWSLYPSDSQVSEEVK	2295.4	2	4.1841	0.3629
ADEPQWSLYPSDSQVSEEVKTR	2552.7	3	3.8694	0.3557
ADEVAPAKK	929.1	2	2.7168	0.151
ADFDNTVAIHPTSSEELVTLR	2316.5	3	4.6565	0.423
ADFPVDEELGLDLGDLSR	1962.1	2	4.1415	0.2483
ADFREPNAEVPRPIPHIGPDYIPTEEER	3246.5	3	3.8	0.3954
ADFSGMSQTDLSLSK	1587.7	2	4.575	0.3509
ADGGAEYATYQTK	1375.4	2	2.4882	0.1504
ADGGTQVIDTK	1105.2	2	3.5302	0.3409
ADGKISEQSDAK	1249.3	2	3.3356	0.314
ADGKISEQSDAKLKEIVTNFLAGFEA	2783.1	3	5.5074	0.3989
ADGLGAGDVAAVLGPLGLQEVASFVTKR	2713.1	3	3.3124	0.2955
ADGTATAPPPR	1054.1	2	2.5696	0.1192
ADGYEPPVQESV	1291.3	2	2.8611	0.2903
ADGYNQPDSK	1095.1	2	2.5879	0.2376
ADGYVDNLAEAVDLLLQHADK	2271.5	2	5.3785	0.4556
ADGYVLEGK	952.0	2	3.0613	0.3223
ADGYVLEGKELEFYLR	1903.1	3	5.145	0.4033
ADGYVLEGKELEFYLRK	2031.3	3	5.1374	0.4313
ADHDFVVQEDFMK	1581.7	2	4.1825	0.3963
ADHGEPIGR	952.0	2	2.5087	0.2389
ADHPPAEVTSHAASGAK	1646.7	3	3.8827	0.3939
ADHQPLTEASYVNLPTIALCNTDSPLR	2941.3	3	5.2176	0.2995
ADIGVAMGIAGSDVSK	1491.7	2	3.1865	0.2858
ADIHLVELLYYVEELDSSLISSFPLLK	3108.6	2	5.2073	0.5221
ADILEDKDGK	1104.2	2	2.9804	0.2539
ADIWSLGITAIELAR	1629.9	2	3.2662	0.2762
ADKDYHFK	1024.1	2	2.4525	0.1682
ADKDYHFKVDNDENEHQLSLR	2574.7	3	6.4756	0.5011

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ADKEGDYYVLNGSK	1559.7	2	3.0465	0.3165
ADKLAEEHSS	1087.1	2	2.9716	0.3473
ADKNEVAAEVAK	1245.4	2	3.4488	0.159
ADKQEAVFENLDKPGETQVISYEMLHVTPPMSPPDVLK	4255.8	3	3.234	0.1383
ADLAAQYTTVGR	1266.4	2	4.0235	0.3615
ADLDELVAAECVYCGELMIR	2214.6	2	2.5362	0.1285
ADLEAQRDVTYEEAKQFAEENGLLFLEASAK	3487.8	3	4.9334	0.3439
ADLIAYLK	907.1	2	2.8006	0.2367
ADLIAYLKK	1035.3	2	2.9131	0.2023
ADLINNLGTIAK	1243.4	2	4.144	0.3422
ADLKQLMVHAFIK	1514.9	2	2.5945	0.1018
ADLLGIVSELQLK	1399.7	2	3.4689	0.1639
ADLLLSTQPGREEGSPLELER	2311.5	3	5.2341	0.4499
ADLNQGIGEPQSPSR	1569.7	2	4.1441	0.2898
ADLQKLKDELASTK	1560.8	2	3.4965	0.384
ADLQNHLDTAQNALQDKQQELNK	2636.8	3	3.495	0.2003
ADLSGITGAR	961.1	2	3.5406	0.3268
ADLSGMSGAR	965.1	2	3.4689	0.343
ADLSGMSGARDIFISK	1668.9	2	3.6398	0.1569
ADLTALFLPR	1117.3	2	2.606	0.2117
ADLTEYLSTHYK	1441.6	2	3.4017	0.3541
ADLTEYLSTHYKAPR	1765.9	3	4.149	0.4793
ADMEDLMSSKDDVGKNVHELEK	2491.7	3	4.5089	0.3716
ADMVIEAVFEDLSLK	1680.9	2	5.2822	0.4226
ADNFEYSDPVDGSISR	1772.8	2	4.635	0.4689
ADNKQKGDVVLQSDHVIETLTK	2439.7	3	3.9641	0.3079
ADPSLLGFSVNASSER	1650.8	2	4.0516	0.513
ADPSQFELLK	1148.3	2	2.797	0.216
ADQEEQIHPR	1223.3	2	3.5188	0.1577
ADQPIDADVTVIGSGPGGYVAAIK	2315.6	2	6.6622	0.5667
ADQTVLTEDEKK	1377.5	2	3.2635	0.1902
ADQTVLTEDEKKELENLAAMDLELQK	2976.3	3	6.4298	0.4042
ADQTVLTEDEKKELENLAAMDLELQKIAEK	3417.8	3	4.9868	0.3357
ADRDESSPYAAMLAAQDVAQR	2266.4	3	5.4323	0.3408
ADSERQNQEYQR	1524.5	3	3.6552	0.2049
ADSLKAAVEQEKR	1445.6	3	3.3639	0.3142

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ADSQAQLLLSTVVGVFTAPGLHLK	2466.9	3	3.2528	0.21
ADSVANQGTKVEGITNQGK	1918.1	3	4.8693	0.3192
ADTGLKLPDFQDSIFEYFNTAPLAHDLTFR	3444.8	3	5.4691	0.3742
ADTIAKNELHK	1240.4	2	2.9822	0.2137
ADTVSKTELQK	1220.4	2	3.2097	0.2672
ADVAFHFNPR	1174.3	2	2.738	0.1961
ADVFHAYLSLLK	1377.6	2	2.8769	0.279
ADVKGGTLTQYEGK	1467.6	2	2.6391	0.1952
ADVLTTGAGNPVGDKLNVITVGPR	2365.7	3	5.1904	0.3746
ADYLKNYEFPHLQNFIK	2141.4	2	4.3043	0.323
AEAAAAPAAASGPNQMSFTFASPTQVFFNGANVR	3400.7	3	7.0864	0.5564
AEAAASALADADADLEERLK	2031.2	3	3.9623	0.2015
AEAAEKLQR	1016.1	2	2.4027	0.1341
AEAARIEGEGSVLQAK	1629.8	3	4.1195	0.288
AEADKNDKAVK	1189.3	2	3.2987	0.2611
AEADKNDKAVKDLVVLLFETALLSSGFSLEDPQTHSNR	4160.6	3	6.0181	0.5159
AEADKNDKSVK	1205.3	2	2.449	0.2187
AEAEAQAEELSFPR	1548.6	2	3.2721	0.2685
AEAEAWYQTKFETLQAQAGK	2271.5	3	4.6237	0.319
AEAEQEKDQLR	1317.4	2	3.2239	0.1009
AEAERLGHELQQAGLK	1750.9	3	3.8448	0.2549
AEAERPEEQAEASGLKK	1844.0	3	5.5587	0.3591
AEAESMYQIK	1170.3	2	3.429	0.2411
AEAESMYQIKYEELQSLAGK	2289.5	3	5.9635	0.4422
AEAESMYQIKYEELQSLAGKHGDDLR	2983.3	3	4.4969	0.3448
AEAESMYQIKYEELQSLAGKHGDDLRR	3139.4	3	4.2933	0.2547
AEAESRAEAARIEGEGSVLQAK	2273.4	3	3.6306	0.1259
AEAETLPSLSITK	1360.5	2	3.7813	0.3069
AEAETLPSLSITKLDLQWVQVLSEGWATPLKGFMR	3917.5	3	4.4651	0.4106
AEAGAGSATEFQFR	1442.5	2	3.5258	0.2739
AEAGDNLGALVR	1186.3	2	4.4401	0.2912
AEAGEQPGTAER	1216.2	2	3.4271	0.1728
AEAGPEGVAPAPEGEK	1509.6	2	4.5944	0.4443
AEAGPEGVAPAPEGEKK	1637.8	2	4.5198	0.4307
AEAGVPAEFSIWTR	1534.7	2	4.1398	0.3935
AEAQEAEDQQAR	1346.3	2	4.4614	0.3418

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AEAQGKQEVESLREK	1702.8	3	4.0759	0.1196
AEASQLGHK	941.0	2	2.8036	0.3653
AEASQLGHKVSQMAQYFEPLTLAAVGAASK	3105.5	3	4.9074	0.3779
AEASSGDHPTDTEMKEEQK	2091.2	3	4.2669	0.4256
AEASSGDHPTDTEMKEEQKSNTAGSQSQVETEA	3481.5	3	5.682	0.333
AEAYLIEEMYDEAIQDYETAQEHNENDQQIR	3760.9	3	5.1437	0.3937
AEDAPLSSGEDPNSR	1545.5	2	3.4154	0.3165
AEDGATPSPSNETPK	1501.5	2	4.1743	0.3448
AEDGATPSPSNETPKK	1629.7	2	2.9988	0.2934
AEDGENYDIKK	1282.3	2	3.2656	0.1531
AEDGHAVAK	898.0	2	3.1486	0.2636
AEDGHAVAKK	1026.1	2	3.2379	0.291
AEDGSSSKEGTSV	1254.2	2	2.7115	0.219
AEDGSVIDYELIDQDAR	1910.0	2	5.4622	0.4028
AEDGSVIDYELIDQDARDLYDAGVK	2771.9	3	4.269	0.3189
AEDGSVIDYELIDQDARDLYDAGVKR	2928.1	3	4.7694	0.4064
AEDGSVIDYELIDQDARDLYDAGVKRK	3056.3	3	4.6976	0.3996
AEDKEWMPVTK	1334.5	2	2.986	0.1964
AEDYPIDLYYLMDLSYSMKDDLENVK	3145.5	3	3.9931	0.29
AEEAQKTESVDNEGE	1636.6	2	3.3707	0.373
AEEDEILNR	1089.1	2	3.0517	0.2328
AEEEQAGSAPGAGGTATKTLDK	2090.2	2	2.6184	0.1943
AEELGLPILGVLR	1380.7	2	2.4258	0.1528
AEERAELSEGQVR	1474.6	2	3.3077	0.2735
AEEREAWSGGYPGGVLAQLWCCALALQGR	3093.5	3	3.2613	0.1877
AEETEQMIEK	1208.3	2	2.6578	0.1872
AEEYEFLTPVEEAPK	1752.9	2	4.0627	0.3614
AEEYEFLTPVEEAPKGMLAR	2281.6	2	4.3834	0.4628
AEFAEVSK	881.0	1	2.5695	0.2509
AEFAEVSKLVTDLTK	1651.9	2	4.7829	0.4681
AEFGPPGPGAGSR	1200.3	2	2.5648	0.2223
AEGDVAALNR	1016.1	2	3.365	0.1763
AEGFVDALHR	1115.2	2	3.3736	0.3357
AEGGGATTSTQVMVIK	1550.8	2	4.1042	0.4767
AEGGQSAAAHSAHTVKQEDIAVTGK	2464.6	3	5.2118	0.4394
AEGNDHIER	1041.1	2	2.6265	0.241

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AEGNNQAPGEEEEEEEEATNTHPPASLPSQK	3321.3	2	3.4572	0.3982
AEGPEVDVNLPK	1268.4	2	3.1684	0.2778
AEGQLQASPPGAAEGHLEKPVPEPQRK	2823.1	3	4.7613	0.3855
AEGQRQAQEYEALLNIK	1962.2	3	5.5505	0.3365
AEGSDVANAVLDGADCIMLSGETAK	2438.7	2	5.6965	0.5241
AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	3439.8	3	5.7556	0.4727
AEGSSTASSGSQLAEGK	1567.6	2	4.1856	0.395
AEGTFPGKI	920.0	2	2.6191	0.1802
AEGTFTSDVSSYLEGQAAK	1962.1	2	5.2058	0.484
AEGYEVAHGGR	1146.2	2	2.8996	0.2458
AEHDSILAEK	1113.2	2	3.2838	0.2452
AEHDSILAEKAEKDSKPIKVTLPDGK	2821.2	3	5.686	0.488
AEIDMLDIR	1076.2	2	3.4262	0.2921
AEIHDLQEEHIKER	1747.9	3	3.4469	0.2866
AEIIADKQSGK	1160.3	2	2.8551	0.2571
AEIIHHLADLLTDQRDEILLANK	2643.0	3	3.5885	0.3141
AEIIHHLADLLTDQRDEILLANKK	2771.2	3	5.6166	0.4633
AEIIHHLADLLTDQRDEILLANKKDLEEAEGR	3671.1	3	5.5673	0.4719
AEISELPSIVQDLANGNITWADVEAR	2813.1	3	5.3471	0.486
AEISNAIDQYVTGTIGEDEDLIK	2495.7	2	5.0221	0.3523
AEISNAIDQYVTGTIGEDEDLIKWK	2810.1	3	4.106	0.3278
AEITLVATKPEK	1300.5	2	3.5121	0.2221
AEKDSKPIKVTLPDGK	1727.0	2	3.6446	0.2866
AEKESLESALMGTHQELEMFGSQPAYPEK	3239.6	3	3.7621	0.1776
AEKEVAEVKS	1090.2	2	2.7548	0.1191
AEKKGDEYIINGQK	1593.8	2	4.0752	0.3264
AEKNGVKITLPVDFVTADKFDENAK	2751.1	3	6.6744	0.4887
AEKPLFSSNPELDNLMIQAIQVLR	2728.2	3	5.5071	0.3322
AEKTEVLSEDLLQIER	1874.1	2	3.3989	0.2209
AELATEEFLPVTPILEGFVILR	2458.9	3	5.2087	0.4242
AELDEVNKSAK	1204.3	2	3.0058	0.1705
AELEEKGHSATGK	1357.5	2	3.1296	0.2828
AELEIQKDALEPGQR	1697.9	2	3.7016	0.2374
AELEKHGYKMETS	1523.7	2	2.949	0.2077
AELGIPLEEVPPEEINYLTR	2283.6	2	2.9563	0.1671
AELINIHHLMVELKK	1789.2	3	3.3083	0.3188

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AELIVQPELKYGDGIQLTR	2144.5	3	4.207	0.34
AELNDKVHK	1054.2	2	2.4649	0.1269
AELNEFLTR	1093.2	2	2.8545	0.1467
AELQTALAHTQHAAR	1618.8	2	3.2199	0.3561
AELRAPPDKIAIIGAGIGGTSAAYYLR	2746.2	3	4.7349	0.4145
AELRDDPIISTHLAK	1679.9	2	3.3524	0.293
AELRDLELEEARLVQELEDVDRNNAR	3097.3	3	3.3229	0.1012
AELSEGQVR	989.1	2	3.0655	0.1197
AEMDQILHGLDK	1370.6	2	2.5545	0.1106
AEMDQILHGLDKVAEEWAQGTFK	2617.9	3	4.2943	0.2596
AEMPASEKYSEKEDKYEEEIKLLSDK	3091.4	3	3.717	0.2295
AENFFILR	1010.2	2	3.2918	0.1688
AENFKQVEYLLIHGTADDNVHFQQSAQISK	3432.7	3	5.1954	0.3525
AENGKLVINGNPITIFQER	2114.4	3	5.0494	0.4256
AENGKLVINGNPITIFQERDPSK	2541.8	3	5.1732	0.4397
AENLQLLTENELHR	1680.8	2	2.7247	0.1937
AENNSEVGASGYGVPGPTWDR	2164.2	2	5.1746	0.4651
AENQVLAMR	1032.2	2	3.2738	0.2761
AENSQLTER	1048.1	2	3.2057	0.2262
AENSSLNLIGK	1146.3	2	2.4694	0.1524
AENYDIPSADR	1251.3	2	3.5257	0.3499
AENYDIPSADRHK	1516.6	2	3.4935	0.338
AEPAKIEAFR	1132.3	2	2.8236	0.2325
AEPAKIEAFRASLSK	1618.9	2	3.7775	0.2261
AEPDVKKLEDQLQGGQLEEVILQAEHELNLAR	3615.0	3	6.4156	0.4226
AEPDVKKLEDQLQGGQLEEVILQAEHELNLARK	3743.2	3	4.5711	0.2625
AEPEDHYFLLTEPPLNTPENR	2483.7	3	3.5176	0.1925
AEPLETFPFDQSK	1509.6	2	2.7967	0.1282
AEPPKAPEQEQAAPGPAAGGEAPK	2299.5	3	4.7027	0.3953
AEQDITTLEQSISRLEGQVLR	2387.6	3	4.3073	0.3288
AEQEEEFISNTLFKK	1814.0	2	3.2922	0.285
AEQINQAAGEASAVLAK	1671.8	2	2.825	0.2645
AEQLAQQAHSNR	1353.4	2	3.8014	0.3871
AEQLAQQAHSNRK	1481.6	2	3.8223	0.2259
AEQLGAEGNVDESQK	1575.6	2	2.7885	0.1965
AEQMASVQNAQR	1333.5	2	2.8921	0.1593

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AEQSKAEEAQR	1247.3	2	2.6963	0.1084
AEQSLHDLQER	1326.4	2	2.5971	0.1217
AERDSALETLQGQLEEKAQELGHSQSALASAQR	3553.8	3	8.5488	0.5163
AERLDVLEQQR	1357.5	2	2.566	0.2027
AERQHQLYVGVLGSK	1685.9	2	2.9998	0.2896
AERVHELNEEIGKLLAK	1950.2	3	4.587	0.1502
AESAPLPVSADDTPEVLNR	1982.1	2	4.3828	0.4787
AESEEMETSQAGSK	1484.5	2	4.3601	0.3998
AESMLQQADK	1121.2	2	2.7689	0.1882
AETAAKHGEAQVK	1340.5	2	3.6767	0.2225
AETGDKVYVHLK	1360.5	2	2.6036	0.1237
AETSEGSGSAPAVPEASASPK	1931.0	2	4.6363	0.4057
AEVDLVVQDLK	1229.4	2	2.8641	0.2952
AEVEGKDLPEHAVLK	1635.8	2	4.5579	0.3392
AEVGEKTEER	1148.2	2	2.8769	0.2766
AEVLGHKTPEPAPR	1502.7	2	3.2704	0.3379
AEVQKLQALANEQAAAAHELEK	2363.6	3	5.4775	0.3485
AEVQNLGGELVVSGVDSAMSLIQAAK	2587.9	3	4.0673	0.2538
AFAAQEDLEKTKEELK	1851.0	3	3.2	0.2501
AFADALEVIPMALSENSGMNPIQTMTEVR	3137.6	2	5.3835	0.483
AFADAMEVIPSTLAENAGLNPISTVTELR	3032.4	2	4.9689	0.44
AFAEKNNLSFIETSALDSTNVEEAFKNILTEIYR	3880.3	3	5.7611	0.4358
AFAETHIK	917.0	2	2.4407	0.1222
AFAETHIKGFTLNDAANSR	2064.2	3	3.3802	0.235
AFAGDIANQLATDAVQILGGNGFNTEYPVEK	3225.5	3	6.1088	0.5034
AFAGDIANQLATDAVQILGGNGFNTEYPVEKLMR	3626.1	3	5.8866	0.4874
AFAHITGGGLLENIPR	1666.9	2	4.019	0.3375
AFAKELFLGK	1124.4	2	3.2257	0.3184
AFAMIIDKLEEDINSSMTNSTAASRPPVTLR	3380.8	3	5.6678	0.4266
AFAMIIDKLEEDISSSMTNSTAASRPPVTLR	3353.8	3	4.6155	0.3811
AFAVVASALGIPSLLPFLK	1915.4	2	3.5641	0.1241
AFDLFNPNFK	1213.4	2	2.8476	0.1563
AFDLIVDRPVTLVR	1614.9	3	3.7872	0.3961
AFDLVPPEAVPEQKDPDPEFPTVK	2667.0	2	2.596	0.1002
AFDRNTESLFEELSSAGSGLIGDVDEGADLLGMGR	3630.9	3	5.1681	0.3656
AFDSGIIPMEFVNK	1568.8	2	4.6322	0.4358

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AFEALLSNIVKPVASDIQAR	2143.5	2	2.9075	0.1933
AFEAVDKAYK	1142.3	2	2.8261	0.3365
AFEEAEKNAPAIIFIDELDAIAPK	2616.9	2	4.962	0.4053
AFEEAEKNAPAIIFIDELDAIAPKR	2773.1	3	5.9709	0.5001
AFEEDQVAGR	1122.2	2	2.6167	0.1908
AFEGQAHGADR	1159.2	2	2.78	0.1874
AFEKNIFNK	1111.3	2	2.6355	0.1864
AFEVMDEFDGR	1316.4	2	3.248	0.3622
AFFESHPAPSAER	1446.5	2	3.0756	0.3232
AFFSEVER	985.1	2	2.5956	0.1255
AFGEGASARPR	1119.2	2	2.4305	0.1341
AFGFNVLFYDPYLSDGVER	2210.4	2	4.7128	0.3857
AFGFSHLEALLDDSK	1650.8	2	5.0621	0.4479
AFGFSHLEALLDDSKELQR	2177.4	3	5.6204	0.4711
AFGHHAVSLLDGGLR	1550.7	2	4.111	0.4397
AFGPGLQGGSAGSPAR	1430.6	2	4.4431	0.3513
AFGPSETNESPAVVLEPPVVSMEVSEPHILETLKPATK	4032.6	3	5.3709	0.4423
AFGYYGPLR	1044.2	2	2.7979	0.3343
AFHEDKKPSK	1187.3	2	2.6429	0.1078
AFHNEAQVNPER	1412.5	2	3.8227	0.3397
AFHNEAQVNPERK	1540.7	3	4.1906	0.3355
AFHPFIAGPYNR	1390.6	2	3.3565	0.3434
AFIDQGKLIPDDVMTR	1820.1	2	3.3098	0.1929
AFIPAIDSFGFETDLR	1800.0	2	4.157	0.3255
AFIPLPSAVVQAVFGR	1673.0	3	3.9062	0.4326
AFITNIPFDVK	1265.5	2	3.9558	0.2622
AFITNIPFDVKWQSLKDLVK	2363.8	3	4.1575	0.2085
AFKAWAVAR	1020.2	2	2.8104	0.2293
AFKDIDIEDLEELDPDFIMAK	2468.8	2	5.9049	0.451
AFKDKVDVASVIVTK	1620.9	2	3.4781	0.2679
AFKEVGIEFMDLYSHLVPVYDVEPLEK	3169.6	3	4.2374	0.2991
AFLADPSAFVAAAPVAAATTAAPAAAAAPAK	2754.1	2	5.7907	0.4382
AFLADPSAFVAAAPVAAATTAAPAAAAAPAKVEAK	3181.6	3	5.2561	0.4037
AFLAQIHAR	1027.2	2	2.8769	0.2141
AFLASPEYVNLPINGNGK	1905.1	2	5.58	0.4309
AFLASPEYVNLPINGNGKQ	2033.3	3	5.3448	0.3863

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AFLDALQNQAEASSK	1593.7	2	5.1483	0.3947
AFLDFHALPYQVVEVNPVR	2215.5	2	4.6735	0.3437
AFLDFHALPYQVVEVNPVRR	2371.7	3	3.3717	0.2242
AFLEENNLDYIIR	1610.8	2	4.0282	0.3018
AFLIEEQKIVVK	1417.7	2	3.689	0.2027
AFLMQHAPANDYLVTSHIHLHVPEGATPK	3196.6	3	4.3126	0.4082
AFLQGGQEATDIALLLR	1817.1	2	3.2136	0.2273
AFLSPPTLLEGPLR	1511.8	2	2.8391	0.2006
AFLSTHPNTETVFEAFLK	2053.3	2	4.0747	0.125
AFLTLAEDILR	1262.5	2	4.6119	0.357
AFLTLAEDILRK	1390.7	2	3.5554	0.2918
AFMTADLPNELIELLEK	1948.3	2	5.2457	0.4237
AFNLVKDSATGLSK	1451.6	2	3.1123	0.268
AFPALTSLDLSDNPGLGER	1974.2	2	5.2152	0.5083
AFQNVFAPR	1050.2	2	2.8816	0.3094
AFQYVETHGEVCPANWTPDSPTIKPSPAASK	3330.7	3	6.0426	0.4229
AFREEAIKFSEEQR	1740.9	3	4.2376	0.3579
AFSDPFVEAEKSNLAYDIVQLPTGLTGIK	3125.5	3	4.5995	0.4118
AFSGYLGTDQSK	1274.4	2	2.8989	0.283
AFSQFGKLER	1183.3	2	2.8103	0.1808
AFSVFLFNTENK	1417.6	2	3.9701	0.3686
AFSVNIFK	926.1	2	2.4473	0.2488
AFSYYGPLR	1074.2	2	2.9624	0.2728
AFTELQAK	908.0	2	2.4138	0.1514
AFTGFIVEADTPGIQIGR	1893.1	2	4.5544	0.4845
AFTGFIVEADTPGIQIGRK	2021.3	2	4.3758	0.3952
AFTGREFDELNPSAQR	1839.0	2	4.2602	0.2879
AFTHTAQYDEAISDYFR	2036.1	2	4.9203	0.4606
AFTHTAQYDEAISDYFRK	2164.3	3	5.447	0.3496
AFVAIGDYNGHVGLGVK	1717.9	2	3.082	0.1219
AFVDFLSDEIKEER	1698.9	2	3.6198	0.3048
AFVEQVANVVLYSSDYYVK	2195.5	3	3.5909	0.1626
AFVGEVGAR	906.0	2	2.4107	0.1841
AFVHWYVGEGMEEGEFSEAR	2331.5	3	3.8362	0.1612
AFVHWYVGEGMEEGEFSEAREDMAALEK	3219.5	3	4.1963	0.2216
AFVRPSGTEDVVR	1433.6	2	3.4752	0.2174

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AFYAELYHIISSNLEK	1899.1	2	5.4815	0.4944
AFYAPVHADDLREGAQYLMQAAGLGR	2822.2	3	3.5372	0.1648
AFYGDTLVTGFAR	1418.6	2	4.2412	0.4582
AFYNNVLGEYEEYITK	1954.1	2	4.4115	0.372
AFYPEEISSMVLTK	1615.9	3	4.4046	0.4599
AFYVNVLNEEQR	1482.6	2	4.2658	0.3689
AGAAGGPEEEAEKPVK	1540.7	2	4.4116	0.3495
AGAAPYVQAFDSLLAGPVAEYLK	2352.7	2	6.1747	0.5239
AGADEERAETAR	1276.3	2	2.7845	0.1769
AGAEVVKQVEHPLLSGLLYPGLQALDEEYLK	3381.9	3	4.7546	0.2998
AGAGSATLSMAYAGAR	1455.6	2	4.7242	0.4531
AGAIAPCEVTVPAQNTGLGPEK	2124.4	2	4.8152	0.3867
AGALNSNDAFVLK	1320.5	2	3.7406	0.3536
AGALNSNDAFVLKTPSAAYLWVGTGASEAEKTGAQELLR	4009.4	3	6.4519	0.4692
AGATLDLLVENMGR	1460.7	2	4.4263	0.395
AGATSEGVLANFFNSLLSK	1927.1	2	5.5968	0.4716
AGATSEGVLANFFNSLLSKK	2055.3	2	4.8864	0.408
AGAVEKGVPLYR	1260.5	2	3.3062	0.2642
AGAVGAHLPASGLDIFGDLK	1910.2	2	2.7366	0.1843
AGAVGAHLPASGLDIFGDLKK	2038.3	3	5.8038	0.4564
AGAVNPTVK	857.0	2	2.8001	0.1721
AGAYDFPSPEWDTVTPEAK	2082.2	2	4.4979	0.4624
AGDEFVEK	894.9	2	2.9371	0.1738
AGDEFVEKTLSTIATSTDAASVVHSTDLVVEAIVENLK	3962.4	3	8.0411	0.5463
AGDEFVEKTLSTIATSTDAASVVHSTDLVVEAIVENLKVKNELFK	4821.4	3	4.7564	0.3803
AGDGDGWVSLAELR	1446.5	2	3.0976	0.2526
AGDKPHMQTYEVDLNK	1847.0	3	4.1623	0.2452
AGDLRDTGIFLDLMHLK	1916.2	3	4.4079	0.1509
AGDMENAENILTVMR	1664.9	2	4.3211	0.3643
AGDPLDLVALAEQVQKADEFIR	2399.7	3	4.6439	0.324
AGEAGKLEEVMQELR	1660.9	2	4.8652	0.3968
AGEARPGPTAESASGPSEDPSVNFLK	2572.7	3	5.7466	0.4142
AGEERAPAHAQSFLAQQR	1968.1	3	4.8901	0.3273
AGEGNEEISNMIHSYIKEIEDLRAK	2848.1	3	4.298	0.342
AGEIKGFTGIDSDYEKPETPER	2440.6	2	5.7918	0.478
AGEKELILTVLSVPPHEADNLDPSDDSLGQSFYDYTEK	4195.5	3	4.5317	0.27

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AGELTEDEVER	1248.3	2	3.3129	0.2954
AGELTEDEVERVITIMQNPR	2301.6	3	3.2644	0.1153
AGEQLAPFLPQLVPR	1636.9	2	3.1057	0.2877
AGEVERDLDKADSMIR	1806.0	3	3.5473	0.2447
AGEVFIHK	901.0	2	3.0315	0.1677
AGEVFIHKDK	1144.3	2	2.8537	0.2018
AGEVFIHKDKGFGFIR	1822.1	2	2.7912	0.1032
AGEVINQPMMMAAR	1519.8	2	3.4532	0.1705
AGFAALQLEYFFTAGPDEVR	2203.4	2	3.3518	0.2907
AGFAGDDAPR	977.0	2	3.6218	0.3928
AGFAGDQIPK	1004.1	2	3.0526	0.1008
AGFALDEGIANPTDAFTVFYSER	2492.7	2	5.1226	0.4056
AGFIQDTSLILYEEVKPNLTER	2537.8	3	3.2756	0.1712
AGFLAFTQLPK	1193.4	2	2.8281	0.1124
AGFLDLKDFLPK	1364.6	2	3.3314	0.1278
AGFLDLKDFLPKEYVK	1884.2	3	4.0697	0.2254
AGFLHHVK	909.1	2	2.8087	0.234
AGGAAQLALDKSDSHPSDALTR	2182.3	3	5.4788	0.4255
AGGAAVVITEPEHTKER	1765.9	2	3.7972	0.2226
AGGADAVQTVTGGLR	1373.5	2	4.0587	0.2667
AGGAGVPAFYTPTGYGTLVQEGGSPIK	2596.9	2	4.8324	0.3126
AGGANYDAQTE	1097.1	1	2.2367	0.1715
AGGDTHLGK	855.9	2	2.5593	0.1404
AGGEELDEGVAKDNAK	1603.7	2	4.4421	0.352
AGGEELDEGVAKDNAKIDGATQSSPAEPK	2886.0	3	4.64	0.214
AGGGAGDPGLGAAAAPAPETR	1764.9	2	4.3831	0.4049
AGGGDRKGK	845.9	2	2.7649	0.1084
AGGGRPSSPSPSVVSEKEKEELER	2513.7	3	6.6898	0.4645
AGGIETIANEFSDR	1480.6	2	3.9371	0.4212
AGGIETIANEYSDR	1496.6	2	3.8373	0.4177
AGGITQVQYILPTLPQQLQVAPAPAPAPGTK	3127.6	3	3.538	0.2772
AGGKEFLETVK	1179.3	2	3.4253	0.2155
AGGKEFLETVKELR	1577.8	3	5.0798	0.3595
AGGKEFLETVKELRK	1706.0	2	3.9204	0.2478
AGGKILTFDQLALDSPK	1775.0	2	4.9265	0.3997
AGGMATTGKEAVLDVIPTDIHQR	2381.7	3	5.2692	0.2685

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AGGPATPLSPTR	1125.3	2	2.6658	0.2445
AGGPGLERGEAGVPAEFSIWTR	2258.5	2	5.1621	0.3803
AGGPLGLSIVGGSDHSSHPFGVQEPGVFISK	3035.4	3	4.311	0.2656
AGGPTTPLSPTR	1155.3	2	3.2986	0.2408
AGGQPPGQSAGGK	1112.2	2	2.6588	0.1549
AGGSAALSPSK	946.0	2	3.3412	0.2703
AGGSASAMLQPLLDNQVGFK	2005.3	3	5.8271	0.4806
AGGSASAMLQPLLDNQVGFKNMQNVEHVPLSLDR	3639.1	3	4.3719	0.3297
AGGSFDLR	822.9	2	2.4577	0.1266
AGGTEIGKTLAEK	1275.4	2	3.3237	0.3225
AGGTKPKKPVGAAK	1310.6	2	2.5399	0.17
AGGVFTPGAAFSK	1210.4	2	2.8335	0.2441
AGGVLAYELLPALDEVLASDSR	2260.5	2	3.1966	0.2033
AGHFDKEIVPVLVSTR	1769.0	2	4.5814	0.4124
AGHGAGKPTAK	995.1	2	2.6431	0.2076
AGHKATLEEAR	1183.3	2	3.8547	0.3557
AGHYAASIIIR	1172.4	2	3.0317	0.2239
AGIAHLYGIAGSTNVTGDQVK	2073.3	3	3.9011	0.3367
AGIDPNAITYGYYNK	1660.8	2	2.6961	0.1692
AGIEVQEIKDSEHKLETSSGR	2314.5	3	4.7874	0.4256
AGIFQSVK	850.0	2	2.8847	0.1304
AGIIASAR	758.9	1	1.6581	0.146
AGIIQDTWHK	1169.3	2	2.8829	0.2265
AGIKVTVAGLAGKDPVQCSR	1971.3	3	4.2161	0.2192
AGIPKEEVKEAYMGNVLQGGEGQAPTR	2831.2	3	5.908	0.4807
AGITSAMATR	979.1	2	2.7902	0.1067
AGIVQEDVQPPGLK	1451.6	2	3.9076	0.3681
AGKDLVSSLTSGLLTIGDR	1904.2	2	6.2529	0.5548
AGKDLVSSLTSGLLTIGDRFGGALDAAAK	2806.2	3	5.5362	0.5045
AGKEPGLQIWR	1255.5	3	4.1311	0.3038
AGKEVLLEVK	1086.3	2	2.5519	0.1667
AGKFPSLLTHNENMVAK	1858.2	3	3.9499	0.3186
AGKITDEEATK	1163.3	2	2.5602	0.1785
AGKLDPHLVLDQLR	1575.8	2	4.6393	0.4303
AGKLIENVDPEKAVQLYQQTANVFENEER	3334.6	3	5.1637	0.3392
AGKLIENVDPEKAVQLYQQTANVFENEERLR	3604.0	3	4.2667	0.2468

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AGKPVICATQMLESMIK	1821.3	3	4.5305	0.4575
AGLAASLAGPHSIVGR	1477.7	2	3.3319	0.279
AGLEPFFDFIVSINGSR	1870.1	2	4.6626	0.4141
AGLGSGLSLSGLVHPELSR	1851.1	2	4.8589	0.4554
AGLGSPERPPK	1109.3	2	2.7588	0.2383
AGLIDWNMFVK	1294.5	2	2.5997	0.1126
AGLLAGDRLVEVNGENVEKETHQQVVSR	3049.3	3	8.5007	0.4357
AGLLEPEVFHLNPAK	1635.9	2	4.2928	0.2868
AGLLGQPR	812.0	2	2.5237	0.1535
AGLLHNILPSQSTDLHHSVGTELLSLVYK	3144.6	3	5.6004	0.3773
AGLLPSGPRPGYAAIQALLSSR	2196.5	3	3.3023	0.2023
AGLLRPDYALLGHR	1552.8	2	2.5766	0.1288
AGLLTEQAPGDTLTAVESK	1902.1	2	3.0274	0.1801
AGLQDASGNLVPLEDVHIK	1977.2	2	2.4478	0.1652
AGLQFPVGR	945.1	2	3.419	0.2015
AGLQSLEASGR	1089.2	2	2.6682	0.1571
AGLQSLEASGRLEDEFDMFALTR	2557.8	3	5.0211	0.3553
AGLQVYNK	893.0	1	3.5259	0.1924
AGLSLKDMDLVEVNEAFAPQYLAVER	2880.3	3	6.6396	0.4381
AGLSQSLFER	1108.2	2	2.6163	0.2843
AGLTDQVSHHAR	1292.4	2	3.0133	0.3059
AGLTHLITMDLHQK	1578.9	3	4.2908	0.4179
AGLTMNDIDAFEFHEAFSGQILANFK	2888.2	3	4.6276	0.332
AGLVDDFEKK	1122.3	1	2.9306	0.2524
AGLVGPEFHEK	1184.3	2	2.6321	0.1335
AGMGAHFR	847.0	2	2.6387	0.1464
AGMSAEQAQGLLEK	1433.6	2	4.3874	0.3044
AGMSYYNSPGLHVQHMGTSHGITRPSPR	3040.4	3	3.2772	0.2686
AGNAIHAILLYR	1312.5	2	3.1019	0.2846
AGNASKDEIDSAVK	1405.5	2	3.2896	0.2998
AGNFIGWLHIDGANLSVLLVEHALSK	2776.2	3	4.1338	0.311
AGNFYVPAEPK	1193.3	2	2.5888	0.1321
AGNILLNTEGHAK	1338.5	2	3.0666	0.2089
AGNKEATDEELEK	1434.5	2	2.9793	0.2112
AGNKEATDEELER	1462.5	2	2.4779	0.1661
AGNLGGGVVTIER	1243.4	2	2.7517	0.1654

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AGNNMLLVGVHGPR	1435.7	2	3.9925	0.3955
AGNYEEALQLYQHAVQYFLHVVK	2722.0	3	3.8015	0.1932
AGNYLRPYPVGEQEIHHTGR	2295.5	3	5.2446	0.3291
AGPAHAGHTAPMRPSYSAQEGLAGYQR	2783.0	3	3.6675	0.2635
AGPESDAQYQFTGIKK	1740.9	2	4.4966	0.3816
AGPGTLSVTIEGPSK	1414.6	2	3.8929	0.3728
AGPGVVR	655.8	1	1.6508	0.243
AGPHKEIYPYVIQELRPTLNELGISTPEELGLDK	3822.3	3	4.9019	0.2762
AGPHKEIYPYVIQELRPTLNELGISTPEELGLDKV	3921.4	3	6.5937	0.547
AGPIWDLR	928.1	2	2.8229	0.1946
AGPKADGEEDEVK	1345.4	2	3.1067	0.2669
AGPPPIQDGEFTFLLPAGR	1984.2	2	4.9809	0.473
AGPPSEILPLVQAVPK	1616.9	2	2.8539	0.1535
AGQAVDDFIEK	1193.3	2	2.8452	0.2208
AGQAVDDFIEKLVPLLDTGDIIIDGGNSEYR	3335.7	3	4.4054	0.3464
AGQAVDDFIEKLVPLLDTGDIIIDGGNSEYRDTTR	3809.1	3	3.6827	0.2406
AGQAVDDFIEKLVPLLDTGDIIIDGGNSEYRDTTRR	3965.3	3	3.4829	0.2332
AGQEHLLR	924.0	2	2.927	0.1363
AGQLLSELFTNRK	1477.7	2	3.669	0.2819
AGQPLQLLDASWYLPK	1801.1	2	3.3164	0.2188
AGQSAAGAAPGGGVDTR	1443.5	2	4.6853	0.5098
AGQSSLGGGHVSER	1342.4	2	3.635	0.4761
AGQSVIGLQMGTNK	1404.6	2	4.8755	0.4018
AGQTQPNPGILPIQPALTPR	2070.4	2	2.9929	0.2804
AGQTTYSGVIDCFR	1518.7	2	3.3174	0.2528
AGQVFLEELGNHK	1442.6	2	4.0127	0.2707
AGRDIFAQR	1034.2	2	2.6527	0.1167
AGREQTGLEAYALGLDTK	1894.1	3	3.8408	0.1659
AGRPHHDLPVILVGNK	1724.0	2	4.1367	0.3402
AGRSEAVVEYVFSGSR	1714.9	2	4.5206	0.4161
AGRVDLVDESGYVSGYK	1816.0	2	3.3821	0.2274
AGSGSQVPTEPK	1158.2	2	3.2828	0.267
AGSMKDPLLDDHGDFIR	1888.1	3	4.4686	0.3667
AGSRYEDFSNLGTTHLLR	2038.2	3	5.6364	0.4483
AGSSTPGDAPPAVAEVQGR	1767.9	2	4.0089	0.4671
AGTEALPDGLSVEDILNLLGMESAANQK	2858.2	2	5.7803	0.4587

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AGTEEAIVYSDIDLKK	1752.9	2	5.0699	0.3792
AGTFQAFEQFGQQLLAHGHYASPEIK	2877.2	3	5.1919	0.4658
AGTGVDNVDLEAATR	1489.6	2	4.5547	0.4564
AGTGVDNVDLEAATRK	1617.7	2	4.0525	0.3946
AGTLSITEFADMLSGNAGGFR	2116.3	2	5.6894	0.4994
AGTLTVEELGATLTSLLAQAQAQAR	2514.8	3	5.7839	0.4159
AGTQIENIEEDFRDGLK	1936.1	2	4.2627	0.3788
AGTQIENIEEDFRDGLKLMLLLEVISGER	3290.7	3	4.1983	0.1304
AGVAPLQVK	883.1	2	2.5345	0.1091
AGVDPLVPLR	1037.2	2	3.1425	0.2926
AGVDTSPDTQK	1119.2	2	3.1568	0.2457
AGVDTSPDTQKILVDSR	1803.0	3	3.4307	0.252
AGVEAMSK	792.9	1	2.1162	0.1492
AGVENGKPTHFTVYTK	1749.9	2	4.1252	0.3643
AGVHIKLPLLSK	1276.6	3	4.4369	0.258
AGVIFPVGR	916.1	1	2.6058	0.1894
AGVIGLTQTAAR	1158.3	2	4.0972	0.3831
AGVKDTENR	990.1	2	2.5412	0.1592
AGVLADDHLIEVNGENVEDASHEEVVEK	3019.2	3	6.4866	0.3148
AGVLAGHDNR	1010.1	2	2.9509	0.2305
AGVLAHLEEER	1224.3	2	3.6404	0.4287
AGVLAHLEEERDLK	1580.8	2	3.8274	0.3112
AGVMALANLLQIQR	1498.8	2	3.8298	0.1618
AGVNTVTTLVENK	1346.5	2	3.1301	0.2221
AGVPMEVMGLMLGEFVDDYTVR	2430.8	2	4.8746	0.4729
AGVSISVVHGNLSEEAAK	1768.9	2	3.8332	0.4028
AGVSSQPVSLADR	1287.4	2	3.2503	0.2845
AGVVGPELHEQLLSAEK	1778.0	2	4.8162	0.455
AGVVTPGITEDQLWR	1642.8	2	3.5539	0.3589
AGYIIPLQGPGLTTTESR	1875.1	2	4.5143	0.3974
AGYQDMPEYENFKHLLQAPLDDAQEILQAR	3505.9	3	4.1302	0.2847
AGYTDKVVIGMDVAASEFFR	2177.5	2	6.1072	0.5689
AGYVDFENGQWATDDIPDDLNSIR	2712.8	3	5.3242	0.4132
AHAAIRENPVYEK	1498.7	2	3.2358	0.3474
AHAHLDTGR	978.0	2	2.6204	0.222
AHATGAGPAGR	966.0	2	2.736	0.2709

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AHATTSNTVSK	1117.2	2	2.9412	0.4913
AHAVEGQVEDVVGNLR	1693.8	2	3.9436	0.4509
AHDERSEASGPQLLPVR	1863.0	3	3.3371	0.2687
AHDGGIYAISWSPDSTHLLSASGDK	2586.8	3	5.078	0.4183
AHDGGIYAISWSPDSTHLLSASGDKTSK	2903.1	3	5.4476	0.4783
AHDILHLVELAAQYR	1750.0	2	4.8091	0.43
AHEAQDAGYR	1118.1	2	2.9807	0.2502
AHEEQLKEAQAVPATLPELEATKASLKK	3032.4	3	5.2212	0.4069
AHEKEFGSVNGDNKPIWMHAEER	2682.9	3	3.2128	0.1156
AHELKEHNGHITGIDWAPK	2154.4	3	3.3603	0.2096
AHEQALAELTKR	1367.5	2	3.6886	0.3121
AHESVVK	769.9	1	1.8241	0.1237
AHESVVKSEDFSLPAYMDR	2182.4	2	5.5097	0.5072
AHESVVKSEDFSLPAYMDRR	2338.6	3	4.1411	0.3663
AHFGLPSVEAEDKEGKPPISVK	2336.6	3	3.9509	0.2524
AHFKELVNAVATVR	1555.8	2	2.4385	0.303
AHFLDADPGFVHSDGTISHHDMYDYLHLSR	3455.7	3	4.5299	0.2981
AHFMHHYENF	1333.5	2	2.9748	0.1901
AHFNLDESGVLSLDRVESVFETLVEDSAEEESTLTK	3998.3	3	6.1165	0.4829
AHFPLDVQWNDLDYMDSR	2223.4	2	5.2569	0.4588
AHFQNFPNGVTDFIK	1735.9	2	2.5046	0.1822
AHFSISNSAEDPFIAIHAESKL	2385.6	3	3.7257	0.3657
AHFSPSNIILDFPAAGSAAR	2043.3	3	3.3694	0.1455
AHGELHEQFK	1196.3	2	3.0606	0.3061
AHGFTFTR	937.0	1	1.7464	0.2385
AHGGYSVFAGVGER	1407.5	2	4.4921	0.5541
AHGLEVEPSALEQGFR	1740.9	3	5.2424	0.394
AHGLLAEENR	1110.2	2	3.1728	0.337
AHGLLAEENRGLGER	1622.8	2	3.1036	0.3467
AHGNVQDR	896.9	1	1.6185	0.1094
AHGPGLEGGLVGKPAEFTIDTK	2195.5	2	6.1936	0.5293
AHGSLKP	709.8	1	1.6543	0.1179
AHGTHPAISTLAR	1332.5	2	2.9552	0.4346
AHGVDK	626.7	1	1.6955	0.1917
AHIKFPIDYPYSPPTFR	2050.3	3	4.3455	0.3857
AHIVFDFHQAADGIQEQQR	2211.4	3	3.9511	0.2488

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AHIVFDFHQAADGIQEQQRQEQAGK	2853.1	3	4.0397	0.2863
AHKETVEQLQAK	1382.5	2	3.5447	0.3558
AHLEKESIAQR	1282.4	2	2.5312	0.1606
AHLEKLEVDLNK	1409.6	2	2.8733	0.3001
AHLESLVASRPSPQPLAETPIPSLPEFPR	3138.6	3	7.0038	0.5503
AHLGTALK	811.0	1	1.9303	0.186
AHLLAAALGPAGER	1347.5	2	2.5347	0.2009
AHLLADMAHISGLVAAK	1719.0	2	5.3638	0.4942
AHLLDNTERLER	1467.6	2	2.4869	0.1542
AHLMEIQVNGGTVAEK	1697.9	2	5.8565	0.5018
AHLVAVFNEYQR	1447.6	2	3.9273	0.4389
AHLVEVQGLQVR	1349.6	2	2.8915	0.2266
AHMGMFTELAILYSK	1713.1	2	3.3561	0.1208
AHPQGLVLVTDAIPALGLGNGR	2170.5	3	4.2881	0.3229
AHQAHAVVAEEVAALTGELER	2202.4	2	3.7257	0.3603
AHQANQLYPFAISLIESVR	2158.4	2	4.6986	0.4981
AHQEKPNFIIK	1325.5	2	2.939	0.2455
AHQITDESLESTRR	1643.7	2	3.425	0.2691
AHQVVEDGYEFFAK	1640.8	2	4.3362	0.4354
AHQVVEDGYEFFAKR	1797.0	2	4.8975	0.4433
AHSDGGDGVVSQVK	1356.4	2	3.6507	0.389
AHSGAQGLLAAQK	1252.4	2	4.0521	0.4517
AHSGSHSGGGLEAK	1295.3	2	3.9178	0.5336
AHSIKDMENTLQLVR	1756.0	2	3.2818	0.3097
AHSIQIMKVEEIAASK	1756.1	2	4.8224	0.4457
AHSQTDRENLR	1327.4	2	3.2023	0.1569
AHSSAGQQVAR	1112.2	2	3.3914	0.2488
AHSSMAEVNLPQKAGGFLMK	2117.5	2	3.0335	0.1138
AHSSMVGVNLPQK	1368.6	2	4.3813	0.4228
AHSSPASLQLGAVSPGTLTPTGVVSGPAATPTAQHLR	3536.9	3	7.5156	0.4814
AHSTGEQPPQLSLATR	1693.8	2	4.2713	0.4929
AHSTMTGSGVDAR	1290.4	2	3.1478	0.3499
AHTDFFEAFK	1213.3	2	2.86	0.3696
AHTKDEAEQLAGK	1398.5	2	3.0594	0.3533
AHTSSTQLQEELEK	1601.7	2	3.1013	0.2919
AHTSSTQLQEELEKVANQIKEEEEKQVVEAEK	3684.0	3	5.3843	0.49

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AHVDEFKSVSK	1247.4	2	3.5224	0.4064
AHVIVMAATNRPNSIDPALR	2147.5	3	3.6285	0.3824
AHVIVMAATNRPNSIDPALRR	2303.7	3	3.9397	0.3282
AHVLAASVEQATENFLEK	1958.2	2	5.1386	0.2895
AHVLAASVEQATENFLEKGDK	2258.5	3	3.5633	0.3952
AHVLAASVEQATENFLEKGDKIAK	2570.9	3	4.6499	0.4491
AHVLHFGK	909.1	2	2.6257	0.2107
AHVQEVAQHNLK	1374.5	3	4.2434	0.393
AHVTHPELK	1032.2	2	2.8105	0.2984
AIAALISEKLETLR	1528.8	2	4.3481	0.3637
AIADTGANVVVTGGK	1373.5	2	4.3833	0.466
AIAELGIYPAVDPLDSTSR	1989.2	3	5.0714	0.5026
AIAELGIYPAVDPLDSTSRIMDPNIVGSEHYDVAR	3787.2	3	3.7526	0.1096
AIAGDEHKR	997.1	2	2.6382	0.2469
AIAGGDEKGAAQVAAVLAQHR	2034.3	3	4.4093	0.3352
AIAGVINQPYYNYEAGPDAVLGR	2452.7	3	6.0265	0.5387
AIAHYEQSADYYKGEESNSSANK	2563.6	3	5.4932	0.428
AIAIPVDLDSQVNNLFLK	1971.3	2	3.291	0.3795
AIANECQANFISIK	1522.8	2	3.441	0.3202
AIAQSQSVQESLESLLQSIGEVEQNLEGK	3116.4	3	5.5021	0.3218
AIATLMSDEVFHDIAYK	1925.2	2	4.8111	0.4829
AIDALREFNEEGALSVLQQFK	2379.7	2	3.3212	0.2093
AIDGLDRNLHYFNSDSFASHPNYPYSDEY	3409.5	3	4.7425	0.3922
AIDIYEQVGTNAMDSPLLK	2079.4	2	3.6841	0.3443
AIDLFTDAIK	1107.3	2	3.1422	0.1944
AIDLFTDAIKLNPR	1587.8	2	4.7031	0.4428
AIDTIYQTTDFSGIR	1701.9	2	3.3036	0.4392
AIDTTQLFSLPK	1334.5	2	3.8556	0.343
AIDTTQLFSLPKDFWEQEVR	2424.7	3	5.0383	0.4825
AIEALHGHELRPGR	1556.8	3	3.2522	0.3028
AIEALKEFNEDGALAVLQQFK	2335.6	2	5.8626	0.5183
AIEALKEFNEDGALAVLQQFKDSDLSHVQNK	3459.8	3	7.5059	0.4307
AIEAVHNTAMR	1213.4	2	3.213	0.3051
AIEEFESSLKEAK	1481.6	2	3.0598	0.2803
AIEENNNFSK	1166.2	2	2.9344	0.2454
AIEGFNQSSHQK	1346.4	2	3.1955	0.1377

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AIEINPDSAQPYK	1446.6	2	3.2523	0.2856
AIEKLAVEALSSLDGDLAGR	2029.3	2	5.8742	0.5014
AIELFSVGQGPAK	1317.5	2	4.0189	0.2859
AIEMLGGELGSK	1205.4	2	3.9142	0.3767
AIEMLGGELGSKIPVHPNDHVNK	2456.8	3	5.6374	0.4353
AIENELLAR	1029.2	2	3.2795	0.1937
AIENIDTLTNLESLFLGK	1992.3	2	6.2222	0.5458
AIEPNDYTGKVSEEIEDIIKKGETQTL	3022.3	3	3.3463	0.1341
AIEPPPLDAVIEAEHTLRELDALDANDELTPLGR	3696.1	3	3.439	0.1982
AIEPQKEEADENYNSVNTR	2208.3	3	3.7825	0.2272
AIEQADLLQEEDESPR	1843.9	2	5.2442	0.3708
AIEQFQTENGVLLPSLQSALPFLDLHGTPR	3293.7	3	3.3458	0.2546
AIETTDIISR	1119.3	2	3.1222	0.2532
AIFDTPDEDPNYNPLPEERPGGFAWGEGQR	3376.5	3	5.0274	0.4242
AIFLADGKVFTTGFSR	1731.0	2	4.4531	0.3559
AIFLADGNVFTTGFSR	1716.9	2	4.3346	0.4309
AIFTGHSAVVEDVAWHLLHESLFGSVADDQK	3380.7	3	3.8346	0.37
AIGAVPLIQGEYMIPCEK	1933.3	2	4.2049	0.3833
AIGDHFYKR	1107.2	2	2.8892	0.2869
AIGGEFSDTNAAVEGTPLPK	1975.1	2	4.7998	0.3035
AIGHVIEEGGVK	1209.4	2	2.4033	0.1704
AIGIEPSLATYHHIIR	1792.1	2	3.0763	0.2822
AIGISNFNHLQVEMILNKPGLK	2437.9	3	4.1895	0.2723
AIGKDNFTAIPEGTNGVEER	2119.3	2	5.8988	0.4542
AIGLLDVDVYGPSVPK	1643.9	2	3.8267	0.3667
AIGPHDVLATLLNNLK	1690.0	2	5.0576	0.3803
AIGPSQTHTIR	1181.3	2	3.3161	0.3376
AIGSASEGAQSSLQEVYHK	1963.1	2	5.4327	0.4598
AIGSTSKPQESPK	1330.5	2	2.9582	0.2375
AIGTDEDLAHSSIR	1485.6	2	4.0891	0.3431
AIGTEPDTDVLSEIMNSFAK	2139.4	2	3.3364	0.3162
AIHDKDYVK	1089.2	2	2.4114	0.1946
AIHDVKATDLGLGK	1438.7	2	3.6319	0.3243
AIHEFLAAQKK	1256.5	2	2.419	0.1571
AIHKETGQIVAIK	1408.7	2	2.5885	0.2483
AIHKIDIPSFDWPIAPFPR	2221.6	3	5.2445	0.4259

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AIHNKVNIVPVIAK	1516.9	2	3.1825	0.1095
AIIEEYLHLNDMK	1589.8	2	2.7573	0.1245
AIIESDQEQGR	1246.3	2	3.3713	0.2731
AIIESDQEQGRK	1374.5	2	3.4213	0.2398
AIIIFVPVPQLK	1338.7	2	3.6776	0.3688
AIIKPQYVDQIPK	1513.8	2	3.1825	0.2722
AIILNTPHNPLGK	1388.6	2	3.4716	0.3318
AIIPSHLAYGKR	1326.6	2	2.841	0.3149
AIISNKDILATNGVIHYIDELLIPDSAK	3038.5	3	4.0351	0.2465
AIKEGDLSTK	1062.2	2	2.5739	0.2032
AIKEGDLSTKYDAPFVFAEVNADVVDWIQQDDGSVHK	4109.5	3	6.0183	0.3668
AIKEKEYEIER	1408.6	2	2.7563	0.2109
AIKELEEWYAR	1408.6	3	3.8026	0.2758
AIKELEEWYARQDEQLQK	2278.5	2	4.267	0.3149
AIKELGDHVTNLR	1466.7	2	4.0897	0.3982
AIKELGDHVTNLRK	1594.8	2	4.4965	0.388
AIKLTVNDFVR	1276.5	2	2.5671	0.2189
AIKQVYEEEYGSSLEDDVVGDTSGYYQR	3202.3	3	7.0046	0.6147
AIKVEQATKPSFER	1604.8	2	3.9523	0.3674
AIKVEQATKPSFESGR	1749.0	3	5.1626	0.4867
AIKVEQATKPSFESGRR	1905.1	2	2.9605	0.2191
AILIFNNHGKPR	1380.6	2	3.2608	0.2702
AILILDNDGDRLFAK	1674.9	2	4.1995	0.3853
AILNYIASK	993.2	2	3.2146	0.3352
AILNYIASKYNLYGK	1732.0	2	4.1022	0.4071
AILQEVLDADLSNEAFPFSTHK	2446.7	2	5.1422	0.4532
AILTESENKLRDLQQEAETYR	2508.7	3	3.3518	0.2131
AILVDLEPGTMDSVR	1616.9	2	4.9038	0.4887
AIMAQLPQEQK	1257.5	2	3.4392	0.1211
AIMEKLEMSKFQPTLLTLPR	2347.9	3	3.2857	0.1805
AIMKDPDDHTVCHLLFANQTEK	2527.9	3	4.2319	0.3098
AIMTYVSSFYHAFSGAQK	2009.3	2	5.4628	0.5314
AIMTYVSSFYHAFSGAQKAETAANR	2723.0	3	3.7582	0.3309
AINEAYKEDYHK	1481.6	2	3.5703	0.3055
AINEAYKEDYHKSLEDALSSDTSGHFR	3085.2	3	7.0799	0.4966
AINEAYKEDYHKSLEDALSSDTSGHFRR	3241.4	3	4.4737	0.2854

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AINFNFGYAK	1145.3	2	3.1087	0.3094
AINGPTSASGDDISK	1433.5	2	2.7238	0.2074
AINIADELPR	1112.3	2	3.3077	0.2733
AINLQMFHK	1102.3	2	2.9532	0.1664
AINQGGLTSVAVR	1286.5	2	3.6809	0.3782
AINQQTGAFVEISR	1534.7	2	4.1692	0.4086
AINTLNGLR	972.1	2	2.6716	0.2442
AINTQEAPVKEK	1328.5	2	2.9228	0.2272
AINTQEVAVKEK	1330.5	2	2.7698	0.2858
AINVQEEKIAALQAFADQLIAAGHYAK	2885.3	3	3.9373	0.2934
AIPDLTAPVAAVQAAVSNLVR	2077.4	2	5.7322	0.6354
AIPELTKLLNDEDQVVVNK	2139.4	2	3.6627	0.2151
AIPLFGNSLKPDSLR	1628.9	2	3.816	0.3819
AIPQLQGYLR	1159.4	2	2.6245	0.2707
AIPTVNHSGTFSPQAPVPTTVPVVDVR	2788.2	3	4.8032	0.3397
AIPVAQDLNAPSDWDSR	1856.0	2	5.0865	0.5049
AIQAYGMKPHDIFEANDLFENGNMTQVQTTLVALAGLAK	4222.8	3	5.347	0.4191
AIQDGTIVLMGTYDDGATK	1970.2	2	3.8468	0.1546
AIQDGTIVLMGTYDDGATKLNDEARR	2825.1	3	4.2714	0.3715
AIQDHLLEVEQSKDQMEK	2142.4	3	3.416	0.2209
AIQDMFPNMDQEVIR	1808.1	2	3.1126	0.199
AIQGGTSHHLGQNFSK	1682.8	2	4.3057	0.4415
AIQIMYQNLQQDGLEK	1893.2	2	5.7643	0.4442
AIQINPAFADAHSNLASIHKDSGNIPEAIASYR	3493.8	3	5.1024	0.3849
AIQTLGYFPVGDGDFPHQK	2091.3	2	4.0363	0.4116
AIRDEAIYHFR	1391.6	2	2.8649	0.2703
AIRDGVIEASINHEK	1652.8	2	4.4378	0.3261
AIRDGVIEASINHEKGYVQSK	2315.6	2	5.5174	0.4859
AIRDYQGPLKEHEVTIFVR	2272.6	2	5.0068	0.3781
AIRLELQGPR	1153.4	2	2.9936	0.143
AISAHFDDSSASSLK	1536.6	2	3.3881	0.3171
AISEAKLEEYTGTMMK	1803.1	2	4.8259	0.3797
AISEQTGK	833.9	2	2.6457	0.1988
AISEQTGKELLYK	1480.7	2	3.7028	0.3273
AISESGVALTSVLVK	1474.7	2	5.1173	0.4247
AISGVHTVR	940.1	2	2.832	0.2952

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AISHEHSPSDLEAHFVPLVK	2214.5	3	5.7661	0.4721
AISHEHSPSDLEAHFVPLVKR	2370.7	3	6.8471	0.5125
AISKDHLYGTLDPNTR	1802.0	2	4.5463	0.4481
AISPDKDNFYFDVKDDFDFGTMGHVIR	3151.5	3	4.2441	0.3291
AISQGHQAFLLEGDSSSR	1904.0	2	5.7015	0.4815
AISQSGVALSPWVIQK	1685.0	2	4.548	0.3082
AISYHLVQKPFSLTK	1733.0	2	3.1938	0.1601
AITDGQAGFGNDTLSKVPGISSIEQGMTGLK	3094.4	3	3.7134	0.2692
AITEKEKIEK	1189.4	2	3.0586	0.148
AITEKEKIEKER	1474.7	2	3.3593	0.2231
AITGASLADIMAK	1262.5	2	4.4213	0.4379
AITGASLADIMAKR	1418.7	2	2.9439	0.2356
AITGFDDPFSGK	1255.4	2	3.53	0.3312
AITHLNNNFMFGQK	1635.9	2	4.7132	0.3894
AITIAGIPQSIIECVK	1657.0	2	3.0226	0.1105
AITIAGVPQSVTECVK	1616.9	2	3.481	0.3045
AITIAGVPQSVTECVKQICLVMLETLSQSPQGR	3502.1	3	5.4929	0.4508
AITISSALQAGTVWVNCYGVVSAQCPFGGFK	3176.7	3	3.9935	0.3192
AITQEQCEAR	1149.3	2	3.0773	0.3309
AITSAYYR	945.1	1	1.9831	0.1024
AITVFSPDGHLFQVEYAQEAVK	2450.7	3	5.0642	0.3984
AITVFSPDGHLFQVEYAQEAVKK	2578.9	2	4.6692	0.4609
AIVAIENPADVSVISSR	1742.0	2	5.4808	0.5064
AIVEDHSLVAEEK	1440.6	2	3.6468	0.3791
AIVHDNKDGTYAVTYIPDKTGR	2435.7	3	5.1028	0.4071
AIWNVINWENVTER	1744.9	2	4.9511	0.4933
AIYDIERPDLITYEPFYTSGYDDKQER	3299.5	3	5.6594	0.4419
AIYFDGDFGQIVR	1501.7	2	4.1685	0.4912
AIYHDLEQSIR	1345.5	3	3.7626	0.2523
AIYKGPGSEAGP	1147.3	2	3.0187	0.3041
AKADAEYYAAHK	1338.5	2	3.1514	0.322
AKADSAYHPSCTCK	1482.7	2	2.5837	0.1041
AKALDQSDNDMSAVYR	1784.9	2	3.8455	0.4173
AKAQALVQYLEEPLTQVAAS	2131.4	2	3.387	0.267
AKAQELIQATNQILSHR	1922.2	3	4.2649	0.2339
AKAVSEKEVDSGNDIYGNPIKR	2391.6	3	4.5076	0.2545

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AKDAELAWIDGVLDMR	1804.1	2	3.8025	0.4209
AKDANNGNLQLR	1314.4	2	3.3852	0.2511
AKDDQTPLHISAR	1452.6	2	3.383	0.1829
AKDEQSAVSMLKK	1435.7	3	4.1152	0.2692
AKDFVFSLLGLVHR	1602.9	2	3.8091	0.3877
AKDGLVVFGK	1034.2	2	2.6064	0.2233
AKDHGLEVLGLVR	1407.6	2	3.1757	0.312
AKDINQEVYNFLATAGAK	1954.2	2	5.8463	0.5162
AKDIPIPNLPPLDFPSPELPLMELSEDILK	3343.9	3	3.4672	0.2177
AKDLEEELER	1232.3	2	3.1711	0.2561
AKDLIVTPATILK	1383.7	2	3.4725	0.1959
AKDLVELDPEVEGTKPSATEMIWAVLAAFNK	3374.8	3	3.9539	0.2251
AKDLVELDPEVEGTKPSATEMIWAVLAAFNKS	3461.9	3	4.9792	0.3625
AKDLYSALIK	1122.3	2	2.718	0.1281
AKDMHLVK	942.2	2	2.7301	0.2123
AKDPFAHLPK	1124.3	2	2.6956	0.1546
AKDQDILDLVGVLHDPETLLR	2361.7	3	5.1566	0.3772
AKDREIATLQEQLMTSEATVHSLQATVHQR	3393.8	3	5.1178	0.3326
AKDYPAHTEEDKQIQTEAAQLLTSFSEK	3180.4	3	6.137	0.4325
AKDYPAHTEEDKQIQTEAAQLLTSFSEKN	3294.5	3	6.5398	0.4703
AKEAAALGSR	974.1	2	2.9173	0.1667
AKEAAEQDVEK	1218.3	2	3.9069	0.3261
AKEAAEQDVEKK	1346.5	2	4.1569	0.3158
AKEAAEQDVEKKK	1474.6	2	4.3749	0.3107
AKEAEGGAATAGPSR	1373.5	2	2.8539	0.3139
AKEALELTDTGLLSGSEER	2020.2	2	6.6377	0.5415
AKEAQDDLVK	1117.2	2	3.4845	0.2067
AKEDVLQKEVR	1315.5	2	2.8601	0.2131
AKEELERQAVDQIK	1657.9	2	4.0133	0.2393
AKEELERQAVDQIKSQEQLAAELAEYTAK	3291.6	3	6.1608	0.4495
AKEEMSLSDLNSQDRVDHEEWEMVPR	3132.4	3	4.4289	0.2897
AKEEQQDDTVYMGK	1642.8	2	4.1708	0.3877
AKEFTNVYIK	1213.4	2	4.1135	0.2796
AKEFTNVYIKNFGEEVDDESLKELFSQFGK	3513.9	3	5.5091	0.3236
AKEIGADLVLQISKESPQEIAR	2396.7	3	5.8459	0.404
AKEILQEEEDLAEIVQLVGK	2255.6	2	6.9172	0.4097

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AKEILTKESNVQEVR	1745.0	2	4.172	0.3367
AKEILTNEESR	1290.4	2	3.1077	0.194
AKEISNLNQLIEEFKK	1905.2	2	5.3191	0.3159
AKELLGQGLLLR	1311.6	2	4.0358	0.2484
AKEQIESLEHDLQASVDELQDVKEER	3040.2	3	4.9644	0.3316
AKESLKELSLAGNELGDEGAR	2188.4	2	5.6117	0.4612
AKETADAITK	1048.2	2	2.9586	0.2006
AKETADAITKEAK	1376.5	2	4.4019	0.3462
AKFDAELLEIKK	1405.7	3	4.1899	0.3283
AKFEELNMDLFR	1513.7	3	4.7695	0.4521
AKFYPEDVAEELIQDITQK	2238.5	2	5.9112	0.504
AKFYPEDVAEELIQDITQKLFFLQVK	3114.6	3	5.1158	0.458
AKFYPEDVSEELIQDITQR	2282.5	2	4.822	0.5087
AKGDAKGDKAK	1089.2	2	3.2054	0.1962
AKGGEEPLPEGLFWLLVTGHIPTEEQVSWLSK	3550.0	3	4.5311	0.1667
AKGHSLSDGLEEVQK	1598.7	3	4.17	0.3449
AKGHSLSDGLEEVQKAEMK	2058.3	3	3.3976	0.2951
AKGPVTIPYPLFQSHVEDLYVEGLPEGIPFR	3471.0	3	3.9988	0.3701
AKGSETPGATPGSK	1288.4	2	4.0566	0.3178
AKHDELTYF	1124.2	2	2.7899	0.2609
AKHHAISAK	963.1	2	2.6448	0.2211
AKHLAEEYGER	1303.4	2	2.8461	0.3019
AKHSGDYFTLLR	1408.6	3	3.5531	0.2178
AKHVYSEAAR	1132.3	2	2.7708	0.2802
AKIAEQVASFQEEK	1578.7	2	4.6635	0.3301
AKIDDPTDSKPEDWDKPEHIPDPDAK	2961.1	3	5.6708	0.3499
AKIEDEKKDEEKEDPK	1932.1	2	4.5349	0.2741
AKIEETITQAR	1260.4	2	2.4769	0.1955
AKIELLGSYDPQK	1462.7	2	3.4097	0.163
AKIIAEGANGPTTPEADKIFLER	2442.8	3	5.2848	0.3927
AKKDDTDDEIAK	1349.4	2	4.7476	0.2166
AKKDDTDDEIAKYDGK	1812.9	2	5.3283	0.5173
AKKDDTDDEIAKYDGKWEVEEMKESK	3089.3	3	5.8735	0.3668
AKKDLEEWNQR	1417.6	2	2.9192	0.1498
AKKDNVAGVTLPVFEHYHEGTDSYELTGLAR	3419.7	3	7.2257	0.568
AKKGEEALFTTR	1351.5	2	3.4538	0.3549

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AKKPAAATVTK	1086.3	2	2.4351	0.2859
AKKVEDMMK	1080.3	2	2.6975	0.2419
AKKYILGNPLTPGVTQGPQIDKEQYDK	3003.4	3	4.6517	0.3185
AKLAEQAERYDDMAAAMK	2013.3	2	4.1899	0.4701
AKLAEVLEAVMPHLDQTPNPLVSSVFHR	3100.6	3	4.9192	0.3177
AKLDNNKELAFFANALEEVSIETIEAGFMTK	3445.9	3	3.2998	0.1893
AKLDSLQDIGMDHQALLK	1997.3	2	5.1175	0.446
AKLEAAIAEAEER	1401.5	2	3.4855	0.3846
AKLEAAIAEAEERGELALK	2013.3	2	6.1757	0.4521
AKLEAAIAEAEERGELALKDAR	2355.6	3	5.5255	0.41
AKLEEAILGSIGAR	1428.7	2	3.5015	0.3182
AKLEEHFK	1002.1	2	2.7584	0.1731
AKLEEHFKNQELR	1642.8	2	4.1935	0.2219
AKLEQLFQDEVAK	1519.7	2	4.0818	0.3691
AKLEQLFQDEVAKAQQLREEQQR	2787.1	3	3.4856	0.2051
AKLGDSHDLQR	1240.4	2	2.577	0.2051
AKLHIDEMDSVPTVR	1712.0	2	3.0117	0.3285
AKLNWLSVDFNNWK	1736.0	2	4.3747	0.3842
AKLPLGLLLHPFR	1475.8	3	3.4571	0.4143
AKLQIELGK	1000.2	2	2.5754	0.1185
AKLSSDVLTLLIK	1401.7	2	3.0846	0.188
AKLTISPDYAYGATGHPGIIPPHATLVFDVELLKLE	3849.4	3	5.0828	0.3526
AKMDAEQDPNVQVDHLNLLK	2279.6	3	3.5114	0.1684
AKNEILDEVISLSQVTPK	1985.3	2	5.4881	0.4864
AKNGHLAVVAPR	1233.4	2	3.5335	0.4119
AKNNTVTPGGKPNK	1426.6	2	3.4624	0.2511
AKPAEAPAAAAPK	1193.4	2	3.0703	0.2357
AKPAMPQDSVPSPR	1481.7	2	3.4582	0.3839
AKPDFKELTVSNNDINEAGVR	2318.5	2	5.6748	0.3407
AKPDHDPNTR	1151.2	2	2.4908	0.1555
AKPKEADESLNFEEQILEAAK	2361.6	3	5.0532	0.3684
AKPLLLQLPIGEAK	1491.8	2	2.869	0.2321
AKPVNSKPDSAYR	1433.6	2	2.8182	0.2793
AKPYEGSILEADCDILIPAASEK	2434.7	2	4.1933	0.2859
AKQDFLKTDSDSDLQLYKEQGEGQGDR	3073.2	2	2.5425	0.1182
AKQDMAR	820.0	1	2.0287	0.1743

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AKQEALVKER	1172.4	2	2.9488	0.2407
AKQEELEAALQR	1386.5	2	4.3659	0.3068
AKQIVWNGPVGVFEWEAFAR	2305.6	3	5.3048	0.4283
AKQNDQVSFASLVEELKK	2035.3	3	5.4107	0.4149
AKQQGDHSLKEHELLEQQK	2247.5	3	4.1028	0.2997
AKQTLENERGELANEVK	1930.1	2	5.6287	0.3782
AKQTLENERGELANEVKVLLQGK	2568.9	3	4.0593	0.125
AKRLEEIPLIK	1310.6	2	2.9295	0.1017
AKRPEVPFPEITR	1540.8	2	3.212	0.2553
AKRPLMVLGSQALLTPTSADK	2198.6	3	4.5327	0.3852
AKRPLMVLGSQALLTPTSADKLR	2468.0	3	5.0419	0.3105
AKSEENTKEEKPDSK	1720.8	2	3.6826	0.2547
AKSELNRLQQEETQLEQSIQAGR	2657.9	3	3.3184	0.2355
AKSHLEVPLEENVNRR	1892.1	2	2.9848	0.2546
AKTALEEQLSR	1246.4	2	2.9588	0.1741
AKTDAGGEDAILQTR	1546.7	2	4.3888	0.377
AKTELLLSAEAAK	1345.6	2	3.3961	0.2993
AKTGTDKTLVK	1162.4	2	2.9117	0.1807
AKTGTDKTLVKEVVQNFAK	2078.4	3	4.0704	0.2925
AKTNADTDGMVK	1251.4	2	3.578	0.363
AKVAAVEMLK	1060.3	2	2.8216	0.1984
AKVAVLGASGGIGQPLSLLLK	1993.4	2	6.6125	0.4981
AKVDEFPLCGHMVSDEYEQLSSEALEAAR	3226.5	3	4.6719	0.4083
AKVETDDVKK	1133.3	2	2.6573	0.2548
AKVGAAEEELQK	1273.4	2	4.0534	0.3442
AKVIAAEGEMNASR	1447.6	2	3.4709	0.3683
AKVKDEPQR	1071.2	2	2.4577	0.2112
AKVNDFLAEIFKK	1523.8	2	3.7993	0.363
AKWDAWNALGSLPK	1557.8	2	3.6715	0.2361
AKWEMPFDPQDTHQSR	1974.1	3	4.3233	0.4073
AKYHGNVMLLR	1302.6	2	2.587	0.2783
AKYIYDSAFHPDTGEK	1843.0	2	5.1988	0.4196
AKYPDYEVTWANDGY	1792.9	2	4.4225	0.3998
AKYPSLGQKPGGSDFLMK	1925.2	2	2.9232	0.2597
AKYVYDSAFHPDTGEKVVLIGR	2466.8	3	4.2034	0.2981
ALAAAGYDVEK	1108.2	2	3.664	0.441

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALAAAGYDVEKNNSR	1579.7	2	4.6796	0.433
ALAAFLKK	862.1	2	2.6319	0.1806
ALAAGGVGSIVR	1071.3	2	4.1265	0.4121
ALAAGGYDVEKNNSR	1565.7	2	4.7712	0.4865
ALAAPAAEEKEEAR	1456.6	2	3.9814	0.4397
ALAAPAAEEKEEAREK	1713.9	2	4.5013	0.4093
ALAAVLLQALDRPASPPAPSGSQQGPEEEAAEALLTETV	3900.3	3	5.158	0.3194
ALAAVLLQALDRPASPPAPSGSQQGPEEEAAEALLTETVR	4056.5	3	6.0272	0.5175
ALADHSMAQTPR	1298.5	2	3.4185	0.3725
ALADILSESLHSLATSLPR	1995.3	2	3.1706	0.2827
ALADVATVLGR	1086.3	2	3.5997	0.2507
ALAEGVLLR	942.1	2	2.9195	0.1863
ALAEIAKAELDDTPMR	1745.0	2	5.2636	0.4477
ALAEIAKAELDDTPMRGR	1958.2	3	3.7767	0.3566
ALAEKRPGKLHQRVLLHHDNAPAHSSHQTR	3406.8	3	3.2607	0.1715
ALAENSGVK	889.0	2	2.49	0.1391
ALAENSGVKANEVISK	1630.8	2	4.6511	0.3436
ALAFHPIEPVLITASEDHTLK	2303.6	3	5.2976	0.373
ALAFHPVEPVLVTASEDHTLK	2275.6	3	5.6376	0.4008
ALAGCDFLTISPK	1336.6	2	2.7112	0.2535
ALAGWLRPEDGGQAEGAEDELEVR	2569.7	3	3.5333	0.3312
ALAHLLEAER	1123.3	2	3.3722	0.3665
ALAHLLEAERQER	1536.7	2	3.5293	0.4829
ALAIYEGQLGPDNPNVAR	1899.1	3	4.778	0.4002
ALALDEAVSQSTQITEFHDKIEPMLETLENLSSR	3818.2	3	3.2004	0.1728
ALAMGYKPK	979.2	2	2.635	0.2498
ALANMHESLEWLASR	1729.0	2	3.2667	0.2706
ALANSLACQGK	1076.3	2	3.7597	0.3805
ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSTAAAPAEEK	3754.2	3	7.1572	0.617
ALAPEYAK	863.0	1	1.7383	0.1348
ALAQALKEGR	1057.2	2	2.6961	0.1077
ALAQEDQGAGEVER	1473.5	2	4.9811	0.2705
ALAQEILPQAPIAVR	1590.9	2	2.8207	0.3094
ALASEKSPTADAKPAPK	1682.9	3	3.6438	0.2823
ALASGGSALDAVESGCAMCER	1999.2	2	4.082	0.277
ALASILLQDHIR	1350.6	2	3.5476	0.2984

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALASLMTYK	998.2	2	3.2145	0.1838
ALASPEQLAQLPSSGVPR	1822.1	2	3.8338	0.3325
ALASQLQDSLK	1174.3	2	2.7129	0.2097
ALAVELLDKVNNPDNHAHYTEADDDDFEPHAIIR	3860.1	3	4.6381	0.4013
ALAVGGLGSIIR	1127.4	2	3.5602	0.3458
ALAVVYGPHEIR	1325.5	2	3.1221	0.1738
ALAYDKLEK	1051.2	2	2.4795	0.1774
ALDDFVLGSAR	1164.3	2	3.9339	0.4122
ALDDISESIKELQFYR	1928.1	2	4.8025	0.4457
ALDDMISTLKK	1235.5	2	2.786	0.1896
ALDEATKYALER	1380.5	2	3.6423	0.3705
ALDEATKYALERK	1508.7	2	3.7621	0.3941
ALDEGDIALLK	1158.3	2	4.242	0.2831
ALDELKQSYLTLESGAVPLLEDTASRIDELFQK	3695.1	3	3.3337	0.1089
ALDELKQSYLTLESGAVPLLEDTASRIDELFQKR	3851.3	3	3.2934	0.2948
ALDEMEKQQR	1248.4	2	2.9381	0.2004
ALDENAKLTQQLEEERIQHQQK	2650.9	3	4.5367	0.2682
ALDEPAKTESVSKDNTLEPPVETPTTLPR	3137.4	3	4.9733	0.3075
ALDEYYDKHFTEFVPLR	2144.4	2	4.9985	0.4776
ALDEYYDKHFTEFVPLRTK	2373.6	3	5.081	0.3312
ALDFAVGEYNK	1227.3	2	3.508	0.3535
ALDFAVGEYNKASNDMYHSR	2289.5	3	3.2257	0.2153
ALDFIASK	865.0	2	2.8899	0.2214
ALDFIASKGVK	1149.4	2	2.9529	0.2439
ALDIDLDKPLADSEKLPIQK	2223.6	3	4.4438	0.299
ALDIDVEKLTQAELEKLLLDDSFETK	2978.3	3	4.3326	0.1438
ALDKLDGTEINGR	1402.5	2	3.8845	0.3231
ALDKSDSHPSDALTR	1613.7	2	4.676	0.2967
ALDLFSDNAPPPELLEIINEDIAK	2639.0	3	4.894	0.404
ALDLFSDNAPPPELLEIINEDIAKR	2795.1	3	5.9105	0.477
ALDLNLKHQILPK	1503.8	2	3.9504	0.2988
ALDLPSSGEGLAFFTFPNIASATK	2455.7	3	5.7237	0.5315
ALDMSYDHKPEDEVELAR	2119.3	2	4.6541	0.3973
ALDQFVNFSEQKEK	1683.8	2	3.7052	0.2917
ALDSNSLENDDLSAPGREPGHFNPESR	2926.0	3	4.1331	0.2216
ALDTMNFDVIK	1267.5	2	3.716	0.3657

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALDVGSGSGILTACFAR	1638.9	2	4.3351	0.4141
ALDVIQAGKEYVEHTVK	1901.2	2	3.1342	0.2469
ALDVIQAGKEYVEHTVKER	2186.5	3	5.0043	0.3889
ALDVNVALR	971.1	2	3.2373	0.3357
ALDVSASDDEIAR	1362.4	2	3.7706	0.3768
ALDYYMLR	1045.2	2	2.5478	0.1147
ALEAAALAH	867.0	2	2.9818	0.1886
ALEAANGELEVK	1244.4	2	4.417	0.3584
ALEAANGELEVKIRDWYQK	2234.5	3	3.2588	0.1472
ALEAFDLDPAQWGVNVQPYSGSPANLAVYTALLQPHDR	4126.5	3	6.1028	0.5776
ALEAGTAVELLDVFLGLETDGEELAGAIAAGNPGAPLRER	4008.4	3	5.2893	0.4359
ALEATKLAIEAGFR	1490.7	2	3.6872	0.3193
ALEATTEHIR	1141.3	2	2.6772	0.1226
ALEATTEHIRQELAVFCSPEPPAK	2639.0	3	3.7026	0.2971
ALEAVFGK	835.0	1	2.4109	0.1755
ALECHPDKHPENPK	1615.8	2	3.2813	0.2001
ALEDAFLAIDAK	1277.4	2	4.0747	0.2924
ALEDDIINHNKHLHQAVSIGQSLK	2682.0	3	4.7517	0.1988
ALEDIDEKISNEVLK	1716.9	2	3.5411	0.2008
ALEDMFDALEGK	1339.5	2	3.7763	0.2664
ALEEALEAKEEFER	1664.8	2	3.2866	0.2516
ALEEALEAKEEFERQNK	2035.2	2	4.3314	0.216
ALEEAMEQK	1049.2	2	3.1733	0.1453
ALEEAMEQKAELER	1647.8	2	4.8963	0.4203
ALEEAMEQKAELERLNK	2003.3	2	5.3163	0.2986
ALEEAMEQKAELERLNKQFR	2434.8	3	3.8997	0.1857
ALEEANMKLESR	1391.6	2	3.3679	0.3157
ALEEEQEAREELER	1731.8	2	3.3837	0.2202
ALEEETKNHEAQIQDMR	2043.2	2	5.3322	0.3596
ALEELATKR	1031.2	2	2.8346	0.1379
ALEENNNFSK	1166.2	2	2.7608	0.1389
ALEEPAVDMLHTVTDMVR	2028.3	2	2.791	0.2386
ALEFVQTESQKDLEITKENLAQAVEHR	3128.4	3	6.7474	0.345
ALEGTLSELAAETDLPVVFVK	2203.5	2	4.3744	0.4253
ALEHAFQLEHIMDLTR	1925.2	3	5.1814	0.4307
ALEHFTDLYDIK	1465.6	2	3.3786	0.3448

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALEHFTDLYDIKR	1621.8	3	4.6091	0.3791
ALEIADFSGNPLSR	1490.6	2	3.4893	0.2998
ALEILLHPSEPHQPHLMLEGGSLSSAEYEAR	3413.8	3	3.6304	0.2245
ALEKAEENAQR	1259.4	2	2.9503	0.1825
ALEKEAASEKQQLVETHLAR	2252.5	3	3.3745	0.1279
ALEKGIEILTDMSRPVELSDRETLLNSATTSLNSK	3834.3	3	5.2482	0.3717
ALEKLDGTEVNGR	1402.5	2	3.1747	0.2677
ALEKNESSFASHK	1448.6	2	3.2469	0.2943
ALELDSNLYR	1194.3	2	3.3159	0.2664
ALELDSNNEK	1133.2	2	3.0936	0.2161
ALELDSNNEKGLFR	1606.8	2	3.4842	0.2585
ALELENDRLLLK	1427.7	2	3.8594	0.1467
ALELFLESLLK	1276.5	2	4.4526	0.2711
ALELTGLKVFGNEIKLEKPK	2228.7	3	4.4558	0.3365
ALENPDTASLLGR	1357.5	2	3.1426	0.2751
ALENVLSGKA	1002.1	1	1.8896	0.1168
ALEPALSDISVDWFVPDTVEALLTPR	2856.2	3	4.1058	0.2193
ALEQALEKTK	1131.3	2	3.1517	0.2191
ALEQFATVVEAK	1306.5	2	3.8125	0.3097
ALEQQVEEMK	1205.4	2	3.6828	0.2691
ALEQQVEEMKTQLEELEDELQATEDAK	3149.4	3	5.0338	0.4463
ALEQQVEEMKTQLEELEDELQATEDAKLR	3418.7	3	5.7826	0.4106
ALEQQVEEMKTQLEELEDELQATEDAKLRLEVNLQAMK	4446.0	3	5.8432	0.4431
ALEQQVEEMR	1233.4	2	2.6968	0.1333
ALEQQVEEMRTQLEELEDELQATEDAKLR	3446.7	3	5.911	0.3057
ALESALKEAKENASR	1617.8	3	3.2624	0.2795
ALESDMAPVLIMATNR	1733.0	2	4.729	0.3919
ALESELQQLR	1187.3	2	3.1824	0.1685
ALESPERPFLAILGGAK	1770.1	3	4.9435	0.1958
ALESSIAPIVIFASNR	1688.9	2	4.6519	0.4556
ALETNTHVK	1013.1	2	2.5521	0.2828
ALEVAEYLTPVLK	1446.7	2	3.2914	0.216
ALEVAEYLTPVLKESK	1791.1	2	2.5973	0.2098
ALEVIKPAHILQEKEEQHQLAVTAYLK	3101.6	3	6.7302	0.5118
ALEVTKLAIEAGFR	1518.8	2	2.8774	0.368
ALEVYDLIR	1092.3	2	3.2071	0.379

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALEYIENLR	1121.3	2	3.3503	0.223
ALFDYDKTKDSGLPSQGLNFK	2345.6	3	3.4231	0.2869
ALFEEVPELLTEAEKK	1847.1	2	3.6888	0.299
ALFLETEQLK	1192.4	2	3.5739	0.1497
ALFLETEQLKK	1320.6	2	2.7621	0.1361
ALFQDIK	835.0	2	2.5799	0.1326
ALFQDIKKPAEDEWGKTPDAMK	2519.9	3	4.7349	0.4521
ALFQDIKKPAEDEWGKTPDAMKAAMALEK	3234.7	3	5.5365	0.2215
ALFVSEEEKK	1180.3	2	2.7018	0.1215
ALGALVDSCAPGLCPDWDSWDASKPVTNAR	3117.5	3	4.8689	0.3155
ALGDPATPTEGPR	1282.4	2	3.1181	0.2869
ALGGHMTTLSGEEISYTGSDGIEGGLLASIR	3094.4	3	3.4472	0.1567
ALGHQLGR	852.0	2	2.4576	0.2502
ALGHRPIPNQPPTAAHTANFLLNASGSTSTPAPSR	3551.9	3	7.7913	0.5339
ALGISPFHEHAEVVFTANDSGPR	2452.7	3	5.8299	0.5446
ALGISPFHEHAEVVFTANDSGPRR	2608.9	3	3.3515	0.3077
ALGKHPVSCK	1040.3	2	2.6422	0.3095
ALGKHPVSCKDTPGFIVNR	2040.4	3	5.0352	0.4953
ALGLGVEQLPVVFEDVVLHQATILPK	2787.3	3	4.4596	0.4179
ALGLKDIFDESKADLSGIASGGR	2321.6	3	4.8171	0.2946
ALGLQFHSR	1029.2	2	2.9475	0.1237
ALGMKLPETNLFETEETRK	2208.5	3	4.4231	0.1009
ALGPGLGTPTPR	1137.3	2	3.3333	0.3088
ALGQAASDNSGPEDAKR	1687.8	2	4.3353	0.3145
ALGQEHDITLFVK	1471.7	2	2.4581	0.1128
ALGQNPTNAEVLK	1355.5	2	3.8786	0.2776
ALGQNPTNAEVLKVLGNPKSDEMNVK	2768.1	3	4.477	0.2892
ALGSAAADAQR	1031.1	2	2.8101	0.1643
ALGSAIEYTIENVFESAPNPR	2279.5	2	3.9776	0.3787
ALGSEVQDASK	1105.2	2	2.7614	0.2186
ALGSQYQNR	1037.1	2	2.8056	0.1849
ALGSVGPVDLLVNNAAVALLQPFLEVTK	2850.3	3	3.6297	0.1656
ALGVEQDLALPAIAVIGDQSSGKSSVLEALSGVALPR	3634.1	3	4.4595	0.3059
ALGVSNFSHFQIEK	1577.8	2	3.55	0.2595
ALGYFAVVTGK	1126.3	2	3.3756	0.4122
ALHAELVQHFR	1321.5	2	3.2812	0.2851

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALHDTGKFTDGQLVSQK	1846.0	3	3.4798	0.1526
ALHEKVNIVPLIAK	1545.9	2	3.9048	0.4371
ALHESGSQNKK	1199.3	2	2.5619	0.1854
ALHFVFK	862.1	2	2.4294	0.1541
ALHHGIDLEK	1133.3	2	2.714	0.1964
ALHLGNNVLQSLPSR	1619.9	2	2.8323	0.2048
ALHLLEEYR	1144.3	2	3.1882	0.1911
ALHPREPLPPIQQHIWNMLNPPAEVTTK	3229.7	3	3.7282	0.1878
ALHSDRPPSASQPR	1519.6	2	3.194	0.2569
ALHSLLLR	923.1	2	2.4171	0.1761
ALHSVLQAVPLNELR	1660.9	2	4.3463	0.4479
ALIAAQLDNAIEKELLER	2011.3	2	4.516	0.4769
ALIAAQYSGAQVR	1348.5	2	4.7279	0.3953
ALIAGGGAPEIELALR	1551.8	2	4.2289	0.3859
ALIDPSSGLPNRLPPGAVPPGAR	2253.6	3	4.0136	0.2183
ALIEILATR	1000.2	2	3.4325	0.2861
ALIEMEKQQQDQVDR	1832.0	3	4.9501	0.3862
ALIEMEKQQQDQVDRNIKEAR	2543.8	3	3.3351	0.113
ALIEVLQPLIAEHQAR	1802.1	2	4.6386	0.3994
ALIGATNPADAPPGTIR	1635.8	2	4.9895	0.3612
ALILVGGYGTR	1120.3	2	3.1325	0.3015
ALILVGLER	984.2	2	3.264	0.2191
ALINADELASDVAGAEALLDR	2128.3	2	5.6886	0.4233
ALINADELASDVAGAEALLDRHQEHKGEIDAHEDSFK	4017.3	3	3.9115	0.211
ALINSPEGAVGR	1184.3	2	3.1364	0.2864
ALIPLALEGTDVGQTK	1626.9	2	4.805	0.5041
ALIPSLEGRFEDEELQQILDDIQTKR	3058.4	3	4.8116	0.2487
ALIVEPSRELAEQTLNNIK	2139.4	2	4.5507	0.2903
ALIVEPSRELAEQTLNNIKQFKK	2671.1	3	4.3948	0.3067
ALIVLAHSER	1109.3	2	2.8796	0.123
ALIVVPYAEGVIPDEAK	1785.1	2	5.0279	0.4686
ALKANGEVIIEIPTR	1624.9	2	2.8746	0.2411
ALKASAPAPGHH	1157.3	2	3.1628	0.2656
ALKDEEKMELQEIQLK	1946.3	2	5.9146	0.3634
ALKDEEKMELQEIQLKEAK	2274.6	2	6.5073	0.3576
ALKDEEKMELQELQLK	1946.3	3	5.9386	0.3583

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALKDEEKMELQELQLKEAK	2274.6	2	6.6791	0.3407
ALKDEIDVLR	1172.4	2	3.0089	0.2501
ALKDKIEKAVVSQR	1585.9	2	3.2102	0.3108
ALKDQINQLELLLKER	1925.3	2	3.1733	0.2614
ALKEASMVITESPAALQLR	2029.4	3	6.5305	0.5302
ALKEAVKEIQTSAK	1516.8	2	4.2149	0.3346
ALKEDDPKAALSSFQK	1749.0	2	4.9027	0.3868
ALKEEIGNVQLEK	1471.7	2	3.8362	0.1301
ALKENKDQLESVLEVLHR	2122.4	3	4.3827	0.3287
ALKGIGTDEFTLNR	1535.7	3	3.5714	0.1951
ALKHELAFK	1057.3	2	2.6337	0.247
ALKLPSTGEGTQFYLFENVDNAQQFK	2947.2	3	5.2439	0.3649
ALKNHQLEVTPK	1378.6	2	2.4019	0.1079
ALKNNSNDIVNAIMELTM	1992.3	2	3.9725	0.3479
ALKPEVDKLNIMAAK	1642.0	2	3.901	0.3269
ALKPMHSLIPLGK	1405.8	2	2.655	0.1919
ALKPPPIKLYR	1296.6	3	3.2899	0.2035
ALKSEFLVR	1063.3	2	2.6585	0.2327
ALKSEVQKLQTLVSEQPNKDVVEQMEK	3100.5	3	3.8391	0.2325
ALKSVLVSAGNVKR	1442.7	2	2.5686	0.16
ALKVLDNYLTSPLPEEVDETSAEDEGVSQRK	3434.7	3	5.1075	0.3695
ALLADAQLMLDHLK	1552.9	2	4.492	0.3848
ALLANQDSGEVQQDPK	1713.8	3	4.9098	0.4213
ALLAPLVAPEAGEAEPGSQER	2106.3	2	4.8847	0.5002
ALLDASETTSTRK	1393.5	2	2.5858	0.2218
ALLDFEDKDGDKVVAGDEWLFEGPGTYIPR	3354.7	3	6.2515	0.4434
ALLDSLQLGPDSLTVHLIHEVTK	2500.9	2	4.0653	0.3991
ALLDYGVTADAR	1265.4	2	3.2915	0.3729
ALLEEAFDNLKDEMFR	1942.2	2	2.9739	0.3677
ALLELQEYFGSLAA	1525.7	2	2.7546	0.2831
ALLELQLEPEELYQTFQR	2221.5	2	5.3383	0.3989
ALLENMEGLFLAVDEIVDGGVILESDPQQVVHR	3608.1	3	6.823	0.5329
ALLEVVQSGGK	1101.3	2	3.8661	0.2662
ALLKDQQPGTFLLR	1600.9	2	2.6806	0.14
ALLKFPDIYGPRPAVTAPEVINYADYSLR	3251.7	3	4.7539	0.4181
ALLLPDYYLVTVMLSGIK	2010.5	2	4.403	0.3032

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALLLSHQFK	1057.3	2	2.7796	0.13
ALLNVVDNAR	1085.2	2	2.6746	0.2299
ALLQEMPLTALLR	1469.8	2	3.8596	0.3274
ALLQMVQQFAVDFEK	1768.1	2	3.6391	0.3345
ALLQMVQQFGVDFEK	1754.0	2	2.4456	0.1569
ALLQMVQQFGVDFEKR	1910.2	2	3.0661	0.3223
ALLQQQPEDDSKR	1528.6	2	3.4077	0.2827
ALLQSGAPAVPQLLHMPDFEGLYPVHLAVR	3241.8	3	4.2567	0.4329
ALLQSSASR	933.0	2	2.6467	0.2982
ALLSAPWYLNR	1304.5	2	3.1014	0.2939
ALLSHDSGSDHLAFVR	1725.9	2	4.3652	0.4312
ALLSSSDDPPAEVDIFELLK	2160.4	2	5.3276	0.5123
ALLSVHDTVAQK	1282.5	2	2.6161	0.2709
ALLTPVAIAAGR	1153.4	2	3.8699	0.3215
ALLVEPVINSYLLAER	1801.1	2	5.481	0.5018
ALLVEPVINSYLLAERDLYLENPEIK	3016.5	2	3.3128	0.2276
ALMAAEDKYSQKEDRYEEEIK	2547.8	3	4.3918	0.2832
ALMAAEDKYSQKEDRYEEEIKVLSDK	3090.4	3	5.1066	0.2544
ALMAAEDKYSQKEDRYEEEIKVLSDKLK	3331.7	3	4.6101	0.2751
ALMDEVVK	905.1	1	1.8437	0.1617
ALMDEVVKATSR	1320.5	2	2.8413	0.3589
ALMGSPQLVAAVVR	1412.7	2	3.3026	0.3126
ALMLQGVDLLADAVAVTMGPK	2114.6	3	6.4054	0.5277
ALMLQGVDLLADAVAVTMGPKGR	2327.8	2	3.1495	0.3327
ALMTVGKEPFPTIYVDSQKENER	2654.0	3	5.1818	0.4013
ALMTVGKEPFPTIYVDSQKENERWNVISK	3381.8	3	4.8763	0.3066
ALNAGYILNGLTVSIPGLER	2072.4	2	4.7348	0.4053
ALNALCDGLIDELNQALK	1915.2	2	5.7843	0.4346
ALNDHHVYLEGTLLKPNMVTAGHACTK	2935.4	3	3.7102	0.1902
ALNEALKLFK	1147.4	2	3.1754	0.2596
ALNEGGFQSIPK	1261.4	2	3.3563	0.3507
ALNEVFIGESLSSR	1522.7	2	3.3112	0.2349
ALNFLVNEFLLK	1421.7	2	3.3803	0.2503
ALNLGYALDYAQR	1468.6	2	2.7853	0.3723
ALNRPPTYPTK	1258.5	2	2.5806	0.141
ALNVEPDGTGLTCSLAPNIISQL	2327.6	2	3.2012	0.215

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALPAMMQWVR	1203.5	2	3.6451	0.3864
ALPDFKGIQTSDPNAVVMGLAPEHFHYQILNQAFR	3927.4	3	4.8494	0.3677
ALPDMEVVGLNFSSATTPELLLK	2446.8	2	5.704	0.5536
ALPESLGQHALR	1292.5	2	3.1047	0.3333
ALPEVHYHLGQK	1392.6	2	2.7704	0.2746
ALPFWNEEIVPQIK	1685.0	2	4.4199	0.3546
ALPFWNEEIVPQIKEGK	1999.3	2	3.6682	0.236
ALPFWNEEIVPQIKEGKR	2155.5	2	3.6533	0.2295
ALPGQLKPFETLLSQNQGGK	2127.4	2	4.8509	0.4277
ALPLALVLHELGAGR	1530.8	2	5.4572	0.5366
ALPLEAEVAPVKDMAQLPETEIAPAKDVAPSTVK	3531.1	3	5.4576	0.4281
ALPLIVGAQLIHADK	1559.9	2	3.4776	0.3742
ALPLIVGAQLIHADKLGEK	1987.4	2	5.2914	0.5301
ALPLIVGAQLIHADKLGEKVEDSTMPIRR	3172.7	3	4.7007	0.3013
ALQALEELRLQAEEAER	1970.2	3	4.6097	0.2545
ALQALQQEHKAEIITVSDGR	2208.5	3	4.7464	0.4326
ALQASALAAWGGK	1244.4	2	4.4754	0.396
ALQASALK	802.0	1	1.8958	0.125
ALQASALNAWR	1201.4	2	3.9466	0.378
ALQATVGNSYK	1152.3	2	3.939	0.2572
ALQDEWDAVMLHSFTLR	2033.3	2	5.0357	0.5264
ALQDFKEGNAIFTFPNTPVK	2238.5	3	4.5906	0.1446
ALQDLENAASGDAAVHQR	1867.0	2	5.1832	0.4498
ALQDLENAASGDATVR	1631.7	2	4.9411	0.4342
ALQDLQLDQGNQKDFIK	1975.2	2	3.5922	0.3463
ALQDPNVAAFMVEPIQGEAGVVVPDPGYLMGVR	3442.0	3	3.3383	0.1192
ALQEALVLSDR	1215.4	2	3.7915	0.2267
ALQEELSQAK	1117.2	2	2.6085	0.1495
ALQEGDLASSR	1147.2	2	3.3487	0.2997
ALQFLEEVK	1077.3	2	3.0278	0.2275
ALQFLEEVKVSR	1419.7	2	3.1777	0.2616
ALQGDYDQSR	1153.2	2	2.9648	0.2803
ALQKYEKEKFEEMIQQIK	2284.7	2	3.2749	0.2296
ALQLLDEVLHTMPIADPQPLD	2330.7	2	3.2691	0.2793
ALQNAVTTFVNR	1334.5	2	3.8087	0.3661
ALQPIVSEEEWAHTK	1738.9	2	2.8156	0.1392

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALQPLEEGEDEEKVSHQAGDHWLIR	2888.1	3	4.191	0.3737
ALQPLEEGEDEEKVSHQAGDHWLIRGPLEYVPSAK	3930.3	3	4.8646	0.4153
ALQQNGAPGIAK	1168.3	2	3.9423	0.2849
ALQQYTLEPSEKPFDLK	2008.3	3	4.7468	0.3246
ALQRPSAAAPQAENGPAAAPAVAAPAATEAPK	2967.3	3	6.4399	0.4543
ALQSVGQIVGEVLK	1441.7	2	4.3022	0.3579
ALQSVGQIVGEVLKQLTEEK	2170.5	2	4.0677	0.3893
ALRAELEALLSSKDDVGK	1916.2	2	3.7588	0.2594
ALRAELEALLSSKDDVGKSVHELER	2767.1	3	7.887	0.5247
ALRDAKLDKAQIHDLVLVGGSTR	2477.8	3	4.9853	0.3133
ALRDAKLDKSQIHDIVLVGGSTR	2493.8	3	4.0078	0.2902
ALRETLPAEQDLTTK	1686.9	3	4.0022	0.3459
ALRETLPAEQDLTTKNVSIGIVGK	2554.9	3	3.3697	0.1447
ALRPDLADKVASVYEAPGFFLDLEPIPGALDAVR	3628.1	3	5.9407	0.4313
ALRPPHGPPRPGALTPTPSLSSQALPSPR	2957.4	3	3.5261	0.4258
ALRQENAGLLGR	1298.5	2	3.0313	0.2625
ALRTDYNASVSVPDSSGPER	2122.2	2	5.5603	0.5085
ALRYPMAVGLNK	1333.6	2	3.3113	0.2001
ALSAIADLLTNEHER	1653.8	2	5.0661	0.4822
ALSDHHIYLEGTLLKPNMVTPGHACTQK	3076.5	3	6.6948	0.5006
ALSEIAGMTLPYDTLDQVR	2094.4	2	5.8887	0.4847
ALSEPRADAKAYSDPSTGEPATYGELQQR	3110.3	3	3.202	0.2247
ALSFLGFSAPTPIQALTLAPAIR	2356.8	2	3.58	0.3933
ALSKDLPK	872.0	2	2.9174	0.1064
ALSLDGEQLIGNKHYAVDSIRPK	2525.8	3	5.1684	0.2882
ALSNLESIPGGYNALR	1675.9	2	3.8587	0.3419
ALSPSDSLEIFTKLEEIQQQILQQK	2888.3	3	5.0323	0.299
ALSRQEMQEVQSSR	1649.8	2	4.4953	0.2481
ALSSEGKPYVTKEELYQNLTR	2427.7	3	5.8433	0.5122
ALSSESFERLPVFNK	1724.9	2	3.2628	0.1393
ALSSGGSITSPPLSPALPK	1781.0	2	3.5226	0.3559
ALSSQHQAR	998.1	2	3.2565	0.3062
ALSTDPAAPNLK	1198.4	2	3.1835	0.2899
ALSTGEKGFGYK	1258.4	2	2.8817	0.3505
ALSTQVEELKDELVTQR	1960.2	3	3.8505	0.2416
ALSVGNIDDALQCYSEAIK	2011.2	2	4.7084	0.1698

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALSVGNIDDALQCYSEAIKLDPHNHVLYSNR	3457.8	3	4.5573	0.3294
ALTAHLYSLLQTQHALGDAFADLSQK	2814.1	3	6.2077	0.4834
ALTDKVTDLLGGLFSK	1679.0	2	3.5621	0.3897
ALTDYRAELRDDPIISTHLAK	2399.7	2	3.183	0.2849
ALTEKNKELEIAQDRNIAIQSQFTR	2918.3	3	3.2334	0.2081
ALTFWNEEIVPQIK	1688.9	2	3.3612	0.3225
ALTFWNEEIVPQIKEGKR	2159.5	2	3.4225	0.2327
ALTGGIAHLFK	1128.3	2	3.6318	0.4023
ALTGHLEEVVLALLK	1606.9	2	4.6198	0.4118
ALTGHLEEVVLALLKTPAQFDADELR	2851.2	3	5.3328	0.2846
ALTHIDHSLSR	1250.4	2	2.6553	0.2858
ALTLDQWLEQHKGDFNLL	2142.4	2	2.5976	0.1175
ALTLGALTLPLAR	1310.6	2	4.1915	0.3163
ALTLHYDRYTTSR	1597.8	2	2.5468	0.1558
ALTQTGGPHVK	1109.3	2	3.433	0.3239
ALTQVLSQANTGGVQSTLLLNNEGSLLAYSGYGDTDAR	3900.2	3	4.3149	0.1498
ALTSEIALLQSR	1302.5	3	4.0403	0.24
ALTSELANAR	1046.2	2	3.3475	0.316
ALTSELANARDESK	1505.6	2	3.5368	0.254
ALTSELANARDESKK	1633.8	2	4.5548	0.3092
ALTSELANARDESKKTANDMIHAENMR	3018.3	3	4.4587	0.2907
ALTSFERDSIFSNLTGQLDYQGFEK	2868.1	3	6.0182	0.3888
ALTSQLTDEELAQGR	1632.8	2	4.2997	0.4193
ALTTMGFR	897.1	2	2.4098	0.1578
ALTVGGFIEEEKEDLLQHFSTANQGPK	2960.2	3	4.2002	0.2156
ALTVPELTQQMFDAK	1693.0	3	4.7055	0.4322
ALTVPELTQQMFDAR	1721.0	2	3.4242	0.4246
ALTVPELTQQMFDSK	1709.0	2	3.9141	0.4461
ALTVPELTQQVFDAK	1660.9	3	4.7168	0.4525
ALVADSHPESER	1311.4	2	3.7247	0.4329
ALVAIGTHDLDTLSGPFTYTAK	2292.6	2	5.8005	0.5188
ALVATPGKK	885.1	1	2.1666	0.228
ALVDELEWEIAQVDPK	1856.1	2	4.0973	0.1336
ALVDELEWEIAQVDPKK	1984.2	2	4.9806	0.2449
ALVDGPCTQVR	1159.3	2	2.8468	0.1833
ALVDHENVISCPHLGASTK	1992.2	3	3.9391	0.3923

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ALVDHHDAEVKEK	1491.6	2	3.6828	0.3233
ALVDLADPR	970.1	2	3.2048	0.2422
ALVDNEQLR	1058.2	2	2.402	0.1148
ALVDNEQLRHELAQLR	1906.1	2	2.9917	0.1085
ALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVK	3898.4	3	4.562	0.3711
ALVERGGVVTSNPLGF	1616.8	2	2.4396	0.1147
ALVEVLGPYEPLLSR	1656.9	2	4.1004	0.3047
ALVFQPVAELKDQTDFEHRIPK	2582.9	3	3.2207	0.287
ALVHERDEAAYGELR	1729.9	2	4.6638	0.3454
ALVLAPEFLESLEPDLPALR	2194.6	3	3.2385	0.1389
ALVLELCCNDESGEDVEVPYVR	2453.7	3	4.1867	0.3122
ALVNLAADPGLHETLLAADPGLPAR	2496.8	3	4.1032	0.2442
ALVNQLHER	1080.2	2	2.979	0.2656
ALVNQLHERVEHIK	1686.9	2	2.4338	0.1141
ALVQNDTLLQVK	1342.6	2	3.8441	0.2734
ALVSAQWVAEALR	1414.6	2	4.1044	0.2683
ALVSAQWVAEALRAPR	1739.0	2	3.1482	0.1563
ALVSEEGEGKNPVDYIQGLLDLK	2488.8	3	4.8284	0.3007
ALVSGKPAESSAVAATEK	1716.9	2	5.5734	0.4732
ALVSGKPAESSAVAATEKK	1845.1	2	5.6326	0.452
ALVSHNGSLINVGSLLQR	1879.2	3	4.0217	0.2714
ALVSTLVPLGLVLAVGAVAVGVAR	2246.8	2	3.0775	0.3685
ALVYGHHGDPAK	1265.4	2	3.0223	0.3316
ALVYGHHGDPAKVVELK	1834.1	2	2.8726	0.2792
ALXEVLQPLIAEHQAR	1802.1	2	2.5306	0.179
ALYAIPGLDYVSHEDILPYTSTDQVPIQHELFER	3932.3	3	4.9761	0.3237
ALYALQDIVSR	1249.4	2	3.2415	0.2532
ALYDTFSAFGNILSCK	1751.0	2	4.3557	0.4236
ALYEQSLHIK	1202.4	2	2.4252	0.1628
ALYESELADAR	1238.3	2	2.7686	0.2235
ALYETELADAR	1252.4	2	2.8961	0.2103
ALYLIATNGTPELQNPEKLSPIFRDFLNR	3332.8	3	4.8524	0.4031
ALYLSDNDFEILPPDIGKLTK	2363.7	3	3.2209	0.1979
ALYPSSVGQPFQGAYLEINKNPK	2522.8	2	4.1663	0.3412
ALYTLSGETEELSR	1569.7	2	2.8476	0.1677
AMAAEAEASR	1007.1	2	3.1505	0.2651

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AMADALLER	990.2	2	3.5677	0.2625
AMADPEVQQIMSDPAMR	1891.2	2	3.4044	0.3194
AMAGDTSLSENYAFAGMYHVFDQHVDEAVPR	3430.7	3	4.5561	0.4076
AMDDGVKELLTVGQEHWK	2057.3	3	4.6521	0.3204
AMDDKRFDEATQLR	1696.9	3	3.5286	0.1295
AMDFYDPAR	1086.2	2	2.9783	0.298
AMDLDQDVLSALAEVEQLSK	2176.4	3	4.665	0.4446
AMDQEITVNPQFVQK	1749.0	2	4.5915	0.3348
AMDSDWFAENYMGR	1693.8	2	3.6445	0.385
AMDVYQK	855.0	1	1.7267	0.1323
AMEAEAAGLREQLEEEAAAR	2146.3	3	5.9064	0.331
AMEEMNGKDLEGENIEIVFAKPPDQK	2934.3	3	4.367	0.295
AMEGAGTDEK	1009.1	2	3.0552	0.3346
AMEGAGTDEKALIEILATR	1990.3	2	5.5621	0.376
AMEGIFIKPSVEPSAGHDEL	2128.4	2	4.2977	0.4767
AMELSFALVNGNNIR	1649.9	3	3.3208	0.1823
AMESHKDEFTIIPVLVGALSESKEQEFGK	3221.6	3	5.0783	0.4051
AMEWITAK	950.1	2	2.4712	0.105
AMGAAQVVVTDLSATR	1590.8	2	2.8762	0.2146
AMGDAEIKDGERLPLAVK	1914.2	2	4.5914	0.325
AMGEQAVALAR	1117.3	2	3.7057	0.2421
AMGIMNSFVNDIFER	1745.0	2	5.2488	0.5294
AMGIMNSFVNDIFERIAGEASR	2429.8	3	4.0976	0.3118
AMGNLQIDFADPSR	1535.7	2	2.7454	0.1787
AMGPLVLTEVLFNEK	1662.0	2	4.5736	0.4031
AMIAYWTNFAK	1316.6	2	3.8983	0.398
AMINLHIQK	1068.3	2	2.7345	0.1817
AMINLHIQKDNPK	1522.8	2	4.0505	0.2847
AMKDEEKMEIQEMQLK	1982.3	2	6.0703	0.2682
AMKDEEKMELQEMQLK	1982.3	2	6.0641	0.2811
AMKEYEEEER	1314.4	2	2.6869	0.2216
AMKGFGTDEQAIVDVVANR	2022.3	2	5.59	0.5336
AMKGLGTDEDAIISVLAYR	2024.3	2	5.3269	0.5581
AMKGLGTDEDTIIDIITHR	2100.4	2	5.4972	0.5309
AMKGLGTDEESILTLLTSR	2036.3	2	5.1016	0.323
AMLDAHPEVR	1139.3	2	3.2608	0.1776

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AMLDQLMGTSR	1223.4	2	3.2173	0.2719
AMLLQGTESLNR	1333.5	2	2.977	0.1166
AMLSGPGQFAENETNEVNFR	2212.4	2	5.6087	0.4883
AMNGESLDGR	1050.1	2	2.6824	0.2695
AMNLHVGNLR	1125.3	2	3.1099	0.309
AMPLPEEVTQILEENSDLIR	2298.6	2	2.698	0.1709
AMQAAGQIPATALLPTMTPDGLAVTPTPVPVVGSQMTR	3791.5	3	5.4451	0.3699
AMQDAEVSK	979.1	1	2.2385	0.1697
AMQDAEVSKSDIGEVILVGGMTR	2407.8	2	5.427	0.4397
AMQGAGTQER	1049.1	2	3.4163	0.2903
AMQHAEVYYK	1240.4	2	2.7952	0.3521
AMQRPETAATLKR	1473.7	3	3.3638	0.1461
AMREENGLKYIEEAIEK	2024.3	2	4.2003	0.2662
AMSLVSNEGEGEQNEIR	1864.0	2	4.7142	0.2997
AMSRPILYSNWLSK	1667.0	2	3.4648	0.3227
AMSTTSISSPQPGK	1392.6	2	3.1285	0.2643
AMSVEQLTDVLMNEILHGADGTSIK	2674.0	3	3.7746	0.4034
AMTILLEEAK	1119.4	2	3.083	0.2134
AMTKDNNLLGK	1205.4	2	3.0955	0.2503
AMTKDNNLLGR	1233.4	2	3.2461	0.288
AMTLQEAEAFVGAER	1623.8	2	4.3035	0.3568
AMTTGAIAAMLSTILYSR	1872.2	2	3.2107	0.3709
AMVASGSELGKK	1178.4	2	3.1671	0.2965
AMVDPAQTVEQR	1345.5	2	2.6969	0.1599
AMVEAVQLIADGKAPR	1670.0	2	2.9394	0.238
AMVEEMQGHLKR	1429.7	2	2.9881	0.2338
AMVEYEIDLQKMPLGK	1866.2	2	3.5697	0.2649
AMVNKDDIQK	1162.3	2	3.1503	0.1712
AMVSNAQLDNEKTNFMYQVDTLKDMLLELEEQLAESR	4319.8	3	5.8863	0.4151
AMYLPDTLSPADQLK	1663.9	2	3.3948	0.2412
AMYTQAVQNIR	1295.5	2	2.9228	0.2075
ANAEYMSPSGKVPFIHVGNQVVSELGPIVQFVK	3544.1	3	4.403	0.2538
ANAGKPKDPTFIPAPIQAK	1965.3	3	3.7629	0.192
ANDHQHIR	991.0	2	2.4273	0.1997
ANDIEKAVQSLDKNGVDLLMK	2302.6	3	5.2725	0.364
ANDTQEFNLSAYFER	1805.9	2	4.4753	0.3715

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ANDTTFGLAAGVFTR	1541.7	2	4.5812	0.4289
ANEAMAIDTLLISDELFR	2023.3	2	3.3131	0.1818
ANEDELKRLDEELEDAEKNLGESEIRDAMMAK	3694.0	3	4.1716	0.2402
ANEFEFVLSQFKDFGVR	2034.3	2	2.6594	0.1703
ANEFLEVGK	1007.1	2	2.5208	0.2233
ANEFLEVGKK	1135.3	2	2.4856	0.1215
ANEFLEVGKKQPALDVLYDVMK	2508.9	3	4.7485	0.3663
ANEQLTDELAQK	1360.5	2	2.7598	0.2329
ANEVEQMIRDLEASIAR	1946.2	3	4.4799	0.3009
ANFDKESER	1096.1	2	2.5093	0.1271
ANFLNSNDVFVLK	1481.7	2	3.523	0.2591
ANGEVIIEIPTR	1312.5	2	3.4832	0.1865
ANGHLLLNSEK	1196.3	2	3.7597	0.2433
ANGQENGHVK	1054.1	2	2.8271	0.2443
ANGTTVHVGIHPSK	1418.6	2	3.7943	0.415
ANHEEVLAAGK	1139.2	2	2.581	0.1978
ANHFFTVTDPR	1305.4	2	2.9444	0.3938
ANHFLILFR	1131.4	2	2.9994	0.1264
ANHGPGMAMNWPQFEEWSADLNR	2659.9	3	5.1919	0.3058
ANHPHNVQSQVVEAFIR	1947.1	2	4.5088	0.4618
ANHPMDAEVTK	1213.3	2	3.2559	0.2738
ANHSAFLFGFGDGGGGPTQTMLDR	2454.7	3	6.1192	0.4559
ANINIEKAFLTLAEDILR	2045.4	2	4.4468	0.4259
ANINVENAFFTLAR	1580.8	2	5.2539	0.4653
ANIPIMDTGENPEVPFPR	1998.2	2	4.5928	0.4749
ANIVAYHDSIMNPDYNVEFFR	2516.8	3	4.8826	0.3849
ANKEFGDSLSLEILQIIK	2019.3	2	4.4694	0.4615
ANKEFGDSLSLEILQIIKESQQQHGLR	3083.4	3	6.042	0.5046
ANKHQIRQAVK	1293.5	2	2.5577	0.3194
ANKITITNDKGR	1331.5	2	3.5553	0.2605
ANKLDHVVTIIK	1351.6	2	3.2242	0.2421
ANLEAFTVDKDITLTNDKPATAIGVIGNFTDAER	3623.0	3	5.7805	0.4593
ANLEKAQAELVGTADEATRAEIQIR	2699.0	3	4.1177	0.2838
ANLPQSFQVDTSK	1435.6	2	3.3081	0.3576
ANLPQSFQVDTSKAGVAPLQVK	2299.6	2	5.1993	0.2985
ANLQIDQINTDLNLER	1871.0	2	5.9246	0.4697

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ANLQIDQINTDLNLERSHAQKNENAR	3007.2	3	4.4979	0.267
ANLVFKEIEK	1191.4	2	3.4541	0.2547
ANLVFKEIEKKLEEEGEQFVK	2508.9	3	5.1916	0.379
ANLVFKEIEKKLEEEGEQFVKK	2637.0	3	3.7532	0.3271
ANMGVSREDVTFEDHPLNPNPDSR	2698.9	3	4.022	0.2672
ANNHQQQQGLQDSSSK	1770.8	2	4.3821	0.4043
ANNLSSLSK	934.0	2	3.1211	0.1639
ANNSQEPSPQLASSVASTR	1945.0	2	3.9094	0.4468
ANNSTYGLAAAVFTK	1528.7	2	5.0152	0.5297
ANNTFYGLSAGVFTK	1590.8	2	5.305	0.5131
ANPDLPILIR	1122.3	2	2.5106	0.245
ANPDPNCCLGVFGLSLYTTER	2271.6	2	2.7926	0.1227
ANPDPNTCLGVFGLSLYTTER	2269.5	2	4.8638	0.3739
ANPFGGASHAK	1057.1	1	2.5447	0.3168
ANPQVGVAFPHIK	1378.6	2	3.631	0.3109
ANPVFDYQLYFQEPGVAEAELEQNLSR	3129.4	3	5.178	0.4266
ANQAIQMACQSLGEPGCTQAQVLSAATIVAK	3104.6	3	3.8064	0.1833
ANQHKEQQLGLK	1394.6	2	2.7778	0.1416
ANQHKEQQLGLKQQIESEVANLKK	2763.1	3	3.9273	0.2582
ANQTKEGLPVALDKHILGFDTGDAVLNEAAQILR	3620.1	3	6.5933	0.4467
ANQTLKDEYDALQITFTALEGK	2470.7	3	3.7529	0.2405
ANQVPGRPR	995.1	2	2.6815	0.1928
ANQYKENHNR	1274.3	2	2.6436	0.2129
ANSALTPPKPESGLTLQESNTPGLR	2579.8	3	4.6229	0.3368
ANSEEFIPIFANNPR	1719.9	2	4.2318	0.3688
ANSFTVSSVAAPSWLHR	1831.0	3	4.4016	0.5032
ANSNLVLQADR	1201.3	2	3.7835	0.2937
ANSSATETINK	1136.2	2	3.5794	0.2195
ANSSATETINKLK	1377.5	2	2.9874	0.2383
ANSTDYGLTAAVFTK	1559.7	2	4.1181	0.3982
ANSTEYGLASGVFTR	1573.7	2	4.2612	0.3891
ANSVFEDLSVTLR	1451.6	2	3.8835	0.4325
ANSVKQEFEKQDELKR	1950.1	2	4.4909	0.3027
ANTAYHLHQR	1211.3	2	3.1973	0.1772
ANTFVAELK	993.1	2	2.7329	0.2898
ANTFVAELKGLDPAR	1602.8	2	4.0191	0.3909

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ANTFVAELKGLDPARVNVPVIGGHAGK	2732.1	3	5.1809	0.4781
ANTNEVLWAVVAAFTK	1735.0	3	3.4498	0.3542
ANTTAFLTPLEIK	1419.6	2	4.1977	0.2619
ANTYEKYWPFYQK	1738.9	3	3.6051	0.3191
ANVAKAEAEK	1031.1	2	2.9154	0.1737
ANVAKAEAEKIKAALEAVGGTVVLE	2482.9	2	2.4322	0.2142
ANVDKVFFDLMR	1455.7	3	3.9259	0.3857
ANVELDHATLVR	1338.5	2	2.7386	0.3126
ANVGAGKKPKE	1099.3	2	2.7033	0.1501
ANVLNKVEYAQQR	1533.7	2	2.8011	0.1898
ANVMSSQLHSLTHFSDISALTGGTVHLDEDQNPIKK	3893.3	3	3.694	0.124
ANWYFLLAR	1154.3	2	2.896	0.3152
ANYEQSKKDPHQTLPLDTPR	2339.5	3	3.264	0.1145
ANYLASPPLVIAYAIAGTIR	2075.4	2	5.1329	0.4984
APAAHPEGQLK	1119.3	2	2.8194	0.2989
APAEILNGKEISAQIR	1711.0	2	4.7896	0.3647
APAHHPAAISTAK	1272.4	2	2.5087	0.2399
APALGGSFAGLEPMGLLWALEPEKPLVR	2921.4	3	5.0115	0.2968
APAPEAEDEEVAR	1384.4	2	2.9043	0.3687
APAQKAPAPK	979.2	2	2.7533	0.1403
APASVLPAATPR	1151.3	2	3.7759	0.4458
APAVQGADNQR	1127.2	2	3.1495	0.2319
APDELHYTYLDTFGRPVIVAYK	2569.9	3	4.0766	0.2432
APDELHYTYLDTFGRPVIVAYKK	2698.1	3	4.9098	0.461
APDFVFYAPR	1183.3	2	3.988	0.4007
APDGAALATAR	1014.1	2	3.1205	0.3044
APDGYIVK	863.0	2	2.6554	0.2544
APDLFPTDFKFDTPVDKLPQL	2405.7	3	4.6136	0.3762
APDPGFQER	1017.1	2	2.4129	0.2346
APDVTTLPR	970.1	2	2.7475	0.1829
APEAWDYGQGFVNEEMIR	2113.3	2	5.7212	0.474
APEDAGPQPGSYEIR	1587.7	2	3.8784	0.2764
APEEHPVLLTEAPLNPK	1856.1	2	4.5224	0.1309
APEIMLNSK	1003.2	2	2.7067	0.1948
APEKKPLVK	1010.3	2	2.7833	0.1186
APELLFRPDLIGEESEGIHEVLVFAIQK	3151.6	3	4.1359	0.3745

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
APEPGPAGDGGPGAPAR	1474.6	2	3.4328	0.4623
APEVSQYIYQVYDSILKN	2131.4	2	6.2093	0.5219
APFDLFENR	1109.2	2	3.054	0.2059
APFPLYALQVDPSTGLLIAAGGGGAAK	2556.9	2	4.8112	0.4278
APGAIGPYSQAVLVDR	1614.8	2	3.9548	0.4122
APGALLAAAGLADAATEIVER	1981.2	2	3.9014	0.4314
APGFAHLAGLDK	1197.4	2	2.6387	0.1152
APGFAQMLK	963.2	2	2.9842	0.2831
APGFGDNR	833.9	2	2.5588	0.351
APGPASGGSGEVDELFDVK	1832.9	2	5.0342	0.4995
APGPGLAQGLPQLHSLVLR	1925.3	3	4.1145	0.4154
APGPQAGPGPGVR	1161.3	2	3.2186	0.3842
APGQLALFSVSDKTGLVEFAR	2207.5	2	5.606	0.5357
APGTPHSHTK	1033.1	2	2.8439	0.1379
APGTPHSHTKPYVR	1548.7	3	3.2444	0.3451
APHLVGPHLGLETGNGGGVINLNAFDPTLPK	3107.5	3	6.0956	0.4937
APHWTSAPLTEASAHSHPPEIK	2365.6	2	4.8268	0.4289
APHWTSAPLTEASAHSHPPEIKDQGGAGEGLVR	3405.7	3	4.0891	0.3368
APHYPGIGPVDESGIPTAIR	2048.3	3	3.5251	0.2747
APIIAVTR	841.0	1	2.0476	0.2079
APIKVGDAIPAVEVFEGEPGNKVNLAELFK	3153.6	3	6.1947	0.5071
APIKVGDAIPAVEVFEGEPGNKVNLAELFKGK	3338.8	3	5.155	0.3005
APILIATDVASR	1227.4	2	3.8054	0.3523
APIRPDIVNFVHTNLR	1863.2	3	5.2227	0.3175
APIRPDIVNFVHTNLRK	1991.3	3	4.7614	0.3242
APKDQVDIAVQELLQLK	1909.2	2	4.9275	0.4743
APKPEDIDEEDDDVPDLVENFDEASKNEAN	3361.4	3	5.1836	0.2656
APLATGEDDDDEVPDLVENFDEASKNEAN	3121.1	3	3.7173	0.171
APLDIPVPDPVKEK	1518.8	2	3.5361	0.4011
APLDIPVPDPVKEKEKEER	2190.5	3	3.2577	0.1089
APLEPVYPGDNATPEQMAQYAADLR	2719.0	3	5.3521	0.415
APLEVAQEH	994.1	2	2.5371	0.1284
APLNVQFNSPLPGDAVK	1768.0	2	4.1523	0.452
APLPLGHIK	946.2	2	2.7751	0.1871
APLVCLPVFVSR	1301.6	2	2.8884	0.2894
APLVKVEEATVEER	1570.8	2	4.5215	0.4933

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
APMVNPTLGVHEADLLK	1806.1	2	3.2291	0.1102
APNDFKLQDFNVGDYIEAVLDR	2540.8	3	4.6079	0.5123
APNDFKLQDFNVGDYIEAVLDRNLAENISR	3438.7	3	4.3305	0.3604
APPAPGPASGGSGEVDELFDVK	2098.3	2	5.1366	0.4976
APPGAPGPGPGSGAPGSQEEEEEPGLVEGDPGDGAIEDPELEAIKAR	4535.8	3	4.197	0.3413
APPGRPEAQPPPLSSEHKEPVAGDAVPGPK	3014.3	3	5.9879	0.4514
APPGRPEAQPPPLSSEHKEPVAGDAVPGPKDGSAPEVR	3826.2	3	6.6885	0.4512
APPHELTEEEKQQILHSEEFLSFFDHSTR	3483.7	3	5.5108	0.4218
APPQTHLPSGASSGTGSASATHGGGSPPGTR	2786.9	3	5.0849	0.5687
APPSVFAEVPQAQPVLVFK	2025.4	2	5.895	0.5212
APQAPLHSVVQQLHGK	1711.0	2	3.2379	0.3751
APQETYADIGGLDNQIQEIK	2204.4	2	6.0854	0.407
APQLLIAPFKEEDEWDSPHIVR	2591.9	3	5.0499	0.3905
APQLVGQFIAR	1200.4	2	2.843	0.196
APQQQPPPQQPPPPQPPPQQPPPPPSYSPAR	3330.7	3	3.9331	0.2606
APQVLVLAPTR	1165.4	2	2.5048	0.199
APREPAIHSEGQWVTLPAPLDTINVHLR	3119.5	3	5.2962	0.3223
APRPAPGGAEQR	1207.3	2	2.4304	0.2348
APRPPKQPNVQDFQFFPPR	2267.6	3	3.3933	0.2418
APSEAEPAADLIDMGPDPAATGNLSSQLAGMNLGSSSVR	3800.1	3	5.5328	0.5113
APSHSESALNNDSK	1457.5	2	4.1913	0.3392
APSIHGGSGGR	996.1	2	2.6066	0.2872
APSIIFIDELDAIGTK	1704.0	2	4.2381	0.468
APSPLYSVEFSEEPFGVIVR	2224.5	2	2.4858	0.249
APSRQDVYGPQPQVR	1698.9	3	3.4086	0.2371
APTEEGKKELLFLSNANPSLLER	2557.9	3	4.4645	0.2894
APTTDEDKKAAEK	1404.5	2	3.2021	0.3521
APTTVEDR	888.9	1	1.8166	0.1514
APTTVEDRVGDSTPVSEKPVSAAVDANASESP	3185.4	3	5.8259	0.4429
APTVHGGAGGAR	1051.1	2	2.4345	0.2178
APVAGTCYQAEWDDYVPK	2014.2	2	6.0998	0.5179
APVDFGYVGIDSILEQMR	2011.3	2	4.1564	0.4924
APVIIIPQSSVSPNAVIADLGLIR	2444.9	3	4.0225	0.336
APVILGSPDDVLEFLK	1714.0	2	4.8131	0.4157
APVILGSPDDVLEFLKVYEK	2233.6	2	3.0522	0.2171
APVIRPGGTLGLSEAADSDAHLFQDSTEPR	3109.4	3	5.038	0.44

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
APVPASELLASGVLSR	1567.8	3	3.2653	0.2546
APVPGTPDSLSSGSSR	1515.6	2	2.7374	0.3736
APVPTGEVYFADSFDR	1771.9	2	4.4782	0.4328
APWIEQEGPEYWDGETR	2064.2	2	5.6231	0.5025
APWIEQEGPEYWDR	1776.9	2	4.4486	0.3936
APYFSGSSTFSPTILSSDKETIEIIDLAK	3119.5	3	4.5462	0.3534
APYYNYKDPAGHFHQVWYDNPQSISLK	3240.5	3	5.7399	0.4897
AQAAAPASVPAQAPK	1378.6	2	4.4363	0.3895
AQAALAVNISAAR	1256.4	2	3.4418	0.3501
AQAALQAVSAVQSGSLALSGGPSNEGTVLPGQSPVLR	3519.9	3	4.9961	0.438
AQAELENVSGALNEAESK	1861.0	2	5.4083	0.5211
AQAELNALKR	1114.3	2	2.6667	0.1263
AQAELVGTADEATR	1432.5	2	4.4421	0.4412
AQAELVGTADEATRAEIQIR	2143.3	3	3.6012	0.192
AQAGEGVRPSPMQLELR	1840.1	3	3.3096	0.228
AQALDRDGNLVEDFVFDAGVGDIGNR	2764.9	3	5.3002	0.3189
AQALNEHLSTR	1240.4	2	3.0351	0.3219
AQALRDNSTMGYMAAK	1729.0	2	3.3736	0.3412
AQALRDNSTMGYMMAK	1789.1	2	3.7648	0.4357
AQAQTDRESLR	1275.4	2	2.83	0.1347
AQASEILLEELQQGLSQAK	2057.3	2	2.6597	0.2112
AQASEILLEELQQGLSQAKR	2213.5	3	3.391	0.3354
AQASSIPVGSR	1073.2	2	2.6168	0.1623
AQAVHPGYGFLSENKEFAR	2122.3	2	4.8982	0.5246
AQAVLEEDHYGMEDVKKR	2119.3	3	4.6042	0.4187
AQAVSEDAGGNEGR	1361.4	2	4.6303	0.444
AQAYQTGK	866.9	1	1.9657	0.1838
AQAYQTGKDISTNYYASQK	2138.3	2	5.2831	0.4945
AQAYQTGKDISTNYYASQKK	2266.5	3	4.8598	0.4283
AQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	3631.9	3	8.2087	0.4799
AQDFVQWLMNTK	1481.7	2	4.4472	0.4118
AQDFVQWLMNTKR	1637.9	2	3.8356	0.302
AQDGSHPLSLQDLIEK	1751.9	2	3.6801	0.2528
AQDGSHPLSLQDLIEKVVILR	2332.7	3	5.1467	0.3689
AQDIEAGDGTTSVVIIAGSLLDSCTK	2565.8	2	5.037	0.3956
AQDLSNLENTVAALKSEFQK	2207.4	3	3.4105	0.1945

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AQDPSEVLTMLTNETGFEISSSDATVK	2872.1	3	4.6726	0.393
AQDQTQDTQLITVDEKLDITTLTGVPEEHIK	3481.8	3	6.1419	0.4937
AQEALDAVSTLEEGHAQYLTSLADASALVAALTR	3487.8	3	5.1071	0.3877
AQEALSHTEQSK	1329.4	2	4.4433	0.3859
AQEALSHTEQSKSELSSR	1989.1	3	5.2417	0.476
AQEALSHTEQSKSELSSRLDTLSAEKDALSGAVR	3616.9	3	5.986	0.4864
AQEAPGQAEPPAAAEVQGAGNENEPR	2589.7	3	5.8001	0.4601
AQEEAEAEER	1162.1	2	3.6212	0.2234
AQEEAEAEERR	1318.3	2	2.7986	0.1206
AQEEAEAEERRLQEQEELENYIEHVLLR	3455.7	3	4.2793	0.3332
AQEEAEAEERRLQEQEELENYIEHVLLRRP	3709.0	3	3.363	0.1557
AQEEAERLEADRMAALR	1960.2	2	2.9671	0.2249
AQEIAMQNR	1061.2	2	2.7871	0.2429
AQEIDRSNEFK	1337.4	2	3.2064	0.2088
AQEIQDESAVLWLDEIQGGIWQSNKDTQEAQK	3659.9	3	3.3346	0.213
AQEKVHEMEK	1229.4	2	3.5005	0.2483
AQELDALDNSHPIEVSVGHPSEVDEIFDAISYSK	3714.0	3	7.3919	0.4917
AQELEGKLNFLTK	1491.7	2	4.0974	0.1568
AQELGHSQSALASAQR	1654.8	2	4.7798	0.4658
AQELQKVQELQQQSAR	1885.1	3	4.4453	0.3616
AQENLNPLVVLNLFK	1713.0	2	3.268	0.3941
AQEQQQQMAELHSK	1656.8	2	4.6452	0.3009
AQFAEATQR	1022.1	2	2.6206	0.251
AQFAQPEILIGTIPGAGGTQR	2126.4	2	5.1903	0.3878
AQFEGIVTDLIR	1362.6	2	4.3241	0.3676
AQGEKPLAGAK	1070.2	2	2.9016	0.2414
AQGEPVAGHESPKIPYEK	1938.1	2	4.5539	0.4694
AQGEPVAGHESPKIPYEKQQLPK	2532.8	3	4.1027	0.2606
AQGGSSDSSLALHER	1515.6	2	3.6227	0.3419
AQGHELGASR	1026.1	2	3.1282	0.313
AQGLLSAGHPEGEQIIR	1777.0	2	3.6352	0.433
AQGPAASAEEPKPVEAPAANSDQTVTVKE	2894.1	3	6.0207	0.4589
AQGPDGGLTASTYSYLGGFDSSSNVLAGQLR	3091.3	3	3.3144	0.3129
AQGWAPLKPLPPSAKDPAQAPQA	2340.7	3	3.3902	0.1488
AQHEDQVEQYKK	1503.6	2	4.4892	0.4218
AQHEDQVEQYKKELEK	2003.2	2	5.3803	0.4311

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AQHEDQVEQYKKELEKTYSAK	2553.8	3	3.8663	0.3469
AQHEENIKK	1097.2	2	2.6162	0.1041
AQHLSPAPGLAQPAAPAQASAAIPAAGK	2563.9	3	7.0054	0.5329
AQHVFQHAVPQEGKPITNQK	2258.5	3	5.9106	0.4993
AQIAGYLYGVSPPDNPQVK	2018.3	2	2.821	0.146
AQIFANTVDNAR	1320.4	2	4.3646	0.3821
AQIHEQNPSVEVVYYNK	2019.2	3	4.9703	0.3691
AQILAGGR	785.9	1	2.0149	0.1604
AQIQQFHSQIAAQTSASVLAEELHK	2737.0	3	4.0628	0.3148
AQISDDTTHPISYYKPEFYTPDDGG	2818.9	3	5.2979	0.4261
AQIWDTAGQER	1275.4	2	3.4625	0.2248
AQKDEEKMEIQEIQLK	1961.2	2	5.8356	0.2926
AQKDEEKMEIQEIQLKEAK	2289.6	3	3.5946	0.1038
AQKLADDLSTLQEK	1560.7	2	2.8365	0.3278
AQLADSFHLQQFFR	1708.9	2	4.6553	0.4465
AQLAKAEDGHAVAK	1409.6	2	4.2925	0.2963
AQLDAAVTFGPSQVAR	1631.8	2	4.9592	0.4695
AQLDPAFIKTYEDIKENLESR	2481.7	3	4.3705	0.3895
AQLDYVDLYLIHSPMSLKPGEELSPTDENGK	3461.8	3	4.0818	0.2826
AQLELEVSK	1017.2	2	2.7853	0.1432
AQLELEVSKAQQLAEVEVKK	2241.6	3	4.2744	0.2085
AQLELEVSKAQQLAEVEVKKFK	2516.9	3	3.5199	0.1098
AQLEPVASPAKKPK	1464.7	2	2.9498	0.2074
AQLEVQASQHR	1267.4	2	3.4784	0.2503
AQLFALTGVQPAR	1372.6	2	3.9909	0.3445
AQLGGPEAAK	942.1	1	2.7651	0.2543
AQLGGPEAAKSDETAAK	1644.8	2	5.0348	0.5059
AQLGPDESKQK	1201.3	2	3.0088	0.1565
AQLGRKEEELQAALAR	1784.0	3	4.4826	0.3045
AQLGVQAFADALLIIPK	1769.1	2	4.8723	0.3789
AQLHDTNMELTDLK	1629.8	2	3.1013	0.1508
AQLHDTNMELTDLKLQLEK	2241.6	3	4.8082	0.3232
AQLHQLQLHAAVLR	1598.9	2	4.7815	0.4865
AQLHVQGLLHEAGSTDDRIVVPQR	2640.9	3	4.1259	0.3972
AQLLELEKEFLFNK	1723.0	2	3.5603	0.3138
AQLLQPTLEINPR	1493.7	2	3.5196	0.3315

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AQLMAEQEK	1048.2	2	2.5841	0.1311
AQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	3155.7	3	4.1265	0.2649
AQLNIGNVLPVGTMPEGTIVCCLEEKPGDRGK	3340.9	3	3.7473	0.1749
AQMALWTVLAAPLLMSTDLR	2202.7	2	2.566	0.1078
AQMKNPILER	1200.4	2	2.8238	0.1796
AQMSEDNHLSNTVR	1602.7	2	4.6117	0.4457
AQMVQEDLEK	1191.3	2	3.0892	0.1806
AQMVQEDLEKTR	1448.6	2	2.5514	0.2015
AQMVQEDLEKTRAELK	1890.2	3	3.4548	0.2226
AQNDLIWNIKDELKK	1829.1	2	4.4117	0.2859
AQNKPFYVVAESFK	1628.9	2	2.8152	0.1131
AQNVTLEAILQNATSDNPVVQLSAVQAAR	3023.3	3	5.5454	0.4194
AQPAQPADEPAEKADEPMEH	2162.3	2	4.4326	0.2173
AQPFVAAANIDDKR	1516.7	2	3.4592	0.3231
AQPLSLEELLAK	1312.5	2	2.6072	0.1649
AQPPEAGPQGLHDLGR	1643.8	2	3.2163	0.3886
AQPSASLGVGYR	1206.3	2	3.4022	0.3279
AQPSVSLGAAYR	1220.4	2	2.9753	0.418
AQPVQVAEGSEPDGFWEALGGK	2273.4	2	6.8918	0.5339
AQQATPGGAAPTIFSR	1573.7	2	4.5756	0.5336
AQQEAEAAQR	1102.1	2	3.3351	0.2426
AQQEFAAGVFSNPAVR	1692.9	2	4.5662	0.4865
AQQEFATGVMSNK	1411.6	2	4.1403	0.3319
AQQEHQSLLEK	1311.4	2	2.7109	0.2362
AQQEQELAADAFK	1449.5	2	3.8581	0.4044
AQQEVLQALEPQVDYLR	2001.2	2	4.4458	0.4597
AQQGIVFLDEVDKIGSVPGIHQLR	2621.0	3	4.6535	0.4357
AQQLAEVEVK	1115.3	2	2.9348	0.2082
AQQLAEVEVKK	1243.4	2	3.6952	0.2688
AQQLREEQQR	1286.4	2	2.5815	0.1235
AQQNNVEHK	1068.1	2	2.6191	0.1609
AQQNNVEHKVETFSGVYK	2079.3	2	5.5832	0.4569
AQQNNVEHKVETFSGVYKK	2207.4	2	5.1977	0.4541
AQQSLELIQSK	1245.4	2	2.7098	0.1607
AQQVAVQEQEIARR	1626.8	2	2.843	0.1946
AQSALHEQK	1012.1	2	2.7895	0.2743

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AQSEAEKLAK	1075.2	2	2.6482	0.197
AQSEAEKLAKERQEAEEAKEALLQASR	3015.3	3	6.927	0.5162
AQSELAAHQK	1083.2	2	3.0077	0.2112
AQSELAAHQKK	1211.4	2	2.7618	0.2608
AQSHSFPNYGLSHGLTSR	1960.1	3	5.1589	0.539
AQSLLSTDREASIDILHSIVK	2297.6	3	5.7467	0.4454
AQSLLSTDREASIDILHSIVKR	2453.8	3	5.8181	0.3886
AQSSQDAVSSMNLFDLGGQYLR	2388.6	2	5.0908	0.4114
AQSVSQINHKLEAQLVDLKSELTETQAEK	3239.6	3	4.0704	0.1673
AQTEGINISEEALNHLGEIGTK	2325.5	2	4.6064	0.4062
AQTGSGGADPTTDVSGQS	1636.6	2	2.5212	0.2115
AQTKAPPKPAR	1165.4	2	2.7289	0.2192
AQTLPTSVVTITSESSPGKR	2060.3	2	4.2167	0.5204
AQTMSNSGIK	1037.2	2	2.4734	0.2334
AQTTNSNSSSSSDVSTHS	1797.7	2	2.9088	0.3189
AQVARPGGDTIFGK	1417.6	2	3.4155	0.3184
AQVEQELTTLR	1288.4	2	2.5117	0.1826
AQVLAGGR	771.9	1	1.9163	0.1736
AQVPFEQILSLPELK	1713.0	2	3.8027	0.2815
AQVSGQSAR	904.0	2	2.4444	0.1403
AQVTELEDELTAAEDAK	1833.9	2	4.5022	0.3603
AQVTSLLGELQESQSR	1746.9	2	3.1171	0.2024
AQVVDLLQQELTAAEQR	1913.1	3	5.5001	0.3707
AQYEDIANR	1080.1	2	3.128	0.282
AQYEEIAQR	1108.2	2	3.2202	0.1035
AQYQDKLAR	1093.2	2	2.428	0.1733
AQYYLPDGSTIEIGPSR	1868.0	2	5.3796	0.4488
ARAEAEQMAK	1105.3	2	2.9851	0.232
ARAEAQEAEDQQAR	1573.6	2	5.1169	0.3531
ARAEEAEAQKR	1259.4	3	3.3261	0.2033
ARAETEELIR	1188.3	2	2.9387	0.1021
ARAHGLEVEPSALEQGFR	1968.2	3	4.7751	0.4099
ARDAILDALENLTAEELKK	2114.4	3	5.04	0.3248
ARDDLITDLLNEAK	1587.8	2	4.5299	0.3536
ARDDLITDLLNEAKQR	1872.1	3	5.4565	0.3473
ARDDTKEWLIEVPGNADPLEDQFAKR	3015.3	3	3.9027	0.1861

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ARDHGLLIYHIPQVEPR	2015.3	3	3.767	0.3549
ARDINAVLIDMER	1516.7	2	3.2755	0.2317
ARDIVPGDIVEVAVGDKVPADIR	2405.7	3	6.4751	0.3586
ARDSLIQSLATQLELDGFER	2263.5	3	5.2911	0.4255
ARDYDAMGSQTK	1343.4	2	3.3952	0.3587
AREEAEAEVASLNR	1545.6	2	5.3944	0.352
AREEEESESSTSDDKR	1855.8	3	4.7403	0.4256
AREETDKEEPASK	1490.6	2	3.6067	0.3852
AREQAEAEVASLNRR	1700.8	3	3.7285	0.2044
AREQEELLAPADGTVELVR	2097.3	2	4.6213	0.322
ARETYGLPNTLPTAWHNLVYR	2473.8	3	3.8385	0.204
ARFEELCSDLFR	1486.7	2	3.6513	0.2898
ARFEELNADLFR	1481.6	2	4.1355	0.3066
ARFEELNADLFRGTLDPVEK	2321.6	2	2.7599	0.1818
ARFEEVLSK	1079.2	2	2.4588	0.1024
ARGDLGAFSR	1050.2	2	2.5481	0.2084
ARGDSEALDEES	1279.3	2	2.8859	0.1781
ARHEVLLISAEQDKR	1766.0	3	5.2081	0.366
ARIVAEEFLK	1176.4	2	2.415	0.1186
ARKEALLVEKERSAKITSLPPPPPTLFENIEVK	3703.3	3	3.2381	0.1271
ARKYTLVSYGTGELER	1844.1	2	2.7261	0.1212
ARLEIEPEWAYGK	1562.8	2	3.7576	0.3208
ARLEIEPEWAYGKK	1690.9	2	4.1934	0.3494
ARNDEYENLFNMIVEIPR	2224.5	3	3.9536	0.357
ARPAEVGGMQLR	1285.5	2	2.7477	0.1841
ARPATVLGAMEMGR	1460.8	2	3.132	0.3365
ARPEDVISEGR	1229.3	2	2.8327	0.1171
ARPEYMLPVHFYGR	1737.0	3	4.2273	0.3579
ARPFPDGLAEDIDKGEVSAR	2144.3	3	6.8115	0.4969
ARPFPDGLAEDIDKGEVSARQELK	2642.9	3	4.8525	0.2862
ARPNIPVYR	1086.3	2	2.4723	0.1878
ARPTDYPTQEQQLHFIR	2101.3	3	5.0376	0.3932
ARPTILSSGLPEEPDQNLSSPEEVFHSGHSR	3375.6	3	5.6312	0.4127
ARPVQIAVYHMLYK	1690.0	3	3.3524	0.1783
ARPVSSAASVYAGAGGSGSR	1808.9	2	5.7687	0.5191
ARQEELYSELQAR	1593.7	2	4.2877	0.2533

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ARQEQLQLINNQLREEDDKWQDDLAR	3226.5	3	3.4442	0.1219
ARQLLDQVEQIQKEQDYQR	2389.6	3	4.9425	0.2964
ARQNALLFAEEEDGEAGAED	2136.2	2	6.0389	0.5788
ARQNLSQVPEADSVSFLQELLALR	2686.0	3	3.9995	0.31
ARQYTSPEEIDAQLQAEKQK	2334.5	3	6.0314	0.306
ARRDHFSIERAQQEAPAVRKLSSKGSFADLGLEPR	3925.4	3	3.4767	0.1662
ARRPESALLGGSEAGER	1756.9	3	4.6152	0.3951
ARSDEGQLSPATR	1388.5	2	3.4547	0.2641
ARVADLVAGRRQHGQR	1791.0	2	2.7029	0.2309
ARVDHGAEIITQSPGR	1707.9	3	3.8918	0.3324
ARVEENFLK	1106.3	2	2.7339	0.1318
ARVEKVESPAK	1214.4	2	3.1702	0.2061
ARVITEEEKNFK	1464.6	2	3.6151	0.2021
ARVVFGPELVSLGPEEQFTVLSLSAGRPK	3085.5	3	4.0514	0.241
ASAAAAAAAAAAAAK	1229.4	2	4.9925	0.3628
ASAAFSSVGSVITK	1325.5	2	4.7545	0.4822
ASAAPKPEPVPVQK	1419.7	2	3.1651	0.2823
ASAELALGENSEVLK	1531.7	2	4.5335	0.2285
ASAELALGENSEVLKSGR	1832.0	2	3.7069	0.385
ASAELIEEEVAKLLK	1643.9	2	4.3874	0.2548
ASAFALQEQPVVNAVIDDTTK	2218.4	2	3.5963	0.1406
ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK	3334.4	3	6.5397	0.4562
ASAGHAVSIAQDDAGADDWETDPDFVNDVSEKEQR	3747.8	3	7.5945	0.5597
ASALIDRPAPYFER	1606.8	2	3.2108	0.2279
ASALRHEEQPAPGYDTHGR	2093.2	3	4.5498	0.4439
ASANMDLMR	1009.2	2	2.6023	0.3189
ASAPAPGHH	844.9	1	1.8529	0.2722
ASASGSGAQVGGPISSGSSASSVTVTR	2366.5	3	5.8866	0.5526
ASASSTNLKDILADLIPK	1858.1	3	5.2978	0.338
ASASSTNLKDILADLIPKEQAR	2342.6	3	6.4245	0.3859
ASDEVPLAPR	1055.2	2	2.626	0.199
ASDGSFSLPLKPVISQPIHDSKSPGASNLK	3079.5	3	3.8029	0.243
ASDPASPHIGR	1108.2	2	2.9651	0.3141
ASDPDEAKLAEDILNTMFDTSYSK	2662.9	2	5.0829	0.4774
ASDSPIDLFYGDFFGDISEAVIQK	2635.9	3	5.6173	0.5159
ASDVHEVR	913.0	2	2.4102	0.129

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ASDVHEVRK	1041.1	2	2.4528	0.1025
ASDVHEVRKVLGEK	1567.8	2	2.9604	0.2508
ASDVVLGFAELEGYLQK	1840.1	2	2.7927	0.2226
ASDVVLGFAELEGYLQKQPYFGAVIGR	2929.3	3	6.3039	0.4312
ASDYGMKLPILR	1364.6	2	3.1841	0.3469
ASEAASPLPDSPGDKLVIVK	1995.3	2	2.8628	0.2242
ASEAKEGEEAGPGDPLLEAVPK	2195.4	3	4.0133	0.2511
ASEAKEGEEAGPGDPLLEAVPKTGDEKDVSV	3126.3	3	5.1376	0.3778
ASEDTTSGSPPKK	1305.4	2	2.7035	0.1738
ASEEAFVKESKEETPGTEWEK	2412.5	3	5.2391	0.2986
ASEEDHTNAACFACILLSHGEENVIYGK	3023.3	3	4.102	0.2748
ASEEHLKQHYIDLK	1711.9	2	3.8872	0.2975
ASEEHLKQHYIDLKDRPFFPGLVK	2869.3	3	5.1721	0.4049
ASEGPAFFPGR	1136.2	2	2.7548	0.2494
ASEHKDQLSR	1171.2	2	2.4431	0.1445
ASEIKEAEAK	1076.2	2	2.4294	0.1088
ASEKLDYITYLSIFDQLFDIPKER	2906.3	3	3.4169	0.1742
ASELHLLETPLVVKK	1678.0	3	3.7163	0.376
ASELPVSEVASILQADLQNGLNK	2397.7	3	4.1786	0.2725
ASEPGLAQLLVDQIYENAMIAAGLVDDPR	3071.5	3	4.5132	0.2153
ASEPGLAQLLVDQIYENAMIAAGLVDDPRAMVGR	3586.1	3	3.8596	0.3692
ASESSKPWPDATYGTGSASR	2056.1	3	4.5803	0.3442
ASEWVQQVSGLMDGK	1635.8	2	4.4719	0.5304
ASFANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIK	3541.0	3	4.6927	0.4201
ASFEEASNQLINHIEQFLDTNETPYFMK	3318.6	3	3.739	0.3093
ASFNHFDKDHGGALGPEEFK	2204.3	3	5.295	0.4113
ASFNHFDRDHSGTLGPEEFK	2292.4	3	4.2994	0.3286
ASGANFEYIIAEK	1413.6	2	4.3142	0.4237
ASGANYSFHK	1082.2	2	2.9832	0.2361
ASGATILSTLANLEGEETFEAAMLGQAEEVVQER	3566.9	3	3.8192	0.1273
ASGDENDNIEIDTNEEIPEGFVVGGGDEL	3036.1	3	5.1378	0.1566
ASGDFQTTK	955.0	2	2.6855	0.2692
ASGDFQTTKLNGFEVFAR	1989.2	3	3.3593	0.109
ASGDGESLDEDSEFTLASDFEIGHFFR	2980.1	3	3.5436	0.1494
ASGDSARPVLLQVAESAYR	1991.2	3	3.2989	0.1728
ASGGGVPTDEEQATGLER	1774.8	2	4.8854	0.4909

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ASGGTSEFITGKDR	1426.5	2	3.4428	0.3659
ASGNLETK	819.9	2	2.9027	0.1865
ASGNYATVISHNPETK	1689.8	2	5.0325	0.4554
ASGNYATVISHNPETKK	1818.0	2	4.3339	0.3833
ASGPGLNTTGVPASLPVEFTIDAK	2343.6	2	5.0995	0.4826
ASGPPVSELITK	1199.4	1	3.252	0.402
ASGTNDKPGGPHYILR	1683.8	2	3.1087	0.1779
ASGVDIEEETEKNLEKVQTIIEHLQEK	3111.4	3	3.6078	0.1062
ASGYQSSQK	956.0	2	2.8885	0.3386
ASGYQSSQKK	1084.2	2	2.6614	0.1671
ASHEEVEGLVEK	1327.4	2	4.1341	0.4182
ASHEEVEGLVEKIR	1596.8	3	4.4546	0.4036
ASHPEDPASVVEAR	1465.6	2	3.2609	0.2896
ASHSTSQLSQK	1174.2	2	2.842	0.3169
ASHTAPQVLFSHR	1451.6	3	4.1658	0.4511
ASHTAPQVLFSHREPPLELK	2258.6	2	3.4439	0.1131
ASHTLLPSHR	1119.3	2	2.6616	0.3117
ASIHEAWTDGKEAMLK	1788.0	2	4.1368	0.4073
ASIKKGEDFVK	1222.4	2	2.4026	0.2402
ASIPFSVVGSNQLIEAK	1761.0	2	4.3065	0.3678
ASITALEAK	904.0	2	3.1064	0.2148
ASITALEAKIAQLEEQLDNETKER	2702.0	3	6.5584	0.4747
ASITPGTILIILTGR	1526.8	2	4.4007	0.3713
ASKELVER	932.1	1	2.1021	0.169
ASKLQNELDNVSTLLEEAEK	2232.4	2	3.38	0.3294
ASKLQNELDNVSTLLEEAEKK	2360.6	3	5.4907	0.5104
ASKLQNELDNVSTLLEEAEKKGIK	2659.0	3	5.6888	0.4874
ASKPLPPAPAPDEYLVSPITGEKIPASK	2875.3	3	4.8757	0.3835
ASKSEVLSESSELLQQELEELRK	2633.9	3	4.8791	0.2478
ASLAETDKITLEVAK	1589.8	2	4.475	0.4267
ASLASLPPLHVAK	1304.6	2	3.1561	0.3008
ASLDRPFTNLESAFYSIVGLSSLGAQVPDAK	3255.6	3	4.1536	0.4345
ASLDRPFTNLESAFYSIVGLSSLGAQVPDAKK	3383.8	3	6.3614	0.4931
ASLDSAGGSGSSPILLPTPVVGGPR	2293.6	2	5.365	0.4718
ASLEAAIADAEQR	1345.4	2	4.9064	0.3193
ASLEAAIADAEQRGELAIK	1957.2	2	5.5076	0.343

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ASLEAAIADAEQRGELAIKDANAK	2456.7	3	5.9338	0.4299
ASLEAAIADAEQRGELAIKDANAKLSELEAALQR	3567.9	3	7.9901	0.4373
ASLEDAPVDDLTR	1402.5	2	3.1574	0.1778
ASLEDAPVDDLTRK	1530.7	2	2.9759	0.1435
ASLEDLGWADWVLSPR	1816.0	2	3.6849	0.203
ASLEEPPDGPSAGQATGPGEGR	2081.1	2	3.932	0.3928
ASLENSLR	890.0	1	2.8671	0.2114
ASLENSLREVEAR	1474.6	2	3.0649	0.1489
ASLHALVGSPIIWGGEPR	1861.1	2	4.0243	0.3572
ASLHGGEPTTIIRQDLGSPEGIAVDHLGR	2998.3	3	4.7075	0.3874
ASLIDDAFALAR	1263.4	2	2.5246	0.25
ASLISAVSDKLR	1260.5	2	3.1064	0.3104
ASLLGDMHFR	1147.3	2	2.8958	0.2289
ASLLHSMPTHSSPR	1521.7	2	3.0101	0.4107
ASLLQNESTNEQLQIHYK	2117.3	3	3.6014	0.3016
ASLLTDEEDVDMALDQR	1922.1	2	2.6831	0.1516
ASLLTGLPQHQNGMYGLHQDVHHFNSFDK	3293.6	3	4.9838	0.353
ASLLTGLPQHQNGMYGLHQDVHHFNSFDKVR	3548.9	3	3.9248	0.1862
ASLPTGEGSISHEEQK	1670.8	2	4.3676	0.3768
ASLSKLGDVYVNDAFGTAHR	2122.3	3	5.7696	0.5221
ASLTLSGGPSALAFDLSK	1736.0	2	3.3684	0.205
ASLVALPEQTASEEETPPPLLTK	2422.7	3	4.0147	0.3518
ASLVHVGSRPYTEFPFGQHSSGEAAQDAVR	3202.4	3	7.1503	0.4888
ASMHPVTAMLVGK	1342.7	3	4.0041	0.3872
ASMHPVTAMLVGKDLKVD	1913.3	3	3.6287	0.3277
ASMMYLENGTPDTAAMALER	2173.5	2	4.6992	0.4218
ASMQQQQQLASAR	1447.6	2	4.3409	0.3905
ASNAMMNNNDLVR	1450.6	2	3.7385	0.3504
ASNDMYHSR	1081.1	2	3.1309	0.3245
ASNEDGDIKR	1105.1	2	3.3376	0.3015
ASNGDAWVEAHGK	1342.4	2	4.0579	0.4829
ASNGDAWVEAHGKLYSPSQIGAFVLMK	2878.3	3	5.9743	0.4233
ASNKVQDSAPVETPR	1599.7	2	4.276	0.3382
ASNLENSTYDLYTIPK	1830.0	2	5.0591	0.4127
ASNLENSTYDLYTIPKDADSQNPDAPEGKR	3311.5	3	4.3415	0.2196
ASNPFLPGGGPATGPSVTNPFQPAPPATLTLNQLR	3487.9	3	5.7559	0.3982

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ASNTADTLFQEVLGR	1622.8	2	3.2821	0.2647
ASNTAEVFFDGVR	1413.5	2	3.8934	0.3507
ASNTAEVFFDGVRVPSENVLGEVGSGFK	2914.2	3	6.1778	0.5043
ASNTAEVFFDGVRVPSENVLGEVGSGFKVAMHILNNGR	4020.5	3	4.6383	0.3149
ASPALVAKDPGTVANKKEEEDLAK	2482.8	3	5.3137	0.5023
ASPALVAKDPGTVANKKEEEDLAKAIELSLKEQR	3651.1	3	4.8944	0.3905
ASPAPGSGHPEGPGAHLDMNSLDRAQAAK	2841.1	3	3.5204	0.3133
ASPATQPPPLLPPSATGPDATVGGPAPTPLLPPSATASVK	3729.2	3	3.379	0.2171
ASPDDPSGLPGRSPDT	1569.6	2	2.5691	0.1378
ASPDQNASTHTPQSSVK	1755.8	2	3.753	0.3505
ASPESQEPLIQLVQAFVR	2013.3	2	5.0845	0.4745
ASPGHSPHYFAASSPTSPNALPPAR	2518.7	3	3.9299	0.1084
ASPGHSPHYFAASSPTSPNALPPARK	2646.9	3	3.4717	0.2264
ASPHATPSTLHFPTSPIIQQPGPYFSHPAIR	3354.8	3	4.823	0.3808
ASPNVEAPQPHR	1303.4	2	3.3197	0.4167
ASPSPQPSSQPLQIHR	1730.9	2	4.3819	0.4373
ASPSTAGETPSGVK	1289.4	2	2.5997	0.2455
ASPTSDFASPTYDLIK	1713.9	2	3.3963	0.2235
ASQGPVYK	850.0	2	2.5285	0.156
ASQKDFENSMNQVK	1626.8	2	4.2548	0.3789
ASQKPQPNFPSPEYMIFDHEFTK	2740.0	3	5.5646	0.475
ASQSTQAHENSR	1316.3	2	3.4974	0.3717
ASRDEIFAQSK	1252.4	2	3.1826	0.2022
ASREEILAQAKENEK	1716.9	2	4.9054	0.3022
ASREEILAQAKENEKK	1845.0	2	4.6335	0.2324
ASSDASKVTSK	1081.2	2	3.2417	0.3888
ASSEGGTAAGAGLDSLHK	1629.7	2	4.5855	0.4862
ASSEGGTAAGAGLDSLHKNSVSQISVLSGGK	2887.1	3	5.8913	0.5295
ASSHSSQTQGGGSVTK	1519.6	2	4.8744	0.4201
ASSHSSQTQGGGSVTKK	1647.7	2	3.8417	0.3928
ASSIIDELFQDR	1394.5	2	4.1188	0.3894
ASSQQEKEDKPAETK	1676.8	2	3.7237	0.3063
ASSQQEKEDKPAETKK	1804.9	3	3.7343	0.3707
ASSRLENLGIPEEELLRQQQELFAK	2900.2	3	5.0691	0.4015
ASSSGSASKSDKDLETQVIQLNEQVHSLK	3088.3	3	7.0365	0.3599
ASSTSPVEISEWLDQK	1777.9	2	4.7214	0.3775

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ASSTSPVEISEWLDQKLTK	2120.3	2	3.2147	0.3345
ASSVSLHAER	1057.1	2	2.4037	0.107
ASTALSNEQQAR	1276.3	2	3.443	0.3086
ASTEGVAIQGQQGTR	1503.6	2	3.6598	0.3249
ASTKVEVDMEKAESLQVTR	2122.4	3	3.5233	0.2574
ASTLLRDEELEEIKKETGFSHSQITR	3019.3	3	6.9156	0.4341
ASTNAMLISAGLPPLK	1584.9	2	2.8252	0.2028
ASTNSETNRGESEK	1510.5	2	3.0512	0.2349
ASTPAILFLDEIDSILGAR	2003.3	2	3.7417	0.3325
ASTYGVAVR	924.0	2	2.6306	0.3514
ASVDSGSSEEQGGSSR	1540.5	2	4.781	0.5405
ASVDTKEAEGAPQVEAGK	1787.9	2	5.4621	0.375
ASVDTKEAEGAPQVEAGKR	1944.1	2	5.5983	0.3872
ASVDTKEAEGAPQVEAGKRLEELR	2584.8	3	4.9129	0.3389
ASVEDADTQSK	1151.2	2	2.7824	0.3524
ASVEDADTQSKVHQLYETIQR	2419.6	3	4.703	0.3874
ASVITQVFHVPLEER	1726.0	2	3.6735	0.2595
ASVITQVFHVPLEERK	1854.1	3	4.2587	0.408
ASVLFDTMQHHLALNR	1854.1	2	4.835	0.3521
ASVSPMDEPVPDSESPIEK	2015.2	2	3.4071	0.2388
ASVSQVEADLK	1147.3	2	2.9807	0.2384
ASVTNDSGPR	1004.0	2	2.7269	0.1776
ASVVTLPVYLNFTR	1580.9	2	2.9842	0.1511
ASWGEFQAR	1052.1	2	3.161	0.2154
ASWSSLSMDEK	1241.4	2	3.0559	0.3452
ASWSSLSMDEKVELYR	1902.1	3	3.2845	0.3787
ASYGHSMVVDPWGTVVAR	1933.2	2	4.2179	0.3508
ASYGVEDPEYAVTQLAQTTMR	2331.5	2	5.3277	0.4742
ASYHFSPEELDENTSPLLGDAR	2449.6	3	4.5247	0.3374
ASYISSAR	854.9	1	2.7067	0.1861
ASYISSARLEQPDPGAVAAAAILR	2428.7	3	4.0362	0.3308
ASYLEIYQEEIRDLLSKDQTK	2543.8	3	3.6824	0.1702
ASYVAPLTAQPATYR	1609.8	2	3.5472	0.2868
ATAAELLKHPFLAK	1510.8	2	4.1944	0.3348
ATAAFILANEHNVALFK	1831.1	2	2.4198	0.1822
ATAAGVKQTESTSFLEK	1768.9	3	3.3997	0.3098

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ATAAPAGAPPQPQDLEFTKLPNGLVIASLENYSPVSR	3822.3	3	5.1191	0.5076
ATAEQISSQTGNK	1335.4	2	4.8134	0.3007
ATAGAYIASQTVK	1281.4	2	4.068	0.3126
ATAGDTHLGGEDFDNR	1676.7	2	4.8522	0.4795
ATAGDTHLGGEDFDNRLVNHFVEEFK	2920.1	3	4.5091	0.4074
ATAGDTHLGGEDFDNRLVNHFVEEFKR	3076.3	3	4.9964	0.4476
ATAGDTHLGGEDFDNRLVNHFVEEFKRK	3204.5	3	3.9585	0.3153
ATAPQTQHVSPMR	1424.6	2	3.4162	0.3953
ATAVMPDGQFK	1165.3	2	2.8724	0.3445
ATAVVDGAFK	979.1	1	2.7772	0.2938
ATAVVDGAFKEVK	1335.5	2	3.4959	0.3146
ATCAPQHGAPGPGPADASK	1733.9	2	4.5967	0.4579
ATDAEADVASLNR	1333.4	2	3.7928	0.2897
ATDAMAHVAGFTVAHDVSAR	2028.2	3	3.8559	0.3269
ATDFVADR	895.0	2	2.9551	0.2707
ATDFVADRAGTFK	1399.5	2	3.0344	0.3238
ATDFVVPGPGK	1088.2	2	2.9715	0.3109
ATDFVVPGPGKVEITYTPSDGTQK	2508.8	3	4.977	0.335
ATDKDITGTLSNPEVFNYGVETHEAYK	3001.2	3	4.6432	0.2735
ATDKSFVEK	1025.1	2	2.6779	0.2853
ATDKTFVEKLVQEQGSHSK	2133.3	2	4.6872	0.3367
ATDLGGTSQAGTSQR	1450.5	2	4.5227	0.4099
ATDLRPIYISVQPPSLHVLEQR	2533.9	3	4.5897	0.4019
ATDSSDPLKPYQDFIIDSREPDATTR	2940.1	3	3.7777	0.1603
ATDVMIAGK	906.1	2	2.7295	0.2363
ATEKDKVEIYK	1324.5	2	2.9846	0.2275
ATEKFQLAVEALEQEKQGLQSQIAQVLEGR	3343.7	3	5.7248	0.4069
ATEKQHITLALEK	1482.7	2	4.1054	0.2662
ATENDIANFFSPLNPIR	1920.1	2	5.2064	0.4914
ATENDIYNFFSPLNPMR	2030.2	2	5.3737	0.4675
ATENDIYNFFSPLNPVR	1998.2	3	5.2217	0.4295
ATENPEQVASEGLPEPVLR	2037.2	3	4.7285	0.4058
ATEPVIAFYEK	1268.4	2	2.4858	0.2638
ATEQEKAAMDSAR	1408.5	2	3.9299	0.4397
ATESGAQSAPLPMEGVDISPK	2086.3	3	3.3357	0.1236
ATEVSKTPEAR	1189.3	2	2.7731	0.1737

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ATFDAISK	853.0	2	2.4306	0.1923
ATFDAISKTYSYLTPDLWK	2221.5	2	4.6003	0.4169
ATFDAISKTYSYLTPDLWKETVFTK	2927.3	3	4.4772	0.2104
ATFDISLVVPK	1190.4	2	2.8591	0.1821
ATFDPDTGLLMEIMNMNQQLLLPVR	2862.4	2	4.1994	0.4096
ATFIKVPQNQNGK	1445.6	2	4.0097	0.1914
ATFLDAWEAMEELVDEGLVK	2267.5	3	5.3116	0.4438
ATFSDSLLIQPTSAGSTDRLPYSK	2556.8	3	3.333	0.2159
ATFYGEQVDYYK	1484.6	2	3.8527	0.4162
ATFYLLIGNANAAKPDLDKVISLK	2577.0	3	4.1602	0.3549
ATFYLNVLEQK	1326.5	2	3.5723	0.1862
ATGASKKLKKATGASKKSVKTPKKAKKPAATRKSSKNPK	4038.8	3	3.6457	0.2013
ATGATQQDANASSLLDIYSFWLK	2501.7	2	2.9547	0.1198
ATGDETGAKVER	1234.3	2	3.3825	0.3726
ATGDETGVKVER	1262.4	2	2.6342	0.1544
ATGEADVEFVTHEDAVAAMSK	2179.4	2	3.1853	0.128
ATGGGLSSVGGGSSTIK	1436.6	2	3.7203	0.4143
ATGQSHKPVPPTQVQK	1703.9	2	4.2384	0.3337
ATGYLELSNWPEVAPDPSVR	2202.4	2	2.8043	0.3189
ATHAVVR	753.9	1	1.7523	0.1586
ATHDGAPELGAGGTR	1410.5	2	3.8058	0.456
ATHGGRIDYIAGLDSR	1702.9	3	3.6621	0.2712
ATHVVQSEVDKYVDDIMKEK	2335.6	3	3.9578	0.2578
ATIAGGGVIPHIHK	1371.6	2	4.4952	0.4689
ATIERDGYAQILR	1506.7	3	4.3103	0.3123
ATIRPWSTFVDQQR	1705.9	2	3.4677	0.1854
ATKEQLKAVMDDFAAFVEK	2142.5	2	5.5389	0.4459
ATKKEPAVLELEGK	1513.8	3	4.0692	0.3447
ATKKEPAVLELEGKK	1641.9	3	3.7138	0.284
ATKQELLQLR	1200.4	2	3.1169	0.1721
ATKSPEEGAETPVYLALLPPDAEGPHGQFVSEK	3466.8	3	5.4825	0.4246
ATKSPEEGAETPVYLALLPPDAEGPHGQFVSEKR	3623.0	3	4.0844	0.2211
ATKVPLVAEKPLKEPK	1749.1	2	4.5012	0.3008
ATLENITNLRPVGEDFR	1946.2	2	3.1243	0.1914
ATLEQDSAKKEQQLQER	2003.2	3	5.3137	0.3536
ATLGPTPTTPPQPPDPSQPPPGPMQH	2644.9	3	3.4658	0.359

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ATLPDADKER	1116.2	2	2.5126	0.2305
ATLPSPDKLPGFK	1371.6	2	2.7342	0.2355
ATLSEDKKHYILNGSK	1805.0	2	4.559	0.3119
ATLSQMLSDLTLQLR	1691.0	2	4.3301	0.2099
ATMDAGKLVSDEMVVELIEK	2179.5	2	2.9108	0.185
ATMEAYSR	929.0	2	2.4496	0.3284
ATMQNLNDR	1063.2	2	2.5881	0.1561
ATNDSVVADK	1020.1	2	2.7462	0.3171
ATNIEVLSNTFQFTNEAR	2056.2	2	3.6013	0.3855
ATNMTVSAIR	1064.2	2	3.3526	0.1882
ATNVTYQAHHVSR	1484.6	2	3.8473	0.4192
ATNVVMNYSEIESK	1585.8	2	3.0119	0.1863
ATNYNAGDR	982.0	2	2.6479	0.1199
ATNYNAGDRSTDYGIFQINSR	2364.5	3	4.3264	0.382
ATPEEKLKLEDFFAR	1795.0	2	3.6728	0.3464
ATPENYLFQGR	1296.4	2	2.8947	0.305
ATPEQYQILKENYGQK	1911.1	2	4.3626	0.3547
ATPEQYQILKENYGQKEAEKVAR	2695.0	3	3.8067	0.4493
ATPMPSRPSTTPFIDKKPTSAKPSSTTPR	3086.5	3	5.4558	0.2278
ATPPQIVNGDQYCGDYELFVEAVEQNTLQEFLK	3761.1	3	4.8512	0.2902
ATPSENLVPSSAR	1329.4	2	3.5427	0.4214
ATQASQEY	897.9	2	2.5504	0.1021
ATQDSDTVKLEVDQELSNGFK	2325.5	3	3.9481	0.3221
ATQELIPIEDFITPLK	1829.1	2	3.4607	0.3257
ATQLLKEAEEEFWYR	1914.1	3	4.7704	0.3383
ATQPETTEEVTDLKR	1718.8	2	3.4949	0.2641
ATQQPFDVSAFNASYSDSGLFGIYTISQATAAGDVIK	3843.2	3	5.3822	0.3716
ATQQPFDVSAFNASYSDSGLFGIYTISQATAAGDVIKAAYNQVK	4618.0	3	4.3329	0.3546
ATQQQHDFTLTQTADGR	1919.0	2	5.0809	0.4321
ATRPSDDPLSLLDPLWTLNKT	2354.6	3	4.3749	0.2279
ATSEIFHSQSFLATGSNLRK	2195.4	3	4.3634	0.2942
ATSETLAADPTPAATIVHFK	2042.3	2	3.2228	0.3113
ATSFATVVKDIEGFMEENQTK	2346.6	3	4.9439	0.2534
ATSFLLALEPELEAR	1660.9	2	5.0348	0.3894
ATSGDKLNNNK	1162.2	2	2.8814	0.2542
ATSHVGEIEQELALAR	1724.9	2	2.7197	0.2678

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ATSLGRPEEEEDELAHR	1940.0	3	3.4346	0.1354
ATSLTLEGGRLKR	1402.6	2	2.4436	0.1195
ATSNVFAMFDQSQIQEFKEAFNMIDQNR	3311.7	3	3.5418	0.141
ATSPADALQYLLQFAR	1766.0	2	4.0365	0.3773
ATSQGGDLMSDLFNK	1584.7	2	2.786	0.1825
ATSSSSGSLSATGR	1269.3	2	3.9232	0.4569
ATSTATSGFAGAIGQK	1468.6	2	4.3796	0.3685
ATTAALLLEAQAATGFLVDPVR	2229.6	2	3.0398	0.3724
ATTADGSSILDR	1207.3	2	2.8063	0.1769
ATTLSNAVSSLASTGLSLTK	1923.2	2	4.4465	0.4595
ATTPVIMVGPGTGVAPFIGFIQER	2459.9	3	3.928	0.2557
ATVAAFAASEGHSHPR	1609.7	2	3.9882	0.5055
ATVASSTQK	893.0	2	2.5949	0.1665
ATVDNKDKLEETSGLK	1748.9	2	4.9976	0.3528
ATVEDEKLQGK	1218.3	2	2.6693	0.1331
ATVHDPETGKLTTAQYR	1889.1	2	4.0255	0.377
ATVKELASLHGTK	1355.6	2	3.5371	0.389
ATVLESEGTRESAINVAEGK	2062.2	2	4.6103	0.2829
ATVLESEGTRESAINVAEGKK	2190.4	3	5.5484	0.4184
ATVLQKTSFTPVGDVFELNFMNVK	2687.1	3	3.3185	0.1239
ATVNLLGEEKK	1202.4	2	2.6701	0.2481
ATVNQDTR	904.9	2	2.4474	0.1965
ATVQSVLLDSAGK	1289.5	2	3.4373	0.3069
ATVSKTENQK	1106.2	2	2.6662	0.19
ATVTPSPVK	900.1	1	1.7552	0.1441
ATVVESSEK	950.0	2	2.4084	0.1262
ATVVYQGER	1023.1	2	2.9252	0.1777
ATWLHQALR	1096.3	2	2.4736	0.1283
AVAAAAAAAVTPAAIAAATTTLAQEEPVAAPEPK	3116.5	3	3.4287	0.1553
AVAALLTIPEAEKSPLMSEFQSQISSNPELAAIFESIQK	4190.8	3	5.2782	0.4785
AVAASKER	831.9	2	2.7238	0.1772
AVAATSTKGQEQSAQK	1605.7	2	3.0438	0.3093
AVADTRDQADGSR	1362.4	2	2.6908	0.1587
AVAEGKADQFLVGTSR	1649.8	2	4.825	0.4549
AVAEIEEMCNILK	1463.7	2	3.1759	0.1375
AVAEQIPLLVQGVR	1493.8	2	3.9174	0.3468

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AVAEQVLHSQSR	1325.5	2	3.4228	0.3217
AVAFQNPQTHVIENLHAAAYR	2351.6	3	6.1557	0.4497
AVAFSPVTELKKDTDFEHR	2191.4	3	3.5222	0.202
AVAGDASESALLK	1232.4	2	3.8098	0.3686
AVAGEYSDPVTLETK	1580.7	2	3.0849	0.2103
AVAGNISDPGLQK	1270.4	2	2.9349	0.2827
AVAGQGELTR	1002.1	2	2.4808	0.1259
AVAHHTDCTFIR	1371.6	2	2.6349	0.2592
AVAHHTTAAFIR	1295.5	2	3.5207	0.3803
AVAIDLPGLGHSK	1278.5	2	3.7185	0.2745
AVALDEAISQSTQFHDKIDQILESLER	3058.3	3	5.0909	0.4617
AVANETGAFFFLINGPEIMSK	2257.6	2	6.077	0.5306
AVANQTSATFLR	1279.4	2	3.1808	0.3914
AVANSRPAK	914.0	2	2.8693	0.2195
AVANYDSVEEGEKVVK	1737.9	2	4.5193	0.4489
AVAPSIIFFDELDALAVER	2077.4	2	4.0217	0.3911
AVAQALEVIPR	1167.4	2	3.5327	0.2892
AVAREESGKPGAHVTVK	1737.0	2	3.8169	0.3038
AVASAAAALVLK	1085.3	2	2.7443	0.1652
AVASLNTPFIPANPNMSPLESIK	2412.8	2	2.9924	0.1996
AVASLSVKLEQAMKEIQR	2002.4	2	2.7963	0.2254
AVASPEATVSQTDENKAR	1875.0	2	3.969	0.4186
AVASQPDSVDAAER	1416.5	2	3.6916	0.2542
AVATGKMDENQFVAVTSTNAAK	2254.5	3	5.2929	0.3586
AVAVVVDPIQSVK	1325.6	2	3.3674	0.331
AVAVVVDPIQSVKGK	1510.8	2	3.4583	0.1793
AVCVLKGDGPVQGIINFEQK	2116.5	2	5.2958	0.4502
AVCVLKGDGPVQGIINFEQKESNGPVK	2828.2	3	4.2509	0.2012
AVCVLKGDGPVQGIINFEQKESNGPVKVWGSIK	3499.0	3	3.725	0.1832
AVDDGVNTFK	1066.1	2	3.4324	0.3238
AVDEAVILLQEIGVLDQR	1982.3	2	2.831	0.1131
AVDEMNGRIVGSKPLHVTLGQARRR	2762.2	3	3.598	0.1836
AVDHATNR	883.9	1	1.7688	0.1489
AVDHINSTIAPALISSGLSVVEQEKLDNLMLELDGTENK	4166.7	3	6.1926	0.5443
AVDHINSTIAPALISSGLSVVEQEKLDNLMLELDGTENKSK	4381.9	3	6.7172	0.5986
AVDIPHMDIEALK	1452.7	2	3.3756	0.3138

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AVDIPHMDIEALKK	1580.9	2	3.4388	0.4023
AVDLGPPKPSDQETGEQVSSPSSHPALHTTTEDSAGVQTEF	4236.4	3	4.5438	0.3102
AVDNQVYVATASPAR	1562.7	2	4.1545	0.4916
AVDQSIEKK	1018.1	2	2.4721	0.1773
AVDSEYPKNIK	1264.4	2	2.4863	0.1628
AVDSLVPIGR	1027.2	2	3.3456	0.2871
AVDSQILPK	971.1	2	2.9623	0.1436
AVDWIFSHIDDLDAEAAMDISEGR	2677.9	2	2.7592	0.2957
AVEAAQLAEDLKVQLEHVQTR	2349.6	3	5.2894	0.4262
AVEDEATKGTR	1177.2	2	2.7863	0.3471
AVEEEDKMTPEQLAIK	1832.1	2	5.1726	0.3828
AVEEKIEWLESHQDADIEDFK	2532.7	3	4.8035	0.421
AVEEKIEWLESHQDADIEDFKAK	2732.0	3	5.6585	0.396
AVEFLASNESR	1223.3	2	3.9562	0.3727
AVEHINKTIAPALVSK	1692.0	2	4.3119	0.4596
AVEILADIIQNSTLGEAEIERER	2570.8	3	3.9214	0.3073
AVEIVTSTSAAK	1177.3	2	2.4823	0.1308
AVEKVEKQVNDAVSK	1644.9	2	3.7665	0.3094
AVELAANTK	917.0	2	2.8379	0.2544
AVELLPDGTANLAK	1412.6	2	3.2096	0.3157
AVENPTATEIQDVCSAVGLNVFLEK	2649.0	3	3.4194	0.2462
AVENSSTAIGIR	1218.3	2	3.4889	0.3307
AVEQHNGKTIFAYFTGSK	1999.2	3	3.3904	0.2367
AVEQLAEGLLSHYLPDLQR	2153.4	2	2.7571	0.1716
AVERGQLEQITGK	1429.6	3	3.8589	0.1636
AVETTAQSDNK	1164.2	2	4.022	0.2757
AVEVAWETLQEEFSR	1794.9	2	3.5834	0.2881
AVEVDPSLLLHMLE	1566.8	2	3.7747	0.4332
AVEYDTLFR	1114.2	2	2.6544	0.2216
AVEYLTLSSVASTDVLATVLEEMPPFPERESSILAK	3895.4	3	3.3075	0.1736
AVFDETYPDPVR	1409.5	2	3.7123	0.4328
AVFDVDKK	922.1	2	2.5911	0.2044
AVFHEEEQR	1145.2	2	2.829	0.1736
AVFPSIVGRPR	1199.4	2	2.9668	0.3056
AVFQANQENLPILK	1585.8	2	3.9095	0.2929
AVFQANQENLPILKR	1742.0	2	4.4149	0.3973

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AVFVDLEPTVIDEIR	1717.0	3	4.3449	0.2593
AVFVDLEPTVIDEIRNGPYR	2304.6	2	2.84	0.1732
AVFVDLEPTVIDEVR	1702.9	2	5.5503	0.4847
AVFVDLEPTVIDEVRTGTYR	2281.6	3	3.2362	0.3295
AVGDKLPECEADDGCPKPPEIAHGYVEHSVR	3320.7	3	4.7104	0.4154
AVGFGGDFDGVPRVPEGLEDVSKYPDLIAELLR	3532.9	3	6.1078	0.5116
AVGFSSGTENPHGVK	1487.6	2	3.3003	0.38
AVGKDNFTLIPEGTNGTEER	2149.3	2	5.8691	0.4155
AVGKDNFTLIPEGVNGIEER	2159.4	2	6.4126	0.4111
AVGKEELGK	931.1	2	2.596	0.1805
AVGKEELGKNINADEAAAMGAVYQAAALSK	2992.4	3	4.5677	0.3437
AVGKVIPELDGK	1226.4	2	3.6619	0.2017
AVGKVIPELDGKLTGMAFR	2003.4	3	4.2444	0.2491
AVGLISHVLEQNQEGDAAYR	2171.4	3	4.896	0.3239
AVGLISHVLEQNQEGDAAYRK	2299.5	3	6.1526	0.4303
AVGMHSFLVVGPQALDPVVR	2093.5	3	3.7301	0.1982
AVGPSGGGGETPR	1142.2	2	3.0222	0.4566
AVGPSSTQLYMVR	1409.6	2	2.6365	0.2502
AVGPTAEADKSAAEK	1445.6	2	4.0304	0.3797
AVGRLEAVSHTSDMHR	1767.0	3	4.1432	0.402
AVGTQTLSGAGLLK	1316.5	2	3.8951	0.3524
AVGVAVATGLHTELGK	1523.8	2	4.2331	0.3806
AVGVAVATGLHTELGKIR	1793.1	2	2.6896	0.1803
AVHAHVNLGYTK	1310.5	2	3.4986	0.4057
AVHANPPTLLLPVAHMLEVGDPDDLAFLR	3123.6	3	5.9283	0.512
AVHANPPTLLLPVAHMLEVGDPDDLAFLRK	3251.8	3	4.4606	0.4367
AVHEQLAALSQGPISKPK	1875.2	3	3.2614	0.2222
AVHHAAFGDEGAVIEVLHR	2029.2	2	5.8503	0.5351
AVHISNPK	866.0	1	2.2376	0.1225
AVHLQGHEGPVYAVHAVYQR	2232.5	3	4.6757	0.2729
AVIDLNNRWFNGQPIHAELSPVTDFR	3011.3	3	4.3015	0.2274
AVIEAEKIAQVAK	1370.6	2	4.0096	0.3313
AVIEHNLLSASK	1282.5	2	2.925	0.2742
AVIFCLSADKK	1195.5	2	2.6619	0.2863
AVIFDRFR	1024.2	2	2.4294	0.1702
AVIHWIMDIPFVLSANLHGGDLVANYPYDETR	3629.1	3	5.9064	0.4913

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AVILFKPMVSEPIHIHR	1988.4	3	4.649	0.4011
AVILIGGPQK	996.2	2	2.4043	0.1533
AVIQGLETLRGEHR	1579.8	2	2.6984	0.1648
AVIQVSQIVAR	1184.4	2	3.1167	0.2566
AVITSLLDQIPEMFADTR	2021.3	2	3.5055	0.241
AVITSLLDQIPEMFADTRETETVFVPVIQAGMEALK	3965.6	3	3.6015	0.2152
AVIYNPATQADWTAK	1649.8	2	3.0679	0.2203
AVKDELLGEKPEVK	1555.8	2	4.172	0.2406
AVKDLVVLLFETALLSSGFSLEDPQTHSNR	3288.7	3	4.39	0.308
AVKESTITLQQAEYEFLSFVR	2460.8	3	3.5521	0.3773
AVKNFTEVHPDYGSHIQALLDK	2483.8	3	4.502	0.3031
AVKNFTEVHPDYGSHIQALLDKYNAEKPK	3314.7	3	3.7981	0.2655
AVKQGESEVSR	1190.3	2	3.1573	0.3565
AVLAELPQQVVQYFK	1734.0	2	3.3884	0.2449
AVLAESYER	1038.1	2	2.4296	0.1388
AVLASMDNENMHTPDIGGQGTTSEAIQDVIR	3272.6	3	7.8836	0.4971
AVLAVHPDKAAGQPYEQHAK	2131.4	3	4.3245	0.2696
AVLDALLEGK	1029.2	2	3.3755	0.2353
AVLDVFEEGTEASAATAVK	1909.1	2	5.8234	0.5055
AVLEEKEKDLANTGK	1645.8	2	4.9144	0.4337
AVLENNLGAAVLR	1340.6	2	3.0097	0.1801
AVLEPIQSTSLIGTLTR	1800.1	2	4.3708	0.4061
AVLEQEETAAASR	1375.5	2	4.3103	0.32
AVLFCLSEDKK	1253.5	2	3.1775	0.3673
AVLGEVVLYSGARPLSHQPGPEAPALPK	2855.3	3	4.7088	0.2776
AVLGMAAAAEELLGQHLVQGVISVPK	2603.1	3	4.0683	0.3296
AVLHVHGGGGPR	1157.3	2	2.699	0.3979
AVLIAGQPGTGK	1112.3	2	3.617	0.3445
AVLIDKDQSPK	1214.4	2	3.0985	0.3075
AVLIPIREVLTPESDISIAHVLAAR	2685.2	3	5.7472	0.4817
AVLKELSEKLELAEK	1701.0	2	4.7685	0.4019
AVLLDLEPR	1026.2	2	2.6873	0.2139
AVLLGPPGAGK	980.2	2	2.7502	0.1896
AVLNPLCQVDYR	1391.6	2	2.5543	0.2032
AVLPVAESFGFADEIR	1721.9	2	4.2469	0.4666
AVLSAEQLRDEEVHAGLGELLR	2406.7	3	6.0685	0.5039

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AVLTPNHVEFSR	1370.5	2	2.4378	0.3384
AVLTVVKDDDHGILDQFSR	2129.4	3	4.6016	0.3798
AVLVALKER	999.2	2	2.7209	0.1391
AVLVDLEPGTMDSVR	1602.8	2	4.4848	0.3971
AVMDDFAAFVEK	1343.5	2	3.8422	0.4157
AVMHFLVNHVK	1295.6	2	2.6454	0.2974
AVMLLHTHTITSR	1480.8	2	3.4606	0.3646
AVNSATGVPTV	1016.1	2	2.72	0.3247
AVNSLRDFVDDDDDDDLER	2225.2	2	3.3272	0.2663
AVNTAPVPGQTPHDESDRRTEPR	2531.7	3	3.4506	0.1995
AVNTQALSGAGILR	1371.6	2	2.7926	0.2667
AVPEGFVIPR	1085.3	2	2.732	0.2383
AVPKEDIYSGGGGGGSR	1607.7	3	3.4624	0.4432
AVPLALALISVSNPR	1521.8	2	2.5009	0.1092
AVPLIHQEGNR	1234.4	2	2.9286	0.255
AVPLNASKQDGPMPKPHSVSLNDTETR	2891.2	3	4.0281	0.3204
AVPLNASKQDGPMPKPHSVSLNDTETRK	3019.4	3	3.5526	0.2503
AVPMAPAPASPGSSNDSSAR	1871.0	2	3.2843	0.2085
AVPREELFVTSK	1376.6	2	2.8793	0.1452
AVPYQKFEAHPNDLYVEGLPENIPFR	3045.4	3	3.7317	0.2033
AVQADGQVK	916.0	2	2.4887	0.105
AVQALCAVYEHWVPR	1743.0	2	3.9035	0.379
AVQAQGGESQQEAQR	1587.6	2	4.9131	0.4426
AVQELVHPVVDR	1362.6	2	2.9537	0.1654
AVQFTEEKFGQAEKTELDAHFENLLAR	3123.4	3	6.1791	0.4158
AVQFTEEKLGQAEKTELDAHLENLLSK	3043.4	3	5.9208	0.4752
AVQGFFTSNNATR	1413.5	2	3.8906	0.3209
AVQGFFTSNNATRDFLLPFLEEPMDTEADLQFRPR	4075.5	3	3.2461	0.1095
AVQGGGATPVVGAVQGPVPGMPPMTQAPR	2729.2	3	3.5066	0.1159
AVQGPEETVTQDCLQLIADSETPTIQK	2916.2	3	4.0534	0.1864
AVQLKPRPPQGLVR	1559.9	2	2.802	0.2516
AVQLYQQTANVFENEER	2040.2	2	3.689	0.3346
AVQQPDGLAVLGIFLK	1670.0	2	5.1305	0.54
AVQSLDKNGVDLLMK	1631.9	2	4.1116	0.3373
AVQSTINHVKEERPEKIPDLK	2432.8	3	3.2023	0.1427
AVQTDVVPYSPAISELIQSVLQK	2486.8	2	2.6453	0.1442

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AVQTLQMELQQIMK	1662.0	3	4.9108	0.3559
AVQVHQDTLR	1167.3	2	2.8462	0.3385
AVRVFEFGGPEVLK	1548.8	2	3.8502	0.2408
AVSDASAGDYGSAIETLVTAISLIK	2453.7	2	5.8884	0.5552
AVSDWIDEQEK	1320.4	2	2.6987	0.1374
AVSDWLIASVEGR	1403.6	2	3.812	0.3161
AVSEEQQPALK	1200.3	2	3.2152	0.2086
AVSEEQQPALKGK	1385.5	2	3.3484	0.2128
AVSEKEVDSGNDIYGNPIKR	2192.4	2	5.1408	0.4465
AVSGASAGDYSDAIETLLTAIAVIK	2437.7	2	4.555	0.3823
AVSILPLLGHGVPR	1429.7	2	3.3979	0.338
AVSIMGNEVFR	1223.4	2	2.5426	0.1959
AVSLFSLNDPALSPDIPPAHSPVHSHLSLER	3305.7	3	3.4098	0.1058
AVSPTEPTPR	1055.2	2	2.5072	0.1589
AVSREDSVKPGAHLTVK	1795.0	2	3.7553	0.2273
AVSREDSVKPGAHLTVKK	1923.2	2	3.5286	0.2047
AVSSAIAQLLGEVAQGNENYAGIAAR	2574.8	2	5.9194	0.3904
AVTDKFLSAIVSSVDKIPYGMR	2398.8	3	5.9858	0.5235
AVTELGRPAAEYWNSQKDILEEKR	2805.1	3	4.6923	0.3483
AVTELGRPDAEYWNSQK	1965.1	3	4.0146	0.1645
AVTELGRPDAEYWNSQKDFLEDR	2740.9	3	4.1945	0.3578
AVTELGRPDAEYWNSQKDFLEDRR	2897.1	3	3.3658	0.2525
AVTELGRPDAEYWNSQKDILEQAR	2791.0	3	6.1752	0.4119
AVTELGRPSAEYWNSQKDFLEDR	2712.9	3	4.9387	0.4004
AVTELNEPLSNEDR	1587.7	2	5.3077	0.4222
AVTELNEPLSNEDRNLLSVAYK	2476.7	2	3.8499	0.3631
AVTELNEPLSNEDRNLLSVAYKNVVGAR	3073.4	3	4.4215	0.4109
AVTEQGAELSNEER	1533.6	2	5.056	0.3973
AVTEQGAELSNEERNLLSVAYK	2422.6	3	4.6751	0.531
AVTEQGAELSNEERNLLSVAYKNVVGGR	3005.3	3	5.1951	0.4317
AVTEQGHELSNEER	1599.6	2	4.874	0.4724
AVTEQGHELSNEERNLLSVAYK	2488.7	2	4.8306	0.4104
AVTEQGHELSNEERNLLSVAYKNVVGAR	3085.4	3	7.613	0.526
AVTGTHTLALAAK	1254.5	2	3.2788	0.252
AVTGYNDPETGNIISLFQAMNK	2384.7	3	3.6659	0.1198
AVTGYNDPETGNIISLFQAMNKELIEKGHGIR	3518.0	3	3.4996	0.1481

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AVTGYRDPYTGQSVSLFQALKK	2430.7	3	5.8531	0.5144
AVTHAIPALQPIVHDLFVLR	2211.6	3	3.9896	0.326
AVTIHDTEK	1014.1	2	2.4321	0.2787
AVTKDEDEWKELEQK	1849.0	3	3.5441	0.1911
AVTKDEDEWKELEQKEVDYSGLR	2769.0	3	4.9847	0.4374
AVTKYTSSK	985.1	2	2.5131	0.2964
AVTLHDQGTAQWADLSSQFYLR	2508.7	3	3.4412	0.1501
AVTLHDQGTAQWADLSSQFYLREEDIGKNR	3450.7	3	3.3358	0.1763
AVTPVPTKTEEVSNLK	1714.0	2	2.9193	0.3509
AVTTVTQSTPVPGPSVPPPEELQVSPGPR	2926.3	3	4.6417	0.4446
AVVDAGITTK	975.1	2	2.6518	0.2872
AVVEVDESGTR	1162.2	2	3.5494	0.4417
AVVGEEALTSDDLLYLEFLQK	2354.6	2	5.8001	0.399
AVVGEEALTSDDLLYLEFLQKFER	2787.1	3	5.5735	0.4386
AVVGVVAGGGR	942.1	2	3.5799	0.3208
AVVHGILMGVPVPFPIPEPDGCKSGINCPIQK	3315.0	3	5.8875	0.4079
AVVHGILMGVPVPFPIPEPDGCKSGINCPIQKDK	3558.2	3	4.2069	0.2832
AVVISGAGK	802.0	1	2.1803	0.1959
AVVIVDDR	887.0	2	2.6296	0.1914
AVVIVDDRGR	1100.3	2	3.0391	0.195
AVVLAANHFGR	1155.3	2	3.3331	0.3357
AVVLAGFGGLNK	1146.4	2	3.8464	0.3777
AVVMTPVPLFSK	1289.6	2	2.58	0.3166
AVVNDATIFKLELPLKQK	2028.4	3	3.3692	0.1684
AVVPAKYLDEDTIYHLQPSGR	2373.6	3	3.9381	0.2447
AVVPGVKPQDWISAAR	1695.0	2	2.8606	0.417
AVVQVFEGTSGIDAK	1521.7	2	5.2258	0.5248
AVVTHSSGNHGQALTYAAK	1913.1	2	4.9755	0.4805
AVVVVDDRGR	1086.2	2	2.5699	0.2316
AVVYSNTIQSIMAIVK	1738.1	2	5.1047	0.4473
AVWPTMVDINSPESLTEAYK	2252.5	2	4.7259	0.411
AVYSDADIFLLDDPLSAVDSHVAK	2562.8	2	3.5206	0.3277
AWDDFFPGSDR	1313.4	2	3.2259	0.2992
AWDQEAEGAGPELGLR	1699.8	2	5.9374	0.3431
AWEEYYKK	1117.2	2	2.8515	0.1389
AWGNNQDGVVASQPAR	1670.8	2	3.4275	0.1916

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AWGPGLEGGVVGK	1227.4	2	3.6168	0.2886
AWGPGLHGGIVGR	1277.5	2	3.5145	0.4014
AWLFQHLTHPYPSEEQKK	2240.5	3	4.641	0.2276
AWQTATTTLNASNLIYPIFVTDVPDDIQPITSLPGVAR	4101.6	3	3.9008	0.435
AWRDPDEPVLLEEPVVLALAEK	2490.8	3	5.9565	0.3718
AWRDPDEPVLLEEPVVLALAEKYGR	2867.2	3	6.0271	0.4135
AYAALAALEK	1021.2	2	3.6212	0.285
AYAALAALEKLFPDTPLALDANKK	2546.0	3	5.7651	0.4296
AYAALAALEKLFPDTPLALDANKKK	2674.1	3	4.9508	0.4431
AYAANSHQGQMLAQYIESFTQGSIEAHKR	3238.5	3	7.1793	0.4667
AYADFYR	906.0	1	1.7403	0.1387
AYAEALKENSYVK	1486.7	2	3.507	0.2848
AYAEALKENSYVKK	1614.8	2	4.2195	0.3985
AYAGDKAEEIGR	1280.4	2	3.131	0.3217
AYALAFAER	1012.1	2	3.3887	0.2435
AYAQGISR	866.0	2	2.4762	0.1612
AYAQQLTEWAR	1337.5	2	3.2447	0.2821
AYASPAKLESIDGAR	1549.7	2	2.872	0.33
AYDATHLVK	1018.1	1	3.038	0.2631
AYDTDAGPVFVK	1283.4	2	3.2076	0.3011
AYEDQTKPVLEYYQK	1876.1	3	4.1478	0.3887
AYEDQTKPVLEYYQKK	2004.2	3	3.691	0.2956
AYFHLLNQIAPK	1415.7	3	4.4089	0.3144
AYGELPEHAK	1115.2	2	2.5824	0.1135
AYGENIGYSEK	1231.3	2	3.2182	0.2888
AYGENIGYSEKDR	1502.6	2	3.7583	0.4105
AYGPGIEPTGNMVK	1434.6	2	3.6591	0.2197
AYGSHCYALFLSPK	1557.8	2	2.7399	0.2309
AYGVESHVLSPAETK	1588.7	2	4.3063	0.3429
AYHEQLSVAEITNACFEPANQMVK	2695.0	3	4.8279	0.4502
AYHLQDDGTQTVR	1504.6	2	3.3698	0.1941
AYINKVEELK	1207.4	2	2.9893	0.2417
AYINKVEELKK	1335.6	2	3.1671	0.2141
AYINKVEELKKK	1463.7	2	3.4311	0.1528
AYIQENLELVEKGFSNLKK	2224.5	3	4.0727	0.3061
AYLDQTVVPILLQGLAVLAK	2126.6	3	5.2624	0.4347

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AYLLGKEDAAR	1207.4	2	3.2741	0.2688
AYLPVNESFGFTADLR	1801.0	2	5.1648	0.5234
AYLRDFMYVSQDPKDQLLLGPTYATPK	3132.6	3	4.2932	0.3338
AYLTEENGQIAVFDATNTTR	2215.4	2	5.6095	0.5034
AYNYVAQEVDDYHAFQTLTHIYNK	2905.1	3	4.1098	0.339
AYPDVAALSDGYWVVSNR	1984.2	3	3.3665	0.2597
AYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHR	4801.4	3	5.3157	0.4508
AYPLADAHLTK	1200.4	2	2.8029	0.3089
AYPLADAHLTKK	1328.5	2	3.5508	0.4212
AYQDRYQDLGAYSSAR	1865.0	2	3.5682	0.2699
AYQGVAAPFPK	1149.3	2	4.121	0.3414
AYQHGGVTGLSQY	1381.5	2	2.4843	0.1972
AYQIDTVINLNVPFEVIK	2077.4	2	4.794	0.3352
AYQIDTVINLNVPFEVIKQR	2361.7	3	4.391	0.2322
AYQKQPTIFQNK	1466.7	2	4.0025	0.1918
AYQKQPTIFQNKK	1594.8	2	3.3197	0.1524
AYQQALSR	937.0	2	2.416	0.1229
AYSDPSTGEPATYGELQQR	2071.1	2	5.6428	0.4766
AYSDQAIVNLLK	1335.5	2	4.202	0.3112
AYSEAHEISK	1135.2	2	3.354	0.2308
AYSEAHEISKEHMQPTHPIR	2362.6	2	5.2274	0.3941
AYSPELIVHPVLDSPNAVHEVEK	2544.8	3	4.8045	0.4075
AYSPELIVHPVLDSPNAVHEVEKWLPR	3097.5	3	3.607	0.2847
AYTALHYLSHLSPGK	1658.9	3	3.7739	0.3623
AYTASLGETAVAFDFGPLAAVPK	2297.6	2	4.8143	0.4525
AYTGREFDDLSPEQQR	1913.0	2	4.8218	0.4244
AYTNFDAER	1087.1	1	2.7089	0.3427
AYTNFDAERDALNIETAIK	2156.3	2	4.5974	0.3726
AYTNFDAERDALNIETAIKTK	2385.6	3	5.3355	0.4274
AYVAVDGIPQGVLER	1587.8	3	3.6265	0.3431
AYVDDTPAEQMK	1368.5	2	3.7529	0.3149
AYVDDTPAEQMKAER	1724.9	2	3.9662	0.2054
AYVFERDQSVGDPK	1611.7	3	3.6625	0.384
AYVFERDQSVGDPKIDLIR	2222.5	3	4.7856	0.3327
AYVRDPYALDLIDKLLVLDPAQR	2659.1	3	4.1288	0.2295
AYVTKSPVDAGK	1236.4	2	3.4063	0.3861

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
AYVVLGQFLVLK	1350.7	2	3.7232	0.3401
AYYEFREEAYHSR	1721.8	2	3.4308	0.2337
AYYHLLEQVAPKGDEEGVPAVVIDMSGLR	3158.6	3	5.167	0.4404
CAGEVSAAANNNICGVGVAYNSK	2213.4	2	3.6904	0.2406
CCTESLVNR	1025.2	2	2.6839	0.1021
CDQDAQNPLSAGLQGACLMETVELLQAK	2948.3	3	3.2857	0.1525
CDVDIRKDLYANTVLSGGTTMYPGIADR	3046.4	3	4.0736	0.2606
CELAFLHTSHCLASGEVMISSLGDVK	2749.2	3	3.8228	0.2294
CESAPGCGVWQRPVIDNPNYK	2334.6	3	3.9214	0.2362
CESAPGCGVWQRPVIDNPNYKGK	2519.8	3	4.5466	0.2279
CEYLMELMTPAACPEPPPEAPTEDDHDEL	3245.6	3	4.586	0.2951
CGILTPGDDFLCLEGKEFNR	2228.5	2	3.0363	0.1106
CHDFQCALLANLFASEGQPGK	2250.5	2	3.9421	0.2953
CHDFQCALLANLFASEGQPGKVIEVK	2819.3	3	5.1334	0.2362
CLAALTECAASGDGNILALAVDASR	2406.7	2	4.6912	0.2015
CNPGGNSLKTNSEVIVAK	1832.1	2	3.6868	0.1169
CPEALFQPSFLGMESCGIHETTFNSIMK	3119.6	2	2.684	0.1723
CPPGVVPACHNSKDTVTISGPQAPVFEFVEQLRK	3653.2	3	5.404	0.2534
CPTDELSLTNCAVVNEKDFQSGQHVIVR	3104.5	3	4.9956	0.2641
CPVTVCGDVHGQFHDLMELFR	2404.8	3	4.3495	0.3482
CQFGLAQECLHHAQDYGGLLLLATASGNANMVNK	3590.1	3	6.1717	0.473
CSRHKVCIAQDSQTAVCISHR	2343.7	2	2.7056	0.1047
CTYLVLDEADRMLDMGFEPQIR	2617.0	3	3.2377	0.1693
CVHCVPLEPFDEDYLNHLEPPVK	2695.1	3	4.3232	0.2695
DAAAPAEPQAQHTR	1463.5	2	3.6115	0.28
DAAAVGNHVAK	1053.2	2	3.0307	0.2792
DAAGIAMEAIAFAR	1407.6	2	2.8519	0.1446
DAAGLECKPRPLHK	1535.8	2	3.279	0.2499
DAAGSGDKPGADTGR	1375.4	2	2.9325	0.2192
DAALATALGDKK	1174.3	2	3.7454	0.3066
DAALATALGDKKSLEGDLEDLKDQIAQLEASLAAAK	3685.1	3	3.2603	0.1083
DAALKQLEALEKEK	1586.8	3	3.7458	0.1952
DAASLESQLQDTQELLQEETR	2405.5	2	5.9463	0.4168
DAASLESQLQDTQELLQEETRQK	2661.8	3	4.0363	0.239
DAASVDKVLELK	1288.5	2	2.8294	0.1208
DAASVDKVLELKEHK	1682.9	2	4.1189	0.2794

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DAASVDKVLELKEHKLDGK	2096.4	2	4.7859	0.3514
DAASVEK	719.8	1	1.7741	0.1123
DAASVEKVLDQKEHR	1725.9	2	3.7849	0.2844
DAATIMQPYFTSNGLVTK	1958.2	2	3.8612	0.3533
DADEAKRVESQLK	1489.6	2	3.0053	0.113
DADPILISLR	1113.3	2	3.0814	0.1365
DADSITLFDVQQK	1480.6	2	3.399	0.2164
DADSITLFDVQQKR	1636.8	2	2.6815	0.1547
DADSQNPDAPEGK	1344.3	2	4.0625	0.233
DADSQNPDAPEGKR	1500.5	2	2.8773	0.3019
DADSSISVLEIHSQK	1629.8	2	2.4295	0.2056
DADVQNFVSFISK	1470.6	2	4.8796	0.4179
DADVQNFVSFISKDSIQK	2042.2	2	3.4462	0.1155
DAEASNVLVGEVDFLDTPFIAFVR	2625.9	2	2.5145	0.1678
DAEAWFTSR	1083.1	2	3.5051	0.3015
DAEAWFTSRTEELNR	1825.9	3	4.6051	0.2296
DAEAWFTSRTEELNREVAGHTEQLQMSR	3293.5	3	3.7381	0.2527
DAEDAMDAMDGAVLDGR	1752.9	2	5.4749	0.4742
DAEEAISQTIDTIVDMIK	1993.2	2	5.9365	0.4545
DAEERASLAGNRNSMVIHIPEEPR	2693.0	2	2.7947	0.1294
DAEFYEHR	1067.1	2	2.6607	0.257
DAEGIAEWLR	1160.3	2	4.085	0.2621
DAELAGSPELLEFLGTR	1819.0	2	4.7789	0.4838
DAEMPATEKDLAEDAPWKK	2146.4	3	3.7391	0.1806
DAENHEAQLK	1155.2	2	2.6729	0.1024
DAESIHQYLLQR	1473.6	2	4.0098	0.3585
DAFADAVQR	993.1	2	3.3156	0.1995
DAFENGEWGR	1181.2	2	2.5288	0.1134
DAFVAIVQSVK	1177.4	2	4.1596	0.3047
DAGAPTYMYEFQYRPSFSSDMKPK	2818.1	3	3.2975	0.1916
DAGDKDKEQELSEEDKQLQDELEMLVER	3321.5	3	6.5287	0.4115
DAGEGGLSLAIEGPSK	1501.6	2	4.3325	0.2874
DAGEGLLAVQITDPEGKPK	1939.2	2	4.7595	0.3045
DAGEGLLAVQITDQEGKPK	1970.2	2	4.5283	0.3488
DAGHPLYPFNDPY	1506.6	2	3.1478	0.2137
DAGIEPGPDTYLALLNAYAEK	2222.4	3	3.9145	0.2759

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DAGMQLQGYR	1139.3	2	3.8678	0.3787
DAGNGPQALR	999.1	2	2.9968	0.1868
DAGQISGLNVLR	1243.4	2	3.9936	0.3738
DAGTIAGLNVLR	1200.4	2	4.3692	0.2921
DAGTIAGLNVMR	1218.4	2	4.1521	0.4055
DAGTITGLNVLR	1230.4	2	3.3404	0.289
DAGVIAGLNVLR	1198.4	2	4.9982	0.3454
DAGYEFDICFTSVQK	1723.9	2	3.5515	0.3281
DAGYGGISLAVEGPSK	1521.7	2	3.5325	0.242
DAHKSEVAHR	1150.2	2	3.1241	0.3694
DAHLLVESK	1012.1	2	2.6715	0.2133
DAHNALLDIQSSGR	1497.6	2	4.5199	0.4236
DAHQSLLATR	1112.2	2	2.5188	0.2466
DAHSVLLSHIFHGR	1589.8	2	4.3965	0.4681
DAIAQAVR	844.0	2	2.7388	0.1965
DAIFKQFHFKDFNR	1814.0	3	3.4485	0.2529
DAILDALENLTAEELKK	1887.1	2	3.9947	0.3449
DAINQGMDEELERDEK	1893.0	2	3.0795	0.2634
DAINQGMDEELERDEKVFLLGEEVAQYDGAYK	3677.0	3	5.766	0.4999
DAINQGMDEELERDEKVFLLGEEVAQYDGAYKVSR	4019.4	3	5.1799	0.3459
DAKDKLESEMEDAYHEHQANLLR	2743.9	3	5.4288	0.389
DAKIYQIYEGTSQIQR	1914.1	2	5.0744	0.4792
DAKLDKAQIHDLVLVGGSTR	2137.4	2	6.3303	0.5007
DAKLDKSQIHDIVLVGGSTR	2153.4	2	6.5271	0.4342
DAKMDKAKIHDIVLVGGSTR	2155.5	3	4.3657	0.3449
DALGAQNASGER	1189.2	2	3.9165	0.3535
DALKSSVDAVK	1133.3	2	2.5551	0.1563
DALKTEFKANAEK	1465.6	2	4.1292	0.3825
DALLLIFANK	1118.4	2	3.8218	0.1779
DALNIETAIK	1088.2	2	3.5932	0.1845
DALNIETAIKTK	1317.5	2	2.8231	0.1428
DALNQATSQVESK	1391.5	2	4.4308	0.4837
DALSDLALHFLNK	1457.7	2	3.9123	0.2595
DALSSVQESQVAQQAR	1717.8	3	3.5385	0.2007
DAMPSDANLNSINK	1490.6	2	2.9609	0.1671
DANGNSFATR	1053.1	2	3.2546	0.3809

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DANLYISGLPR	1219.4	2	3.0963	0.3083
DANNGNLQLR	1115.2	2	2.9146	0.12
DAPEEEDHVLVLRK	1650.8	2	4.5234	0.3585
DAPQDFHPDR	1198.2	2	2.9001	0.2619
DAPQDFHPDRVK	1425.5	2	3.0028	0.163
DAPWTASSSEKAPDMSSSEEFPSFGAQVAPK	3243.5	3	6.139	0.475
DAQDVQASQAEADQQQTR	1990.0	2	6.8239	0.5485
DAQELYAAGENR	1337.4	2	4.3778	0.4368
DAQGLVLFDVTGQVR	1618.8	2	4.7237	0.4337
DAQGQPGLER	1071.1	2	2.7089	0.2505
DAQISEGASR	1034.1	2	2.5148	0.1857
DAQLIKELGLR	1256.5	2	3.3011	0.138
DAQSNAARDFVNYLVR	1840.0	3	4.7186	0.2877
DAQVVQVVLDGLSNILK	1812.1	2	2.4581	0.1417
DAQYAPGYDKVKDISEVVTPR	2352.6	3	3.8464	0.2214
DASDQNFDYMFK	1481.6	2	3.8234	0.1974
DASIVGFFDDSFSEAHSEFLK	2349.5	2	5.0785	0.5276
DASLMVTNDGATILK	1549.8	2	4.3429	0.3631
DASTLQSQK	978.0	1	1.8094	0.2694
DASTLQSQKAEGTGDAK	1707.8	2	4.1131	0.3868
DASVAEAWLLGQEPYLSSR	2093.3	2	5.616	0.3387
DASVPLIDVTNLPTPR	1708.9	2	3.1121	0.2747
DATLTALDRGQQQVFK	1792.0	2	3.7882	0.3538
DATNDQVTKDAAEAIKK	1819.0	2	4.5188	0.1944
DATNDQVTKDAAEAIKKHNVGVK	2453.7	3	5.5118	0.363
DATNVAAAFEEAVR	1464.6	2	2.6308	0.2655
DATNVGDEGGFAPNILENK	1962.1	2	5.9826	0.4275
DATNVGDEGGFAPNILENKEGLELLK	2745.0	3	4.4299	0.1273
DATNVGDEGGFAPNILENKEGLELLKTAIGK	3215.6	3	5.0876	0.3808
DATNVGDEGGFAPNILENSEALELVK	2703.9	2	5.4001	0.5047
DATNVGDEGGFAPNILENSEALELVKEAIDK	3260.5	3	4.6606	0.3275
DATNVGDEGGFAPNILENSEALELVKEAIDKAGYTEK	3910.2	3	5.3955	0.3274
DATSKDQLISELK	1448.6	2	2.9699	0.1397
DATSKVALVYGQMNEPPGAR	2105.4	3	3.7646	0.222
DAVGQPPRETDFMAFHQEHEVR	2597.8	3	4.8219	0.3729
DAVLLVFANK	1090.3	2	3.8804	0.2641

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DAVSNTTNQLESK	1407.5	2	4.0713	0.2788
DAVTTTVTGAK	1064.2	2	2.5587	0.1971
DAVTYTEHAK	1135.2	2	3.3453	0.3497
DAVTYTEHAKR	1291.4	2	2.8718	0.1931
DAVVYPILVEFTR	1522.8	3	4.702	0.3837
DAVVYPILVEFTREVEEEPGIHSLK	2871.2	3	3.8076	0.3186
DAYSGGAVNLYHVR	1522.6	2	3.8871	0.4
DAYTHPQFVTDVMKPLQIENIIDQEVQTLSGGELQR	4115.6	3	3.9918	0.188
DAYVSRLNAIYQNNLTK	1984.2	3	3.5792	0.1339
DCGEDGLCISDLVLDVR	1823.0	2	3.0615	0.1319
DCIGGCSDLVSLQQSGELLTR	2195.5	2	4.4997	0.195
DCIKDCTSALALVPFSIKPLLR	2404.9	3	4.0872	0.2306
DCYVGDEAQSK	1215.3	2	2.5234	0.1323
DDEAAAVALSSLIHALDDLDMVAIVR	2725.1	3	4.8008	0.3631
DDEFTHLYTLIVRPDNTYEVK	2569.8	3	3.7296	0.1922
DDETDEPKPK	1174.2	2	2.9515	0.2328
DDEVDVDGTVEEDLGK	1735.7	2	5.8845	0.4836
DDEVDVDGTVEEDLGKSR	1979.0	2	4.6292	0.4209
DDEVQVVR	960.0	2	2.9037	0.2028
DDFKRELDSITPEVLPGWK	2246.5	3	5.0992	0.3429
DDFSSGTSSR	1059.0	2	2.9314	0.2757
DDGLFSGDPNWFPK	1595.7	2	4.71	0.4355
DDGLFSGDPNWFPKK	1723.9	2	4.1914	0.42
DDGLSAAAR	875.9	2	2.635	0.1837
DDGSWEVIEGYR	1426.5	2	4.1948	0.3939
DDGTGQLLLPLSDAR	1571.7	2	3.6374	0.3319
DDGVFVQEVTQNSPAAR	1833.9	2	4.6644	0.2822
DDIENMVK	964.1	2	2.4842	0.1194
DDILNGSHPVSFDK	1544.6	2	4.0708	0.3515
DDILNGSHPVSFDKACEFAGFQCQIQFGPHNEQK	3809.2	3	3.7613	0.2267
DDKASYVAWGHSTVVNPWGEVLAK	2630.9	3	3.3698	0.1743
DDKHGSYEDAVHSGALND	1930.9	2	4.1228	0.4417
DDLVTVKTPAFAESVTEGDVRWEK	2693.9	3	4.6988	0.4416
DDNGKPYVLPSVR	1460.6	2	2.5704	0.1031
DDNMFQIGK	1068.2	2	2.4651	0.1884
DDNSNPGGKTDEPK	1474.5	2	2.9521	0.1744

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DDPLTNLNTAFDVAEK	1763.9	2	4.7319	0.3498
DDPVTNLNNAFEVAEK	1776.9	2	3.7797	0.3207
DDRLLQALVDILNEEN	1871.0	2	3.2427	0.1789
DDSIRPFKVETSDEEIHDLHQR	2667.8	3	5.5648	0.3502
DDSNESDVVESLDEIYHTGTFAQIHEMQDLGDKLR	4009.2	3	4.114	0.2494
DDSTKPKPEEEVKPVKEPDIKPQK	2763.1	3	5.0259	0.2383
DDTIYEDEDVKEAIR	1811.9	2	3.7575	0.3684
DDVGKNVHELEK	1383.5	2	3.6074	0.2742
DDVGKSVHELEK	1356.5	2	3.5211	0.2746
DDYELIDVLVNNAK	1621.8	2	2.8407	0.1531
DEAAYGELR	1024.1	2	3.2501	0.1351
DEDKDKVGNVEYFGLGNSPGFPLQYYPYYGK	3561.9	3	5.0533	0.3344
DEFEGLFKQPAENVNQYLTDPK	2583.8	3	6.1245	0.351
DEGNYLDDALVR	1380.4	2	3.8991	0.4025
DEHEHTYQDKEEVVLWMNTVGPYHNR	3228.5	3	6.4024	0.3206
DEILPTTPISEQK	1471.6	2	3.1257	0.1191
DELADEIANSSGK	1349.4	2	4.5925	0.3485
DELEEGAPSQAMLR	1546.7	2	3.3329	0.2477
DENSVELTMAEGPYK	1683.8	2	4.3633	0.3488
DEPSVAAMVYPFTGDHK	1865.1	2	4.0485	0.3136
DEQGFGGAFPAR	1252.3	2	3.3878	0.2325
DEQQISAAVEK	1218.3	2	2.6358	0.2144
DESLKVDEHLAK	1384.5	2	3.381	0.2207
DESLKVDEHLAKQDAQILYK	2344.6	3	5.2235	0.3366
DETKKTQNDVLHAENVK	1970.1	2	4.8504	0.3344
DETNYGIPQR	1193.2	2	3.7228	0.3387
DFAEKELFPIAAQVDKEHLFPAAQVK	2943.3	3	4.8675	0.4292
DFAEKELFPIAAQVDKEHLFPAAQVKK	3071.5	3	3.6269	0.1126
DFAVLEDHTLAHSLQEQEIEHHLASNVQR	3368.6	3	6.6315	0.4928
DFDPAVTEYIQR	1454.6	2	3.5838	0.2881
DFEGAVDLLDKLNHYLEDKPSPPPVKELR	3336.7	3	3.926	0.248
DFEQPLAISR	1176.3	2	3.1808	0.2469
DFFLANASR	1041.1	1	2.6148	0.2154
DFFNYLPLSSQDPAPVR	1967.2	2	4.1421	0.3164
DFFQSYGNVVELR	1574.7	2	3.5902	0.2613
DFGDLSFTPVPKDDLYNNLIVNPR	2751.0	3	3.7326	0.2949

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DFGDSLAR	880.9	1	2.2702	0.2913
DFGGAVQDYFK	1247.3	2	2.4482	0.1276
DFGGVTNGKPEDK	1364.4	2	2.8294	0.1531
DFGNYLFNFASAATK	1666.8	2	5.0832	0.3862
DFGSFDK	815.9	1	2.5199	0.1158
DFGSFDKFK	1091.2	2	3.0994	0.307
DFGSFDKFKEK	1348.5	1	3.7745	0.2757
DFHINLFQVLPWLK	1771.1	2	3.4631	0.1396
DFIATLEAEAFDDVVGETVGK	2227.4	2	5.3681	0.4773
DFIATLEAEAFDDVVGETVGKTDYIPLLDVDEK	3630.0	3	4.1648	0.3192
DFIATLEAEAFDDVVGETVGKTDYIPLLDVDEKTGNSESK	4333.7	3	4.5223	0.335
DFIETHYLNEQVK	1636.8	2	4.3485	0.222
DFIGVDSTGKR	1195.3	2	2.5586	0.1598
DFINWLIQTK	1278.5	2	3.9403	0.2396
DFKPGDLIFAK	1251.5	2	2.8526	0.3361
DFLAGGIAAAISK	1234.4	2	5.6618	0.3656
DFLAGGVAAAISK	1220.4	2	4.9623	0.3762
DFLAGGVAAAVSK	1206.4	2	4.4723	0.3005
DFLASHAHGPSAGGAPSLLLLLPCALLHR	2936.4	3	3.3032	0.1671
DFLDEYIFLAVGR	1558.8	2	2.4159	0.1587
DFLGKSDPFLEFFR	1718.9	2	3.621	0.2844
DFLLKPELLR	1244.5	2	2.7719	0.1697
DFLLPFLEEPMDTEADLQFRPR	2681.0	2	3.4842	0.208
DFLLQQTMLR	1265.5	2	3.2612	0.2067
DFLMLAQTHSK	1291.5	2	3.1541	0.3367
DFLTPPLLSVR	1258.5	2	2.5032	0.1385
DFMYVSQDPK	1230.4	2	3.8344	0.2472
DFMYVSQDPKDQLLLGPTYATPK	2629.0	2	5.1048	0.4271
DFNHINVELSLLGK	1599.8	3	4.6943	0.4355
DFNHINVELSLLGKK	1728.0	3	4.4046	0.2637
DFPEEVAIVEELGR	1603.8	2	5.1611	0.364
DFPEEVAIVEELGRR	1759.9	1	3.8954	0.3982
DFPLSGYVELR	1296.5	2	3.5453	0.3729
DFPVESVKLTEVPVEPVLTVHPESK	2777.2	3	3.3668	0.2463
DFQQYLPLVIEPLIK	1817.2	2	2.7778	0.2468
DFQSGQHVIVR	1286.4	2	3.0503	0.2856

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DFQYNEEEMKADKEEMNR	2307.5	3	3.5739	0.2551
DFSALESQLQDTQELLQEENR	2494.6	2	6.9208	0.4648
DFSALESQLQDTQELLQEENRQK	2750.9	3	4.9505	0.392
DFSALESQLQDTQELLQEENRQKLSLSTK	3380.7	3	5.3535	0.3806
DFSAPLTISR	1107.2	2	2.9076	0.2936
DFSEDQGYPDPPNPCPVGK	2063.2	2	4.4638	0.4659
DFSLEQLR	1008.1	2	2.9828	0.2001
DFSPSGIFGAFQR	1429.6	2	4.2109	0.5013
DFSPSSAK	838.9	1	1.7823	0.2134
DFSRYNYLSLDSAK	1679.8	2	2.8787	0.1832
DFSSVFQFLR	1246.4	2	3.6043	0.3295
DFSSVFQFLREEETF	1882.0	2	3.6538	0.3267
DFTATDLSEFAAK	1416.5	2	4.5927	0.4635
DFTATFGPLDSLNTR	1655.8	2	2.9799	0.2539
DFTFDLYR	1077.2	2	2.6297	0.2296
DFTFNKDGFRDFPAMVQELHQGGR	2814.1	3	4.8182	0.4341
DFTPVCTTELGR	1339.5	2	2.5144	0.2336
DFTSLENTVEER	1440.5	2	3.6019	0.2932
DFTSLENTVEERLTELTK	2126.3	2	3.1803	0.2392
DFTVSALHGDMDQK	1564.7	2	3.3472	0.2991
DFTVSALHGDMDQKER	1850.0	2	3.8746	0.44
DFTVSAMHGDMDQK	1582.7	2	2.7176	0.1355
DFTVSAMHGDMDQKER	1868.0	2	4.4825	0.4302
DFVAEPMGEKPVGSLAGIGEVLGK	2401.8	2	4.5923	0.4379
DFVAEPMGEKPVGSLAGIGEVLGKK	2529.9	3	4.6564	0.3795
DFVDHIDLVDPVDGVVLVDPEYLKER	2998.3	3	4.9979	0.3838
DFVNYLVR	1026.2	2	3.2122	0.2773
DFVSEQLTSLLVNGVQLPALGENKK	2701.1	3	4.57	0.3111
DFYMTDSISR	1235.3	2	2.4034	0.1154
DFYVVEPLAFEGTPEQK	1970.2	2	3.2956	0.2516
DGADFAK	723.8	1	2.1939	0.1434
DGADFAKWR	1066.2	2	2.7407	0.2335
DGADIHSDLFISIAQALLGGTAR	2342.6	2	5.2968	0.5186
DGAESLAAQR	1018.1	2	3.3931	0.262
DGAGFLINLIDSPGHVDFSSEVTAALR	2803.1	3	3.4837	0.225
DGALTLLLDEFENMSVTR	2025.3	2	3.8129	0.2749

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DGALTQLNVAFSR	1392.5	2	3.3242	0.272
DGANIVIAAK	972.1	2	3.8039	0.3271
DGDFENPVPYTGAVK	1609.7	2	4.388	0.3733
DGDILGKYVD	1095.2	2	2.9036	0.2177
DGEDQTQDTELVETR	1736.7	2	4.2425	0.248
DGEDQTQDTELVETRPAGDGTFQK	2638.7	2	4.3135	0.4125
DGEDQTQDTELVETRPAGDR	2233.2	3	3.4502	0.1109
DGEDQTQDTELVETRPAGDRTFQK	2737.8	3	4.5286	0.2952
DGEEAGAYDGPR	1237.2	2	3.9368	0.3773
DGEIVGLSGR	1003.1	2	3.2717	0.2275
DGELPVEDDIDLSDVELDDLGKDEL	2759.9	2	5.824	0.4943
DGENYVVLLDSTLPR	1691.9	2	3.5754	0.3019
DGEQIEQEEDDEKYIFSDDSSQLTIK	3063.1	3	4.1725	0.2893
DGETPDPEDPSR	1315.3	2	2.5366	0.1527
DGFGGLAAAR	935.0	2	3.3408	0.1913
DGFRDFPAMVQELHQGGR	2061.3	3	5.6804	0.2852
DGFSLASQLKSEELNLPEGK	2163.4	3	5.953	0.4563
DGGAWGTEQR	1077.1	2	3.0448	0.1183
DGGDKKEPTQAVVEEQVLDKEEPLPEEQR	3294.5	3	4.581	0.3181
DGGEALVSPDGTVTEAPR	1771.9	2	3.1354	0.2686
DGGLQNMELHGMIMLR	1816.2	2	4.9486	0.4043
DGGNPFAEPSELDNPFQDPAVIQHRPSR	3092.3	3	4.2518	0.3008
DGGNQEVEIAR	1188.2	2	3.8002	0.2349
DGGQEYVVK	995.1	2	3.2003	0.2909
DGGQTESNEEGKENR	1650.6	2	4.1065	0.351
DGGSGNSTIIVSR	1263.3	2	3.5087	0.3427
DGHNLISLLEVLSGDSLPR	2036.3	2	5.5212	0.4842
DGHPVVVNILIGR	1389.6	2	3.8008	0.3748
DGIEPGHIPGTVNIPFTDFLSQEGLEKSPEEIR	3624.0	3	5.2839	0.4526
DGIFSESTFNSPQGVAIMNNIIYVADTENHLIR	3668.0	3	5.252	0.4277
DGKALER	788.9	1	2.0387	0.209
DGKDQGVNVR	1088.2	2	2.5622	0.1456
DGKLVSESSDVLPK	1474.6	2	4.2712	0.3356
DGKNNVAFMSYFLQGK	1820.1	2	3.138	0.2186
DGKTLNDELEIIEGMK	1806.0	2	4.6023	0.435
DGKTLNDELEIIEGMKFDR	2224.5	3	5.2957	0.2985

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DGKYDLDFK	1101.2	2	2.5838	0.1324
DGKYDLDFKSPTDPSR	1842.0	3	3.4844	0.2451
DGKYSQVLANGLDNKLREDLER	2534.8	3	3.4209	0.314
DGLAFNALIHR	1227.4	2	2.7987	0.2807
DGLALGPGPFVTALEYATDTK	2137.4	2	4.1039	0.4259
DGLGGLPDIVR	1112.3	2	3.3862	0.2987
DGLILTSR	875.0	2	2.4724	0.135
DGLLPENTFIVGYAR	1665.9	2	3.0332	0.3316
DGLQGPGQRLHVLLGRAELRR	2342.7	3	3.5932	0.117
DGLQNEK	803.8	1	2.0092	0.1385
DGLQNEKNIVSTPVK	1642.8	2	4.512	0.3534
DGLSEAAAQSR	1105.1	2	3.8491	0.2925
DGLTDVYNK	1025.1	2	3.279	0.3232
DGLVVFGK	835.0	2	2.8969	0.2108
DGMAFNALIHK	1217.4	2	2.4639	0.1654
DGMDNQGGYGSVGR	1413.5	2	4.3265	0.3975
DGMVSFHDNPEKYNNPAMLHNIDQEMLK	3289.7	3	5.632	0.361
DGNASGTTLLEALDCILPPTRPTDKPLR	2966.4	3	4.751	0.3985
DGNASGTTLLEALDCILPPTRPTDKPLRLPLQDVYK	3923.5	3	5.382	0.4589
DGNDLHMTYK	1194.3	2	3.2371	0.3367
DGNVLLHEMQIQHPTASLIAK	2316.7	3	5.6949	0.5011
DGPAAGDSGPR	1000.0	2	2.81	0.1236
DGPGETDAFGNSEGK	1481.5	2	4.0152	0.4389
DGPGETDAFGNSEGKELVASGENK	2409.5	3	5.8794	0.456
DGPGETDAFGNSEGKELVASGENKIK	2650.8	3	3.798	0.2628
DGPGFYTTR	1014.1	2	2.4864	0.1904
DGPVRPQNAEEEKR	1625.7	3	3.4122	0.3143
DGQAMLWDLNEGK	1477.6	2	4.3035	0.2768
DGQEGITAFLQK	1307.4	2	2.8452	0.3124
DGQVINETSQHHDDLE	1837.8	2	4.0638	0.3936
DGQYLLTGGDR	1195.3	2	3.2221	0.313
DGRGALQNIIPASTGAAK	1740.9	2	5.1029	0.388
DGRISVAGVTSSNVGYLAHAIHQVTK	2682.0	3	6.512	0.4649
DGSAFEDGLRHPFIVNHPK	2137.3	2	3.8178	0.3233
DGSATLSGIQLATR	1390.5	2	3.5854	0.2852
DGSAVEIVGLSK	1175.3	2	2.9286	0.2575

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DGSDVIYPAR	1093.2	2	3.1993	0.2068
DGSFSDEMNTILDNLAAR	1970.1	2	5.1504	0.4661
DGSLASNPYSGDLTK	1525.6	2	3.8968	0.3535
DGSTTAGNSSQVSDGAAAILLAR	2163.3	2	6.0264	0.477
DGSVAIASKPR	1101.2	2	3.0973	0.1159
DGTFPLPIGESVTVTR	1689.9	2	2.99	0.3564
DGTGVVEFVR	1079.2	2	2.4356	0.1729
DGTIDFTPGSELLITK	1707.9	2	4.0704	0.2711
DGTVLCELINALYPEGQAPVKK	2359.7	2	3.4626	0.3223
DGTVTAGNASGVADGAGAVIIASEDAVK	2517.7	2	6.9096	0.5228
DGTVTAGNASGVADGAGAVIIASEDAVKKHNFTPLAR	3582.9	3	4.7511	0.3581
DGTYAVTYIPDK	1343.5	2	2.9084	0.2223
DGVGGLPTFLENSFIGSAR	1938.1	2	4.44	0.4642
DGVIEASINHEK	1312.4	2	2.6054	0.1919
DGVLTLANNVTPAKDVPPLSETEATPVPIKDMEIAQTQK	4133.7	3	5.6167	0.4437
DGVREVFEMATR	1410.6	2	2.798	0.2779
DGVVEITGK	918.0	1	2.5012	0.3368
DGVVEITGKHEER	1469.6	2	4.0251	0.3858
DGVVEITGKHEERQDEHGYISR	2555.7	3	4.4865	0.3139
DGVYVLDLAAK	1164.3	2	3.2688	0.3222
DGYADIVDVLNSPLEGPDQK	2146.3	2	4.947	0.5081
DGYAQILR	936.0	2	2.9278	0.2258
DGYDYDGYR	1124.1	2	2.4625	0.2147
DGYNYTLSK	1061.1	2	2.7668	0.2723
DHAISLSEPR	1125.2	2	2.6176	0.2241
DHANEELDELKR	1469.5	3	4.3597	0.4359
DHASIQMNVAEVDKVTGR	1971.2	3	6.2023	0.5558
DHATLNGALQFATK	1487.6	2	2.8354	0.1872
DHAVVVGVYRPLPK	1550.8	3	3.3819	0.286
DHAVVVGVYRPPPK	1534.8	2	4.2064	0.4507
DHDTFLAVR	1074.2	2	2.4739	0.1792
DHEKDAFEHIVTQFSSVPVSVVSDSYDIYNACEK	3861.2	3	5.1541	0.2327
DHFALDRPSETHADYLLR	2157.3	3	3.7102	0.4461
DHFEEAMR	1035.1	2	2.4712	0.1552
DHFQLGTLSHTLNIK	1724.9	2	4.8003	0.3343
DHGLLIYHIPQVEPR	1788.0	2	4.4626	0.415

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DHIKDSFHSLR	1355.5	3	3.2239	0.337
DHINLPGFSGQNPLRGPNDER	2334.5	3	3.2821	0.2379
DHLPPPEEEPLVLMCGPPPMIQYACLPNLDHVGHPTER	4244.9	3	3.3266	0.2248
DHPESYHSFMWNNFFK	2087.3	2	4.6307	0.4113
DHPHTAAYLQELGR	1608.7	2	2.9245	0.3189
DHPLPEVAHVK	1242.4	3	3.5669	0.3238
DHQEVETEGPESADTGDKSESPDEANVGKHPK	3421.5	3	5.3455	0.4227
DHSAIPVINR	1122.3	2	2.4332	0.3492
DHSKPISNPSDNKELPK	1907.1	2	3.7617	0.1814
DHSPDLYSLELAGLDEIGKR	2229.4	3	4.1012	0.4294
DHSSLLQGTLAEHFGVLPGPR	2232.5	3	3.3811	0.2432
DHTDQTSETAPDASVPPSVKPK	2308.4	3	4.1451	0.1976
DHYEATAMHR	1231.3	2	2.8919	0.3044
DIAANEENRK	1160.2	2	2.8645	0.1982
DIAQQLQATCTSLGSSIQGLPTNVKDQVQQAR	3400.8	3	5.7839	0.4781
DIASTPHELYR	1302.4	2	2.7029	0.2018
DICNDVLSLLEK	1362.6	2	4.6357	0.3208
DIDEVSSLLR	1147.3	2	3.6026	0.2663
DIDIHEVR	997.1	2	2.9325	0.2214
DIDKAITISSALQAGTVWVNCYGVVSAQCPFGGFK	3648.2	3	6.7192	0.482
DIDNLVQR	973.1	2	2.8678	0.1793
DIDPQNDLTFLR	1447.6	2	3.9141	0.4171
DIDSFVPSK	1008.1	2	2.5818	0.2363
DIDTAAK	733.8	1	2.4081	0.2495
DIDTHTHR	995.0	2	2.6017	0.2565
DIEDVFYK	1029.1	2	2.6669	0.1617
DIEEIIDELK	1217.3	2	3.1271	0.1013
DIELVMSQANVSR	1462.7	2	2.7636	0.1016
DIEQSIKSETSGSFEDALLAIVK	2481.7	3	4.2017	0.4
DIETFYNTSIEEMPLNVADLI	2428.7	2	4.177	0.3978
DIETFYNTTVEEMPMNVADLI	2446.7	2	3.5774	0.2699
DIFNKGFGFGLVK	1442.7	2	3.8366	0.1689
DIFNKGFGFGLVKLDVK	1898.2	3	3.4944	0.291
DIGAIAQVHAENGDIIAEEQQR	2378.5	3	4.0111	0.206
DIGEGNLSTAAAAALAAAAVK	1886.1	2	4.7443	0.3934
DIGFIKLD	921.1	2	3.1938	0.2694

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DIGIWYNILRGIGKLAVIINAFVISFTSDFIPR	3724.4	3	3.4552	0.165
DIHELFVPENKLDHVR	1962.2	3	3.5353	0.2746
DIHTLAQLISAYSLVDPEK	2114.4	2	2.9797	0.2946
DIHTLAQLISAYSLVDPEKAK	2313.6	2	6.2757	0.4734
DIIALNPLYR	1188.4	2	3.1451	0.2458
DIIHDPGRGAPLAK	1460.7	2	2.5664	0.1789
DIILQSNPLLEAFGNAK	1844.1	2	2.6459	0.2742
DIISDTSGDFRK	1354.4	2	3.0881	0.1967
DIISIAEDEDLR	1389.5	2	3.8209	0.3742
DIISIAEDEDLRVHFEESSKLEDLLR	3073.4	3	5.5009	0.4219
DIKDTTVGTLSQR	1434.6	2	4.1884	0.371
DIKPAATHHYLVVPK	1690.0	3	3.4355	0.2037
DIKPDNVLLDVNGHIR	1819.1	3	3.6422	0.2029
DIKPQLELIEDEEKLKETEPVEAYVIQK	3328.8	3	4.8221	0.358
DILAQVKPLGPQLADPEVFLPQGELLDSP	3101.5	3	3.7963	0.2549
DILIQYDR	1036.2	2	2.6801	0.124
DILIVVGNEIIEAPMAWR	2040.4	3	5.1599	0.3236
DILVATDVAGR	1130.3	2	2.7377	0.2259
DIMEDTIEDKLDTK	1666.8	2	2.6867	0.1088
DIMEIEGEPAPDHR	1609.7	2	2.9484	0.2594
DINAVLIDMER	1289.5	2	3.0465	0.2764
DINAYNCEEPTEK	1526.6	2	3.488	0.3007
DINAYNCEEPTEKLPFPIIDDR	2593.9	3	3.7635	0.1372
DINEIDINMNDPLFTK	1893.1	2	5.0892	0.4078
DINLASFIEQVAVSMT	1739.0	2	4.2243	0.4625
DINLQDEDWNEFNDINK	2123.2	2	4.724	0.3837
DINQEVYNFLATAGAK	1754.9	2	5.4737	0.4845
DIPGLTDTTVPR	1285.4	2	2.7067	0.3105
DIPNMFMDSAGSVSK	1599.8	2	4.8599	0.5934
DIPVLVATDVAAR	1340.6	2	3.8865	0.4068
DIPVTAQPSKDVHVVK	1734.0	2	2.8885	0.2959
DIPVVHQLLTR	1291.5	2	2.9083	0.2796
DIQDLKFGVEQDVDMVFASFIRK	2702.1	3	3.537	0.3059
DIQENDEEAVQVK	1517.6	2	4.0257	0.2829
DIQENDEEAVQVKEQSILELGSLLAK	2900.2	3	5.1708	0.2896
DIQNTQCLLNVEHLSAGCPHVTLQFADSK	3183.6	3	3.9475	0.2306

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DIQNTQCLLNVEHLSAGCPHVTLQFADSKGDVGLGLVK	4022.6	3	5.4659	0.4481
DIQTLLSR	946.1	2	2.5504	0.1784
DIRGETLNHHVNAR	1632.8	2	2.7944	0.1395
DIRPGAAFEPTYIYR	1770.0	2	2.6591	0.1595
DISEASVFDAYVLPK	1654.8	2	4.2943	0.3373
DISEVVTPR	1016.1	2	2.5097	0.1564
DISILQCHGDCDPLVPLMFGSLTVEK	2832.3	3	3.5688	0.1063
DISPVLKDPASFR	1445.6	2	3.2102	0.3193
DISQAYYTVYKK	1479.7	2	3.3062	0.3106
DISTLNSGKK	1063.2	1	2.6372	0.2049
DISTNYYASQK	1290.4	2	3.6161	0.338
DISTNYYASQKK	1418.5	2	3.7442	0.3273
DISTTLNADEAVAR	1476.6	2	3.9076	0.3746
DITDTLVAVTISEGAHHLDLR	2277.5	3	3.7498	0.1277
DITPLQVVLPNTALHLK	1873.2	2	3.971	0.307
DITYFIQQLLR	1410.6	2	4.1477	0.3416
DITYFIQQLLRDREVGIPPEQSLETAK	3161.6	3	3.9892	0.2238
DIVHSGLAYTMER	1492.7	2	2.946	0.3666
DIVIAETLEDLDR	1502.6	2	4.7493	0.406
DIVLVAYSALGSQR	1492.7	2	3.6352	0.3066
DIVPGDIVEIAVGDKVPADIR	2192.5	2	4.5219	0.4139
DIVPGDIVEVAVGDKVPADIR	2178.5	2	4.9008	0.4709
DIVQFVPFR	1121.3	2	2.8779	0.2448
DIVQFVPYR	1137.3	2	2.6908	0.2312
DIVVLGVEKK	1100.3	2	2.7416	0.1191
DIWFGTPEGEFVSMGVISDGNSYGVPDDLLYSFPVVIK	4152.6	3	4.0012	0.1024
DKAGPHKEIYPYVIQELRPTLNELGISTPEELGLDKV	4164.7	3	5.7165	0.388
DKAILDIERPDLMIYEPHFTYSLLEHVELPR	3755.3	3	5.6636	0.3409
DKAKETADAITK	1291.4	2	3.4418	0.2766
DKANMQHR	1000.1	2	2.5351	0.1892
DKAPGQLECETAIAALNSCLRDLDQASLAAVSQQLAPR	3969.5	3	4.3128	0.3379
DKAPVQPQQSPAAAPGGTDEKPSGK	2462.7	3	4.3699	0.2836
DKASDASDKQR	1221.3	2	2.5068	0.1853
DKASQEGGDVLGAR	1403.5	2	2.9144	0.1254
DKDAIYGHPLFPLLALVFEK	2287.7	3	4.543	0.2034
DKDAYSSFGSR	1233.3	2	2.5506	0.2444

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DKDDQEWESPSPPKPTVFISGVIAR	2800.1	3	3.8981	0.2536
DKDFAIDIIK	1178.4	2	3.1642	0.1931
DKDPVNK	815.9	1	2.453	0.1315
DKDTDKFK	997.1	1	2.1257	0.2901
DKEEKESSR	1108.1	2	2.853	0.1164
DKENALMPNWLHLPVGYHGR	2348.7	3	4.0663	0.3376
DKETTENENTK	1309.3	2	3.3441	0.3088
DKETTENENTKFEVR	1840.9	2	4.9256	0.4028
DKEVGNLYDMFHTR	1725.9	2	3.7301	0.2976
DKEVNSQVYSR	1325.4	2	2.9858	0.2029
DKEVQQLQENLDSTVTQLAAFTK	2607.9	3	4.1686	0.2258
DKFSFDLGKGEVIK	1583.8	2	3.954	0.3493
DKGEYTLVVK	1152.3	2	2.4331	0.1143
DKGIVVGIKVDKGVVPLAGTDGETTTQGLDGLSER	3526.9	3	4.8771	0.3395
DKGLQTSQDAR	1219.3	2	2.506	0.2239
DKGLVEKLTAYAMTIPFVR	2153.6	3	3.8686	0.3048
DKGNEVNAER	1132.2	2	2.7337	0.2524
DKGTGREQQIVIQSSGGLSKDDIENMVK	3034.3	3	5.7926	0.3778
DKIIFLHGK	1071.3	2	2.4934	0.1618
DKIIVNDR	973.1	1	2.5266	0.1864
DKILGATIENSR	1317.5	2	3.6165	0.1985
DKLDGNELDLSLSDLNEVPVKELAALPK	3037.4	3	6.4506	0.47
DKLESEMEDAYHEHQANLLR	2429.6	3	6.1345	0.4455
DKLEYFEERPFAAASIGQVHLAR	2649.0	3	5.7356	0.4429
DKLKSELVANNVTLPAGEQR	2183.5	3	5.1375	0.248
DKLLAAVKEDAAATK	1544.8	2	4.0246	0.3204
DKLNNLVLFDK	1319.5	2	3.5559	0.3217
DKLNNLVLFDKATYDKLCK	2242.6	3	3.3204	0.3431
DKLPQPVQPDPVSHCK	1789.0	2	3.2527	0.2875
DKLTELQLR	1116.3	2	2.7354	0.1276
DKLVGAIVYYDGQHNDAR	2035.2	2	5.9008	0.4371
DKLVYVHTNGPK	1371.6	2	2.7563	0.2002
DKMMNGGHYTYSENR	1804.0	2	4.984	0.4417
DKMMNGGHYTYSENRVEK	2160.4	2	4.0425	0.261
DKMMNGGHYTYSENRVEKDGLILTSR	3016.4	3	3.357	0.1313
DKNALQNIILYHLTPGVFIGK	2355.8	3	3.3608	0.2394

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DKNEATVSTGK	1150.2	2	3.0216	0.2629
DKPELQFPFLQDEDTVATLLECK	2681.0	3	3.8576	0.359
DKPHVNVGTIGHVDHGK	1811.0	2	3.9864	0.4018
DKPHVNVGTIGHVDHGKTTLTAAITK	2712.1	3	4.3676	0.3658
DKPLKDVIIADCGK	1515.8	2	4.6227	0.3922
DKPNPQLIYDDEIPSLKIEDTVFHVFDK	3317.7	3	4.7242	0.36
DKPSGDTAAVFEEGGDVDDLLDM	2397.5	2	5.2044	0.5087
DKPSGDTAAVFEEGGDVDDLLDMI	2510.7	2	4.5747	0.3836
DKPTAAETTLAVR	1373.5	2	3.5715	0.3788
DKPVKTETKPSVTEK	1687.9	2	3.532	0.3392
DKPVYDELFYTLSPINGK	2100.4	2	2.8315	0.2432
DKRPEGYNLKEEDGR	1806.9	3	3.2178	0.2365
DKRPLSGPDVGTPQPAGLASGAK	2220.5	3	3.559	0.3028
DKSFLAMVVDIVQELK	1836.2	2	4.2273	0.4317
DKSFLAMVVDIVQELKQQNPR	2459.9	3	3.2692	0.1182
DKSYQDAVLEDIFKK	1800.0	3	4.1959	0.2821
DKTSPFELYQFFVR	1778.0	2	3.1593	0.2445
DKTYSYLNKLPVK	1569.8	3	4.3568	0.3112
DKTYSYLNKLPVKSEYPSIK	2374.7	3	4.0488	0.3341
DKVAGHSLGYGFVNYVTAK	2027.3	2	5.4403	0.3946
DKVFQGNFDNDTHRK	1821.9	2	3.5838	0.3253
DKVLTDSGSLDSTIPGIENTITVTTEQLTTASFPVGSKK	4053.5	3	6.1274	0.4137
DKVMSEFNNNFR	1501.6	2	3.5178	0.2546
DKVVALAEGR	1058.2	2	2.7739	0.2108
DKYEPAAVSEQGDKK	1665.8	2	4.4847	0.3868
DKYGKDATNVGDEGGFAPNILENSEALELVK	3295.6	3	5.2382	0.1892
DKYGKDATNVGDEGGFAPNILENSEALELVKEAIDKAGYTEK	4501.9	3	3.5733	0.1002
DKYPNLQVIGGNVVTAAQAK	2087.4	3	5.0339	0.369
DLAAFDKSHDQAVR	1573.7	2	2.6897	0.1053
DLAALEDKVK	1102.3	2	2.6456	0.1889
DLAALGDKVNSLGETAER	1860.0	2	5.1295	0.5035
DLADELALVDVIEDKLKGEMMDLQHGSLFLR	3516.0	3	5.4327	0.4859
DLAEDLYDGQVLQK	1607.7	2	3.5468	0.2003
DLAEITTLDR	1147.3	2	3.6847	0.2445
DLAEVGEGGGHSQAR	1483.5	2	3.5757	0.3455
DLAGIIAIQR	1070.3	2	3.2885	0.1869

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DLAGSIIGK	874.0	1	1.9731	0.2502
DLAGSIIGKGGQR	1272.4	2	2.9145	0.2381
DLAKDITSDTSGDFR	1641.7	2	4.2302	0.4096
DLANIAEVEVSIPAKLHNSLIGTK	2533.9	3	3.5357	0.1196
DLANQVTGWLDGSAIYGSSHSWSDALR	2908.1	3	3.2753	0.2718
DLAQALINR	1014.2	2	3.2931	0.1723
DLAQYDAAHHEEFKR	1830.9	2	4.9108	0.4799
DLASVQALLR	1086.3	2	2.6404	0.1428
DLATDLSLIEVK	1317.5	2	4.2401	0.259
DLAVAGPEMQVK	1258.5	2	3.376	0.2871
DLDEDEILGALTEEELR	1961.1	2	4.6971	0.2184
DLDELSRYPEDKITPENLPQILLQLK	3082.5	3	5.9259	0.3357
DLDELSRYPEDKITPENLPQILLQLKR	3238.7	3	6.0108	0.4031
DLDIIDNYDYSHTVK	1811.9	2	4.7043	0.354
DLDKADSMIR	1164.3	2	2.4236	0.1781
DLDLKKPIYQR	1389.6	2	2.8812	0.2409
DLDNAGELGR	1060.1	2	3.0776	0.1492
DLDQASLAAVSQQLAPR	1784.0	2	4.3936	0.3183
DLDRIAGQVAAANK	1442.6	2	4.0232	0.1992
DLDRIAGQVAAANKKH	1707.9	2	4.041	0.2768
DLEADIIGDTSGHFQK	1746.9	2	5.3816	0.4111
DLEAEHVEVEDTTLNR	1871.0	2	5.2863	0.548
DLEAHIDSANK	1213.3	2	3.9359	0.3649
DLEAHIDSANKNR	1483.6	2	4.0161	0.3259
DLEAHIDSANKNRDEAIK	2040.2	2	4.1649	0.3703
DLEASIAR	875.0	2	2.8353	0.1093
DLEDKEGEIQAGAK	1503.6	2	4.0076	0.3243
DLEDSLAR	919.0	2	2.5863	0.1869
DLEEAEGR	918.9	1	2.1271	0.1206
DLEEELDMKDR	1393.5	2	2.5205	0.1856
DLEEFFSTVGK	1272.4	2	3.6569	0.2502
DLEFTIYDDDDVSPFLEGLEERPQR	3000.2	3	3.7142	0.2839
DLEFTIYDDDDVSPFLEGLEERPQRK	3128.3	3	3.8121	0.2703
DLEGLHRAEQSLHDLQER	2147.3	3	4.2326	0.3124
DLEGLSQRHEEKVAAYDKLEK	2459.7	3	5.126	0.3043
DLEGSDIDTR	1121.1	2	3.3955	0.2083

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DLEIQALHAR	1166.3	2	3.3697	0.2385
DLEKPFLLPVEAVYSVPGR	2130.5	2	5.0578	0.4028
DLELLIQTATR	1273.5	2	4.0558	0.3746
DLEPLKRTEEEPLEEPLDEALVR	2722.0	3	4.871	0.2372
DLEQAISQR	1060.1	2	2.8365	0.1677
DLEQPTYR	1022.1	2	2.5248	0.2468
DLESLREYVESQLQR	1866.0	2	4.3551	0.2566
DLFAEGLLEFLRPAVQQLDSHVHAVR	2962.4	3	5.3593	0.4787
DLFDPIIEDR	1233.4	2	2.4014	0.2667
DLFEDELVPLFEK	1594.8	2	4.556	0.3678
DLFHGATFVPR	1260.4	2	2.4372	0.2066
DLFLHHKK	1038.2	2	2.5736	0.1407
DLFQVAFNR	1110.2	2	3.6151	0.3868
DLFQVIYNVK	1239.4	2	2.597	0.1416
DLFSTFTITR	1201.4	2	3.5104	0.4167
DLGAQDAPAIAFGGSYGGMLSAYLR	2502.8	3	4.2948	0.3701
DLGDVGPPIPSPGFSSFPGVDSSSSFSSSSR	3058.2	3	4.986	0.4166
DLGEEALNEYLK	1394.5	2	3.246	0.1417
DLGEELEALKTELEDTLDSTAAQQELR	3019.2	2	5.389	0.542
DLGEELEALRGELEDTLDSTNAQQELR	3046.2	3	6.3477	0.4776
DLGHAQMVVDELFSSHSDLDSDSELDR	3019.2	3	3.5469	0.2434
DLGKFQVATDALK	1406.6	2	4.0303	0.283
DLGLAADLPGGAEGAAAQPQAVLRQPELR	2886.2	3	4.3438	0.3912
DLGLAQDSATSTK	1307.4	2	4.2347	0.2865
DLGLAQDSATSTKSPILLGSLAHQIYR	2857.2	3	7.0245	0.5331
DLGLSESGEDVNAAILDESGK	2120.2	2	3.6881	0.3177
DLGLSESGEDVNAAILDESGKK	2248.4	2	5.0902	0.4733
DLGMVTILVQDTDTALKELEK	2333.7	2	4.5429	0.2812
DLGPHAEGQLAPR	1361.5	2	2.4054	0.2139
DLGTESQIFISR	1366.5	2	4.0766	0.4064
DLHDQFQHQLR	1437.5	2	3.3181	0.2042
DLHIQSHISENRDEVEAVK	2220.4	2	5.5888	0.4453
DLHIQSHISENRDEVEAVKNLYPSYK	3086.4	3	5.9998	0.3385
DLIADLKYELTGK	1479.7	2	4.2922	0.3877
DLIADLKYELTGKFER	1912.2	3	3.8135	0.2472
DLIGHIVEFSQDQHGSR	1939.1	3	3.6532	0.1887

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DLIHDQDEDEEEEEGQR	2087.0	2	3.0376	0.204
DLIHGAPVGKPAANR	1516.7	2	2.6899	0.2804
DLIQDQNMDEK	1349.5	2	2.7624	0.2421
DLISHDEMFSDIYK	1713.9	2	4.3999	0.418
DLISHDEMFSDIYKIR	1983.2	3	4.8771	0.4224
DLISNSPR	902.0	2	2.6741	0.1569
DLKPENILLDEEGHIK	1864.1	3	5.2732	0.2093
DLKPENLLLASK	1341.6	2	3.1348	0.2613
DLKPENVLLDAHMNAK	1809.1	3	4.3526	0.2687
DLKPSNIFLVDTK	1490.7	2	2.676	0.2002
DLKPSNILYVDESGNPESIR	2247.4	2	3.0523	0.154
DLKVENLLLSNQGTIK	1786.1	2	3.8251	0.2394
DLLDDLKSELTGK	1447.6	2	3.9446	0.3516
DLLDDLKSELTGKFEK	1852.1	2	4.6585	0.4111
DLLDLLVEAK	1129.3	2	2.8124	0.1319
DLLDTVLPHLYNETK	1772.0	2	4.5667	0.3647
DLLEVADVLEK	1244.4	2	3.854	0.2871
DLLFQALGR	1033.2	2	3.7462	0.3062
DLLGETLAQLIR	1342.6	2	4.3245	0.1385
DLLGTVWGGPANLEAIAK	1826.1	2	2.4847	0.1765
DLLHPSLEEEK	1310.4	2	2.7408	0.1938
DLLHPSLEEEKKK	1566.8	3	3.4896	0.2878
DLLHPSPEEEK	1294.4	2	3.0836	0.1428
DLLHPSPEEEKR	1450.6	2	2.7783	0.1957
DLLHPSPEEEKRK	1578.8	2	3.2282	0.2602
DLLIAYYDVDYEK	1620.8	2	5.0128	0.4434
DLLLNTMSQEEK	1421.6	2	3.1078	0.2132
DLLNGVKPQDIDFATTATPTQMKEMFQSAGIR	3526.0	3	4.4491	0.2249
DLLPSDMAVALLEAQAGTGHIIDPATSAR	2935.3	3	4.5567	0.4076
DLLQIIFSFSK	1311.6	2	3.3798	0.2745
DLMLMSHLQDNIQHADPPVQILYNR	2963.4	3	4.0948	0.1126
DLMTDLKSEISGDLAR	1765.0	3	5.0189	0.3926
DLMVGDEASELR	1335.5	2	3.2062	0.2438
DLNFEVR	893.0	2	2.5111	0.1467
DLNKDGKLDKDEIR	1659.8	2	4.4724	0.3766
DLNPDVNVFQR	1317.4	2	3.4582	0.3071

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DLNPEDFWEIIGELGDGAFGK	2323.5	2	5.4135	0.4417
DLNQLFQQDSSSR	1538.6	2	3.4654	0.3133
DLNSDMDSILASLK	1522.7	1	4.4458	0.4328
DLNSDMDSILASLKLPPKSEVSSDEDIQFR	3351.7	3	5.4222	0.3221
DLPEEYLSAIYNEIAGK	1926.1	2	2.975	0.2099
DLPEHAVLK	1022.2	1	1.9711	0.2165
DLPELALDTPRAPQLVGQFIAR	2421.8	3	4.1755	0.421
DLPETLNELHLDHNK	1788.9	2	3.1311	0.1675
DLPETLNELHLDHNKIQAIELEDLLR	3083.4	3	5.2763	0.3927
DLPGALDEKELIEK	1570.8	2	3.4047	0.1348
DLPLAQGIKFQ	1230.4	2	3.2471	0.2754
DLPLLLFR	987.2	2	2.7834	0.1557
DLPQDPVELAMFGLR	1702.0	2	2.8571	0.2397
DLPQTMDQIQDQFNDLVISDGSSLEDLVVK	3364.7	3	5.1053	0.2546
DLPSAGEEILEVESEPR	1871.0	2	3.7278	0.2967
DLPVTEAVFSALVTGHAR	1884.1	2	4.7669	0.4668
DLQAHINHR	1104.2	2	2.6419	0.1025
DLQGRDEAGEER	1375.4	2	2.5055	0.152
DLQGRDEQSEEKKK	1690.8	3	4.081	0.2159
DLQHPNEFIR	1269.4	2	2.5398	0.192
DLQLVLPDYFPER	1605.8	2	3.1325	0.2961
DLQNVNLTLR	1186.3	2	4.0442	0.2311
DLQQYQSQAK	1209.3	2	3.5428	0.2194
DLQSNVEHLTEK	1413.5	2	2.619	0.1217
DLRNDEHTR	1156.2	2	2.4633	0.2183
DLRQDEHTR	1170.2	2	2.4412	0.2168
DLSAAGIGLLAAATQSLSMPASLGR	2372.7	2	4.799	0.44
DLSDGIHVVK	1083.2	2	2.4838	0.2489
DLSDGIHVVKDAR	1425.6	2	2.7726	0.2591
DLSEELEALKTELEDTLDTTAAQQELR	3063.3	2	5.3174	0.4872
DLSELGSVR	976.1	2	3.2045	0.126
DLSENNDQRQQLQALSEPQPR	2467.6	3	4.2046	0.325
DLSFKDTQLKEYEELLASVR	2385.7	3	4.9689	0.4667
DLSKPIGVVNPK	1267.5	2	2.5056	0.1116
DLSLEEIQKKLEAAEER	2002.2	3	4.7188	0.3287
DLSLLSHGGR	1055.2	2	2.8638	0.2948

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DLSLNKLGIQTDDKGHIIVDEFQNTNVK	3156.5	3	6.5073	0.4936
DLSQVRDHLAEAKEK	1739.9	3	3.365	0.1036
DLSSHQLNEFLAQTLQR	2001.2	2	2.7812	0.2004
DLSSSEKQEHVK	1387.5	2	3.8251	0.3284
DLSSSEPVHAK	1170.3	2	3.0435	0.2012
DLSSVQTLLTK	1205.4	2	3.5213	0.2947
DLSTVEALQNLK	1331.5	2	3.7	0.268
DLTALSNMLPK	1203.4	2	3.192	0.2373
DLTDYLMK	999.2	1	2.9391	0.2685
DLTEYLSR	997.1	2	3.032	0.2131
DLTGQVPTPVVK	1254.5	2	4.2091	0.3783
DLTQLPVITSNTIVR	1670.9	2	2.696	0.2407
DLTQNTVVSINFKDPQFAEDYIFK	2834.1	3	4.2163	0.1641
DLTQTASSTAR	1151.2	2	3.1325	0.3173
DLVDYITTHYK	1368.5	2	2.4264	0.2225
DLVEAVAHILGIR	1406.7	2	3.4059	0.3598
DLVGELGTALR	1144.3	2	3.9822	0.3559
DLVGMGHHFLPSEPTKWNVEDVYEFIR	3217.6	3	3.4416	0.2466
DLVHSNKKEQEFR	1630.8	2	3.4904	0.3447
DLVPDLSNFYAQYK	1673.8	2	3.9094	0.4594
DLVSSLTSGLLTIGDR	1647.9	2	4.5135	0.423
DLVSSLTSGLLTIGDRFGGALDAAAK	2549.9	3	4.6013	0.3513
DLVVLLFETALLSSGFSLEDPQTHSNR	2990.3	3	3.27	0.2243
DLWASKNENEEILERPAQLANAR	2668.9	3	3.3362	0.2885
DLYANNVLSGGTTMYPGIADR	2229.5	2	3.7096	0.2556
DLYANNVMSGGTTMYPGIADR	2247.5	3	3.9735	0.2421
DLYANTVLSGGTTMYPGIADR	2216.5	2	5.9896	0.5538
DLYDDKDGLRKEELNAISGPNEFAEFYNR	3420.6	3	4.8791	0.4189
DLYEDELVPLFEK	1610.8	2	4.1552	0.3234
DLYIDRPLPYLIGSK	1764.1	2	2.7412	0.1831
DLYLENPEIK	1234.4	2	3.5006	0.1802
DLYLENPEIKIR	1503.7	2	3.1686	0.2692
DMAEAHKEAMSR	1376.5	2	3.6075	0.3071
DMAGAQAAAVALNEEFLR	1878.1	2	4.4329	0.4011
DMAIATGGAVFGEEGLTLNLEDVQPHDLGK	3099.4	3	5.6363	0.4103
DMALATKTEVALAK	1462.7	2	3.522	0.2288

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DMALSDVTEESEIISELVQTVSLGGNYLLNIGPTK	3738.2	3	3.5652	0.1435
DMANPTALLLSAVMMLR	1848.3	2	3.9489	0.3478
DMDDAYDRLTR	1371.5	2	2.5398	0.1341
DMDLTEVITGTLWNLSSHDSIK	2476.7	2	5.3854	0.4497
DMDLVEVNEAFAPQYLAVER	2310.6	2	6.1888	0.4725
DMDSIIAEVKAQYEDIANR	2182.4	2	4.4488	0.4309
DMEALLPLMNMVIYSIDK	2097.5	2	2.8163	0.2688
DMESPTKLDVTLAK	1548.8	2	3.7616	0.3542
DMGGYSTTTDFIK	1436.6	2	2.8699	0.3185
DMIDLEANFEKIENELKEINTNQEALKR	3349.7	3	6.8683	0.3798
DMIILPEMVGSMVGVYNGK	2054.5	2	5.5373	0.485
DMILNFAEQNSFK	1557.8	2	3.2813	0.147
DMLGGNGISDEYHVIR	1777.0	2	4.6329	0.3324
DMLLANKVPAAAR	1370.6	2	3.4931	0.1922
DMLLANPHELSLLK	1594.9	2	3.0073	0.1828
DMMELVQPSISGVDLDKFR	2181.5	2	3.3858	0.2304
DMNQVLDAYENKKPFYLYTGR	2566.9	3	4.914	0.2788
DMQGLSLDAASQPSKGGLLER	2174.4	3	3.3721	0.249
DMQGTEEEKAPLALFGHTLVASLEDMK	2962.3	3	4.2714	0.2457
DMQHLTVLTSK	1273.5	2	3.0911	0.3258
DMQHLTVLTSKR	1429.7	3	3.8945	0.3807
DMQHLVVWTSEYDPLANNPGWK	2601.9	3	4.5591	0.2926
DMQHLVVWTSEYDPLANNPGWKK	2730.1	3	4.2725	0.2396
DMQPSMESDMALVKDMELPTEKEVALVK	3166.7	3	3.9481	0.1035
DMRQTVAVGVIK	1317.6	2	2.8351	0.1562
DMSGHYQNALYLGDVSER	2056.2	2	5.4016	0.4353
DMSISNTTMDEFRQHLQATGVSLGGVDLTVR	3380.8	3	4.2461	0.2895
DMSLYASLTSEKVQSLEGEKLSPK	2642.0	3	3.2443	0.1386
DMTLPPETNVILTK	1572.8	2	2.8797	0.1776
DMTMFVTASKDNTAK	1660.9	2	4.1031	0.3622
DMTSEQLDDILK	1408.6	2	2.4248	0.147
DMTSEQLDDILKYHTEIVFAR	2525.8	3	3.6053	0.1418
DMVGIAQTGSGK	1164.3	2	3.6272	0.3582
DMVGQVAITR	1090.3	2	3.528	0.2936
DNAGAATEEFIK	1266.3	2	3.71	0.2792
DNAGAATEEFIKR	1422.5	2	3.0304	0.3361

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DNALELSQLENR	1402.5	2	2.8874	0.1811
DNEETGFGSGTR	1270.2	2	3.1393	0.3878
DNERVVGFHVLGPNAGEVTQGFAAALK	2798.1	3	3.9407	0.2688
DNFHGLAIFLDTYPNDETTER	2469.6	3	4.135	0.1518
DNFTLIPEGVNGIEER	1804.0	2	2.9203	0.159
DNGKHALIIYDDLSK	1702.9	2	3.9382	0.4075
DNGKHALIIYDDLSKQAVAYR	2391.7	3	6.3588	0.4279
DNHLLGTFDLTGIPPAPR	1935.2	2	5.6476	0.4506
DNHVVAAGGVEK	1196.3	2	3.4425	0.288
DNIISDYDQIIDYVER	1972.1	2	2.4688	0.1329
DNIQGITKPAIR	1326.5	2	3.6872	0.2932
DNLAEDIMR	1077.2	2	2.9371	0.1819
DNLAQQSFNMEQANYTIQSLKDTK	2789.0	3	4.0514	0.1782
DNLEFFLAGIGR	1352.5	2	4.2031	0.3495
DNLTLWTSDMQGDGEEQNKEALQDVEDENQ	3453.5	3	5.1019	0.4363
DNLTLWTSDQQDDDGGEGNN	2195.1	2	4.1233	0.4479
DNLTLWTSDTQGDEAEAGEGGEN	2410.4	2	6.1575	0.3897
DNLTLWTSENQGDEGDAGEGEN	2352.3	2	5.4193	0.5381
DNMNDNFLEGEEENELTLNEK	2498.6	2	5.6957	0.436
DNNGVIGLLEPMKK	1528.8	2	2.6416	0.2851
DNNQFASASLDR	1338.4	2	3.1543	0.2457
DNPGNFVKTEETLFEIQGIDPIASAIQNLK	3303.7	3	3.906	0.3505
DNQLSEVANKFAK	1464.6	2	3.5298	0.2324
DNSNIILLGDSQGDLR	1730.9	2	3.9729	0.372
DNSTMGYMAAK	1189.3	2	3.5779	0.3459
DNSTMGYMAAKK	1317.5	2	2.7017	0.235
DNSTMGYMMAK	1249.5	2	3.3222	0.2525
DNTINLIHTFR	1344.5	2	3.4336	0.3261
DNTNEIYSGK	1141.2	2	3.0025	0.2667
DNTQLLINQLWQLPTERVEEAIVAR	2951.3	3	3.7032	0.2189
DNTYLVELSSLLVR	1622.8	2	3.9861	0.3236
DNVTSPLPSLLVVIAAIFIGFFLGK	2633.2	3	3.8928	0.2126
DNYPPGFSYADFGPQFTAR	2151.3	2	4.9466	0.5139
DNYVPEVSALDQEIIEVDPDTK	2490.7	2	5.276	0.4445
DNYVPEVSALDQEIIEVDPDTKEMLK	2992.3	2	3.5473	0.1855
DPADASEAHESSSR	1459.4	2	4.3523	0.4603

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DPAGMPHPETK	1180.3	2	2.6036	0.1974
DPDAGIDEAQVEQDAQALFQAGELK	2659.8	2	5.9682	0.4917
DPDAQPGGELMLGGTDSK	1788.9	2	5.5433	0.5203
DPDAQPGGELMLGGTDSKYYK	2243.4	2	4.413	0.4219
DPDQTDGLGLSYLSSHIANVER	2388.5	3	4.4546	0.372
DPEAPIFQVADYGIVADLFK	2209.5	3	3.4518	0.3615
DPENFPFVVLGNK	1476.7	2	4.2264	0.3057
DPENFPFVVLGNKIDLENR	2217.5	3	3.9078	0.2856
DPFAHLPK	925.1	2	2.4227	0.222
DPGENYNLLGGVAGATPEVLQALK	2427.7	2	3.7952	0.2898
DPGTVANKKEEEDLAK	1744.9	2	3.1991	0.2979
DPGVITYDLPTPPGEK	1699.9	2	4.1696	0.4461
DPLVIELGQK	1112.3	2	3.8	0.2484
DPNGLPPEAQK	1166.3	2	3.3268	0.2474
DPNIVIAK	870.0	1	2.4863	0.1271
DPNLPLLPTRNLSTVK	1779.1	2	2.7302	0.1017
DPNSPLYSVK	1120.2	2	2.8387	0.1576
DPSQELEFIADILNQDAK	2047.2	2	4.7183	0.3958
DPSQQELPR	1070.1	2	2.8602	0.2208
DPVASSLSPYFGTK	1469.6	2	2.8884	0.2246
DPVQEAWAEDVDLR	1643.7	2	3.3029	0.3771
DPVRDFPFELIPEPPEGGLPGPWALHR	3040.4	3	4.1241	0.1348
DQALTEEHAR	1170.2	2	2.5597	0.1718
DQAVENILVSPVVVASSLGLVSLGGK	2552.9	3	5.5129	0.5048
DQAVFPQNGLVVSSVDVQSVEPVDQR	2814.1	3	4.7627	0.333
DQEGQDVLLFIDNIFR	1923.1	2	5.877	0.4854
DQETLHSHGVR	1279.3	2	3.1508	0.3067
DQGELERQLLQANPILEAFGNAK	2555.8	3	4.1134	0.1626
DQGGAGEGLVR	1059.1	2	2.4859	0.1466
DQGTYEDYVEGLR	1545.6	2	3.7765	0.454
DQHDTFFLRDPAEALQLPMDYVQR	2907.2	3	5.6807	0.3858
DQHPSKIPVIIER	1532.8	3	3.4342	0.3767
DQITAGNAAR	1017.1	2	3.2476	0.2025
DQKKTQEQLALEMAELTAR	2204.5	3	5.5958	0.4774
DQLLLGPTYATPK	1417.6	2	3.8071	0.2896
DQLNDQYLELLEK	1621.8	2	3.2588	0.1583

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DQLQTFSEEHPVLLTEAPLNPR	2535.8	3	5.6264	0.3526
DQLQTFSEEHPVLLTEAPLNPSK	2594.9	3	4.9977	0.3056
DQLSDDVSKVIAYLK	1694.9	2	2.9579	0.1911
DQLSDDVSKVIAYLKR	1851.1	3	4.9262	0.363
DQLSVLENGVDIVVGTPGR	1969.2	2	4.6123	0.2911
DQLSVLENGVDIVVGTPGRLDDLVSTGK	2898.2	3	4.4976	0.3334
DQLSVLENGVDIVVGTPGRLDDLVSTGKLNLSQVR	3709.2	3	5.8539	0.4012
DQNGNHVVQK	1139.2	2	2.6579	0.111
DQNILLGTTYR	1294.4	2	3.5067	0.1554
DQNTVETLQR	1204.3	2	3.3862	0.3045
DQNVFVAQK	1049.2	2	2.8426	0.2707
DQPLDSSHIASIR	1439.6	2	2.6383	0.2975
DQQEAALVDMVNDGVEDLR	2118.3	2	6.6827	0.5739
DQQQKPLYHHFTTAINTENIR	2555.8	3	4.1598	0.3519
DQQVEAAQR	1045.1	2	3.175	0.1934
DQTASAPATPLVNK	1413.6	2	2.761	0.212
DQTDDQVTIDSALATQK	1849.9	2	5.6133	0.4581
DQTVSDNELQEMSNQGSK	2011.1	2	5.7902	0.4916
DQVANSAFVER	1236.3	2	3.932	0.3574
DQWEDRIQVWHAEHR	2006.1	3	3.7095	0.3034
DRADQTVLTEDEKKELENLAAMDLELQK	3247.6	3	6.5015	0.396
DRAEAEAR	917.9	1	1.6565	0.1312
DRANMQHR	1028.1	2	2.8214	0.1762
DRDHFQLGSLSHLLNAK	1952.2	3	4.4697	0.2611
DRDNDSDDVESNLLLPAGIALR	2399.6	2	3.2231	0.1504
DRDNQDREENDKDPER	2032.0	2	3.4461	0.2159
DRDVDVLSAALKEQLSHSR	2140.3	3	3.4493	0.1819
DRDVTFSPATIENELIK	1949.2	2	4.4728	0.3475
DRDYSDHPSGGSYR	1612.6	2	3.6648	0.3071
DREAAEGLGSHER	1427.5	2	4.2461	0.2751
DREDDQYSHLQGNQLR	1975.0	2	3.0551	0.1655
DREEALHQFR	1301.4	2	3.5428	0.2633
DREGFFTNGLTLGAK	1626.8	2	5.0741	0.4305
DREVGIPPEQSLETAK	1769.9	2	4.7032	0.4597
DRFHEQFHSLR	1472.6	2	3.0208	0.2682
DRFSAEDEALSNIAREAEARLAAKRAAR	3089.4	3	4.3446	0.1289

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DRGSGLLGSQPQPVIPASVIPEELISQAQVVLQGK	3613.1	3	4.0003	0.3992
DRHFAGDVLGYVTPWNSHGYDVTK	2736.0	3	5.0831	0.3394
DRKESLDVYELDAK	1681.8	2	4.1941	0.3401
DRLLLATMESMNGGK	1636.9	2	4.808	0.4018
DRLPDAAAPESLPGQGR	1750.9	2	2.6158	0.114
DRLTSKEEELKDIQNMNFLLK	2565.9	3	4.5304	0.1203
DRLVPGPVFGSK	1272.5	2	3.1759	0.1272
DRPFFAGLVK	1150.4	2	2.8226	0.2338
DRPFFPGLVK	1176.4	2	2.7296	0.2505
DRPFKPYNFLAHGVLPDSGHLHPLLK	2970.4	3	4.4679	0.3273
DRPMEESLLLFEAMR	1838.1	2	3.4194	0.1271
DRTQIALSPNNHEVHIYKK	2264.5	3	3.4225	0.1905
DRVPTYQYNMNFEK	1806.0	2	3.23	0.2039
DRVTSAVEALLSADSASR	1849.0	3	3.5918	0.2383
DRYDSFIELQEK	1543.7	2	3.5815	0.1016
DRYFVEETVEVIR	1655.8	2	2.8175	0.1669
DSAAAVVVYDITNVNSFQQTTK	2372.6	3	4.0526	0.1712
DSAIGFSR	852.9	2	2.5697	0.1469
DSALETLQGQLEEKAQELGHSQSALASAQR	3197.4	3	6.3856	0.4741
DSALNLFNDPMWNQQWYLQDTR	2757.0	3	3.4076	0.1501
DSAQESVITR	1106.2	2	3.2225	0.1929
DSAQTSVTQAQR	1292.3	2	3.6926	0.2942
DSASFNPELLTHILDGSPEK	2171.3	2	4.335	0.3025
DSASFNPELLTHILDGSPEKTR	2428.6	3	3.2438	0.1161
DSAVAISGADSR	1149.2	2	3.7539	0.4848
DSDEADLVLAK	1176.3	2	2.4187	0.1726
DSDLSHVQNK	1143.2	2	3.2094	0.1896
DSDSSVLTR	980.0	2	2.4899	0.1109
DSEMGQQSLLFQIDYPEIAEGIMPR	2869.2	2	3.1653	0.1936
DSENKGPAFVNPLIPESPEEEELFR	2845.1	3	3.4708	0.1012
DSEQVAELKQELATLK	1803.0	2	4.2817	0.3759
DSEQVAELKQELATLKSQLNSQSVEITK	3118.4	3	6.874	0.5211
DSESADAGGAQR	1164.1	2	3.2152	0.3414
DSETGENIR	1021.0	2	2.5967	0.1639
DSFDDRGPSLNPVLDYDHGSR	2363.4	3	4.9778	0.2223
DSFKAGGSASAMLQPLLDNQVGFK	2482.8	2	5.6443	0.4961

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DSFLKDGQPFR	1310.4	2	2.9452	0.246
DSFQEVLR	994.1	1	2.251	0.1184
DSGEEAAEPSAPSR	1403.4	2	2.6002	0.1187
DSGKSEESSHYSTEKESEK	2145.1	3	3.7295	0.2717
DSGPLSDPITGKPYVPLLEAEEVR	2583.9	3	3.6268	0.1979
DSGQAFSLEQLRPLLASSLPLAAR	2541.9	3	3.5664	0.2015
DSGSDGHSVSSR	1191.1	2	3.2125	0.3568
DSGTLQSQEAK	1164.2	2	3.7868	0.2359
DSHGVAQVR	969.0	1	2.5406	0.263
DSHRDVQAGSHDYPGEGIYLLK	2458.6	3	4.0367	0.2443
DSHTDSHLHTR	1306.3	2	2.8367	0.1795
DSIFSNLTGQLDYQGFEK	2063.2	2	5.7076	0.5055
DSIFSNLTGQLDYQGFEKADMVIEAVFEDLSLK	3725.1	3	4.1505	0.3209
DSIFSNLTGQLDYQGFEKADMVIEAVFEDLSLKHR	4018.5	3	4.6969	0.3498
DSIKLDDDSER	1293.3	2	2.8238	0.3173
DSIVAELDREMSR	1521.7	2	3.0072	0.1792
DSIVHQAGMLKR	1355.6	2	2.7041	0.1038
DSLAEATR	862.9	2	2.4568	0.1259
DSLALARPK	971.1	2	2.7574	0.1354
DSLDPSFTHAMQLLTAEIEK	2247.5	2	5.902	0.4709
DSLGAYASQDANEQGQDLGKR	2224.3	3	3.4689	0.2549
DSLIFLVDASK	1208.4	2	4.3749	0.4349
DSLIQSLATQLELDGFERGPFSER	2709.9	3	3.5189	0.2932
DSLLQDGEFSMDLR	1626.8	2	4.8137	0.3822
DSLSEEDWMR	1268.3	2	3.5059	0.257
DSLSVNEFKELVTQQLPHLLK	2439.8	3	4.2687	0.2997
DSLYAQGR	910.0	2	3.1071	0.3444
DSNFAGDLVR	1094.2	2	3.2534	0.1426
DSNGAILVYDITDEDSFQK	2131.2	2	4.6444	0.3896
DSNTILLPSNPGDVTSMVAQAMGVYGALTK	3052.5	3	3.9538	0.3842
DSNYHLLMSVQESLER	1922.1	2	5.3471	0.336
DSNYHLLMSVQESLERK	2050.3	3	3.9082	0.1892
DSPLFDFIESCLR	1542.7	2	3.3305	0.2676
DSPLQGSGQQNSQAGQR	1758.8	2	4.2357	0.4451
DSPSVWAAVPGK	1214.4	1	2.5055	0.2568
DSPSYGSLSR	1069.1	2	2.8205	0.3059

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DSQDAGGFGPEDR	1351.3	2	3.6455	0.2428
DSQDGSSYR	1015.0	2	2.5621	0.1391
DSQEDLQER	1120.1	2	2.6519	0.1221
DSQEEEKTEALTSAK	1666.7	2	4.3279	0.2485
DSQGHGRDLSAAGIGLLAAATQSLSMPASLGR	3110.5	3	3.7001	0.3227
DSQLYAVDYETLTRPFSGR	2219.4	3	3.7196	0.3555
DSQMQNPYSR	1226.3	2	3.1032	0.2187
DSQNPLLMWAAPDPATGQNGPR	2337.6	3	4.5486	0.3384
DSQSPNTATQR	1205.2	2	2.7324	0.3142
DSQTQAILTK	1105.2	2	2.4186	0.2334
DSREHEEPTTSEMAEETYSPK	2454.5	3	5.0483	0.3734
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK	3142.2	3	6.1158	0.4783
DSSDQNFDYMFK	1497.6	2	2.7153	0.1534
DSSGNKIMHPVSGK	1457.6	2	3.2388	0.3052
DSSGNLHGYVAEGGAK	1562.6	2	3.2772	0.2903
DSSGQHVDVSPTSQR	1600.6	2	3.6631	0.4372
DSSLEADHVISAIPASVLSELLPAEAAPLAR	3144.5	3	3.4576	0.1426
DSSPHFQAEQR	1302.3	2	2.7135	0.3166
DSSQVHPLAVLLLTDGDVHIR	2286.6	3	3.8861	0.2688
DSSRLPSEGPRPAHVVVGDVLQAADVDK	2916.2	3	3.6333	0.4094
DSSSTNLESMDTS	1374.4	2	3.5129	0.3093
DSSTSPGDYVLSVSENSR	1900.9	2	2.5164	0.1219
DSTIHVEENGQSSESR	1775.8	3	3.8388	0.3189
DSTLIMQLLR	1190.4	2	3.6715	0.1671
DSTVAVVVYDITNLNSFQQTSK	2430.7	3	3.9761	0.1459
DSVAAGKPK	873.0	2	3.0645	0.1073
DSVADPHNLK	1096.2	2	2.6579	0.2158
DSVPKPSVLFLHPDLGVGGAER	2291.6	3	3.3109	0.1463
DSVVLNFNPFMAFNPDPK	2053.3	3	4.006	0.2934
DSVVLNFNPFMAFNPDPKSEYNDQLTR	3160.5	3	3.8106	0.2464
DSYESYGNSR	1178.1	2	3.3994	0.3699
DSYLILETLPTEYDSR	1916.1	2	5.187	0.3569
DSYVGDEAQSK	1199.2	2	3.7627	0.4199
DSYVGDEAQSKR	1355.4	2	3.5406	0.4355
DTANWLEINPDTGAISTR	1975.1	2	2.7624	0.1995
DTAQQGVVNFPYDDFIQCVMSV	2477.8	2	3.2249	0.1096

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DTASLSTTPSESPR	1449.5	2	3.5703	0.2934
DTAVQGNIR	974.1	2	2.5804	0.103
DTDAAVGDNIGYITFVLFPR	2185.4	3	4.3993	0.3898
DTDISIKPEGVREPDKPAPVEGK	2478.7	3	3.7839	0.1966
DTEEEDFHVDQVTTVK	1893.0	2	5.072	0.3792
DTEGHLVR	927.0	2	2.4053	0.1555
DTFNHLTTWLEDAR	1719.8	2	3.6036	0.3916
DTFYKEQLER	1329.4	2	2.6053	0.2593
DTFYKQPMFYHLGHFSK	2147.4	2	3.3605	0.3017
DTGAALLAESR	1104.2	2	3.4064	0.2823
DTGEGYQTPNIILDIQPGGNHVIEDSHKK	3177.4	3	4.0454	0.2977
DTGEKLTVAENEAETKLQAILEDIQVTLFTR	3477.9	3	6.4134	0.4621
DTGIFLDLMHLK	1403.7	2	4.312	0.3205
DTGKTPVEPEVAIHR	1649.8	3	4.8745	0.3952
DTGNIGQER	990.0	2	2.7276	0.1658
DTGQLYAALHHR	1382.5	2	3.0974	0.3069
DTHEDHDTSTENTDESNHDPQFEPIVSLPEQEIK	3936.0	3	5.9088	0.375
DTHLTITPTVLGER	1553.7	2	3.1663	0.26
DTIGKETFHPFVPEHHLIK	2246.6	2	3.0091	0.2
DTINLLDQR	1088.2	2	3.6555	0.1567
DTLENTIGHR	1156.2	2	2.8249	0.2085
DTLNKDHGNDKESNVLHQ	2065.1	3	3.6333	0.1549
DTLVQGLNEAGDDLEAVAK	1959.1	2	4.8515	0.2628
DTLYEAVR	967.1	2	2.6194	0.2331
DTLYEAVREVLHGNQR	1901.1	3	4.5237	0.3607
DTNGENIAESLVAEGLATR	1961.1	2	5.3577	0.38
DTNGSQFFITTVK	1458.6	2	4.5725	0.4265
DTPALFNFTTQELSSNPPLATILIPPHAR	3163.6	3	3.2169	0.1728
DTPGFIVNR	1019.1	1	2.717	0.2672
DTPGLHIGKPENK	1406.6	2	2.7291	0.1839
DTPTSAGPNSFNK	1336.4	2	3.3008	0.3829
DTQSGSLLFIGR	1294.4	2	3.9722	0.2887
DTSASAVAVGLK	1119.3	2	3.8534	0.3561
DTSASAVAVGLKQGK	1432.6	2	3.4388	0.3808
DTSFLGSDDIGK	1255.3	2	2.8096	0.1453
DTSFLGSDDIGNIDVR	1724.8	2	3.0057	0.1816

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DTSFSGLSLEEYK	1476.6	2	3.6112	0.448
DTSNHFHVFVGDLSPEITTEDIK	2602.8	3	4.6028	0.2741
DTSPGSAYQEGGGLYALGLIHANHGGDIIDYLLNQLK	3873.2	3	3.8663	0.3209
DTSSSTVVSTQR	1268.3	2	3.4795	0.2905
DTSYLFITGPDVVK	1555.8	2	3.7999	0.3043
DTVATQLSEAVDATR	1577.7	2	4.2122	0.4239
DTYIENEK	1012.1	2	2.6084	0.1263
DTYIENEKLISGK	1510.7	2	3.696	0.2259
DVAFTVGEGEDHDIPIGIDK	2128.3	2	3.6141	0.3117
DVAHGILNEAYRK	1486.7	2	3.5874	0.2921
DVAPQAPVHFLVIPK	1631.9	2	3.1028	0.2562
DVAQLGDVVHGVESLVELLGWTEEMRDLVQR	3494.9	3	3.6132	0.1192
DVAVAEEVR	988.1	2	2.8747	0.1648
DVAYQYVK	986.1	1	2.1883	0.1773
DVDAAYMSK	1000.1	1	2.5611	0.3238
DVDAAYMSKVELEAKVDALNDEINFLR	3070.4	3	6.4964	0.4801
DVDEAYMNK	1085.2	1	3.2905	0.3555
DVDEAYMNKVELESR	1799.0	2	4.5597	0.4786
DVDEAYMNKVELESRLEGLTDEINFLR	3200.5	3	5.1706	0.4672
DVDEIEAWISEKLQTASDESYKDPTNIQSK	3441.7	3	3.4171	0.1142
DVDFEGTDEPIFGK	1569.7	2	2.8836	0.1699
DVDFELIKVEGK	1392.6	2	3.7845	0.2575
DVDIIDHHDNTYTVK	1785.9	2	3.5634	0.395
DVDLEFLAK	1050.2	2	2.9052	0.1955
DVDRIIGLDQVAGMSETALPGAFK	2504.8	3	3.5921	0.2901
DVDRTDNQDMFTSSHIR	2038.1	2	2.8812	0.1561
DVEDFLSPLLGK	1333.5	2	3.8539	0.3477
DVEFLVQLK	1091.3	2	2.9449	0.1453
DVESDSAKQFLQAAEAIDDIPFGITSNSDVFSK	3546.8	3	5.9891	0.4804
DVFANYLTSNFQAPGVK	1872.1	2	2.759	0.1877
DVFISAAERDVYTGDALR	1999.2	2	3.0187	0.211
DVFLGMFLYEYAR	1624.9	2	4.0653	0.4282
DVFLPKPTWGNHTPIFR	2026.3	3	3.5513	0.364
DVFNKGYGFGMVK	1462.7	2	3.5302	0.2868
DVFQHSQSR	1104.2	2	2.658	0.1457
DVFTKGYGFGLIK	1445.7	2	3.4374	0.3426

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DVGAQILLHSHK	1318.5	2	2.7936	0.1398
DVGAQILLHSHKK	1446.7	2	4.0096	0.3548
DVGAYSK	739.8	1	2.3944	0.2201
DVGGEGVQQGLLK	1300.4	2	3.8776	0.2854
DVGLEVLDNALLALQGPTAAQVLQAGVADDLRK	3375.8	3	3.678	0.2445
DVGLKKEDIAMWEVNEAFSLVVLANIK	3033.5	3	4.6635	0.2579
DVGPHRDLVGELGTALR	1806.0	3	4.7433	0.3049
DVGPLSKKGFYLAFQDVGACIALVSVRVFYK	3393.0	3	3.2304	0.2505
DVGRPQPGRENFQNWLK	2042.2	2	3.3575	0.2339
DVHNIYGLYVHMATADGLR	2146.4	3	5.1552	0.4401
DVIAQSQSGTGK	1191.3	2	3.0588	0.2543
DVIEEYFK	1043.2	1	2.1575	0.2051
DVILADLLPSLAVYLR	1772.1	2	2.6463	0.2107
DVISQTIPNPDLDWVKNAQK	2282.5	3	3.3498	0.1084
DVKDGKYSQVLANGLDNKLREDLER	2877.2	3	3.5598	0.1794
DVKDKETTENENTK	1651.7	2	4.8215	0.2803
DVKDKETTENENTKFEVR	2183.3	3	3.8282	0.2696
DVKGESLFHSK	1247.4	2	2.5148	0.1782
DVKPSNILVNSR	1342.5	2	2.7433	0.1007
DVLFLKDCVGPEVEKACANPAAGSVILLENLR	3385.9	3	4.8936	0.3677
DVLNDTAPR	1001.1	2	2.7081	0.2198
DVLSVAFSSDNR	1310.4	2	4.368	0.4853
DVMQQQLAEYQELLDVK	2051.3	2	4.4567	0.307
DVNAAIAAIK	986.1	2	3.6509	0.2784
DVNAAIATIK	1016.2	2	3.6678	0.3269
DVNAAIATIKTK	1245.5	2	3.9268	0.219
DVNFEFPEFQL	1385.5	2	3.644	0.2471
DVNGELIAVQR	1214.4	2	2.6185	0.2408
DVNQQEFVR	1135.2	2	2.9467	0.1546
DVPAVEITHTFWER	1700.9	2	3.4413	0.3867
DVPAYSQDTFKVHYENNSPFLTITSMTR	3263.6	3	4.7984	0.2396
DVPDLTLIDLPGITR	1638.9	2	3.5381	0.2907
DVPFSVVYFPLFANLNQLGR	2297.6	2	3.0366	0.3297
DVPLTIKDPAVGFLETISPGYSIHTYLWR	3290.8	3	3.9122	0.2711
DVPRPILLGASAPLK	1547.9	2	3.2778	0.1881
DVPTGGIFQLR	1203.4	2	3.321	0.3175

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DVPVAEEVSALFAGELNPVAPK	2253.5	2	4.0122	0.3659
DVPVYLFSR	1096.3	2	2.626	0.2015
DVPYPPPLSPAIEAIQK	1836.1	2	2.7516	0.2333
DVQAMK	691.8	1	1.8455	0.1178
DVQELLTQYTK	1338.5	2	4.2519	0.3766
DVQFEHGYR	1151.2	2	2.6177	0.2257
DVQGTDASLDEELDR	1663.7	2	4.9924	0.4829
DVQGTDASLDEELDRVK	1891.0	2	3.2274	0.3423
DVQMLQDAISK	1248.4	2	3.8813	0.2542
DVQNTFYDIVAELGAMEHAQAVDYIK	2942.2	3	4.1342	0.3138
DVQNTFYDIVAELGAMEHAQAVDYIKK	3070.4	3	3.7454	0.2883
DVRDTVLEPYADPYYDYEIER	2622.8	3	3.597	0.1969
DVRQQYESVAAK	1394.5	2	3.0003	0.2338
DVSELTGFPEMLGGR	1608.8	2	4.4763	0.3106
DVSKEDHSKR	1201.3	2	2.8298	0.1295
DVSLGTYGSR	1055.1	2	3.1348	0.3399
DVSSALDKLKEFGNTLEDKAR	2337.6	3	5.4919	0.403
DVTADFEGQSPK	1294.3	2	3.673	0.301
DVTATVDSLPLITASILSK	1945.2	2	3.9927	0.3236
DVTFSPATIENELIK	1677.9	2	4.0236	0.3993
DVTGAEALLER	1174.3	2	2.9052	0.2206
DVTGPDEESFLYFAYGSNLLTER	2624.8	2	4.3339	0.4405
DVTLENR	846.9	1	2.1221	0.1445
DVTNFTVGGFAPMSPR	1696.9	2	3.022	0.1221
DVTNNVHYENYR	1524.6	2	4.0833	0.2243
DVTRGQAAVQQLQAEGLSPR	2125.3	2	5.4818	0.3183
DVTYEEAK	955.0	1	2.1102	0.2715
DVTYEEAKQFAEENGLLFLEASAK	2703.9	3	4.7072	0.3383
DVVFLIDGSQSAGPEFQYVR	2228.4	3	5.8327	0.5057
DVVFNYLHATAFQGTPLAQAVEGPSENVRK	3260.6	3	5.4358	0.4681
DVVICPDASLEDAKK	1603.8	2	2.7789	0.2799
DVVMMENFHHIFATLSR	2048.4	2	2.8531	0.1985
DVYGGAHQTLGLSGNLIASSFGK	2293.5	3	4.6273	0.4416
DVYKEHFQDDVFNEK	1914.0	2	5.0179	0.3804
DVYKEHFQDDVFNEKGWNYILEK	2918.2	3	5.1156	0.2781
DVYKEHFQDDVFNEKGWNYILEKYDGHLPIEIK	4084.5	3	3.8466	0.2003

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DVYKKFDLGQDVIDFTGHALALYR	2786.1	3	4.3851	0.311
DVYLSPR	850.0	1	2.3218	0.1229
DVYLSPRDDGYSTK	1616.7	2	3.1154	0.2942
DVYVQLYLQHLTAR	1720.0	2	4.2539	0.4249
DVYVVTDQIPVFVTMFQK	2130.5	2	5.6039	0.5279
DWKLDPVLYR	1305.5	2	2.5156	0.1758
DWSHYFK	983.1	2	2.467	0.1921
DYDAMGSQTK	1116.2	2	2.6695	0.3146
DYDDMSPR	999.0	2	2.591	0.3023
DYDRDKDDKISWEEYK	2106.2	3	4.0864	0.3245
DYDSLAQPGFFDR	1531.6	2	4.2912	0.5119
DYEGPAIAPK	1061.2	2	2.5896	0.1503
DYEPPSPSPAPGAPPPPPQR	2055.2	3	4.4231	0.4878
DYETATLSDIK	1256.3	2	3.2135	0.3124
DYFEEYGKIDTIEIITDR	2221.4	2	4.8401	0.4181
DYFGAHTYELLAKPGQFIHTNWTGHGGTVSSSSYNA	3916.2	3	5.5192	0.337
DYGHSSSRDDYPSR	1642.6	2	2.7325	0.1027
DYGKESQAKDVIEEYFK	2050.2	2	4.8798	0.3262
DYGNSPLHR	1059.1	2	2.5048	0.2015
DYGVLLEGSGLALR	1463.7	2	5.3374	0.4728
DYGVYLEDSGHTLR	1625.7	2	4.2087	0.453
DYHFKVDNDENEHQLSLR	2260.4	3	3.4604	0.1863
DYILEGEPGK	1121.2	2	2.6383	0.1443
DYILEGEPGKVSNLQYLHSYLTYIK	2945.3	3	5.3475	0.3723
DYIQKHPELNISEEGITK	2115.3	3	3.8449	0.2981
DYKGFSPSVDWETVDFDSAPSIQELPVQSAITEPR	3913.2	3	5.876	0.4042
DYKVDQEIINIMQDR	1881.1	2	4.4112	0.439
DYLDLTASNNFFVDDYAR	2140.3	2	3.6412	0.4609
DYLGDFIEHYAQLGPSQPPDLAQAQDEPR	3272.5	3	4.5401	0.2332
DYLGDFIEHYAQLGPSQPPDLAQAQDEPRR	3428.7	3	4.84	0.3609
DYLHLPPEIVPATLRR	1891.2	3	3.2584	0.243
DYLIDGSR	939.0	2	2.4336	0.1353
DYNKYEEGINIHLAK	1808.0	3	3.561	0.3398
DYNLNDILLQLGIEEAFTSK	2297.5	2	6.7189	0.5701
DYNVTANSK	1012.1	2	3.2351	0.362
DYPDFSPSVDAEAIQK	1782.9	2	4.5597	0.4565

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
DYPVVSIEDPFDQDDWAAWSK	2484.6	2	3.0168	0.1707
DYPVVSIEDPFDQDDWGAWQK	2511.6	3	5.2529	0.3637
DYQDNKADVILK	1422.6	2	3.7529	0.2989
DYQDNKADVILKYNADEAR	2242.4	3	4.5639	0.3172
DYQGPLKEHEVTIFVR	1932.2	3	4.4233	0.5133
DYSGQGVVK	953.0	1	1.6433	0.1638
DYSGQGVVKLDVQPK	1633.8	2	3.4364	0.2352
DYSHYYTTIQDLR	1675.8	2	3.8867	0.4151
DYSHYYTTIQDLRDK	1919.0	3	4.0154	0.2918
DYSHYYTTIQDLRDKILGATIENSR	2974.2	3	4.9244	0.5039
DYSKKPTPDK	1179.3	2	2.5036	0.1966
DYSNFDQEFLNEK	1649.7	2	3.608	0.2132
DYTGALAVFTR	1214.4	2	3.2191	0.3689
DYTGEDVTPQNFLAVLR	1939.1	2	3.9094	0.2906
DYTQMNELQR	1298.4	2	3.0418	0.2708
DYTSGAMLTGELKK	1514.7	2	3.4711	0.294
DYTYEELLNR	1316.4	2	2.883	0.3569
DYVAPTANLDQK	1335.4	2	3.7628	0.3766
DYVAPTANLDQKDKQFVAK	2152.4	2	5.1918	0.4392
DYVQKAQTK	1081.2	2	2.621	0.1992
EAAAALVEEETRR	1445.6	2	2.7593	0.2106
EAAAATQKRQELEAELAK	1958.2	2	4.1763	0.3299
EAAAATQKRQELEAELAKVR	2213.5	3	4.1858	0.2939
EAAAQQQAER	1102.1	2	2.7517	0.2264
EAADKEEPPSKK	1329.4	2	2.7439	0.2288
EAADPLASKLNK	1257.4	2	3.4555	0.3369
EAAEMGK	735.8	1	1.8535	0.1435
EAAENSLVAYK	1195.3	2	3.0572	0.2659
EAAEQDVEK	1019.0	2	2.5564	0.2312
EAAEQDVEKK	1147.2	2	3.3169	0.1993
EAAEQDVEKKK	1275.4	2	3.0417	0.1321
EAALGAGFSDK	1066.1	2	2.8358	0.2858
EAALKAQSER	1103.2	2	2.9945	0.1636
EAALSTALSEK	1120.2	2	3.3417	0.2814
EAALSTALSEKR	1276.4	2	2.8955	0.3134
EAALTSEEVGADLEQVEVLQK	2259.5	2	6.5644	0.4064

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EAANAMKLER	1133.3	2	2.4043	0.1182
EAAPDAGAEPITADSDPAYSSK	2164.2	2	4.7084	0.4259
EAATAVEQEKEILLEMIHSIQNSQDMR	3115.5	3	4.8129	0.3558
EAATQAQQTLGSTIDKATGILLYGLASR	2879.2	3	5.5289	0.4099
EAAVSHAGSMHR	1253.4	2	3.0963	0.349
EAAWDQALHR	1197.3	2	2.8516	0.2409
EAAYHPEVAPDVR	1454.6	2	3.0777	0.2641
EADDIVNWLK	1203.3	2	2.7701	0.2724
EADDIVNWLKK	1331.5	2	3.3614	0.2626
EADDIVNWLKKRTGPAATTLPDGAAAESLVESSEVAVIGFFK	4405.9	3	3.6657	0.1925
EADESLNFEEQILEAAK	1937.1	2	5.6774	0.4007
EADESLNFEEQILEAAKSIAAATSALVK	2950.2	3	3.4473	0.3265
EADGILKPLPK	1181.4	2	2.6293	0.2275
EADGSETPEPFAAEAK	1649.7	2	4.7326	0.4285
EADLAAQEEAAKK	1374.5	2	3.3983	0.2363
EADLPMTAASHSSAFTPVTAAASPVSLPR	2884.2	3	4.3439	0.2345
EADPALNVETEIEILK	1785.0	2	3.3225	0.2053
EADYVAQATR	1124.2	2	2.7186	0.2517
EAEAAIYHLQLFEELR	1933.2	2	4.6236	0.403
EAEAAIYHLQLFEELRR	2089.3	2	3.7724	0.3468
EAEAAMFHR	1062.2	2	2.7852	0.2695
EAEAAMFHRK	1190.4	2	2.8975	0.3113
EAEALLQSMGLTPESPIVPPPMSPSSK	2795.2	3	4.3785	0.1539
EAEDLQVGQVELGGGP	1598.7	2	4.9618	0.3791
EAEDLQVGQVELGGGPGAGS	1871.0	2	5.3242	0.3783
EAEDLQVGQVELGGGPGAGSLQ	2112.2	2	5.2721	0.3012
EAEDLQVGQVELGGGPGAGSLQP	2209.4	2	6.2005	0.459
EAEDLQVGQVELGGGPGAGSLQPL	2322.5	2	7.4185	0.5039
EAEDLQVGQVELGGGPGAGSLQPLA	2393.6	2	6.476	0.5143
EAEDLQVGQVELGGGPGAGSLQPLAL	2506.8	2	6.364	0.5125
EAEDLQVGQVELGGGPGAGSLQPLALEGS	2780.0	2	6.4973	0.5441
EAEDLQVGQVELGGGPGAGSLQPLALEGSL	2893.2	3	7.3754	0.5305
EAEDLQVGQVELGGGPGAGSLQPLALEGSLQ	3021.3	3	7.8163	0.5414
EAEDLQVGQVELGGGPGAGSLQPLALEGSLQK	3149.5	2	8.7087	0.5822
EAEDLQVGQVELGGGPGAGSLQPLALEGSLQKR	3305.6	3	7.2682	0.5519
EAEFTKSIAKFFDHSGTLVMDAYEPEISR	3320.7	3	3.422	0.269

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EAEGAPQVEAGK	1186.3	2	2.5902	0.1567
EAEGSSAEYKK	1199.2	2	2.7769	0.3221
EAEGSSAEYKKEIEELKELLPEIR	2792.1	3	3.2792	0.1884
EAEGTEEGGEEEDDEEMDPQTIDSLIELSTK	3427.5	2	6.1347	0.3947
EAEHLYHTLESSYQK	1836.0	2	3.8265	0.2914
EAEKLESEHPDQAQAILSR	2152.3	3	6.1716	0.4172
EAELDVNEELDKK	1532.6	2	3.8809	0.2681
EAELKEAEKELHEK	1683.8	2	3.5378	0.2256
EAELKEAEKELHEKFDLLKR	2456.8	3	3.417	0.1811
EAENPEGEEKEAATLEVERPLPMEVEK	3055.3	3	6.1693	0.4487
EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	3199.6	3	4.7356	0.3547
EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK	3199.6	3	5.018	0.4152
EAESLIAKK	989.1	2	2.8533	0.1529
EAESSPFVER	1151.2	2	3.2055	0.2372
EAETEPHEGKR	1283.3	2	2.5062	0.2958
EAETLREQLSSANHSLQLASQIQK	2682.9	3	4.8101	0.2932
EAEVLLLQQR	1199.4	2	3.7218	0.2051
EAEYFELPELVR	1495.7	2	3.8067	0.4261
EAFDEVDMAHR	1320.4	2	2.6311	0.2983
EAFLNTEDKGDSLDSVEALIK	2295.5	2	5.5545	0.4302
EAFQLFDR	1026.1	2	2.7709	0.156
EAFRVFDKDGNGYISAAELR	2259.5	2	4.2081	0.294
EAFSLFDKDGDGTITTK	1846.0	2	4.0037	0.3928
EAFTNKPNVFTVVTR	1724.0	2	3.5706	0.2589
EAGAGGLAIAVEGPSK	1427.6	2	4.3051	0.27
EAGAGGLAIAVEGPSKAEISFEDR	2375.6	3	3.3803	0.2744
EAGAGGLAIAVEGPSKAEISFEDRK	2503.8	3	4.87	0.4154
EAGAGGLSIAVEGPSK	1443.6	2	2.8746	0.1533
EAGAGGLSIAVEGPSKAEITFDDHK	2500.7	3	3.2122	0.1777
EAGEGGEAEAPAAEGGK	1530.5	2	5.324	0.3098
EAGELKPEEEITVGPVQK	1954.2	2	4.3746	0.3116
EAGEQGDIEPR	1201.2	2	3.2894	0.2191
EAGFKRPVVLFGPIADIAMEK	2289.7	3	5.064	0.4061
EAGFLRPVTIFGPIADVAR	2030.4	3	5.0374	0.2798
EAGFPPGVVNIVPGYGPTAGAAISSHMDIDK	3069.4	3	3.5898	0.1976
EAGFPPGVVNIVPGYGPTAGAAISSHMDIDKVAFTGSTEVGK	4146.6	3	4.5394	0.362

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EAGFPPGVVNIVPGYGPTAGAAISSHMDIDKVAFTGSTEVGKLIK	4501.1	3	4.2657	0.3035
EAGGAFGK	736.8	1	1.6588	0.2262
EAGGGGVGGPGAK	1014.1	2	3.5201	0.2126
EAGHGTQKEEIPEEELAEDVEEIDHAER	3191.3	3	5.2886	0.4189
EAGHGTTKEEITK	1401.5	2	2.4406	0.114
EAGIPEFYDYDVALIK	1844.1	2	3.9119	0.4357
EAGISDYLTIEELVK	1680.9	2	3.0207	0.2067
EAGITEK	747.8	1	2.151	0.1239
EAGITEKVVFEQTK	1579.8	2	3.6361	0.3558
EAGKEPAEGGGGDGSHR	1611.6	2	3.9931	0.3194
EAGLVAQHPPAR	1246.4	2	2.8064	0.1677
EAGTKEEPVTADVINPMALR	2142.4	2	3.2092	0.193
EAGVEKFIHVSHLNANIK	2007.3	2	3.4663	0.2683
EAGVEMGDEDDLSTPNEK	1937.0	2	5.2529	0.3787
EAHEPLAVADAK	1251.4	2	2.7898	0.2795
EAHFVR	758.8	1	1.6096	0.1083
EAIAELEREKEKLQQEAK	2143.4	3	4.5227	0.2022
EAIDKAGYTEK	1225.3	2	2.5132	0.3069
EAIDSYIKADDPSSYMEVVQAANTSGNWEELVK	3661.9	3	5.9009	0.4235
EAIEGTYIDKK	1267.4	1	2.7462	0.1929
EAIENATTNAEVLR	1531.7	2	3.5401	0.2456
EAIHSQLLEK	1168.3	2	2.4084	0.1428
EAILAIHKEAQR	1379.6	2	3.2856	0.1766
EAILEYILHQK	1357.6	2	2.6772	0.2105
EAILNDEIYCPPETAVLLASYAVQAK	2823.2	3	3.4581	0.2197
EAINVEQAFQTIAR	1590.8	2	4.5645	0.4515
EAIQHPADEKLQEK	1636.8	2	3.9539	0.2821
EAKPDELMDSKLR	1532.7	2	2.6301	0.1682
EAKQQEEKIEK	1360.5	2	2.705	0.1175
EALAQTVLAEVPTQLVSYFR	2236.6	3	6.1296	0.4979
EALATLKPQAGLIVPQAVPSSQPSVVGAGEPMDLGELVGMTPEIIQK	4769.5	3	4.6196	0.4406
EALDHMVEYVAQNTPVTWLVGPFAPGITEK	3314.8	3	4.0119	0.3373
EALDVLDAVLK	1186.4	2	2.6291	0.2172
EALEKTEKQLEAIDQLHLEYAK	2600.9	3	3.6846	0.2559
EALEKTEKQLEAIDQLHLEYAKR	2757.1	3	4.5168	0.285
EALENANTNTEVLK	1546.7	2	4.4234	0.2819

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EALGGQALYPHVLVK	1595.9	2	2.8483	0.2252
EALGHWLGLLNADGWIGREQILGDEAR	2991.3	3	3.7599	0.2655
EALKDEYDDLSDLTAAQQETLSDWESQFTFK	3625.8	3	6.9966	0.5383
EALKEAVILPIKFPHLFTGK	2252.7	3	4.6001	0.3093
EALKQREEMLEK	1504.7	2	3.5806	0.1317
EALLSSAVDHGSDEVK	1657.8	2	4.4495	0.3969
EALLSSAVDHGSDEVKFR	1961.1	3	3.5491	0.3828
EALLSSAVDHGSDEVKFRQDLMNIAGTTLSSK	3421.8	3	6.4411	0.4832
EALLVANGTPR	1141.3	2	3.5204	0.3651
EALNVFGNDYDTEDGTGVRDYIHVVDLAK	3227.4	3	4.8709	0.4506
EALNVINTHTK	1240.4	2	2.7865	0.2817
EALQEKEEQKTMK	1592.8	2	4.3987	0.3514
EALRGEVGHLGLALEELQAQVQATSTQLALEELR	3675.1	3	5.5534	0.4103
EALTYDGALLGDR	1394.5	2	2.9163	0.1747
EAMDPIAELLSQLSGVR	1830.1	2	4.3006	0.3366
EAMEDGEIDGNK	1308.4	2	3.4474	0.312
EAMEDGEIDGNKVTLDWAKPK	2347.6	3	4.8221	0.3047
EAMEHPYFYTVVKDQAR	2085.3	3	4.2413	0.353
EAMQQADDWLGIPQVITPEEIVDPNVDEHSVMTYLSQFPK	4573.1	3	5.9229	0.3823
EAMQQADDWLGVPQVITPEEIIHPDVDEHSVMTYLSQFPK	4596.1	3	4.66	0.366
EAMRIGAEVYHNLK	1631.9	3	3.5847	0.2944
EANAHLAAVHR	1189.3	2	3.1179	0.3064
EANELQQWINEK	1502.6	2	3.6136	0.1881
EANELQQWINEKEAALTSEEVGADLEQVEVLQK	3743.0	3	5.8167	0.3197
EANHNVSAPYGR	1315.4	2	2.4677	0.2822
EANNFLWPFK	1266.4	2	2.7297	0.1427
EANNYEEDPNKPTSWTENQAGKIPEK	2991.1	3	3.9427	0.2455
EANSKADPSLNPEQLK	1741.9	2	4.2302	0.3297
EANSKADPSLNPEQLKK	1870.1	2	4.5351	0.3376
EANVDAATKKGNTALHIASLAGQAEVVK	2808.1	3	5.769	0.4731
EANYIGSDKYFHAR	1671.8	2	3.6862	0.4012
EAPAGPLEEDDLEPLTLAPAPAPRPPQDLIGLR	3460.9	3	4.3584	0.4203
EAPAKLESQAGQQVSR	1699.8	2	3.6632	0.3585
EAPAPPKAEAK	1109.3	2	2.4627	0.1029
EAPKVVEEQESR	1401.5	2	2.633	0.2096
EAPPMEKPEVVK	1354.6	2	2.9549	0.2708

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EAPPMEKPEVVKTHLR	1862.2	3	3.6452	0.153
EAPPRELTEEEKQQILHSEEFLIFFDR	3332.7	3	5.4898	0.3449
EAPVDVLTQIGR	1298.5	2	3.6029	0.3815
EAQAALAEAQEDLESER	1860.9	2	5.1971	0.5353
EAQGKIDVLQAEVAALK	1784.0	2	2.6014	0.1691
EAQKELEALIQNLDNVVEDSMLVDPK	2942.3	3	5.4872	0.3122
EAQLEEQFYLQALKLPNQTHPDVPVGDESQAR	3653.0	3	5.0681	0.258
EAQNQPIDKAR	1270.4	2	3.1242	0.2628
EAQQALGSAAADATEAK	1632.7	2	4.1291	0.4237
EAQSDLNKTR	1162.2	2	2.9261	0.1128
EAQTSFLHLGYLPNQLFR	2135.4	3	4.0943	0.4495
EASDIILTDDNFTSIVK	1882.1	2	3.8244	0.2443
EASDPQPEEADGGLK	1543.6	2	3.8067	0.2638
EASEEAFSGSAQPRPPSVVHESR	2455.6	3	4.0916	0.2959
EASHVLEVK	1012.1	2	2.6345	0.189
EASIDILHSIVK	1325.5	2	2.7298	0.31
EASIYTGITLSEYFR	1750.9	2	4.4984	0.4488
EASRPPEEPSAPSPTLPAQFK	2237.5	3	3.695	0.166
EASSVSEELHKEVQEAFLTLHK	2512.8	3	4.4023	0.3427
EATADDLIKVVEELTR	1803.0	2	5.025	0.4142
EATAHFQITLDEIQAQLEQHDIHNAK	3002.2	3	4.3337	0.3166
EATDAIGHLDR	1198.3	2	3.2534	0.39
EATNPPVIQEEKPK	1580.8	2	3.7141	0.3431
EATNPPVIQEEKPKK	1708.9	2	3.2852	0.3842
EATNPPVIQEEKPKKK	1837.1	2	3.2973	0.3687
EATQEAFMKR	1211.4	2	2.4203	0.1125
EATQILSVPKVDDEILGFISEATPLGGIQAASTESCNQQLDLALCR	4847.4	3	3.6664	0.2392
EATSDPSRTPEEEPLNLEGLVAHR	2648.8	3	4.938	0.4117
EATSVPHIYAIGDVVEGRPELTPIAIMAGR	3164.6	3	3.7502	0.2506
EATTDFTVDSRPLTQVGGDHIK	2388.6	2	3.7111	0.3876
EATTEFSVDAR	1226.3	2	2.6619	0.1231
EATTLANGVLASLNLPAAIEDVSGDTVPQSILTK	3410.8	3	5.2906	0.4891
EATVKPFAIDIFPVTNK	1891.2	2	3.5073	0.2725
EATVKPFAIDIFPVTNKDFR	2309.6	3	4.2444	0.464
EATWVVDVK	1047.2	1	1.8458	0.1565
EAVAHENNR	1040.1	2	2.4417	0.3015

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EAVANKGPVSVGVDAR	1569.7	2	4.0952	0.399
EAVAPVQEESDLEK	1544.6	2	3.2048	0.3852
EAVEEPSSK	976.0	1	2.0919	0.1948
EAVEKEFEPLLNWMK	1864.2	2	4.8983	0.3816
EAVEKEFEPLLNWMKDK	2107.4	3	4.5924	0.3976
EAVELPLTHFELYK	1689.9	2	3.6237	0.337
EAVFFQSHSAR	1279.4	2	2.5362	0.1547
EAVIAQISSHVK	1282.5	2	3.2437	0.2528
EAVILPIKFPHLFTGK	1811.2	2	3.4485	0.38
EAVKAASDELSK	1248.4	2	2.5089	0.1699
EAVKEESIKR	1189.3	2	2.7345	0.2098
EAVKEIQTSAK	1204.4	2	2.8687	0.1701
EAVKHIGYDDSSKGFDYK	2060.2	2	4.4976	0.4661
EAVLAALALR	1027.2	2	2.8809	0.2283
EAVLDVIPTDIHQR	1606.8	2	4.7391	0.2561
EAVLIDPVLETAPR	1523.8	2	4.5517	0.3624
EAVQLMAEAEKR	1375.6	2	2.7972	0.2692
EAVSSAFFSLLQTLSTQFK	2105.4	2	3.2599	0.4631
EAVTEILGIEPDREK	1699.9	2	4.0473	0.2594
EAVTFLRK	964.1	2	2.7216	0.2381
EAWKIWADIPAPK	1525.8	2	3.795	0.2917
EAYGAVTQTVR	1195.3	2	3.1311	0.2324
EAYMGNVLQGGEGQAPTR	1879.0	2	4.9187	0.498
EAYPDHTQFEK	1365.4	2	2.6397	0.1959
EAYPEEAYIADLDAK	1698.8	2	4.5533	0.4793
EAYPGDVFYLHSR	1554.7	2	3.5593	0.412
EAYVNANQAR	1136.2	2	2.5868	0.2212
EDAQEVELQEGK	1375.4	2	2.7821	0.1445
EDAQVAAEILEIADTPSGDK	2073.2	2	3.787	0.2915
EDAQVAAEILEIADTPSGDKTSLETR	2760.9	3	4.6387	0.3669
EDAVSKEVTR	1134.2	2	2.5372	0.1868
EDDFLNNAMSSLYSGWSSFTTGASR	2744.9	2	3.8254	0.4399
EDDLNSFNATDLKDLSSHQLNEFLAQTLQR	3464.7	3	6.7579	0.521
EDDSIRPFKVETSDEEIHDLHQR	2796.9	3	5.7552	0.4936
EDEEEEEGENYQKGER	1970.9	2	3.2794	0.3969
EDGNEEDKENQGDETQGQQPPQR	2629.6	3	5.1553	0.4079

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EDGNEEDKENQGDETQGQQPPQRR	2785.8	3	4.2595	0.4067
EDGTFYEFGEDIPEAPER	2102.2	2	3.9924	0.3866
EDHGRGYFEYIEENKYSR	2293.4	3	4.7043	0.3291
EDHSLEHR	1023.0	2	2.4421	0.206
EDIDTAMK	923.0	1	2.0039	0.2894
EDILENQFMDSR	1497.6	2	2.828	0.1678
EDITHSAQHALR	1378.5	2	2.9549	0.1837
EDITQSAQHALR	1369.5	2	3.3604	0.3637
EDLHILFSNHGEIK	1652.8	2	4.121	0.3055
EDLRLPEGDLGKEIEQK	1970.2	2	4.7353	0.2345
EDLTEIRDMLLANKVPAAAR	2227.6	3	4.038	0.2751
EDLVFIFWAPESAPLK	1863.1	2	2.6255	0.1911
EDMAALEK	907.0	1	2.5211	0.2007
EDPNLVPSISNK	1313.4	2	2.7831	0.2844
EDQSILCTGESGAGK	1495.6	2	4.0168	0.3927
EDQTEYLEER	1312.3	2	3.357	0.3411
EDSARPGAHAK	1139.2	2	2.4166	0.203
EDSERPGAHLTVK	1439.6	2	3.4344	0.12
EDSKEAEKSGEATDGARPQALPEPMQESK	3117.3	3	4.5593	0.3632
EDSQRPGAHLTVK	1438.6	2	2.9531	0.1304
EDSRADVKRNNVTR	1660.8	2	2.7311	0.1441
EDSVKPGAHLTVK	1381.6	2	3.4465	0.2555
EDSVKPGAHLTVKK	1509.7	2	3.2217	0.1462
EDTEEHHLRDYFEEYGKIDTIEIITDR	3368.6	3	4.7694	0.2855
EDTESLEIFQNEVAR	1780.9	2	4.157	0.3388
EDTLAFSEWGSPHAAVPR	1971.1	2	3.1755	0.1871
EDTNNLFSVQFR	1470.6	2	3.5073	0.3332
EDYKFHHTFSTEIAK	1854.0	2	3.6278	0.2122
EEAAEHIPLLFFAFPSAK	2018.3	2	2.8011	0.1705
EEAAVDAQQQK	1217.3	2	3.1497	0.2038
EEADEYIDIGALNGIFVLGR	2195.4	2	5.7482	0.4635
EEAENTLQSFR	1324.4	2	3.0881	0.3843
EEAENTLQSFRQDVDNASLAR	2394.5	3	3.974	0.3705
EEAQAEIEQYR	1366.4	2	3.9911	0.3962
EEASDYLELDTIK	1526.6	2	3.8906	0.2489
EEASGSSVTAEEAKK	1523.6	2	3.5272	0.2731

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EECDKYALQSQQR	1598.7	2	2.4044	0.2667
EECLLGR	819.9	1	1.787	0.1042
EEDDVVSEDLVQQDVQDLYEAGELK	2867.0	3	4.9026	0.3412
EEDEVYPPGPYHPFPNYIRPR	2573.8	3	3.2266	0.3264
EEDSANLKPSELKK	1588.7	2	3.7055	0.1622
EEEAIQLDGLNASQIR	1786.9	2	4.8732	0.4393
EEEEEEEEEAEAGEEAVPEEEGPTVVLNPHPSLGYK	3983.1	3	6.6559	0.5086
EEEEEEEEEAEAGEEAVPEEEGPTVVLNPHPSLGYKEI	4225.3	3	6.4536	0.4672
EEEEEEEEEAEAGEEAVPEEEGPTVVLNPHPSLGYKEIR	4381.5	3	5.6377	0.5057
EEEEKKAEFER	1424.5	2	2.9692	0.2831
EEEEVLDQGDFYSLLSK	2002.1	2	5.096	0.3758
EEEGSANRRPEDQELESLSAIEAELEK	3060.2	3	3.4993	0.1352
EEEGSANRRPEDQELESLSAIEAELEKVAHQLQALR	4077.4	3	4.0749	0.3623
EEFASTCPDDEEIELAYEQVAK	2517.7	2	4.5238	0.4703
EEFTAFLHPEEFEHMK	2022.2	2	3.1821	0.2811
EEGGENLDQAR	1218.2	2	2.8213	0.2918
EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	3487.9	3	5.3211	0.4276
EEIFGPVQQIMK	1419.7	2	3.4682	0.2833
EEIKDDNPHLK	1338.4	2	3.5922	0.2464
EEILAQAKENEK	1402.5	2	4.0588	0.2006
EEITMEHLEPHLQAEIVETIDNGFGHSR	3233.5	3	4.228	0.2967
EEIVQFFSGLEIVPNGITLPVDFQGR	2906.3	3	3.3569	0.2404
EEKEESDDEAAVEEEEEEKKPK	2607.6	3	5.4725	0.3289
EEKKEEEEKKEVMLQNGETPKDLNDEKQKK	3633.0	3	4.4047	0.1424
EEKPGSKKVEEDLKADK	1931.1	2	2.9055	0.1493
EELAQQYEAILR	1463.6	2	3.7108	0.3403
EELDKYWSQQIEESTTVVTTQSAEVGAAETTLTELRR	4201.5	3	3.7704	0.2803
EELDSLMTDETIANVPILILGNK	2529.9	2	2.513	0.1249
EELEEELDEAVER	1590.6	2	4.8695	0.4408
EELEEEQRTEE	1421.4	2	3.8471	0.1941
EELEEVIKDI	1217.3	2	2.8888	0.1278
EELEQASQAHGAR	1426.5	2	4.3975	0.3179
EELSNVLAAMR	1233.4	2	2.987	0.2643
EELTAFLHPEEFPHMR	1984.2	2	3.8563	0.3966
EELVKNLGTIAK	1315.5	2	3.6691	0.2718
EENKGGEDKLK	1247.3	2	3.1175	0.1601

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EENLSMHQMLDQTLLELNNM	2404.7	2	4.6734	0.3159
EENVKADVFHAYLSLLK	1977.2	3	4.8638	0.3474
EESGKPGAHVTVK	1339.5	2	3.4673	0.359
EESGKPGAHVTVKK	1467.7	2	3.3539	0.1727
EESLVEELSPASEK	1547.6	2	3.3879	0.3247
EESREPAPASPAPAGVEIR	1964.1	3	3.2518	0.2499
EESTSSGNVSNR	1267.2	2	2.9247	0.4436
EETQPPVALKK	1240.4	2	2.9566	0.1382
EEVEVLKEQIK	1344.5	2	3.1708	0.1154
EEVKEAYMGNVLQGGEGQAPTR	2364.6	3	4.0489	0.1667
EEYEGPNKKPR	1347.5	2	3.0776	0.3848
EEYPDRIMNTFSVVPSPK	2110.4	3	3.2728	0.2709
EFADSLGIPFLETSAK	1725.9	2	4.7827	0.4297
EFATLIIDILSEAK	1563.8	2	2.923	0.2531
EFDDLSPEQQR	1364.4	2	3.3273	0.2348
EFDELNPSAQR	1306.4	2	2.7897	0.2464
EFDLTKEEDLAALRHEIELR	2428.7	3	3.4691	0.2554
EFDYVINDLTAVPISTSPEEDSTWEFLR	3275.5	2	2.7531	0.1834
EFEETMDALQADIDQLEAEKAELK	2768.0	2	2.582	0.207
EFELEESYNGR	1373.4	2	2.505	0.1837
EFEPLLKPHVAVK	1507.8	2	3.2436	0.2621
EFESVLVDAFSHVAR	1706.9	2	3.9116	0.4215
EFFNGKEPSR	1211.3	2	3.0871	0.302
EFGEEALNSLQK	1365.5	2	3.1741	0.2724
EFGGGHIKDEVFGTVKEDVSLHGYKK	2878.2	3	4.6483	0.4056
EFHHGPDPTDTAPGEQAQDVASSPPESSFQK	3295.4	3	5.2087	0.2782
EFHLNESGDPSSK	1447.5	2	3.7997	0.33
EFHSHEFHSHEDMLVVDPK	2321.5	2	4.1174	0.4174
EFIAWLVK	1006.2	1	2.5713	0.2201
EFIEKYDKSLHQAIEGDTSGDFLK	2772.0	3	5.3939	0.3508
EFIGSFLEMFGPEGALK	1873.2	2	2.8533	0.2503
EFLGKSEPEHQH	1438.5	2	2.9993	0.3214
EFLGTYNKLTETCFLDCVKDFTTR	2846.2	3	4.0429	0.345
EFLHAQEEVKR	1386.5	2	3.1407	0.4358
EFNAETFTFHADICTLSEK	2204.4	2	4.0777	0.498
EFNAEVHRK	1130.2	2	3.0089	0.2593

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EFNEEGALSVLQQFK	1739.9	2	3.5311	0.1813
EFNGQHFILEEAITGDFALVK	2379.7	2	2.8918	0.2911
EFNKYDTDGSK	1304.3	2	2.9718	0.1937
EFPGFLENQKDPLAVDK	1948.2	2	4.2228	0.2992
EFPVYLWQPFFR	1629.9	2	3.3004	0.2639
EFQASPLLLPVPTQVPQPVGR	2274.6	3	4.6824	0.4849
EFQDAGEQVVSSPADVAEK	2007.1	2	5.1968	0.5011
EFQLHQHLFDPEHDYPGLGK	2408.6	3	5.5081	0.4289
EFQLHQHLFDPEHDYPGLGKWNK	2837.1	3	3.7013	0.2241
EFQLHQHLFDPEHDYPGLGKWNKK	2965.3	3	5.7995	0.3797
EFRFEPSSQMIEVQEGQNLK	2397.6	3	4.4752	0.2035
EFRGQENGLDGTK	1451.5	2	3.9985	0.29
EFSHIAFLTIK	1306.5	2	3.3357	0.3156
EFSHLGKEDFTSLSLVLYSR	2329.6	3	4.3693	0.368
EFSIDVGYER	1215.3	2	2.7084	0.3763
EFSITDLVPYSITLR	1755.0	2	4.1045	0.4935
EFSITDVVPYPISLR	1737.0	2	4.5138	0.491
EFSPFGTITSAK	1285.4	2	2.8109	0.3316
EFTEAVEAK	1024.1	1	1.7502	0.1244
EFTKLEEVLTNK	1451.6	2	3.6711	0.3359
EFTKLEEVLTNKK	1579.8	2	4.444	0.3233
EFTLEFSR	1029.1	2	2.5615	0.2936
EFVEREVIDFAR	1510.7	2	2.4221	0.2218
EFVGQLVAPLPLGTGALR	1839.2	2	2.7238	0.141
EFVISDRKELEEDFIK	1998.2	3	3.6196	0.3028
EFVISDRKELEEDFIKSELKK	2583.9	3	5.8189	0.329
EGAAHAFAQYNLDQFTPVKIEGYEDQVLITEHGDLGNGK	4277.6	3	5.3048	0.4109
EGAAHAFAQYNMDQFTPVKIEGYEDQVLITEHGDLGNSR	4353.7	3	5.8291	0.4123
EGAIHREELVYELNPLDHR	2291.5	3	5.0279	0.2315
EGAPGAEGSPGR	1085.1	2	3.3904	0.3963
EGASEEEIRLSK	1348.4	2	3.7815	0.1445
EGASLPKPKP	1024.2	2	2.4478	0.1332
EGDIVKR	816.9	1	1.907	0.114
EGDLIAAQAR	1044.1	2	3.1988	0.1785
EGDLLFTVAKDPIVNVWYSVNGER	2723.0	3	4.5978	0.3374
EGDLSTKYDAPFVFAEVNADVVDWIQQDDGSVHK	3797.0	3	5.8065	0.2846

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EGDNVNYDWIHWDPEHSYEFK	2681.8	3	3.6737	0.2035
EGDQTSNNIPADIVFVLK	1961.2	2	3.8907	0.3784
EGDTVIFASDDEQDR	1697.7	2	3.7181	0.2393
EGDVLTLLESER	1361.5	2	3.9287	0.2944
EGDVLTLLESEREAR	1717.9	2	3.1768	0.1494
EGDYVLFHHEGGVDVGDVDAK	2259.4	2	5.0813	0.4412
EGDYVLFHHEGGVDVGDVDAKAQK	2586.8	3	6.3486	0.4192
EGEEAGPGDPLLEAVPK	1708.8	2	3.8273	0.3909
EGEFVAQFK	1055.2	2	2.5774	0.3244
EGENPPDGFMAPK	1389.5	2	2.9577	0.1192
EGEPGWVHPRGVEQRNKALDWLR	2731.0	3	3.3689	0.1533
EGESVTVLR	990.1	1	2.0153	0.1741
EGFFTNGLTLGAK	1355.5	2	3.3109	0.3327
EGFHFEETLTGFK	1542.7	2	2.8469	0.2808
EGGDGEEQDVGDAGR	1491.4	2	3.6395	0.3824
EGGFSPHISPFTAVNDLGHLLGR	2422.7	3	4.7427	0.3988
EGGGAIEEEAKEK	1347.4	2	2.7115	0.2192
EGGGEGGPHLAVLHSVLHR	1923.1	2	2.9781	0.2287
EGGGNNLYGEEMVQALK	1810.0	2	3.769	0.2683
EGGLGPLNIPLLADVTR	1736.0	2	4.8481	0.4891
EGGLLTLAGAK	1030.2	2	2.694	0.2461
EGGPNNHLLK	1079.2	1	1.8408	0.1003
EGGQTAPASTR	1075.1	2	3.5608	0.3807
EGGSAGLIPSQFLEEK	1662.8	2	3.7199	0.1985
EGGSIPVTLTFQEATGK	1735.9	2	3.7721	0.4225
EGGTVVYGGK	967.1	2	2.4344	0.2724
EGGVLKVHPTSTR	1381.6	2	2.7764	0.1736
EGHLPSVLAMIHVK	1531.8	2	3.6007	0.2911
EGHPVTSEPSRPEPAVFK	1965.2	2	3.8579	0.3828
EGHPVYPQLRPGYIPIPVLHEGAENR	2940.3	3	5.2005	0.3748
EGIDPTPYYWYTDQRK	2033.2	2	2.8972	0.2553
EGILNDDIYCPPETAVLLASYAVQSK	2811.2	2	4.6247	0.3403
EGILSDEIYCPPETAVLLGSYAVQAK	2768.1	2	4.4369	0.4109
EGINIFLDGYVPTENLR	1951.2	2	3.0259	0.1703
EGIPALDNFLDKL	1445.6	2	3.9478	0.4385
EGIREETVSLRKD	1532.7	3	3.5265	0.1636

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EGITVYSMQFGGYAK	1651.9	2	2.9999	0.3068
EGIVTATEQEVKEDIAK	1861.0	2	4.2105	0.4063
EGKAAEAVAAAVGTGATTAAVMAAAGIAAIGPAKELEAER	3668.1	3	3.9768	0.3021
EGKDVNSSSPVMLAFK	1709.9	2	4.1001	0.2761
EGKEHDLSVSSDSTHVTFYGLLR	2578.8	3	3.4819	0.2954
EGKHEPVQPSAHHSAEPAEAGK	2294.4	2	4.5309	0.5031
EGKHEPVQPSAHHSAEPAEAGKAETSEGSGSAPAVPEASASPK	4206.4	3	3.752	0.3563
EGKLIMGIGHR	1211.5	2	3.0246	0.2164
EGKLQPHEFQGGTFTISNLGMFGIK	2738.1	3	4.3818	0.382
EGKNLDAVHDITVAYPHNIPQSEK	2676.9	3	4.224	0.3189
EGKPEIEGKPESEGEPGSETR	2243.3	3	3.9966	0.4023
EGKQFSSADEAALKEPIIK	2062.3	2	5.2203	0.4243
EGKQFSSADEAALKEPIIKKFEEEGNPYYSSAR	3721.0	3	6.362	0.4981
EGKVVDAK	846.0	1	1.9596	0.2374
EGLDKLVSDANEQYKLVSDTIGQRVDEIDAAIQR	3791.1	3	3.5619	0.2181
EGLELPEDEEEK	1417.5	2	2.7265	0.2571
EGLELPEDEEEKK	1545.6	2	3.11	0.1564
EGLELPEDEEEKKK	1673.8	2	3.0929	0.2622
EGLELPEDEEEKKKMEESK	2278.5	2	3.9752	0.267
EGLELPEDEEEKKKQEEK	2188.3	2	4.1956	0.2489
EGLELPEDEEEKKKQEEKK	2316.5	2	4.0332	0.2707
EGLISQDGSSLEALLR	1688.9	2	3.9308	0.2824
EGLISQDGSSLEALLRTDPLEKR	2528.8	3	3.7229	0.1602
EGLLATHPRPGQERPGVAR	2042.3	3	3.4224	0.2158
EGLNSVIKPTQYKPVPDEEPNSTDVEETLER	3515.8	3	4.9397	0.3542
EGLPVALDKHILGFDTGDAVLNEAAQILR	3077.5	3	7.7616	0.6112
EGLPVEQRNEILTAILASLTAR	2395.7	3	3.5301	0.2315
EGLTSIEEVTKNLQK	1689.9	2	3.1515	0.2576
EGLVMVEVRK	1160.4	2	2.9894	0.2289
EGMAALQSDPWQQELYR	2023.2	2	5.0452	0.3774
EGMLQHWELGQALR	1668.9	2	4.1814	0.3594
EGMNIVEAMER	1279.5	2	3.0758	0.2949
EGMTAFVEKR	1168.3	2	2.8055	0.2585
EGNASGVSLLEALDTILPPTRPTDKPLR	2962.3	3	4.432	0.3636
EGNASGVSLLEALDTILPPTRPTDKPLRLPLQDVYK	3919.5	3	5.0249	0.4647
EGNDLYHEMIESGVINLK	2062.3	2	5.4105	0.4214

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EGNDLYHEMIESGVINLKDATSK	2564.8	2	5.6605	0.4675
EGNDLYHEMIESGVINLKDATSKVALVYGQMNEPPGAR	4148.6	3	6.1567	0.3596
EGNGTVMGAEIR	1234.4	2	3.2345	0.2992
EGNLELLKIPNFLHLTPVAIKK	2489.0	3	4.0456	0.2758
EGNNPAENGDAK	1216.2	2	3.0066	0.2822
EGNNPAENGDAKTDQAQK	1887.9	2	2.8606	0.1955
EGNNPAENGDAKTDQAQKAEGAGDAK	2587.6	3	3.5985	0.285
EGNSPSFFNPEEAATVTSYLK	2289.4	2	2.8382	0.2631
EGPAHEPK	864.9	1	2.0441	0.1816
EGPAVVGQFIQDVK	1487.7	2	2.8584	0.246
EGPEGANLFIYHLPQEFGDQDLLQMFMPFGNVVSAK	4041.6	3	3.9361	0.2822
EGPYDVVVLPGGNLGAQNLSESAAVK	2585.9	3	5.221	0.4682
EGPYDVVVLPGGNLGAQNLSESAAVKEILKEQENR	3726.1	3	4.5917	0.3903
EGPYDVVVLPGGNLGAQNLSESAAVKEILKEQENRK	3854.3	3	4.4494	0.3631
EGPYSISVLYGDEEVPR	1911.1	2	4.5657	0.3546
EGPYSISVLYGDEEVPRSPFK	2370.6	2	5.7001	0.5034
EGQEDQGLTK	1105.1	1	2.2229	0.2172
EGQEDQGLTKDFSNSPLHR	2159.3	3	4.464	0.2826
EGQEDQGLTKDYGNSPLHR	2145.2	2	4.4695	0.4561
EGRGESENAGTNQETR	1735.7	2	4.7647	0.396
EGRPSGEAFVELESEDEVKLALKK	2661.9	3	3.5475	0.1106
EGRPSGEAFVELESEEEVKLALKK	2676.0	3	5.1671	0.3155
EGSALTEGAKEEGGEEVAKAVLEQEETAAASR	3248.4	3	5.3998	0.4296
EGSGGGGGMDDIFSHIFGGGLFGFMGNQSR	2993.2	3	4.1752	0.1916
EGSGIGAIDSNLDWSHNFTNMLGYTDHQFTELTR	3829.1	3	5.5417	0.3909
EGSGNPTPLINPLAGR	1593.8	2	2.4474	0.3038
EGSGSSGTGEQKEDQKEEK	2011.0	2	3.4642	0.2517
EGSGSSGTGEQKEDQKEEKQ	2139.1	2	3.9429	0.2057
EGSIEIDIPVPK	1297.5	2	3.0669	0.1049
EGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASR	3657.9	3	4.4245	0.3555
EGSRTDDEVVQR	1391.4	2	3.6185	0.2265
EGSRTDDEVVQREEEAIQLDGLNASQIR	3159.3	3	4.9349	0.3169
EGSRTDDEVVQREEEAIQLDGLNASQIRELR	3557.8	3	3.6718	0.1546
EGSTHNWQHITDQIGMFCFTGLKPEQVER	3390.8	3	4.7714	0.3045
EGTAPSENGETKAEEAQKTESVDNEGE	2837.8	3	3.7852	0.2258
EGTEASASKGLEKK	1435.6	2	3.1354	0.2049

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EGTETFADHREGILK	1703.8	2	3.2199	0.2982
EGTFTSDVSSYLEGQAAK	1891.0	2	5.2888	0.5597
EGTGSTATSSSSTAGAAGK	1628.6	2	4.5206	0.4822
EGTINVHDVETQFNQYK	2023.1	2	2.928	0.2081
EGTKITFPKEGDQTSNNIPADIVFVLK	2963.3	3	3.665	0.1633
EGTLTQVPLAPPPPGAPPSPAPAR	2319.6	3	3.6531	0.3032
EGVHGGGLNK	968.0	1	2.6204	0.3081
EGVHGGLINK	1024.2	1	2.7257	0.2393
EGVHGGLINKK	1152.3	2	3.0175	0.1701
EGVIGVTEEQVHHIVK	1775.0	2	3.6993	0.3659
EGVKFDESEK	1168.2	2	2.7142	0.2822
EGVKFDESEKTK	1397.5	2	3.4207	0.2744
EGVKVMPNAIVQSVGVSSGK	1987.3	3	3.9717	0.335
EGVLPLTAASTAPISFGFTR	2036.3	2	3.0762	0.2716
EGVREVFEMATR	1424.6	2	3.5239	0.3268
EGVVGPELHHK	1202.3	2	2.6686	0.2116
EGYLQIGANTQAAQK	1592.7	2	4.7922	0.301
EGYNNPPISGENLIGLSR	1931.1	2	3.3655	0.2561
EGYSALPQLDIER	1491.6	2	3.4284	0.2657
EHAALEPR	923.0	1	2.2278	0.2637
EHALAQAELLK	1223.4	2	2.612	0.2454
EHALAQAELLKR	1379.6	2	3.3207	0.3859
EHALLAYTLGVK	1315.5	2	4.2902	0.4236
EHALTSGTIK	1057.2	1	2.9673	0.333
EHAMLAK	800.0	1	1.7373	0.1556
EHAPSIIFMDEIDSIGSSR	2105.3	3	4.1715	0.4766
EHASGSGAQSEAAGR	1415.4	2	4.4427	0.5524
EHDPVGQMVNNPK	1465.6	2	3.4494	0.4384
EHDVKKEDGTFYEFGEDIPEAPER	2839.0	3	4.2781	0.3611
EHEEPTTSEMAEETYSPK	2096.2	2	4.7006	0.4411
EHEKEVLQK	1140.3	2	2.4988	0.1856
EHFAQFGHVR	1228.3	2	3.5161	0.4271
EHFGTVK	817.9	1	1.8095	0.1115
EHFQHVAAPYIAK	1511.7	2	3.9972	0.4923
EHFQSYDLDHMEK	1679.8	2	4.4565	0.4043
EHGAFDAVK	974.1	2	2.4028	0.3066

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EHGGPEGMDPDGVIESNWNEIVDNFDDMNLK	3475.7	3	6.7768	0.5243
EHGGPEGMDPDGVIESNWNEIVDNFDDMNLKESLLR	4074.4	3	5.9251	0.4244
EHGIR	611.7	1	1.6042	0.2158
EHGIRFFETSAK	1422.6	2	3.2143	0.3355
EHGLIFMETSAK	1363.6	2	3.1534	0.3179
EHHFEAIALVEK	1423.6	2	4.0005	0.4417
EHHFEGIALVEK	1409.6	2	2.6329	0.1808
EHHFGSSGMTLHER	1625.8	2	3.4768	0.3681
EHIIHLER	1047.2	2	2.4141	0.1909
EHIMQMLQNPDWK	1670.9	2	2.8082	0.2643
EHLAMLLSSVLEAKPLLGDQSHAGSELLQR	3244.7	3	4.1604	0.3891
EHLGHESDNLLFVQITGK	2038.2	3	3.7717	0.1519
EHLHIVK	876.0	1	2.2933	0.1402
EHLHIVKR	1032.2	2	2.4437	0.2772
EHLLAQWELEVFER	1800.0	2	3.0519	0.1058
EHLLTNHLK	1105.3	2	2.5897	0.1735
EHLNEPGTR	1053.1	2	2.4062	0.1485
EHLNKVQTANEVK	1510.7	2	3.9434	0.2991
EHLNQGSSQETDK	1473.5	2	3.4492	0.241
EHMQPTHPIR	1246.4	2	3.0309	0.3053
EHMSSSSSLQSR	1336.4	2	2.7413	0.2691
EHPSLELLHLYFNELSSEGR	2371.6	3	3.5154	0.1425
EHPVLALPGAPAQFPVLEEHRPLQK	2775.2	3	3.544	0.1931
EHQAHVENLEADIKR	1789.9	3	3.982	0.3179
EHQEALHQQR	1276.3	2	3.2357	0.3891
EHQHEEIQNVR	1419.5	2	3.5325	0.3808
EHRSELNLR	1154.3	2	2.9533	0.237
EHSLIKPYQGVGSSSMPLWDFQGSTMLTSQYVR	3732.2	3	5.0451	0.3325
EHSSLGHADLDALQQNPQPLIFHMEMLK	3201.6	3	5.9939	0.2994
EHTAYYIK	1025.1	1	2.1968	0.1862
EHTQLLQQSSSQKDEILQTVKEEQSR	3071.3	3	6.0479	0.3729
EHTSHLEAELEK	1423.5	2	3.7874	0.3656
EHVKEVQQLQGK	1423.6	2	4.0661	0.355
EHVPSGQFPDTEAPATSETSNSR	2445.5	3	4.4534	0.2444
EHVVAASK	840.9	1	2.5739	0.2436
EHYVDLKDRPFFAGLVK	2035.3	2	2.5991	0.1508

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EIADLGEALATAVIPQWQKDELRETLK	3039.4	3	3.8446	0.2408
EIAEEYGGVMVSFPR	1684.9	2	3.1283	0.2538
EIAITHHVK	1048.2	2	2.4189	0.2376
EIAQDFKTDLR	1336.5	1	3.1963	0.2842
EIATLKQHLSNMEVQVASQSSQR	2585.9	3	4.2261	0.2951
EIDDYIVQAK	1194.3	2	2.6622	0.1335
EIDGGLETLR	1103.2	2	2.6843	0.1948
EIDIAATLEHVR	1367.5	2	3.308	0.1725
EIDTDSTSQGESK	1397.4	2	3.4726	0.4426
EIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR	3835.1	3	5.0568	0.3444
EIEDPEDRKPEDWDERPK	2284.4	3	3.4696	0.1304
EIEELKELLPEIR	1611.9	2	3.8206	0.2137
EIEELKQELIQAEIQNGVK	2212.5	3	5.5009	0.2827
EIEELQSQAQALSQEGK	1889.0	2	3.1958	0.2936
EIEIAEQDMSALISLR	1819.1	2	2.4082	0.166
EIEIAEQEMPALMALR	1845.2	2	3.0151	0.2532
EIEIDIEPTDKVER	1686.8	2	3.5574	0.3234
EIEKNPPAQGK	1211.3	2	2.8991	0.2292
EIEMASEERPPAQALEIMMGLK	2474.9	3	3.5906	0.1852
EIENQKTDAASKPFAEVR	2034.2	3	3.5488	0.2901
EIEQEAAVELSQLRDPQHDLDR	2592.8	3	3.9282	0.1078
EIFDSRGNPTVEVDLFTSK	2155.4	2	4.3752	0.3757
EIFEQPESVVNTMR	1679.9	2	4.8866	0.416
EIFLRELISNASDALDKIR	2204.5	3	4.7653	0.2193
EIFLSQPILLELEAPLK	1954.3	2	5.5599	0.4899
EIFVDFAPFLSR	1441.7	2	4.2884	0.3963
EIGELTQLKELHIQGNR	1979.2	3	3.9009	0.3583
EIGELTQLKELHIQGNRLTVLPPELGNLDLTGQK	3769.3	3	3.7204	0.2457
EIGGDVQKHAEMVHTGLKLER	2348.7	3	3.7082	0.2281
EIGQSVDEVEKLIK	1587.8	2	3.7271	0.2997
EIGQSVDEVEKLIKR	1744.0	2	3.631	0.2666
EIGTHKPLPGITVGDIGPK	1930.2	2	3.4096	0.3775
EIGWTDVGGWTGQGGSILGTK	2120.3	2	2.9847	0.3109
EIHQDWANR	1169.2	2	2.6136	0.2006
EIIDPVLDR	1070.2	2	2.4548	0.2749
EIIGVVSQEPVLFATTIAENIR	2400.8	3	3.3193	0.2147

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EIIHQLSIKPMAHSELVK	2074.5	2	3.2913	0.314
EIIQDVTLHDLDVANARPQGGQDILSMMGQLMKPK	3864.5	3	5.0712	0.3958
EIISFGSGYGGNSLLGK	1699.9	2	2.8059	0.1595
EIKDAISGIGTDEK	1476.6	2	3.7296	0.35
EIKDAKEQVSPLETTLEKFQQEKEELINKK	3575.0	3	3.9653	0.2278
EIKDILIQYDR	1406.6	2	3.0773	0.2953
EIKDSLAEVEEK	1390.5	2	3.4246	0.3351
EIKEVIELPVKHPELFEALGIAQPK	2829.3	3	5.5232	0.3577
EIKNYIQGINLVQAK	1732.0	2	3.5089	0.4013
EIKTVESITDIR	1404.6	2	2.6597	0.104
EIKTVESITDIRADIDKK	2075.3	2	3.9932	0.2876
EILDKFTEEVVK	1450.7	2	4.1879	0.3685
EILDKFTEEVVKQTQR	1964.2	3	3.6793	0.3321
EILDSRGNPTVEVDLYTAK	2121.3	2	4.5286	0.3463
EILGTAQSVGCNVDGR	1619.8	2	4.1818	0.4899
EILGTAQSVGCNVDGRHPHDIIDDINSGAVECPAS	3591.9	3	4.7775	0.3233
EILHHVNQAVR	1316.5	2	3.1041	0.3804
EILKEQENRK	1287.4	2	3.0582	0.1523
EILLKGPDWILGEIK	1725.1	2	3.469	0.2396
EILNLTSELLQK	1401.6	2	3.454	0.1936
EILQEEEDLAEIVQLVGK	2056.3	2	5.484	0.4137
EILSVDCSTNNPSQAK	1706.9	2	4.5285	0.383
EILVGDVGQTVDDPYATFVK	2167.4	2	5.7927	0.5294
EIMLAAK	776.0	1	2.0091	0.1339
EINTNQEALKR	1316.4	2	3.1939	0.2192
EIPAKIIFEDDR	1446.6	2	3.1289	0.296
EIQALKDTKPQVQTK	1728.0	2	4.3933	0.3529
EIQEKLDAFIEALHQEK	2042.3	3	5.0867	0.318
EIQELQSKPDR	1343.5	2	2.9966	0.2629
EIQKLETELQEATKEFQIKEDIPETK	3119.5	3	5.9431	0.4737
EIQNASHR	955.0	2	2.857	0.1764
EIQNAVNGVK	1072.2	2	2.5348	0.1558
EIQTAVR	816.9	1	1.8787	0.104
EIQTAVRLLLPGELAK	1752.1	2	4.2694	0.3221
EIQTAVRLLLPGELAKHAVSEGTK	2562.0	3	5.69	0.3914
EIQTTTGNQQVLVR	1587.8	2	4.2741	0.37

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EIQVIPLQRDDED	1570.7	2	2.5016	0.132
EIQVQHPAAK	1121.3	2	2.9874	0.1601
EIRPTYAGSK	1122.3	2	3.0396	0.2879
EISEVFPDQFIHLGGDEVEFK	2436.7	2	3.8773	0.4095
EISGHTSGIKK	1157.3	2	2.9933	0.31
EISGLWNELDSLKDAVEHQR	2340.5	3	3.3053	0.3024
EISITHHVK	1064.2	2	2.4492	0.2332
EISLWFKPEELVDYK	1897.2	2	3.4833	0.3776
EISNLNQLIEEFKK	1705.9	2	2.5597	0.1695
EISQANKNEDTK	1377.4	2	2.5281	0.1884
EISYENTQISR	1340.4	2	3.1707	0.3009
EISYLESEMYQLSHLLTEQK	2442.7	2	4.0213	0.3669
EITALAPSTMK	1162.4	2	2.9757	0.3097
EITALAPSTMKIK	1403.7	2	3.1032	0.1079
EITFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVAR	4600.1	3	3.8935	0.2773
EITSLDTENIDEILNNADVALVNFYADWCR	3458.8	3	5.8373	0.4397
EIVDPLYGIAEVEIPNIQK	2141.4	2	3.3599	0.2072
EIVDSYLPVILDIIK	1731.1	2	4.895	0.5028
EIVHIQAGQCGNQIGAK	1767.0	2	4.9935	0.3785
EIVHLQAGQCGNQIGAK	1767.0	2	5.0534	0.3431
EIVTNFLAGFEA	1311.5	2	2.6057	0.2017
EIYKDNR	938.0	2	2.5226	0.1655
EIYPYVIQELRPTLNELGISTPEELGLDKV	3430.9	3	7.1622	0.5855
EKAANSLEAFIFETQDK	1942.1	2	4.6684	0.5054
EKADIQLLVYTIDDLIDK	2106.4	3	4.3049	0.3649
EKADIQLLVYTIDDLIDKLSTIVN	2734.1	2	3.5244	0.4288
EKAEGDVAALNR	1273.4	2	3.396	0.3403
EKAPSIIFIDELDAIGTK	1961.2	2	4.687	0.4818
EKAPSIIFIDELDAIGTKR	2117.4	3	3.945	0.3129
EKDFLLKEAVESQR	1692.9	2	2.9162	0.1685
EKDFSPEALKK	1292.5	2	3.3133	0.1924
EKDILVLPLDLTDTGSHEAATK	2367.6	3	5.2204	0.4198
EKDIQEESTFSSR	1556.6	2	4.0909	0.3908
EKDKHIEEVR	1283.4	2	2.806	0.2203
EKDKHIEEVRK	1411.6	2	2.8846	0.2345
EKDLEDLFYK	1300.4	2	3.0436	0.143

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EKDLTEVSTLKDLFGLASNEHDLSMAK	2993.3	3	5.4729	0.2696
EKDNIDITLQWLIQHSK	2082.3	3	4.4615	0.2974
EKDPFEVDLSHVYLAYTEESLR	2641.9	3	3.9626	0.208
EKDRDPEAQFEMPYVVR	2110.3	3	3.8484	0.2798
EKDTAVQGNIR	1231.3	2	2.8402	0.2464
EKDVFDDIPKWEGK	1706.9	2	3.1582	0.3483
EKDVQFEHGYR	1408.5	2	3.1879	0.3107
EKEAAEQAER	1161.2	2	2.7358	0.2208
EKEAAYQER	1124.2	2	2.5757	0.2156
EKEDDVPQFTSAGENFDKLLAGK	2539.7	3	4.166	0.31
EKEEFAVPENSSVQQFKEEISKR	2740.0	3	3.7911	0.3631
EKEELELLKEDVQDYSEDLQEIKK	2952.2	3	5.3002	0.3144
EKEELETGKK	1191.3	2	2.626	0.1483
EKEELMLR	1048.2	2	2.4786	0.1112
EKEFEETMDALQADIDQLEAEKAELKQR	3309.6	3	4.1134	0.1898
EKEISGLWNELDSLKDAVEHQR	2597.8	3	4.3583	0.4107
EKEKEEPPGEK	1300.4	2	2.8348	0.1597
EKEKEPEKLDKLENSAAPK	2184.4	2	4.6287	0.4401
EKEKPSYDTETDPSEGLMNVLK	2511.7	3	3.3558	0.1388
EKEPEKPAKPLTAEK	1695.9	2	3.7669	0.2228
EKEPEYTLLTER	1508.7	2	3.1259	0.116
EKEPIVGSTDYGKDEDSAEALLK	2495.7	3	3.6339	0.267
EKEPVVVETVEEKKEPILVCPPLR	2762.3	3	4.0176	0.2303
EKEQNEAEER	1262.3	2	2.4634	0.119
EKETLAVNYEKEEEFLTNELSR	2672.9	3	4.1309	0.3727
EKEVEAIQAQAK	1344.5	2	3.089	0.1542
EKFENLGIQPPK	1400.6	2	2.5569	0.2394
EKGKFEDMAK	1183.4	2	2.7072	0.3123
EKGPTLLKHPPAPAEPSSDLASK	2371.7	3	4.3054	0.4183
EKGSETDSAQDQPVK	1619.7	2	3.7233	0.4493
EKGTWVQLKR	1245.5	2	2.7607	0.1121
EKHAHSILQFQFAEVK	1913.2	2	3.9139	0.38
EKHGEEFFPTSNSLLHGTHVPSTEEIDR	3195.4	3	3.3295	0.201
EKIDFADTVTK	1267.4	2	2.6453	0.188
EKIDLENTLEQEQEALVNR	2272.5	2	5.8904	0.4009
EKIEDAKESQR	1333.4	2	2.8707	0.2436

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EKISALQSAGVVVSMSPAQLGTTIYKEFEK	3213.7	3	6.1689	0.4651
EKIVAPISDSPKPPPQR	1860.1	2	3.9035	0.4486
EKKDELDSLITAITTNGAHPSK	2369.6	3	3.6156	0.2767
EKKEESHSNDQSPQIR	1913.0	2	4.504	0.3416
EKLAPVPFFSLLQYE	1782.1	2	3.8049	0.3842
EKLCFLDKVEPHATIAEIK	2185.6	2	4.6212	0.2989
EKLCYVALDFEQEMATAASSSSLEK	2752.1	2	2.4383	0.1018
EKLDQLKQEFEFWYPVDLR	2484.8	3	5.0875	0.4278
EKLDSVIEFSIPDSLLIR	2075.4	2	5.0109	0.4308
EKLDSVIEFSIPDSLLIRR	2231.6	3	3.2606	0.3004
EKLEATINELV	1259.4	2	3.6192	0.2883
EKLEAYQHLFYLLQTNPTYLAK	2685.1	3	5.5098	0.4507
EKLEDFFKNMVK	1528.8	2	2.9139	0.2215
EKLEMEMEAAR	1337.5	2	3.3379	0.1607
EKLEMEMEAARHEHQVMLMR	2499.9	3	3.8104	0.2455
EKLHIPWGDNSNQQHGDK	2104.2	3	3.7168	0.1455
EKLILPHVDIQLK	1546.9	2	4.0913	0.2734
EKLKEEENTVGR	1432.6	2	2.9351	0.1583
EKLKSLKDSCSWAGPTPHTR	2242.5	2	3.119	0.1389
EKLQEEMLQREEAENTLQSFR	2609.9	2	4.4442	0.3474
EKLQEEMLQREEAENTLQSFRQDVDNASLAR	3680.0	3	3.3019	0.3229
EKLVLTTLDFQK	1435.7	2	2.994	0.1095
EKMDLTAK	936.1	1	2.0956	0.1778
EKMDLTAKELTEEKESAFEFLSSA	2735.0	2	3.0995	0.1911
EKNHLQEQK	1154.3	2	2.6017	0.1853
EKNLEEAKK	1089.2	2	3.0157	0.169
EKNQPKPSPK	1153.3	2	2.5127	0.1786
EKNVQGIIEILK	1384.6	2	3.8554	0.2126
EKPEEESLAAPTWLVHLQQVER	2590.9	3	3.5594	0.2571
EKPKSDKTEEIAEEEETVFPK	2464.7	3	3.7594	0.1574
EKPLALYVFSHNHK	1683.9	2	4.8029	0.3927
EKPLIQHPIDSQVAMSEFPAAQPLYDER	3211.6	3	3.3783	0.2182
EKPQTLPSAVKGDEK	1627.8	2	3.8541	0.3468
EKPSKPTEKTEESK	1618.8	2	3.1658	0.3161
EKPYFPIPEEYTFIQNVPLEDR	2726.0	3	6.2709	0.409
EKQAKGDTEF	1153.2	2	2.7962	0.157

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EKQAQLAQTLQQQEQASQGLR	2384.6	3	5.7192	0.487
EKQDTFALASQQK	1494.6	2	4.3703	0.264
EKQEEIDNYKK	1424.5	2	3.5022	0.1527
EKQLAAENR	1059.2	2	2.6877	0.2578
EKQLSPEAQAR	1257.4	2	2.9126	0.1073
EKQPVAGSEGAQYR	1520.6	2	3.8311	0.3524
EKQPVTGTEGAFYR	1583.7	2	3.2348	0.218
EKQSDDEVYAPGLDIESSLKQLAER	2822.0	3	3.3162	0.2176
EKRDPGVITYDLPTPPGEKK	2241.5	3	3.7968	0.1311
EKRPEAAQLLEDVQAALKPFSVK	2569.0	3	6.9232	0.5132
EKSNLAHSLQVAQQQAEELRQER	2693.9	3	4.0575	0.2369
EKSSQESGEEAGSQENHPQESK	2403.4	3	5.1089	0.4418
EKTHVADFAPEVAWVTR	1957.2	2	4.4915	0.5132
EKTLLQKPHVDITDPEKPHQPK	2579.9	3	5.3364	0.27
EKTPDEKKDEIEK	1589.7	2	3.777	0.2496
EKTPSPKEEDEEPESPPEKK	2311.4	3	4.0087	0.162
EKTVQQHAGETDPVTTMR	2029.2	3	3.7587	0.2433
EKVDLVLLGK	1114.4	2	2.7515	0.318
EKVESELR	990.1	1	2.2258	0.1447
EKVFDVIIR	1119.3	2	2.6721	0.3515
EKVGEVTYVELFKDAEGK	2042.3	2	4.0638	0.4219
EKVGEVTYVELLMDAEGK	2011.3	2	4.7931	0.5221
EKVHEYNVLLETLSR	1831.1	2	3.7657	0.4716
EKVLATVTKPVGGDK	1542.8	2	4.6532	0.3879
EKVLATVTKPVGGDKNGGTR	2028.3	3	3.4334	0.2977
EKVLGADHPDVAK	1379.5	2	3.503	0.255
EKVLGTNHPDVAK	1408.6	2	3.9972	0.3359
EKVMYEKEAK	1255.5	2	2.8583	0.2196
EKVNVDIINFGEEEVNTEKLTAFVNTLNGK	3366.7	3	3.4593	0.1918
EKVSSIDLEIDSLSSLLDDMTKNDPFK	3041.4	3	3.6852	0.2095
EKVTEQHR	1027.1	2	2.5679	0.2471
EKVVPLADIITPNQFEAELLSGR	2540.9	3	6.0757	0.3937
EKVWAHYEEQPVEEVMPVLEEK	2700.0	3	4.8035	0.2872
EKVWAHYEEQPVEEVMPVLEEKER	2985.3	3	6.1106	0.4176
EKYEKDIAAYR	1386.5	2	3.7008	0.2827
EKYGIVDYMIEQSGPPSKEILTLK	2740.2	3	4.2636	0.4123

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EKYGKDATNVGDEGGFAPNILENK	2567.7	3	4.8069	0.3046
EKYGKDATNVGDEGGFAPNILENKEGLELLK	3350.7	3	7.3608	0.5505
EKYGKDATNVGDEGGFAPNILENKEGLELLKTAIGK	3821.2	3	5.1303	0.3823
EKYIDQEELNK	1409.5	2	4.0687	0.2868
EKYPSHSFIGEESVAAGEK	2066.2	2	3.4224	0.1276
EKYQEEFEHFQQELDKK	2256.4	2	3.4793	0.208
EKYQEEFEHFQQELDKKKEEFQK	3046.3	3	4.9233	0.249
EKYSIGEPTVPSTLAEEFTYNPFMR	2908.2	3	4.4527	0.3409
ELAEDDSILK	1133.2	2	2.8277	0.2324
ELAEDGYSGVEVR	1424.5	2	4.1733	0.4251
ELAEEFGVTEYPTLK	1726.9	2	4.914	0.4546
ELAEEKREGYER	1509.6	2	2.7091	0.1568
ELAEQKATEKQHITLALEK	2181.5	3	4.0455	0.325
ELAEQLGLSTGEKEKLPGELEPVQATQNK	3138.5	3	6.1737	0.342
ELAESDFASTFR	1373.4	2	3.4005	0.3431
ELAILLGMLDPAEKDEK	1886.2	2	3.8704	0.3169
ELAKVEEEIQTLSQVLAAK	2100.4	3	4.4479	0.23
ELALPGELTQSR	1314.5	2	2.9866	0.2211
ELALQPKDDIVDRAK	1711.9	3	3.7095	0.3047
ELAPYDENWFYTR	1704.8	2	2.7701	0.1898
ELAQNASSDTPMDPVTFIQTLPSDLRR	3004.3	3	4.3099	0.3024
ELAQQVQQVAAEYCR	1736.9	2	3.9082	0.3601
ELAQQVQQVADDYGK	1692.8	2	5.0341	0.4258
ELASALKSALSGHLETVILGLLK	2364.8	3	3.7156	0.3255
ELASALKSALSGHLETVILGLLKTPAQYDASELK	3569.1	3	6.3694	0.4347
ELASLHGTK	956.1	1	2.6503	0.2516
ELASQPDVDGFLVGGASLKPEFVDIINAK	3031.4	3	4.4575	0.4564
ELASQPDVDGFLVGGASLKPEFVDIINAKQ	3159.5	3	4.5578	0.3654
ELASTTQIDFWKPDSVTQIKPHSTVDFR	3248.6	3	4.9613	0.4135
ELAVQIYEEARK	1449.6	2	3.8153	0.2371
ELCHTQSSHASLR	1469.6	2	3.5261	0.3826
ELCQGLGQPGSVLR	1457.7	2	3.2528	0.1872
ELDAFFLHMLMK	1495.8	2	4.4313	0.3786
ELDALDANDELTPLGR	1742.9	2	4.3539	0.3657
ELDALGHELPVLAPQWEGYDELQTDGNR	3167.4	3	5.6352	0.3783
ELDDATEANEGLSR	1520.5	2	5.1186	0.4433

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ELDDTRASREEILAQAKENEK	2446.6	3	3.5969	0.1583
ELDEEGSDPPLPGR	1511.6	2	2.5092	0.2159
ELDELMASLSDFK	1498.7	2	3.1256	0.3992
ELDESLQVAER	1289.4	2	3.501	0.3397
ELDESLQVAERLTR	1659.8	2	2.7214	0.1714
ELDFVSHHVR	1239.4	2	3.1184	0.4095
ELDIMEPKVPDDIYKTHLENNR	2671.0	3	5.0247	0.4258
ELDLPVDLDDISEADLDHPDLFQNR	2896.1	2	3.7707	0.2491
ELDLVSHHVR	1205.3	2	3.5519	0.4107
ELDPTNMTYITNQAAVYFEK	2349.6	3	4.2956	0.3899
ELDPTNMTYITNQAAVYFEKGDYNK	2927.2	3	3.2342	0.1317
ELDRDTVFALVNYIFFK	2091.4	3	4.0123	0.3131
ELDRNYLNYGEEGAPGK	1926.0	2	4.5797	0.307
ELDRNYLNYGEEGAPGKWQQQGDLQDTK	3254.4	3	5.675	0.4634
ELDRNYLNYGEEGAPGKWQQQGDLQDTKENR	3653.8	3	4.7506	0.3006
ELDRNYLNYGEEGAPGKWQQQGDLQDTKENREEAR	4139.3	3	4.3797	0.2617
ELDSITPEVLPGWK	1584.8	2	4.0647	0.3476
ELDSLQTEAESLDNTVKELAEQLEFIK	3094.4	3	3.8245	0.2447
ELDSNPFASLVFYWEPLNR	2298.5	2	4.1622	0.3099
ELDTNTLKNAGDLLNR	1788.0	2	3.0405	0.1174
ELEAASAPEER	1202.3	2	2.6327	0.1833
ELEAENYHDIKR	1517.6	2	3.9554	0.3423
ELEALDEVFTK	1294.4	2	3.6411	0.3392
ELEDAQAGSGTIGR	1404.5	2	4.1032	0.3737
ELEDATETADAMNR	1566.6	2	4.6852	0.4832
ELEDATETADAMNREVSSLK	2210.4	2	4.469	0.3973
ELEDATETADAMNREVSSLKNK	2452.6	2	4.654	0.3586
ELEDFKLQHGSILGFPK	1959.2	3	4.8497	0.3975
ELEDKVIELHK	1353.5	2	3.5252	0.217
ELEDLEHLQLDFWR	1844.0	2	2.8522	0.2335
ELEDVTESAESMNR	1610.7	2	4.4872	0.4251
ELEDYIDNLLVR	1492.7	2	4.1986	0.3322
ELEEAMAGER	1135.2	2	2.7618	0.3105
ELEEIVQPIISK	1398.6	2	4.3341	0.2926
ELEEQLENETLHKEIHNLK	2347.6	3	4.3423	0.3083
ELEEVSPETPVVPATTQRTLAR	2424.7	3	3.3612	0.1098

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ELEKTYSAKLDNAR	1638.8	2	3.5419	0.4037
ELELKVPLVVR	1295.6	2	3.2497	0.2358
ELELQKEQR	1173.3	2	2.6358	0.1176
ELELVYAR	993.1	1	2.2513	0.2606
ELENIIQETEKELDPDGLKK	2342.6	3	3.6495	0.2947
ELENLAAMDLELQK	1617.8	2	5.4247	0.3536
ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK	3000.3	3	5.6381	0.4902
ELESAHHPFTAPHPSDIHLLYTEPK	2868.2	3	3.9437	0.1968
ELESQISELQEDLESER	2035.1	3	5.5953	0.5273
ELESVCVVEAGPGTCTFDHRHLYTK	2793.1	3	3.2023	0.1729
ELETVAAHQFPEVR	1626.8	2	2.5937	0.126
ELEVQHPAAK	1122.3	2	3.2668	0.3138
ELFPIAAQVDKEHLFPAAQVK	2352.7	3	3.5476	0.1576
ELFSNLQEFAGPSGK	1624.8	2	4.4725	0.3851
ELFSPLHALNFGIGGDGTQHVLWR	2666.0	3	4.8433	0.4131
ELFSPLHALNFGIGGDTTR	2046.3	2	5.4873	0.5193
ELGDHVTNLR	1154.3	2	2.6688	0.3023
ELGEDGLKAYTEVK	1552.7	2	3.1842	0.2007
ELGENLTDEELQEMIDEADRDGDGEVSEQEFLR	3812.9	3	5.2105	0.4174
ELGEYGFHEYTEVK	1701.8	2	3.9956	0.4461
ELGEYGLQAYTEVK	1600.8	2	4.0784	0.4596
ELGIETYKVNVSER	1637.8	2	3.6765	0.4106
ELGITALHIK	1095.3	2	3.1572	0.2451
ELGIWEPLAVK	1255.5	2	3.1647	0.2671
ELGLEKDDKDAIEEK	1732.9	2	4.6126	0.3365
ELGLETYKVNEVER	1679.9	2	3.7678	0.3281
ELGLGRHENAIK	1337.5	2	2.6784	0.1057
ELGLPEELVSRHPFPGPGLAIR	2385.7	3	4.5371	0.3843
ELGQSLAQEVK	1202.3	2	2.5744	0.1418
ELGSSVALYSR	1182.3	2	2.9637	0.3801
ELGVGIALR	928.1	2	2.7373	0.1849
ELGVGIALRK	1056.3	2	3.0248	0.3221
ELHDLFNLPHDRPYFK	2042.3	2	3.4127	0.2654
ELHEQLVALDKQNK	1665.9	2	5.1921	0.3342
ELHINLIPNKQDR	1590.8	2	4.0303	0.3485
ELHLDNNKLAR	1323.5	2	3.5887	0.2904

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ELHLDNNKLTR	1353.5	2	2.4153	0.1026
ELHPPATSHEAPGTK	1572.7	2	3.007	0.287
ELHSEFSEVMNEIWASDQIR	2421.6	2	5.6275	0.4621
ELIAEHKPHIDK	1430.6	2	3.1478	0.2592
ELIEIISGAAALD	1315.5	2	3.666	0.3271
ELIEKNSQLEQENNLLK	2043.3	3	3.5015	0.1808
ELIIGDRQTGK	1230.4	2	3.2137	0.1981
ELIKVLEEANQAINPK	1810.1	2	4.3898	0.3108
ELIPTEEALRLLDAQLATGGIVDPR	2692.1	3	4.3178	0.3168
ELIQKELTIGSK	1359.6	2	3.8974	0.2595
ELIQKELTIGSKLQDAEIAR	2256.6	3	3.4317	0.2387
ELIQTSALNFLTPLR	1717.0	2	2.9702	0.1349
ELISNASDALDK	1276.4	2	3.2986	0.2931
ELISNASDALDKIR	1545.7	2	4.0443	0.4132
ELISNASDALDKIRYESLTDPSKLDSGK	3067.4	3	4.653	0.2933
ELISNASDALDKIRYESLTDPSKLDSGKELK	3437.8	3	4.9714	0.339
ELISNASDALEKLR	1559.7	2	2.9371	0.2234
ELISNSSDALDK	1292.4	2	3.3039	0.301
ELISNSSDALDKIR	1561.7	2	4.0377	0.3199
ELKDDLKGDLSGHFEHLMVALVTPPAVFDAK	3394.9	3	4.4142	0.284
ELKDLLTELQK	1330.6	2	3.0281	0.2094
ELKEALGIPAAASFK	1545.8	2	4.0282	0.3542
ELKELIQKELTIGSK	1730.0	2	4.0904	0.3318
ELKELIQKELTIGSKLQDAEIAR	2627.0	3	4.6157	0.3993
ELKGYSIPFMGSDVSVVR	1985.3	2	3.4102	0.3271
ELKIDIIPNPQER	1565.8	2	3.2559	0.3055
ELKKDPKPSVSR	1384.6	2	2.8394	0.2323
ELKLLESIFHR	1385.6	2	3.0104	0.2649
ELKQQMQDIQAEIDAHNDIFK	2515.8	3	4.6232	0.3042
ELKREPAVGEPAEVTTTVLVR	2295.6	3	3.4352	0.196
ELKTDNLPNQAR	1399.5	2	3.2531	0.2647
ELKTDSSPNQAR	1346.4	2	2.7843	0.1812
ELLAEYQDLTFLTK	1684.9	2	2.4366	0.22
ELLFHPALFEVPSLK	1741.1	2	4.2481	0.3673
ELLHSVHPESPNLK	1600.8	2	4.123	0.3823
ELLIFLAQYLCNEYQK	1989.3	2	2.4511	0.1058

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ELLIIGGVAAR	1112.3	2	2.9592	0.2256
ELLKDVEVVRPLEK	1668.0	2	3.3312	0.1385
ELLKPNASVALHK	1420.7	2	3.3773	0.1155
ELLLDKLLETPSTLHDQKR	2250.6	3	3.6141	0.103
ELLLQPVTISR	1269.5	2	3.3641	0.1733
ELLLTGPGLEER	1327.5	2	3.5635	0.3175
ELLMGIFEMGWEKPSPIQEESIPIALSGR	3259.8	3	4.9688	0.4024
ELLPLIYHHLLR	1517.8	2	3.2839	0.3993
ELLPVKKFESEILEAISQNSVVIIR	2856.3	3	3.3005	0.1204
ELLQHPFLK	1125.3	2	2.4495	0.201
ELLQHQFLK	1156.4	2	2.9341	0.1692
ELLREETGAALKPR	1583.8	3	4.8404	0.2803
ELLTEFGYKGEETPVIVGSALCALEGRDPELGLK	3636.1	3	3.7681	0.2767
ELLTTMGDR	1036.2	2	2.6783	0.292
ELLTTMGDRFTDEEVDELYR	2433.6	3	5.3645	0.4521
ELLTTMGDRFTDEEVDELYREAPIDKK	3215.5	3	3.3278	0.1617
ELLVIELSDNPGVHEPGEPEFK	2449.7	3	4.5813	0.4309
ELMLHAADVEALQAAK	1711.0	2	3.4497	0.3277
ELNARPLEVFMCSVLK	1850.2	2	2.9056	0.1572
ELNARPLEVFMCSVLKR	2006.4	3	5.1576	0.3157
ELNARPMEVFMCSVLKR	2024.5	3	3.7792	0.2013
ELNEDKLEKLEELTMDGAK	2206.5	2	4.893	0.3403
ELNELVSAIEEHFFQPQK	2159.4	2	5.2174	0.4348
ELNELVSAIEEHFFQPQKYNLQPK	2903.2	3	4.2147	0.2483
ELNHMLSDTGNR	1387.5	2	3.091	0.3669
ELNHMLSDTGNRK	1515.7	2	2.7241	0.244
ELNITAAK	860.0	1	1.9153	0.1442
ELNITAAKEIEVGGGR	1657.9	2	4.2159	0.4535
ELNITAAKEIEVGGGRK	1786.0	2	3.9691	0.3984
ELNKEEAAQQK	1288.4	2	3.3323	0.1778
ELNKEMAAEK	1163.3	2	2.5328	0.111
ELNKEMAAEKAK	1362.6	2	3.6521	0.285
ELNKPVQGPLAHR	1459.7	2	2.8981	0.301
ELNWDDYKKQEQLETAR	2167.3	3	3.8442	0.2299
ELNYFAKALESPERPFLAILGGAK	2636.0	2	3.095	0.1253
ELPAAVAPAGPASLAR	1491.7	2	3.9042	0.4461

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ELPESGIQLGTPR	1397.6	2	2.7601	0.1101
ELPLSPAFFGEDGIFR	1796.0	2	3.6112	0.3271
ELPPGVEELLNKGQDPLADRGEKDTAK	2921.2	3	3.4685	0.2913
ELPTAFDYVEFTR	1588.7	2	3.8272	0.46
ELPTEPPYTAYVGNLPFNTVQGDIDAIFK	3211.6	3	5.9471	0.4411
ELPTEPPYTAYVGNLPFNTVQGDIDAIFKDLSIR	3796.2	3	4.2932	0.4424
ELPVPGSAEEEPPSGGGR	1765.9	2	2.9609	0.3475
ELQAAGKSPEDLER	1543.7	2	4.4546	0.3545
ELQALGFQPGPITDTTR	1845.0	2	4.0553	0.4063
ELQAQIAELQEDFESEK	2008.1	2	4.6178	0.318
ELQDAQEHDAR	1312.3	2	3.0415	0.3268
ELQDLALQGAK	1186.3	2	3.7752	0.29
ELQDLALQGAKER	1471.6	2	4.161	0.2534
ELQEALPEAPAPLLPHITATSLLGTREPDTEVITVEK	3981.5	3	3.3974	0.1503
ELQELQDSLNAEREK	1802.9	2	3.5685	0.1449
ELQELSSSIKDLVLK	1703.0	2	4.7881	0.3125
ELQELVQYPVEHPDK	1825.0	2	3.8814	0.3208
ELQELVQYPVEHPDKFLK	2213.5	2	4.9788	0.4045
ELQHAALGGTATR	1325.5	2	3.5055	0.4476
ELQKANQEQYAEGK	1636.7	2	3.8022	0.2751
ELQKPDSFHSLTPTFAAVLVHIDNLR	2950.3	3	4.3698	0.3039
ELQLEYLLGAFESLGK	1811.1	2	2.9877	0.1932
ELQNTVANLHVR	1394.6	2	3.7501	0.3638
ELQPQQQPR	1124.2	2	2.4022	0.1459
ELQPSEEVTWK	1346.5	2	2.5638	0.1385
ELQSQISDTSVVLSMDNSR	2110.3	2	6.7978	0.5947
ELQTLHNLRK	1252.4	2	2.703	0.3025
ELQVGIPVADEAGQR	1582.7	2	3.3418	0.3314
ELRDHADSNIVIMLVGNK	2025.3	2	3.0939	0.171
ELRDLVLQGHHTR	1574.8	3	4.2867	0.2675
ELRENTQTTIK	1333.5	2	3.359	0.236
ELREQLKELTK	1387.6	2	2.9135	0.1201
ELREVIELPLTNPELFQR	2197.5	3	4.345	0.1891
ELRFEIGEGENLDLPYGLER	2350.6	3	5.4866	0.3376
ELSAERPLNEQIAEAEED	2044.1	2	5.152	0.3629
ELSAERPLNEQIAEAEEDKI	2285.5	2	4.994	0.3485

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ELSAERPLNEQIAEAEEDKIKK	2541.8	3	5.0699	0.3746
ELSAQPEVHR	1166.3	2	2.8128	0.2108
ELSAVTFPDIIR	1361.6	2	3.2451	0.214
ELSDFISYLQR	1371.5	2	4.1758	0.4113
ELSDIAHR	941.0	1	2.3092	0.2798
ELSDPAGAIIYTSR	1493.6	2	2.7665	0.1958
ELSEALGQIFDSQR	1593.7	2	4.7341	0.4696
ELSEIAQSIVANGK	1459.6	2	4.1124	0.4293
ELSEIAQSIVANGKGILAADESVGTMGNR	2932.3	3	4.2873	0.2194
ELSGLGSALKNPFGNAGLLLGEAGK	2414.7	3	5.5009	0.4077
ELSGLPSGPSAGSGPPPPPPGPPPPPVSTSSGSDESASR	3592.8	3	5.9952	0.5451
ELSHEDLEPPPEHIPPPPRPPKR	2666.0	3	4.2051	0.3242
ELSHLQSENDAAKDEVKEVLQALEELAVNYDQK	3758.1	3	4.0986	0.2854
ELSLAGNELGDEGAR	1531.6	2	3.8254	0.3826
ELSQLQELSNHQK	1554.7	2	4.0009	0.3443
ELSSTEAQLHDAQELLQEETRAK	2627.8	3	4.1899	0.2825
ELSYMVVSRGQLVAVGK	1837.2	2	2.8045	0.1144
ELTALLHHYYPIEIDPHR	2218.5	3	3.6903	0.2719
ELTDEEAERLQLEIDQKKDAENHEAQLK	3324.6	3	5.7624	0.3454
ELTEEKESAFEFLSSA	1817.9	2	4.1187	0.4291
ELTIGSK	747.9	1	1.7257	0.2576
ELTLQAMADGVNK	1390.6	2	4.6443	0.4122
ELTNQQEASVER	1404.5	2	3.6847	0.327
ELTPQVVSAAR	1171.3	2	2.4611	0.229
ELTQIKQKVDSLLENLEK	2129.4	2	2.643	0.1769
ELTSELKENFIR	1479.7	2	3.7211	0.3053
ELTVSNNDINEAGVR	1631.7	2	4.4714	0.3784
ELVAENLSVR	1130.3	2	2.5338	0.2247
ELVASGENKIK	1188.4	2	3.0161	0.2429
ELVDDSVNNVR	1260.3	2	3.4086	0.3487
ELVDDSVNNVRKDDPTLLSSGR	2430.6	3	3.6392	0.2413
ELVDYFLNVATAQGR	1696.9	2	4.7006	0.5006
ELVEKSEAVR	1160.3	2	2.4691	0.2669
ELVEPVSR	929.1	1	1.9649	0.1004
ELVFKEDGQEYAQVIK	1897.1	2	5.0713	0.3712
ELVLDNSR	946.0	2	2.7189	0.1816

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ELVSCSNCTDYQAR	1589.7	2	2.7687	0.1614
ELVSDANQHVK	1240.3	2	2.6584	0.2067
ELVSLKQEQQAFK	1548.8	2	3.8383	0.3539
ELVSLKQEQQAFKEAADTER	2321.5	2	4.6954	0.4205
ELVSLKQEQQAFKEAADTERLALQALTEK	3289.7	3	5.6701	0.4175
ELVVTQLGYDTR	1394.6	2	3.2662	0.3429
ELVYPPDYNPEGK	1521.7	2	2.9936	0.2034
ELWFSDDPNVTK	1451.6	2	3.5641	0.3594
ELYERPPHLFAIADAAYK	2105.4	3	4.5748	0.3594
ELYLSHNGIEVIEGLENNNKLTMLDIASNR	3401.8	3	4.1671	0.3193
ELYSILQHK	1131.3	2	2.7831	0.1587
ELYVPENKLHLAK	1554.8	2	3.5499	0.2675
EMAEKEKEKIER	1520.7	2	2.8572	0.1335
EMAGDNKLLGQFTLIGIPPAPR	2339.7	2	2.9111	0.1915
EMAPAWEALAEKYQDHEDIIIAELDATANELDAFAVHGFPTLK	4786.3	3	4.7091	0.322
EMDEAATAEER	1252.3	2	2.6246	0.2834
EMDEEDKAFK	1242.3	2	3.1856	0.2346
EMDEEDKAFKQK	1498.6	2	2.9521	0.1046
EMDEQIR	921.0	1	1.9679	0.123
EMDPVTQLYTMTSTLEYK	2151.4	2	2.5416	0.1936
EMDQTMAANAQK	1338.5	2	4.2673	0.3763
EMDQTMAANAQKNK	1580.8	2	3.2047	0.1472
EMDRETLIDVAR	1448.6	2	3.2806	0.1564
EMDSDIETMQQTIEDLEVASDPLYVPDPDPTKFPVNR	4237.6	3	4.7601	0.351
EMEAELEDER	1251.3	2	2.9301	0.2727
EMEAELEDERK	1379.5	2	3.6815	0.3348
EMEAELEDERKQR	1663.8	2	3.5059	0.1252
EMEDTLNHLK	1230.4	2	2.7376	0.1954
EMEENFAVEAANYQDTIGR	2188.3	2	6.1736	0.5312
EMEENFAVEAANYQDTIGRLQDEIQNMKEEMAR	3905.3	3	5.5917	0.4276
EMFNPMYALFR	1419.7	2	3.1713	0.2824
EMGSEVSEDSEEKDVVNVLQAVGESLAK	2980.2	3	4.5277	0.3572
EMIDIYSTREPQLAFHQR	2235.5	3	5.0647	0.3073
EMIQLPGARPILDPVDFLGLQDKIK	2808.3	3	3.9161	0.2225
EMKPGFYHGHVSYLDFAK	2127.4	2	3.664	0.1745
EMLNLYIENEGK	1453.6	2	3.2307	0.2714

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EMLNSVMQELEDYSEGGPLYK	2433.7	2	2.7441	0.1447
EMNADAVFAFQLR	1512.7	2	2.6199	0.2072
EMNDAAMFYTNR	1463.6	2	4.0661	0.398
EMNLSETAFIR	1311.5	2	3.1643	0.2343
EMQENDASMR	1211.3	2	2.674	0.2866
EMQENDASMRDVVFNYLHATAFQGTPLAQAVEGPSENVR	4324.7	3	6.1708	0.4351
EMQNLSQHGR	1200.3	2	3.1626	0.2615
EMQPTHPIR	1109.3	1	2.4444	0.2805
EMSGDLEEGMLAVVK	1608.9	2	3.9361	0.2927
EMSGDVRDAFVAIVQSVK	1952.2	3	4.2996	0.2074
EMSKEFIEAEMK	1472.7	2	2.7323	0.1525
EMTNEEKNIITNLSK	1765.0	2	4.0665	0.3077
EMVELPLRHPALFK	1681.0	2	4.3383	0.4344
EMYKTDLEKDIISDTSGDFR	2364.6	2	4.5834	0.3561
EMYKTDLEKDIISDTSGDFRK	2492.7	3	4.5444	0.2887
ENAEVDGDDDAEEMEAK	1867.8	2	3.4433	0.3805
ENAPAIIFIDEIDAIATK	1945.2	2	4.437	0.3829
ENAPAIIFIDEIDAIATKR	2101.4	3	3.3331	0.2879
ENDFDRLVLQYAPSA	1738.9	2	3.1221	0.1884
ENERHAFTCRVAGGPGTPR	2056.3	2	2.7055	0.1555
ENESLTHSTDR	1289.3	2	3.2745	0.3695
ENFIPTIVNFSAEEISDAIR	2266.5	2	4.9037	0.468
ENGDESHLPER	1283.3	2	2.5752	0.2531
ENGHVTISESPEELGTPGPSLPDVPGIESR	3102.3	3	4.2164	0.2272
ENGTVTAANASTLNDGAAALVLMTADAAK	2763.0	2	4.5417	0.4386
ENGTVTAANASTLNDGAAALVLMTADAAKR	2919.2	3	4.8584	0.3689
ENGVTHPIDYHTTDYVDEIKK	2475.7	3	4.6365	0.4131
ENISNAQALLEYHLSYLQEVEQLR	2862.1	3	3.3345	0.174
ENIVEAIIHSPELIR	1734.0	2	3.1707	0.3399
ENKEVVLQWFTENSK	1852.0	3	3.6161	0.1481
ENLATVEGNFASIDER	1765.9	2	3.4673	0.1867
ENLKAAQEEYVK	1422.6	2	3.8147	0.3119
ENLKAAQEEYVKR	1578.8	2	3.7877	0.3746
ENLLEEQGSIALRQEQIDNQTR	2585.8	3	3.417	0.2997
ENLNKDLLTAAEKYPNVK	2061.3	3	4.3362	0.2862
ENLSDEDKLNNAK	1490.6	2	4.0323	0.27

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ENNAVYAFLGLTAPPGSK	1850.1	2	4.343	0.4395
ENPHDAVVFHPK	1390.5	2	2.7343	0.2036
ENPLDSSVEFMQIWR	1852.1	2	3.8118	0.2823
ENPVYEKKPK	1232.4	2	2.7169	0.1253
ENPYYDSR	1044.1	2	2.6182	0.2618
ENQWFDVGVIK	1335.5	2	3.0428	0.1932
ENTEGEYSGIEHVIVDGVVQSIK	2503.7	3	4.2225	0.3134
ENTQQHITAR	1198.3	2	2.8616	0.217
ENVFQEHQTLK	1373.5	2	3.4986	0.2746
ENVFQEHQTLKEKELETGPK	2385.6	3	4.4152	0.3027
ENVLIGDGAGFK	1220.4	2	3.1046	0.1529
ENYSHHTQDDR	1402.4	2	2.8076	0.323
EPAAEIEALLGMDLVR	1728.0	2	4.3114	0.4337
EPAHLMSLFGGKPMIIYK	2033.5	2	4.0331	0.3434
EPAIHSEGQWVTLPAPLDTINVHLR	2795.1	3	3.3198	0.2012
EPAVYFKEQFLDGDGWTSR	2246.4	2	4.5505	0.4817
EPEKEIRPALELLEPIEQK	2262.6	3	4.12	0.2308
EPESILQVLSQMEK	1631.9	2	2.8823	0.1241
EPFTLEAYYSSPQDLPYPDPAIAQFSVQK	3303.6	3	5.1985	0.3671
EPLPPIQQHIWNMLNPPAEVTTK	2655.1	3	3.9198	0.225
EPLPSLEAVYLITPSEK	1887.2	2	3.6102	0.3351
EPPPEFEFIADPPSISAFDLDVVK	2661.0	3	3.457	0.2095
EPQDTYHYLPFSLPHR	2001.2	2	3.3447	0.3736
EPQPIKEVTIMEEKER	1957.2	3	3.3048	0.1391
EPSLATWEATWSEGSK	1779.9	2	2.4703	0.1739
EPSLQPRREATLLPATVAETQQAPRDR	3032.4	3	3.6602	0.1357
EPVGDDESVPENVLSFDDLTADALANLK	2975.2	3	3.4724	0.1809
EPVRAPAVAVAPTPVQPPIIVAPVATVPAMPQEK	3443.1	3	4.6192	0.1797
EPWDGRDGELPVEDDIDLSDVELDDLGKDEL	3500.6	3	4.0523	0.1443
EQADFAIEALAK	1306.4	2	3.0259	0.3481
EQAEAEVASLNR	1317.4	1	2.807	0.1295
EQAGGDATENFEDVGHSTDAR	2207.2	2	5.4041	0.4531
EQDLQLEELR	1273.4	2	2.4139	0.1551
EQDLQLEELRQQVSTLK	2058.3	2	4.3678	0.3971
EQEELENYIEHVLLR	1915.1	2	4.5155	0.3369
EQEHMINWVEK	1443.6	2	2.4005	0.1831

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EQEITAVQAR	1145.2	2	3.0081	0.2868
EQELQQTLQQEQSVLDQLRGEAEAAR	2999.2	3	5.0075	0.377
EQELQQTLQQEQSVLDQLRGEAEAARR	3155.4	3	3.4858	0.2302
EQEMTEMRDVMQQQLAEYQELLDVK	3086.5	3	4.3723	0.2511
EQESEKPSQELLEYNIQQK	2321.5	3	4.1353	0.1848
EQFDKTQAISISK	1495.7	2	3.5602	0.3936
EQFDTLTPEPPVDPNQEVPPGPPR	2657.9	3	3.8079	0.2694
EQFEFALTAVAEEVNAILK	2123.4	2	2.4274	0.2627
EQFLDGDGWTSR	1411.5	2	3.5713	0.4361
EQGFLSFWR	1170.3	2	2.5146	0.3036
EQGGSGLGSGSSGGGGSTSGLGSGYIGR	2387.4	3	5.5828	0.4672
EQHLLDELSRAQAWSGPSR	2181.4	2	2.4179	0.1487
EQHLTKEER	1170.3	2	2.4919	0.1138
EQHLYYQDQLLPVSR	1890.1	2	4.4671	0.3977
EQHQHSDLDSNQTHSSGTVTSSSSTANIDDLKK	3556.6	3	4.9198	0.3408
EQIESLEHDLQASVDELQDVK	2426.6	2	2.7806	0.1807
EQIGKVDEIFGQLR	1632.8	2	2.6412	0.2195
EQISDIDDAVR	1261.3	2	2.6659	0.2707
EQIVPKPEEEVAQK	1624.8	2	3.5397	0.338
EQIVPKPEEEVAQKK	1753.0	2	2.882	0.2045
EQIVVDLSHPGVSEDDQVSR	2210.3	2	5.9071	0.5299
EQLAIAEFAR	1148.3	2	2.9442	0.3177
EQLDKIQSSHNFQLESVNK	2245.4	3	3.2197	0.291
EQLEEEEEAKHNLEK	1855.9	2	4.8132	0.2968
EQLEHIKTHELHL	1627.8	2	3.0235	0.2965
EQLIDMNAEGDETGVMDSLLEALQSGAAFR	3212.5	3	4.26	0.3557
EQLIDMNAEGDETGVMDSLLEALQSGAAFRR	3368.7	3	3.697	0.3164
EQLKAVMDDFAAFVEK	1842.1	2	4.0012	0.4481
EQLLLEELVSLVNQR	1784.0	2	2.6141	0.1982
EQLMREEAEQK	1391.5	2	3.1332	0.1422
EQLPPMSEDFLLDALSEDFSGPQNASSLK	3167.4	3	3.7113	0.2889
EQLRQEQALLEEIER	1885.1	2	3.4642	0.314
EQLSLLDRFTEDAK	1665.8	2	3.264	0.3348
EQLSLLDRFTEDAKR	1822.0	3	3.2609	0.2177
EQLYEMFQNILGIK	1727.0	2	4.5231	0.3588
EQNGDSLVHAAFVAESAVAGSAEANAFSVLQHVLGAGPHVK	4087.5	3	5.0343	0.3877

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EQPLDEELKDAFQNAYLELGGLGER	2836.1	3	4.583	0.4807
EQPPRFAQPGSFEYEYAMR	2304.5	2	3.9424	0.3463
EQPPRFAQPGTFEFEYASR	2258.4	3	4.163	0.2209
EQQAQVEKEDFSDMVAEHAAK	2391.6	3	5.5626	0.4397
EQQEAIEHIDEVQNEIDRLNEQASEEILKVEQK	3936.2	3	4.409	0.3027
EQQIEEHR	1069.1	2	2.449	0.1349
EQQIVIQSSGGLSK	1474.6	2	4.1092	0.3182
EQQIVIQSSGGLSKDDIENMVK	2419.7	2	4.3793	0.4916
EQQLAEIEAR	1187.3	2	2.7634	0.1619
EQRDPTVHDDVLELEMDELNR	2554.7	3	4.4142	0.233
EQSILELGSLLAK	1401.6	2	3.1807	0.2332
EQSQLTATQTR	1263.3	2	3.3446	0.3523
EQTADGVAVIPVLQR	1596.8	2	4.3523	0.4247
EQTKQVEELSK	1319.4	2	3.2311	0.2233
EQTLSPTITSGLHNIAR	1839.0	2	3.6457	0.3349
EQTVSVSGAFQINTFDLR	2013.2	2	2.7998	0.1543
EQVANSAFVER	1250.3	2	2.8324	0.3291
EQVLQPVSAELLELDIR	1953.2	2	2.9964	0.2361
EQWDTIEELIR	1432.6	2	2.8516	0.2639
EQWDTIEELIRK	1560.7	2	3.1247	0.2268
EQWTKYEEENFYLEPYLK	2410.6	2	4.33	0.45
EQWTKYEEENFYLEPYLKEVIR	2908.2	3	3.9584	0.1867
ERADEPQWSLYPSDSQVSEEVK	2580.7	3	4.0179	0.262
ERDFTSLENTVEER	1725.8	2	4.2936	0.3652
ERDFTSLENTVEERLTELTK	2411.6	3	4.7769	0.3476
ERDSASFNPELLTHILDGSPEK	2456.7	3	4.9196	0.2658
ERDSASFNPELLTHILDGSPEKTR	2713.9	3	4.6951	0.3004
EREEFLIPIYHQVAVQFADLHDTPGR	3082.4	3	3.4864	0.2381
EREEQETTSSK	1324.3	2	3.0249	0.2943
EREHLEMELEK	1443.6	2	3.4383	0.1795
EREHLEMELEKAEMER	2060.3	3	4.2067	0.2125
ERELQHAALGGTATR	1610.8	2	4.1749	0.354
ERELQNTVANLHVR	1679.9	2	4.1763	0.3579
EREMAEMR	1052.2	2	2.518	0.1424
EREMQNLSQHGR	1485.6	2	4.4616	0.3319
EREVLQLQEEVKNFITR	2132.4	3	4.8724	0.2846

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ERGDYVLAVK	1150.3	2	2.9675	0.1954
ERGEVVPLGPGVPALVANGFLALDVAANR	2903.3	3	4.9139	0.4016
ERHGNVASLVQR	1366.5	2	3.0142	0.3753
ERHPGSFDVVHVK	1507.7	3	3.959	0.4052
ERHPGSFDVVHVKDANGNSFATR	2541.7	3	4.5005	0.3109
ERIDNLIDPGSPFLELSQFAGYQLYDNEEVPGGGIITGIGR	4452.9	3	4.968	0.3346
ERIPEAPAGPPSDFGLFLSDDDPKK	2700.0	3	5.458	0.4552
ERIPEAPAGPPSDFGLFLSDDDPKKGIWLEAGK	3554.9	3	3.6665	0.1939
ERISEQTYQLSR	1510.6	2	3.9423	0.3154
ERLAGLFNEQR	1333.5	2	2.4745	0.145
ERLEHPVLHVSWNDAR	1959.2	2	3.5138	0.2743
ERLEQDLQQMQAK	1617.8	2	4.235	0.3188
ERLEQQVPVNQVFGQDEMIDVIGVTK	2973.4	3	5.6943	0.4667
ERLQEELSQAESTIDELKEQVDAALGAEEMVEMLTDR	4208.6	3	6.4529	0.479
ERMEPTYQLSR	1410.6	2	2.5198	0.151
ERNDLIVFLADQNAPYFKPK	2379.7	3	6.8956	0.506
ERNTDQASMPDNTAAQK	1878.0	2	5.3347	0.4621
ERPAYAVHGNMLHYVK	1886.2	3	4.5992	0.3349
ERPDLEAPAPGSPFR	1639.8	3	3.3393	0.2336
ERPGEQSEVAQLIQQTLEQER	2469.7	3	4.6185	0.2237
ERPPEEVAAR	1154.3	2	2.6533	0.2425
ERPPEEVAARLAQQEKQEQVKIESLAK	3106.5	3	3.4635	0.1224
ERPPNPIEFLASYLLK	1888.2	2	4.9236	0.4745
ERPSQPEGLR	1169.3	2	2.5968	0.1799
ERPTDEEGFLHPPGEK	1839.0	2	2.8577	0.1078
ERQEAEEAKEALLQASR	1959.1	2	4.9996	0.42
ERQEEQSAAIHISETLEQKPHFESSTVK	3240.5	3	6.1264	0.4201
ERQRMHKLNNAFQALREVIPHVRADKK	3286.8	3	3.3651	0.1091
ERQTNPSAMEVEEDDPVPEIR	2442.6	3	4.1083	0.3636
ERQTNPSAMEVEEDDPVPEIRR	2598.8	3	4.1524	0.2322
ERSDTFINLR	1251.4	2	3.1461	0.2027
ERSGVSLAALKK	1259.5	3	3.6897	0.135
ERVEAVNMAEGIIHDTETK	2143.4	2	4.1824	0.3504
ERVWLGPWSHPVLLR	1846.2	3	3.2494	0.1341
ERWEQGQADYMGADSFDNIKR	2517.7	3	4.9193	0.3664
ESADPLGAWLQDAR	1529.6	2	3.1131	0.2862

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ESAEALATKLNKENK	1646.8	2	4.1511	0.2028
ESAFEFLSSA	1088.1	2	2.8226	0.1572
ESAINVAEGKK	1146.3	2	2.8567	0.3402
ESALFSTELSVLHNFFSPSPK	2338.6	2	3.3678	0.2617
ESAREEEEAEQER	1592.6	2	4.3831	0.2715
ESAREEEEAEQERR	1748.7	2	4.2216	0.2889
ESDDPMAYIHFTAEGEVTFK	2288.5	2	2.9685	0.3094
ESDITKER	978.0	1	1.71	0.1265
ESDLSHVQNK	1157.2	2	3.1982	0.2341
ESDLSSKTQLLQDVQDENKLFK	2566.8	3	4.6579	0.3316
ESDRLEEKGSLTEGALAHSGNPVSK	2612.8	3	4.6285	0.2947
ESDVPLKTEEFEVTK	1751.9	2	3.6717	0.3211
ESEAVEWQQK	1234.3	2	2.5786	0.1147
ESEIIDFFLGASLKDEVLK	2154.4	2	3.1105	0.2621
ESEKELALVKR	1302.5	2	2.5203	0.1054
ESESVDKVMDQK	1395.5	2	3.4775	0.2778
ESESVDKVMDQKEHK	1789.9	2	4.0256	0.2446
ESEVKREFK	1152.3	1	2.3618	0.1028
ESGLKYVAVMPPHIGDQPLTGAYTVTLDGR	3187.6	3	3.2099	0.1592
ESGTDDFNVWIGLHDPK	1931.1	2	4.177	0.3542
ESGTDDFNVWIGLHDPKK	2059.2	2	3.7729	0.3607
ESGYMHIQCTKPDTVGSALNDSPVGLAAYILEK	3510.0	3	3.9419	0.1739
ESHAKADSAVSQEQLR	1756.9	3	4.1997	0.1301
ESHATLVFHNLLGEIDQQYSR	2458.7	3	4.5947	0.4646
ESHPATVFILFSDLNPLVTLGGNKESFQQPEVR	3672.1	3	4.3579	0.3372
ESHPHGVK	891.0	1	2.185	0.1486
ESHRLPVDIAYKR	1584.8	3	4.3701	0.2545
ESIAEHKPHIDK	1404.6	2	3.2072	0.3103
ESKDQLSDDVSK	1351.4	2	3.4984	0.414
ESKDQLSDDVSKVIAYLKR	2195.5	3	3.2523	0.1463
ESKEETPEVTK	1277.4	2	2.7228	0.1034
ESKEQLPPMSEDFLLDALSEDFSGPQNASSLK	3511.8	3	4.427	0.2275
ESKEQLPPMSEDFLLDALSEDFSGPQNASSLKFEDAK	4102.4	3	3.299	0.1822
ESKFFEHFIEGGR	1583.7	2	2.8999	0.2351
ESKKEDLVFIFWAPESAPLK	2335.7	3	5.7537	0.5232
ESKKEDLVFIFWAPESAPLKSK	2550.9	3	3.9816	0.3292

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ESKPLTAQQTTK	1332.5	2	2.7624	0.2081
ESLAPAAPADPGPASPR	1604.7	2	2.7004	0.2918
ESLDVYELDAK	1282.4	2	3.5556	0.3075
ESLHEVSKSDLGR	1457.6	2	2.9697	0.271
ESLKELSLAGNELGDEGAR	1989.1	2	5.3651	0.4313
ESLKPAAKPLPSK	1366.6	2	2.5963	0.2055
ESLQQMAEVTR	1292.4	2	3.2735	0.3241
ESLREVQLEELEAARDLVSK	2315.6	3	4.1488	0.225
ESLRQDGHVLAVEVAEEKEQK	2395.6	3	4.7066	0.2413
ESLSEEEAQK	1150.2	2	2.7985	0.1921
ESLSTHTSPSQSPNSVHGSR	2096.2	3	3.5556	0.2157
ESLTLIVEGKPQIK	1555.8	2	3.8257	0.2416
ESNGPVKVWGSIK	1401.6	2	3.4326	0.273
ESNTVFSFLGLKPR	1595.8	2	2.7394	0.3773
ESPESEGPIYEGLIL	1633.8	2	3.9556	0.3657
ESPEVLLTLDILK	1470.7	2	3.3682	0.2887
ESQAKDVIEEYFK	1586.7	2	4.3213	0.3597
ESQLAHIKDEPPPLSPAPLTPATPSSLDPFFSR	3545.0	3	6.3511	0.4443
ESQPLLGTVIDGMLLLK	1828.2	2	3.5605	0.3006
ESQSPDTTIQR	1262.3	2	2.5631	0.2057
ESREAVEKEFEPLLNWMKDK	2479.8	3	4.3134	0.1737
ESRKEELMFFLWAPELAPLK	2435.9	3	3.8934	0.1634
ESRQEEMNSQQEEEEMETDAR	2586.6	3	4.528	0.227
ESSEKPPEKPAKPER	1709.9	2	3.055	0.2178
ESSETPDQFMTADETR	1844.9	2	4.6223	0.4833
ESSLILAVTPANMDLANSDALK	2274.6	2	3.3475	0.2233
ESSLPSKEALEPSGENVIQNKESTG	2631.8	3	4.4619	0.3137
ESSPLYSPTFSDSTSAVKEK	2161.3	2	4.2211	0.3936
ESSSSLVLKEILQEAPELITEQLAHR	2922.3	3	5.0216	0.4149
ESSTDDSNVWIGLHDPK	1901.0	2	4.5122	0.4055
ESSTDDSNVWIGLHDPKK	2029.2	2	4.2331	0.4418
ESSTESSQSAKPVSGQDTSGNTEGSPAAEK	2955.0	3	4.6286	0.3512
ESSTVFELKR	1196.3	2	2.7896	0.1254
ESTGAQVQVAGDMLPNSTER	2091.2	2	5.9093	0.4246
ESTITLQQAEYEFLSFVR	2162.4	2	4.3857	0.4941
ESTLHLVLR	1068.3	2	3.1321	0.3301

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ESTYQGHHTPPVQK	1609.7	2	2.8102	0.2061
ESVDHLTIPSR	1254.4	2	2.5335	0.173
ESVFTVEGGHR	1218.3	2	3.0268	0.3769
ESVLQMMQAGQR	1378.6	2	3.1227	0.115
ESVLTATSILNNPIVK	1700.0	2	3.624	0.2452
ESVNAAFEMTLTEGSKLEK	2085.3	2	3.6371	0.3893
ESVNYLVSQQNMLLIPTSFSPLK	2610.0	2	5.0856	0.3715
ESVPPSIIMSSQK	1403.6	2	2.4718	0.1207
ESVQVPDDQDFR	1435.5	2	2.4146	0.1852
ESWHGKPLPK	1179.4	2	2.7582	0.2172
ESYDDVSSFR	1205.2	2	2.8356	0.2261
ESYSIYVYKVLKQVHPDTGISSK	2643.0	3	4.3799	0.3647
ESYSVYVYK	1138.3	1	2.2673	0.2892
ESYSVYVYKVLKQVHPDTGISSK	2629.0	3	4.6069	0.4545
ESYSVYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFER	4355.0	3	3.2082	0.1121
ESYVETELIFALAK	1613.8	2	4.8987	0.4313
ETAAVIFLHGLGDTGHSWADALSTIR	2740.0	3	6.2944	0.5127
ETADAITK	848.9	1	1.802	0.1299
ETADAITKEAKK	1305.5	2	2.6354	0.2238
ETAEADVASLNR	1276.3	2	3.8713	0.3761
ETAENYLGHTAK	1334.4	2	2.6634	0.1889
ETAGLGRAKAWKGGWNGFLVFSRVPSAGFFASAQVPQGPGALRRSR	4848.5	3	3.4274	0.2671
ETAGNSGSTHEGR	1303.3	2	2.8785	0.2278
ETAHWKPPPWNDVDPPKDTIVK	2571.9	3	4.7019	0.1854
ETAIELGYLTAEQFDEWVKPK	2468.7	2	4.433	0.3523
ETAKRPVGGFLLDGFQGNPTTLEAR	2676.0	3	3.2629	0.238
ETDLLLDDSLVSIFGNR	1908.1	2	5.2602	0.4694
ETDQKKEAVAPVQEESDLEKK	2402.6	3	3.7233	0.2404
ETEAEEELDAEVLEVFHPTHEWQALQPGQAVPAGSHVR	4238.5	3	4.4628	0.2818
ETEFKDDSLPIKR	1578.7	2	3.5299	0.3176
ETEGDVTSVKDAK	1379.5	2	3.6138	0.3816
ETEYKDKIPLLQQPK	1831.1	2	3.7676	0.244
ETFASTASQLHSNVVNYVQQIVAPK	2733.0	3	3.6455	0.1897
ETGDPGGQLVLAGDPR	1582.7	2	2.5673	0.1226
ETGEHLVHVK	1149.3	2	2.6996	0.3344
ETGERPSNEEIMR	1548.7	2	2.6524	0.1532

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ETGVDLTKDNMALQR	1691.9	2	3.8133	0.3087
ETGYVVERPSTTK	1467.6	2	3.1189	0.2666
ETHQQVVSR	1084.2	2	2.7055	0.2466
ETHSIGRD	914.9	1	2.2395	0.2032
ETIEDVEEMLNNLPGVTSVHSR	2470.7	3	4.2028	0.272
ETIEQEKQAGES	1349.4	2	3.7211	0.2376
ETIEQERQAGES	1377.4	2	2.75	0.1705
ETIPLQETSLYTQDR	1794.9	2	3.1548	0.1637
ETKTFGGGGGGAR	1195.3	2	2.4614	0.2515
ETLAQLQQEFQR	1491.6	2	2.8046	0.2086
ETLEKHYGNKPIGMGGTFIIQK	2462.9	3	4.4627	0.2611
ETLKRKVSGNRCASPVTGPGSK	2273.6	2	2.4309	0.113
ETLPAEQDLTTK	1346.5	2	2.5677	0.2009
ETLRPLAYSTLADLVHHVR	2192.5	3	4.0058	0.2605
ETLVYLTHLDYVDTER	1968.2	2	3.382	0.4089
ETMVTSTTEPSR	1339.5	2	3.4199	0.4117
ETNELLKELGSLPLPLSTSEQR	2455.7	3	3.6623	0.2084
ETNEPVKTK	1046.2	1	1.8534	0.1439
ETNLDSLPLVDTHSK	1669.8	2	4.3672	0.3851
ETNLDSLPLVDTHSKR	1826.0	2	3.8207	0.3445
ETPAATEAPSSTPK	1387.5	2	2.4248	0.32
ETPHSPGVEDAPIAK	1548.7	2	3.4028	0.3337
ETPLPIDPSMFPTWPAK	1928.2	2	2.5987	0.2386
ETPSQENGPTAK	1259.3	2	2.5019	0.1542
ETRLVLEVAQHLGESTVR	2038.3	3	4.7185	0.4429
ETSGNLEQLLLAVVK	1614.9	2	4.1431	0.4215
ETSGSIWQAR	1135.2	2	2.4087	0.1382
ETSKDTETVLK	1251.4	2	2.7907	0.1586
ETSMVHELNR	1216.4	2	3.1304	0.3281
ETSNLYKIQFHNVKPEYLDAYNSLTEAVLPK	3627.1	3	4.2839	0.2617
ETSSALTHAGAHLDLSAFSSWEELASLGLDR	3273.5	3	4.669	0.2413
ETSSDVALASHILTALR	1785.0	2	3.4527	0.3819
ETSVTPSNLWGGQGLLGVSIR	2172.4	2	3.7018	0.2969
ETTDTDTADQVIASFK	1742.8	2	4.4987	0.3783
ETTEESIKETER	1452.5	2	2.5881	0.2526
ETVEEQASTTER	1380.4	2	3.1879	0.1882

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ETVEREKEQMMR	1566.8	2	2.7505	0.1608
ETVFTK	724.8	1	2.1416	0.137
ETVFTKSPYQEFTDHLVK	2170.4	3	4.8278	0.398
ETVSEESNVLCLSK	1538.7	2	4.1734	0.3361
ETVSQRPGATVPTDFATFPSSAFLR	2684.0	3	4.1313	0.2933
ETVVEVPQVTWEDIGGLEDVKR	2499.8	2	4.1727	0.4525
ETVVQQKETLGAQR	1587.8	2	3.7076	0.2038
ETYEVLLSFIQAALGDQPR	2151.4	2	3.5659	0.2194
ETYLAILMDR	1225.4	2	2.6372	0.2104
ETYQKLNQEK	1281.4	2	2.4997	0.1144
EVAAFAQFGSDLDAATQQLLSR	2339.5	2	7.2861	0.5705
EVAAFAQFGSDLDAATQQLLSRGVR	2651.9	3	3.6793	0.3276
EVAAQVK	744.9	1	2.1362	0.1003
EVAEAATGEDASSPPPK	1656.7	2	4.3024	0.5126
EVAEAATGEDASSPPPKTEAASDPQHPAASEGAAAAAASPPLLR	4196.5	3	4.5165	0.4094
EVAFFNNFLTDAK	1516.7	2	3.1236	0.3775
EVAGAKPHITAAEGK	1479.7	2	3.9952	0.4231
EVAGHTEQLQMSR	1486.6	2	4.3784	0.4753
EVAGLRQLLLESQSQLDAAKSEAQKQSDELALVR	3726.1	3	4.7447	0.3664
EVAKPSPGEGEVLLK	1553.8	2	4.0109	0.3273
EVALDLSQHK	1140.3	2	2.8349	0.2171
EVAPDGPLQESSTR	1486.6	2	3.4369	0.4725
EVAQQAVDADVHAVGVSTLAAGHK	2374.6	3	3.901	0.2788
EVARLEAPLEELR	1525.7	2	3.4099	0.3119
EVATNSELVQSGK	1362.5	2	3.9719	0.4606
EVDDLEQWIAER	1503.6	2	3.2351	0.2675
EVDDLGPEVGDIK	1386.5	2	4.244	0.2571
EVDDLGPEVGDIKIIPLYSTLPPQQQQR	3150.5	3	4.5974	0.3736
EVDEQMLAIQSK	1391.6	2	3.7355	0.2527
EVDEQMLNVQNK	1447.6	2	4.4984	0.2447
EVDIGIPDATGR	1243.3	2	3.1173	0.3427
EVDIGIPDATGRLEILQIHTK	2319.6	2	4.3068	0.3274
EVDPLVYNMSHEDPGNVSYSEIGGLSEQIR	3336.6	3	6.0228	0.4606
EVDVEKVSAFENPYVDAIK	2153.4	3	3.8146	0.1995
EVDVGLAADVGTLER	1544.7	2	3.086	0.1099
EVDVGLAADVGTLQR	1543.7	2	4.2577	0.1787

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EVDVNLPKADIDVSGPKVDVEVPDVSLEGPEGK	3447.8	3	3.863	0.2191
EVEEDEYK	1041.0	1	2.7702	0.1997
EVEEDEYKAFYK	1550.6	2	3.8751	0.2933
EVEEEPGIHSLK	1367.5	2	4.0215	0.3532
EVEEQHEVNEQLQAR	1838.9	2	4.2322	0.3089
EVEERPEKDFTEK	1636.7	2	3.9125	0.2341
EVEHFLKAEPEKNGEVVHTPETSV	2706.9	3	3.3847	0.2343
EVEKVKLDQK	1216.4	2	2.8447	0.1294
EVEQFTQVAK	1179.3	2	2.8156	0.214
EVERVVVDALSGLKGDLAGR	2084.4	3	5.1437	0.369
EVESMGAHLNAYSTR	1665.8	2	3.9258	0.2571
EVFEDAAEIR	1179.3	2	2.5543	0.1197
EVFEMATR	983.1	1	2.3786	0.1943
EVFLPSTPGLGMHVEVKDPDGK	2353.7	2	4.8821	0.3542
EVFPFPEVSQDELNEINQFLGPVEK	2906.2	3	6.1503	0.3612
EVGEHLVSIKK	1239.4	2	2.4696	0.1575
EVGHNIYILALQLSR	1727.0	2	3.1449	0.3212
EVGKDVSDEKLR	1375.5	2	3.0641	0.202
EVGLLKDMSPLSETEMALGKDVTPPPETEVVLIK	3668.3	3	5.1601	0.2824
EVGSHFDDFVTNLIEK	1851.0	2	3.6202	0.3716
EVGVYEALKDDSWLK	1752.9	2	4.4839	0.4193
EVGVYEALKDDSWLKGEFVTTVQQR	2899.2	3	5.3057	0.4014
EVHKQVVESAYEVIK	1759.0	2	3.9527	0.3183
EVIDLLKPDQVEGIQK	1825.1	2	4.7644	0.4143
EVIELPLTNPELFQR	1799.1	2	4.8046	0.3953
EVIELPVKHPELFEALGIAQPK	2458.9	2	3.4719	0.2766
EVIKTNNVSEHEDTDKYR	2178.3	2	3.8802	0.3362
EVIRNDGVLLLQALTR	1811.1	2	4.0165	0.3517
EVKEHVGTDQFGNK	1588.7	2	4.2628	0.4217
EVKEHVGTDQFGNKYYYIPQYK	2708.0	3	3.2242	0.2319
EVKEMEQFVK	1267.5	2	2.4413	0.1869
EVKEMEQFVKK	1395.6	2	3.3279	0.225
EVKKEEGEAFAR	1393.5	2	2.8802	0.2663
EVKYEAPQATDGLAGALDAR	2076.3	2	5.0002	0.454
EVLAELEALER	1272.4	2	3.5054	0.1717
EVLAGRPLFPHVLCHNCAVEFNFGQK	2927.4	3	6.9558	0.474

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EVLDKNDMVELLGPRPFAEK	2301.6	3	3.3063	0.2269
EVLDYSTPTTNGTPEAALSEDINLIR	2821.0	3	4.5348	0.3823
EVLHGNQR	953.0	1	2.3976	0.188
EVLLFPAMKPEDKK	1646.0	2	3.1843	0.2611
EVLPEHVSVLQGVDLSPDITR	2304.6	3	4.1607	0.2982
EVLPLAFLGMHEIADEEK	2042.3	2	2.9132	0.3083
EVLTGNDEVIGQVLSTLKSEDVPYTAALTAVRPS	3575.0	3	6.3055	0.4766
EVLTGNDEVIGQVLSTLKSEDVPYTAALTAVRPSR	3731.2	3	4.8241	0.401
EVMQEVAQLSQFDEELYK	2187.4	2	4.3022	0.4816
EVMQEVAQLSQFDEELYKVIGK	2584.9	2	4.3117	0.3202
EVMSPLQAMSSYTVAGR	1828.1	2	3.0796	0.2752
EVMVDDRLVTMQIWDTAGQER	2493.8	3	5.1691	0.2862
EVNGHEVGNNPK	1294.4	2	3.5349	0.3528
EVNKFQMAYSNLLR	1714.0	3	3.9191	0.4376
EVPEYLHHVNK	1365.5	2	3.1046	0.191
EVPEYLNHVSK	1315.5	2	2.6057	0.1394
EVPMVVVPPVGAK	1322.6	2	3.2043	0.2555
EVPNYKLITPAVVSER	1816.1	2	3.9226	0.2594
EVQGFESATFLGYFK	1723.9	2	4.6861	0.4612
EVQGNESDLFMSYFPR	1920.1	2	4.6107	0.4354
EVQISTEKQQK	1318.5	2	2.8475	0.1818
EVQKFTEDLVGSVVHVLSHR	2280.6	3	3.792	0.3749
EVQLAQIFEPLSR	1530.8	2	2.8041	0.3436
EVQQGEEFER	1251.3	2	3.0015	0.1911
EVQQKYNMGLPVDFDQYNELHLPAVILK	3303.8	3	4.4833	0.2444
EVQTNDLK	947.0	1	2.3511	0.1088
EVQTNDLKEVVNK	1516.7	2	4.8825	0.2763
EVQTNDLKEVVNKLIPDSIGKDIEK	2826.2	3	5.9069	0.305
EVQTNELKAEK	1289.4	2	3.7109	0.2504
EVRDLEEQIETELGKK	1917.1	3	4.7746	0.1851
EVSDGIIAPGYEEEALTILSK	2235.5	3	4.8595	0.2876
EVSGIKAAYEAELGDARK	1908.1	2	4.1941	0.3284
EVSMDDHK	961.0	1	1.8955	0.1438
EVSMDDHKLSLDELHR	1925.1	2	3.6028	0.2268
EVSMDDHKLSLDELHRK	2053.3	3	3.5311	0.2609
EVSMKAEDAQR	1264.4	2	2.4651	0.1966

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EVSPAPAVAGQSK	1241.4	2	2.7404	0.1673
EVSQPDWTPPPEVTLVLTK	2137.4	2	3.4717	0.1731
EVSSSFDHVIK	1248.4	2	3.1711	0.271
EVSSSFDHVIKETTR	1735.9	2	4.4706	0.4714
EVSTYIK	840.0	1	1.8955	0.1319
EVTAIETKLEQK	1389.6	2	2.9123	0.1169
EVTDEIVKEFMTPR	1694.9	2	4.1623	0.4347
EVTDKEQEFAAR	1423.5	2	3.3387	0.3888
EVTHNIHYETYR	1562.7	2	3.1815	0.3615
EVTINQSLLAPLR	1454.7	2	3.726	0.2964
EVTINQSLLAPLRLDADPSLQR	2450.8	3	3.6015	0.451
EVTSHFQVTLNDIQLQMEQHNER	2798.0	3	4.2701	0.1648
EVVAEVVKAPQVVAEAAK	1838.1	2	4.6008	0.3383
EVVAGSHELGQDYEHVTMLQER	2528.7	3	5.3566	0.3986
EVVDYIIFGTVIQEVK	1853.1	2	4.6133	0.3101
EVVEAHVDQK	1154.3	2	3.0851	0.3103
EVVEAHVDQKNK	1396.5	2	3.5884	0.2486
EVVEDINKLLK	1300.5	2	3.4223	0.123
EVVEEAENGR	1132.2	2	2.9087	0.2635
EVVETPLLHPER	1419.6	2	2.9316	0.2216
EVVIFGAASELFTK	1511.7	2	4.6955	0.4593
EVVILEDPGLPALYPCPACEEKLALPTAALYGLR	3627.3	3	4.1334	0.3727
EVVIVSATR	974.1	2	2.8888	0.2388
EVVKPLLVSTLGEK	1512.8	2	3.8135	0.3567
EVVKPVPITSPAVSK	1551.9	2	3.5835	0.4022
EVVLQWFTENSK	1480.6	2	3.4228	0.3397
EVVQEILQFQEDPQTKEEVASLR	2717.0	3	4.6587	0.4071
EVWYFGLHYVDNK	1670.8	2	3.1264	0.2235
EVYQQQQYGSGGR	1500.6	2	4.3125	0.4755
EWHHFLVVNMK	1440.7	2	3.251	0.2139
EWNRDVQYR	1266.3	2	2.5008	0.1158
EWSGLLEELAR	1303.4	2	3.3231	0.3037
EWVTQASGVWFAK	1509.7	2	4.3197	0.5096
EWVTQATALWTANK	1619.8	2	4.416	0.2114
EYFGGFGEVESIELPMDNK	2162.4	2	5.338	0.4874
EYFSWEGAFQHVGK	1685.8	2	3.3394	0.2677

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
EYGGLDVLVNNAGIAFK	1781.0	2	5.4017	0.3731
EYGGLNVLVNNAAVAFK	1780.0	2	2.8433	0.2386
EYGMIYLGKDTNGENIAESLVAEGLATRR	3172.5	3	4.384	0.4246
EYGSLKDSTKDDNSNPGGKTDEPK	2583.7	3	5.2543	0.314
EYIEIITSSIKK	1424.7	2	3.1234	0.1588
EYIPGQPPLSQSSDSSPTR	2047.2	2	3.3605	0.5146
EYKAGDLVFAK	1241.4	2	2.8366	0.2815
EYKYGAHNYHPLPVALER	2158.4	2	3.4299	0.3436
EYLDNVQLGHILER	1699.9	2	3.0793	0.308
EYLTAEILELAGNAAR	1734.9	2	5.0177	0.3359
EYQDLLNVK	1122.3	1	2.6542	0.1563
EYQELMNVK	1154.3	2	2.5796	0.1966
EYQLNDSAAYYLNDLER	2078.2	2	5.3148	0.46
EYSKEGWEYVK	1418.5	2	3.2918	0.1485
EYSSELNAPSQESDSHPR	2034.0	2	4.2795	0.3928
EYTAGREADDIVNWLK	1881.0	2	2.7129	0.1735
EYTINIHKR	1174.3	2	2.8565	0.116
EYVESQLQR	1152.2	2	2.7453	0.1443
EYVNSTSEESHDEDEIRPVQQQDLHR	3142.2	3	5.4801	0.4369
EYYSEADASHCIQQILESVNHCHLNGIVHR	3467.8	3	3.6575	0.2669
FAAATGATPIAGR	1204.4	2	4.279	0.3859
FAADAVKLER	1120.3	2	3.4972	0.3525
FAAEEFKVPAATSAIITNDGIGINPAQTAGNVFLK	3578.0	3	6.5539	0.5089
FAAEHTIFASNTSSLQITSIANATTR	2754.0	3	4.5184	0.3793
FAAKGEGQLGPAER	1431.6	2	4.316	0.3661
FAALDNEEEDKEEEIIKEKEPPKQGK	3045.3	3	4.8221	0.2966
FAANPNQNKNVALLSQLYHSPAR	2554.8	3	4.4697	0.2804
FAASGGFLHHMAGLSSSK	1806.0	2	4.262	0.3792
FAATTVEEILAK	1293.5	2	3.4349	0.2188
FAAYFQQGDMESNGK	1693.8	2	5.0137	0.4593
FAAYFQQGDMESNGKYITK	2199.4	2	4.5863	0.3456
FACESIVEEYEDELIEFFSR	2456.7	2	4.3357	0.3406
FADEFNKLAEDFLQ	1687.8	2	3.7419	0.24
FADEHVPGSPFTVK	1531.7	2	3.6972	0.2216
FADLSEAANR	1094.2	2	4.1647	0.2314
FADTEKER	996.1	2	2.8382	0.2368

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FADTRPWDPLNDMIQFEKDGVIQTK	2966.3	3	4.9752	0.3347
FAEAFEAIPR	1151.3	2	4.0072	0.383
FAEEADVVIVGAGPAGLSAAVR	2100.4	3	4.5672	0.3542
FAEEDKK	866.9	1	2.5143	0.1438
FAEEDKKLKER	1393.6	2	3.6553	0.4014
FAEFQYLQPGPPR	1550.7	2	3.7498	0.3223
FAEKYDSDRTELGFTNYIR	2326.5	3	3.841	0.1997
FAELAQIYAQR	1310.5	2	3.3448	0.2347
FAELRSPNEFK	1338.5	2	2.6228	0.2326
FAENPKAGDEFVEK	1581.7	1	4.1443	0.2519
FAENPKAGDEFVEKTLSTIATSTDAASVVHSTDLVVEAIVENLK	4649.1	3	4.5006	0.3577
FAEQDAKEEANK	1380.4	2	3.2948	0.198
FAEVEHVVNAILFLLSDR	2073.4	2	2.8965	0.2616
FAFDYATKK	1091.2	2	2.4618	0.1684
FAFQAEVNR	1082.2	2	3.323	0.2572
FAGDKGYLTK	1100.2	2	3.1797	0.3222
FAGDKGYLTKEDLR	1613.8	2	3.5723	0.308
FAGGDYTTTIEAFISASGR	1965.1	2	4.9161	0.4608
FAGGLHFSGPK	1118.3	2	2.8782	0.2588
FAGHNFRNPSVL	1359.5	2	2.4609	0.1474
FAGHSEAGGGSGDR	1305.3	2	3.4564	0.4177
FAGLHFFNPVPVMK	1604.9	2	4.6124	0.4193
FAGSGNEENRNNAYPHK	1906.0	2	3.3011	0.2957
FAGVFHVEKNGR	1361.5	2	2.7532	0.267
FAHIDGDHLTLLNVYHAFK	2212.5	2	4.948	0.5085
FAHTNVESLVNEYDDNGEGIILFR	2754.0	3	5.8373	0.4916
FAHTNVESLVNEYDDNGEGIILFRPSHLTNK	3531.8	3	6.5851	0.5511
FAHTNVESLVNEYDDNGEGIILFRPSHLTNKFEDK	4051.4	3	6.3494	0.4743
FAHTNVESLVNEYDDNGEGIILFRPSHLTNKFEDKTVAYTEQK	4972.4	3	4.0566	0.3945
FAIQDISVEETSAK	1538.7	2	3.9871	0.3378
FAKDAASLESQLQDTQELLQEETR	2751.9	3	5.5295	0.3922
FAKDAASLESQLQDTQELLQEETRQK	3008.2	3	4.7603	0.2785
FALGIFAINEAVESGDVGK	1938.2	2	5.8047	0.4766
FALGIFAINEAVESGDVGKTLSALR	2579.9	3	3.543	0.2304
FALGLSGGSLVSMLAR	1579.9	2	2.9925	0.2296
FALKEEDISR	1208.3	2	3.0944	0.2875

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FALPSPQHILGLPVGQHIYLSAR	2515.9	3	6.1495	0.492
FALPTAHHTLGLPVGK	1660.0	2	4.0389	0.403
FALQLGDPSTGLLIR	1601.9	2	3.5914	0.1061
FALVPKLVKEEVFWRNYFYRVSLIK	3146.8	3	3.3802	0.1962
FAMEPEEFDSDTLR	1687.8	2	3.8891	0.3244
FAMEPEEFDSDTLREFVTAFK	2510.8	2	3.9678	0.4174
FAMEPEEFDSDTLREFVTAFKK	2638.9	3	3.3605	0.2168
FAMVAPDVQIEDGKGTILISSEEGETEANNHKK	3559.9	3	4.9326	0.4274
FANLNEQAAR	1134.2	2	3.1073	0.1714
FANPFPAAVR	1090.3	2	2.4249	0.1066
FANSEVEVK	1023.1	2	2.6739	0.2157
FANSLPINDPLQTVYQLMSGR	2365.7	2	4.1014	0.4429
FANSLVGVQQQLQAFNTYR	2185.4	3	4.8288	0.2908
FANYIDKVR	1126.3	2	3.2765	0.3306
FAPAIMQALK	1090.4	2	3.0713	0.1857
FAPKGPEEDHKA	1326.4	2	2.6885	0.1917
FAPNHTKELEDKVIELHK	2149.4	2	3.0984	0.3603
FAPPLVIKEDELR	1527.8	2	3.3997	0.3659
FAPVVAPKPK	1054.3	2	2.5074	0.1898
FAQENELMFLETSALTGENVEEAFLK	2962.3	3	3.863	0.1387
FAQEQIAPLVSTMDENSK	2009.2	2	4.6182	0.2363
FAQHGTFEYEYSQR	1763.8	2	4.9415	0.4758
FAQPGSFEYEYAMR	1696.9	2	4.7153	0.5064
FAQPGTFEFEYASR	1650.8	2	3.6992	0.3352
FAQQHQAR	986.1	2	2.6275	0.1982
FAQQITGMR	1052.2	2	3.145	0.2551
FAQVSDPTVGVDFFSR	1772.9	2	3.8619	0.1904
FAREEIIPVAAEYDKTGEYPVPLIR	2878.3	3	6.1573	0.4597
FASEIAGVDDLGTTGR	1609.7	2	5.2523	0.4472
FASFEAQGALANIAVDK	1752.9	2	3.9441	0.268
FASFEAQGALANIAVDKANLEIMTK	2654.0	3	4.0112	0.2262
FASFIDKVR	1083.3	2	3.5113	0.1579
FASFPDYLVIQIK	1541.8	2	3.2809	0.3752
FASFPDYLVIQIKK	1670.0	2	3.0636	0.1473
FASYLTFSPSEVK	1476.7	2	4.4241	0.4412
FATEAAITILR	1206.4	2	3.4562	0.368

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FATHAAALSVR	1144.3	2	3.271	0.4692
FATLQNELQSSLDAQKESTGVTTLR	2739.0	3	4.3274	0.3608
FATSLVDNSVPLLR	1532.8	2	3.8695	0.417
FATVEVTDKPVDEALR	1791.0	2	4.346	0.4184
FAVEEIIQKQVK	1432.7	2	3.1318	0.2346
FAVGIVIGR	932.1	2	2.5742	0.1131
FAYGYIEDLK	1219.4	2	3.2355	0.3137
FCDVKDETYDLLYQQCDAQPGASGSGVYVR	3329.6	3	3.8158	0.2627
FDADEKGYIEEK	1444.5	2	3.755	0.3573
FDADEKGYIEEKELDAFFLHMLMK	2921.3	3	6.6574	0.5265
FDAGELITQR	1150.3	2	3.8001	0.2755
FDAMPFTLR	1098.3	2	3.1991	0.2172
FDAQTGADR	981.0	2	2.9298	0.2852
FDASFFGVHPK	1252.4	3	3.2737	0.3401
FDATQAFVGELSQFNIWDR	2245.4	2	4.6772	0.4128
FDCSSAPDICSNLYVFQPSLAVFK	2653.0	3	4.3068	0.2189
FDDAVVQSDMK	1255.4	2	3.931	0.3601
FDDAVVQSDMKHWPFMVVNDAGRPK	2891.3	3	4.924	0.3804
FDDGAGGDNEVQR	1380.4	2	4.2583	0.4277
FDDPGLMLMGFKPLVLLKK	2163.7	3	3.5967	0.2732
FDDPLLGPR	1030.2	2	2.5519	0.3246
FDEAALSIQKEK	1379.5	2	3.2717	0.2281
FDEATQLR	980.1	2	2.7708	0.1707
FDEGRADFPVDEELGLDLGDLSR	2566.7	3	4.2223	0.2476
FDEHQSKPEILNLVK	1798.0	2	3.565	0.2553
FDEHQSKPEILNLVKR	1954.2	3	3.4284	0.2377
FDEILEASDGIMVAR	1666.9	2	3.9654	0.2346
FDESEKTKESR	1356.4	2	3.1437	0.2563
FDGALNVDLTEFQTNLVPYPR	2410.7	2	5.8172	0.4712
FDGATEVEPR	1121.2	2	3.0747	0.2099
FDGGEEVLISGEFNDLRK	2026.2	3	3.7991	0.2753
FDGGVEAIATR	1136.2	2	3.4599	0.3827
FDGILGMAYPR	1240.5	2	3.9973	0.5046
FDGWDKVVFNTLQGGK	1812.0	2	4.3453	0.3599
FDHIFYTGNTAVGK	1570.7	2	3.446	0.3223
FDHLVAIER	1100.3	2	2.8854	0.2247

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FDIEMSMRGDIFER	1747.0	2	3.1421	0.1291
FDKDHDVMLFLK	1508.8	3	4.6256	0.2406
FDKKDEESGGGSNPFQHLEK	2250.4	3	5.4721	0.4093
FDKKDEESGSGSNPFQHLEK	2280.4	3	4.2464	0.3296
FDKKDEESGSGSNPFQHLEKSAVLQEAR	3135.3	3	3.8599	0.1356
FDKLSHASSGAGH	1314.4	2	3.1911	0.3252
FDKRSEAEEAITSFNGHKPPGSSEPITVK	3160.4	3	3.9389	0.327
FDLEKYNQLKDAIAQAEMDLKR	2641.0	3	4.3753	0.25
FDLGQDVIDFTGHALALYR	2152.4	2	6.0307	0.544
FDLLASNFPPLPGSSSR	1806.0	2	2.878	0.1023
FDLPDMKETK	1224.4	2	2.8392	0.2138
FDNSYSLLR	1115.2	2	2.8425	0.316
FDNTYSFIHAK	1343.5	2	3.326	0.2894
FDPTWESLDAR	1337.4	2	2.8005	0.2571
FDPVGPLPGPNPILPGR	1744.0	2	3.0972	0.318
FDPYEHEALFHTPVEGK	2017.2	3	3.6164	0.1925
FDPYEHEALFHTPVEGKEPGTVALVSK	2999.3	3	5.6338	0.3923
FDQGDTTR	939.9	2	2.4808	0.1553
FDQKQELGR	1121.2	2	2.9558	0.1431
FDQLFDDESDPFEVLK	1945.1	2	5.5144	0.4585
FDQLLAEEK	1093.2	2	2.8346	0.1995
FDQLLAEEKTISAK	1593.8	2	4.265	0.3437
FDREVDIGIPDATGR	1661.8	2	3.18	0.2274
FDRGYISPYFINTSK	1809.0	3	4.1754	0.3734
FDSASSSYYLDMHSLPHVINPVESR	2853.1	3	3.835	0.2942
FDSDAASPR	966.0	2	3.2305	0.3595
FDSDAASQR	997.0	2	3.1221	0.2149
FDSDVGEYR	1088.1	2	2.8982	0.255
FDSDVGVYR	1058.1	2	2.8356	0.3904
FDSKDEILLTLEK	1551.8	2	3.7622	0.3239
FDSNNVVLIEDNGNPVGTR	2061.2	2	5.5817	0.4277
FDTEEEFKKR	1329.4	2	2.6757	0.1938
FDTGNLCMVTGGANLGR	1727.0	2	2.526	0.1012
FDTQYPYGEK	1248.3	2	2.9993	0.1619
FDTQYPYGEKQDEFKR	2052.2	2	3.8496	0.4484
FDVNTSAVQVLIEHIGNLDR	2241.5	2	3.0022	0.2343

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FDVPGDENAEMDAR	1566.6	2	3.2592	0.2933
FDVQLKDLEK	1235.4	2	3.2887	0.1923
FDVQLKDLEKWQNNLLPSR	2344.7	3	5.6876	0.3667
FDVSGYPTIK	1127.3	2	3.2452	0.35
FDVSGYPTLK	1127.3	2	2.8588	0.2561
FDYSGVGSSDGNSEESTLGK	2037.0	2	4.9286	0.4567
FEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR	3940.4	3	6.7243	0.4633
FEAPLFNAR	1065.2	2	2.4199	0.206
FEDENFILK	1155.3	2	3.1727	0.1356
FEDHEGLPTVVK	1371.5	2	2.932	0.2313
FEDKTVAYTEQK	1459.6	2	4.4593	0.3089
FEDPKFEVIEKPQA	1677.9	2	4.3449	0.3764
FEELNADLFR	1254.4	2	3.3034	0.2612
FEELNADLFRGTLDPVEK	2094.3	2	3.062	0.1159
FEELNMDLFR	1314.5	2	3.5353	0.2768
FEELTNLIR	1135.3	2	2.5165	0.1433
FEGGDRDLEHLSK	1503.6	2	2.8638	0.1816
FEGGDRDLEHLSKFIEEHATK	2459.7	3	3.4201	0.1541
FEGKPLLQR	1088.3	2	2.525	0.133
FEHCNFNDVTTR	1483.6	2	2.9354	0.2216
FEIGEGENLDLPYGLER	1952.1	2	4.9101	0.4195
FEKEAAEMGK	1140.3	2	2.9966	0.2034
FEKNFYVEHPEVAR	1765.9	2	4.3534	0.4058
FELGKLMELHGEGSSSGK	1907.1	2	3.921	0.3646
FELGKLMELHGEGSSSGKATGDETGAKVER	3122.4	3	3.6573	0.3741
FENAFLSHVVSQHQALLGTIR	2368.7	3	6.1528	0.5412
FENAFLSHVVSQHQALLGTIRADGK	2740.1	3	5.9466	0.42
FENIHTNNKPGLLGEPPAVVLQTALGIGSVLPLKK	3667.3	3	4.4156	0.3322
FEQIYLSKPTHWER	1835.1	2	2.5134	0.1393
FEREQLLGVQQHLSNTLK	2141.4	3	5.2232	0.3621
FESDPATHNEPGVR	1556.6	2	3.4136	0.3588
FETEKNNGAGYFLEHLAFK	2216.4	3	5.1337	0.4619
FETEKNNGAGYFLEHLAFKGTK	2502.8	3	4.4547	0.3981
FETFCLDPSLVTK	1500.7	2	3.4021	0.2329
FETLQAQAGK	1093.2	2	3.273	0.3613
FETLQAQAGKHGDDLR	1786.9	2	3.9482	0.3104

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FEWELPLDEAQR	1533.7	2	3.5803	0.3777
FFALPYVDHFLR	1525.8	2	3.1457	0.244
FFDANYDGKDYDPVAAR	1965.1	2	4.8432	0.4163
FFDANYDGKDYNPLLAR	2020.2	2	4.1651	0.3435
FFDDPMLLELAK	1439.7	2	2.8191	0.3266
FFDEESYSLLR	1406.5	2	3.8672	0.4159
FFDEESYSLLRK	1534.7	2	3.3859	0.2952
FFDENESPVDPQHGSK	1833.9	2	4.1704	0.3833
FFDHSGTLVMDAYEPEISR	2215.4	2	6.3225	0.537
FFDKVIEKR	1182.4	2	2.7206	0.2673
FFEDYGLFMR	1325.5	2	2.7063	0.2382
FFEEPEDPSSR	1340.4	2	3.1097	0.2668
FFEHFIEGGR	1239.4	2	3.162	0.3538
FFESFGDLSTPDAVMGNPK	2060.3	2	5.0469	0.526
FFEVILIDPFHK	1505.8	2	3.5335	0.3029
FFFDVGSNK	1061.2	2	2.4235	0.2064
FFFDVGSNKYGVFMR	1815.1	2	3.6309	0.4617
FFGDSAASMAIK	1245.4	2	2.9626	0.2754
FFGDSAASMAIKNPK	1584.8	2	4.143	0.4361
FFGKDISTTLNADEAVAR	1956.1	2	5.3195	0.5377
FFGKELSTTLNADEAVTR	2000.2	2	5.4655	0.4979
FFGNSWAETYR	1378.5	2	2.775	0.3488
FFGPNAEISQPPALSQLVNLYLGR	2633.0	3	3.2389	0.1789
FFGTFPGNYVK	1277.5	2	3.1581	0.3383
FFHETEAPRPK	1359.5	2	3.4012	0.3537
FFHETEAPRPKDFLSK	1950.2	2	3.9756	0.3543
FFHLAFEEEFGR	1529.7	2	2.8476	0.1568
FFHPEEWADLFQAAGAK	1965.2	3	4.8577	0.3552
FFLKDISTTLNADEAVAR	2012.3	2	2.4161	0.1327
FFLQDPQSQELDVQVK	1922.1	3	4.6127	0.3437
FFLQDPQSQELDVQVKDDSR	2395.6	3	3.9072	0.2539
FFLQGIQLNTILPDAR	1847.2	2	3.2372	0.1358
FFLQGIQLNTILPDARDPAFK	2405.8	3	4.8692	0.1947
FFLSHPAYR	1138.3	2	2.6831	0.2763
FFLSHPSYR	1154.3	2	2.4124	0.2667
FFLSSGLIDKVDNFK	1731.0	2	4.2023	0.2865

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FFNIPFLQLQR	1423.7	2	3.6668	0.3291
FFNLNKLEDSR	1383.5	2	3.6629	0.2903
FFPASADRTVIDYNGER	1959.1	2	3.2413	0.1736
FFPFGLVQLSSDLSK	1685.9	2	4.9745	0.4903
FFPFGLVQLSSDLSKK	1814.1	2	2.6358	0.2812
FFPLESWQIGK	1352.6	2	3.1842	0.3643
FFPYYVYNIIGGLDEEGK	2125.4	2	2.8368	0.2499
FFQKEQALSTLQLEHTSTQALVSELLPAK	3259.7	3	5.1218	0.4496
FFQPTEMAAQDFFQR	1864.1	2	3.6962	0.4116
FFQPTEMASQDFFQR	1880.1	2	2.9832	0.3532
FFQSFSDALIDEDPQAALEELTK	2615.8	2	5.5786	0.37
FFREVLLEVQK	1408.7	3	3.4402	0.1477
FFRPHFLQAPGDLTVQEGK	2188.5	3	5.5499	0.4128
FFSDKETFHDIAQVASEFPGAQHYVGGNAALIGQK	3782.1	3	5.9764	0.4396
FFTDDLFQYAGEK	1581.7	2	3.4509	0.3698
FFTEEVDSR	1130.2	2	2.8391	0.3992
FFTGQITAAGK	1141.3	2	2.4545	0.2254
FFTNFESR	1048.1	2	2.57	0.311
FFTREPQDTYHYLPFSLPHR	2552.8	3	4.8501	0.444
FFTVKLPVALDPGAK	1603.9	2	4.5217	0.4162
FFTYGNFPLEQHLK	1742.0	2	3.4993	0.295
FFVADTANEALEAAK	1597.8	2	5.1562	0.5058
FFVADTANEALEAAKR	1753.9	2	5.4581	0.5472
FFVNFVVGQDPGSDVAFHFNPR	2497.8	3	4.1399	0.2749
FFVSSSQGR	1015.1	2	2.9353	0.3696
FFVTTLPAFFHAK	1526.8	2	3.9738	0.3588
FFWGNAETLKHEPR	1732.9	2	2.4847	0.222
FFYSDQNVDSRDPVQLNLLYVQAR	2889.2	3	5.5793	0.3532
FGAFHSPALEDADFDGKPMVLVAGQYSTGK	3157.5	3	5.373	0.3379
FGALTAEK	837.0	2	2.6192	0.1115
FGANAILGVSLAVCK	1463.8	2	3.8722	0.3918
FGAPPHAGGGIGLER	1436.6	2	3.6019	0.4068
FGAQLAHIQALISGIEAQLGDVR	2408.7	2	6.7829	0.5386
FGAQLAHIQALISGIEAQLGDVRADSER	2967.3	3	4.9608	0.4838
FGAQLAHIQALISGIEAQLGDVRADSERQNQEYQR	3914.3	3	4.2804	0.2187
FGAQNEEMLPSILVLLK	1903.3	2	4.7896	0.2251

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FGAQNEEMLPSILVLLKR	2059.5	3	5.1077	0.349
FGAQNESLLPSILVLLQR	1999.3	2	4.5431	0.3216
FGDPVVQSDMK	1223.4	2	3.0765	0.4084
FGDPVVQSDMKHWPFQVINDGDKPK	2886.2	3	5.1235	0.2898
FGDQLLQIDGR	1262.4	2	3.9659	0.2693
FGDRFPAMSDAYDR	1648.8	2	3.3105	0.3073
FGDSNTVMR	1027.1	2	2.5623	0.2137
FGDYNKEVHK	1237.3	2	2.9658	0.2292
FGDYNKEVHKSGYLSSER	2117.3	2	4.1762	0.4497
FGEGVSSPK	908.0	2	3.4965	0.2933
FGEGVSSPKTHLGEALAPLSK	2126.4	3	4.2899	0.3161
FGELVMTK	925.1	2	2.8306	0.1115
FGELVMTKESK	1269.5	2	2.4761	0.2174
FGEMQLDFR	1143.3	2	2.7218	0.2255
FGESTTGFNFSFK	1469.6	2	3.3063	0.3497
FGEVVDCTIK	1111.3	2	2.6648	0.201
FGEVVDCTLKLDPITGR	1864.2	3	4.5279	0.3741
FGFGLLNAK	967.1	2	3.3684	0.2755
FGFPEGSVELYAEK	1573.7	2	3.2207	0.4113
FGGAAVFPNQEQAR	1492.6	2	3.5726	0.1777
FGGALDAAAK	921.0	2	3.0969	0.2293
FGGEHVPNSPFQVTALAGDQPSVQPPLR	2947.3	3	4.5077	0.4024
FGGGNPELLTQMVSK	1578.8	2	4.812	0.3948
FGGGNPELLTQMVSKGFLGR	2109.4	2	3.6723	0.378
FGGNPGGFGNQGGFGNSR	1727.8	2	4.425	0.4027
FGGPVHHQAQR	1234.4	2	3.178	0.2264
FGGSGSQVDSAR	1168.2	2	3.8582	0.3664
FGHEFLEFEFRPDGK	1856.0	2	4.2318	0.396
FGHGSDYSR	1026.0	2	2.7855	0.3016
FGIDDQDYLVSLTR	1642.8	2	4.7036	0.4314
FGIDDQDYQNSVTR	1658.7	2	4.3327	0.4587
FGIEKEVR	978.1	2	2.6993	0.1702
FGISSVPTK	936.1	2	2.4528	0.1041
FGIVTSSAGTGTTEDTEAK	1873.0	2	5.4834	0.5038
FGKHGGTIPIVPTAEFQDR	2071.3	2	4.4005	0.4197
FGKPDPIVSVIFKDEK	1820.1	3	4.3212	0.3243

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FGLALAVAGGVVNSALYNVDAGHR	2372.7	2	5.4845	0.4491
FGLGSVAGAVGATAVYPIDLVK	2106.5	2	6.2662	0.5304
FGLLDEDGKKTFFR	1673.9	2	2.5584	0.2258
FGLNIDR	834.9	2	2.7079	0.15
FGLNVSSISR	1080.2	2	3.2539	0.3333
FGLSVGHHLGK	1152.3	2	3.321	0.2662
FGLYLPLFKPSVSTSK	1785.1	2	4.2291	0.3668
FGMAAALAGTMR	1197.5	2	3.5533	0.3753
FGMDFKEIELIGSGGFGQVFK	2307.7	2	2.9787	0.2027
FGMFEFLSNHMR	1516.8	3	3.3809	0.3963
FGMLDATDGPGTEDAALR	1838.0	2	3.0817	0.2584
FGNAFLNR	939.1	2	2.6487	0.3006
FGNEVIPVTVTVK	1403.6	2	3.6501	0.2853
FGNPLLVQDVESYDPVLNPVLNR	2599.9	2	6.1116	0.5366
FGNQADHFLGSLAFAK	1723.9	3	4.1192	0.4054
FGPGVAFR	851.0	2	2.576	0.3093
FGPIPLGSLGWK	1272.5	2	2.8413	0.2084
FGPVVAPKPK	1040.3	2	2.4681	0.1179
FGPYESYDSR	1221.3	2	2.5832	0.1988
FGPYYTEPVIAGLDPK	1768.0	2	3.7586	0.3103
FGQAATMEGIGAIGGTPPAFNR	2164.4	2	5.9985	0.5484
FGQDFSTFLEAGVEMAGQAPSQEDR	2718.9	3	3.8432	0.1486
FGQGDLPKPINSDFR	1691.9	3	3.2869	0.3206
FGQGGAGPVGGQGPR	1342.4	2	4.3754	0.4397
FGQHLIKPSVVFLK	1614.0	2	2.7671	0.1338
FGQMLGSNMTEFHSQISK	2043.3	3	3.2876	0.2463
FGQVPDQPAGLR	1285.4	2	2.688	0.1155
FGQVTPMEVDILFQLADLYEPR	2583.0	3	3.3176	0.174
FGRFDREVDIGIPDATGRLEILQIHTK	3098.5	3	4.0747	0.1712
FGSAIAPLGDLDQDGFNDIAIAAPYGGEDKKGIVYIFNGR	4187.6	3	4.2444	0.3992
FGSDHTGVGR	1033.1	2	2.4308	0.2516
FGSGMNMGR	957.1	2	2.7376	0.2593
FGSLLPIHPVTSG	1325.5	2	2.991	0.1933
FGTVLTEHVAAAELGAR	1743.0	2	4.9217	0.4368
FGVAPDHPEVK	1196.3	2	3.216	0.2674
FGVAPDHPEVKNVINTFTQTAHSGR	2724.0	3	4.4364	0.4205

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FGVEQDRMDK	1225.4	2	2.8886	0.2826
FGVEQDRMDKSAVGHEYQSK	2312.5	3	5.6015	0.3286
FGVEQDVDMVFASFIR	1861.1	2	5.877	0.5649
FGVEQDVDMVFASFIRK	1989.3	3	5.5108	0.4855
FGVQMDRVDQSAVGFEYQGKTEK	2620.9	3	4.0658	0.2046
FGVQTDRQDK	1194.3	2	2.756	0.1897
FGVVLDEIKPSSAPELQAVR	2156.5	2	4.9248	0.3154
FGVVVVGVGR	989.2	2	3.7906	0.3111
FGYDEIDNGYLK	1434.5	2	3.8375	0.3178
FGYHFTQQGPR	1338.5	2	3.2253	0.3581
FGYRLPAEGLK	1251.5	3	3.6513	0.3398
FGYVDFESAEDLEK	1649.7	2	3.9367	0.373
FGYVDFESAEDLEKALELTGLK	2475.7	2	4.5734	0.4447
FGYVDFESAEDLEKALELTGLKVFGNEIK	3263.6	3	3.3845	0.1688
FHALGPIYYR	1237.4	2	2.6406	0.154
FHCVGGSVQDPEKIPSTGK	1987.2	2	5.4399	0.308
FHDFLGDSWGILFSHPR	2032.2	3	5.4827	0.5147
FHDIDDVKK	1117.2	2	2.8603	0.147
FHDIISDAEIEIVKDLAKPR	2310.6	2	3.7529	0.1896
FHDKRDAEDAMDAMDGAVLDGR	2436.6	3	4.9339	0.4185
FHDLLSQLDDQYSR	1737.9	2	4.8314	0.3843
FHDLRPDEVADLFQTTQR	2189.4	3	4.2596	0.2859
FHDNFGFDDLVR	1482.6	2	2.6904	0.2174
FHDPDSAVVAQHLTNTVFVDR	2369.6	3	5.822	0.488
FHEERKTKLSLLLDNERWKQADVPA	3025.4	2	4.508	0.1299
FHEFHSPALEDADFDNKPMVLLVGQYSTGK	3394.8	3	5.6068	0.4735
FHEFHSPALEDADFENKPMILLVGQYSTGK	3422.8	3	7.0336	0.4184
FHEQFHSLR	1201.3	2	3.0671	0.1813
FHFASALKR	1077.3	2	2.6053	0.1758
FHFTHTIQQK	1287.5	2	2.8929	0.1639
FHFVDLAGSER	1278.4	2	2.9524	0.2898
FHGGNLFFLPGGAR	1490.7	2	3.3235	0.3466
FHHTFSTEIAK	1318.5	2	2.9663	0.309
FHLATAEWIAEPVR	1640.9	2	3.7646	0.3125
FHMDSETHDPIDLQTK	1915.1	3	3.6216	0.3611
FHMVDGNVSGEFTDLVPEK	2122.3	2	2.6427	0.2282

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FHNELNAHIK	1223.4	2	2.5475	0.1098
FHNLEGFLEEFADIAKEDQIKK	2622.9	3	3.4919	0.1509
FHPDTDDVPVPAPAGDQKEVDTSEK	2695.8	3	5.0665	0.4091
FHPDTDDVPVPAPAGDQKEVDTSEKK	2824.0	3	4.6404	0.4039
FHPEPYGLEDDQR	1603.7	3	3.4912	0.3127
FHPIKETVVEEPVDITPYLDQLDESLRDK	3427.8	3	5.3518	0.2938
FHQLDIDDLQSIR	1600.8	3	4.4427	0.3222
FHQLLDDESDPFDILR	1961.1	2	4.1802	0.3844
FHQNQLLSSLKGEPAPALSSR	2281.6	3	3.9067	0.2438
FHSEDYIDFLQR	1570.7	2	2.7452	0.2309
FHSFPNVYHELSK	1605.8	3	3.2756	0.2632
FHSGWEPPVDVLQEAPWEVEGLASAPIEEVSPVSR	3846.2	3	5.0029	0.4454
FHSPQHPPEEFGFGFSFSPGGGIR	2619.8	3	4.4768	0.2716
FHTSRPESFAIYK	1583.8	2	2.5071	0.1044
FHTVSGSK	863.0	1	2.301	0.2068
FHVEEEGK	975.0	1	2.8606	0.1487
FHVEEEGKGKDASGNK	1732.8	2	5.631	0.4164
FHVEEEGKGKDASGNKVK	1960.1	2	5.7718	0.4822
FHYKTDQGIK	1237.4	2	2.6464	0.1491
FIADQLDHLNVTK	1514.7	2	4.3461	0.3443
FIADQLDHLNVTKK	1642.9	2	2.8496	0.1347
FIAEEAAASGAK	1165.3	2	3.2299	0.1951
FIAVGYVDDTQFVR	1630.8	2	5.2177	0.464
FIAVGYVDDTQFVRFDSDAASPR	2577.8	3	4.3419	0.3173
FIAVGYVDDTQFVRFDSDAASQR	2608.8	3	3.5397	0.3361
FICTTSAIQNR	1254.4	2	3.3688	0.3586
FIDFFK	817.0	2	2.4237	0.1597
FIDTTSK	811.9	1	2.006	0.1341
FIDTTSKFGHGR	1366.5	2	3.8154	0.3762
FIEAEQVPELEAVLHLVIASSDTR	2668.0	3	4.9666	0.3368
FIEEHATK	975.1	2	2.5649	0.1965
FIEEHATKLSR	1331.5	2	3.3665	0.2754
FIEQEKAKLEQLFQDEVAK	2294.6	3	6.0965	0.3339
FIEQEKAKLEQLFQDEVAKAQQLREEQQR	3561.9	3	3.427	0.1196
FIGELGKLDLIHESILHK	2063.4	2	5.1003	0.4076
FIHDQTSPNPK	1284.4	2	3.3441	0.1889

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FIHNSHDLTYFAYLIK	1983.3	3	4.1183	0.2468
FIHQQPQSSSPVYGSSAK	1949.1	2	3.9751	0.3537
FIHVSHLNANIK	1393.6	2	3.2405	0.3377
FIIHAPPGEFNEVFNDVR	2102.3	3	4.6369	0.3985
FIKPLSNAYHELAQVYSTNNPSELR	2893.2	3	6.549	0.5075
FILNLPTFSVR	1307.6	2	3.417	0.1334
FIPHENGVHTIDVK	1606.8	2	4.115	0.4065
FIPLSEPAPVPPIPNEQQLAR	2314.7	3	4.2485	0.3504
FIQENIFGICPHMTEDNKDLIQGK	2792.2	3	4.4439	0.2944
FIQFEPEEDIKRK	1679.9	2	3.6719	0.1018
FISDKDASIVGFFDDSFSEAHSEFLK	2940.2	2	7.3972	0.5519
FISEQVSHHPPISAFHSEGLNHDFLFHGSIYPK	3777.2	3	3.9701	0.229
FISGHTSELGDFR	1466.6	2	3.1292	0.2157
FISNPNSIILAVTAANTDMATSEALK	2694.1	3	4.5864	0.2671
FISVGYVDDTQFVR	1646.8	2	4.6363	0.5278
FITHAPPGEFNEVFNDVR	2090.3	3	4.5464	0.4195
FIVDGWHEMDAENPLHQPSPSLNK	2763.0	3	6.4259	0.4136
FIVDGWHEMDAENPLHQPSPSLNKLVAENK	3417.8	3	4.8846	0.3663
FIVDGWHEMDAENPLHQPSPSLNKLVAENKFGK	3750.2	3	4.6788	0.422
FIVLSNNYLQIR	1480.7	2	3.596	0.2618
FIWYNNVINPTLPR	1748.0	2	4.1595	0.2889
FIYITPEELAAVANFIR	1968.3	3	4.791	0.4181
FKAADLNGDLTATR	1493.6	2	2.867	0.2364
FKARPELEELLAK	1544.8	2	3.827	0.2162
FKATISALEAK	1179.4	2	2.9228	0.2968
FKAVSAK	750.9	1	1.8211	0.1245
FKDFLLSLK	1111.4	2	3.1084	0.168
FKDHVEGK	960.1	2	2.8807	0.1952
FKDIFQEIFDK	1430.6	2	3.7202	0.286
FKDIFQEIFDKHYK	1859.1	2	4.7994	0.3559
FKDIFQEIYDK	1446.6	2	4.1622	0.2838
FKDIFQEIYDKQYK	1866.1	2	4.8951	0.4131
FKDKSSEEAVR	1296.4	2	3.3057	0.2482
FKDLEDKKVNQQPNTSDKK	2263.5	3	4.2195	0.2347
FKDLGEENFK	1227.3	2	3.764	0.299
FKDPGLVDQLVK	1359.6	2	3.8623	0.2623

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FKDPLKDGEAK	1248.4	2	2.8812	0.1004
FKDPNAPK	917.0	1	1.7523	0.1275
FKEANNFLWPFK	1541.8	2	4.1209	0.2645
FKEDLLNNGQPR	1431.6	2	3.3648	0.2735
FKEHVQNNLPR	1382.6	2	3.1046	0.2757
FKEIAEAYDVLSDPR	1753.9	2	3.5805	0.329
FKEMELPAK	1093.3	2	2.5555	0.1887
FKEPAHALAFQQK	1515.7	2	4.0895	0.3336
FKEQLTPSQIMSLEKEIMDK	2396.8	3	5.4382	0.3567
FKEREENVK	1179.3	2	2.7676	0.1445
FKESFAEMNR	1259.4	2	3.0705	0.2925
FKEVIPISDPELK	1515.8	2	2.4231	0.1335
FKEVIPISDPELKQK	1772.1	3	3.883	0.1048
FKFLFNLPLNIER	1652.0	2	3.9676	0.2888
FKFTIGDHSR	1208.4	2	3.138	0.3434
FKFTVGDHSR	1194.3	2	3.0522	0.2833
FKGDETVVIGQGKPYVFDR	2156.4	3	3.3755	0.3522
FKGFDPNQLSVATLLFEGDREK	2512.8	3	3.9432	0.2798
FKGFPQPILSEDGSR	1678.9	2	3.5609	0.3822
FKGPFTDVVTTNLK	1567.8	2	4.0885	0.3485
FKIGDQEFDHLPALLEFYK	2311.6	2	4.726	0.4266
FKILDAVVAQEPLHR	1737.0	2	4.7217	0.4327
FKIPGSPPESMGR	1403.6	2	2.8773	0.2465
FKKDPPLAAVTTAVQELLR	2098.5	3	4.7307	0.353
FKKEDEIPETVSLEMLDAAK	2294.6	3	4.7537	0.336
FKKGDSVGLR	1107.3	2	2.4857	0.1012
FKKYEEIDNAPEER	1768.9	2	5.086	0.3901
FKLDLDFPNLPYLLDGK	2009.3	2	5.5516	0.3359
FKLEESYDMESVLR	1747.0	2	4.5477	0.3149
FKLEESYTLNSDLAR	1787.0	2	4.4406	0.426
FKLGLDFPNLPYLIDGTHK	2189.5	3	5.7194	0.4511
FKLITEDVQGK	1278.5	2	3.3589	0.1532
FKLPTKNEFIPTNFEILPLEK	2520.0	3	3.8706	0.1232
FKLQDVADSFKK	1426.6	3	3.7586	0.2624
FKLWYTLDR	1242.5	2	2.8472	0.2065
FKNTEAIGNEVTR	1479.6	2	3.3734	0.2196

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FKNWDDVLTVDYTR	1772.9	2	3.0053	0.2028
FKPFTVEIVDSVEAYATMLR	2317.7	3	3.4188	0.2369
FKPGVISEELQDALGVTDK	2047.3	2	2.5246	0.1453
FKPLSDKIQQQR	1488.7	2	3.6341	0.1647
FKPLWIEEPTSPDDILGHATISK	2595.9	3	5.2815	0.2852
FKPSLFQHVGTHSSLAGK	1942.2	2	2.7019	0.1726
FKQAETLYKEILTR	1741.0	2	2.8188	0.1597
FKQESTVATER	1296.4	2	3.4318	0.2599
FKQLQDER	1064.2	2	2.6913	0.1085
FKQLQDEREAVQK	1619.8	2	4.5209	0.1533
FKQMTEAIGPSTIR	1579.8	2	3.8911	0.3386
FKQMTEAIGPSTIRDLAVAGPEMQVK	2819.3	3	4.7201	0.3291
FKSESDIHLAEHHK	1678.8	2	4.1522	0.336
FKSHTDQLVLIFAGK	1705.0	2	4.0261	0.3395
FKSLDDVIK	1065.2	2	3.1147	0.125
FKSLDDVIKR	1221.4	3	3.5401	0.3168
FKTEKEFMQHAR	1552.8	2	3.5917	0.3066
FKTEQENEAK	1224.3	2	3.1551	0.2028
FKTIEEVVGR	1178.4	2	3.4259	0.2587
FKTQLNLLLDKLR	1602.9	2	2.4347	0.1217
FKVDLTPYPTISSINKR	1980.3	2	4.2351	0.3181
FKVLMTQQPRPVL	1557.9	2	2.622	0.1143
FKVSGGLPLMHVR	1441.8	2	3.8485	0.3494
FLAAGTHLGGTNLDFQMEQYIYE	2619.9	3	6.0944	0.1257
FLAAGTHLGGTNLDFQMEQYIYER	2776.1	3	5.7666	0.1879
FLAAGTHLGGTNLDFQMEQYIYK	2618.9	3	5.2517	0.2381
FLADQQSEIDGLK	1464.6	2	3.4258	0.2507
FLAELLSEPNQTENDALEPEDLSQAAEQDEMR	3634.8	3	5.2964	0.4457
FLALLREEGASPLDFD	1794.0	2	3.8925	0.3274
FLASVLHNGLGR	1284.5	2	3.4974	0.3528
FLATTPNSLLVSWQPPR	1928.2	3	4.1201	0.2604
FLAVGLVDNTVR	1304.5	2	3.7925	0.2372
FLCTGGVSPYADPNTCRGDSGGPLIVHKR	3019.4	3	4.1699	0.2846
FLDAGHKLNFAVASR	1646.9	2	4.8533	0.4524
FLDGDELTLADCNLLPK	1878.1	2	3.5219	0.1464
FLDGIYVSEK	1171.3	2	3.6838	0.3117

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FLDPLPTSGITPGATVLTASGQTVGK	2529.9	3	4.7196	0.3571
FLDRYFYNQEESVR	1867.0	2	3.6471	0.3428
FLDTAFNLQAFEGK	1601.8	2	4.8362	0.4305
FLEDTFGNDGRPR	1524.6	2	2.7842	0.226
FLEEHPGGEEVLR	1512.6	2	4.0954	0.3276
FLEEHPGGEEVLREQAGGDATENFEDVGHSTDAR	3700.8	3	6.0555	0.5171
FLEEYLSSTPQR	1470.6	2	3.476	0.3272
FLEFQYLTGGLVDPEVHGR	2178.4	3	5.1575	0.4626
FLEHKGPVFAPPYEPLPENVKFYYDGK	3183.6	3	6.5915	0.524
FLEHLSGAGK	1059.2	2	2.6861	0.1985
FLEQQNKILLAELEQLKGQGK	2428.8	3	7.3596	0.2874
FLEQQNKLLETKWTLLQEQK	2518.9	3	3.3151	0.1552
FLEQQNKMLETK	1509.8	2	3.1187	0.1812
FLEQVHQLYDDSFPMEIR	2268.5	2	3.8478	0.4139
FLESGGQDGAGDDDDLEDLEEAEEPDMEEDDDQK	3759.7	3	6.6457	0.4639
FLESGGQDGAGDDDDLEDLEEAEEPDMEEDDDQKAVKDEL	4415.4	3	5.8556	0.4216
FLESVEGNQNYPLLLLTLLEK	2434.8	2	4.5091	0.4068
FLEVIKPFCVILPEIQKPER	2399.9	3	4.4249	0.3417
FLEVQYLTGGLIEPDTPGRVPLDEALQR	3128.5	3	5.5775	0.4002
FLFENQTPAHVYYR	1786.0	2	2.4489	0.1789
FLFPFFDSAYQGFASGNLER	2314.5	2	4.2688	0.4667
FLGEGHHR	953.0	2	2.5105	0.2038
FLGGDMEHTHLVK	1484.7	2	2.6995	0.2311
FLGLTERDVELLYPVKEK	2150.5	3	4.0134	0.177
FLGLYRDEHQDFMDEQKR	2328.5	3	4.2093	0.2765
FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR	4261.8	3	3.9456	0.3127
FLGRDPKQDAFLLSK	1736.0	2	3.9455	0.2181
FLGTEPEPDAVGLDSGHIR	2011.2	3	4.9112	0.4893
FLGTVEKEATFSNPK	1668.9	2	3.1504	0.2697
FLIDGFPR	965.1	2	2.7343	0.1376
FLIPNASQAESK	1305.5	2	2.521	0.2365
FLIPNASQAESKVFYLK	1956.3	2	3.3755	0.2394
FLITHNPTNATLNKFTEELKK	2460.8	3	4.2339	0.2763
FLIVAHDDGR	1143.3	2	3.0221	0.2709
FLKEEPHKLDSLLK	1698.0	2	3.3332	0.2577
FLKGDTTDLLK	1251.5	2	2.6334	0.1547

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FLKNEVER	1035.2	2	2.4242	0.106
FLLDHQGELFPSPDPSGL	1970.2	2	4.0583	0.2895
FLLDNPYTHTYSYSCSGSAITCSSK	2747.0	3	5.378	0.3456
FLLDTLKASPSEVVFLDDIGANLKPAR	2931.4	3	5.6908	0.3572
FLLGYFPWDSTKEER	1889.1	2	2.9115	0.1123
FLLHQETLPEQLLAEK	1910.2	2	3.4183	0.3894
FLLSDQSLLLLPEYHQR	2073.4	2	2.7824	0.2166
FLLYTNENPNNFQEVAADSSSISGSNFK	3095.3	3	5.9321	0.5035
FLLYTNENPNNFQLITGTEPDTIEASNFQLDRK	3845.2	3	4.163	0.1762
FLNALTLNMIR	1306.6	2	4.1054	0.3295
FLNEHPGGEEVLLEQAGVDASESFEDVGHSSDAR	3629.8	3	6.3335	0.4936
FLNRHDLDLICR	1515.8	2	2.926	0.229
FLNSFASMHR	1210.4	2	2.9387	0.2182
FLNVLSPR	946.1	2	2.4983	0.1494
FLNYVQSQHQR	1420.6	2	3.4849	0.3566
FLPREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK	4001.5	3	5.4263	0.4093
FLPSYQAVEYMR	1504.7	2	4.2841	0.4184
FLQDPYSTTFSSFSR	1783.9	2	4.6948	0.3885
FLQDYFDGNLK	1360.5	2	4.0346	0.3185
FLQDYFDGNLKR	1516.7	2	4.2956	0.3015
FLQEHGSDSFLAEHK	1745.9	2	4.7038	0.4214
FLQEHGSDSFLAEHKLLGNIK	2384.7	3	4.9099	0.3179
FLQEHGSDSFLAEHKLLGNIKNVAK	2797.2	3	3.2078	0.1552
FLQEHLAPK	1083.3	2	2.8784	0.2077
FLQESNVLYQHNLR	1762.0	2	3.6052	0.1127
FLQHGTLVGLLPVPHPILIR	2221.7	2	4.1132	0.3056
FLQLESLQELMK	1479.8	2	3.3626	0.1572
FLQSSASVQNHEFLLVHHLQR	2491.8	3	3.2378	0.1177
FLRDLPDGLFTR	1450.7	2	2.5527	0.1591
FLRENPYYDSR	1460.6	2	3.4706	0.2814
FLREWVESMGGK	1439.7	2	3.0051	0.2019
FLREWVESMGGKVPPATQK	2161.5	3	4.4368	0.4602
FLSDPQVHTVLVER	1640.9	2	4.6868	0.4407
FLSGLELVK	1006.2	2	2.4981	0.168
FLSHLVDGVKR	1271.5	2	2.6816	0.1062
FLSHSLVELLNQISPTFKK	2202.6	2	3.3224	0.1508

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FLSLDLQGDPRESQPLLGTVIDGMLLLKTPEELQAER	4124.7	3	4.6262	0.3547
FLSNGHVTIPGQQDK	1641.8	2	4.9982	0.293
FLSNGHVTIPGQQDKDMFQETMEAMR	3012.4	3	5.6866	0.4634
FLSPQDTFEALKR	1552.8	2	2.9779	0.1185
FLSPVVPNYDNVHPNYHK	2141.4	2	3.928	0.424
FLSPVVPNYDNVHPNYHKEPFLQQLK	3125.5	3	3.3302	0.2227
FLSQPFQVAEVFTGHMGK	2024.3	2	4.7138	0.4688
FLSSAAAVSKEHPVVISK	1871.2	3	3.5123	0.2479
FLTAGRTDPAHDVR	1556.7	2	3.3078	0.2982
FLTALAQDGVINEEALSVTELDR	2505.8	3	4.4537	0.3816
FLTALAQDGVINEEALSVTELDRVYGGLTTK	3325.7	3	5.1759	0.3767
FLTAVNLEHPEMLEK	1772.1	2	4.8841	0.3542
FLTGPLNLNDPDAK	1515.7	2	3.7411	0.2897
FLTKGDNNAVDDR	1465.6	2	2.9622	0.1423
FLTLPPVLHLQLMR	1679.1	2	2.5832	0.2133
FLTVLCSR	939.2	2	2.4602	0.2089
FLVFVANFDENDPK	1655.8	2	4.589	0.3254
FLVGFTNK	926.1	2	2.7969	0.1579
FLVGFTNKGTEDFIVESLDASFR	2593.9	3	3.4682	0.2762
FLVGPYQNTIGAAFVAK	1797.1	2	3.6526	0.3852
FLVLDEADGLLSQGYSDFINR	2373.6	3	6.0817	0.5679
FLVTHSMR	991.2	2	2.4628	0.1667
FLYLGDDRNIEEVYVGGK	2088.3	2	3.9663	0.3309
FLYVGGALHALPTGLR	1686.0	2	3.0904	0.313
FMATNDLMTELQK	1542.8	2	2.5276	0.1631
FMATNDLMTELQKDSIKLDDDSER	2817.1	3	4.6186	0.3994
FMDEFFEQVEEIR	1719.9	2	4.2879	0.3799
FMEDTAAEKLHK	1420.6	2	2.8497	0.2145
FMELLEPLNER	1391.6	2	3.4901	0.1879
FMETVAEK	955.1	1	2.5781	0.2464
FMETVAEKALQEYR	1716.0	2	4.6895	0.4678
FMHVLYPR	1063.3	2	2.6999	0.1706
FMLQDVIDLR	1250.5	2	3.6763	0.2596
FMNPFNMPNLYQK	1644.9	2	3.723	0.3798
FMQASEDLLKEHYVDLKDRPFFAGLVK	3198.7	3	4.6694	0.2696
FMQDASDVMQLLLK	1640.0	2	4.203	0.3485

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FMQDPMEIFVDDETKLTLHGLQQYYVK	3290.8	3	3.8011	0.3475
FMQTFVLAPEGSVANK	1740.0	2	4.3428	0.4369
FMQTFVLAPEGSVPNK	1766.1	2	2.8695	0.2081
FMRDNYPPGFSYADFGPQFTAR	2585.8	3	4.13	0.3559
FMVQTIFAPPNTSDMEAVWKEAKPDELMDSKLR	3827.4	3	4.3515	0.3224
FNADEFEDMVAEK	1545.7	2	3.0122	0.2384
FNADEFEDMVAEKR	1701.8	3	3.9781	0.3103
FNADEFEYVVAEK	1561.7	2	3.38	0.3318
FNAHEFATLVIDILSDAK	2005.3	2	3.9558	0.3036
FNAHGDANTIVCNSK	1591.7	2	4.0575	0.4213
FNALFAQGNYSEAAK	1631.8	2	5.0368	0.44
FNALKVPVPEDKYTAQVDAEEKEDVK	2964.3	3	5.8052	0.4241
FNASQLITQR	1178.3	2	3.9078	0.2195
FNDEHIPESPYLVPVIAPSDDAR	2582.8	2	4.0291	0.2469
FNDGKVDPAGR	1176.3	2	3.1432	0.2674
FNDGSDEKK	1040.1	2	2.6248	0.1367
FNDGSDEKKK	1168.2	2	3.0343	0.2438
FNEELRAVDSEYPKNIK	2053.3	3	3.427	0.1904
FNEKDGHVER	1231.3	2	3.4687	0.2796
FNFFALLPHQR	1390.6	2	3.2844	0.2238
FNFGAYHTLEEISQEMDNLVAEHPGLVSK	3277.6	3	6.229	0.4648
FNFLAPELPAVSEFSTSETMGHSADR	2842.1	2	3.4115	0.4272
FNGGGHINHSIFWTNLSPNGGGEPK	2638.8	3	5.4485	0.5137
FNGGGHINHSIFWTNLSPNGGGEPKGELLEAIK	3492.8	3	5.9316	0.3246
FNGGGHINHSIFWTNLSPNGGGEPKGELLEAIKR	3649.0	3	5.8946	0.4104
FNGGHSPTHSPEK	1395.5	2	3.3532	0.2376
FNGSHVVGSPFK	1276.4	2	3.7984	0.2993
FNGTHIPGSPFK	1302.5	2	2.9317	0.152
FNHNLLPSETAHKPDLSSK	2136.4	2	4.7579	0.4504
FNILGTHTK	1031.2	2	2.4435	0.1176
FNISNGGPAPEAITDK	1631.8	2	4.1977	0.266
FNISNGGPAPEAITDKIFQISK	2348.6	3	3.7852	0.2561
FNKLFLNEDDKPHNPMVNAGAIVVTSLIK	3226.7	3	5.353	0.3759
FNKPFVFLMIEQNTK	1857.2	2	5.8284	0.3124
FNLLAHLADDLGHVVPNSR	2089.3	2	5.222	0.4276
FNLTGLNEQVPHYR	1688.9	2	2.5385	0.2321

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FNLTYVSHDGDDKKRPVIVHR	2497.8	3	4.2017	0.2557
FNNWGGSLSLGHPFGATGCR	2079.3	2	2.5199	0.1071
FNPETDYLTGTDGK	1558.6	2	3.7653	0.3312
FNPETDYLTGTDGKK	1686.8	2	3.7465	0.3015
FNPFVTSDR	1083.2	2	2.6292	0.2363
FNQLVEQYKQK	1425.6	2	2.8822	0.1641
FNRYPLIIDPSGQATEFIMNEYKDR	3019.4	3	5.3092	0.3165
FNRYPLIIDPSGQATEFIMNEYKDRK	3147.6	3	4.6141	0.4643
FNTANDDNVTQVR	1494.5	2	3.953	0.3454
FNVGEDCPVFDGLFEFCQLSTGGSVASAVK	3125.5	3	4.4642	0.285
FNVGEDCPVFDGLFEFCQLSTGGSVASAVKLNK	3480.9	3	3.7444	0.2688
FNVIQPGPIK	1113.3	2	2.8145	0.1761
FNVLHWHIVDDQSFPYQSITFPELSNK	3263.6	3	4.683	0.2834
FNVLQYVVPEVK	1435.7	2	3.9034	0.233
FNVTGTPEQYVPYSTTR	1961.1	2	3.8772	0.4245
FNVWDTAGQEK	1295.4	2	2.4258	0.1639
FNYGFEYLGVQDK	1580.7	2	4.0538	0.3174
FNYGFEYLGVQDKLVQTPLTDR	2604.9	3	3.5597	0.2334
FNYSGSGGR	945.0	2	2.6649	0.1747
FPAEDEFPDLSAHNNHMAK	2171.3	3	4.966	0.4404
FPEHELTFDPQR	1516.6	2	3.2997	0.2663
FPELESLVPNALDYIR	1877.1	2	3.0095	0.2106
FPFIPMPLDYILPELLK	2047.5	2	4.7939	0.4247
FPFLGVHFTPR	1318.6	2	3.4539	0.2018
FPGINYPVLTPNLK	1573.9	2	3.5891	0.252
FPGLHSFAPDKPGGILMMDLKEEKPR	2912.4	3	4.7065	0.3893
FPGQLNADLR	1131.3	2	2.4563	0.1522
FPGQLNADLRK	1259.4	2	2.9287	0.1742
FPGYDSESKEFNAEVHRK	2141.3	2	4.4534	0.4181
FPLDYYSIPFPTPTTPLTGR	2284.6	2	3.2289	0.263
FPNQNQTR	1005.1	2	2.4948	0.1197
FPPEASGYLHIGHAK	1624.8	2	2.6947	0.2562
FPSHFSSDLKDLLR	1662.9	2	3.7733	0.3286
FPVFNPATEEELCQVEEGDKEDVDK	2869.1	3	3.6736	0.2135
FPVFNPATEEELCQVEEGDKEDVDKAVK	3167.4	3	4.9656	0.3362
FPVGPPKNDDTPNR	1554.7	2	3.7541	0.3947

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FPVGPPKNDDTPNRQYWDEDLLMK	2877.2	3	3.4624	0.1444
FQAHQQQGNK	1186.3	2	2.8216	0.2165
FQAKLEHEYIQNFK	1796.0	2	5.1698	0.3675
FQAPISAPEYTVTPSPQQAR	2189.4	2	2.6531	0.134
FQDDPDGLHQLDGTPLTAEDIVHK	2662.8	3	5.0281	0.4228
FQDGDLTLYQSNTILR	1885.1	2	6.2014	0.4992
FQDLGAAYEVLSDSEK	1772.9	2	4.6457	0.3621
FQDLGAAYEVLSDSEKR	1929.1	2	2.4568	0.2353
FQDNFEFVQWFK	1635.8	2	3.6782	0.3834
FQDNLDFIQWFK	1601.8	2	3.0757	0.196
FQDNLDFIQWFKK	1730.0	2	3.9405	0.3458
FQDTAEALAAFTALMEGK	1915.2	2	5.4467	0.48
FQDTDGKHLLPK	1399.6	2	3.2686	0.3107
FQDVGPQAPVGSVYQK	1720.9	2	5.4442	0.4618
FQEAKGDSPQEK	1364.4	2	3.7387	0.2121
FQEHIIQAPKPVEAIK	1849.2	2	5.1614	0.3355
FQEHIIQAPKPVEAIKRPSPDEPMTNLELK	3458.0	3	4.8679	0.3952
FQELDSR	895.0	1	2.2626	0.1084
FQELIFEDFAR	1415.6	2	3.6779	0.2942
FQELLQDLEKKER	1676.9	2	4.2716	0.2195
FQESEERPKLFEELGK	1967.2	2	4.0549	0.2864
FQESEERPKLFEELGKQIQQYMK	2887.3	3	3.5012	0.1561
FQETFEDVFSDR	1520.6	2	3.6273	0.3832
FQEYHIQQNEALAAK	1791.0	2	5.4568	0.4184
FQFPPSWLYIDNIEGEWGAFNDIMR	3047.4	3	4.1535	0.2362
FQFPSHVTDVSEEAKDLIQR	2347.6	3	4.6835	0.2459
FQGEDTVVIASKPYAFDR	2044.3	2	5.333	0.4768
FQHPSHELLK	1236.4	2	2.5792	0.1765
FQIGDYLDIAITPPNR	1834.1	2	3.1286	0.1637
FQIPPNAELKYELHLK	1941.3	2	3.6281	0.3348
FQKELKEIQYGIR	1652.9	3	3.3678	0.1807
FQKENPGFDFSGAEISGNYTK	2337.5	2	5.3742	0.4255
FQKTLYVEEVVPNVIEPSFGLGR	2623.0	3	4.1947	0.286
FQLAVEALEQEKQGLQSQIAQVLEGR	2914.3	3	6.2083	0.4377
FQLLEGPPESMGR	1461.7	2	4.368	0.276
FQLTSDEMSLLR	1440.6	2	3.0924	0.2559

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FQMAYSNLLR	1243.5	2	3.0969	0.256
FQMPDQGMTSADDFFQGTK	2152.4	2	5.536	0.4782
FQMTQEVVCDECPNVK	1871.1	2	4.4167	0.2475
FQNALLVR	961.1	2	2.9797	0.2338
FQNIDFAEEVYTR	1632.8	2	3.3772	0.2658
FQPGETLTEILETPATSEQEAEHQR	2843.0	2	4.8307	0.4433
FQQAVDAVEEFLR	1552.7	2	3.8626	0.3016
FQQLANISMSGNNLAEILPPALQDIKELQHDVQK	3805.3	3	4.3335	0.1015
FQQQLEQLNAMGFLNREANLQALIATGGDINAAIERLLGSQPS	4643.2	3	5.3319	0.3206
FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	3382.8	3	6.0301	0.4951
FQSAAIGALQEASEAYLVNLFEDTNLCAIHAK	3439.8	3	4.5961	0.2545
FQSKYEPR	1055.2	2	2.5786	0.2586
FQSLGVAFYR	1188.4	2	3.6713	0.2506
FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	3458.9	3	4.595	0.353
FQSSHHPTDITSLDQYVER	2261.4	3	5.941	0.4888
FQSVESGANNVVFIR	1667.8	2	4.602	0.4819
FQSVPAQPGQTSPLLQYFGILLDQGQLNK	3189.6	3	4.7288	0.3232
FQTHAEAQAAINTLHSSR	1983.1	3	4.9579	0.325
FQVDKVNFHMFDVGGQR	2025.3	2	3.1693	0.3906
FQVDPSGEIVELAK	1532.7	2	3.0155	0.1636
FQVIVYNPLGR	1306.5	2	3.708	0.2695
FQVWDYEEGEVEALLDR	2099.2	2	2.8784	0.2498
FQVWDYEEGEVEALLDRYFEADPPGQVAASPDPTT	3944.2	3	4.9225	0.4542
FRAPDEPQQAQVPHVWGWEVAGAPALR	3014.3	3	4.5263	0.2826
FRAPELLFQPDLVGDESEGLHEVVAFAIHK	3365.8	3	6.7764	0.587
FRAPELLFRPDLIGEESEGIHEVLVFAIQK	3455.0	3	4.3026	0.3667
FRCPEALFQPSFLGMESCGIHETTFNSIMK	3423.0	3	4.7739	0.3399
FRDEELEHHDIGLDHDAELAPAYAVLK	3105.4	3	4.8098	0.307
FRDEFVIPHLHK	1538.8	2	2.8922	0.2707
FREALGDAQQSVR	1477.6	2	4.0618	0.2386
FREDHPDLIQNAK	1583.7	2	4.5826	0.3578
FREFVYQEAAGPHQTLAR	2121.3	3	4.5698	0.2066
FRELAEEAAR	1192.3	2	3.3347	0.2082
FRELLLYGR	1167.4	2	3.4296	0.2141
FREMIPFAVVGSDHEYQVNGK	2424.7	3	5.8854	0.3885
FRENVQDVLPALPNPDDYFLLR	2633.0	3	4.2259	0.1484

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FRFDGQPINETDTPAQLEMEDEDTIDVFQQQTGG	3874.1	3	5.855	0.4446
FRFNFLAPELPAVSEFSTSETMGHSADR	3145.5	3	6.1123	0.4931
FRFPHIDLVVQR	1527.8	2	3.2004	0.276
FRGCLAGALLGDCVGSFYEAHDTVDLTSVLR	3287.7	3	4.259	0.2567
FRGHGSEASVSK	1262.4	2	2.9294	0.1878
FRGHLDNISNNLLIGAINIENGK	2523.8	3	5.4463	0.2731
FRGHLDNISNNLLIGAINIENGKANSVR	3051.4	3	6.8341	0.4236
FRGPFTDVVTTNLK	1595.8	2	4.4673	0.2962
FRHENIIGINDIIR	1711.0	3	4.5032	0.2984
FRHHLGDDVVLFTTDGAHK	2166.4	3	4.3825	0.2451
FRHNIAYFPQIVSVAAR	1990.3	3	4.7067	0.4404
FRIDELEPR	1175.3	2	3.0702	0.2371
FRISHELDSASSEVN	1691.8	2	3.9128	0.46
FRLEAPDADELPKGEFDPGQDTYQHPPK	3199.4	3	3.9484	0.2026
FRLEAPDADELPKGEFDPGQDTYQHPPKDSSGQHVDVSPTSQR	4781.0	3	3.7949	0.4064
FRLENDLEELALYQIQLLK	2349.7	2	5.1713	0.297
FRLENDLEELALYQIQLLKDLR	2734.1	3	5.2115	0.3379
FRLPPGEYVVVPSTFEPNKEGDFVLR	2994.4	3	7.2497	0.5443
FRNPPGGDNLEER	1501.6	2	3.2884	0.2253
FRPAGAAPRPPPKPM	1590.9	2	3.4891	0.3274
FRPFYLSQLEESVEEDVK	2216.4	3	3.9695	0.1479
FRPLNEAEILR	1358.6	2	3.0254	0.1475
FRPSDEHHPEVK	1478.6	2	3.1359	0.2439
FRPSEPHFTLDGNSFYK	2043.2	3	3.6245	0.3002
FRQDLMNIAGTTLSSK	1783.0	3	4.5656	0.4413
FRRPDIQYPDATDEDITSHMESEELNGAYK	3529.7	3	5.9014	0.4098
FRSETITEEELVGLMNK	1997.3	2	5.6152	0.4365
FRSETITEEELVGLMNKFVEDTK	2717.0	3	3.9814	0.2097
FRSHEGETAYIR	1466.6	3	3.984	0.2632
FRTEAAAAAPQR	1289.4	2	3.3723	0.3767
FSALQQAVPTESTDNRR	1921.1	2	3.3184	0.125
FSAQSQAR	895.0	2	2.5702	0.1777
FSASLAPHFNSLPR	1544.7	2	3.1629	0.3508
FSATEVTNKTLAAEMQELR	2140.4	2	4.1154	0.3517
FSDEPPEVYGDFEPLVAK	2040.2	2	4.4933	0.4284
FSDFLGLHSK	1151.3	2	3.2093	0.1253

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FSDFLGLYEK	1219.4	2	2.7481	0.2669
FSDHVALLSVFQAWDDAR	2078.3	2	3.1442	0.2502
FSELTAEK	925.0	2	2.5966	0.12
FSELTAEKLGFAGLVQEISFGTTKDK	2818.2	3	4.8221	0.3327
FSESTIVCNSLDGSNWGQEQREDHLCFSPGSEVK	3788.0	3	3.2087	0.1101
FSFSGNTLVSSSADPEGHFETPIWIER	3012.2	3	4.0758	0.3303
FSGEELDKLWR	1380.5	2	2.6445	0.2573
FSGTWYAMAK	1162.3	2	2.7602	0.135
FSGWYDADLSPAGHEEAK	1981.1	2	5.3051	0.4929
FSGWYDADLSPAGHEEAKR	2137.3	3	5.1592	0.5205
FSHEEIAMATVTALR	1676.9	2	4.8551	0.49
FSHEEIAMATVTALRR	1833.1	2	3.8255	0.3626
FSHLAADTIINGGATSHLAPTDPADR	2649.9	3	3.8155	0.2192
FSIFGKDFLLNYPFSTSVK	2211.5	3	5.7579	0.4684
FSILTVNNDITLLK	1591.9	2	4.8049	0.3889
FSKEFEEASSKLEEFVNGLDK	2434.6	3	4.0782	0.3274
FSKGEILQIVNR	1404.6	2	2.823	0.3852
FSLDALITHVLPFEK	1731.0	2	3.8752	0.2673
FSLDALITNILPFEKINEGFDLLR	2780.2	3	3.9269	0.2741
FSLENNFLLQHNIR	1746.0	2	3.4918	0.3917
FSLFAGGMLR	1099.3	2	3.7607	0.3673
FSLVPHNYGLVLYENK	1894.2	3	4.6625	0.4031
FSLYFLAYEDKNDIPKEKDEK	2593.9	3	4.4062	0.2897
FSMPGFKAEGPEVDVNLPK	2063.4	2	3.5316	0.2397
FSMPGFKGEGPEVDMNLPK	2081.4	2	2.5681	0.2061
FSMVVQDGIVK	1223.5	2	3.9195	0.361
FSNAEPEPR	1047.1	2	2.622	0.172
FSPAGPVLSIR	1144.3	2	2.511	0.1688
FSPDGELYASGSEDGTLR	1902.0	2	3.9854	0.3734
FSPDGNRFATASADGQIYIYDGK	2494.7	3	4.2896	0.4626
FSPDLWGVSVCTVDGQR	1867.1	2	2.4152	0.2386
FSPGAPGGSGSQPNQK	1516.6	2	2.6252	0.2778
FSPLTTNLINLLAENGR	1874.1	2	5.3105	0.3362
FSPPILQLDEVDFYYDPK	2187.4	2	3.0542	0.2501
FSQLYPER	1040.2	2	2.4831	0.1247
FSQMLHPIFEEASDVIKEEFPNENQVVFAR	3553.0	3	6.5663	0.5049

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FSQQQSFVQILQEVNDFAGQR	2470.7	3	4.5701	0.3338
FSSAPLIPLPTPPIIPVLPQQFVPPTNVR	3137.7	3	4.2633	0.2462
FSSASGASARINSSSVK	1656.8	2	2.978	0.1424
FSSQQAATK	968.0	2	2.538	0.1285
FSSSTEQSSASR	1274.3	2	2.9829	0.249
FSTEHRTELLTEALR	1804.0	3	3.8061	0.2685
FSTETTFLVDKYEIL	1807.0	2	2.4966	0.1604
FSTEYELQQLEQFKK	1919.1	2	2.8124	0.1551
FSTEYELQQLEQFKKDNEETGFGSGTR	3170.3	3	5.6168	0.4097
FSTGGDKPAIWLDAGIHAR	2013.2	2	3.622	0.1735
FSTSGLSISGLNPLPNPSYLLPPR	2528.9	3	3.9051	0.3684
FSTYTSDKDENKLSEASGGR	2193.3	3	4.3691	0.2953
FSVCVLGDQQHCDEAKAVDIPHMDIEALK	3213.7	3	5.5047	0.3676
FSVCVLGDQQHCDEAKAVDIPHMDIEALKK	3341.8	3	4.8643	0.1908
FSVLLLHGIR	1155.4	2	3.7371	0.3739
FSVSGAKGEETGIDVTLPTGEVTVPGVSGDVSLPEIATGGLEGK	4259.7	3	4.508	0.3414
FSVSPVVR	891.0	1	1.7066	0.2464
FTANVGIQIVGDDLTVTNPK	2103.4	2	4.5824	0.3383
FTASAGIQVVGDDLTVTNPK	2034.3	2	5.7996	0.4823
FTASAGIQVVGDDLTVTNPKR	2190.4	3	5.1204	0.5395
FTDDDKTDHLSWEWNLTIK	2365.5	3	5.0535	0.4001
FTDEEVDELYR	1416.5	2	4.4584	0.3851
FTDEYQLFEELGK	1619.8	2	4.3895	0.4294
FTDEYQLFEELGKGAFSVVR	2336.6	3	4.6102	0.2856
FTDEYQLFEELGKGAFSVVRR	2492.8	3	3.645	0.1077
FTDFDEVRQEIEAETDRVTGTNK	2701.8	3	3.6676	0.2816
FTDLKHYSDELQSVISHLLR	2402.7	3	3.7102	0.299
FTEDAKR	866.9	1	1.9244	0.1366
FTELKAQLSTILEEEKAQQEER	2621.9	3	4.7392	0.4009
FTEYETQVK	1145.2	2	3.0142	0.2556
FTFGLDWVPK	1210.4	2	2.8048	0.3058
FTFRPPNNEK	1250.4	2	2.6291	0.1959
FTGLSKEELLK	1265.5	2	3.2289	0.2698
FTHSEKFTFHLEPQAQATQVSDVPATSR	3161.4	3	4.9438	0.3025
FTHVLTAGGIGPTHDDVTFEAVAQAFGDELKPHPK	3705.1	3	4.5298	0.2202
FTIDSDAVSASSPEK	1554.6	2	2.5758	0.1196

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FTIGDHSR	933.0	2	2.4831	0.196
FTITPSTTQVVGILK	1605.9	2	3.1777	0.3898
FTLGSVAGAVGATAVYPIDLVK	2150.5	2	5.7511	0.5472
FTLTEKLEHR	1274.5	2	2.9521	0.2885
FTMELAKK	968.2	2	2.488	0.1194
FTMVQVWPVR	1263.5	2	3.3742	0.2204
FTNEDHLAVHK	1311.4	2	3.3508	0.2817
FTNLLTSILDSAETKN	1768.0	2	5.2002	0.3452
FTPGTFTNQIQAAFR	1699.9	2	4.5116	0.4349
FTPSLDSDFTFTLPAGQK	1973.2	2	5.1169	0.4368
FTQAGSEVSALLGR	1436.6	2	5.0799	0.3519
FTQAGSEVSALLGRIPSAVGYQPTLATDMGTMQER	3685.1	3	8.0005	0.5918
FTQDTQPHYIYSPR	1753.9	2	4.422	0.4666
FTQHQNTVK	1103.2	2	2.5546	0.2854
FTQISPVWLQLK	1460.7	2	3.2499	0.266
FTQNMMMPIIHYPNEVIVK	2306.8	3	3.6351	0.1166
FTRNEFNLESK	1385.5	2	3.2582	0.2115
FTRPEHLGSSAK	1330.5	2	2.9023	0.2967
FTSGKYQDVYVELSHIK	2015.3	3	3.7366	0.2015
FTSLDKGENGTLSR	1525.6	2	3.4795	0.3209
FTTDLDSPR	1052.1	2	2.5363	0.2589
FTVLLMPNGPMR	1376.7	2	3.2777	0.1759
FTVTFESDKFKVK	1576.8	2	3.7741	0.3474
FTYRSDSFENPVLQQHFR	2272.5	3	5.1437	0.3518
FVADGIFK	897.1	2	2.4924	0.1677
FVADGIFKAELNEFLTR	1971.2	3	5.6807	0.4324
FVAFSGEGQSLR	1298.4	2	3.4006	0.2799
FVAKENEVQSLHSK	1616.8	2	4.3982	0.4568
FVAKENEVQSLHSKLTDTLVSK	2474.8	3	3.4927	0.2334
FVASKNEQESR	1295.4	2	2.8084	0.3046
FVATQAAVPPAEELAFTDSLITR	2448.8	3	3.4488	0.1098
FVDGEWYR	1072.2	2	2.9187	0.2157
FVDGLMIHSGDPVNYYVDTAVR	2469.8	2	2.7833	0.1714
FVDHVFDEQVIDSLTVK	1992.2	2	5.4351	0.4283
FVDKLYTGLIQGQR	1638.9	2	3.6776	0.3458
FVDLYGAQK	1041.2	2	3.0361	0.2472

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FVEDTKKGVHQK	1416.6	2	3.66	0.3309
FVEFFGPGVAQLSIADR	1854.1	2	5.2694	0.4767
FVEGLPINDFSR	1394.6	2	3.5709	0.4345
FVEKPQVFVSNK	1422.7	2	2.4005	0.1784
FVEKYTELQKLGETDEEKLFVETGK	2962.3	3	4.9731	0.2951
FVETSPSGLDPNASVYQPLK	2150.4	3	4.3559	0.3286
FVFSLVDAMNGK	1328.6	2	4.2978	0.4116
FVFWKILKTK	1310.7	2	2.9065	0.1386
FVGGAENTAHPR	1256.4	2	3.1172	0.3582
FVGGSGQVSER	1123.2	2	2.6588	0.2589
FVGIKDEDQLEAFLKK	1881.2	3	4.6758	0.3798
FVHFIDAPSLALIMPIVQR	2168.6	3	5.2797	0.2216
FVHSENQHLVSPEALDFLDK	2326.5	3	5.5501	0.4664
FVHSENQHLVSPEALDFLDKLLR	2709.1	3	4.761	0.3505
FVHTSVHGVGHSFVQSAFK	2072.3	2	5.258	0.6032
FVIATSTK	867.0	1	2.1155	0.1894
FVIGGPQGDAGLTGR	1445.6	2	3.676	0.2072
FVIGGPQGDAGLTGRK	1573.8	2	3.957	0.3096
FVIHCNSPVWGADK	1573.8	2	2.5829	0.1178
FVIHCNSPVWGADKCEELLEK	2418.8	3	3.4254	0.2165
FVIKPIDKK	1088.4	2	2.4407	0.2634
FVIKPIDKKAPDFVFYAPR	2252.7	3	4.5664	0.2897
FVIKRPELLTHSTTEVTQPR	2353.7	3	5.3731	0.4663
FVINYDYPNSSEDYVHR	2119.2	2	3.3092	0.4167
FVIPDFMSFTSHIDELYESAK	2477.8	2	4.1522	0.4227
FVIPDFMSFTSHIDELYESAKK	2605.9	2	3.267	0.3024
FVKKPDDGKMK	1293.6	2	2.4069	0.144
FVLCPECENPETDLHVNPK	2185.5	2	4.6524	0.3147
FVLINWTGEGVNDVR	1719.9	2	4.3131	0.373
FVLKNYGENPEAYNEELKKLELLR	2911.3	3	3.9039	0.2857
FVLPAVLNPR	1126.4	2	2.6269	0.2098
FVLQDGAHHMVDSNEISFIR	2316.6	3	4.6253	0.459
FVLSSGK	737.9	1	1.8148	0.155
FVLSSGKFYGDEEKDKGLQTSQDAR	2807.0	3	5.9796	0.2733
FVLVKFDTQYPYGEKQDEFKR	2639.0	3	3.9392	0.2938
FVMQEEFSR	1173.3	1	2.9563	0.291

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FVMQEEFSRDGK	1473.6	2	2.7598	0.2622
FVNLGIEPPKGVLLFGPPGTGK	2238.7	2	5.0174	0.4387
FVNQHLCGSHLVEALYLVCGER	2488.9	3	5.6658	0.5011
FVNQLKGESR	1178.3	2	2.5185	0.1786
FVNVVPTFGK	1108.3	2	2.7335	0.1955
FVPFAAVAAANCINIPLMR	2019.5	3	3.6532	0.2424
FVQIKEMVPEFVVPDLTGFK	2324.8	2	3.6463	0.3538
FVQLQHGEIDKR	1470.7	2	3.817	0.2914
FVRNPLGSTHPEATLK	1768.0	2	3.6845	0.2766
FVSAIEGMHPNQEDHETFVDINPLTGIILK	3366.8	3	7.4649	0.461
FVSDEHYDENEDDLVSHVDGSVISR	2864.9	3	5.6766	0.3232
FVSISDLLVPK	1218.5	2	3.6879	0.3676
FVSISDLLVPKDLGTESQIFISR	2565.9	3	5.155	0.4308
FVSKEMENMYIEELKSSVNLLMANLESMPVSK	3693.3	3	5.7609	0.4845
FVSLEGFAQPVAIFLGIPFAKPPLGPLR	2983.6	3	4.1982	0.343
FVSSSSSGAYGGGYGGVLTASDGLLAGNEK	2810.0	2	6.2216	0.5211
FVSSSSSGAYGGGYGGVLTASDGLLAGNEKLTMQNLNDR	3896.2	3	6.0048	0.4999
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK	2796.0	2	5.7431	0.4929
FVSSSSSGGYGGGYGGVLTASDGLLAGNEKLTMQNLNDR	3882.2	3	4.3535	0.3313
FVTDIDELGKDLLLK	1720.0	2	3.3311	0.2334
FVTSNTQELGKDK	1467.6	2	3.4643	0.3115
FVTTEFEPCFDAADFIR	2009.2	2	4.3807	0.4613
FVTVQTISGTGALR	1450.7	2	4.5179	0.3805
FVVDLSDQVAPTDIEEGMR	2122.3	2	5.6501	0.5072
FVVEKAEQQK	1206.4	2	2.4607	0.1253
FVVEKAEQQKK	1334.5	2	3.3296	0.1855
FVVQNVSAQKDGEK	1549.7	2	3.9074	0.386
FVWNGHLLR	1142.3	2	2.5928	0.2205
FVYKEEHPFEK	1453.6	2	3.767	0.2886
FWAHEHWGLDDPADVMTFSK	2390.6	3	5.274	0.4421
FWANFAR	912.0	2	2.6114	0.234
FWEGDFHRDMEALNVLPPDVLTR	2759.1	3	3.209	0.1654
FWEVISDEHGIDPAGGYVGDSALQLER	2962.2	3	5.3937	0.3192
FWEVISDEHGIDPSGNYVGDSDLQLER	3079.2	3	6.499	0.4819
FWEVISDEHGIDPTGSYHGDSDLQLER	3104.2	3	5.2574	0.2166
FWEVISDEHGIDPTGTYHGDSDLQLDR	3104.2	3	6.3383	0.407

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FWEVISDEHGIDPTGTYHGDSDLQLER	3118.3	3	5.7792	0.4704
FWKEHHFEAIALVEK	1885.2	3	4.0298	0.3193
FYALRPDRDIELTLR	1879.2	2	2.5735	0.1651
FYALSASFEPFSNK	1608.8	2	5.2483	0.4661
FYAYNPLAGGLLTGK	1585.8	2	4.3606	0.4619
FYCDYCDTYLTHDSPSVR	2186.4	2	4.0236	0.29
FYDANYDGKEYDPVEAR	2053.1	3	3.3992	0.2499
FYDDAIVSQK	1186.3	2	3.257	0.2135
FYDLSSKYYQTIGNHASYYKDALR	2905.2	3	5.904	0.455
FYDSKETVNNQK	1473.6	2	2.9715	0.2038
FYEDNGQLDDAR	1443.5	2	3.4171	0.3931
FYEEEENGGVWEGFGDFSPTDVHR	2804.9	3	4.3525	0.3412
FYEEVHDLER	1337.4	2	2.4146	0.1504
FYEEVHDLERK	1465.6	2	4.3337	0.3726
FYEQFSK	949.0	2	2.8214	0.1701
FYEQMNGPVAGASR	1527.7	2	4.7065	0.4912
FYFDPKQTDVLQQLSIQMANAK	2586.9	3	4.6179	0.2282
FYFENLLAK	1145.3	2	3.1041	0.2853
FYFVGDEDLLEIIGNSK	1960.2	2	4.8524	0.4487
FYGDEEKDK	1131.2	2	2.5418	0.2508
FYGDEEKDKGLQTSQDAR	2088.2	2	6.0946	0.4913
FYGPAGPYGIFAGR	1473.7	2	4.7641	0.5402
FYGPEGPYGVFAGR	1517.7	2	3.4495	0.5001
FYHDWNDKEIEVLNK	1951.1	3	3.8031	0.2376
FYIDPYKLLPLQR	1667.0	2	3.5229	0.3103
FYKELQAHGADELLKR	1919.2	2	4.1446	0.3543
FYKENLGQGWMTQK	1731.0	2	3.9665	0.3788
FYNELTEILVR	1397.6	2	4.2132	0.3508
FYPEDVAEELIQDITQK	2039.2	3	5.8666	0.4359
FYPEDVSEELIQDITQR	2083.2	3	4.2876	0.3809
FYQAEMEELDFISAVEK	2050.3	2	4.6781	0.2843
FYQDLKDR	1085.2	2	2.4599	0.2084
FYQDLKDRDVTFSPATIENELIK	2744.0	3	5.1606	0.3712
FYREASSGAAK	1187.3	2	3.039	0.1576
FYSFLVLKK	1145.4	2	2.6012	0.1235
FYSVNVDYSK	1222.3	2	2.6374	0.21

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
FYTDPSYFFDLWK	1729.9	2	2.928	0.2348
FYTLIPHDFGMK	1469.7	2	3.4833	0.2269
FYVHNDIFR	1211.4	2	2.7475	0.3182
FYVHNDMFR	1229.4	2	2.4314	0.2694
FYVPPTQEDGVDPVEAFAQNVLSK	2651.9	3	5.6638	0.4583
FYWGHKEILIPVFK	1778.1	3	3.2595	0.2272
GAAAAHGSESSPGLETGAALGAGGATCVPLLR	2851.1	3	3.3931	0.1
GAAAEAAGILQDAVSKLDDPLHLR	2432.7	3	5.5568	0.4546
GAAAHPDSEEQQQR	1524.5	2	4.0904	0.3813
GAAAQGQTQTVAAQAQALAAQAAAAAHAAQAHR	3083.3	3	5.7171	0.4366
GAAASPEPAR	927.0	2	2.5223	0.2155
GAAATTTTTEHR	1217.3	2	2.8838	0.3037
GAADVEKVEEK	1175.3	2	3.0607	0.1966
GAAEPEAQLSNHLAEEGPAEGSGEAAR	2649.7	3	5.3275	0.2279
GAAGALLVYDITRR	1476.7	2	2.4572	0.2682
GAAGALMVYDITRR	1494.7	2	2.9142	0.3176
GAAGGAEQPGPGGR	1182.2	2	3.8686	0.2584
GAANHDLTDTTR	1272.3	2	2.8125	0.3999
GAAPPKQEFLDIEDP	1627.8	2	3.188	0.2
GAAPYVQAFDSLLAGPVAEYLK	2281.6	2	5.2908	0.5059
GAASGVVGELAR	1087.2	2	2.9869	0.2013
GAAVDGGKLDVGNAEVKLEEENR	2371.5	3	6.1572	0.4916
GAAVDGGKLDVGNAEVKLEEENRSLKADLQK	3255.6	3	5.3127	0.3648
GAAYAHAEESIKK	1375.5	2	2.9178	0.2656
GADCCVLVFDVTAPNTFK	1901.2	2	3.7624	0.3197
GADFLVTEVENGGSLGSK	1780.9	2	6.582	0.4376
GADFLVTEVENGGSLGSKK	1909.1	2	5.4218	0.4075
GADINAPDKHHITPLLSAVYEGHVSCVK	2973.4	3	6.3401	0.4966
GADKTVKGPDGLTAFEATDNQAIK	2448.7	3	4.9752	0.3442
GADKVNTFSALLLEPYKPPSAQ	2347.7	2	4.7997	0.2931
GADMSVPDEKGNPPLWLALANNLEDIASTLVR	3408.8	3	4.6584	0.2951
GADPGMPEPTVLSLLWG	1741.0	2	2.501	0.2179
GAEAANVTGPDGVPVEGSR	1783.9	2	4.9031	0.4352
GAEAANVTGPGGVPVQGSK	1696.8	2	5.3283	0.2593
GAEADQIIEYLK	1350.5	2	3.6291	0.2963
GAEADQIIEYLKQQVSLLK	2147.5	2	5.6793	0.3683

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GAEADQIIEYLKQQVSLLKEK	2404.7	3	4.1154	0.2582
GAEEMETVIPVDVMR	1676.9	2	4.7391	0.346
GAEHITTYTFNTHK	1620.7	2	3.7963	0.3825
GAEIEYAMAYSK	1333.5	2	3.5437	0.331
GAEILADTFKDYAVSTVPVADGLHLK	2732.1	3	5.127	0.4656
GAEILEVLHSLPAVR	1604.9	2	3.9193	0.2795
GAEIVADTFRDFAVSTVPVSGPSHLR	2730.0	3	4.9105	0.2894
GAELEYESLKRQELESENKK	2381.6	3	3.2071	0.1314
GAEVNQVKEQLLQSNPVLEAFGNAK	2685.0	3	6.6565	0.449
GAFGEATLYR	1085.2	2	2.6721	0.2115
GAFGKPQGTVAR	1189.3	2	2.9239	0.1528
GAFHRPVLGGFR	1314.5	2	2.4475	0.1589
GAFPPVWNPIAYLDYNNLWR	2407.7	2	4.5394	0.4465
GAFSRLDPTGTFEKEMIGR	2113.4	3	3.9983	0.1068
GAFTFQGSMIDMPLLK	1757.1	2	3.6647	0.3634
GAGAESSHPVR	1068.1	2	3.2017	0.2515
GAGAFGYFEVTHDITK	1713.9	2	3.573	0.3643
GAGALLQHGLVNFTFNK	1788.0	2	4.3237	0.4625
GAGATGKDTMGDLPRDPGHVVEQLSR	2665.9	3	4.2802	0.339
GAGATLEHQQEISK	1469.6	2	4.0752	0.291
GAGAVIHTHSK	1078.2	2	3.7552	0.3767
GAGGALFVHRDTPENNPDTPFDFTPENYKR	3364.6	3	5.5492	0.407
GAGGEENKENERPSAGSK	1817.9	2	3.9976	0.4148
GAGGQGKLDVTILSPSRK	1785.0	3	4.2166	0.2603
GAGHMVPTDKPLAAFTMFSR	2135.5	3	4.7885	0.4276
GAGIGGLGITVEGPSESK	1629.8	2	4.7281	0.4875
GAGKAPLNVQFNSPLPGDAVK	2081.4	3	3.6451	0.1686
GAGKAPLNVQFNSPLPGDAVKDLDIIDNYDYSHTVK	3874.3	3	5.0733	0.3253
GAGTDDHTLIR	1156.2	2	3.2862	0.1784
GAGTDDSTLVR	1092.1	2	3.1736	0.2975
GAGTDEKTLTR	1149.2	2	3.7675	0.3085
GAGTGGLGLAVEGPSEAK	1571.7	2	4.7624	0.3989
GAGTNEDALIEILTTR	1674.8	2	5.2391	0.3682
GAGTNEKVLTEIIASR	1659.9	2	3.7098	0.3062
GAGYTFGQDISETFNHANGLTLVSR	2656.8	2	4.7981	0.471
GAHLTALEMLTAFASHIR	1940.3	2	6.2764	0.5712

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GAHNGQGLGNAFLSHISACDGIFHLTR	2795.1	3	5.0706	0.3837
GAHPSGGADDVAK	1182.2	2	3.1758	0.3092
GAHSVGLMWWMLAR	1616.0	2	4.528	0.4586
GAIETYQEVASLPDVPADLLK	2230.5	2	4.7898	0.4506
GAILTGPPGTGK	1069.2	2	2.5669	0.1769
GAIQFVTHYQHSSTQR	1861.0	2	4.4905	0.3921
GAIREYQTQLIQR	1576.8	2	3.646	0.3607
GAIVHYTILNNHVYR	1771.0	2	4.3322	0.4622
GAKAEEILEK	1088.2	1	2.4881	0.1118
GAKEEHGGLIR	1167.3	2	3.1469	0.2299
GAKEGIILFK	1076.3	2	2.7331	0.1848
GAKEHGAVAVER	1224.4	2	2.5204	0.2834
GAKPHFITSSVEHDSIR	1882.1	2	4.2974	0.4169
GAKWTTAPKPTMADELYNQDYPIHSVEDR	3335.6	3	5.7511	0.4315
GALALAQAVQR	1098.3	2	2.583	0.167
GALEAYVQSVR	1193.3	2	2.6191	0.1368
GALFGANANR	991.1	2	2.8321	0.2628
GALFQAHAR	971.1	2	2.4224	0.2707
GALINVPPPFLGLPR	1561.9	2	3.1696	0.2842
GALLLSSIELEELKAENEKLSSQITLLEAQNR	3542.0	3	5.4575	0.411
GALLVFAEHR	1113.3	2	3.306	0.3169
GALPLDTVTFYK	1325.5	2	3.7181	0.3926
GALPLDTVTFYKVIPK	1763.1	2	4.543	0.3291
GALQNIIPASTGAAK	1412.6	2	4.2115	0.319
GALQQGEAFQR	1205.3	2	2.6446	0.1663
GALQYLVPILTQTLTK	1760.1	2	5.3324	0.389
GALVLGSSLK	945.1	2	2.5013	0.146
GALVVVNDLGGDFK	1404.6	2	4.2588	0.3888
GALVVVNDLGGDFKGVGK	1746.0	2	5.5408	0.497
GAMAATYSALNR	1226.4	2	3.5088	0.1507
GAMAATYSALNSSKPTPQLKPIESSILAQR	3132.6	3	4.7659	0.3923
GAMPPAPVPAGTPAPPGPATMMPDGTLGLTPPTTER	3454.0	3	3.8817	0.3757
GAMSHALNFIK	1189.4	2	2.8634	0.1879
GANFLTQILLRPGASDLTGSFR	2335.6	3	4.0316	0.2399
GANIQLLDLPGIIEGAAQGK	1979.3	2	5.492	0.4599
GANPGFHEAIGDVLALSVSTPEHLHK	2698.0	3	5.6165	0.4582

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GANPVEIR	856.0	1	1.9218	0.2035
GANQHATDEEGKDPLSIAVEAANADIVTLLR	3220.5	3	5.13	0.3652
GANVIAGVWLEEAGQK	1642.8	2	3.6865	0.2599
GAPAAATAPAPTAHK	1332.5	2	4.2807	0.4182
GAPGQPGTILR	1067.2	2	2.4612	0.1184
GAPLVKPLPVNPTDPAVTGPDIFAK	2515.9	3	3.8958	0.1553
GAPPKIPGGATLVFEVELLK	2037.4	3	4.6663	0.3022
GAPPSSNIEDFHGLLPK	1780.0	2	3.8406	0.4817
GAPQHYPK	898.0	2	2.5827	0.1667
GAPVGGHILSYLLEK	1554.8	2	4.5809	0.3883
GAQAAIVVYDITNEESFAR	2055.2	2	2.5632	0.1514
GAQAAIVVYDITNTDTFAR	2027.2	2	4.7037	0.4481
GAQATLSSTTK	1065.2	2	3.3471	0.3407
GAQGVILVYDVTR	1391.6	2	2.9478	0.214
GAQVEEIWSLEPENFEK	2006.2	2	3.326	0.2116
GASGAGGPGGAAR	986.0	2	3.0097	0.1539
GASGSFVVVQK	1079.2	2	2.5463	0.1492
GASGTREDPNLVPSISNK	1843.0	2	4.438	0.2785
GASGTREDPNLVPSISNKR	1999.2	2	3.2881	0.2849
GASIVEDK	818.9	1	1.8696	0.1224
GASIVEDKLVEDLR	1544.7	2	3.7756	0.3646
GASIVEDKLVEDLRTR	1802.0	3	3.7421	0.4032
GASKEILSEVER	1318.5	2	3.8024	0.2621
GASNKYLVEFR	1284.4	2	3.2172	0.2287
GASQAGAPQGR	1000.1	2	3.4419	0.24
GASQAGMLAPGTR	1217.4	2	3.1648	0.249
GASQAGMTGYGMPR	1384.6	2	4.1753	0.5039
GASYILKLANRLYGEKTYNFLPEFLVSTQK	3466.0	3	4.6324	0.3255
GATELTHEDYMEGILEVQAK	2235.5	3	4.2301	0.2032
GATLKITLDNAYMEK	1668.9	2	2.827	0.2002
GATLSHYNIVNNSNILGER	2073.3	3	4.0877	0.2035
GATPAPQAGEPSPGLGAR	1634.8	2	4.2639	0.4774
GATQQILDEAER	1331.4	2	4.0012	0.3219
GATRPNGPNTGNK	1284.4	2	2.7195	0.1742
GATYGKPVHHGVNQLK	1706.9	3	3.2491	0.2517
GAVAEDGDELRTEPEAK	1787.9	2	4.1998	0.3571

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GAVAEDGDELRTEPEAKK	1916.0	3	3.2773	0.2744
GAVASVTFDDFHK	1394.5	2	3.618	0.2921
GAVASVTFDDFHKNSAR	1823.0	2	4.5874	0.51
GAVDAAVPTNIIAAK	1411.6	2	3.5064	0.2821
GAVDALAAALAHISGASSFEPR	2112.3	3	5.3024	0.3948
GAVDGGLSIPHSTK	1339.5	2	4.2895	0.3633
GAVDGGLSIPHSTKR	1495.7	2	3.6635	0.3808
GAVEALAAALAHISGATSVDQR	2109.3	3	4.9538	0.4768
GAVGALLVYDIAK	1290.5	2	4.7071	0.3608
GAVHQLCQSLAGK	1312.5	2	3.4348	0.2641
GAVLHHLVNK	1088.3	2	2.9818	0.1618
GAVNMPFMDFLTEDGFEKGPEELR	2731.1	2	4.3798	0.4343
GAVPWYTINLDLPPYKR	2004.3	2	3.557	0.2113
GAVQGAAGVK	858.0	2	2.5284	0.1412
GAVQSGVDKTK	1090.2	2	2.8863	0.1842
GAVSAEQVIAGFNR	1419.6	2	3.8632	0.3719
GAVTGSVEKTK	1077.2	2	2.7645	0.1936
GAVWGATLNKDATK	1432.6	2	4.3333	0.3339
GAVYSFDPVGSYQR	1546.7	2	3.1351	0.3474
GAYGGGYGGYDDYGGYNDGYGFGSDR	2661.6	3	5.0395	0.2181
GAYGGGYGGYDDYGGYNDGYGFGSDRFGR	3022.0	3	4.8727	0.2666
GAYGGGYGGYDDYNGYNDGYGFGSDRFGR	3079.1	3	5.1382	0.3959
GAYIYNALIEFIR	1543.8	2	4.2445	0.3256
GAYREHPYGR	1206.3	2	2.553	0.182
GAYTQVIFLAR	1239.4	2	3.4242	0.2984
GDAAVRDELMAAVR	1474.7	2	3.5956	0.3164
GDADQASNILASFGLSAR	1793.9	2	5.51	0.5011
GDAEKPEEELEEDDDEELDETLSER	2922.9	3	3.5152	0.1866
GDARPAEIDSLWEISK	1788.0	3	3.9444	0.2054
GDASKEDIDTAMK	1381.5	2	4.2815	0.3939
GDATPEGEKATEK	1333.4	2	2.6715	0.2058
GDATPEGEKATEKENGDKSEAQKPSEK	2862.0	3	5.6845	0.3724
GDATVSYEDPPTAK	1451.5	2	3.8027	0.3869
GDDETLHKNNALK	1455.6	2	3.5272	0.2071
GDDLSTAILK	1033.2	2	2.9219	0.1105
GDDTPLHLAASHGHR	1584.7	2	4.4232	0.4857

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GDEELDSLIK	1119.2	2	3.2885	0.2853
GDEELDSLIKATIAGGGVIPHIHK	2471.8	3	6.9827	0.4033
GDELADSALEIFK	1408.5	2	3.7789	0.2786
GDFCIQVGR	995.1	2	2.5679	0.2669
GDFFPPERPQQLPHGLGGIGMGLGPGGQPIDANHLNK	3821.3	3	6.1589	0.4325
GDFITIGSR	966.1	2	2.4561	0.1111
GDFLASLENDIKPAFGTNQEDYASYIMNGIIK	3536.9	3	5.9347	0.4447
GDFNYLEEFK	1262.3	2	2.9199	0.2637
GDGPVQGIINFEQK	1502.7	2	4.1451	0.3669
GDGVVLVAPPLR	1193.4	2	3.1438	0.3783
GDGVVLVAPPLRVG	1349.6	2	3.5482	0.1973
GDHVWDGNSFDSK	1464.5	2	3.7242	0.3896
GDKAQIEKR	1045.2	2	2.5572	0.1481
GDKAQLEKR	1045.2	2	2.6045	0.1181
GDKEEVAYEER	1325.4	2	2.8076	0.1684
GDLEEYGQDLLHTVFK	1865.0	2	2.9232	0.1398
GDLENAFLNLVQCIQNKPLYFADR	2783.2	3	4.3669	0.3748
GDLGIEIPAEK	1142.3	2	3.2694	0.3168
GDLGIEIPAEKVFLAQK	1829.1	2	4.677	0.4142
GDLPFVVPR	1000.2	2	3.0457	0.1945
GDNITLLQSVSN	1261.4	2	3.0117	0.1229
GDNNEVDDR	1034.0	2	2.7538	0.1338
GDNPNKPMNPLITGVFGAIAGAASVFGNTPLDVIK	3498.0	3	4.0251	0.2123
GDNVAVIGEIDEETDSALDLGNIR	2516.7	2	4.4388	0.3315
GDNVYEFHLEFLDLVKPEPVYK	2653.0	3	3.737	0.2265
GDPAHAGLAELGHR	1401.5	2	3.5293	0.3994
GDPEEEEEEEEELVDPLTTVR	2445.5	2	5.4617	0.4327
GDPESPRPPALDDAFSILDLFLGR	2599.9	3	4.1212	0.2324
GDPGDQTKAEGSSTASSGSQLAEGK	2366.4	3	3.3164	0.2966
GDPSLLFVNAGMNQFKPIFLGTVDPR	2835.3	3	3.5335	0.2034
GDRSEDFGVNEDLADSDAR	2069.0	3	3.8247	0.2481
GDSKKDDEENYLDLFSHK	2141.2	3	4.8128	0.3225
GDSPSPLPPPPPPTSLQPGAPPAARAWPGER	3099.4	3	3.3258	0.2401
GDSSIRYFEITDESPYVHYLNTFSSKEPQR	3567.8	3	4.799	0.3292
GDSVIVVLRNPLIAGK	1652.0	2	3.4782	0.1087
GDTPGHATPGHGGATSSAR	1734.8	3	3.3122	0.4255

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GDTSGDYKK	971.0	2	2.8537	0.2566
GDTVDLAKK	947.1	2	2.4783	0.1846
GDTVLLKGK	931.1	2	2.6389	0.1857
GDVAEGDLIEHFSQFGTVEK	2179.3	2	4.211	0.2776
GDVCDLKVQVVMEKK	1692.0	2	2.5013	0.1685
GDVCQDCIQMVTDIQTAVR	2096.4	2	5.6186	0.2538
GDVDPFYYDYETVR	1739.8	2	4.1992	0.3513
GDVFHVLDTLHPGPGQSHAR	2141.3	2	4.1011	0.37
GDVGSADIQDLEK	1347.4	2	4.2001	0.2752
GDVQAQVGLGQLHLHGGR	1843.0	2	3.9609	0.3562
GDVSGVLIAGGENGNIILYDPSK	2289.5	2	2.6745	0.1527
GDVTAEEAAGASPAK	1374.4	2	3.6009	0.2538
GDVTAQIALQPALK	1425.7	3	6.4123	0.3598
GDVVNQDDLYQALASGK	1793.9	2	3.1625	0.2308
GDVVPKDVNAAIAAIK	1581.8	2	3.1012	0.333
GDYPLEAVR	1020.1	2	2.7697	0.2623
GEAAAERPGEAAVASSPSK	1785.9	2	4.6761	0.3885
GEAAGAVQELAR	1172.3	2	3.9665	0.3533
GEAGAPGEEDIQGPTK	1556.6	2	4.4434	0.4133
GEAGAPGEEDIQGPTKADTEK	2101.2	2	5.0693	0.4944
GEAGVPAEFSIWTR	1520.7	2	3.6531	0.2624
GEALKFHKPGENYK	1618.8	2	3.8935	0.3532
GEALSALDSK	991.1	2	3.3958	0.2227
GEATVSFDDPPSAK	1421.5	2	4.4421	0.4149
GEDEEENNLEVR	1433.4	2	3.6877	0.3149
GEDFPANNIVK	1204.3	2	3.6336	0.2785
GEDSSEEKHLEEPGETQNAFLNER	2746.8	3	4.0958	0.1734
GEEAAGGDRLIHEQDLEWLQQADVVVAEVTQPSLGVGYELGR	4536.9	3	4.777	0.3069
GEEGHDPKEPEQLR	1621.7	2	3.1199	0.2642
GEEHCGHLIEAHK	1460.6	2	3.3983	0.302
GEEILSGAQR	1060.1	2	3.7859	0.2539
GEELGGGQDPVQLLSGFPR	1957.1	2	4.1607	0.3496
GEESAVMLEPR	1218.4	2	3.1756	0.1528
GEFKDEEETVTTK	1513.6	2	3.6081	0.3154
GEFVTTVQQR	1165.3	2	3.9654	0.283
GEGERPAQNEK	1215.3	2	3.168	0.2753

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GEGGILINSQGER	1330.4	2	3.696	0.2825
GEGKDEEKYIDVVINK	1837.0	2	3.1248	0.2266
GEGPEAGAGGAGGR	1143.1	2	3.6142	0.3686
GEGQLGPAER	1014.1	2	3.2962	0.3059
GEGYAKPNEGAIVEVALEGYYKDK	2601.8	3	4.111	0.3075
GEHPGLSIGDVAK	1280.4	2	2.9479	0.3148
GEHPGLSIGDVAKK	1408.6	3	3.5173	0.4443
GEHSIVYLKPSYAFGSVGK	2040.3	2	4.9551	0.4538
GEHSIVYLKPSYAFGSVGKEK	2297.6	3	4.5308	0.2735
GEHVHSLPEASVSSKPDEGRTEQSSQTR	3037.2	3	4.3576	0.3783
GEKLDDLVSK	1104.2	2	3.4141	0.2199
GEKSDEDKDKEGEALEVK	2007.1	3	5.8335	0.3025
GELAIKDANAK	1130.3	2	3.8967	0.3319
GELAIKDANAKLSELEAALQR	2241.5	3	5.9385	0.4437
GELFWDDGESLEVLER	1895.0	2	5.1138	0.4468
GELLEAIKR	1029.2	2	3	0.1384
GELSGDFEK	982.0	2	2.5855	0.2238
GENHPHFEGGVK	1308.4	2	2.7459	0.2092
GENLEHLR	968.0	2	2.5569	0.1558
GEPAAAAAPEAGASPVEK	1623.7	2	4.5522	0.4509
GEPEKLGQALTEVYAK	1733.9	2	3.0997	0.1198
GEQEHSQQKEEEEEMAVVPQGLFR	2816.0	3	5.6943	0.4811
GERNFHVFYQLLSGASEELLNK	2552.8	3	3.2089	0.1257
GESLGIKHEEAPGHRPTTNPNASK	2528.7	3	3.6794	0.1789
GESLSLPGPSPPPDGTEQVIISR	2334.6	2	2.6687	0.3542
GETGDDGRDGVGSEGR	1564.5	2	2.7759	0.203
GETGPSGPVGPAGAVGPR	1563.7	2	3.4497	0.2995
GETPRVEEVGPYTYR	1753.9	2	4.203	0.3231
GETSGRVDDNEETIKK	1778.9	2	3.7008	0.2444
GEVLGDVLQLETLKQEAATLAANNTQLQAR	3196.6	3	3.5233	0.1351
GEVQVSDKER	1147.2	2	3.3045	0.1729
GFAFISFHR	1082.2	2	3.0148	0.2685
GFAFVEFSHLQDATR	1725.9	2	2.8979	0.3466
GFAFVEYESHR	1342.4	2	3.045	0.3041
GFAFVQYVNER	1330.5	2	4.6135	0.4024
GFAFVTFDDHDSMDKIVIPK	2283.6	3	3.6505	0.3107

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GFAFVTFDDHDSVDK	1700.8	2	4.7481	0.3637
GFAFVTFDDHDSVDKIVIQK	2282.5	2	4.715	0.4142
GFAFVTFDDHDTVDKIVVQK	2282.5	2	4.9363	0.3921
GFAFVTFESPADAK	1487.6	2	4.7501	0.3923
GFAFVTFESPADAKDAAR	1901.1	2	4.9163	0.4521
GFAFVYFER	1136.3	2	3.1521	0.3367
GFALVGVGSEASSK	1309.5	2	2.6181	0.1694
GFALVGVGSEASSKK	1437.6	2	3.3341	0.3011
GFAYVQFEDVR	1331.5	2	2.625	0.2639
GFAYVQFEDVRDAEDALHNLDR	2581.7	3	5.8034	0.4362
GFAYVQFEDVRDAEDALHNLDRK	2709.9	3	5.0874	0.4346
GFCFITFKEEEPVKK	1803.1	2	4.4778	0.3975
GFDEYMKELGVGIALRK	1927.3	3	4.3184	0.3734
GFDKAYVVLGQFLVLK	1798.2	2	4.6703	0.4179
GFDPLLNLVLDGTIEYMR	2067.4	2	3.0262	0.1589
GFDPLLNLVLDGTIEYMRDPDDQYK	2929.3	3	3.2133	0.2317
GFDPLLNLVLDGTIEYMRDPDDQYKLTEDTR	3645.0	3	3.446	0.307
GFDPSSPVLHELTFQAMSYDLLPIENDVYKYETSGIGEAR	4491.9	3	4.3753	0.3814
GFEATLVQEAPIPAEPGALQER	2324.6	3	3.4847	0.2038
GFEDELSEVLENQSSQAELK	2253.4	2	5.2265	0.4105
GFELTFK	842.0	2	2.4376	0.119
GFENVIHDKLPLQESEEEEREER	2814.0	3	4.0183	0.308
GFESKVDAILNR	1349.5	2	3.0911	0.2053
GFESPSDNSSAMLLQWHEK	2164.3	2	3.3959	0.282
GFFDPNTEENLTYLQLK	2030.2	2	4.9169	0.4102
GFFDPNTHENLTYLQLLER	2308.5	3	3.9478	0.2298
GFFDPNTHENLTYR	1711.8	2	3.0669	0.3323
GFFEGTIASK	1057.2	2	3.1618	0.3742
GFFELFPSLSHNLLVD	1836.1	2	2.8167	0.2863
GFFIKPTVFGGVQDDMR	1915.2	3	4.8119	0.4041
GFFYTPK	860.0	1	2.2033	0.1972
GFGDGYNGYGGGPGGGNFGGSPGYGGGR	2496.5	3	5.9411	0.4244
GFGDHIHWR	1125.2	2	3.2268	0.3306
GFGDLKSPAGLQVLNDYLADK	2222.5	2	5.0082	0.4959
GFGFGLVKLDVK	1280.5	2	2.4385	0.1726
GFGFGQGAGALVHSE	1434.5	2	4.0532	0.4846

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GFGFIKLESR	1154.3	2	2.9312	0.188
GFGFILFK	929.1	2	3.2997	0.2227
GFGFILFKDAASVEK	1629.9	2	4.5001	0.4202
GFGFITFTNPEHASVAMR	1983.2	2	4.358	0.4359
GFGFVDFNSEEDAK	1562.6	2	4.4063	0.486
GFGFVDFNSEEDAKAAK	1832.9	2	4.1962	0.4366
GFGFVLFK	915.1	2	3.1014	0.2417
GFGFVLFKDAASVDK	1601.8	2	3.7551	0.4114
GFGFVSFER	1046.2	2	3.1314	0.2533
GFGFVSFERHEDAQK	1754.9	2	3.0603	0.2382
GFGFVTFADPASVDK	1558.7	2	2.9694	0.2044
GFGFVTFADPASVDKVLGQPHHELDSK	2900.2	3	4.4781	0.3416
GFGFVTFADPASVDKVLGQPHHELDSKTIDPK	3454.8	3	3.7406	0.3186
GFGFVTFDDHDPVDK	1696.8	2	4.1026	0.41
GFGFVTFDDHDPVDKIVLQK	2278.5	2	5.408	0.4715
GFGFVTFENEDVVEK	1717.9	2	4.075	0.3265
GFGFVTFENIDDAKDAMMAMNGK	2510.9	2	5.3186	0.5272
GFGFVTFSSMAEVDAAMAAR	2066.3	2	3.7958	0.3585
GFGFVTFSSMAEVDAAMAARPHSIDGR	2829.2	3	3.5639	0.3383
GFGFVTYATVEEVDAAMNAR	2149.4	2	5.5884	0.2035
GFGFVTYATVEEVDAAMNARPHK	2511.8	2	4.6571	0.5264
GFGFVTYATVEEVDAAMNTRPHKVDGR	2969.3	3	4.5387	0.418
GFGFVTYSCVEEVDAAMCARPHK	2518.9	3	3.366	0.1848
GFGFVTYSCVEEVDAAMCARPHKVDGR	2946.3	3	3.2368	0.2336
GFGFVYFQNHDAADK	1716.8	2	3.9254	0.3667
GFGFVYFQNHDAADKAAVVK	2185.4	2	4.6558	0.4528
GFGGAMTDAAALNILALSPPAQNLLLK	2669.1	3	4.2008	0.2525
GFGGIGGILR	947.1	2	2.9487	0.1167
GFGGITHGPPEK	1197.3	2	4.023	0.3944
GFGGITHGPPEKK	1325.5	2	3.7419	0.3811
GFGGLTGQIVAALSTAK	1591.8	2	3.9617	0.3705
GFGHGAGLLAHQR	1321.5	2	3.55	0.2855
GFGSDKEAILDIITSR	1722.9	2	5.7721	0.418
GFGSFRFPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG	3873.9	3	5.5304	0.4687
GFGSLPALEVLDLTYNNLSENSLPGNFFYLTTLR	3778.2	3	5.887	0.4385
GFGTDEQAIVDVVANR	1691.8	2	5.4012	0.4846

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GFGTDFKKLESFYIQK	1909.2	3	3.7787	0.2282
GFGVDHGQVAEQSAGVLHLR	2078.3	3	4.889	0.302
GFGYAEFEDLDSLLSALSLNEESLGNRR	3104.3	3	3.8112	0.3465
GFHQEVFLGK	1162.3	2	2.8398	0.2046
GFHQEVFLGKDLGGFDEDAEPR	2464.6	3	5.6102	0.4145
GFHQEVFLGKDLGGFDEDAEPRR	2620.8	3	4.2033	0.2956
GFHQVPFAPIVFIER	1758.1	3	4.0049	0.2974
GFIDKIAENVEEVKRK	1876.1	3	3.3233	0.2227
GFIGPGIDVPAPDMSTGER	1917.1	2	5.227	0.4552
GFIYPMLPGGPGGPGAEDVAVWTRAQR	2801.2	3	3.3146	0.1269
GFKDQIYDIFQK	1502.7	2	4.2863	0.3138
GFKEQIYDVYR	1418.6	2	2.8381	0.224
GFKFDETEQALANER	1755.9	2	4.1889	0.4939
GFKGELIHVFNK	1389.6	3	3.9034	0.3561
GFKGELIHVFNKHDGALR	2039.3	2	3.2504	0.2168
GFKNSPTIFGEALAR	1608.8	2	2.502	0.1504
GFLEFVEDFIQVPR	1696.9	2	3.6821	0.3315
GFLFGPSLAQELGLGCVLIR	2091.5	2	2.8558	0.1817
GFLIDGYPR	1038.2	2	3.2285	0.3291
GFLNSSELSGLPAGPDREGSLKDQLALAIGK	3142.5	3	4.7121	0.2348
GFLSGLLDNVKQELAK	1733.0	2	4.6088	0.3257
GFLSGPMGSGMR	1197.4	2	2.936	0.2508
GFLWDEGFHQLVVQR	1832.1	2	5.1067	0.4301
GFNEGLWEIENNPGVK	1804.0	2	3.7797	0.3622
GFPGYMYTDLATIYER	1898.1	2	5.6326	0.5528
GFPLITITVR	1117.4	2	3.2664	0.3264
GFPTDATLDDIKEWLEDKGQVLNIQMR	3134.5	3	5.3793	0.4399
GFPTIYFSPANK	1342.5	2	3.5041	0.2912
GFPTIYFSPANKK	1470.7	2	3.6127	0.281
GFPTIYFSPANKKLNPK	1923.2	2	4.0223	0.3553
GFQALGDAADIR	1234.3	2	2.9565	0.2451
GFQHLLHTLNLPGHGLETR	2141.4	3	3.2367	0.2574
GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	3352.8	2	3.8057	0.3649
GFQQILAGEYDHLPEQAFYMVGPIEEAVAKADK	3667.1	3	5.8547	0.3413
GFQQILAGEYDHLPEQAFYMVGPIEEAVAKADKLAEEHSS	4420.9	3	4.8252	0.342
GFQRPVYLFHK	1392.6	3	3.7041	0.3228

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GFQSSQALR	994.1	2	2.6455	0.2869
GFQVAPEHHNDHK	1516.6	2	2.5899	0.2436
GFSDKLDFLEGDQKPLAQR	2165.4	3	4.1252	0.2068
GFSEGLWEIENNPTVK	1821.0	2	3.8059	0.1946
GFSLEELR	951.1	2	2.4685	0.1582
GFSLLATEDKEALKK	1650.9	2	4.1205	0.2049
GFSQEELETCMINQAPGCPDYSILSFMGAFHGR	3638.1	3	5.7643	0.4242
GFSVVADTPELQR	1419.6	2	4.2885	0.4182
GFTGIDSDYEKPETPER	1942.0	2	4.8243	0.4503
GFTIPEAFR	1038.2	2	2.4808	0.1719
GFVEFAAKPPAR	1290.5	2	2.656	0.1663
GFVFITFKEEEPVKK	1799.1	2	4.4441	0.4443
GFVLQDTVEQLR	1405.6	2	3.3214	0.1302
GFVPDTPVGVAHFLLQR	1854.1	2	3.5134	0.1428
GFVPSPTSQPGGHESLVDR	1968.1	2	3.9564	0.3801
GFVQVDDGRK	1121.2	2	2.9196	0.2525
GFVTADMIR	1010.2	2	2.4657	0.2759
GFVVQGSNGEFPFLTSSER	2059.2	2	3.6709	0.3582
GFYEALFDGHPPGKVR	1791.0	3	3.6929	0.3179
GFYIYQEGVK	1204.4	2	3.0736	0.309
GGAARPNGPAAGNK	1238.3	2	3.2381	0.2447
GGAEQFMEETER	1384.5	2	3.8877	0.3727
GGAEVQIFAPDVPQMHVIDHTK	2390.7	2	4.6178	0.3437
GGAEVQIFAPDVPQMHVIDHTKGQPSEGESR	3318.6	3	4.8883	0.3437
GGAGVGSMTK	865.0	2	3.1268	0.2907
GGARVEPADASGTEK	1445.5	2	4.2588	0.3808
GGARVEPADASGTEKAFEPATGR	2275.4	2	4.7939	0.4638
GGDAPAAGEDA	930.9	1	2.4848	0.2726
GGDKVLLHFVQK	1341.6	2	3.3255	0.313
GGDLMAYDR	998.1	2	3.4642	0.2981
GGDPSKEPERVVHYEI	1813.0	2	2.5216	0.1572
GGDSIGETPTPGASK	1374.4	2	3.5134	0.2818
GGEDGPAIAIDLSGINETNDLKR	2356.5	3	5.0349	0.3612
GGEERVGEEDEEAAEAEAEAEEEAER	2692.6	2	5.8047	0.4681
GGEERVGEEDEEAAEAEAEAEEEAERAR	2919.9	3	6.2411	0.3929
GGEIQPVSVK	1014.2	2	3.5058	0.1778

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GGEIQPVSVKVGDKVLLPEYGGTK	2471.8	3	3.5133	0.1399
GGELVYTDSEARDVFEK	1916.0	2	3.976	0.3649
GGENVKAINQQTGAFVEISR	2119.3	3	4.1422	0.3688
GGFCNFMHLKPISR	1607.9	2	3.3685	0.239
GGFKDTTPDELLSAVMTAVLK	2194.5	3	3.8988	0.282
GGFLPPEEIKER	1372.6	2	2.6646	0.1838
GGFNMSSFK	975.1	1	3.0851	0.2691
GGFSFGNVEPASLPSASVFVLGR	2296.6	2	4.9431	0.4396
GGFVLLDGETFEVK	1511.7	2	4.1325	0.288
GGGAFVQNSQPVAVR	1487.6	2	4.7284	0.3942
GGGAMGHMLLPFR	1344.6	2	2.7093	0.1817
GGGDLPNSQEALQK	1414.5	2	3.2465	0.2263
GGGEELAQLAGVPFLGSVPLDPALMR	2596.0	2	3.5307	0.2369
GGGEQETQELASK	1334.4	2	4.048	0.338
GGGGFGAGPGPGGLQSGQTIALPAQGLIEFR	2869.2	3	5.7495	0.3505
GGGGFRGRGGGGGFQRYENRGPPGGNRGGFQNR	3338.5	3	3.6463	0.2006
GGGGGGGGGGGLGGGLGNVLGGLISGAGGGGGGGGGGGGGGGGGGGTAMR	3583.7	3	8.1271	0.5513
GGGGGGGKKSLSARNAAVER	1830.0	2	2.6728	0.2046
GGGGGGPGEGFDVAK	1262.3	2	3.0131	0.2993
GGGGGQDNGLEGLGNDSR	1660.6	2	4.6505	0.4235
GGGGNFGPGPGSNFR	1378.4	2	3.2597	0.3901
GGGGPGGGGPGGGSAGGPSQPPGGGGPGIRK	2399.5	3	3.5654	0.3131
GGGGYGGSGDGYNGFGNDGGYGGGGPGYSGGSR	2875.8	3	6.0976	0.5086
GGGHVAQIYAIR	1242.4	2	3.1163	0.3393
GGGKDVSAQATGK	1176.3	2	3.7349	0.3123
GGGLTGLLVGTLDVVLDSSAR	2001.3	2	3.423	0.3454
GGGPQAQSHGEAR	1252.3	2	3.0564	0.3694
GGGPTSSEQIMK	1192.3	2	2.8241	0.3232
GGGQIIPTAR	970.1	2	2.6448	0.1229
GGGVGGFLPAMK	1091.3	2	2.7928	0.2116
GGHAAYSSAVNILLGHGTR	1882.1	2	2.712	0.3849
GGHFAAFEEPELLAQDIR	2001.2	2	6.2729	0.477
GGHFAAFEEPELLAQDIRK	2129.4	3	6.3984	0.4988
GGHFYSAKPEILR	1475.7	2	3.7932	0.3755
GGHGAASPSEK	998.0	2	2.9416	0.3385
GGHMDDGGYSMNFNMSSSR	2051.2	3	6.0413	0.5833

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GGHPPAIQSLINLLADNR	1887.1	3	4.5123	0.4397
GGHSGQLGPSSVAPSFRPEDELEHLTK	2834.1	3	4.8031	0.3367
GGHSGQLGPSSVAPSFRPEDELEHLTKK	2962.2	3	5.1327	0.4566
GGHSSSLFGNIK	1204.3	2	3.6461	0.4362
GGHVDLTMLGAMQVSK	1644.9	2	3.7106	0.1381
GGIMLPEK	845.0	2	2.5674	0.1071
GGIMLPEKSQGK	1245.5	2	3.557	0.224
GGIREGSLDLGHAPLGPYAR	2037.3	2	3.3342	0.109
GGIVDEGALLR	1100.3	2	3.104	0.2652
GGIVGMTLPIAR	1185.5	2	4.1552	0.3403
GGKAVANYDSVEEGEKVVK	1980.2	3	4.4022	0.3703
GGKEFVEAVLELR	1447.7	2	4.333	0.3831
GGKEFVEAVLELRK	1575.8	3	3.7731	0.2445
GGKPEPPAMPQPVPTA	1574.8	2	3.6698	0.3821
GGKSGELEQEEER	1448.5	2	4.5264	0.3539
GGKSGELEQEEERLSKEWEDS	2423.5	2	4.9733	0.3835
GGKSGELEQEEERLSKEWEDSKR	2707.8	3	4.9894	0.257
GGLDVTHGQTGVESVYTTFR	2125.3	3	3.4381	0.1828
GGLGGGYGGASGMGGITAVTVNQSL	2182.4	2	4.3762	0.4031
GGLGGGYGGASGMGGITAVTVNQSLLSPLVLEVDPNIQAVR	3927.4	3	7.1545	0.5929
GGLGLILKR	927.2	2	2.8545	0.1322
GGLGLSGAK	759.9	1	1.6715	0.1307
GGLKLNPNFLVDFGKEPLGPALAHELR	2904.4	3	4.473	0.1966
GGLPITQLFR	1102.3	2	2.5121	0.2679
GGLPLEEVTVAEVLAAR	1725.0	2	5.6841	0.3706
GGLRKPEASHSFENR	1685.8	2	3.9705	0.3265
GGLVDEKALAQALKEGR	1756.0	3	4.9868	0.4138
GGMGSGGLATGIAGGLAGMGGIQNEK	2262.6	2	6.1943	0.4755
GGMGSGGLATGIAGGLAGMGGIQNEKETMQSLNDR	3337.7	3	5.9813	0.4782
GGMGSGGLATGIAGGLAGMGGIQNEKETMQSLNDRLASYLDR	4156.6	3	4.2406	0.2838
GGNEESTKTGNAGSR	1465.5	2	4.0975	0.3926
GGNFGFGDSR	1014.0	2	3.204	0.1838
GGNIGDGGGAADR	1117.1	2	3.9887	0.3179
GGNIGDGGGAADRVINQILTEMDGMSTK	2779.1	2	4.8231	0.2469
GGNIGDGGGAADRVINQILTEMDGMSTKK	2907.2	3	4.1444	0.1572
GGNLRDKLDGNELDLSLSDLNEVPVKELAALPK	3535.0	3	6.116	0.4963

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GGNNSFTHEALTLK	1489.6	2	3.777	0.3018
GGNRFEPYANPTKR	1607.8	3	4.0438	0.2498
GGNVGINSFGFGGSNVHIILRPNTQPPPAPAPHATLPR	3860.3	3	5.0643	0.3716
GGNVPQLDAPISQFYADR	1949.1	3	4.7165	0.4632
GGPASVPSSSPGTSVK	1415.5	2	3.1757	0.2303
GGPDFSNLEK	1064.1	2	2.6065	0.1217
GGPEETITQQGR	1273.3	2	3.7333	0.2488
GGPEKHEVTGWVLVSPLSK	2021.3	3	5.3184	0.4074
GGPNIITLADIVKDPVSR	1866.2	2	4.5951	0.4807
GGPNYQEGLR	1091.2	2	3.4886	0.1997
GGPPFAFVEFEDPRDAEDAVYGR	2542.7	2	3.8081	0.3971
GGPPFAFVEFEDPRDAEDAVYGRDGYDYDGYR	3647.8	3	3.3197	0.3193
GGPSPGDVEAIKNAIANASTLAEVERLK	2809.1	3	3.4585	0.4106
GGPTPQEAIQR	1154.3	2	3.076	0.2435
GGPVQVLEDEELKSQPEPLVVK	2391.7	3	5.3017	0.3397
GGQIGLQAPGLSVSGPQGHLESGSGK	2419.6	3	3.3565	0.1431
GGQLQEQLTQQLSQALSSAVAGR	2371.6	3	4.2666	0.3661
GGQLQEQLTQQLSQALSSAVAGRLER	2770.1	3	5.9492	0.4572
GGQTHLGLPVFNTVK	1568.8	2	4.1809	0.4219
GGQTHLGLPVFNTVKEAK	1897.2	2	4.6506	0.3827
GGQVIQIPVADITVGDIAQVK	2122.5	3	3.2097	0.1958
GGQVVNLMNQR	1216.4	2	2.8952	0.1754
GGQVYATNTR	1067.1	2	3.3444	0.3123
GGRGDVGSADIQDLEK	1617.7	2	3.8333	0.255
GGRGDVGSADIQDLEKWLAK	2116.3	3	6.4521	0.2571
GGRHPSAHDVILEGAGLR	1843.0	2	3.9815	0.4359
GGSAAATSNPHHDNVR	1591.6	2	4.7111	0.4411
GGSASVWSER	1036.1	2	3.2017	0.2388
GGSDGYGSGR	912.9	2	3.5252	0.389
GGSGSGPTIEEVD	1205.2	2	3.3021	0.3498
GGSGSHNWGTVKDELTESPK	2087.2	3	5.075	0.4646
GGSHDAPENTLAAIR	1509.6	2	2.9662	0.2271
GGSLPKVEAK	986.1	2	2.6405	0.1046
GGSLPSHHQTR	1177.3	2	3.0608	0.3034
GGSMHMYAK	982.2	2	2.5521	0.2911
GGSPFAIVITQQHQIHR	1890.1	2	3.6763	0.2599

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GGSRGEEVGELSR	1333.4	2	3.4611	0.1314
GGSSEIAFHTIPVIQR	1712.9	2	3.7209	0.234
GGTLKDDDWGNIK	1419.5	2	3.5439	0.3334
GGTQEPAPVPAEPFDNTTYK	2120.3	2	3.8512	0.2892
GGTWFAGFGR	1056.2	2	3.2529	0.4312
GGVADALLYR	1035.2	2	3.8862	0.2811
GGVASGFKHVVPNEVVVQR	1980.3	2	4.427	0.4389
GGVDHAAAFGR	1058.1	2	3.0862	0.3792
GGVDTAAAPAGGAPPAHAPGPGR	1953.1	3	3.8244	0.2365
GGVHLTKDPNVVGQLAK	1734.0	2	4.5585	0.4342
GGVVAGNVAHILDSNHGK	1745.9	2	2.7793	0.2565
GGVVAGNVAHILDSNHGKK	1874.1	2	4.1397	0.3581
GGVVGIKVDK	972.2	2	2.6733	0.198
GGVVGIKVDKGVVPLAGTNGETTTQGLDGLSER	3226.6	2	7.3336	0.2803
GGVVNAAKEEHETDEKR	1870.0	3	3.3921	0.2801
GGVVTSNPLGF	1048.2	2	2.8356	0.2337
GGYFLVDFYAPTAAVESMVEHLSR	2661.0	3	3.8921	0.3038
GGYIGSTYFER	1250.3	2	2.9819	0.155
GGYVLHIGTIYGDLK	1606.8	2	4.2532	0.3325
GHAAFTSDPKPTIEVSGK	1843.0	2	5.6435	0.5223
GHAAFTSDPKPTIEVSGKK	1971.2	2	5.4167	0.443
GHAAPILYAVWAEAGFLAEAELLNLR	2797.2	3	3.6393	0.195
GHAAPILYAVWAEAGFLAEAELLNLRK	2925.4	3	4.0889	0.3817
GHADSVTGLSLSSEGSYLLSNAMDNTVR	2883.1	3	4.5261	0.3408
GHAGNPRDPTDEGIFISK	1912.1	2	3.4382	0.3369
GHASAPYFGKEEPSVAPSSTGK	2205.4	3	4.2191	0.3104
GHAVGDIPGVR	1078.2	2	2.6129	0.2243
GHAVNLLDVPVPVAR	1557.8	2	3.5702	0.4422
GHDEREHPFLVK	1464.6	2	3.2126	0.2032
GHDFHEGVR	1054.1	2	2.8819	0.2886
GHDHVLQFLVSIPSYEPQETDSLSQMETK	3317.6	3	5.2334	0.4209
GHDLMSNTPDSVPPEELKPYHIR	2633.9	3	4.3067	0.3667
GHDQYAYDGKDYIALNEDLR	2357.5	3	4.3716	0.1959
GHEAEESR	914.9	2	2.6242	0.2589
GHEFYNPQKK	1248.4	2	3.1586	0.2486
GHEKEALQLMATYLPK	1830.1	2	3.5794	0.3037

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GHETTGHTYER	1288.3	2	3.1489	0.2872
GHFASVWQR	1088.2	2	2.5745	0.2568
GHFDYQSLLMR	1367.6	2	3.5867	0.4008
GHFEEEKQQLSSLITDLQSSISNLSQAK	3119.4	3	4.531	0.2798
GHFEEEKQQLSSLITDLQSSISNLSQAKEELEQASQAHGAR	4526.8	3	5.7879	0.4319
GHFGPINSVAFHPDGK	1680.8	3	4.3181	0.4393
GHFNIQPNKK	1183.3	2	3.1195	0.2229
GHFTSLELVPPSTLTTTHLKAEPLTK	2820.2	3	4.1088	0.1864
GHGAGGASILTFWDAR	1616.8	2	3.6498	0.3761
GHGFITPADGGPDIFLHISDVEGEYVPVEGDEVTYK	3862.2	3	5.6186	0.432
GHGVLHTLIR	1103.3	2	2.6033	0.2276
GHHLPSENLGKEPLDPDPSHSPSDK	2691.9	3	3.7586	0.2068
GHHLPSENLGKEPLDPDPSHSPSDKVGR	3004.2	3	4.6542	0.2615
GHHVAQLDPLGILDADLDSSVPADIISSTDK	3201.5	3	7.4386	0.6006
GHIASVLNAWPEDVIK	1750.0	2	2.5053	0.1386
GHIAVSAAVFPTGTK	1456.7	2	3.648	0.3256
GHITAGSNK	885.0	1	2.7993	0.2374
GHKEIINAIDGIGGLGIGEGAPEIVTGSR	2832.2	3	5.6871	0.3449
GHLAAAANHR	1018.1	2	2.6131	0.2273
GHLDNISNNLLIGAINIENGK	2220.5	3	6.092	0.4285
GHLDNISNNLLIGAINIENGKANSVR	2748.0	3	5.1045	0.4036
GHLDPTWALQQLQQLR	1905.1	3	4.3671	0.3208
GHLENNPALEK	1222.3	2	3.6034	0.3861
GHLENNPALEKLLPHIR	1952.2	2	4.0606	0.3865
GHLESSLLSHLVDPK	1632.8	2	4.2224	0.4199
GHLESSLLSHLVDPKDLEPR	2243.5	3	4.194	0.421
GHLHLLETSIDGILADVK	1932.2	2	3.6283	0.3508
GHLLYVALSPGQHR	1548.8	2	4.0615	0.4431
GHLQIAACPNQDPLQGTTGLIPLLGIDVWEHAYYLQYK	4238.8	3	6.5893	0.575
GHLSRPEAQSLSPYTTSANR	2173.3	2	4.613	0.3951
GHMPPLTSAQQALTGTINSSMQAVQAAQATLDDFDTLPPLGQDAASK	4797.3	3	5.5515	0.3075
GHNGWVTQIATTPQFPDMILSASR	2628.9	3	4.5493	0.3296
GHNPLGLMYHDASR	1568.7	2	3.3251	0.4315
GHNSALLQIHQLQAELEALR	2242.5	3	5.5544	0.4011
GHNTNVGAIVFHPK	1491.7	3	3.8025	0.4157
GHNVGSLFHMADDLGR	1726.9	2	2.4847	0.2634

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GHPDLQGQPAEEIFESVGDR	2182.3	2	4.5577	0.4698
GHPDRLSLQLALTELETLAEK	2335.6	3	3.7125	0.2119
GHPSSPPVVDTVHGK	1514.7	3	4.7796	0.3465
GHQAALGLMER	1183.4	2	3.5201	0.4433
GHQAFDVGQPR	1212.3	2	3.4263	0.3946
GHQLLSADVDIKELAVETK	2067.3	3	4.6562	0.3946
GHQQLYWSHPR	1409.5	2	4.0116	0.4794
GHREEEQEDLTK	1471.5	2	2.7657	0.1355
GHRIEEVPELPLVVEDK	1960.2	2	4.6854	0.3462
GHRIEEVPELPLVVEDKVEGYK	2536.9	2	5.5459	0.4444
GHRIEEVPELPLVVEDKVEGYKK	2665.0	3	7.4866	0.5187
GHRIEEVPELPLVVEDKVEGYRK	2693.1	3	5.2437	0.3294
GHSAAVHSFAFSNDSR	1690.8	2	4.3819	0.4201
GHSEKEVADAIR	1312.4	2	3.5172	0.3667
GHSGGSGGGGSGSGPGIKK	1541.6	2	3.2861	0.453
GHSLSDGLEEVQK	1399.5	2	3.2821	0.33
GHSLSDGLEEVQKAEMK	1859.1	3	3.941	0.3471
GHTELLTVEQALADFAELLR	2227.5	2	6.236	0.5674
GHTEVIVPHLTESYNSHRDPPEEEIPFCTLK	3576.9	3	3.3269	0.1365
GHTFAEELQK	1160.3	2	2.5935	0.336
GHTPTQPGALNQR	1377.5	2	3.1108	0.2489
GHVAHLEDDEGDDDESKHSTLK	2435.5	3	4.9577	0.3819
GHVDILAPTVQELAALEK	1905.2	2	4.1899	0.3116
GHVDILAPTVQELAALEKEAQTSFLHLGYLPNQLFR	4021.6	3	3.8343	0.2048
GHVFEESQVAGTPMFVVK	1963.2	2	6.7829	0.5199
GHVQDPNDRR	1194.2	2	2.747	0.1335
GHVSLAAELSK	1112.3	2	3.0985	0.3092
GHYNNVSCAVFHPR	1601.8	3	4.4437	0.41
GHYTEGAELVDAVLDVVR	1944.1	2	6.1031	0.4689
GHYTEGAELVDAVLDVVRK	2072.3	3	6.078	0.4884
GHYTEGAELVDSVLDVVR	1960.1	2	7.3734	0.555
GHYTEGAELVDSVLDVVRK	2088.3	2	6.6113	0.4839
GHYTIGK	775.9	1	1.6304	0.1369
GHYTIGKEIIDLVLDR	1843.1	2	5.3489	0.4316
GHYTIGKEIIDLVLDRIR	2112.5	3	3.26	0.185
GHYTIGKEIIDPVLDR	1827.1	3	5.1418	0.4099

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GHYTIGKEIIDPVLDRIR	2096.4	3	3.6751	0.3043
GHYTIGKEIVDLVLDR	1829.1	2	3.7747	0.2337
GIAAPHAGANVKPR	1359.6	2	3.2774	0.3845
GIAEENKLVTSPNFVVTQALVALLADKGAK	3098.6	3	3.4324	0.1463
GIAGEKFDIVKK	1305.5	2	3.2915	0.2325
GIAGRQDILDDSGYVSAYK	2029.2	3	5.1951	0.4385
GIAGRQDILDDSGYVSAYKNAGTYDAK	2850.0	3	4.1592	0.2368
GIALIFNHER	1170.3	2	3.4426	0.2803
GIAPAPALSVSPQNNHSPDPGLSNLAASYLNPVK	3398.8	3	4.9215	0.3139
GIATNDVGIQK	1116.3	2	3.3557	0.3785
GIATNDVGIQKDGAPK	1584.8	2	3.2474	0.1836
GIAYIEFKTEADAEKTFEEKQGTEIDGR	3177.4	3	4.998	0.4915
GIAYVEFVDVSSVPLAIGLTGQR	2392.7	3	4.4013	0.3231
GIDEGPEGLKLISDIIR	1826.1	2	3.8041	0.2799
GIDEGPEGLKLISDIIREK	2083.4	2	2.6591	0.1444
GIDIHGVPYVINVTLPDEKQNYVHR	2878.2	3	5.8694	0.4653
GIDIIIEMLANVNLSKDLSLLSHGGR	2780.2	3	4.4281	0.295
GIDLTQVK	874.0	2	2.641	0.1408
GIDPFSLDALSK	1263.4	2	3.1862	0.1893
GIDPFSLDALSKEGIVALR	2002.3	3	3.9326	0.2057
GIDRYNPENLATLER	1761.9	2	4.2955	0.2803
GIDVQQVSLVINYDLPTNR	2145.4	3	5.4307	0.3124
GIDVQQVSLVINYDLPTNRENYIHR	2958.3	3	3.8588	0.2889
GIDYDKLIVR	1192.4	2	2.9297	0.3333
GIEAGSEDIDILPNGLAFFSVGLK	2463.8	3	4.5171	0.3563
GIEGVQVIPLIPGAGEIIIADNIIK	2544.0	3	3.5518	0.135
GIEILTDMSRPVELSDRETLLNSATTSLNSK	3392.8	3	5.8729	0.5159
GIEKNLGIGK	1029.2	1	2.8198	0.1745
GIEKNLGIGKVSSFEEK	1836.1	3	4.1513	0.1978
GIEKPPFELPDFIKR	1787.1	3	4.3792	0.3179
GIELAYLEQLHGQHEAWLIHK	2486.8	3	4.7442	0.4654
GIEMSEVRLNLDK	1504.7	2	3.5578	0.1816
GIEMSEVRLNLDKMMEQK	2152.5	2	3.4279	0.3377
GIEQAVQSHAVAEEEAR	1824.9	2	5.5934	0.5463
GIFEALRPLETLPVEGLIR	2124.5	3	4.3063	0.2911
GIFGDHPGHSYGDLPGPSPAQLFQDSGLLYLAQELPAPSR	4207.6	3	6.4627	0.4792

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GIFLHLSNQHEFGR	1655.8	2	3.6059	0.2925
GIFNGFSVTLKEDGVR	1740.0	2	4.1034	0.4483
GIFTKEDALK	1122.3	2	2.7631	0.3211
GIFTKEDALKLVQLK	1704.0	2	4.3364	0.3175
GIFTSEIGTK	1053.2	2	2.9943	0.3438
GIGFLTSGWR	1094.2	2	3.0891	0.2724
GIGHVIKVPDNYGDEIAIELR	2309.6	3	5.148	0.4375
GIGIENIHYLNDGLWHMK	2111.4	3	4.59	0.4398
GIGIHHGGLLPILK	1425.7	2	3.9108	0.3136
GIGMGNIGPAGMGMEGIGFGINK	2179.6	2	5.8487	0.5115
GIGQVLPTHLMEER	1580.8	2	2.4863	0.1588
GIGTDEFTLNR	1223.3	2	2.914	0.3612
GIGTDEKMLISILTER	1777.1	2	5.3281	0.3383
GIHDAFVK	887.0	2	2.4164	0.1023
GIHFCHDLVSLCNFHNYDNLR	2518.8	3	3.9978	0.3384
GIHNSIGDYR	1132.2	2	2.8057	0.328
GIHPTIISESFQK	1457.7	3	4.3659	0.3487
GIHQSTIDLKNELK	1596.8	2	4.2319	0.397
GIHSAIDASQTPDVVFASILAAFSK	2546.9	3	6.4186	0.5219
GIHVEVPPAEAER	1404.6	2	2.8801	0.2134
GIHVEVPPAEAERLGPLQVAR	2239.6	2	3.3428	0.2938
GIIDPTKVVR	1098.3	2	2.811	0.2671
GIIDSTVGEHR	1184.3	2	2.7194	0.3301
GIIGYDV	736.8	1	1.6491	0.1263
GIIPNSFAHIFGHIAK	1723.0	2	2.573	0.2665
GIIRPGTAFELLEAQAATGYVIDPIKGLK	3043.5	3	5.9558	0.4267
GIIVHTMAAVEALGAK	1581.9	2	2.9201	0.4659
GIIWGEDTLMEYLENPKK	2137.4	2	4.9331	0.4379
GIKGEEIVQQLIENSTTFR	2163.4	2	2.5422	0.2667
GIKPVTLELGGK	1212.5	3	4.0036	0.3655
GIKTVFDEAIR	1249.4	2	2.436	0.221
GILAADESTGSIAK	1333.5	2	4.8282	0.4686
GILAADESTGSIAKR	1489.7	2	4.5909	0.4831
GILAADESVGSMAK	1349.5	2	3.3448	0.343
GILAADESVGTMGNR	1491.7	2	4.5467	0.4608
GILDKEEAEAIKR	1472.7	3	4.5201	0.3868

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GILEEPLPSTSSEEEDPLAGISLPEGVDPSFLAALPDDIRR	4334.7	3	3.5267	0.294
GILEQGWQADSTTR	1562.7	2	3.3132	0.2745
GILEYLTVAEVVETMEDLVTYTK	2618.0	2	4.3532	0.4739
GILFVGSGVSGGEEGAR	1592.7	2	5.8839	0.4458
GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK	4039.3	3	7.49	0.5886
GILLFGPPGTGK	1157.4	2	3.4544	0.2964
GILLYGPPGTGK	1173.4	2	3.4698	0.2052
GILSGTSDLLLTFDEAEVR	2037.3	2	5.6106	0.4218
GILSGTSDLLLTFDEAEVRK	2165.4	2	4.3275	0.292
GILTLKYPIEHGIITNWDDMEK	2588.0	2	4.2077	0.377
GILTLKYPIEHGIITNWDDMEKIWHHTFYNELR	4085.6	3	5.9492	0.4937
GILTLPKPVHFK	1350.7	2	2.6634	0.1979
GILTVDELLAIR	1313.6	2	3.1144	0.2354
GIMGEDTYPYQGK	1459.6	2	2.961	0.1887
GINDSKDLPEEYLSAIYNEIAGK	2540.8	3	3.5791	0.1617
GINDSKDLPEEYLSAIYNEIAGKK	2668.9	3	6.4505	0.427
GINDSKDLPEEYLSSIYEEIEGKK	2758.0	3	6.0918	0.4204
GINTLVTYDMVPEPK	1677.9	2	4.6675	0.4335
GINVALANGK	957.1	2	2.9003	0.2037
GIPEFWFTIFR	1413.6	2	2.9605	0.3742
GIPEFWLTVFK	1337.6	2	3.061	0.3259
GIPHLVTHDAR	1216.4	2	2.9341	0.3612
GIPIEVIPMAYVPVSR	1742.1	2	2.9209	0.2423
GIPKQAPFRSPTAPSVFSPTGNRTPIPPSR	3162.6	3	3.9026	0.2078
GIPLATGDTSPEPELLPGAPLPPPKEVINGNIK	3333.8	3	5.2044	0.4832
GIPVLVGLLDHPK	1358.7	2	2.6748	0.2681
GIPVLVGLLDHPKK	1486.8	2	3.5105	0.3453
GIPVLVGLLDHPKKEVHLGACGALK	2566.1	3	3.3566	0.3108
GIQTSDPNAVVMGLAPEHFHYQILNQAFR	3255.7	3	3.5317	0.2602
GIQVEIYSFPKDPEIHLSGPLEAGKPITVK	3264.8	3	5.2638	0.2345
GIRHEVININLK	1406.7	3	3.9069	0.2485
GIRPAINVGLSVSR	1439.7	2	3.38	0.3382
GISCMNTTLSESPFK	1615.9	2	3.3972	0.215
GISDLAQHYLMR	1404.6	2	4.0673	0.385
GISDLVLKEYLDNVQLGHILER	2525.9	3	6.0755	0.5024
GISEDSHLESLQDVGQSAAPTFMISPETITGTGK	3505.8	3	5.2706	0.3492

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GISEDSHLESLQDVGQSAAPTFMISPETVTGTGK	3491.8	3	5.7991	0.2926
GISEDSHLESLQDVGQSAAPTFMISPETVTGTGKK	3620.0	3	7.4458	0.5041
GISEETTTGVHNLYK	1649.8	2	4.1763	0.4125
GISEFIVMAADAEPLEIILHLPLLCEDKNVPYVFVR	4056.8	3	4.0598	0.1773
GISHVIVDEIHER	1504.7	2	4.2979	0.4571
GISLNPEQWSQLK	1500.7	2	4.1691	0.3063
GISLNPEQWSQLKEQISDIDDAVR	2743.0	2	4.6058	0.418
GISLNPEQWSQLKEQISDIDDAVRK	2871.2	3	3.974	0.2659
GISLNPEQWSQLKEQISDIDDAVRKL	2984.3	3	3.2219	0.1817
GISQEQMQEFR	1353.5	2	3.6741	0.3699
GISTKPVYIPEVELNHK	1925.2	2	4.0372	0.3422
GISTKPVYIPEVELNHKLIK	2279.7	3	3.9282	0.2133
GISVHISNAEPK	1252.4	2	2.9477	0.2363
GITEQQKEGLEIVK	1572.8	2	3.5221	0.1627
GITFDSGGISIK	1195.3	2	3.0067	0.3783
GITGVDLFGTTDAVVK	1593.8	2	4.6811	0.4572
GITGVDLFGTTDAVVKHVLEGHDR	2537.8	3	4.7537	0.427
GITGVEDKESWHGKPLPK	1979.2	2	4.459	0.4163
GITHIGYTDLPSR	1430.6	2	4.4113	0.4673
GITINAAHVEYSTAAR	1674.8	2	5.4024	0.5102
GITLHPELFSIDNGLLTPTMK	2298.7	3	3.8237	0.2894
GITSFLVDRDTPGLHIGKPENK	2395.7	3	4.9799	0.4133
GITVTAYSPLGSPDRPWAKPEDPSLLEDPKIKEIAAK	3992.5	3	3.8183	0.1428
GIVAAQETQIQELAAANQESSHVQQQALALEQQFLER	4079.4	3	5.524	0.4633
GIVDLIEER	1044.2	2	2.6588	0.1336
GIVDQSQQAYQEAFEISK	2042.2	2	6.155	0.5174
GIVDQSQQAYQEAFEISKK	2170.4	2	4.8303	0.4185
GIVDSITGQR	1046.2	2	2.598	0.2668
GIVEESVTGVHR	1283.4	2	3.097	0.4
GIVEFASKPAAR	1246.4	2	2.7832	0.3514
GIVEFSGKPAAR	1232.4	2	3.2251	0.4029
GIVEQCCTSICSLYQLENYCN	2384.7	2	4.1468	0.47
GIVFEDVKVPK	1231.5	2	2.8634	0.2854
GIVFEDVKVPKENVLIGDGAGFK	2432.8	3	4.815	0.4413
GIVKDIIHDPGR	1320.5	2	3.7754	0.3395
GIVKDIIHDPGRGAPLAK	1858.2	2	4.0066	0.374

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GIVLLEELLPK	1224.5	2	3.7413	0.1923
GIVNAVKDPDANGK	1398.5	2	3.7882	0.3733
GIVNEQFLLQR	1317.5	2	3.0506	0.1492
GIVNGAAPELPVPTGGPAVGAR	2001.3	2	4.8022	0.4634
GIVQNLHSMLPIQQLQEWGVER	2577.0	3	3.2911	0.1269
GIVVGIKLDQGGAPLAGTNKETTIQGLDGLSER	3309.7	3	6.549	0.531
GIVVGIKVDKGVVPLAGTDGETTTQGLDGLSER	3283.7	3	3.2743	0.2603
GIVVTAYSPLGSPDRPWAKPEDPSLLEDPR	3264.6	3	4.4634	0.4009
GIVVYTGDR	980.1	2	2.9532	0.2666
GIVYDTGGLSIK	1223.4	2	2.8212	0.2996
GIYAYGFEKPSAIQQR	1829.0	2	4.8728	0.4897
GIYKDDIAQVDYVEPSQNTISLK	2597.9	3	4.8323	0.1766
GIYTLNEHDKYNIR	1736.9	2	2.6556	0.1885
GKADAGKDGNNPAK	1343.4	2	4.0877	0.3188
GKADAGKEGNNPAENGDAK	1843.9	2	4.2866	0.436
GKADAGKEGNNPAENGDAKTDQAQK	2515.6	3	3.9161	0.1493
GKADAGKEGNNPAENGDAKTDQAQKAEGAGDAK	3215.3	3	3.4129	0.1298
GKAEEQAVR	988.1	2	3.1034	0.1753
GKAHAAVWNAQEAQADFAK	2014.2	3	4.4362	0.274
GKATISNDGATILK	1389.6	3	4.3134	0.406
GKDAFPVAGQK	1118.3	2	3.0608	0.2365
GKDEAMAIGGHWSPSLDGPDPEKDPSVLIK	3148.5	3	4.3918	0.382
GKDFLALALLDGR	1389.6	2	2.7684	0.1703
GKDGVGAVMDSMELER	1694.9	2	2.8672	0.1689
GKDHVVSDFSEHGSLK	1742.9	2	5.1476	0.4859
GKDIGKPIEK	1085.3	2	2.4322	0.1292
GKDILYIGDHIFGDILK	1918.2	3	4.7182	0.3106
GKDKEYAEIIRK	1450.7	3	3.4313	0.1225
GKDLIGVQNLLK	1298.6	2	2.8023	0.1259
GKDLIGVQNLLKK	1426.7	2	3.8466	0.2883
GKDMVVDIQR	1161.4	2	3.0279	0.1669
GKDSLYAQGK	1067.2	2	3.2526	0.204
GKDSLYAQGR	1095.2	2	3.6975	0.3721
GKDSYETSQLDDQSAETHSHK	2364.4	3	5.8437	0.508
GKDSYETSQLDDQSAETHSHKQS	2579.6	3	5.0673	0.302
GKDYYQTLGLAR	1385.6	2	3.0776	0.2636

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GKEADKEINK	1132.2	2	3.1672	0.223
GKEALESEFR	1166.3	2	3.1095	0.3175
GKEDEGEEAASPMLQIQR	1989.2	2	6.3499	0.3709
GKEFEFSQLPLKVEFLECSAK	2430.8	2	3.9284	0.2057
GKEGQLGHGDVLPR	1463.6	2	3.29	0.3393
GKEGSALSHVR	1141.3	2	2.4731	0.2346
GKEGSALTEGAKEEGGEEVAK	2077.2	2	6.2706	0.4246
GKEHDDIFDK	1204.3	2	3.0313	0.2817
GKEHDDIFDKLK	1445.6	2	3.759	0.3146
GKELDSNPFASLVFYWEPLNR	2483.8	2	3.6899	0.3245
GKELFIQQER	1248.4	2	3.0522	0.1695
GKELQPGSHIQSDKEIDAFVR	2355.6	3	4.6048	0.3255
GKELSGLGSALKNPFGNAGLLLGEAGK	2600.0	3	6.919	0.3576
GKESEKELALVKR	1487.7	2	4.1111	0.4115
GKEVDNFVDKLK	1392.6	2	3.4741	0.2359
GKEVDNFVDKLKSEGETIMSSSMGKR	2874.2	3	3.823	0.3058
GKFEDMAK	926.1	1	2.0544	0.11
GKFGHEFLEFEFRPDGK	2041.3	2	4.839	0.3991
GKFIYITPEELAAVANFIR	2153.5	2	5.1657	0.4299
GKFLEMCNDLLAR	1510.8	2	2.536	0.1524
GKFNFPYKIDDILSAPDLQK	2310.6	3	5.2955	0.3842
GKFPVQLENVDSFVELGQVALR	2446.8	3	3.7823	0.2687
GKFQDNFEFIQWFK	1835.1	2	4.3144	0.4315
GKFQDNFEFVQWFK	1821.0	2	3.2604	0.1686
GKFQDNFEFVQWFKK	1949.2	3	3.7726	0.3437
GKFSEGEATLR	1195.3	2	3.0823	0.3149
GKGASGSFVVVQK	1264.5	2	4.144	0.4278
GKGDKAQIEKR	1230.4	2	3.5719	0.2588
GKGDKAQLEKR	1230.4	2	3.2006	0.2554
GKGEGDLSQLSK	1219.3	2	2.5352	0.1642
GKGEITPAAIQK	1213.4	2	3.1793	0.2329
GKGFSVVADTPELQR	1604.8	2	4.6628	0.429
GKGGEIQPVSVK	1199.4	2	3.9903	0.3332
GKGGTQVDTEIEEKDEETKAFEALLSNIVKPVASDIQAR	4218.6	3	5.2901	0.3608
GKGIYLWDVEGR	1393.6	2	3.1505	0.367
GKGLLNAIVIK	1126.4	2	3.4452	0.2665

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GKGPLKNTSDVISAAK	1586.8	2	3.8003	0.4446
GKGPLKNTSDVISAAKK	1715.0	3	3.4075	0.1093
GKGSLEVLNLKDVEEGDEKFE	2336.5	2	5.551	0.477
GKGYYDAYLKR	1334.5	2	3.2034	0.3774
GKHGFSDNQK	1118.2	2	2.547	0.1949
GKIEEAVNAFK	1206.4	2	3.3472	0.2493
GKIEEAVNAFKELVR	1704.0	2	3.2719	0.278
GKIEEDSEVLMMIK	1622.9	2	4.5668	0.344
GKIFHIDTNALHVPR	1719.0	2	3.5072	0.339
GKITDLANLSAANHDAAIFPGGFGAAK	2628.9	3	5.7152	0.5192
GKITFADFHR	1192.4	2	3.1703	0.2969
GKIYSLNEGYAKDFDPAVTEYIQR	2779.1	3	4.3491	0.3443
GKKEEKQEAGK	1232.4	2	2.7496	0.1763
GKKEEKQEAGKEGTEN	1762.9	2	4.2112	0.2235
GKKPIEDPANDTVDFPK	1872.1	3	3.9779	0.3112
GKKPIEDPANDTVDFPKR	2028.3	3	4.6487	0.401
GKLDGNQDLIR	1229.4	2	3.38	0.248
GKLDVQFSGLTK	1293.5	2	2.8951	0.2101
GKLEAIITPPPAK	1335.6	2	4.1086	0.3423
GKLEAIITPPPAKK	1463.8	2	4.4356	0.3086
GKLEQHLTGR	1139.3	2	2.9682	0.1938
GKLGELVDGLVVPSALVTAILEAPVTEPR	2945.4	3	4.4535	0.3568
GKLGLVGVNLTLDGVK	1583.9	3	4.819	0.4738
GKLHVLLFK	1055.3	2	2.8367	0.1927
GKLHVLLFKEEGEVPASAFQK	2328.7	3	5.5893	0.3817
GKLLATQTAAELSK	1431.7	2	3.5613	0.3954
GKLLSNDEVTIK	1317.5	2	3.496	0.2933
GKLNHLCGADFVK	1402.6	2	3.5989	0.3198
GKLPIVNEDDELVAIIAR	1966.3	2	4.0025	0.3553
GKMSSYAFFVQTCR	1625.9	2	3.18	0.3305
GKNASDMPETITSR	1507.7	2	3.8933	0.3399
GKNASELFPAVVK	1360.6	2	3.3095	0.3396
GKNENESEKR	1191.2	2	2.4681	0.1602
GKNLFFSTNIDDAIKEADLVFISVNTPTK	3199.6	3	7.7154	0.5766
GKNNTVGLIQLNRPK	1652.9	2	4.4451	0.394
GKNPEDLIWHTPEGISIKPLYSK	2624.0	3	4.7194	0.3388

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GKNVIHPFLSR	1268.5	2	3.1856	0.2652
GKNVLINKDIR	1270.5	3	3.4333	0.2666
GKNVVHQLSVTLEDLYNGATR	2315.6	3	3.9329	0.1464
GKNVVHQLSVTLEDLYNGVTK	2315.6	3	3.5084	0.1477
GKPASGAGAGAGAGK	1157.3	2	2.8679	0.3437
GKPASGAGAGAGAGKR	1313.4	2	2.9763	0.4264
GKPAVAALGDLTDLPTYEHIQTALSSK	2798.1	3	5.1312	0.3997
GKPIHHFLGTSTFSQYTVVDENAVAK	2848.2	3	5.1907	0.4017
GKPSSDTVPKPK	1241.4	2	2.6133	0.2588
GKPTEASIEAR	1159.3	2	2.5992	0.137
GKQAEVANQETK	1303.4	2	4.0207	0.3022
GKQAEVANQETKEDLPAENGETK	2487.6	3	3.7149	0.2042
GKQDFLKEIVETFANK	1868.1	2	4.9881	0.4423
GKQDIGDILQQIMTITDQSLDEAQAK	2861.2	3	3.9211	0.1576
GKQEIENLKEEVESLNSLINDLQK	2772.1	3	5.6223	0.3508
GKQFAQALR	1019.2	2	2.5658	0.259
GKQFAQALRK	1147.4	2	2.6593	0.1949
GKQLIVANAGDSR	1329.5	2	3.4657	0.2952
GKQTMQVDEHARPQTTLEQLQK	2567.9	3	4.3135	0.2763
GKSETILSPPPEK	1383.6	2	3.7855	0.3782
GKSETILSPPPEKR	1539.8	2	3.8768	0.3325
GKSGPLFNFDVHDDVR	1804.0	2	2.9551	0.1799
GKSLESLDTSLFAK	1496.7	2	3.4038	0.2692
GKSPGIIFIPGYLSYMNGTK	2144.5	3	3.4006	0.2057
GKSTEEARKELQAAGK	1703.9	2	4.1681	0.3326
GKSTEEARKELQAAGKSPEDLER	2530.7	3	4.7546	0.3428
GKTEAYLEAIR	1251.4	2	3.1892	0.2727
GKTEAYLEAIRK	1379.6	3	4.2363	0.2253
GKTEQQTADQLLAR	1559.7	2	3.7112	0.298
GKTHSQLLIIDR	1381.6	3	3.3923	0.3421
GKTVGFGTNNSEHITYLEHNPYEK	2736.9	3	3.4819	0.1736
GKTVPEELVKPEELSK	1784.0	2	4.7748	0.3592
GKVLIDIR	914.1	2	2.6121	0.1481
GKVPITYLELLN	1360.6	2	3.5963	0.3249
GKVQFQGKK	1020.2	2	2.7248	0.1845
GKVRDKLNNLVLFDK	1760.1	3	4.109	0.2579

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GKWERPFEVKDTEEEDFHVDQVTTVK	3150.4	3	6.7831	0.4175
GKWKPPMIDNPSYQGIWKPR	2399.8	3	3.2372	0.2031
GKYKEELIEK	1237.4	2	3.4343	0.2081
GKYKEETIEK	1225.4	3	3.5198	0.2532
GKYLELLGYR	1212.4	2	3.173	0.166
GKYSEVFEAINITNNEK	1957.1	2	3.2188	0.2507
GKYYAVNYPLRDGIDDESYEAIFKPVMSK	3370.8	3	4.6513	0.2183
GLAAALENKR	1043.2	2	2.9087	0.1969
GLAAGDAIAEIRR	1313.5	2	2.487	0.2229
GLAAHYFFPR	1179.4	2	2.9691	0.4434
GLAEPGSFLDYPSTEPQPGPELPPGDGALEPETPMLPR	3961.4	3	3.6777	0.3156
GLAFIQDPDGYWIEILNPNK	2304.6	2	6.0973	0.4269
GLAFTDVDVDSIK	1380.5	2	3.9302	0.4175
GLAGAVSELLR	1086.3	2	3.7783	0.2454
GLAGLGDVAEVR	1157.3	2	3.0457	0.19
GLAGLGDVAEVRK	1285.5	2	3.3944	0.305
GLAITFVSDENDAK	1480.6	2	5.3202	0.4502
GLAPDLPEDLYHLIK	1695.0	2	4.0919	0.3863
GLAPDLPEDLYHLIKK	1823.1	2	3.707	0.2957
GLAPEQPVTLR	1181.4	2	2.7608	0.3302
GLAPEVADRIGDYVQQHGGVSLVEQLLQDPK	3333.7	3	5.1957	0.35
GLAPVQAYLHIPDIIK	1749.1	2	3.5385	0.1941
GLAVFISDIR	1091.3	2	4.0128	0.3165
GLCGAIHSSIAK	1157.4	2	3.4271	0.302
GLDAHLEQIFQEAHGMVAR	2123.4	3	5.5408	0.3867
GLDDSTGGTPLTPAAR	1529.6	2	2.613	0.1538
GLDGAVDMGAR	1062.2	2	3.5018	0.3961
GLDIKQEELGDLVDKEMAATSAAIETATAR	3148.5	3	4.7621	0.3485
GLDISHISQR	1126.2	2	3.3427	0.3045
GLDISNVKHVINFDLPSDIEEYVHR	2911.2	3	6.0814	0.3613
GLDKLEENLPILQQPTEK	2066.3	2	5.2235	0.3549
GLDLGGRGGVQVPAVDISSSLGGR	2268.5	3	5.3874	0.3022
GLDPARVNVPVIGGHAGK	1758.0	3	4.542	0.3108
GLDPYNVLAPK	1187.4	2	3.2983	0.3163
GLDQDHAR	911.9	2	2.5236	0.2641
GLDRIEERLPILNQPSTQIVANAK	2677.1	3	3.972	0.2104

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GLDSNKNEVNHAIDR	1682.8	2	2.6001	0.319
GLDTVVALLADVVLQPR	1780.1	2	3.6598	0.2391
GLDVDSLVIEHIQVNK	1780.0	2	4.8421	0.3862
GLDVDSLVIEHIQVNKAPK	2076.4	2	3.9806	0.2903
GLDVEDVK	875.0	1	2.0088	0.2083
GLDVEDVKFVINYDYPNSSEDYIHR	2989.2	3	5.9511	0.2776
GLDVEDVKFVINYDYPNSSEDYVHR	2975.2	3	4.8603	0.4614
GLDVPQVSLIINYDLPNNR	2141.4	2	5.1025	0.4333
GLDVPQVSLIINYDLPNNRELYIHR	2953.3	3	3.3545	0.1312
GLDYYTGVIYEAVLLQTPAQAGEEPLGVGSVAAGGR	3624.0	3	4.2375	0.3316
GLEAAQIKELEELRQTVK	2056.3	3	3.4616	0.2385
GLEDVRPSVESLLDELESSVPSPVPAITVNQGEMSSPQR	4151.6	3	3.7537	0.208
GLEETVAKELQTLHNLR	1952.2	2	4.447	0.41
GLEETVAKELQTLHNLRK	2080.4	2	2.6774	0.2053
GLEFPMTDLDMLSPIHTPQR	2299.7	2	4.2819	0.3915
GLEHVTVDDLVAEITPK	1837.1	2	4.7507	0.4379
GLEISGTFTR	1081.2	2	3.2485	0.3648
GLELEPGAGLFVAQAGGADPDKFQGVIAELK	3099.5	3	3.4603	0.2576
GLEMALLPHLHEHNLVK	1952.3	2	3.786	0.2585
GLEQLLVGGSHLK	1351.6	2	3.8148	0.2592
GLEQLLVGGSHLKENK	1723.0	3	3.9206	0.3701
GLESDVAELR	1089.2	2	3.6052	0.2769
GLESDVAELRAQLAKAEDGHAVAK	2479.7	3	3.9149	0.1248
GLESLPPLRPQQNPVLPVAGER	2368.7	2	2.6491	0.1352
GLETTATYDPETQEFILNSPTVTSIK	2857.1	3	3.7167	0.1706
GLEVTAYSPLGSSDR	1552.7	2	4.6567	0.5023
GLEVTDDSPK	1061.1	2	2.6991	0.2382
GLFDEEMNEILTDPSDDTK	2170.3	2	3.9182	0.1987
GLFDEYGSK	1016.1	2	2.6532	0.3809
GLFDEYGSKK	1144.3	2	2.5347	0.1632
GLFDEYGSKKSDYIK	1750.9	2	3.5842	0.3481
GLFGGGAQSLDREELFGESSSGK	2329.5	3	3.6403	0.2775
GLFHHISK	939.1	2	2.4745	0.2643
GLFIIDDK	921.1	2	2.9504	0.17
GLFIIDDKGILR	1360.6	2	3.821	0.3747
GLFIIDDKGILRQITVNDLPVGR	2554.0	3	5.117	0.4807

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GLFIIDGKGVLR	1288.6	2	3.2296	0.2428
GLFIIDPNGVIK	1286.5	2	3.4134	0.1982
GLFIIDPNGVIKHLSVNDLPVGR	2474.9	3	5.1308	0.4259
GLFLPEDENLREK	1560.7	2	3.448	0.1311
GLFSAITRPTAVNSLISK	1876.2	2	3.2103	0.2243
GLFSSDSGIEMTPAESTEVNK	2200.4	2	6.056	0.4527
GLFSSDSGIEMTPAESTEVNKILADPLDQMKAEAYK	3888.3	3	3.7509	0.2689
GLFTGLTPR	962.1	2	2.8334	0.3046
GLGAFVIDSDHLGHR	1594.8	2	3.9885	0.4675
GLGAGAGAGEESPATSLPR	1698.8	2	4.679	0.3373
GLGAVILVHAENGDLIAQEQKR	2332.6	3	4.1062	0.3768
GLGDHDLKVHDSNIYIKPFLSSAPEVR	3009.4	3	5.1923	0.3571
GLGDRPAPK	911.0	2	2.4437	0.1183
GLGDSGSEGHSSLSSHSNSEELAAAAK	2586.6	3	5.259	0.38
GLGEFTPLYPMLFGGGQER	2070.4	2	4.5398	0.4503
GLGGEVPGSHQGPDPYR	1723.8	2	4.0837	0.3635
GLGGEVPGSHQGPDPYRQLR	2121.3	2	3.2132	0.1562
GLGGILLEDIEEALPNSQK	1997.2	2	4.8183	0.3965
GLGGLIVVSK	943.2	2	2.4122	0.1479
GLGHQVATDALVAMEK	1640.9	2	5.0478	0.3521
GLGILSLKQQEMMAALTDAIQDKK	2604.1	3	4.8908	0.3582
GLGLDDALEPR	1156.3	2	3.3638	0.317
GLGMTLSYLFR	1258.5	2	2.9137	0.3481
GLGSTVQEIDLTGVK	1517.7	2	4.2257	0.4424
GLGSTVQEIDLTGVKLVLPK	2068.4	2	2.6543	0.1334
GLGTDDNTLIR	1175.3	2	3.5775	0.417
GLGTDEDAIISVLAYR	1693.9	2	5.7327	0.5116
GLGTDEDSLIEIICSR	1721.9	2	4.5466	0.4662
GLGTDEDTIIDIITHR	1769.9	2	5.3229	0.4545
GLGTDEDTLIEILASR	1703.9	2	5.509	0.3713
GLGTDEESILTLLTSR	1705.9	2	5.577	0.5026
GLGVEIAK	786.9	1	1.6071	0.14
GLGVEIAKNIILGGVK	1581.9	2	4.3254	0.387
GLGVHLSFVR	1085.3	2	3.0106	0.3047
GLGWVQFSSEEGLR	1565.7	2	3.5468	0.3171
GLGWVQFSSEEGLRNALQQENHIIDGVK	3126.4	3	5.0069	0.3016

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GLHEAHQLYGR	1281.4	2	2.8935	0.3062
GLHGPLTLNSPLTPEKIR	1944.3	2	3.8831	0.5285
GLHLQALKPTKPGLLPSLFK	2159.6	2	4.0804	0.2971
GLHNVVYGIQR	1256.4	2	2.7646	0.2524
GLHPRPQAVLSEQQNGLAVGGGEK	2443.7	3	5.2264	0.3314
GLHQSIEEFR	1216.3	2	3.6419	0.3035
GLHVVEVTYDDVPIPNSPFK	2227.5	2	5.1048	0.4606
GLIAAICAGPTALLAHEIGFGSK	2211.6	2	6.2656	0.5958
GLIDGVVEADLVEALQEFGPISYVVVMPK	3089.6	3	7.0541	0.4952
GLIENPALLR	1096.3	2	3.3763	0.2006
GLIEVKTDEFPR	1404.6	2	3.0375	0.37
GLIHPDDSVK	1081.2	2	2.5897	0.3646
GLILKDHGIR	1122.3	2	3.0756	0.3308
GLIPSSPQNEPTASVPPESDVYR	2441.6	2	3.5315	0.2483
GLISKQPGTCDPYVKISLIPEDSR	2618.0	3	3.3259	0.1013
GLIVYQLENQPSEFR	1794.0	2	3.2996	0.2452
GLIVYQLENQPSEFRR	1950.2	3	4.1569	0.2485
GLKAELMER	1047.3	2	2.6731	0.2035
GLKDNFADVQVSVVDCPDLTKEPFTFPVKGICGK	3669.2	3	4.0066	0.1892
GLKEGIPALDNFLDK	1630.9	2	2.6738	0.1961
GLKEGIPALDNFLDKL	1744.0	2	4.4583	0.3822
GLKLTFDSSFSPNTGKK	1828.1	2	4.5821	0.4571
GLKNVFDEAILAALEPPEPK	2152.5	2	5.4044	0.5231
GLKNVFDEAILAALEPPEPKK	2280.6	3	4.8478	0.4406
GLKSGENFKLLYDLADQLHAAVGASR	2775.1	3	5.8576	0.4517
GLKTLENLLASIR	1428.7	2	3.5936	0.3058
GLKYELISETGGSHDKR	1891.1	2	4.9534	0.4568
GLKYQEGGVESAFHK	1650.8	3	4.608	0.3242
GLLEFEHQR	1129.3	2	3.2645	0.156
GLLENELKLMEEFVK	1793.1	2	4.2672	0.3547
GLLGDAPNDPRGGTLLSVTGEVEPR	2521.8	3	4.3251	0.2931
GLLGELILLQQQIQEHEEEARR	2603.9	3	3.2624	0.2501
GLLHPQQLHLLSR	1512.8	2	3.9248	0.3551
GLLLFVDEADAFLR	1579.8	2	5.3893	0.5031
GLLLYGPPGTGK	1173.4	2	3.3042	0.3146
GLLNDAFQKGGPEGATTR	1833.0	3	3.2904	0.1657

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GLLPEELTPLILATQK	1737.1	2	4.3583	0.3851
GLLPGLLPAPADKLTPK	1702.1	2	4.0827	0.4082
GLLQSGQIPGR	1126.3	2	2.7249	0.1421
GLLQTEPQNNQAK	1441.6	2	3.1823	0.164
GLLRPHVPPAAITTLAR	1784.1	2	3.0826	0.1882
GLLSDSMTDVPVDTGVAAR	1905.1	2	5.3473	0.4024
GLLSQGSPLSWEETKR	1789.0	2	3.4885	0.26
GLLSSLDHTSIR	1299.5	2	3.0985	0.4049
GLLTIRYPMEHGVVR	1742.1	3	3.3841	0.3197
GLLTYTSWEDALSR	1612.8	2	4.2805	0.1744
GLNISAVR	830.0	2	2.6606	0.1708
GLNSQSSDDHLNKR	1571.6	2	2.612	0.1173
GLNTIPLFVQLLYSPIENIQR	2429.8	3	5.4433	0.5017
GLNVDQLNMLGEK	1431.6	2	3.1558	0.1869
GLPDFASFSAKL	1253.4	2	3.1006	0.369
GLPDNISSVLNK	1257.4	2	2.8479	0.2071
GLPDNISSVLNKLVVVK	1796.1	2	3.5191	0.283
GLPEGFAHPK	1053.2	2	2.5796	0.2432
GLPFEAENKHVIDFFK	1892.1	2	3.8594	0.3977
GLPFQANAQDIINFFAPLKPVR	2457.9	2	4.4308	0.3575
GLPFRATENDIANFFSPLNPIR	2490.8	3	4.7169	0.4073
GLPLFPLVKPHINFMAAKL	2107.6	2	2.7404	0.2277
GLPLLVALLDHPR	1414.7	2	3.7646	0.3342
GLPLLVALLDHPRAEVR	1870.2	2	2.6082	0.1616
GLPLVDDGGWNTVPISK	1769.0	2	4.2221	0.3604
GLPQLGTLGAGNHYAEIQVVDEIFNEYAAK	3219.5	3	4.8791	0.3327
GLPSPYNMSSAPGSR	1521.7	2	2.4938	0.2172
GLPTGDSPLGPMTHR	1536.7	2	3.6936	0.3476
GLPVLVELLQSETDKVVR	1996.3	2	3.9276	0.3494
GLPWSCSVEDVQNFLSDCTIHDGAAGVHFIYTR	3640.0	3	4.4681	0.3601
GLPYKATENDIYNFFSPLNPVR	2556.9	3	5.3013	0.4993
GLPYRATENDIYNFFSPLNPMR	2616.9	3	4.9857	0.3678
GLPYRATENDIYNFFSPLNPVR	2584.9	2	4.1559	0.4374
GLQAQIASSGLTVEVDAPK	1885.1	2	6.315	0.5015
GLQATQLAR	958.1	2	3.1054	0.2343
GLQDLKQQVEGTAQEAVSAAGAAAQQVVDQATEAGQK	3698.0	3	3.9666	0.1276

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GLQEAAEER	1003.0	2	2.6538	0.2072
GLQEAAEERESAREEEEAEQER	2576.6	3	4.6315	0.2839
GLQEAAEERESAREEEEAEQERR	2732.8	3	4.2542	0.2374
GLQEAAEERESAREEEEAEQERRGGEER	3261.3	3	4.8287	0.1952
GLQHLYALVLVNNK	1582.9	2	3.1342	0.2587
GLQKEEVVLLTHGDSVDKVADGFK	2585.9	3	3.9954	0.2102
GLQQITGHGGLR	1237.4	2	3.1956	0.3434
GLQSIFQEQGMAESVHTWQDHGYLATYTNK	3441.7	3	4.0273	0.2284
GLQTVHINENFAK	1471.6	2	3.1794	0.373
GLRKPEVGGVIR	1281.5	3	3.6521	0.2031
GLSAASPPLAETGAPR	1495.7	2	3.4193	0.2442
GLSAEPGWQAK	1144.3	2	2.8293	0.1777
GLSDIHHR	935.0	2	2.4353	0.1422
GLSEDTTEETLKESFDGSVR	2201.3	2	4.8688	0.4784
GLSGLELDGMAELMAGLMQGVDHGVAR	2729.2	3	4.1415	0.3732
GLSGTAVLDLR	1102.3	2	2.9031	0.2478
GLSQSALPYR	1092.2	2	2.5867	0.1934
GLSSDNKPMVNLDK	1518.7	2	3.9443	0.2496
GLSSLLYGSIPK	1235.5	2	3.8146	0.3168
GLSVREILAELTGR	1514.8	2	3.1945	0.2368
GLSYETAENPRPVGQLADRPEVK	2527.8	3	4.4791	0.3989
GLTAVSNNAGVDNFGLGLLLR	2102.4	2	5.4841	0.5199
GLTEFVEPIIQIK	1487.8	2	3.7826	0.2015
GLTEGLHGFHVHEFGDNTAGCTSAGPHFNPL	3221.5	3	4.9269	0.3437
GLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSR	3464.7	3	8.348	0.5331
GLTGSPGSPGPDGK	1227.3	2	2.5157	0.1194
GLTLIELWEGLTVDDVQK	2030.3	2	3.6678	0.2973
GLTMLDHEQVTPEDPGAQFLIR	2468.8	3	5.4032	0.4388
GLTPSQIGVILR	1254.5	2	3.0844	0.3161
GLTQADPSLDPTSTPVDNLAAEILPAELRETLLR	3619.0	3	5.1117	0.3878
GLTQKDLATK	1075.2	2	3.0796	0.2481
GLTSVINQK	960.1	2	3.0321	0.2532
GLVAVITGGASGLGLATAER	1814.1	2	6.1797	0.5838
GLVDGGEAVEAR	1173.3	2	3.9109	0.3376
GLVDKFNQGMVDTAKK	1752.0	2	3.7468	0.3209
GLVDKFPLFMAVYK	1629.0	2	4.211	0.4476

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GLVEKLTAYAMTIPFVR	1910.3	2	2.8194	0.3294
GLVEPVDVVDNADGTQTVNYVPSR	2545.7	3	5.9826	0.5281
GLVEPVNVVDNGDGTHTVTYTPSQEGPYMVSVK	3491.8	3	6.3443	0.4872
GLVGEIIKR	985.2	2	2.7314	0.1534
GLVGPELHDR	1093.2	2	2.6572	0.2217
GLVLDHGAR	938.1	2	2.4538	0.1492
GLVLGPIHK	934.2	2	2.9693	0.1798
GLVLGPIHKNQKDDVAQTDLLQIDPNFGSKEDFDSLLQSAK	4497.0	3	4.2787	0.3262
GLVMVKPGSIKPHQK	1620.0	2	3.6782	0.3245
GLVNLQSGAPKPEENPSLNIQFK	2481.8	3	4.6879	0.4057
GLVQALGLSNFNSR	1476.7	2	4.8546	0.4076
GLVREDAVLYLLEIPKGEMVTILAQSR	3015.6	3	5.0517	0.3481
GLVSSDELAKDVTGAEALLER	2174.4	2	5.0105	0.4362
GLVSTLQSATEQMAATVAGSVR	2178.5	2	5.2644	0.4975
GLVVDMDGFEEER	1496.6	2	4.1552	0.2525
GLVVDMDGFEEERK	1624.8	2	4.0542	0.4142
GLVVTDLKAESVVLEHR	1866.2	2	4.4211	0.4665
GLVYETSVLDPDEGIR	1763.9	2	4.5282	0.4723
GLYDGPVCEVSVTPK	1564.8	2	3.9035	0.4258
GLYGIKDDVFLSVPCILGQNGISDLVK	2865.3	3	4.1513	0.2782
GLYPAPLKIIDVVK	1526.9	2	2.7632	0.3104
GLYQLTINSVTTDDDAEYTVVAR	2545.7	3	3.2401	0.1355
GMAFLHTLEPLIPR	1595.9	2	3.7813	0.3569
GMAFTLQER	1053.2	2	2.813	0.1365
GMDKILLSSGR	1177.4	2	3.1965	0.2816
GMDKILLSSGRDASLMVTNDGATILK	2708.1	3	3.6631	0.2136
GMDKLIVDGR	1104.3	2	2.5362	0.1125
GMEDLIPLVNR	1257.5	2	3.0335	0.2074
GMELSVLDSLNAR	1405.6	2	3.9846	0.2203
GMENSISDASR	1167.2	2	3.4501	0.3162
GMFTAEDLR	1040.2	2	2.4202	0.1995
GMGEAVQEFVDKEEKDAIEELVK	2594.9	3	5.3106	0.3249
GMGEAVQEFVDKEEKDAIEELVKYQLEK	3256.6	3	4.2067	0.1296
GMGGAFVLVLYDEIKK	1741.1	2	4.3608	0.4001
GMGGAFVLVLYDEIKKYT	2005.4	2	4.4059	0.4387
GMGGAFVLVLYDELKK	1741.1	2	4.0383	0.3832

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GMGGAMDLVSSAK	1224.4	2	2.4708	0.141
GMGGHGYGGAGDASSGFHGGHFVHMR	2544.7	3	5.2357	0.4572
GMGGLFSVGETTAK	1355.5	2	3.8271	0.3955
GMGTVTFEQAIEAVQAISMFNGQFLFDRPMHVK	3702.3	3	3.5704	0.1675
GMLHQDHITFAMLLAR	1855.2	3	4.8796	0.3816
GMLKDNAMLEYLK	1526.8	2	4.0406	0.3949
GMLREDAVLEYLK	1537.8	3	3.3243	0.1047
GMLSAITNVVQNTGK	1533.8	2	4.253	0.443
GMNFSVVVFDTAPTGHTLR	2050.3	2	2.5393	0.2843
GMNMYLTK	958.2	2	2.6036	0.1676
GMQLMHANAQR	1257.5	2	4.0675	0.3461
GMSEEEVFTEVANLFR	1859.0	2	3.2902	0.2816
GMSLNLEPDNVGVVVFGNDK	2105.4	2	5.7305	0.5249
GMSLNLEPDNVGVVVFGNDKLIK	2459.8	2	4.5942	0.391
GMSLNLEPDNVGVVVFGNDKLIKEGDIVKR	3257.8	3	4.4	0.3494
GMSVSDLADKLSTDDLNSLIAHAHR	2667.9	3	6.8015	0.5388
GMSVSDLADKLSTDDLNSLIAHAHRR	2824.1	3	4.9154	0.3609
GMSVYGLGR	940.1	2	2.8199	0.212
GMTLVTPLQLLLFASK	1733.2	2	4.1394	0.4085
GMTPGEAEIHFLENAK	1745.0	2	3.8425	0.2149
GMTTVDDFFQGTK	1447.6	2	3.2955	0.3442
GMTVEGLKQFIAAQGSSR	1881.1	3	3.9553	0.1972
GMTYDALHVFDWIK	1697.0	2	2.8087	0.2428
GMVKEAIDSYIK	1354.6	2	3.2155	0.2498
GMVKEAIDSYIKADDPSSYMEVVQAANTSGNWEELVK	4077.5	3	4.957	0.2989
GMYDGPVFDLTTTPK	1642.9	2	4.6349	0.5005
GMYDGPVYEVPATPK	1624.8	2	4.7249	0.4502
GNAGGIQPDLLISLTAPK	1766.0	2	3.3023	0.2942
GNAHLGYSLVTHIPAGAR	1835.1	3	4.1099	0.3962
GNAMVEEGHFAAEDVK	1704.8	2	5.1258	0.4063
GNDISSGTVLSDYVGSGPPK	1951.1	2	6.4476	0.5505
GNDISSGTVLSDYVGSGPPKGTGLHR	2572.8	3	5.7776	0.4854
GNDVAFHFNPR	1274.4	2	3.2054	0.3377
GNEEAQIFRPLK	1402.6	2	2.7843	0.184
GNEEAQIFRPLKFNTTSVIK	2293.6	3	3.4908	0.2818
GNEFLFSHLWPLIEK	1831.1	2	3.6189	0.2996

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GNEIVLSAGSTPR	1301.4	2	3.463	0.3187
GNEMSEVLRDFPELTMEVDGKVESIMKR	3241.7	3	3.3703	0.1394
GNEQESMAR	1022.1	2	2.8709	0.2657
GNEQESMARLKKLMTIMDSMNDQELDSTDGAK	3589.0	3	3.236	0.1188
GNFGGSFAGSFGGAGGHAPGVAR	2036.2	2	6.1569	0.5965
GNFNYIEFTR	1261.4	2	3.5874	0.4389
GNFNYVEFTR	1247.3	2	3.2848	0.2493
GNFSSFMQKEIFEQPESVVNTMR	2707.0	3	5.0925	0.3278
GNFYIFDVLDQDGNIVSPSEIQAHLK	2921.2	3	5.9889	0.4445
GNGPLPLGGSGLMEEMSALLAR	2171.5	2	3.3577	0.3782
GNHAAFQADVSEAR	1473.5	2	3.7447	0.3178
GNHDGAVQQYIR	1358.4	2	2.7866	0.2116
GNHVIRDEEVSSADISSSSEVISQHLVSYR	3302.5	3	5.9965	0.401
GNILIPGINEAVAAVTEEEHK	2205.5	2	2.432	0.1923
GNIMLSQK	891.1	2	2.409	0.1061
GNKEDYDLSK	1169.2	2	2.9151	0.3058
GNKEPNPMVQLSIQDVTQESK	2343.6	3	4.4222	0.2749
GNLANVIR	857.0	2	2.848	0.234
GNLEVLLFTIQSK	1462.7	2	3.3943	0.2867
GNLEVVHHR	1061.2	2	2.727	0.1504
GNLGAGNGNLQGPR	1325.4	2	3.1087	0.4086
GNLGVYQETR	1137.2	2	3.229	0.3669
GNLLHFPSSQGEEEKEKLEGDHTIR	2852.1	3	3.6975	0.1198
GNNFLYTNGK	1128.2	2	3.7354	0.3923
GNNIRYFILPDSLPLDTLLVDVEPK	2843.3	3	5.1809	0.3661
GNNLSTISDTSPMKRSASVLGPKARR	2745.1	3	3.5159	0.1942
GNPTVEVDLFTSK	1407.6	2	3.9772	0.3004
GNPTVEVDLYTAK	1407.6	2	4.0877	0.2119
GNQDKDAHFPPPSK	1538.6	2	4.2122	0.3863
GNQLQEFAAMLMPHQK	1844.2	2	4.1938	0.342
GNRPVILTYHDIGLNHK	1948.2	3	3.7379	0.2678
GNRPVILTYHDIGMNHK	1966.3	3	4.1586	0.3913
GNSGQSVYSASK	1185.2	2	2.8926	0.1264
GNSIIMLEALER	1346.6	2	3.623	0.3672
GNSIIMLEALERV	1445.7	2	3.6193	0.261
GNSLQEILER	1159.3	2	3.3432	0.2351

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GNSSESIEAIREYEEEFFQNSK	2594.7	3	4.1291	0.3067
GNSTVYEWR	1112.2	2	2.9429	0.3401
GNTAAYLLYAFTR	1461.6	2	2.9854	0.3511
GNTESKTDGDDTETVPSEQSHASGK	2578.6	3	4.7099	0.348
GNTPATGTTQGK	1133.2	2	2.9891	0.453
GNTSGSHIVNHLVR	1491.6	2	4.4116	0.4731
GNVFSSPTAAGTPNKETAGLK	2048.2	2	4.3656	0.472
GNVGFVFTK	969.1	2	2.9922	0.3733
GNVGFVFTKEDLTEIR	1826.0	3	4.7076	0.4633
GNVGFVFTKEDLTEIRDMLLANK	2612.0	3	3.8178	0.3509
GNVGFVFTKEDLTEIRDMLLANKVPAAAR	3177.7	3	6.5344	0.4688
GNVYIHPTAK	1100.3	2	3.1551	0.3403
GNWDEQFDKENTEER	1897.9	2	4.5616	0.4354
GNWGHLDQVAALR	1437.6	2	3.2967	0.3697
GPAAAQGSAAAPAEPK	1394.5	2	4.6541	0.3097
GPADSLSTAAGAAELSAEGAGK	1932.0	2	3.6512	0.313
GPAGPQGPR	836.9	2	2.4817	0.1855
GPAGPSGPAGK	896.0	2	3.1342	0.2408
GPAHPGSPIDVR	1203.3	2	4.0193	0.3604
GPALTPIRDEEWGGHSPR	1976.1	3	3.4557	0.243
GPAPVLEYDYYGAYGSR	1879.0	2	3.9675	0.4368
GPAYGLSR	820.9	2	2.7507	0.3338
GPDALTLLEYTETR	1579.7	2	4.5337	0.4152
GPDFTPAFADFGR	1398.5	2	2.7241	0.1728
GPDGLTAFEATDNQAIK	1748.9	2	5.731	0.5437
GPDNSMGFGAER	1238.3	2	3.2032	0.3914
GPDWILGEIK	1128.3	2	3.0072	0.1044
GPEAGYVATPIAMVQAAMTLLSDASHLPK	2941.4	3	3.8017	0.3828
GPEEKKDCEVVMMIGLPGAGK	2189.6	3	3.7429	0.2187
GPEGHPLHEVLLEQAK	1755.0	3	3.4942	0.2759
GPESESEDHR	1143.1	2	2.799	0.2855
GPFLLGIK	845.1	2	3.0224	0.1885
GPFLVALGK	902.1	2	3.2866	0.3034
GPFPPVWNPITYLDHNNFWR	2471.8	2	3.3597	0.2826
GPFTDVVTTNLK	1292.5	2	3.921	0.346
GPGASGEQPEPGEAAAGGAAEEAR	2167.2	3	6.1596	0.5391

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GPGASVHDR	895.9	2	2.914	0.2484
GPGGSSLLIEALSNSSHK	1754.9	2	3.0682	0.3015
GPGLGSTQGQTIALPAQGLIEFR	2312.6	2	6.2938	0.5783
GPGPLGPGAPPPLLFLNK	1743.1	2	3.3188	0.2974
GPGQVPTATSALSLELQEVEPLGLPQASPSR	3131.5	3	4.8912	0.376
GPGTSFEFALAIVEALNGK	1922.2	2	6.524	0.5576
GPGTSFEFALAIVEALNGKEVAAQVK	2648.0	3	6.3423	0.5365
GPGTSFEFALAIVEALNGKEVAAQVKAPLVLKD	3384.9	3	5.0436	0.3562
GPHFNPSAIHNFYDNIGFVGPVPPKPK	2948.3	3	4.0766	0.2902
GPHHLDNSSPGPGSEAR	1715.8	2	4.1244	0.3338
GPHLVQSDGTVPFWAHAGNAIPSSDQIR	2959.2	3	5.3815	0.4566
GPIKFNVWDTAGQEK	1690.9	3	3.9934	0.2828
GPKPAFGQQHQQQPK	1676.9	2	3.6948	0.3192
GPLEHLYSLHIPNCDKHGLYNLK	2663.1	3	3.2382	0.2251
GPLEYVPSAK	1061.2	2	2.8888	0.3037
GPLEYVPSAKVEVVEER	1902.1	2	5.2515	0.3633
GPLGLTDLELAQQLQQEEYQQQQAAQPVR	3281.6	3	5.4277	0.4466
GPLKTPIAAGHPSMNLLLR	1987.4	3	4.6491	0.4985
GPLLVQDVVFTDEMAHFDR	2190.5	3	3.3766	0.3187
GPLMMYISK	1040.3	2	3.189	0.3902
GPLPAAPPVAPER	1272.5	2	3.3623	0.3571
GPLPLSSQHR	1092.2	2	3.0769	0.3789
GPLPLSSQHRGDADQASNILASFGLSAR	2867.1	3	6.0708	0.5468
GPLQSVQVFGR	1188.4	2	2.9452	0.3046
GPLQTASVSPSMPFSASLLGTLPIGAR	2657.1	2	3.0345	0.2659
GPMDSDDSHGSVLR	1473.6	2	4.1173	0.3906
GPNGESSVIHDR	1268.3	2	2.8955	0.3006
GPNGYGFHLHGEK	1413.5	2	3.754	0.3881
GPNKHTLTQIK	1237.4	2	2.6979	0.1652
GPPASSPAPAPK	1077.2	2	2.7427	0.3427
GPPLREGEELVMDEEAYVLYHR	2603.9	3	3.4322	0.1359
GPPPAPRPTSR	1133.3	2	2.4906	0.1834
GPPQEEEEEEDEEEEATKEDAEAPGIR	3044.0	3	5.541	0.4092
GPPQEEEEEEDEEEEATKEDAEAPGIRDHES	3512.4	3	5.898	0.362
GPPQQHGHHNEFDDEFEDDDPLPAIGHCK	3283.4	3	5.0443	0.3727
GPPRPRPAPAVGEAEDKENQQATSGPNQPSVR	3339.6	3	5.8945	0.3226

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GPQAQIASSGLTVEVDAPK	1869.1	2	2.4763	0.1125
GPQEVAVYVQELQK	1588.8	2	3.0992	0.1483
GPQGVEDGDRPQPSSK	1654.7	2	4.1735	0.4188
GPQLAAQNLGISLANLLLSK	2022.4	2	5.0938	0.542
GPQVQQPPPSNR	1305.4	2	2.5163	0.229
GPRASVTNDSGPRLVSIAGTRPSVR	2551.8	2	2.4724	0.1875
GPSAAGEQEPDKESGASVDEVAR	2287.3	2	2.6967	0.1791
GPSFDVQVGLHELLGHGSGK	2035.2	3	3.8405	0.3322
GPSGLGFNIVGGTDQQYVSNDSGIYVSR	2889.1	3	5.6675	0.4608
GPSGLLTYTGK	1094.2	2	3.1738	0.2262
GPSGLLVYQGK	1119.3	2	4.1003	0.2973
GPSGYGFNLHSDK	1379.5	2	3.3912	0.3123
GPSHPLDLGTSSPNTSQIHWTPYR	2649.9	3	4.6829	0.4274
GPSLNPVLDYDHGSR	1627.7	2	3.6892	0.4538
GPSSEAMHVGHLIPFIFTK	2069.4	2	2.793	0.3104
GPSSHEMR	901.0	2	2.5144	0.3023
GPSSVEDIK	932.0	2	3.0232	0.2465
GPSSVEDIKAK	1131.3	2	3.7062	0.334
GPSWDPFR	962.0	2	2.6683	0.1861
GPSWDPFRDWYPHSR	1904.0	3	4.4133	0.3393
GPTEADELMKR	1247.4	2	2.6922	0.2588
GPTLLKHPPAPAEPSSDLASK	2114.4	3	5.0405	0.4327
GPTPGQAPAGGAGAEGK	1423.5	2	3.2686	0.3021
GPVDHGVQIR	1078.2	2	3.0726	0.3223
GPVEGYEENEEFLR	1668.7	2	4.0481	0.5025
GPVGLEGLLTTK	1185.4	2	3.2146	0.3414
GPVGTVSEAQLAR	1285.4	2	2.8269	0.2881
GPVKPTGGPGGGGTQTQQQMNQLK	2367.6	3	4.8428	0.3147
GPVRAPAEKPR	1178.4	2	2.8482	0.2241
GPVREGDVLTLLESER	1771.0	3	5.0422	0.3581
GPVREGDVLTLLESEREAR	2127.3	3	4.9224	0.3326
GPVSGTEPEPVYSMEAADYR	2156.3	2	4.5804	0.4913
GPVYIGELPQDFLR	1604.8	2	4.5216	0.4077
GQAAQPEPSTGFTATPPAPDSPQEPLVLR	2961.2	3	4.2651	0.4126
GQAAVQQLQAEGLSPR	1653.8	2	5.1627	0.4063
GQAGGKLHIIEVGTPPTGNQPFPK	2444.8	3	4.3693	0.1635

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GQAVDYEGSR	1082.1	2	2.6087	0.1813
GQAVDYEGSRTQEEIVAK	1981.1	2	4.8627	0.3072
GQDEASAGGIWGFIK	1536.7	2	3.7675	0.4117
GQDIRIPTPVIHTK	1575.8	3	3.3269	0.2716
GQDIRIPTPVIHTKH	1713.0	3	4.5827	0.4602
GQDMETEAHQNKLEEMINELAVAMTAVK	3132.5	3	5.1338	0.3972
GQEEAGAGGR	931.9	2	2.4505	0.1943
GQESAGIVTSDGSSVPTFK	1868.0	2	3.6572	0.3975
GQESFKKQEK	1209.3	2	3.3666	0.1952
GQETSTNPIASIFAWTR	1880.1	2	5.1437	0.4772
GQFETYLRDCPDPCIGW	2001.2	3	3.2356	0.2221
GQFSTDELVAEVEKR	1708.9	2	4.4068	0.5102
GQGPGEVDPK	984.0	2	2.4914	0.122
GQGSSPVAMQK	1090.2	2	2.8866	0.2018
GQGVYLGMPGCLPVYDALAGEFIR	2527.9	3	3.8571	0.2637
GQHEPSKPPPAGETVTGGFGAK	2150.3	3	3.5921	0.224
GQHLGEQLGFEFFETSAK	2026.2	2	6.0687	0.5038
GQHLSDAFAQVNPLK	1625.8	2	4.9902	0.5084
GQHVPGSPFQFTVGPLGEGGAHK	2305.5	3	3.2405	0.2408
GQHVTGSPFQFTVGPLGEGGAHK	2309.5	3	5.6355	0.4888
GQKAPAQKAPAPK	1292.5	2	3.3919	0.2596
GQKIPIFSAAGLPHNEIAAQICR	2435.8	3	5.0988	0.4264
GQKLGDLEER	1145.2	2	2.9928	0.1839
GQKVLDSGAPIKIPVGPETLGR	2233.6	3	4.9472	0.4054
GQLEALQVDGGR	1243.4	2	4.1982	0.3515
GQLEANLLQVLEKVEEFR	2116.4	2	3.4938	0.3523
GQLEQITGK	974.1	2	2.9815	0.1663
GQLGNWMSPADFQR	1607.8	2	4.1975	0.4565
GQLKQWLDLHLHQEIPTSLLILSR	2840.3	3	3.3827	0.2324
GQLLAEQLGFDFFEASAK	1972.2	2	6.5321	0.4845
GQLPDYTSPVVLPYSR	1793.0	2	3.5378	0.3314
GQLTTDQVFPYPSVLNEEQTQFLK	2784.1	3	5.9681	0.483
GQLTTDQVFPYPSVLNEEQTQFLKELVEPVSR	3694.1	3	5.3419	0.4094
GQLVPLETVLDMLR	1584.9	2	4.4077	0.4712
GQLVPLETVLDMLRDAMVAK	2200.7	2	3.0299	0.2831
GQMQKPFEDASFALR	1726.0	2	4.0222	0.4042

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GQNDLMGTAEDFADQFLR	2029.2	2	5.7264	0.5876
GQNLLLTNLQTIQGILER	2025.3	2	5.6632	0.5045
GQNSLALHK	968.1	2	2.8668	0.2043
GQPDEELKPK	1141.3	2	2.8884	0.1987
GQPDLPEGSLPIATVEELTDTFYYR	2813.1	3	3.338	0.1928
GQPDVVVKEDEEYK	1635.8	2	3.5544	0.2397
GQPDVVVKEDEEYKR	1791.9	2	4.8587	0.4219
GQPDVVVKEDEEYKRVDFSKVPK	2693.0	3	4.5321	0.3495
GQPFWLTLHFEGR	1588.8	2	3.8844	0.336
GQPIYIQFSNHK	1432.6	2	3.5881	0.326
GQPIYIQFSNHKELK	1803.1	2	3.8928	0.1994
GQPLGPAGVQVSLR	1379.6	2	3.5294	0.3618
GQPLQAAVEKDSLR	1512.7	2	3.0858	0.2163
GQQLVMMPNKHNVEVLGILSDDVETDTVAPGENLK	3793.3	3	6.0149	0.4129
GQQVFLKDIWPTRDEIQAVER	2529.8	3	3.6699	0.2735
GQREEVEQMK	1234.4	2	2.5876	0.1481
GQRGFSQEELETCMINQAPGCPDYSILSFMGAFHGR	3979.5	3	4.6841	0.3023
GQRPETLHER	1223.3	2	2.4127	0.173
GQSEDPGSLLSLFR	1506.6	2	4.4001	0.4576
GQSEEIQK	919.0	2	2.5126	0.1074
GQSLAVKSFSR	1180.3	2	2.43	0.1607
GQTEGKIPELLASGMVDNMTK	2220.6	3	4.7875	0.4117
GQTEGKIPELLASGMVDNMTKLVLVNAIYFK	3382.0	3	6.0254	0.4949
GQTHTLEDFQR	1332.4	3	3.8138	0.4349
GQTLVVQFTVK	1220.4	2	3.4759	0.3385
GQTNVGQDGR	1032.1	2	2.6355	0.204
GQVAKLEAALGEAK	1385.6	2	3.293	0.1605
GQVFDVGPR	975.1	2	2.8025	0.2153
GQVGGQVSVEVDSAPGTDLAK	2015.2	2	5.6184	0.5068
GQVLNSDELQELYEGLR	1964.1	2	5.3783	0.528
GQVLNSDELQELYEGLRLNNMNKYDYVLTGYTR	3911.3	3	4.4187	0.155
GQVPENEANVVITTLK	1712.9	2	3.4244	0.2948
GQVPPLVTTNFLVK	1513.8	2	2.7758	0.4211
GQVQEVGWHDVAGWLGR	1895.1	2	5.7468	0.5328
GQVVGFISQEPVLFGTTIMENIR	2536.9	3	3.9022	0.2298
GQVWINGFNLGR	1361.5	2	2.5836	0.1092

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GQYFGELALVTNKPR	1693.9	2	3.2325	0.34
GQYISPFHDIPIYADKDVFHMVVEVPR	3174.6	3	7.2813	0.5506
GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	3465.8	3	5.7983	0.4103
GRAEGSEKEESR	1335.4	2	3.1721	0.1874
GRAEVLISTVGPEDCVVPFLTRPK	2585.0	3	3.8069	0.3495
GRAQADLALEK	1172.3	2	3.0762	0.2221
GRASSHSSQTQGGGSVTK	1732.8	2	5.0591	0.3254
GRDEVSKNQALK	1345.5	2	2.9157	0.1554
GRDIVVLGVEK	1185.4	2	3.0702	0.2944
GRDKYEPAAVSEQGDKK	1879.0	2	4.7512	0.4111
GRDPALPTLLNPK	1392.6	2	2.8952	0.2143
GRDWNVDLIPK	1313.5	2	2.5278	0.1649
GREEESDQIR	1219.2	2	3.189	0.1494
GREEYEGPNKKPR	1560.7	2	4.2322	0.2989
GREFGNLTR	1050.2	2	3.1802	0.2066
GREGPVQFEEDPFGLDKFLEEAK	2638.9	3	3.5839	0.1817
GRELPTAFDYVEFTR	1802.0	2	5.0853	0.4506
GREMFEVTGLHDVDQGWMR	2264.5	3	4.0173	0.2481
GRENYSSYSSFSSPHMKPAPVGSR	2629.8	3	4.2111	0.2565
GRFEELSAWTEK	1453.6	2	3.0667	0.2297
GRFQDNLDFIQWFK	1815.0	2	3.4494	0.2954
GRGDASGLKR	1017.1	2	2.523	0.1762
GRGELVTHFLTTDVDSLSYLKK	2480.8	3	3.8509	0.3019
GRGFGSEEGSR	1139.2	2	2.6778	0.2777
GRGLEYLYLNVHDEDRDDQTR	2565.7	3	3.934	0.2219
GRHLVLLDTAQAAAAGHR	1858.1	3	5.1765	0.4378
GRHVVLGAIENKVESK	1737.0	3	4.0682	0.2785
GRKPGSVVAAAAAEAK	1483.7	2	4.3486	0.3739
GRLDNGQVGLYPANYVEAIQ	2178.4	2	5.1334	0.4515
GRLDYLSSLK	1152.3	2	2.9987	0.296
GRLGEEDAGAR	1131.2	2	2.4939	0.1694
GRLHPDLQSNLLQVDSEFTEEEIEFLEAR	3416.7	3	6.0805	0.3604
GRLNVLANVIR	1225.5	2	2.8849	0.2112
GRLPLLLVANAGTAAVGHTDK	2075.4	3	4.9073	0.4402
GRLPLLLVANAGTAAVGHTDKIGR	2401.8	3	4.3562	0.209
GRLVQTQR	958.1	2	2.468	0.132

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GRLYPWGVVEVENPEHNDFLK	2499.8	3	6.0636	0.3154
GRPAPGFHHGDGPGNAVQEIMIPASK	2641.9	3	4.931	0.3766
GRPDSLLAYLEQAGASPHR	2039.2	2	3.4981	0.2879
GRPEPLDLHLGMFLPTLLHQATAEQQER	3199.6	3	6.1973	0.4581
GRPGAPGPAGAR	1064.2	2	2.486	0.2295
GRPGLPGAAGAR	1080.2	2	2.8016	0.3661
GRPGPIGVLLMK	1238.6	2	2.7759	0.1982
GRPGPVAGHHQMPR	1497.7	3	3.9251	0.3765
GRPLAEESEQER	1401.5	2	4.2797	0.4363
GRPPKPLGGGTPK	1262.5	2	2.8129	0.2731
GRPTSTNPIASIFAWTR	1876.1	3	4.6454	0.5184
GRPVPMMIPDELAPTYSLDTR	2360.7	3	4.1044	0.1483
GRPYDYNGPR	1195.3	2	2.6987	0.2795
GRQLADHLGFEFFEASAK	2024.2	3	4.0261	0.3469
GRQNISPDKIPWSALK	1811.1	3	4.0165	0.2539
GRQQNPVVNNHIGGK	1618.8	2	3.582	0.2847
GRRAEDGSVIDYELIDQDAR	2279.4	3	3.8399	0.2223
GRRAEDGSVIDYELIDQDARDLYDAGVK	3141.4	3	4.8764	0.3385
GRRDFPEEVAIVEELGR	1973.2	3	5.2589	0.4474
GRRDFPEEVAIVEELGRR	2129.4	3	5.26	0.3329
GRSEADSDKNATILELR	1876.0	3	3.3821	0.1599
GRSLHPVIYHLGQLALLGKSSHLTACGGRGKRSLD	3700.3	3	3.8647	0.1204
GRTAAEDNVR	1089.1	2	2.5933	0.1821
GRVEVLYR	992.2	2	2.6473	0.2603
GRVNFDDYTVNLGGLKDHIK	2262.5	3	4.925	0.3595
GRVPEMADLHR	1281.5	2	2.6752	0.2144
GRVSIAELAQASNSLIAWGR	2100.4	2	2.703	0.3148
GSAADSEESPAIEAIHLLR	1967.1	2	4.5251	0.4812
GSAADSEESPAIEAIHLLRK	2095.3	2	3.7501	0.4248
GSAFSTSISKQETELSPEMISSGSWR	2804.0	3	4.4652	0.2525
GSAITGPVAK	901.0	2	3.0653	0.1432
GSAKELLQHPFLK	1468.7	2	3.9207	0.164
GSAKELLQHQFLK	1499.7	3	3.2755	0.2048
GSAPPGPVPEGSIR	1321.5	2	2.5496	0.3467
GSASMVQK	807.9	2	2.8093	0.138
GSATKDFSVFFQK	1462.6	2	3.6118	0.3206

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GSCSTEVEKETQEK	1555.6	2	3.8925	0.3595
GSDALSETSSVSHIEDLEKVER	2389.5	3	4.2963	0.2707
GSDEPPVFLEIHYK	1631.8	2	3.7994	0.4221
GSDEPPVFLEIHYKGSPNANEPPLVFVGK	3139.5	3	4.5609	0.2843
GSDHSASLEPGELAELVR	1868.0	3	5.4076	0.4884
GSDSPAADVEIEYVTEEPEIYEPNFIFFK	3337.6	3	3.9384	0.2335
GSDSPAADVEIEYVTEEPEIYEPNFIFFKR	3493.8	3	4.5069	0.4461
GSDVIIMLVGNKTDLADKR	2046.4	3	4.1254	0.3334
GSDWLGDQDAIHYMTEQAPAAVVELENYGMPFSR	3800.1	3	4.7006	0.3975
GSEGKPSLTLPASAPGPEEALTTVTVAPAPR	3003.4	3	3.6858	0.1362
GSEGLYMVNGPPHFTESTVFPR	2423.7	3	3.4059	0.1185
GSEIEDLVLLDEESRPVNLPPALKHPQELL	3352.8	3	3.4622	0.1033
GSEIPKHMLADVFSVK	1759.1	3	3.4075	0.3571
GSEKSDDNSYDEK	1474.4	2	3.6926	0.3548
GSELEITLTR	1119.3	2	3.0876	0.1743
GSELSERIESFVETLKR	1981.2	3	3.9232	0.2834
GSELWLGVDALGLNIYEQNDR	2363.6	2	2.6044	0.2455
GSEQESVKEFLAK	1452.6	2	3.3666	0.1914
GSETDSAQDQPVKMNSLPAER	2261.4	3	3.3875	0.2955
GSFGAMDDPFKNK	1414.6	2	2.8775	0.1881
GSFLDKISPSVLR	1419.7	2	2.7254	0.1132
GSFMGSDEVFTYFYK	1779.0	2	3.1715	0.2724
GSFRYAWVLDK	1342.5	3	4.5491	0.2997
GSFSDEMNTILDNLAAR	1855.0	2	4.8718	0.3869
GSFSDTGLGDGK	1141.2	2	3.3318	0.3794
GSFSEQGINEFLR	1484.6	2	4.4033	0.4036
GSFSEQGINEFLRELSFGR	2174.4	3	3.2619	0.3403
GSFTSSSNFMSIR	1421.6	2	2.4663	0.1709
GSFVNGVFEVHKK	1448.7	2	2.7333	0.3068
GSGDGEMGKPR	1091.2	2	2.7096	0.4054
GSGDPSSSSSSGNPLVYLDVDANGKPLGR	2835.0	3	4.1887	0.4048
GSGGGGGGGGQGSTNYGK	1455.4	2	3.9085	0.3088
GSGIFDESTPVQTR	1494.6	2	3.562	0.3163
GSGKGEEVEAGAAK	1290.4	2	3.1978	0.1168
GSGNLEAIHIIK	1252.4	2	3.0005	0.1707
GSGNLEAIHIIKK	1380.6	2	3.2633	0.163

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GSGSSFEQSFNFNFDDLFK	2174.3	2	2.9785	0.2811
GSGTAEVELK	991.1	2	3.4914	0.278
GSGTAEVELKK	1119.3	2	3.4012	0.2609
GSGTAEVELKKGATLK	1589.8	2	4.6512	0.309
GSGVAQSPQQPPPQQQQQPPQQPTPPK	2990.2	3	4.15	0.4385
GSHFFPGNNVIYEK	1609.8	2	4.0503	0.408
GSHLVEALYLVCGER	1646.9	2	5.1408	0.5302
GSIDEVDKR	1019.1	2	2.4056	0.216
GSIFVVFDSIESAK	1499.7	2	3.9198	0.3767
GSIFVVFDSIESAKK	1627.9	2	3.1305	0.3512
GSIHDFPGFDPNQDAEALYTAMK	2525.7	3	5.5836	0.5012
GSIHDFPGFDPNQDAEALYTAMKGFGSDKEAILDIITSR	4229.6	3	3.2994	0.2846
GSILDAMRPQQLHATEITSSGFR	2516.8	3	3.5254	0.156
GSILDPSPEAAVVGGNVLTSQR	2168.4	2	2.8505	0.3521
GSITISAEEIKDNR	1533.7	2	3.5802	0.3363
GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	3717.1	3	6.0402	0.5042
GSIVWQEVFDDKAK	1622.8	2	3.5302	0.3085
GSKEPSTKEPSTHIPPLDSK	2136.3	3	3.9742	0.3723
GSKGGHGAASPSEK	1270.3	2	3.2005	0.301
GSKPVRPPAPGHGFPLIK	1856.2	2	2.563	0.1797
GSKSPDLLMYQGPPDTAEIIK	2261.6	2	5.2608	0.378
GSLAADKVVEEIR	1387.6	2	4.2137	0.3617
GSLAADKVVEEIRR	1543.8	2	3.9793	0.2783
GSLAAVAHAQSLVEAQPNVDKLVEDHLAVQSLIR	3581.0	3	8.9084	0.6005
GSLAEAVGSPPPAATPTPTPPTR	2173.4	3	4.5371	0.3591
GSLASLDSLR	1019.1	2	2.8395	0.207
GSLASLDSLRK	1147.3	2	2.4895	0.1922
GSLGATGEIKGPTVGGGLPGIGVQGLEGNLQMPGIK	3361.9	3	3.3901	0.1397
GSLLEDVVPPIKPPKEIEDPNDKKPEEWDER	3601.0	3	4.057	0.2417
GSLLIDSSTIDPAVSKELAKEVEK	2530.9	3	4.4354	0.4174
GSLLIDSSTIDPAVSKELAKEVEKMGAVFMDAPVSGGVGAAR	4205.8	3	4.8333	0.3314
GSLLWNQQDGTLSLSQR	1904.1	2	5.1975	0.4528
GSLQILDQLLLPK	1438.7	2	3.6455	0.1674
GSLTFEPLTLVPIQTK	1745.1	2	5.0963	0.3979
GSLVKDSQYEMDSEFEGELADDLAGFYR	3173.4	3	4.8495	0.3455
GSMAGSTGVHDTVVNQLLSK	2002.2	2	3.1718	0.2873

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GSMYMQQQQPLLSTQDFNMAADIDPQNADVYHHR	3952.3	3	5.333	0.3595
GSNIKHTEAEIAAACETFLK	2134.4	3	4.1522	0.2924
GSNMDFREPTEEER	1697.8	2	2.7699	0.1586
GSNNVALGYDEGSIIVK	1736.9	2	3.6989	0.2495
GSNPHLQTFTFTR	1506.6	2	3.7108	0.3755
GSNTTSHLHQAVAK	1451.6	2	4.3623	0.4379
GSNVLGPKSVAHIAKRKK	1891.3	2	2.4914	0.2099
GSPAINVAVHVFR	1367.6	2	4.3701	0.4548
GSPAINVAVHVFRK	1495.8	2	4.7222	0.4526
GSPAPAVLAEEAR	1268.4	2	2.5691	0.1026
GSPFPEVAESVQQELESYR	2153.3	2	4.2392	0.4811
GSPFQVTRGDYAPILQK	1878.1	3	4.0232	0.3236
GSPLGEVVEQGITR	1442.6	2	3.191	0.2212
GSPLNAAPYGIESMSQDTEVR	2223.4	2	3.2092	0.3264
GSPLVVISQGK	1085.3	2	3.7271	0.2629
GSPMEISLPIALSK	1443.7	2	3.8293	0.3769
GSPQQIDHAK	1081.2	2	3.2782	0.3198
GSPRPQAPK	938.1	2	2.6711	0.1501
GSQAQPDSPSAQLALIAASQSFLQPGGK	2756.0	3	5.9765	0.4922
GSQFTSKEER	1169.2	2	2.8449	0.3282
GSQGPLPFHEK	1197.3	2	2.5769	0.1503
GSQLGPVPVTIR	1224.4	2	2.9367	0.2604
GSQNERKKQTGLRLPEMQK	2229.6	2	2.441	0.1851
GSSAGFDRHITIFSPEGR	1935.1	3	4.2683	0.3433
GSSCFECTHYQSFLEYR	2058.2	2	4.1981	0.286
GSSCFECTHYQSFLEYREVVDGLEK	2928.2	3	3.3514	0.2346
GSSGGSGAKPSDAASEAARPATSTLNR	2504.6	3	3.6491	0.2173
GSSGPTQINQVVSHPNQPLTITAHDDR	2871.1	3	3.712	0.2329
GSSKQQSEEDLLLQDFSR	2068.2	2	5.5111	0.4307
GSSLSGTDDGAQEVVKDILEDVVTSAIKEAAEK	3363.6	3	3.9921	0.2331
GSSNHNLLAAPR	1237.4	2	3.327	0.3473
GSSNSYAIK	927.0	2	2.58	0.251
GSSVDAPPRPCHTTPDSQFGTEHVLR	2793.0	3	4.8421	0.3089
GSTAPVGGGAFPTIVER	1616.8	2	4.7188	0.4721
GSTDDKGPVAGWINALEAYQK	2221.4	3	5.073	0.5305
GSTDNLMDDIER	1366.4	2	2.9708	0.2333

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GSTDNLMDDIERAVDDGVNTFK	2413.6	2	4.5195	0.4013
GSTHPQPGVSPPAAPAAPGPK	1922.1	3	5.36	0.4945
GSTIETEQKEDKGEDSEPVTSK	2395.5	3	5.0769	0.345
GSTPYGGVKLEDLIVK	1676.9	2	4.0271	0.236
GSTPYGGVKLEDLIVKDGLTDVYNK	2683.0	3	5.9345	0.5227
GSVAGGAVYLVYDQELLGPSDK	2239.5	3	4.3451	0.2969
GSVAGGAVYLVYDQELLGPSDKSQAALQK	2966.3	3	4.5698	0.3629
GSVAYHADDGKIFHGSGVGDPFGPR	2544.7	3	3.5886	0.3165
GSVSHDTVQPR	1183.3	2	2.8174	0.3024
GSYGDLGGPIITTQVTIPK	1918.2	2	5.5381	0.4895
GSYGDLGGPIITTQVTIPKDLAGSIIGK	2773.2	3	4.7933	0.4967
GSYGDLGGPIITTQVTIPKDLAGSIIGKGGQR	3171.6	3	4.496	0.2054
GSYNPVTHIYTAQDVKEVIEYAR	2654.9	3	4.9374	0.3563
GSYNTLWTSGMQGDGEEQNKEALQDVEDENQ	3474.5	3	4.9515	0.1635
GSYSLSHVYTPNDVR	1695.8	2	4.4835	0.4528
GSYTIGRDAQADAK	1453.5	2	3.7743	0.3035
GSYVSIHSSGFR	1297.4	2	3.3375	0.3962
GSYVSIHSSGFRDFLLKPELLR	2522.9	3	3.6432	0.2022
GTADVTHDLQEMKEESR	1947.1	3	3.3888	0.2165
GTAVVNGEFKDLSLDDFK	1956.1	2	3.2213	0.3663
GTAYTFFTPGNLK	1417.6	2	4.0841	0.393
GTAYVVYEDIFDAK	1591.7	2	3.761	0.451
GTAYVVYEDIFDAKNACDHLSGFNVCNR	3123.4	3	3.4188	0.1884
GTDDSPKDSQEDLQER	1820.8	3	4.5253	0.3452
GTDLWLGVDALGLNIYEKDDKLTPK	2776.1	3	3.6247	0.1559
GTDVPKWISIMTER	1633.9	3	4.2215	0.4587
GTEAPAVVTEEEDDDEETAPPVIAPRPDHTK	3317.5	3	5.1692	0.4061
GTEDELDKYSEALKDAQEKLELAEK	2854.1	3	5.3887	0.299
GTEDELDKYSEALKDAQEKLELAEKK	2982.2	3	5.0051	0.3904
GTEDFIVESLDASFR	1686.8	2	5.3817	0.436
GTEDITSPHGIPLDLLDR	1950.1	2	3.3642	0.3357
GTEDITSPHGIPLDLLDRVMIIR	2563.0	3	3.8315	0.3226
GTEHSGSTVPSILNR	1555.7	2	4.2242	0.4338
GTEIGVLAK	888.0	2	3.1361	0.2217
GTEITHAVVIK	1168.4	2	2.6857	0.2
GTEITHAVVIKK	1296.5	2	3.8707	0.3385

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GTEVQVDDIKR	1260.4	2	3.3316	0.2678
GTEWVDPEDPTVIAENELLGAAAAIEAAAK	3053.3	3	5.7633	0.4703
GTFADKEK	896.0	1	2.1946	0.1418
GTFDNAETKKEFGPVVIDYGK	2316.6	3	3.857	0.288
GTFDNAETKKEFGPVVIDYGKVQSK	2759.1	3	4.6302	0.392
GTFESGLKGGVK	1180.3	2	2.4081	0.2531
GTGARPYTGK	1008.1	2	2.5714	0.1944
GTGASGSFK	811.9	1	1.8145	0.2354
GTGASGSFKLNK	1167.3	2	3.1588	0.2238
GTGASGSFKLNKK	1295.5	2	4.0614	0.2791
GTGGVDTAATGGVFDISNLDR	2024.1	2	5.8712	0.574
GTGGVDTAATGGVFDISNLDRLGK	2322.5	3	3.3787	0.163
GTGGVDTAAVGGVFDVSNADR	1966.1	2	5.6115	0.4991
GTGGVDTAAVGGVFDVSNADRLGFSEVELVQMVVDGVK	3797.2	3	4.9328	0.416
GTGIVSAPVPK	1026.2	2	2.985	0.3271
GTGKWTAISALEYGVPVTLIGEAVFAR	2808.2	3	4.556	0.288
GTGLDEAMEWLVETLK	1793.0	2	4.581	0.4491
GTGLQPGEEELPDIAPPLVTPDEPK	2600.9	2	3.3371	0.4726
GTGRIPDQLVILDMK	1657.0	3	4.5659	0.2957
GTGRIPDQLVILDMKHGVEAK	2278.7	3	4.9392	0.3179
GTGYIKTELISVSEVHPSR	2074.3	3	3.7405	0.2188
GTHMENVYDFYKPNLASEYPIVDGK	2889.2	3	5.1157	0.4561
GTHNFHNFTSQK	1418.5	2	3.5532	0.3503
GTHTAVSSNDR	1145.2	2	2.7946	0.3131
GTIEILSDVQLIK	1429.7	2	4.2658	0.2923
GTINFLHADCDKFR	1637.8	2	3.019	0.3508
GTIQVITQGTSLK	1346.6	2	3.6161	0.3359
GTITDAPGFDPLRDAEVLRK	2172.4	3	3.9564	0.2661
GTITIQDTGIGMTQEELVSNLGTIAR	2720.1	3	4.1179	0.2114
GTITVHKTDSSNEPPKTFTFDTVFGPESK	3169.4	3	3.6515	0.2205
GTITVSAQELKDNR	1532.7	2	3.5866	0.266
GTKALMDEVVK	1191.4	2	3.0417	0.2689
GTKNENKPYLFYFNIVK	2076.4	3	3.5458	0.2997
GTKVILHLKEDQTEYLEER	2302.6	3	3.239	0.2309
GTLDPVEKALR	1199.4	2	2.5681	0.1425
GTLGGLFSQILQGEDIVR	1904.2	2	5.5909	0.4338

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GTLGGMFGMLK	1112.4	2	3.1519	0.4007
GTLKGHNGWVTQIATTPQFPDMILSASR	3028.4	3	5.1185	0.1868
GTLKPDSTHSNEFDSDVDVGDLQMVK	2836.0	3	4.9975	0.3827
GTLLAFAEAR	1049.2	2	3.4804	0.1386
GTLQSYLD	897.0	1	1.9771	0.1371
GTLSDEHAGVISVLAQQAAK	1996.2	3	4.3146	0.1213
GTLSGWILSK	1062.2	2	3.6269	0.2669
GTLVQTK	746.9	1	1.7997	0.1358
GTMTTGHNVADLVVILK	1770.1	2	3.8243	0.3551
GTMVTIEGPR	1061.2	2	2.8677	0.2913
GTNDMKQQHVIETLIGK	1913.2	3	3.4507	0.2547
GTNVNQLNYR	1179.3	2	2.7937	0.1612
GTPGPPPAHGAALQPHPR	1759.0	2	4.3463	0.4772
GTPMKPNTQATPP	1340.5	2	2.4945	0.1441
GTPSQSPVVGR	1085.2	2	2.5744	0.2821
GTPSSLLVSTAPHHR	1560.7	2	3.5857	0.4338
GTQGAEEVLR	1060.1	2	3.0479	0.1407
GTQGAEEVLRAHEEQLKEAQAVPATLPELEATK	3545.9	3	5.0627	0.3051
GTQGAEEVLRAHEEQLKEAQAVPATLPELEATKASLK	3945.4	3	4.1804	0.319
GTQGATAGASSELDASK	1551.6	2	5.0951	0.457
GTQGVVTNFEIFR	1468.6	2	3.8452	0.4071
GTRPFVISR	1033.2	2	2.6452	0.1723
GTSAEQDNRFSNK	1454.5	2	3.378	0.2667
GTSFDAAATSGGSASSEK	1631.6	2	4.1463	0.2934
GTSFDAAATSGGSASSEKASSTSPVEISEWLDQK	3390.5	3	6.6923	0.4978
GTSFDAAATSGGSASSEKASSTSPVEISEWLDQKLTK	3733.0	3	5.2623	0.379
GTSKEDAMK	967.1	2	2.4933	0.3076
GTSQLHGMDLLVLLDLIGAPNPTFPNFFPNSAR	3555.1	3	4.7739	0.3435
GTSYQSPHGIPIDLLDRLLIVSTTPYSEKDTK	3547.0	3	4.1203	0.2449
GTTITLVLKEEASDYLELDTIK	2453.8	2	4.407	0.395
GTVAYVGATLFATGK	1456.7	2	3.4997	0.3252
GTVEPQLEAR	1100.2	2	2.9961	0.162
GTVGFSGAELENLVNQAALK	2019.2	2	3.1202	0.2025
GTVIKVPLKVEQANNAR	1838.1	3	3.4778	0.3336
GTVLDQVPVNPSLYLIK	1857.2	2	3.4744	0.1117
GTVPDDAVEALADSLGKK	1787.0	2	2.7651	0.3442

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GTVQALHATGAR	1182.3	2	3.3938	0.3447
GTVRDYPDFSPSVDAEAIQK	2196.4	2	5.7315	0.3769
GTVRPANDFNPDADAK	1688.8	2	3.846	0.3479
GTVTDFPGFDER	1341.4	2	4.0639	0.4878
GTVTDFPGFDERADAETLR	2098.2	2	3.0421	0.22
GTVTDFPGFDERADAETLRK	2226.4	2	2.8373	0.2424
GTVVMKDGK	935.1	2	2.4662	0.2645
GTVVTGTLER	1033.2	2	2.7315	0.2191
GTWIHPEIDNPEYSPDPSIYAYDNFGVLGLDLWQVK	4151.5	3	4.4003	0.3203
GTYLATFHQR	1194.3	2	2.6956	0.2211
GVAALTSDPAVQAIVLDTASDVLDK	2470.8	2	6.4871	0.4917
GVAALTSDPAVQAIVLDTASDVLDKASSLIEEAK	3399.8	3	4.7374	0.3552
GVAALTSDPAVQAIVLDTASDVLDKASSLIEEAKK	3528.0	3	4.4316	0.2733
GVAASAGSSGENKK	1263.3	2	3.385	0.3351
GVAGAHGLLCLLSDHVDKR	1962.3	2	4.6787	0.5526
GVAGALRPLVQATVPATPEQPVLDLK	2642.1	3	4.1338	0.2416
GVAGALRPLVQATVPATPEQPVLDLKRPFLSR	3399.0	3	3.7443	0.2582
GVAGLRDGKEVTPVSSIPVETHR	2405.7	3	4.4919	0.3304
GVAINFVKNDDIR	1461.6	2	2.5612	0.1647
GVAINFVTEEDKR	1478.6	2	3.3477	0.366
GVAINMVTEEDKR	1462.7	2	3.5002	0.3485
GVALLRPEPLHR	1358.6	2	2.6899	0.3331
GVAVDYLPER	1119.3	2	2.7844	0.1133
GVAVKVEEPR	1084.3	2	3.0542	0.2326
GVDDLDFFIGDEAIEKPTYATK	2445.7	2	5.1117	0.4575
GVDEATIIDILTK	1388.6	2	4.0144	0.2888
GVDEGPNGLKLISEVIGER	1983.2	2	4.7745	0.3885
GVDEVTIVNILTNR	1543.7	3	5.1986	0.4132
GVDIVMDPLGGSDTAK	1575.8	2	5.1497	0.5394
GVDIVMDPLGGSDTAKGYNLLKPMGK	2678.1	2	4.5615	0.4896
GVDLDQLLDMSYEQLMQLYSAR	2589.9	2	5.5963	0.4595
GVDLFESFFPYQVTER	1935.1	2	3.615	0.1822
GVDLHEQSQQNK	1383.4	2	2.9587	0.2092
GVDLQENNPASR	1300.4	2	2.7845	0.1633
GVDLSGNDFKGGYFPENVK	2044.2	2	4.0973	0.3121
GVDNTFADELVELSTALEHQEYITFLEDLK	3441.7	3	4.722	0.3698

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GVDNTFADELVELSTALEHQEYITFLEDLKSFVK	3903.3	3	6.6586	0.5173
GVEAGPDLLQ	999.1	2	2.9154	0.1517
GVEEEEEDGEMRE	1538.5	2	4.5295	0.3601
GVEGLIDIENPNR	1426.6	2	3.5833	0.1209
GVEHGPAAIR	1007.1	2	2.7155	0.2518
GVEKPPHLAALILAR	1585.9	3	5.2579	0.4569
GVENVYTQHQPFLHETLDHLIK	2619.9	3	4.0627	0.3368
GVEPSPSPIKPGDIKR	1677.9	2	2.8449	0.3245
GVETIANDVVSLATK	1517.7	2	4.208	0.4003
GVEVTVGHEQEEGGKWPYAGTAEAIK	2744.0	2	5.5919	0.4278
GVFHQTVSR	1031.2	2	2.6964	0.1959
GVFVQSVLPYFVATK	1656.0	2	3.7307	0.2525
GVGAAATAVTQALNELLQHVK	2092.4	3	6.0208	0.5264
GVGASGSFR	837.9	2	2.8743	0.2052
GVGDDQLGEESEERDDHLLPM	2342.4	2	3.1419	0.3915
GVGGSQPPDIDKTELVEPTEYLVVHLK	2922.3	3	5.5024	0.3689
GVGIISEGNETVEDIAAR	1831.0	2	5.3818	0.4722
GVGIISEGNETVEDIAARLNIPVSQVNPR	3049.4	3	4.8585	0.4202
GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGK	4336.9	3	6.1413	0.4771
GVGPVKENDEIEAGIHGLVSMTFK	2528.9	3	5.373	0.4452
GVGPVKENDEIEAGIHGLVSMTFKVEKPEY	3274.7	3	4.215	0.261
GVHFIFNKENF	1352.5	2	2.6676	0.3036
GVHKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASR	4079.4	3	6.586	0.5065
GVIDMGNSLIER	1304.5	2	3.1321	0.3258
GVIFGQTSSTFTFADLAK	1891.1	2	2.6938	0.2146
GVIINTASVAAFEGQVGQAAYSASK	2440.7	3	5.9681	0.5596
GVIKDKYGKDATNVGDEGGFAPNILENSEALELVK	3693.1	3	5.1886	0.4092
GVIKDKYGKDATNVGDEGGFAPNILENSEALELVKEAIDK	4249.7	3	5.3332	0.4589
GVIKDKYGKDATNVGDEGGFAPNILENSEALELVKEAIDKAGYTEK	4899.4	3	3.2928	0.239
GVILREMQEVETNLQEVVFDYLHATAYQNTALGR	3910.4	3	6.8689	0.5048
GVINIIPGSGGIAGQR	1509.7	2	3.8608	0.3796
GVIPNSFDHIFTHISR	1841.1	2	3.1512	0.3774
GVIPSSLFLQDDEDDDELAGK	2264.4	2	5.201	0.412
GVIPSSLFLQDDEDDDELAGKSPEDLPLR	3172.4	3	3.3107	0.3226
GVITVKDGK	917.1	2	2.5436	0.2386
GVIVDKDFSHPQMPK	1699.0	2	5.0504	0.3693

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GVKEIDIAATLEHVR	1651.9	3	5.0125	0.3692
GVLETFSGTETNKIWPYVYAFLQTK	2894.3	3	4.7829	0.3264
GVLFASGQNLAR	1233.4	2	2.8672	0.2258
GVLFGVPGAFTPGCSK	1537.8	2	3.3038	0.3025
GVLHQVMVLDSEALR	1668.0	2	3.5886	0.3568
GVLKEWTLMLHGTQSAPYIDQVVR	2743.2	3	5.7509	0.472
GVLKVFLENVIR	1387.7	2	3.6475	0.3131
GVLKVFLENVIRDAVTYTEHAK	2503.9	3	5.1325	0.4559
GVLLDIDDLQTNQFK	1719.9	2	4.9944	0.3921
GVLLYGPPGTGK	1159.4	2	3.2441	0.3118
GVLSTHQNIR	1125.3	2	2.4522	0.133
GVLTGPEYEALDALPDAER	2017.2	2	4.0043	0.3176
GVLTTEKQNFLLFDMTTHPLTNNNIK	2991.4	3	5.0693	0.3565
GVMGGQSAGPQHTEAETIQK	2027.2	2	4.6067	0.4072
GVMINKDVTHPR	1367.6	2	3.6198	0.3881
GVMLAVDAVIAELK	1429.8	2	5.1631	0.3706
GVMLAVDAVIAELKK	1557.9	2	5.2283	0.4643
GVNADKVGIEAAEMLLANLR	2085.4	2	5.5057	0.4864
GVNAIVYMIDAADREK	1766.0	2	4.2778	0.3344
GVNASAQK	774.8	1	1.8826	0.1296
GVNIGGAGSYIYEKPLAEGPQVTGPIEVPAAR	3212.6	3	8.1797	0.5829
GVNIGGAGSYIYEKPLAEGPQVTGPIEVPAARAEER	3698.1	3	4.8383	0.365
GVNLPGAAVDLPAVSEK	1637.9	2	5.5587	0.468
GVNLPGAAVDLPAVSEKDIQDLK	2350.7	2	5.1087	0.4937
GVNLPGAAVDLPAVSEKDIQDLKFGVEQDVDMVFASFIR	4192.7	3	5.3934	0.5545
GVNLPGAAVDLPAVSEKDIQDLKFGVEQDVDMVFASFIRK	4320.9	3	6.139	0.556
GVNLQEFLNVTSVHLFK	1946.2	2	3.2347	0.3405
GVNTFSPEGR	1064.1	2	2.4949	0.1663
GVNTGAVGSYIYDRDPEGK	1999.1	2	4.4727	0.4509
GVNTGAVGSYIYDRDPEGKVQP	2323.5	3	3.938	0.1897
GVNVSALSR	903.0	2	3.1849	0.2099
GVNWAAFHPTMPLIVSGADDR	2255.5	2	4.942	0.435
GVPAGNSDTEGGQPGR	1499.5	2	3.5637	0.4342
GVPESLASGEGAGAGLPALDLAK	2081.3	2	5.9354	0.4636
GVPLVYEAFNWR	1451.7	2	2.5002	0.3481
GVPQIEVTFDIDANGIVHVSAK	2310.6	2	3.5772	0.3925

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GVPQIEVTFEIDVNGILR	2000.3	2	4.3417	0.4418
GVPTGFILPIR	1170.4	2	2.5322	0.2003
GVPVLHLIPSPFPEVWHTMDDNEENLDESTIDNLNK	4117.5	3	4.5202	0.3402
GVPYRPTDLFDELVAHEVAR	2285.5	3	4.1762	0.1687
GVQGIIVVNTEGIPIK	1637.9	2	3.3673	0.3045
GVQGPPGPAGPR	1090.2	2	3.1469	0.1824
GVQKHQDDLQDVIGR	1708.9	2	3.3208	0.1252
GVQLQTHPNVDK	1336.5	2	3.4352	0.3009
GVQLQTHPNVDKK	1464.7	2	3.7295	0.3101
GVQPLLDAVLEYLPNPSEVQNYAILNKEDDSKEK	3831.2	3	5.2267	0.3635
GVQVETISPGDGR	1315.4	2	3.7995	0.301
GVQVETISPGDGRTFPK	1789.0	2	3.5779	0.203
GVQYLNEIKDSVVAGFQWATK	2354.6	2	5.3854	0.4568
GVRPVSFSDWEKLDAEEVAR	2291.5	3	3.9489	0.2136
GVSFYEVPPHLFAVADTVYR	2268.6	2	2.4072	0.1111
GVSKAVEHINK	1182.4	2	3.0644	0.1807
GVSQMPLR	888.1	2	2.4278	0.1769
GVSSESSGDREK	1238.2	2	2.8706	0.3052
GVSSPDHIFLPIPNWEHKENPETEEDVGPVVQHIYELR	4409.8	3	4.9678	0.3262
GVSSQETAGIGASAHLVNFK	1974.2	2	5.3014	0.3123
GVTDHTQR	914.0	2	2.4274	0.1535
GVTDVVITREEAER	1574.7	2	2.7414	0.1235
GVTFLFPIQAK	1221.5	2	3.2452	0.2728
GVTFNVTTVDTK	1282.4	2	2.7379	0.2557
GVTHNIALLR	1094.3	2	3.0454	0.2064
GVTHTVPIYEGYALPHAILR	2208.5	3	5.7182	0.439
GVTIASGGVLPNIHPELLAK	1987.3	2	5.7385	0.53
GVTIASGGVLPNIHPELLAKK	2115.5	2	5.4275	0.4657
GVTIASGGVLPR	1127.3	2	3.5495	0.2918
GVTIGIMDDGIDYLHPDLASNYNAEASYDFSSNDPYPYPR	4455.7	3	5.235	0.4158
GVTIIGPATVGGIKPGCFK	1816.2	2	3.4584	0.2849
GVTIPYRPKPSSSPVIFAGGQDR	2430.7	3	4.2666	0.4042
GVTSEEFDKFLEER	1686.8	2	3.538	0.2964
GVTSVSQIFHSPDLAIR	1828.1	2	3.4251	0.2454
GVTVGEGVR	874.0	2	2.6712	0.1737
GVVDEQANSAALKEQLK	1801.0	2	4.2167	0.1622

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GVVDSDDLPLNVSR	1486.6	2	4.9417	0.4375
GVVDSEDIPLNLSR	1514.7	2	4.7411	0.3466
GVVDSEDLPLNISR	1514.7	1	4.542	0.3822
GVVEVTHDLQK	1225.4	2	3.6319	0.1952
GVVEVTHDLQKHLAGLGLTEAIDKNKADLSR	3329.8	3	4.9648	0.4569
GVVFDVTSGKEFYGR	1661.8	2	3.966	0.4793
GVVGGVTGIITKPVEGAK	1683.0	2	4.1652	0.4275
GVVGPGPAAIAALGGGGAGPPVVGGGGGR	2283.6	2	2.7275	0.2895
GVVHVYTR	931.1	1	1.7806	0.2054
GVVKDEPETR	1130.2	2	2.5899	0.1345
GVVPLAGTDGETTTQGLDGLSER	2274.4	2	5.407	0.3984
GVVPLAGTNGETTTQGLDGLSER	2273.4	2	5.5655	0.6229
GVVQELQQAISK	1300.5	2	3.9222	0.3877
GVVQELQQAISKLEAR	1770.0	2	4.3407	0.4514
GVVVLAKSYNEQR	1463.7	2	3.523	0.2529
GVYSEETLR	1054.1	2	2.8439	0.2541
GWDEALLTMSK	1251.4	2	3.5494	0.3019
GWDEALLTMSKGEK	1565.8	2	2.9771	0.2327
GWDENVYYTVPLVR	1711.9	2	3.837	0.3865
GWEEGVAQMSVGQR	1534.7	2	3.3198	0.2397
GWKEVHELYK	1289.5	2	3.3672	0.1969
GWNYILEKYDGHLPIEIK	2189.5	2	5.5516	0.363
GWQDVTATSAYK	1327.4	2	4.3857	0.3878
GWQDVTATSAYKK	1455.6	2	3.6777	0.2818
GWTGQESLSDSDPEMWELLQR	2465.6	2	3.6875	0.2802
GWTQWIEGDELHLEMR	2001.2	2	3.8082	0.4118
GWVLGPNNYYSFASQQQKPEDTTIPSTELAK	3471.8	3	3.991	0.2347
GYADIVQLLLAK	1304.6	2	4.0193	0.3064
GYADSPSK	824.9	1	2.1312	0.2697
GYAFIEYEHER	1414.5	2	3.2492	0.337
GYAFNHSADFETVR	1614.7	2	3.8131	0.2977
GYAFVQYSNER	1334.4	2	3.448	0.3989
GYAVNVFDIQQGFDNPQVR	2168.4	2	4.553	0.1248
GYAWGLNELKPISK	1576.8	2	3.064	0.3269
GYAYVEFENPDEAEK	1761.8	2	5.3585	0.4793
GYAYVEFENPDEAEKALK	2074.2	2	5.1625	0.4562

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GYDQSAYDGKDYIALNEDLR	2307.4	3	4.2204	0.128
GYDSDNPR	923.9	2	2.4361	0.1335
GYDVIAQAQSGTGK	1395.5	2	5.1753	0.1715
GYEDYLQSPLQPLMDNLESQTYEVFEKDPIK	3692.1	3	4.0437	0.1949
GYEEVHVPALKPKPFGSEEQLLPVEK	2922.3	3	3.8807	0.3244
GYEEVHVPALKPKPFGSEEQLLPVEKLPK	3260.8	3	3.2804	0.1689
GYEEWLLNEIR	1422.6	2	3.9105	0.2355
GYEIDEDIVSR	1296.4	2	2.8998	0.324
GYELAHQR	974.1	2	2.4883	0.3814
GYELLFQPEVVR	1450.7	2	3.6484	0.3452
GYELVPNLEIPTVNPVAIKPGTVAIPAIGAQYSMFPAAPAPK	4305.0	3	4.4135	0.2005
GYEVIYLTEPVDEYCIQALPEFDGKR	3049.4	3	4.1403	0.3763
GYFEYIEENKYSR	1698.8	2	3.9908	0.3966
GYFIQPTVFGDVQDGMTIAKEEIFGPVMQILK	3574.2	3	4.1361	0.1966
GYFNEELSEILSDPSDDTKGFFDPNTEENLTYLQLK	4171.4	3	5.5284	0.3515
GYFPRFEEPAPLSYDSRPR	2285.5	3	3.4541	0.3296
GYFVQPTVFSNVTDEMR	1991.2	2	6.1177	0.5359
GYGFGLIKLDLK	1324.6	2	3.6426	0.2709
GYGHSRPPDRDFPADFFER	2267.4	3	3.2897	0.1451
GYGPDGHFGMFPANYVELIE	2214.4	2	4.0123	0.2771
GYGYGQGAGTLSTDKGESLGIK	2160.3	2	3.4203	0.3128
GYGYGQGAGTLSTDKGESLGIKHEEAPGHRPTTNPNASK	3985.2	3	4.884	0.3438
GYHQYAYDGKDYIALK	1906.1	2	5.1753	0.408
GYHQYAYDGKDYIALKEDLR	2419.6	2	5.9705	0.4854
GYIEEKELDAFFLHMLMK	2215.6	3	5.6078	0.4377
GYIFLEYASPAHAVDAVK	1952.2	2	5.3514	0.5242
GYIGVVNR	878.0	1	2.0666	0.2244
GYISPYFINTSK	1390.6	2	4.2581	0.4207
GYIWNYGTLPQTWEDPHEKDK	2578.8	3	3.4736	0.1767
GYKHPVLLLHPLGGWTK	1917.3	3	4.3853	0.4112
GYKHPVLLLHPLGGWTKDDDVPLDWR	3029.4	3	4.2685	0.3969
GYKIPVIENLGATLDQFDAIDFSDNEIR	3155.5	3	5.508	0.3758
GYKIPVIENLGATLDQFDAIDFSDNEIRK	3283.6	3	4.1448	0.252
GYKLSPEDYTLK	1414.6	3	3.2929	0.3266
GYKLSPEDYTLKVSQAGK	1985.2	2	4.9097	0.4035
GYKQQLVEK	1093.3	2	2.4654	0.1781

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
GYLADPAKFPEAR	1435.6	2	3.3624	0.2561
GYLDKLEPSK	1150.3	2	2.6557	0.2155
GYLDKLEPSKITK	1492.7	2	4.0506	0.264
GYLEDEHAAAHAEEAFFNTILPAFDPALR	3217.5	3	3.4183	0.1723
GYLGPEQLPDCLK	1433.7	2	2.9826	0.1487
GYLGPEQLPDCLKGCDVVVIPAGVPR	2697.2	3	4.595	0.2673
GYLNKDTHDQLSEPSEVR	2089.2	2	6.2749	0.4598
GYLPSHYER	1122.2	2	2.6149	0.1423
GYLSETVSNALGPQGR	1649.8	2	3.8177	0.3044
GYLVTQDELDQTLEEFKAQFGDKPSEGRPR	3455.7	3	5.5255	0.3915
GYNDDYYEESYFTTR	1923.9	2	5.0428	0.5197
GYNPGLLVHPDLAYLQAEGGGDR	2413.6	3	3.7617	0.2848
GYPEEKKEEEGSANR	1723.8	2	4.3447	0.3963
GYPEEKKEEEGSANRRPEDQELESLSAIEAELEK	3892.1	3	4.9916	0.3501
GYPEEKKEEEGSANRRPEDQELESLSAIEAELEKVAHQLQALR	4909.3	3	4.2427	0.2563
GYPGVQAPEDLEWER	1746.9	2	4.4375	0.3313
GYPHLCSICDLPVHSNK	1884.2	2	3.0582	0.1537
GYPHLCSICDLPVHSNKEWSQHINGASHSR	3374.7	3	4.6715	0.2681
GYPHWPARIDEMPEAAVK	2068.3	2	4.4009	0.3121
GYPTFHYYHYGK	1533.7	2	2.588	0.288
GYPTLLLFR	1080.3	2	2.6835	0.2393
GYPTLLWFR	1153.4	2	2.4497	0.338
GYQGDPSSALLELLDPEQNANFLDHYLDVPVDLSK	3875.2	3	5.9658	0.4898
GYRDINEIDINMNDPLFTK	2269.5	3	4.9189	0.2689
GYRLPTSALVNLSHGSR	1829.1	3	4.34	0.2685
GYSFSLTTFSPSGK	1479.6	2	4.9187	0.4157
GYSFTTTAER	1133.2	2	3.698	0.4499
GYSFTTTAEREIVR	1630.8	2	2.5812	0.1223
GYSFVTTAER	1131.2	2	2.6661	0.178
GYTSWAIGLSVADLAESIMK	2113.4	2	5.5862	0.5582
GYVAKSPDEAYAIAKK	1711.9	3	3.3519	0.2526
GYVKEQFAWR	1284.4	2	2.7045	0.268
GYWASLDASTQTTHELTIPNNLIGCIIGR	3146.5	3	4.2085	0.1232
GYYEQTGVGPLPVVLFNGMPFER	2571.9	2	5.1035	0.4399
HAAENPGK	823.9	1	1.7687	0.1391
HAAENPGKYNILGTNTIMDK	2188.5	2	6.0234	0.4658

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HAAEVARDNLAEELEGVAGR	2108.3	3	4.0866	0.3842
HAAGVLAQEDLVGLLEPINTR	2217.5	2	4.9894	0.5133
HAALVSQPETTK	1282.4	2	3.5388	0.3644
HAASTVQILGAEK	1325.5	2	4.0896	0.4542
HAAVALGQAR	994.1	2	2.7116	0.2439
HAAVLVETIKK	1209.5	2	3.0578	0.4169
HADDDRPPR	1079.1	2	2.5987	0.3099
HADDHTPK	920.9	2	2.6749	0.236
HADEFLLDLGHHER	1689.8	2	2.8291	0.258
HADGSFSDEMNTILDNLAAR	2178.3	2	6.6238	0.5604
HADGSFSDEMNTILDNLAARDFIN	2667.8	2	4.6637	0.3354
HADGSFSDEMNTILDNLAARDFINWLIQTK	3437.8	2	5.2362	0.419
HADHSSLTLGSGSSTTR	1714.8	2	4.7284	0.5024
HADIVTTTTHK	1224.3	2	3.2354	0.3581
HADLEIR	853.9	1	2.7762	0.232
HADQYKEQMEK	1407.5	2	3.9108	0.3198
HADVGVALLANAPER	1533.7	2	2.8621	0.1902
HAEATLGSGNLR	1226.3	2	3.9871	0.4357
HAEELER	883.9	2	2.5749	0.1743
HAEEPWVHLHYYGLR	1908.1	2	2.7825	0.2876
HAEGQLSFIQHSLINPEIFCFADYPCHTVATDILK	3960.5	3	4.982	0.3594
HAEGTFTSDVSSYLEGQ	1828.9	2	4.3271	0.3904
HAEGTFTSDVSSYLEGQAAK	2099.2	2	6.4406	0.6536
HAEGTFTSDVSSYLEGQAAKEFIAWLVK	3086.4	3	7.8184	0.5967
HAEGTFTSDVSSYLEGQAAKEFIAWLVKGR	3299.6	3	5.3118	0.4117
HAEKAPTNIVYK	1371.6	2	2.8513	0.2498
HAEKIEEVKK	1211.4	2	3.1072	0.2313
HAEMVHTGLK	1123.3	2	2.8597	0.4201
HAEPEQNWEAVDGSQTETEKK	2414.5	3	3.9814	0.2854
HAEQERDELADEITNSASGK	2201.3	3	5.6916	0.4073
HAESVGDGER	1057.1	2	2.9799	0.2754
HAFEIFR	920.0	2	2.4951	0.1573
HAFEIFRR	1076.2	2	2.4268	0.2348
HAFEIIHLLTGENPLQVLVNAIINSGPREDSTR	3656.1	3	5.5065	0.3832
HAFFEGLNWENIR	1633.8	2	3.0568	0.3523
HAGGGVHIEPR	1130.2	2	2.8676	0.3422

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HAGGVTGGWDNLLAVIPGGSSTPLIPK	2616.0	3	4.4782	0.3153
HAGNLTLHANSVR	1390.5	2	3.056	0.3419
HAGNNESHSSR	1196.2	2	2.5579	0.2942
HAGTYDQK	920.0	2	2.4633	0.2478
HAHGDQYK	956.0	1	2.3109	0.1807
HAHGDQYKATDFVADR	1831.9	2	3.9282	0.4259
HAHSILQFQFAEVK	1655.9	3	4.5429	0.3649
HAIPNLVK	892.1	2	2.7604	0.1025
HAIYDKLDDDGLIAPGVR	1969.2	2	5.8031	0.5012
HAKPPDVDLK	1120.3	2	3.0134	0.3568
HAKPPDVDLKK	1248.5	2	2.9717	0.3777
HALDAHQQSIPAVLEIPSK	2055.3	3	3.5609	0.222
HALDAHQQSIPAVLEIPSKEHPYDAAK	2967.3	3	7.1961	0.4987
HALDAHQQSIPAVLEIPSKEHPYDAAKDSILR	3552.0	3	6.7034	0.4537
HALIIYDDLSK	1288.5	2	3.5824	0.2765
HALIIYDDLSKQAVAYR	1977.3	3	5.4612	0.4686
HALKGAGTNEK	1126.2	2	2.8621	0.2769
HALLEADVAAHQDR	1546.7	3	3.2518	0.3
HALLEADVAAHQDRIDGITIQAR	2514.8	3	3.4623	0.301
HALNSR	697.8	1	1.8674	0.1546
HALPPGFVLKK	1207.5	3	3.8837	0.1884
HAMNLEAVNTYEGTHDIHALILGR	2677.0	3	5.497	0.4997
HANAKPFEVPFLK	1498.8	2	4.2899	0.4129
HANAKPFEVPFLKF	1645.9	2	3.5934	0.2554
HANEEEKKAAATTAQEYLK	2133.3	2	3.6729	0.3408
HANPGGPIYFLK	1314.5	2	2.9714	0.3243
HAPGLIAALAYETANFYQK	2079.3	2	4.156	0.5194
HAPINSAQHLDNVDQTGPK	2043.2	3	3.7356	0.1282
HAPSLHGSTELLPLSR	1715.9	2	3.6994	0.3298
HAQANGFSVVR	1186.3	2	2.7765	0.3372
HAQAQYAYPGAR	1333.4	2	3.1439	0.1679
HAQAVEELTEQLEQFKR	2057.3	3	4.7076	0.3396
HAQGTVLHR	1019.1	2	2.7922	0.363
HAQTISGHALR	1191.3	2	2.8413	0.3296
HARPPDPPASAPPDSSSNSASQDTK	2518.6	3	3.5096	0.2401
HASAPSHVQPSDSEK	1577.6	2	2.5455	0.1465

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HASAVASKEDSWTLFKPPPVFPVDNSSAK	3114.5	3	4.3725	0.1465
HASLQNSQR	1041.1	2	2.7693	0.256
HASPEDIKK	1025.1	2	2.5341	0.2455
HASPILPITEFSDIPR	1794.0	3	4.7465	0.4223
HASQKDYSSGFGGK	1469.5	2	2.4842	0.252
HASSGSFLPSANEHLK	1682.8	2	5.3207	0.4251
HASSGSFLPSANEHLKEDLNLR	2423.6	3	4.9966	0.4231
HATAEEVEEEER	1429.4	2	2.8566	0.3458
HATALEELSEQLEQAK	1797.9	2	4.733	0.4903
HATALEELSEQLEQAKR	1954.1	3	7.1276	0.5275
HATGNYIIIMDADLSHHPK	2134.4	3	4.5045	0.3524
HAVGNNEFGTVDHER	1682.7	2	4.1088	0.4763
HAVSDPSILDSLDLNEDEREVLINNINR	3192.4	3	4.3781	0.4272
HAVSDPSILDSLDLNEDEREVLINNINRR	3348.6	3	3.7246	0.2639
HAVSEGTK	828.9	2	3.0726	0.3944
HAVSEGTKAVTK	1228.4	2	4.3002	0.5146
HAVTEAEIQQLKR	1523.7	2	4.3999	0.3438
HAVVNLINYQDDAELATR	2043.2	2	6.1522	0.4874
HAVVVGR	737.9	1	1.8443	0.2771
HAYGDQYR	1010.0	2	2.5948	0.3105
HAYGLGEHYNSVTR	1604.7	2	3.8047	0.4608
HCAEPFTEYWTCIDYTGQQLFR	2710.0	3	4.5434	0.2936
HDADGQATLLNLLLR	1650.9	2	5.2609	0.4731
HDDFFPYADGPHQFWTGYFSSRPALK	3088.3	3	3.5552	0.2771
HDDYLVMLK	1134.3	2	3.1004	0.4173
HDEFER	832.8	1	2.5373	0.1479
HDEFERHAEGTFTSDVSSYLEGQAAK	2913.0	3	6.8143	0.5405
HDEFERHAEGTFTSDVSSYLEGQAAKEFIAWLVK	3900.2	3	6.9712	0.5597
HDFSTVLTVFPILR	1645.9	2	4.5933	0.4491
HDGHDDDVIDIEDDLDDVIEEVEDSKPDTTAPPSSPK	4062.1	3	7.3969	0.5803
HDGITVAVHK	1077.2	2	2.7851	0.3124
HDGKEVDEGAWETK	1601.7	3	3.9231	0.431
HDGYGSHGPLLPLPSR	1703.9	2	4.1595	0.4358
HDHAVSLLTAASPTIALLLER	2229.6	3	4.2337	0.3272
HDKVEDALNLKEEFDRLDSSAVLDTGK	3046.3	3	4.7986	0.3265
HDKYMADMDELFSQVDEK	2202.4	2	4.5844	0.391

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HDLGHFMLR	1126.3	2	2.4256	0.2378
HDLPLHPAVVKPHLGHVPDYLVPPALR	2989.5	3	3.4948	0.3118
HDNEEAMK	974.0	2	2.5987	0.2343
HDNFPHNQR	1165.2	2	2.5268	0.1558
HDPQAEEALAK	1209.3	2	3.2917	0.3116
HDSEQDNSDNNTIFVQGLGENVTIESVADYFK	3587.7	3	7.1421	0.3848
HDSPEDVK	927.0	2	2.949	0.2207
HDSPEDVKR	1083.1	2	2.8718	0.2744
HDSPEDVKRR	1239.3	2	2.6311	0.2195
HDSSWVEELLMLHR	1753.0	3	5.4148	0.3367
HDVKFPLDSTGSELKQK	1930.2	3	4.0325	0.3197
HEAFESDLAAHQDR	1626.7	3	3.6298	0.2525
HEAFESDLAAHQDRVEQIAAIAQELNELDYYDSPSVNAR	4417.7	3	5.7118	0.4156
HEALKENGVTHPIDYHTTDYVDEIK	2926.1	3	5.2767	0.3513
HEALKENGVTHPIDYHTTDYVDEIKK	3054.3	3	5.9981	0.4878
HEAPMQMASAQDAR	1543.7	2	3.717	0.4254
HEDLKDMLEFPAQELR	1972.2	2	2.8996	0.2192
HEDLKDMLEFPAQELRK	2100.4	3	4.1466	0.2731
HEEAPGHRPTTNPNASK	1843.9	2	3.477	0.2675
HEEEEAKAER	1228.3	2	3.1943	0.3027
HEEEKFFLNAK	1392.5	2	3.1542	0.2812
HEEFKKYEMMK	1500.8	2	3.3879	0.2655
HEEKVAAYDKLEK	1560.7	2	4.239	0.3882
HEEQPAPGYDTHGR	1594.6	2	3.8586	0.4388
HEERPDEHGFVAR	1579.7	3	3.3153	0.2002
HEERQDEHGFISR	1640.7	2	3.2684	0.2434
HEERQDEHGYISR	1656.7	3	4.1477	0.3649
HEHQLMLMR	1195.4	2	2.8172	0.2603
HEHQVMLMR	1181.4	2	2.6893	0.3749
HEIKDTFLR	1159.3	2	2.4512	0.2837
HEILQWVLQTDSQQ	1725.9	2	2.5612	0.2881
HEIVQTLSLKDGLIPLEIR	2175.6	2	5.2887	0.4869
HELAEIVFK	1086.3	2	2.8402	0.2291
HELELPHLTSALHPVHPDIK	2284.6	2	2.607	0.1795
HELLQPFNVLYEK	1630.9	2	4.0727	0.3772
HELLQPFNVLYEKEGEFVAQFK	2667.0	3	4.7151	0.3796

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HELQANCYEEVKDR	1734.9	3	5.6117	0.4883
HEMLPASLIQAQR	1494.7	2	3.4096	0.4616
HEMLPEFYK	1194.4	2	2.8181	0.2846
HEMPPHIYAISESAYR	1902.1	3	3.5621	0.3537
HEMPPHIYAITDTAYR	1916.1	2	5.1275	0.4296
HEQEYMEVR	1221.3	2	2.7051	0.2453
HEQILVLDPPTDLK	1618.9	2	4.6206	0.4119
HEQILVLDPPTDLKFKGPFTDVVTTNLK	3167.6	3	5.2176	0.4197
HEQNIDCGGGYVK	1420.5	2	4.362	0.3931
HESENLYSIACDKPQQVR	2118.3	3	4.684	0.3626
HESGASIK	828.9	1	2.0953	0.1737
HESGASIKIDEPLEGSEDR	2070.2	2	5.1211	0.4978
HESGASIKIDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	4642.1	3	5.7974	0.4978
HESQMDSVVK	1160.3	2	2.7837	0.3782
HETLTSLNLEK	1285.4	2	2.7617	0.2393
HETLTSLNLEKK	1413.6	2	3.315	0.3475
HETWSGHVISS	1240.3	2	2.5311	0.2877
HEVEKSEISENTDASGK	1860.9	3	4.2434	0.3503
HEVGYVLGQLQHEAAVPQLAAALAR	2643.0	3	3.6273	0.4303
HEVININLK	1080.3	2	2.7263	0.2781
HEVLLISAEQDKR	1538.7	3	4.3119	0.381
HEVPPHVYAVTEGAYR	1826.0	3	4.6879	0.4021
HEYGSPGILEFFHHQLK	2040.3	3	3.2864	0.277
HFAAHEREDLVQQLER	1979.1	2	2.647	0.1403
HFAESETLDQLPLTNPEHFGTPVIGKK	3007.3	3	4.3965	0.2706
HFAGDVLGYVTPWNSHGYDVTK	2464.7	3	3.4893	0.1566
HFCPNVPIILVGNKK	1680.1	3	4.2776	0.2824
HFDETVNR	1018.1	2	3.0598	0.2183
HFDETVNRYK	1309.4	2	2.6116	0.1955
HFEANNGKLPDNK	1484.6	2	3.6618	0.28
HFEANNGKLPDNKVIASELGSMPELK	2840.2	3	3.2054	0.1618
HFEDLEFQQLEHESR	1945.0	2	3.2929	0.271
HFELGGDK	903.0	2	2.531	0.1769
HFELGGDKK	1031.1	2	2.8464	0.1543
HFESQSDDPHFHEK	1740.8	2	3.8044	0.3342
HFFLYGEFPGDER	1614.7	2	2.7435	0.1929

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HFGEKAPAPQPPSLPDRSPRPQR	2566.9	3	3.2199	0.2007
HFGKAPGTPHSHTKPYVR	2018.3	3	3.3145	0.2873
HFHGTSLTFSMQDGPEAGQTVK	2376.6	3	5.2863	0.2812
HFHPLFEYFDYESR	1888.0	3	3.3457	0.2426
HFHVPDQGINIYR	1596.8	2	3.3152	0.2859
HFIDVGAGVIDEDYR	1706.8	2	4.5216	0.4455
HFLDFQGSAIPQAMQK	1819.1	2	3.7116	0.2334
HFLIETGPR	1070.2	2	2.5039	0.1391
HFLLEEDKPEEPTAHAFVSTLTR	2668.9	3	5.7778	0.4068
HFLPEMLSK	1102.3	2	2.4298	0.175
HFNALGGWGELQNSVK	1757.9	2	4.3806	0.4021
HFNAPSHIR	1079.2	2	2.6065	0.2358
HFNLLSSK	946.1	2	2.4062	0.2395
HFNSMSGPATLRK	1446.7	2	3.6635	0.2958
HFPSVNWLISYSK	1578.8	2	3.2031	0.1975
HFRPELEER	1213.3	2	2.7993	0.1669
HFSEHPSTSK	1157.2	2	2.9397	0.284
HFSGLEEAVYR	1308.4	1	3.2353	0.3485
HFSPEELKVK	1214.4	2	2.8008	0.2299
HFSQGSALILHQR	1494.7	2	3.642	0.3426
HFSSDAVPHPR	1250.3	2	2.9846	0.4871
HFSVEGQLEFR	1349.5	2	3.3573	0.4762
HFSVTAEGGLSPAQVTGAR	1886.1	2	6.6315	0.5057
HFTEDIQTR	1147.2	2	2.6168	0.184
HFTILDAPGHK	1236.4	3	3.4051	0.2993
HFTQALSTVTPR	1358.5	2	3.4723	0.2876
HFTQPHAQDFLR	1497.6	3	3.722	0.3181
HFVALSTNTTK	1219.4	2	3.4804	0.3072
HFVDSHHQKPVNAIIEHVR	2264.5	3	4.3175	0.2799
HFVGMLPEKDCR	1432.7	2	2.7693	0.1683
HFVGYPTNSDFELK	1654.8	2	3.8041	0.4233
HFVTISSPLATQIPQAVGAAYAAK	2442.8	3	4.1556	0.3319
HFYQPIWTLVGAGAK	1689.0	2	5.0174	0.4178
HFYVVIPQIYK	1407.7	2	3.2324	0.2899
HFYWYLTNEGIQYLR	2004.2	2	4.6306	0.4669
HGAEVIDTPVFELK	1555.8	2	3.7694	0.3675

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HGAEVIDTPVFELKETLMGK	2215.6	3	4.431	0.3237
HGAGAEISTVHPEQYAK	1795.9	2	5.2377	0.4415
HGAGAEISTVHPEQYAKR	1952.1	2	4.9223	0.3986
HGAGAEISTVNPEQYSKR	1945.1	2	5.2151	0.3891
HGAPSPSHPISAPQAAAAAALR	2079.3	3	4.6239	0.43
HGAPSPSHPISAPQAAAAAALRR	2235.5	3	3.333	0.4815
HGASPELQK	967.1	2	3.308	0.2441
HGATHVFASK	1055.2	2	3.2659	0.1972
HGATHVFASKESEITDEDIDGILER	2770.9	3	4.522	0.2894
HGAVCHTGAPDATLHTVHPDSVSSSYSSR	2978.2	3	5.5271	0.4837
HGDDLRR	868.9	2	2.6604	0.1997
HGDEIYIAPSGVQK	1514.7	2	4.5816	0.4583
HGDEIYIAPSGVQKER	1800.0	3	4.6545	0.4113
HGDGTTLDIMLK	1301.5	2	3.6788	0.2381
HGDLPDIQIK	1136.3	2	3.2509	0.2119
HGDLTHFVANNLQLK	1707.9	2	4.4967	0.3333
HGDPGDAAQQEAK	1324.3	2	4.2695	0.4384
HGDQHEGQHYNISPQDLETVFPHGLPPR	3207.4	3	5.963	0.4986
HGDSAMHLALR	1208.4	2	3.1999	0.3978
HGEAQVK	768.8	1	2.0053	0.1893
HGEEGVEAEKK	1213.3	2	3.4295	0.2803
HGEEVTPEDVLSAAMYPDVFAHFK	2691.0	3	5.3785	0.4362
HGEGGHYHYDTTPDIVEYLGYFLPAEFLYR	3561.9	3	3.2475	0.1338
HGEIDYEAIVK	1274.4	2	3.5939	0.2696
HGEISFLNEEVK	1402.5	2	2.5486	0.1455
HGENEHNLQGR	1291.3	2	3.3069	0.4053
HGENIIDTLGAEVDRLEK	2010.2	3	6.3197	0.4276
HGERDVEVER	1226.3	2	2.7293	0.3088
HGESAWNLENR	1313.4	2	3.7002	0.4384
HGESEFNLLGK	1231.3	2	4.0106	0.3975
HGESGSMAVFHQTQGPSYSESK	2352.5	3	4.7831	0.4134
HGEVCPAGWKPGSDTIKPDVQK	2350.6	3	3.3124	0.2219
HGFEAASIKEER	1374.5	2	3.9814	0.4105
HGFEAASIKEERGDEVMVELAENGKK	2875.2	3	5.3915	0.4002
HGFFVNPSDSVAVIAANIFSIPYFQQTGVR	3283.7	3	4.0445	0.257
HGFLEEFITPIVK	1530.8	2	4.1886	0.2338

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HGFPYQPSALAFDPVQK	1903.1	3	4.9092	0.3635
HGFRQEYLDTLYR	1698.9	2	2.7297	0.2406
HGFSDNQK	933.0	2	2.7293	0.3237
HGGGPPPEPR	1001.1	2	2.4817	0.2672
HGGGTESLFFDKVR	1550.7	2	3.0036	0.2924
HGGLALQPGPPGLHPFPFHPSLGPLER	2827.2	3	4.8677	0.3096
HGGLSLVQTTDFFYPLVEDPYMMGR	2875.3	3	4.1385	0.2086
HGGNYLLFNLSER	1520.7	2	3.8907	0.4432
HGGNYVPAPK	1040.2	2	2.4187	0.2055
HGGPKDEER	1025.1	2	3.3927	0.3409
HGGPLPYHR	1034.2	2	2.9193	0.2662
HGGTIPIVPTAEFQDR	1738.9	2	4.3709	0.4492
HGGYKPSDEHKTDLNPDNLQGGDDLDPNYVLSSR	3755.9	3	6.5211	0.489
HGHVDTLK	907.0	2	2.7668	0.236
HGHYPNTIAEK	1267.4	2	2.476	0.2793
HGIEFSVISSSEV	1391.5	2	3.1156	0.206
HGIILNSEIATNGETSDTLNNVGYQGPTK	3045.3	3	3.7119	0.314
HGITQANELVNLTEFFVNHILPDLK	2864.2	3	3.284	0.1184
HGIVEDWDLMER	1500.7	2	3.7631	0.2314
HGKAPILIATDVASR	1549.8	2	4.1216	0.383
HGKELGGESNFGDALLDAGESMK	2363.5	3	4.9493	0.4249
HGKELGGESNFGDALLDAGESMKR	2519.7	3	4.4445	0.3846
HGKNPVMELNEK	1396.6	2	4.6236	0.3038
HGKYMACCLLYRGDVVPK	2054.5	2	2.7721	0.1704
HGLAHDEMK	1038.2	2	2.7818	0.181
HGLANLTAELLQQGANPNLQTEEALPLPK	3082.5	3	4.4368	0.3675
HGLANSISSYLIKPVQR	1884.2	2	3.4136	0.3273
HGLEAISIMDSR	1329.5	2	3.3647	0.3534
HGLEKPISFVK	1255.5	2	3.239	0.317
HGLEQYLSR	1103.2	2	2.6942	0.1891
HGLEVIYMIEPIDEYCVQQLKEFEGK	3112.6	3	6.169	0.4459
HGLGYSLLER	1145.3	2	2.693	0.2939
HGLINAGYR	1001.1	2	2.4007	0.1392
HGLLLPASPVR	1160.4	2	3.1302	0.2143
HGLLVPNNTTDQELQHIR	2086.3	3	5.3258	0.4786
HGLPLVTLTLPSRK	1532.9	2	3.0369	0.313

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HGLPPSETIAIVEHINAK	1927.2	3	4.5388	0.4502
HGLQHEGIFR	1194.3	2	2.9214	0.2957
HGLQSLGK	840.0	2	2.8819	0.2783
HGLTEADVGITK	1241.4	2	2.7289	0.1771
HGLTTTPQQK	1111.2	2	2.9293	0.2244
HGLVPFAFVR	1143.4	2	2.9751	0.2236
HGLYLPTR	957.1	2	2.6217	0.3556
HGNQYIQVNEPWKR	1769.9	3	5.2752	0.4207
HGNRGETGPSGPVGPAGAVGPR	2028.2	3	6.0823	0.4679
HGNVASLVQR	1081.2	2	3.2799	0.3127
HGPATGPQGVPEVR	1402.5	2	2.9031	0.2955
HGPINVNHYASK	1337.5	2	3.0579	0.3414
HGQALGELAEQLEQAR	1750.9	2	4.8586	0.4262
HGQALGELAEQLEQARR	1907.1	3	4.3846	0.3746
HGQTPTTLPR	1108.2	2	2.4278	0.1254
HGRPGIGATHSSR	1333.4	3	3.5707	0.1532
HGSFLVR	815.9	2	2.5114	0.2309
HGSGAFYSPELLEALTLR	1962.2	2	3.4287	0.3279
HGSGTQYVSTR	1193.3	2	2.9137	0.2165
HGSIIYHPSILPR	1490.7	2	4.2846	0.421
HGSIIYHPSLLPR	1490.7	2	4.4952	0.3722
HGSLGFLPR	984.1	2	3.4617	0.3995
HGSNIEAMSK	1074.2	2	3.3118	0.3936
HGSSEDYLHMVHR	1568.7	3	3.2096	0.2333
HGSSKPTDGTK	1115.2	2	2.4108	0.2331
HGSVSADEAAR	1100.1	2	3.287	0.4151
HGSYEDAVHSGALND	1572.6	2	4.6301	0.4606
HGTEEQKATYLPQLTTEK	2075.3	3	4.3565	0.4142
HGVEAK	640.7	1	1.7397	0.1308
HGVEAKNYEEIAKVEK	1845.0	3	4.8328	0.4192
HGVFLVR	828.0	2	2.5359	0.2156
HGVIVAADSR	1025.1	2	3.1649	0.1632
HGVSHKVDDSSGSIGR	1638.7	2	5.1249	0.4916
HGVVPLATYMR	1244.5	2	3.1271	0.2554
HGVYNPNK	929.0	2	3.2257	0.3124
HGVYNPNKIFGVTTLDIVR	2144.5	2	5.832	0.5742

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HGWEELVYYTVPLIQEMESR	2480.8	2	3.6423	0.3499
HGYEKPTPIQTQAIPAIMSGR	2296.6	3	3.9874	0.2943
HGYIGEFEIIDDHRAGK	1958.1	2	2.5934	0.1538
HHAAYVNNLNVTEEK	1739.9	2	5.3689	0.5013
HHAAYVNNLNVTEEKYQEALAK	2543.8	2	7.2695	0.4836
HHAAYVNNLNVTEEKYQEALAKGDVTAQIALQPALK	3950.4	3	6.6365	0.547
HHEEEIVHHKKEIER	1951.1	3	3.7395	0.212
HHEGFTNWPSPVSWNWNSK	2311.5	3	5.282	0.2871
HHGDVMDLQFFDQER	1875.0	2	2.7078	0.1465
HHGPISTTPGIIPQK	1583.8	2	2.7389	0.121
HHGPQTLYLPVTLSSIPVFQR	2391.8	2	4.886	0.4659
HHGQEGSILVTKVEEPSK	1976.2	3	4.2876	0.2624
HHHENFVGYQDDNLFQDEMR	2532.6	3	3.7146	0.365
HHIETGGGQLPAK	1345.5	2	2.5285	0.1855
HHISIAEIYETELVDIEK	2140.4	2	5.1637	0.4147
HHLDLGHNSQAYEALTQIPDSSR	2590.7	3	3.4944	0.1945
HHLENEKTQLIQQVEQLKQEVSR	2816.1	3	3.9216	0.2661
HHLGAATPENPEIELLR	1898.1	2	4.344	0.379
HHLGDDVVLFTTDGAHK	1863.0	2	4.954	0.3814
HHLGHLLSVPDESSALEDR	2113.3	2	3.3663	0.2705
HHLPQPEGPPDAR	1451.6	2	3.4677	0.2787
HHNQSTAINLNNPESQSMHLETR	2659.8	2	6.0595	0.4468
HHPDFEVFVFDVGQK	1802.0	3	3.5274	0.2784
HHPEDVEPALRK	1428.6	2	2.4894	0.1077
HHSDGSVSLSGHLQPPPVTTEQHGAR	2732.9	3	4.8212	0.4339
HHSLGGQYGVQGFPTIK	1827.0	2	4.7187	0.4236
HHTAAFEER	1098.2	2	2.6344	0.2653
HHVLGTITTDK	1222.4	2	3.1497	0.2501
HHVLQNDVLAHQSTVEAVNK	2240.5	3	4.1056	0.2943
HHVPSDFNVNVK	1393.5	3	3.3055	0.1089
HHVTLRQQISGPELLSR	1972.2	2	2.4734	0.1299
HHYEQQQEDLAR	1554.6	2	3.535	0.3588
HHYESLQTAK	1214.3	2	2.4587	0.201
HIADLAGNSEVILPVPAFNVINGGSHAGNK	3013.4	3	7.3043	0.5397
HIADLAGNSEVILPVPAFNVINGGSHAGNKLAMQEFMILPVGAANFR	4903.6	3	5.5233	0.5237
HIAEDADR	927.0	2	2.6196	0.2056

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HIAEDADRKYEEVAR	1802.9	2	3.7203	0.4045
HIAEDSDRKYEEVAR	1818.9	2	2.755	0.1217
HIAEEADR	941.0	1	2.9602	0.2486
HIAEEADRK	1069.2	2	2.4402	0.1663
HIAEEADRKYEEVAR	1817.0	2	3.8576	0.3801
HIAEEADRKYEEVARK	1945.1	2	3.3642	0.222
HIAEVSQEVTR	1269.4	2	3.3642	0.3224
HIANYISGIQTIGHR	1680.9	2	3.7905	0.5097
HIAQLAGNSDLILPVPAFNVINGGSHAGNK	3026.4	3	6.6555	0.5172
HIAQTSK	784.9	1	2.34	0.1035
HIAVLQAEVYGAR	1427.6	2	3.5664	0.4299
HIDALEDKIDEEVRR	1839.0	3	3.5384	0.2997
HIDCAAIYGNEPEIGEALKEDVGPGK	2727.0	3	3.2808	0.1067
HIDFSLR	888.0	2	2.5753	0.2058
HIDLVEGDEGR	1240.3	2	3.7554	0.3569
HIDSAHLYNNEEQVGLAIR	2180.4	3	6.171	0.5954
HIDYFNNQIIVDLVEQQHK	2354.6	3	6.4813	0.4567
HIEEENLIDEDFQNLK	1987.1	2	6.1781	0.4608
HIEEENLIDEDFQNLKLR	2256.5	2	4.7574	0.4486
HIEEGLGR	911.0	2	2.5876	0.1692
HIEHMESDELGLQK	1666.8	2	3.3401	0.3108
HIEIFTDLSSR	1318.5	2	3.2802	0.2374
HIEVQVAQETR	1310.4	2	3.1252	0.2165
HIEWESVLTNTAGCLR	1830.1	2	4.2884	0.4189
HIFALFNTEQR	1376.5	2	3.7898	0.3484
HIFDHVIGPEGVLAGK	1689.9	2	3.0014	0.2306
HIGFVYHPTK	1199.4	2	2.6579	0.3359
HIGKPLLGGPFSLTTHTGER	2119.4	3	4.863	0.4622
HIGLVYSGMGPDYR	1565.8	3	4.3179	0.4658
HIHITQATETTTTR	1610.8	2	4.1289	0.3378
HIHSQVTVQINSAEQEIK	2062.3	3	4.5114	0.3025
HIIENAKQDVDDEYGVSQALAR	2472.7	2	4.267	0.3717
HIILVLSGK	980.2	2	2.5133	0.2632
HIITTTR	842.0	1	1.74	0.1159
HIITVDGKPPTWSEFPK	1953.2	2	3.1822	0.2424
HIKENDYYTPTGEFR	1871.0	2	4.4656	0.2982

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HILGFDTGDAVLNEAAQILR	2154.4	2	5.5778	0.5108
HILGSIVQSEGSYVESLKR	2103.4	3	5.3668	0.5181
HILLAVANDEELNQLLK	1934.2	3	5.988	0.4721
HILLAVANDEELNQLLKGVTIASGGVLPNIHPELLAK	3902.5	3	8.5364	0.5943
HILLAVANDEELNQLLKGVTIASGGVLPR	3042.5	3	7.2993	0.5479
HILQFVAIK	1069.3	2	2.934	0.1804
HILQFVAIKR	1225.5	2	2.9414	0.2061
HIMGQNVADYMR	1435.7	2	4.1516	0.3399
HINMDGTINVDDFK	1619.8	2	3.1402	0.3623
HINSIKSVFGGLVNYFK	1924.2	2	2.534	0.1602
HIPDEIFLLTAEQIAQEVSEQHLSQGR	3090.4	3	3.6299	0.2627
HIQDAPEEFISELAEYLIKPLNK	2699.1	3	5.7887	0.4845
HIQEHYGGTATFYLSQAADGAK	2366.5	3	4.7326	0.3741
HIQHDTIGYLLTR	1567.8	2	3.0026	0.2343
HISDLYEDLRDGHNLISLLEVLSGDSLPR	3278.6	3	4.9527	0.4154
HISDLYEDLRDGHNLISLLEVLSGDSLPREK	3535.9	3	3.4969	0.1761
HISESHEKGENVK	1494.6	2	3.8382	0.3172
HISETETLKR	1214.4	2	2.8896	0.3217
HISPQAK	780.9	1	2.1012	0.1148
HISPSAKPFENGQYLDIYGITR	2507.8	3	3.9819	0.3237
HISQISVAEDDDESLLGHLMIVGK	2607.9	3	7.6991	0.5168
HISQISVAEDDDESLLGHLMIVGKK	2736.1	3	8.2924	0.5494
HISVLAETIKK	1239.5	2	2.6071	0.1658
HITDSGLAAR	1041.1	2	2.7271	0.34
HITESVNSIR	1156.3	2	2.4244	0.2249
HITGSYK	805.9	1	2.1888	0.341
HITIFSPEGR	1157.3	2	3.0509	0.3819
HITLIFNPTR	1212.4	2	2.8067	0.2804
HITTPREPLPPIVTFQLIPK	2298.8	3	3.4936	0.2657
HIVAVLPEIDPVLFQGK	1876.2	2	3.8729	0.3731
HIVLSGGSTMYPGLPSR	1773.0	2	5.1816	0.4957
HIVNHAVVNEDPNAR	1685.8	2	4.518	0.4139
HIYDTK	776.9	1	1.9025	0.1356
HIYYITGETK	1225.4	2	3.4322	0.3634
HIYYITGETKDQVANSAFVER	2442.7	3	6.4603	0.5855
HKAGFLDLKDFLPK	1629.9	2	3.7298	0.3786

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HKALEEDIENHATDVHQAVK	2285.5	3	3.4993	0.1903
HKASVEDADTQSK	1416.5	2	4.2491	0.3238
HKASVEDADTQSKVHQLYETIQR	2684.9	3	5.7548	0.4786
HKDAAIYLVTSLASK	1617.9	3	4.8001	0.5108
HKDIIDDLVK	1196.4	2	3.4897	0.2867
HKDLQQQLVDAK	1423.6	2	3.9021	0.4132
HKDSMDELFSHR	1502.6	2	3.6274	0.4485
HKDVAEEIANYRPTLDTLHEQASALPQEHAESPDVR	4069.4	3	5.2423	0.5109
HKEALIISNTK	1254.5	2	3.2781	0.3503
HKEAVTILSQQR	1410.6	2	3.7147	0.4467
HKEDLQPYK	1158.3	2	2.8138	0.2752
HKEDTLAFSEWGSPHA	1812.9	2	5.0913	0.4438
HKEDTLAFSEWGSPHAAVPR	2236.4	2	7.1164	0.6271
HKEDVYENLHTK	1513.6	2	4.274	0.3823
HKELAPYDENWFYTR	1970.1	3	5.1587	0.5276
HKELFALHPSPDEEEPIER	2274.5	3	5.274	0.4848
HKELFDELVKK	1386.6	3	3.3339	0.3182
HKELQKEYEILLQSYENVSNEAER	2951.2	3	3.9477	0.1158
HKELSVLLLEMK	1440.8	2	3.9607	0.3404
HKEVEAAQGVK	1196.3	2	3.0404	0.2512
HKFPDEDSYQK	1394.5	2	2.7945	0.1716
HKGPPVFTQEER	1425.6	2	2.6386	0.1579
HKGSPFPEVAESVQQELESYR	2418.6	3	5.2214	0.4306
HKIISIFSGTEK	1360.6	2	3.5349	0.2621
HKIPVMALVGNDAGWTQISR	2194.5	2	5.4367	0.5068
HKLANPPPMVEGEGLASR	1904.2	3	3.5091	0.3491
HKLDVTSVEDYK	1434.6	2	3.7906	0.418
HKLDVTSVEDYKALQK	1875.1	3	5.1524	0.3896
HKLTLESLYQAVCDR	1777.0	2	2.5067	0.1377
HKLVSDGQALPEMEIHLQTNAEK	2589.9	3	6.8913	0.4649
HKMTIAALESK	1229.5	2	3.1958	0.3465
HKNVIQLVDVLYNEEK	1942.2	2	2.4358	0.2773
HKPAFTEEDVLNIFPVVK	2084.4	2	3.931	0.374
HKPDFISLFK	1232.5	2	2.7104	0.291
HKPGIVQETTFDLGGDIHSGTALPTSK	2808.1	3	5.4045	0.3857
HKPQVSQQEELK	1451.6	2	2.6394	0.1268

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HKQEFLDKPEDVLLK	1840.1	3	4.9809	0.4628
HKQELTEKDATIASLEETNR	2314.5	3	4.6262	0.412
HKQPALTADFVNYYFER	2100.3	3	4.5318	0.3746
HKQSLEEAAK	1141.3	2	2.9008	0.3029
HKSDFGK	818.9	2	2.7472	0.1404
HKSDVEIPATVTAFSFEDDTVPLSPLK	2945.3	3	4.5255	0.4359
HKSEFFEK	1052.2	2	2.5233	0.1188
HKSETDTSLIR	1287.4	2	3.4679	0.3749
HKTELESLK	1085.2	2	2.7116	0.2055
HKTTIFTDAK	1162.3	2	2.6257	0.2916
HKTVALDGTLFQK	1458.7	2	4.0375	0.3477
HKVISGTTLGYLSPK	1601.9	2	3.5025	0.3016
HKVNEHEQDGNELQTTPEFR	2409.5	3	4.7645	0.3304
HKWEAAHVAEQLR	1575.8	3	3.5748	0.4193
HKYNFIADVVEK	1463.7	2	2.7541	0.1677
HLAAALENLNK	1194.4	2	2.5348	0.2078
HLAAVEER	925.0	2	2.8566	0.2374
HLADHGQLSGIQR	1432.6	2	3.7749	0.4566
HLAEEYGER	1104.2	2	2.495	0.1291
HLAEHSPYYEAMK	1576.8	2	2.5291	0.2364
HLAELNHQK	1090.2	2	2.7612	0.2055
HLAGEVAK	824.9	1	2.181	0.1644
HLAGLGLTEAIDK	1338.5	2	2.8789	0.3223
HLAGLGLTEAIDKNK	1580.8	2	5.2357	0.489
HLAGLGLTEAIDKNKADLSR	2123.4	2	6.4841	0.4849
HLAILGAGLMGAGIAQVSVDKGLK	2320.8	2	4.6539	0.4496
HLAISNMPLVK	1223.5	2	2.7577	0.1852
HLALNLQEK	1066.2	2	2.5817	0.1251
HLANMMGEDPETFTQEDIDR	2350.5	2	4.4206	0.4021
HLAPDYR	872.0	2	2.4602	0.2057
HLAPPGLHPVPGGVFPVPPAAVVLMK	2599.2	3	3.3167	0.116
HLAPPPLLSPLLPSIKPTVR	2147.6	3	3.6653	0.3121
HLAQVGDSMDR	1229.3	2	3.3765	0.1632
HLASDAIINENYDYLKGFLEDLAPPER	3105.4	3	4.0269	0.3568
HLATHFNLLIGAEAQHQK	2029.3	2	3.0784	0.1638
HLAVMPHPER	1187.4	2	2.8225	0.3229

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HLDFLKQPLATQK	1539.8	2	4.7962	0.3912
HLDFLKQPLATQKDLTGQVPTPVVK	2775.2	3	4.8462	0.4151
HLDHVAALFPGDVDR	1662.8	2	4.9494	0.4737
HLDHVAALFPGDVDRLR	1932.2	3	3.6874	0.3155
HLDLSNVAGYK	1217.4	2	3.5253	0.2828
HLDQIIPR	992.2	2	2.508	0.2167
HLDRVDAVLVTHPGADSLPGLNSLLR	2767.1	3	5.1348	0.4439
HLDRVDSILLTHIGDDNLPGINSMLQR	3044.4	3	5.4988	0.3752
HLDSVLSDHTR	1280.4	3	3.4131	0.3422
HLDTLHNFVSR	1339.5	2	2.885	0.2588
HLEAAALLSER	1210.4	2	2.5334	0.2839
HLEEAFTSEHWLVR	1754.9	2	3.0424	0.2728
HLEEEEER	1071.1	2	3.0071	0.1062
HLEEEKER	1070.1	2	2.6851	0.1016
HLEEENR	927.0	2	2.5601	0.1561
HLEEIVEK	997.1	1	2.4853	0.1584
HLEEKDLKPIFEQFGR	1987.2	2	3.6224	0.2143
HLEELDKSHLEGELRPK	2031.3	3	4.4105	0.3237
HLEEPGETQNAFLNER	1885.0	2	4.9823	0.396
HLEFLGQLR	1113.3	2	2.5822	0.2526
HLEFMNQLK	1160.4	2	2.5324	0.252
HLEFSHDQYR	1332.4	2	3.0057	0.3261
HLEFSHDQYRELQR	1859.0	2	3.2287	0.176
HLEIIYAINQR	1370.6	2	3.5674	0.2757
HLEINPDHPIVETLR	1784.0	3	4.5955	0.4437
HLEINPDHSIIETLR	1788.0	2	5.0065	0.497
HLEINPDHSIIETLRQK	2044.3	3	3.9464	0.2697
HLELGKK	825.0	1	2.1768	0.1005
HLENGKETLQR	1325.5	2	3.5249	0.366
HLEQRDEPQEPSNKVPEQQR	2445.6	3	4.758	0.1879
HLETFEHPNVVR	1478.6	2	3.4692	0.3067
HLFAQVLDINQADAGTLPLDSSQKVR	2838.2	3	4.0317	0.3253
HLFEKELAGQSR	1415.6	2	3.7361	0.3113
HLFKDHAYALAVSSTK	1789.0	2	4.431	0.448
HLGGHEGTIPSKV	1332.5	2	3.1044	0.3643
HLGIVDAFQQGK	1313.5	2	3.2717	0.3668

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HLGNAIK	752.9	1	1.8696	0.1407
HLGQIENYLQTSSLLASDHHLTEEER	3022.2	3	4.9882	0.4171
HLGSPATSVPGMGLHPPGPPLARPILPR	2824.3	3	4.6521	0.4219
HLGTLNFGGIR	1185.4	2	2.6954	0.3067
HLHAILGPMLLNRPLDGVTNSLPSPEQLK	3162.7	3	3.8319	0.1706
HLHESLLQQLQDSVQNLDGHVR	2567.8	3	4.0606	0.4631
HLHFVDVDDLHIIVQELR	2199.5	2	2.7945	0.1203
HLHPIQTSFQEATASK	1796.0	2	3.2532	0.3779
HLHTLIFNAAR	1293.5	2	2.7019	0.3067
HLIATQLLSNLEDIMR	1868.2	2	3.2066	0.3208
HLIEMGYLQGGK	1346.6	2	2.7548	0.2652
HLIIENFIPLEEK	1595.9	2	3.8514	0.3021
HLIKAEEPKKKK	1449.8	2	2.4957	0.1908
HLILPEKYPPPTELLDLQPLPVSALR	2951.5	3	4.6639	0.4627
HLIPAANTGESK	1238.4	2	2.645	0.1087
HLIPMNPNDDSLFK	1641.9	2	3.5248	0.2564
HLISTHFAPGDFQGFALVNPQR	2453.7	3	5.7507	0.4528
HLITTQTEHK	1208.3	2	2.7409	0.1248
HLIVLINK	950.2	2	2.7634	0.1097
HLKAEVDAEKPGATDR	1737.9	2	4.3871	0.4554
HLKEETIQIITK	1453.7	2	3.2948	0.3171
HLKEGGLLTLAGAK	1408.7	2	4.2461	0.3264
HLKLFGYEPTIYYPK	1870.2	3	3.525	0.2899
HLKQTKPEFDQVLQGTAASTK	2328.6	3	4.3451	0.2782
HLLDDNGQDKPVKPPTK	1903.1	2	4.71	0.3678
HLLDDNGQDKPVKPPTKK	2031.3	3	3.481	0.3146
HLLETPGQYLVYNGDLVEYDADHMAQLQR	3390.7	3	6.7984	0.4135
HLLFQSHMATK	1313.6	2	2.6939	0.2782
HLLGVEDLLQK	1265.5	2	3.2298	0.2539
HLLIGVSSDR	1097.3	2	3.0669	0.3116
HLLNQAVGEEEVPK	1563.7	2	2.6278	0.2735
HLLQAPLDDAQEILQAR	1932.2	3	4.7308	0.2651
HLLQAPVDDAQEILHSR	1943.2	3	5.3381	0.5146
HLLSQPLFTESQK	1528.7	2	3.634	0.2802
HLLVHAPEDKK	1287.5	2	3.4118	0.3412
HLLVSNVGGDGEEIER	1724.9	2	3.2062	0.2022

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HLLYGRPAVLYR	1458.7	2	3.1879	0.3422
HLMHLELDISDSK	1538.8	2	3.0157	0.2021
HLMLPDFDLLEDIESK	1916.2	2	5.8851	0.4522
HLNATVNNLQAK	1323.5	2	3.6583	0.3502
HLNDDDVTGSVK	1300.4	2	2.7653	0.2269
HLNDDVVK	940.0	2	2.8132	0.1554
HLNDDVVKIDFEDVIAEPEGTHSFDGIWK	3327.6	3	4.9463	0.3406
HLNDETTSK	1045.1	1	2.5955	0.3822
HLNDETTSKQIK	1414.5	2	3.5267	0.259
HLNDPNSNPK	1136.2	2	2.553	0.2257
HLNEIDLFHCIDPNDSK	2011.2	2	4.2715	0.4406
HLNFLTSEQALADFAELIK	2161.4	2	6.5134	0.507
HLNLAENSSYIHVYR	1817.0	2	2.6858	0.1736
HLNLEYHSSMIADAVK	1829.1	2	3.7989	0.4741
HLNLEYHSSMIADAVKK	1957.2	2	4.6356	0.4502
HLNQEVAVR	1066.2	2	2.8938	0.1815
HLNRPTLDDSSEEEHAIEITTQEITQLFHR	3561.8	3	4.67	0.3295
HLNYTEFTQFLQELQLEHAR	2518.8	3	5.5345	0.3947
HLPASIVEFQPTLR	1608.9	2	2.4324	0.1375
HLPNLQTHKENPVLDVVSNPEQTAGEER	3153.4	3	5.0049	0.4236
HLPSTEPDPHVVR	1484.6	2	2.5113	0.1664
HLQDLFAPLVVR	1408.7	2	3.2889	0.2871
HLQDLMEGLTAK	1356.6	2	2.9272	0.2389
HLQDLSGR	926.0	1	1.9799	0.1368
HLQENTQSHMR	1381.5	2	2.854	0.2238
HLQFIPVVPPR	1303.6	2	2.4104	0.2019
HLQIEIEGLIDQMIDK	1896.2	2	3.6967	0.2926
HLQINQTFEELR	1528.7	2	3.0594	0.2944
HLQKFPTEGLSSVVR	1698.9	3	3.9437	0.3478
HLQLAIR	851.0	2	2.4521	0.1096
HLQLAIRGDEELDSLIK	1951.2	2	4.1177	0.4785
HLQLAIRGDEELDSLIKATIAGGGVIPHIHK	3303.8	3	5.7448	0.4754
HLQLAIRNDEELNK	1693.9	2	4.7872	0.4041
HLQLAIRNDEELNKLLGGVTIAQGGVLPNIQAVLLPK	3947.6	3	5.8935	0.4818
HLQLAIRNDEELNKLLGK	2105.4	3	5.3203	0.4299
HLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPK	4018.7	3	3.8045	0.182

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HLQLAIRNDEELNKLLGRVTIAQGGVLPNIQAVLLPK	4046.8	3	4.2223	0.3295
HLQLAVR	837.0	1	2.7082	0.1644
HLQLAVRNDEELNK	1679.9	2	3.8153	0.2245
HLQLAVRNDEELNKLLGGVTIAQGGVLPNIQAVLLPK	3933.6	3	5.489	0.4368
HLQLKEESVK	1211.4	2	2.756	0.2217
HLQLKEQK	1024.2	2	2.4754	0.1122
HLQLQTQLEQLQEETFRLEAAKDDYR	3204.5	3	4.0781	0.2581
HLQLSFQEPHFYLR	1816.1	2	4.8046	0.3573
HLQPGMVLTVEPGIYFIDHLLDEALADPAR	3332.8	3	6.8524	0.5259
HLQTGENHTSVDPR	1591.7	2	3.5727	0.3851
HLQTYGEHYPLDHFDK	2001.1	3	4.3507	0.3726
HLQVIFGHLAASR	1449.7	3	4.1115	0.4839
HLQVNVTNPVQCSLHGK	1875.1	2	4.4903	0.4619
HLRDEGLR	996.1	2	2.7218	0.2524
HLRDQADFSVLHYAGK	1858.0	3	5.1256	0.3908
HLREEEEEGEKHR	1678.7	2	4.1363	0.3997
HLREYQDLLNVK	1528.7	3	5.2124	0.3098
HLREYQELLNVK	1542.8	2	2.7946	0.1849
HLSASQK	770.9	1	2.4265	0.1966
HLSDHLSELVEQTLSDLEQSK	2409.6	2	6.2321	0.4358
HLSDSINQK	1042.1	2	2.4874	0.1033
HLSDSINQKHFEQAIER	2053.2	2	5.0436	0.4784
HLSIAQEQGDKVGEAR	1738.9	2	2.908	0.2025
HLSIILEKDQLIQEAAAENNK	2378.7	2	5.0033	0.39
HLSIILEKDQLIQEAAAENNKLKEEIR	3147.6	3	5.7838	0.4973
HLSLLTTLSNR	1255.4	2	3.388	0.3563
HLSPYATLTVGDSSHK	1713.9	2	4.3527	0.464
HLSQSSLLLEHLLSSWEQIPK	2446.8	3	5.2689	0.3477
HLSSGDLLRDNMLR	1627.9	2	3.5772	0.3703
HLSSLTDNEQADIFER	1876.0	2	4.0438	0.4042
HLSTFSHQVLQTR	1554.7	2	4.1221	0.4218
HLSVNDLPVGR	1207.4	2	2.9928	0.3398
HLSVVTLAAK	1039.3	2	2.527	0.2164
HLTDAYFK	995.1	2	2.8322	0.1882
HLTDAYFKK	1123.3	2	2.9517	0.2763
HLTDTSHGVR	1123.2	2	2.4951	0.2315

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HLTGEFEKK	1089.2	2	2.4935	0.2476
HLTHENVQR	1134.2	2	2.5996	0.2487
HLTVEELFGTSLPK	1571.8	2	3.3725	0.2221
HLTYAEFTQFLLEIQLEHAK	2432.8	3	3.9262	0.2656
HLTYENVER	1161.2	2	2.527	0.2479
HLVAGGGAGAVSR	1152.3	2	3.4453	0.2441
HLVDPIDDLFLAAK	1567.8	2	3.0899	0.2495
HLVESTNEMAPLKVWQLQDLSFQTAAR	3114.5	3	5.7523	0.4414
HLVFNPSHR	1107.2	2	2.6206	0.2365
HLVFPLLEFLSVK	1542.9	2	3.461	0.2802
HLVGGERDPMNLFAFGDVDGVGINAK	2730.1	3	5.0618	0.4103
HLVGLWTADNATATNLLKR	2095.4	3	3.887	0.3635
HLVGVDSLIGPETQIGEK	1893.1	2	5.485	0.3793
HLVLLDTAQAAAAGHR	1644.9	2	5.6782	0.4949
HLVMGDIPAAVNAFQEAASLLGK	2353.7	3	4.8068	0.4834
HLVMGDIPAAVNAFQEAASLLGKK	2481.9	3	4.5162	0.4638
HLVPGAPFLLQALVR	1632.0	3	4.5009	0.216
HLVSAGYVHVNR	1352.5	2	3.5535	0.3502
HLVSPEALDLLDKLLR	1833.2	3	4.3524	0.4195
HLVYESDKNKDEK	1605.7	2	5.0021	0.3332
HLVYESDQNKDGK	1533.6	2	4.2481	0.4014
HLWDYTFGPEK	1393.5	2	2.949	0.2879
HLYDFVGNIR	1234.4	2	2.4308	0.2212
HLYDTGETKDIHLEMESLVNSR	2588.8	3	4.2482	0.3331
HLYHSSQNELAK	1427.5	2	2.8994	0.2866
HLYTKDIDIHEVR	1639.8	3	4.7304	0.4654
HMDGGQIDGQEITATAVLAPWPRPPPR	2912.3	3	4.4498	0.3918
HMEASLQELK	1186.4	2	2.7965	0.3151
HMEASLQELKASPR	1597.8	3	3.7088	0.3267
HMGIGK	642.8	1	1.9601	0.1639
HMGLFDHAAR	1155.3	2	2.6424	0.2965
HMGVMAGDIYSVFR	1583.9	2	4.0807	0.4777
HMLEEEGTLDLLGLKR	1855.1	2	2.8714	0.2268
HMMAFIEQEANEK	1578.8	2	4.279	0.4533
HMMAFIEQEANEKAEEIDAK	2335.6	2	5.791	0.418
HMMAFIEQEANEKAEEIDAKAEEEFNIEK	3425.7	3	7.1066	0.5142

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HMNLILCDCDEFRK	1738.0	2	3.0726	0.1163
HMNSAGVLATLR	1270.5	2	3.5669	0.4324
HMQANPEPPKKNNDK	1748.9	2	3.5491	0.335
HMQEWLETR	1230.4	2	2.6036	0.2185
HMQFPPMYEENSR	1666.9	2	3.4146	0.2867
HMVFLGGAVLADIMK	1603.0	2	4.6952	0.5047
HMYHSLYLK	1192.4	2	2.8616	0.3371
HMYVFGDFKDVLIPGK	1867.2	3	5.5566	0.495
HMYVFGDFKDVLIPGKLK	2108.5	3	3.6262	0.1267
HNAEVAAFHLDR	1380.5	2	2.552	0.2962
HNAQGQGNGLR	1152.2	2	3.0476	0.2994
HNEETGDNVGPLIIK	1636.8	2	5.1891	0.3276
HNEETGDNVGPLIIKK	1765.0	3	5.4277	0.2819
HNEFDFISGTR	1323.4	2	3.6716	0.3583
HNEFNPQHSLLVQFR	1867.1	2	3.9515	0.2679
HNELTGDNVGPLILK	1620.8	2	4.358	0.4532
HNESVVKEMLELAK	1627.9	2	4.5644	0.4392
HNFLQAHNGQGLR	1492.6	2	3.9369	0.3681
HNFPALFGDVK	1245.4	2	2.8667	0.2945
HNGPNDASDGTVR	1340.3	2	3.4966	0.3514
HNGTGGKSIYGEKFEDENFILK	2484.7	3	4.8419	0.3203
HNHDLSSYQDTIQQLENELR	2441.6	3	3.5209	0.2207
HNIAGTTHSGAEK	1323.4	2	4.1478	0.3304
HNIAYFPQIVSVAAR	1686.9	2	4.8383	0.3718
HNIICLQNDHK	1335.5	3	4.8181	0.2659
HNIMDFAMPYFIQVMK	1986.4	2	4.2669	0.4453
HNIQFSSFDIFSDEEVR	2071.2	2	4.7327	0.4529
HNIRHTEKKPFK	1535.8	2	2.5703	0.1934
HNKEFLLSMANR	1460.7	2	3.3785	0.2943
HNKPEVEVR	1108.2	2	3.1338	0.324
HNKTTAQVLIR	1281.5	2	2.5122	0.2516
HNLEQDLVREELNKR	1894.1	2	2.9952	0.1492
HNLITEMVALNPDFKPPADYKPPATR	2937.4	3	6.0371	0.4585
HNLLRPETVESLFYLYR	2151.5	3	4.2982	0.3865
HNLQDFINIK	1242.4	2	3.8025	0.2433
HNLYSSESEDR	1337.3	2	2.6215	0.3077

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HNNLDLVIIR	1207.4	2	3.0841	0.3114
HNNLDLVIIREQTEGEYSSLEHESAR	3041.2	3	4.0391	0.244
HNPTGAVLFMGQINKP	1725.0	2	2.4637	0.1567
HNPTVTGHQEQTYLQK	1882.0	2	4.6425	0.4879
HNQLPLVIEFTEQTAPK	1966.2	3	5.2525	0.4479
HNSEKPPEPVKPEVK	1715.9	2	3.7462	0.2825
HNSFADFLQAHLHTADLER	2223.4	2	3.6717	0.3698
HNSSGSILFLGR	1288.4	2	3.5313	0.4198
HNSTTSSTSSGGYR	1442.4	2	2.8881	0.2987
HNSTTSSTSSGGYRR	1598.6	2	2.9169	0.2028
HNTALLAATDLLK	1381.6	2	3.0346	0.3599
HNTALLAATDLLKR	1537.8	3	5.147	0.4205
HNTEDFTLFTLDDVDAAFDKIQQLK	2926.2	3	5.8143	0.4228
HNTPEDAK	911.9	2	3.0505	0.2569
HNVMISTEWAAPNVLR	1839.1	2	4.6958	0.384
HNYELDEAVTLQR	1588.7	2	4.6568	0.4544
HNYELGGPMTLQR	1516.7	2	3.9321	0.3536
HNYGVGESFTVQR	1494.6	2	3.5935	0.442
HNYGVVESFTVQR	1536.7	2	3.7226	0.3545
HPDASVNFSEFSKK	1593.7	2	4.3555	0.3505
HPDFLPYDHAR	1368.5	3	3.2108	0.2731
HPDSHQLFIGNLPHEVDK	2084.3	2	3.1869	0.2898
HPDSHQLFIGNLPHEVDKSELK	2541.8	3	5.0678	0.418
HPDSHQLFIGNLPHEVDKSELKDFFQSYGNVVELR	4097.5	3	5.1729	0.414
HPDVEVDGFSELR	1500.6	2	2.5461	0.1083
HPDYSVVLLLR	1312.5	2	2.8301	0.2898
HPEAEMAQNSVR	1369.5	2	2.6263	0.1376
HPELADK	809.9	1	2.2701	0.1396
HPELADKNVPNLHVMK	1843.1	2	3.9052	0.397
HPFFLDDRR	1203.3	2	2.5337	0.1856
HPFLLLGTTANR	1340.6	2	2.5974	0.2082
HPGAHQGNLASGLHSNAIASPGSPSLGR	2691.9	3	3.7788	0.3388
HPGHYAVYNLSPR	1511.7	2	2.8515	0.3362
HPGSFDVVHVK	1222.4	3	4.1888	0.3278
HPGSFDVVHVKDANGNSFATR	2256.4	2	3.4441	0.4091
HPHDIIDDINSGAVECPAS	1991.1	2	4.5556	0.3752

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HPLLHIQK	986.2	1	2.3353	0.2259
HPLQNR	764.9	1	1.7716	0.2031
HPNVHFVLNQESMTLTGLPNHLAK	2699.1	3	4.0308	0.3288
HPPAPAEPSSDLASK	1504.6	2	3.2494	0.3139
HPQAHVDIYEK	1337.5	2	2.4804	0.2081
HPQELLASADFQPVPSIVGVNNNEFGWLIPK	3418.8	3	3.8194	0.1646
HPSHSTTPSGPGDEVAR	1732.8	2	5.0009	0.3777
HPSSPPVVDTVHGK	1457.6	3	5.3338	0.4522
HPTPLALGHFHTVTLLR	1911.2	3	3.3113	0.3377
HPVISESEVFQQFLNFR	2078.3	2	3.9973	0.3988
HPVLLLHPLGGWTK	1568.9	2	3.8959	0.3515
HPVSCKDTPGFIVNR	1670.9	2	3.9037	0.4065
HPVSLEQYLMEGSYNK	1896.1	2	3.7009	0.4635
HPWDDISYVLPEHMSM	1958.2	2	3.8279	0.3162
HPWIVHWDQLPQYQLNR	2231.5	3	3.2834	0.1805
HPYFYAPELLFFAK	1744.0	3	4.2838	0.3266
HPYFYAPELLFFAKR	1900.2	3	3.9222	0.3517
HQAFEAELHANADR	1609.7	2	4.7967	0.4656
HQAFMAELASNKEWLDKIEK	2389.7	2	4.5759	0.3884
HQALQAEIAGHEPR	1557.7	2	4.9635	0.4942
HQAQIDHYLGLANK	1608.8	2	5.1029	0.4804
HQAQIDQYLGLVR	1541.7	2	3.3593	0.3526
HQASINELKR	1196.3	2	3.2679	0.341
HQASISELKR	1169.3	2	2.7146	0.2489
HQAVQLPR	949.1	2	2.5232	0.2197
HQAVQLPREGQEDQGLTKDFSNSPLHR	3089.3	3	4.4843	0.3168
HQDDLQDVIGR	1296.4	2	3.1634	0.3857
HQDLQFAGLLNPLDSPHHMR	2327.6	3	4.9946	0.1986
HQDVATR	826.9	2	2.7201	0.1587
HQDVFSSAQRLDPVYFVAPAK	2376.7	3	3.3779	0.2846
HQDVPSQDDSKPTQR	1738.8	2	4.3399	0.3882
HQEAEMAQNAVR	1384.5	2	3.5971	0.2822
HQEGEIFDTEK	1333.4	2	2.5987	0.3035
HQEGEIFDTEKEK	1590.7	2	4.0071	0.3844
HQEGEIFDTEKEKYEITEQR	2510.7	3	5.6595	0.477
HQEGEIFDTEKEKYEITEQRK	2638.8	3	3.704	0.1092

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HQEHILR	933.0	1	1.6865	0.1312
HQEHKGEIDAHEDSFK	1908.0	2	4.268	0.3795
HQELETLKDLYNQDDNHQELGSFHIR	3181.4	3	4.8019	0.3757
HQEQHHPELEDK	1527.6	2	4.5562	0.336
HQEQHHPELEDKDLDFK	2146.3	3	3.2579	0.2256
HQEQHHPELEDKDLDFKNK	2388.5	3	4.4579	0.2861
HQEYLNSILQHAK	1581.8	3	4.2918	0.3011
HQFGQEKDVFAPR	1559.7	2	3.5343	0.3661
HQFGTDKDVFGPR	1504.6	2	3.0932	0.236
HQGAEELLDEESR	1513.5	2	3.2711	0.2541
HQGALYSLFPDHHVK	1750.0	2	3.9248	0.4128
HQGMTVGMGQK	1174.4	2	2.7666	0.129
HQGVMVGMGQK	1172.4	1	3.4515	0.4405
HQGVMVGMGQKDCYVGDEAQSK	2368.7	2	3.9182	0.3778
HQGVMVGMGQKDCYVGDEAQSKR	2524.8	3	3.5587	0.301
HQGVMVGMGQKDSYVGDEAQSK	2352.6	2	6.429	0.5744
HQGVMVGMGQKDSYVGDEAQSKR	2508.8	3	5.3051	0.5178
HQGVMVSMGQKDSYVGDEAQSK	2382.6	3	4.6896	0.3682
HQGVMVSMGQKDSYVGDEAQSKR	2538.8	3	5.4644	0.4163
HQILEQAVEDYAETVHQLSK	2339.5	3	7.1114	0.5555
HQITYLIHQAK	1352.6	2	3.287	0.3265
HQIVEVAGDDKYGR	1587.7	2	5.1628	0.4872
HQIVEVAGDDKYGRK	1715.9	2	5.4747	0.4401
HQKIIEEAPAPGIK	1531.8	2	2.5051	0.1905
HQKVVEIAPAAHLDPQLR	2023.3	3	3.5285	0.2196
HQLILPAFEHEYR	1653.9	3	4.6163	0.3764
HQLVVSSPPRPVR	1472.7	2	2.6765	0.1412
HQNLKEFALTNPEK	1669.9	2	4.3807	0.3674
HQNLLKELQDLALQGAK	1920.2	2	6.0462	0.4767
HQNLLKELQDLALQGAKE	2049.3	2	4.8252	0.3745
HQNLLKELQDLALQGAKER	2205.5	3	4.4248	0.4496
HQNQNTIQELLQNCSDCLMR	2389.7	2	3.6711	0.2073
HQNVQLPR	992.1	2	3.2369	0.2281
HQNVQLPREGQEDQGLTK	2078.2	2	2.8894	0.1442
HQNVQLPREGQEDQGLTKDYGNSPLHR	3118.3	3	4.8062	0.3329
HQPADLLEFALQHFTR	1924.2	3	4.8214	0.4433

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HQPQEFPTYVEPTNDEICEAFRK	2780.0	3	3.5998	0.3011
HQPTAIIAK	979.2	1	2.5681	0.1505
HQPTLKTDATTAIIK	1638.9	2	3.3314	0.3951
HQQALEVVNNNEEKAK	1852.0	3	3.8111	0.2042
HQQELLEHQR	1318.4	2	3.3909	0.2814
HQQISGR	825.9	2	2.4392	0.1065
HQQLLEEKNILAEQLQAETELFAEAEEMR	3442.8	3	4.4085	0.2142
HQQLSDLHK	1106.2	2	2.706	0.1992
HQQLSGLHK	1048.2	2	2.7942	0.147
HQQTVTIPPKSSLSVPYVIVPLKTGLQEVEVK	3517.1	3	4.6097	0.4334
HQQVPHILQGLLSPR	1724.0	2	3.2534	0.4134
HQSDGNEIAHTR	1365.4	2	2.5739	0.1634
HQSFGAAVLSR	1173.3	2	2.5822	0.3575
HQSFVLVGETGSGK	1446.6	2	4.0191	0.3056
HQTLQGLAFPLQPEAQR	1935.2	2	4.955	0.5091
HQTLQGVAFPISR	1454.7	2	3.4162	0.3983
HQTNISELKR	1226.4	2	3.3701	0.3399
HQTVQLPR	979.1	2	2.4057	0.1822
HQVEQLSSSLK	1256.4	2	3.1307	0.2973
HQVLFIADEIQTGLAR	1812.1	2	4.4954	0.4266
HQVQLLGR	951.1	2	2.5795	0.2069
HRADHPPAEVTSHAASGAK	1940.1	3	3.2819	0.1698
HRAEAPPLEREDSGTFSLGK	2198.4	3	3.2318	0.1693
HRDFVAEPMGEKPVGSLAGIGEVLGK	2695.1	3	6.9279	0.4649
HRDGGEALVSPDGTVTEAPR	2065.2	3	4.5247	0.4698
HRDILQDYTHEFHK	1840.0	3	4.3206	0.2834
HRDLLHNEDR	1305.4	2	2.7251	0.2335
HRDYETATLSDIK	1549.7	2	4.3201	0.4111
HRDYKVDLESK	1390.5	2	2.9324	0.1788
HREEEQLLVQR	1437.6	3	3.4186	0.1506
HREELEQSK	1156.2	2	2.5524	0.1451
HREELSDYEERIEELENLLQQGGSGVIETDLSK	3818.1	3	4.0515	0.298
HRELSGGAEAGTVPTSPGKVPEDSLAR	2719.9	3	4.6993	0.3081
HRFDPVETK	1129.3	2	2.5658	0.1781
HRFEVNPNLIK	1367.6	2	2.473	0.1433
HRGEGENEAVTPK	1424.5	2	3.4614	0.2856

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HRGPGLASGQLYSYPAR	1831.0	2	4.2672	0.4609
HRGPSEVLPPHPEVELLR	2063.3	2	3.9173	0.4086
HRGQAAQPEPSTGFTATPPAPDSPQEPLVLR	3254.6	3	4.7821	0.3571
HRGYLSETVSNALGPQGR	1943.1	2	2.6939	0.1112
HRHPDEAAFFDTASTGK	1888.0	2	2.7835	0.2006
HRLDLGEDYPSGK	1487.6	2	5.068	0.3241
HRLEDMEQALSPSVFK	1888.1	2	4.2577	0.4073
HRLEVEVHQLQDR	1659.8	3	3.2372	0.1679
HRLPDLQAILR	1332.6	3	4.0238	0.1811
HRLQAQLDLIEKDYADR	2085.3	3	4.4436	0.3114
HRPDLIDFDK	1256.4	2	3.1574	0.2224
HRPDLIDFDKLK	1497.7	2	3.3047	0.2705
HRPDLLDFDSLSKDNVFENNR	2532.7	3	3.3178	0.1153
HRPEDVVQFLVSK	1554.8	2	4.2378	0.3619
HRPEDVVQFLVSKK	1682.9	3	3.8686	0.275
HRPELIDYGK	1228.4	2	3.793	0.3276
HRPELIEYDK	1300.4	2	3.2645	0.2263
HRPELIEYDKLR	1569.8	3	5.0942	0.4066
HRPELIEYDKLRKDDPVTNLNNAFEVAEK	3455.8	3	3.8064	0.3008
HRPFPEEVDKIPFVK	1839.1	3	5.2333	0.2862
HRPLNLGPFVVR	1405.7	3	3.5795	0.1826
HRPSEADEEELAR	1539.6	3	4.1191	0.3602
HSAEVAGYQDSIGQLENDLR	2203.3	2	4.2239	0.483
HSAEVAGYQDSIGQLENDLRNTK	2546.7	3	5.0161	0.4921
HSAGGGNVQIVTK	1268.4	2	3.7919	0.3902
HSAILASPNPDEK	1379.5	2	4.4203	0.4203
HSALTIPPTAGPHPFASFHPGLNPLER	2863.2	3	3.2873	0.2517
HSASLIFLHGSGDSGQGLR	1940.1	2	5.3574	0.5399
HSDELTSLLGYFPNKK	1850.1	3	5.528	0.4078
HSDENDGGQPHKR	1477.5	2	4.0319	0.3632
HSDGIFTDSYSR	1385.4	2	2.7089	0.1698
HSEAATAQR	971.0	2	2.43	0.2436
HSEAATAQREEWK	1543.6	2	4.2411	0.393
HSEAFEALQQK	1288.4	2	4.0798	0.291
HSEDQHPTILKK	1433.6	2	2.8013	0.1787
HSEIIKLENSIR	1439.6	2	4.0526	0.3261

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HSEIQQLER	1140.2	2	2.8964	0.2003
HSELLQKVEPLQK	1549.8	2	4.1691	0.2423
HSELSELNVK	1156.3	2	2.9505	0.123
HSELVHVHAELLR	1540.8	2	4.5869	0.4214
HSEVQQANLK	1154.3	2	3.7122	0.3512
HSEYNPQHSLLAQFR	1828.0	3	4.7604	0.4195
HSFDPFADASKGDDLLPAGTEDYIHIR	2989.2	3	5.1645	0.3184
HSFFSGVNWQDVYDKK	1958.1	2	3.0487	0.2345
HSFFSTIDWNK	1382.5	2	3.4334	0.2607
HSFGPLDYESLQQELALK	2076.3	2	4.8795	0.4984
HSFGPLDYESLQQELALKETVWKK	2848.2	3	5.5167	0.4284
HSFSAGPELLR	1214.4	2	2.9704	0.3348
HSGASAEVQKEEEKK	1657.8	2	4.3206	0.3318
HSGDYFTLLR	1209.3	2	2.7575	0.2928
HSGFEDELSEVLENQSSQAE	2236.2	2	5.4215	0.3936
HSGFEDELSEVLENQSSQAELK	2477.6	2	6.2573	0.3969
HSGFEDELSEVLENQSSQAELKEAVEEPSSK	3434.6	3	7.8972	0.4803
HSGFEDELSEVLENQSSQAELKEAVEEPSSKDV	3648.8	3	6.5937	0.5218
HSGFEDELSEVLENQSSQAELKEAVEEPSSKDVM	3780.0	3	5.6447	0.488
HSGFEDELSEVLENQSSQAELKEAVEEPSSKDVME	3909.1	3	6.682	0.4766
HSGFEDELSEVLENQSSQAELKGR	2690.8	3	5.6916	0.393
HSGGFLSSPADFSQENKAPFEAVKR	2707.9	3	4.8362	0.3271
HSGNITFDEIVNIAR	1686.9	2	4.9328	0.553
HSGPNSADSANDGFVR	1631.6	2	4.3504	0.5154
HSGSSHLPQQLK	1319.5	2	4.2226	0.3132
HSGYLWAIGK	1132.3	2	2.4339	0.1016
HSHQDSGLITDYR	1529.6	2	3.0416	0.2812
HSIDKVTSR	1043.2	2	2.5602	0.2692
HSILDTHGR	1036.1	2	2.7887	0.2468
HSISGPISTSKPLTALSDKRPNYGEIPVQEHLLR	3743.2	3	4.6584	0.3995
HSLASSEYPVR	1246.4	2	3.232	0.3619
HSLASTDEKR	1144.2	2	3.3444	0.2752
HSLDASQGTATGPR	1398.5	2	4.7961	0.5038
HSLEQKPTDAPPK	1448.6	2	3.2952	0.1788
HSLEQKPTDAPPKESLELEDPSSGLGVTK	3091.4	3	5.1815	0.3972
HSLEQKPTDAPPKESLELEDPSSGLGVTKQDLGPVPM	3929.4	3	3.3817	0.251

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HSLHEEENNIFKR	1653.8	2	3.7386	0.3142
HSLLPVDDAINGLSEEQR	1994.2	2	6.0341	0.5058
HSLLQTLYK	1103.3	2	3.2059	0.2858
HSLLQTLYKV	1202.4	2	3.8492	0.3778
HSLPDLPYDYGALEPHINAQIMQLHHSK	3226.6	3	5.6051	0.4353
HSLPSGLGLSETQITSHGFDNTK	2427.6	3	5.9077	0.5509
HSLTGHSDIR	1123.2	2	2.6131	0.1749
HSMAYQDLHSEITSLFK	2008.2	2	5.4833	0.5665
HSMNILNR	985.1	2	2.6826	0.1039
HSMNPFCEIAVEEAVR	1833.1	2	2.9048	0.2214
HSNLMLEDLDKSQEEIKK	2158.4	3	3.2038	0.1813
HSNLMLEELDKAQEDILK	2127.4	3	3.7931	0.385
HSPFHLLAGLQDGTLAAYPR	2165.4	3	5.5937	0.476
HSPSHPVGPKPHLDNMVPNALNVGLPDLQTK	3311.8	3	3.3237	0.1912
HSPTEDEESAK	1230.2	2	3.0393	0.3864
HSPTEDEESAKAEADAYIR	2120.2	3	3.6616	0.3685
HSPTSEPTPPGDALPPVSSPHTHR	2502.7	3	4.6433	0.2353
HSQAQSKPTTPEKTDLTNGEHAR	2534.7	3	3.3871	0.2331
HSQAVEELAEQLEQTK	1841.0	2	5.4193	0.4306
HSQAVEELAEQLEQTKR	1997.2	2	6.5796	0.493
HSQDLAFLSMLNDIAAVPATAMPFR	2718.1	3	5.3694	0.389
HSQDLAFLSMLNDIAAVPATAMPFRGYAVLGGER	3621.1	3	3.5122	0.2354
HSQEELLQR	1140.2	2	2.984	0.328
HSQEIAQFQAELAEAR	1829.0	2	2.9368	0.2378
HSQFIGYPITLFVEK	1780.1	3	5.0298	0.502
HSQFIGYPITLFVEKER	2065.4	3	6.6639	0.5169
HSQFIGYPITLYLEK	1810.1	2	4.9039	0.513
HSQFIGYPITLYLEKER	2095.4	3	6.0077	0.478
HSQFLGYPITLYLEK	1810.1	2	5.1652	0.4081
HSQFLGYPITLYLEKER	2095.4	2	7.0194	0.5031
HSQGTFTSDYSK	1358.4	2	4.399	0.4665
HSQNGFIVPPPPEK	1547.7	2	4.3043	0.3982
HSQPATPTPLQSR	1420.6	2	3.4219	0.3728
HSQYHVDGSLEK	1400.5	2	3.3675	0.2577
HSQYHVDGSLEKDR	1671.8	2	3.8388	0.4084
HSRASLQVLGTVGEPINPEAWLWYHRVVGAQR	3629.1	3	3.5116	0.1021

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HSSALGGASLGAR	1184.3	2	3.3535	0.376
HSSDINHLVTQGR	1464.6	2	4.5315	0.4963
HSSHGSDVSLSQILKPNR	1963.1	2	4.9719	0.481
HSSLAGCQIINYR	1462.7	2	4.2941	0.4647
HSSLITPLQAVAQR	1521.7	2	3.7518	0.3412
HSSLITPLQAVAQRDPIIAK	2159.5	3	3.3081	0.221
HSSQTSNLAHK	1210.3	2	3.2301	0.3092
HSSSAPPPPPPGRR	1440.6	2	3.0389	0.1581
HSSVYPTQEELEAVQNMVSHTER	2672.9	3	5.9008	0.4746
HSSYTCICGSGENSAVLHYGHAGAPNDR	2905.1	3	3.3159	0.1585
HSTENDSPTNVQQ	1457.4	2	2.6329	0.2193
HSTFGQSLTQR	1262.4	2	3.4198	0.4278
HSTGDTKVPFCLQSCVKPLK	2189.6	3	3.4823	0.1542
HSTIVPENAAHQGANR	1702.8	2	2.4007	0.3855
HSTLDFMLGAK	1220.4	2	2.8175	0.3035
HSTPHAAFQPNSQIGEEMSQNSFIK	2787.0	3	6.3428	0.4411
HSTVLENTDGK	1201.3	2	2.9101	0.2291
HSTYSSVRPASR	1348.4	2	2.6696	0.1138
HSVASAQLQEK	1198.3	2	3.3315	0.309
HSVATAADLELK	1255.4	2	3.1009	0.3318
HSVESMITTLDPGMAPYIK	2091.4	2	5.3697	0.5217
HSVGVVIGR	924.1	1	2.643	0.1847
HSVHTLVFR	1096.3	2	2.4218	0.2267
HSVPLPTELSSEAK	1495.7	2	3.1206	0.2955
HSVPVYFPAQDPR	1513.7	2	2.6308	0.2887
HSVVAGGGGGEGR	1140.2	2	3.5289	0.4591
HSYFEKPKVDDEPMDVDKGPGSTK	2708.0	3	5.6197	0.2904
HSYTASYDIYDLNKR	1847.0	3	4.6842	0.4725
HTAAGQLVQDLLTQVR	1751.0	2	3.5613	0.2548
HTAAPTDPADGPV	1249.3	2	3.4916	0.3633
HTAFIGDRN	1031.1	1	1.9424	0.1114
HTALAANTQSQQNMHTTTLAR	2296.5	3	4.3975	0.4139
HTAMVSWGGVSIPNSPFR	1944.2	2	4.7419	0.509
HTATGDTIVSSK	1217.3	2	2.6774	0.3027
HTDNTVQWLR	1270.4	2	3.0582	0.301
HTDNVIQWLNAMDEIGLPK	2195.5	2	6.3514	0.6082

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HTEHVFALRPVGFR	1666.9	2	2.4452	0.1315
HTELKEK	885.0	2	2.556	0.1232
HTENEEDKVSSSSFR	1752.8	2	5.1419	0.4502
HTENTFSRPGGR	1359.4	2	2.9779	0.3401
HTGAVLK	725.9	1	1.8105	0.1748
HTGAVLKGPFSR	1270.5	2	2.6327	0.3369
HTGFLEISQHSQEFINR	2044.2	2	5.555	0.4384
HTGPGILSMANAGPNTNCSQCFICTAK	2738.1	3	5.8539	0.3942
HTGPGILSMANAGPNTNGSQFFICTAK	2736.1	3	5.9506	0.4929
HTGPNSPDTANDGFVR	1685.7	3	4.5563	0.5072
HTGYVIELQHVVK	1523.8	3	4.8539	0.4329
HTGYVIELQHVVKGPSGCVESLEVTCR	2942.4	3	4.0622	0.2756
HTHVQDGEAGGITQQIGATNVPLEAINEQTK	3258.5	3	7.9082	0.4768
HTIAVVWGGVNIPHSPYR	2004.3	2	3.8002	0.4164
HTLADNFNPVSEER	1629.7	2	5.2529	0.5507
HTLDQYVESDYTLLYLHHGLTSDNKPSLSWLR	3804.2	3	4.4504	0.3248
HTLEQHNWNIEAAVQDR	2062.2	3	3.298	0.1898
HTLGENIADNGGLK	1439.6	2	3.654	0.3866
HTLNQIDEVK	1197.3	2	2.7964	0.1784
HTLQQHQETPK	1347.5	2	3.4088	0.4626
HTLSFVDVGTGK	1261.4	2	2.9053	0.375
HTLSYVDVGTGK	1277.4	2	3.1305	0.2455
HTMMFSATFPK	1298.6	2	3.2894	0.4106
HTNLTK	713.8	1	1.6994	0.1028
HTNYTMEHIR	1302.4	3	3.8582	0.3617
HTPLVEFEEEESDKRESE	2191.3	3	3.297	0.356
HTQLEQMFR	1190.4	2	2.94	0.2206
HTRPTFSGQQIFALEK	1861.1	2	4.2777	0.3631
HTTDLDASK	988.0	2	2.4782	0.2894
HTTDLDASKIR	1257.4	2	2.7794	0.2188
HTTDLDASKITQGQFDEHYVLSSR	2749.9	3	3.5327	0.2826
HTTEAAAGALQNITAGDRR	1954.1	2	3.4837	0.2396
HTTSIFDDFAHYEK	1711.8	2	4.3909	0.3937
HTTSIFDDFSHYEK	1727.8	2	3.5961	0.2608
HTVDDGLDIR	1141.2	2	2.5619	0.2953
HTVDDGLDIRK	1269.4	2	2.9344	0.3655

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HTVPIYEGYALPHAILR	1951.3	3	5.2225	0.4699
HTVTMIPGDGIGPELMLHVK	2146.6	3	5.2699	0.3654
HTVYPKPEEWPK	1511.7	2	3.3205	0.2785
HTYLPLEVCNIVAGQR	1814.1	2	2.7213	0.2762
HVAAASLIR	938.1	2	2.599	0.2406
HVAAGTQQPYTDGVR	1600.7	2	4.9002	0.4504
HVAEDLGK	869.0	1	2.3781	0.2311
HVAEDLGKVFGER	1457.6	2	4.1396	0.4
HVAEVLEYTKDEQLESLFQR	2435.7	3	6.0181	0.467
HVAVTNMNEHSSR	1482.6	2	4.1877	0.4284
HVDAHATLNDGVVVQVMGLLSNNNQALR	2987.3	3	3.3387	0.1033
HVDAHATLSDGVVVQVMGLLSNSGQPERK	3046.4	3	5.5997	0.3617
HVDNIMFENHTVADR	1799.0	2	4.761	0.5241
HVDNPNGDGR	1081.1	2	2.9429	0.3012
HVDSLSQR	942.0	2	2.7601	0.2836
HVEASGGSGPGDSGPSDPR	1766.8	3	3.6399	0.3411
HVEAVAYYKK	1208.4	2	3.2338	0.3061
HVEDGNVTVQHAALSALR	1918.1	3	3.4794	0.242
HVEKDVLIPK	1178.4	2	3.3204	0.2039
HVENDGYK	962.0	1	1.6935	0.1575
HVENDGYKTIYFFGDK	1934.1	2	4.8188	0.4538
HVEPGNAAIR	1064.2	2	2.5327	0.3213
HVEPGNAAIREK	1321.5	3	3.6167	0.2866
HVETNSYDVQR	1348.4	2	3.1712	0.3904
HVEVQVFGDHHGNAVYLFER	2354.6	3	3.6762	0.2391
HVFAIFNTEQR	1362.5	2	3.6325	0.3833
HVFGESDELIGQK	1459.6	2	4.3021	0.49
HVFGQPVK	912.1	2	2.5064	0.2882
HVFIHTGEKPFQCSQCDMR	2264.6	3	3.6068	0.3025
HVFLTGPPGVGK	1209.4	2	2.4795	0.1995
HVFWGSGSHTLPALLENLK	2107.4	2	2.7874	0.2029
HVGDLGNVTADK	1226.3	2	3.3887	0.3791
HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR	3666.0	3	7.1218	0.5886
HVGKTDPGTVFVMNK	1630.9	2	2.6555	0.2309
HVGMAVAGLLADAR	1381.6	2	4.7486	0.4647
HVGNQQYNVTYVVK	1649.8	2	4.167	0.4238

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HVHLENATEYATLR	1654.8	2	3.8006	0.269
HVHPTTAPDVTSSLPEEK	1946.1	2	4.6281	0.437
HVIDFFK	906.1	2	2.8332	0.2405
HVINFDLPSDIEEYVHR	2084.3	3	5.6719	0.491
HVISYSLSPFEQR	1563.7	2	4.3676	0.4259
HVLDTLIQLAK	1251.5	2	3.5352	0.3237
HVLFGTVGVPEHTYR	1712.9	2	4.4028	0.4095
HVLFPLK	854.1	2	2.4549	0.1097
HVLFPLKSEFVILRDEK	2071.5	3	3.5543	0.3855
HVLGILDR	923.1	2	2.6088	0.1365
HVLQTFGPIPEFSR	1628.9	2	3.7354	0.3892
HVLSVLSK	883.1	2	2.8526	0.1123
HVLTTLGEK	998.2	2	2.5704	0.1338
HVLVILTDMSSYAEALR	1919.2	2	5.4526	0.4279
HVLVTLGEK	996.2	2	2.8503	0.2655
HVMDVVDEELSKLGLLDNHSSEFNVTR	3085.4	3	3.5619	0.1555
HVNALISPGQK	1164.3	2	2.8403	0.1554
HVNEDSQEKK	1214.3	2	2.8594	0.2309
HVNGQDQIVPGLYACGEAACASVHGANR	2839.1	3	6.9143	0.4412
HVNKDLGNMEENK	1528.7	2	3.6193	0.2706
HVNKDLGNMEENKK	1656.8	2	4.4456	0.4683
HVNPVQALSEFK	1369.6	2	2.6512	0.2317
HVNTNPLCDLTPIFKDYEK	2248.5	3	4.1235	0.2644
HVPGGGNVQIQNK	1348.5	2	2.748	0.3776
HVPGGGSVQIVYKPVDLSK	1981.3	2	2.9196	0.2355
HVPVVYVDYPGPASLTQIYGTFNR	2695.0	3	4.946	0.4905
HVQETTDSILSHFQSLSYSLAER	2649.9	2	4.5925	0.3842
HVQGILR	823.0	2	2.6022	0.1627
HVQGPEPAKEVLLKDLLETR	2273.6	3	4.8997	0.3838
HVQSLEPDPGTPGSER	1706.8	2	3.762	0.239
HVSDDMK	831.9	1	2.3824	0.2857
HVSDDMKTHKNPALK	1722.0	3	3.3993	0.2851
HVSHGEELR	1064.1	2	2.7099	0.2495
HVSIQEAESYAESVGAK	1805.9	2	5.5307	0.51
HVSLPSFNQLFGLSDPVNR	2128.4	2	2.6943	0.2751
HVSPAGAAVGIPLSEDEAK	1849.0	2	5.6738	0.532

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HVTAQQPSR	1024.1	2	2.4532	0.1939
HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	3615.2	3	8.4994	0.6243
HVVFGEVTEGLDVLR	1670.9	2	3.4957	0.3714
HVVFGFVK	933.1	2	2.4146	0.2869
HVVFYPTLK	1104.3	2	2.6276	0.2665
HVVLGAIENKVESK	1523.8	2	4.8273	0.3824
HVVPAQVHVNGGALASER	1842.1	2	3.9805	0.4894
HVVPNEVVVQR	1276.5	2	3.2825	0.425
HVVQPGYPAHR	1261.4	2	2.9057	0.2182
HVVQSISTQQEK	1384.5	2	4.3648	0.3814
HVVQSISTQQEKETIAK	1927.1	3	5.7623	0.4529
HWILPQDYDHAQAEAR	1951.1	2	4.8274	0.4091
HWLDSPWPGFFTLDGQPR	2157.4	3	3.364	0.2558
HWMLDKLTGVFAPR	1672.0	2	3.8496	0.4344
HWMLDKLTGVFAPRPSTGPHK	2376.8	3	3.2862	0.2151
HWNHPDSEELPGPPVVKPQSVTVR	2707.0	3	4.8084	0.3958
HWPFMVVNDAGRPK	1654.9	3	4.8663	0.4056
HWPFQVINDGDKPK	1681.9	3	5.2449	0.3904
HYAGDVVYSVIGFIDK	1784.0	2	3.9364	0.2209
HYAMQEAK	978.1	2	2.6253	0.2075
HYASEEIKEK	1234.3	2	3.2329	0.2462
HYASHTGGAVGASSVLLVLPEELDTETINNKVPPR	3674.1	3	5.1058	0.3033
HYCTVANPVSR	1247.4	2	2.4644	0.2051
HYCYPHFTCAVDTENIR	2070.3	2	2.8997	0.1237
HYDLDLVR	1031.1	2	2.7989	0.1654
HYDLSYDTGDK	1314.3	2	3.1646	0.2764
HYEAEHEYYER	1526.5	2	2.6685	0.2386
HYEDGYPGGSDNYGSLSR	1975.0	3	5.2381	0.5102
HYEGLSYNVDSLHQK	1790.9	3	4.6374	0.4001
HYEGSTVPEKK	1275.4	2	3.1838	0.2695
HYFQNTQGLIFVVDSNDR	2154.3	2	4.7733	0.4376
HYFQNTQGLIFVVDSNDRER	2439.6	3	4.1766	0.269
HYGGLTGLNK	1060.2	2	3.4375	0.3519
HYGGLTGLNKAETAAK	1631.8	2	4.7123	0.4732
HYGNKPIGMGGTFIIQK	1862.2	2	4.8761	0.4486
HYGPGWVSMANAGK	1475.7	2	3.9851	0.4621

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
HYGPGWVSMANAGKDTNGSQFFITTVK	2915.2	3	3.6165	0.1297
HYGYNSYSVSNSEK	1635.7	2	4.8898	0.5258
HYGYNSYSVSNSEKDIMAEIYK	2599.8	2	5.9711	0.4697
HYGYSLYSAIK	1302.5	2	3.0975	0.4169
HYHHALPPSR	1215.3	2	2.8922	0.2918
HYIFNPR	947.1	2	2.4076	0.2054
HYILDLLR	1043.2	2	2.6355	0.1592
HYLDFINHYANLFHEK	2062.3	2	5.5571	0.3959
HYLFDVQR	1078.2	2	2.883	0.2954
HYLGHNDDIK	1212.3	2	2.6149	0.1224
HYLHIIENKPLYPVIYDSNGVVLSMPPIINGDHSR	4003.6	3	4.1592	0.2872
HYLHPEEPEYLGK	1612.8	2	2.912	0.2006
HYLLAAVNRQPK	1410.6	2	3.9033	0.234
HYLLSQGWWDEEQEK	1949.1	2	4.153	0.415
HYNEEGSQVYNDAHILEK	2147.2	3	5.4621	0.3996
HYNGEAYEDDEHHPR	1869.8	2	5.8184	0.5151
HYQGTVDK	948.0	2	2.4008	0.1001
HYQHVLAVDPEK	1436.6	2	3.5385	0.3425
HYQTGQPLPK	1169.3	2	2.6748	0.1522
HYSDELQSVISHLLR	1798.0	2	5.6728	0.4493
HYSVVLPTVSHSGFLYK	1935.2	3	4.6517	0.4412
HYTEAIKR	1018.2	1	2.1942	0.1385
IAAAGLDVTSPEPLPTNHPLLTLK	2469.9	3	4.9917	0.4668
IAAAILNTPDLR	1268.5	2	3.8868	0.301
IAAAILNTPDLRK	1396.7	2	3.3735	0.3
IAAEEKKKQDELKR	1686.9	2	4.1577	0.2577
IAAGEKIPLSQEEITLQGHAFEAR	2609.9	3	5.7704	0.3983
IAAGLPMAGIPFLTTDLTYR	2122.5	2	3.7583	0.2506
IAAHPNVQK	978.1	2	2.5799	0.1874
IAALQAFADQLIAAGHYAK	1973.3	3	5.4212	0.4905
IAAPLTKVDEIVVLSGDNSK	2070.4	3	3.5427	0.2027
IAAQDLLLAVATDFQNESAAALAAAATR	2788.1	3	4.6031	0.3184
IAAVHNVPLSVLIRPLPSVLDPAK	2521.0	3	3.8011	0.2676
IADDKYNDTFWKEFGTNIK	2306.5	2	5.0985	0.4771
IADFGLARVFSPDGSR	1708.9	2	2.9531	0.1718
IADGSVKREDIFYTSK	1830.0	3	3.3669	0.254

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IADGYEQAAR	1094.2	2	4.0218	0.3704
IADLPPANPDHIGGYR	1706.9	2	3.561	0.4203
IADMGHLK	885.1	2	2.5773	0.1832
IADNHTPK	896.0	2	2.7096	0.1299
IADRLGLELGK	1185.4	2	2.9755	0.2271
IADRLGLELGKVVTK	1612.9	2	3.4982	0.2153
IAEANKLK	887.1	2	2.5399	0.1277
IAEESNFPFIK	1295.5	2	3.2165	0.2083
IAEFAFEYAR	1217.4	2	3.3962	0.2115
IAEFTTNLTEEEEK	1654.8	2	4.6927	0.403
IAEFTTNLTEEEEKSK	1870.0	2	5.0781	0.4606
IAEGAQQGDPLSR	1342.4	2	3.1313	0.2719
IAEGEHPKDIR	1265.4	2	2.6057	0.1409
IAEGGAAHR	882.0	2	2.4447	0.173
IAEIHESR	955.1	2	2.4005	0.149
IAEKDDDLKR	1203.3	2	2.6867	0.1176
IAELEMGLLHLQQNIEIPEISLPIHPMITNVAK	3707.4	3	6.149	0.4039
IAELLENVTLIHKPVSLQPR	2271.7	3	4.2351	0.4078
IAELLSPGSVDPLTR	1568.8	2	5.0327	0.371
IAEMTDIKPILR	1400.7	2	2.6242	0.2073
IAENPANPPVGGK	1264.4	2	3.341	0.3191
IAEQQKAQAEVEGLGKGVAR	2083.3	3	4.9979	0.1849
IAEQVASFQEEK	1379.5	2	4.1275	0.3459
IAESLGGSGYSVER	1425.5	2	2.7242	0.3363
IAESNHIK	912.0	2	2.9137	0.1787
IAETDFEKR	1109.2	2	2.472	0.1028
IAEVDASVVR	1059.2	2	3.1133	0.2843
IAEVGAGGNK	916.0	2	2.5478	0.1867
IAEVGGVPYLLPLVNQK	1811.2	2	4.8273	0.3353
IAEVGGVPYLLPLVNQKK	1939.3	2	3.7139	0.2376
IAFAITAIK	948.2	2	3.3446	0.1753
IAFGGETDEATR	1267.3	2	3.6711	0.3388
IAFIMDESNVLDSGFLER	2057.3	2	4.1563	0.3462
IAGAGLLFVGGGIGGTILYAK	1949.3	2	4.8304	0.3753
IAGDQSTLQR	1089.2	2	3.3039	0.2426
IAGHPLAQNER	1206.3	2	3.0483	0.2726

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IAGLEEEKQK	1145.3	2	2.6984	0.1878
IAGMDPVVHSALQEER	1753.0	2	3.2221	0.2589
IAGPGLGSGVR	984.1	2	2.938	0.2828
IAGQVAAANK	943.1	2	3.2557	0.2399
IAGQVAAANKKH	1208.4	2	3.2518	0.2069
IAGYVTHLMK	1133.4	2	3.4338	0.3738
IAHFDLKPENIMLLDKNVPNPR	2576.0	3	3.6759	0.1123
IAHIMGPPDR	1107.3	2	2.6508	0.168
IAHLAGVKDQLTKENEELKQR	2421.7	3	3.5937	0.1816
IAIDNLEKAELLQGGDLLR	2082.4	2	2.6531	0.3247
IAIIVDDIIDDVDSFLAAAETLKER	2747.1	2	4.6406	0.5435
IAIIVDDIIDDVESFVAAAEILKER	2759.1	2	4.1077	0.3363
IAILDIEPQTLK	1354.6	2	3.2455	0.3135
IAILGFAFKK	1108.4	2	2.5118	0.2021
IAILHENFTTVKPEDAYEDFIVKPPVR	3143.6	3	6.1806	0.5238
IAILHENFTTVKPEDAYEDFIVKPPVRK	3271.8	3	5.6104	0.3931
IAILTCPFEPPKPK	1554.9	2	2.7845	0.2845
IAIPGLAGAGNSVLLVSNLNPER	2276.6	2	5.7671	0.5298
IAIVNHDK	910.1	2	2.5752	0.1986
IAIYELLFK	1110.4	2	2.659	0.1336
IAIYELLFKEGVMVAK	1825.2	2	3.4874	0.2589
IAKEEIFGPVQEILR	1743.0	2	3.0347	0.2296
IAKEEIFGPVQPILK	1683.0	2	3.9583	0.297
IAKEEIFGPVQPLFK	1717.0	2	4.5457	0.2343
IAKEEIFGPVQPLFKFK	1992.4	2	2.4389	0.1087
IAKEEIFGPVQQIMK	1732.1	3	5.2468	0.4018
IAKEEIFGPVQQIMKFK	2007.4	3	3.7624	0.2345
IAKEIQVIPLQRDDED	1883.1	2	4.1976	0.1809
IALDKNPETRPSAAQLLEHPFVSSITSNK	3165.5	3	5.5045	0.4155
IALLEEAKK	1015.2	2	2.6986	0.1758
IALLEEAR	915.1	2	2.9009	0.1299
IALLPLLQAETDRR	1609.9	2	2.6106	0.125
IALLQSLLDDANLR	1555.8	2	2.8618	0.2594
IALTDNALIAR	1171.4	2	3.6653	0.3363
IALVITDGR	958.1	2	2.8835	0.2045
IAMENDDGRTEEEKHSAVQR	2316.5	3	4.5195	0.3316

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IANAIMK	761.0	1	1.9292	0.1059
IANATEGSSER	1135.2	2	3.5212	0.3237
IANAVVQNLERGPVQTHISEVIR	2544.9	3	4.1517	0.2385
IANAYIIKEHFEK	1576.8	2	4.0819	0.2922
IANDNSLNHEYLPILGLAEFR	2400.7	3	5.7728	0.5162
IANEVIGEMNLKPEEVFLAQGTLRPDLIESASLVASGK	4041.6	3	5.9614	0.4495
IANFKIEPPGLFR	1502.8	2	3.8746	0.1946
IANILKDKDPPIPVAK	1733.1	3	3.6478	0.3965
IANKLFGEK	1020.2	2	2.4786	0.2331
IANLLKPDK	1012.2	2	2.8161	0.1276
IANLLKPDKEIVQDGDHMIIR	2419.8	3	6.9573	0.5105
IANLQTDLSDGLR	1416.6	2	4.1663	0.4114
IANPVEGSSGR	1087.2	2	2.9024	0.3211
IANPVEGSTDR	1159.2	2	3.1474	0.3589
IANPVEGSTDRQVTITGSAASISLAQYLINVR	3346.7	3	3.3395	0.1298
IAPLAEGALPYNLAELQR	1940.2	2	4.9276	0.3721
IAPLEEGTLPFNLAEAQR	1970.2	2	5.4634	0.5106
IAPNHLNVYINLANLIR	1949.3	2	2.7871	0.2338
IAPVHIDTESISALIK	1708.0	2	2.6248	0.1098
IAQDLEMYGINYFEIK	1948.2	2	4.9636	0.3314
IAQDLEMYGVNYFSIK	1892.2	2	3.4031	0.3744
IAQFLSDIPETVPLSTVNR	2101.4	2	5.1056	0.475
IAQITGPPDR	1068.2	2	2.4397	0.2158
IAQLEEELEEEQGNTELINDR	2473.6	2	6.8265	0.4242
IAQLEEELEEEQGNTELINDRLK	2714.9	3	6.0538	0.4258
IAQLEEELEEEQSNMELLNDR	2533.7	3	5.3713	0.2316
IAQLEEELEEEQSNMELLNDRFR	2837.1	3	3.8503	0.2302
IAQLEEQLDNETK	1531.6	2	4.8285	0.3527
IAQLEEQLDNETKER	1816.9	2	5.3842	0.3496
IAQNDHDLGDMSTVADPSVISHLFSHR	2964.2	3	6.2904	0.4795
IAQNFGLQHLSSGHFLR	1926.2	2	4.9214	0.4885
IAQSAELADREK	1331.5	2	2.5938	0.1248
IAQSDYIPTQQDVLR	1747.9	2	4.2133	0.3411
IAQSEAELISDEAQADLALR	2144.3	2	5.3309	0.331
IARDEGGK	845.9	2	2.6968	0.1822
IARELAEDDSILK	1473.7	3	4.2823	0.2819

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IASDEEIQGTK	1191.3	2	3.054	0.1803
IASDEEIQGTKDAVIQDLER	2231.4	3	5.3332	0.2216
IASGLGLAWIVGR	1313.6	2	3.5065	0.3976
IASHYYITNDTVQTYNQLLKPTLSEIELFR	3573.0	3	4.539	0.4256
IASLEVENQSLR	1359.5	2	4.3673	0.343
IASLEVENQSLRGVVQELQQAISK	2641.0	3	6.0813	0.4026
IASLEVENQSLRGVVQELQQAISKLEAR	3110.5	3	6.0391	0.3833
IASNSATAFR	1038.1	2	2.9328	0.2672
IASQVAALDLGYKPGVEAIR	2072.4	3	4.0426	0.3227
IASWADLVNAHVVPGSGVVK	2020.3	2	2.9486	0.2563
IATEKDFLEAVNK	1478.7	2	2.8556	0.2332
IATEKDFLEAVNKVIK	1819.1	3	4.6952	0.3522
IATKNDVDVQIDQESYLPEDIAGGVEIYNGDR	3538.8	3	5.9771	0.2711
IATNALKGHAK	1124.3	2	3.5036	0.3025
IATSLDGFDVASVQQQR	1836.0	2	4.8886	0.3841
IATTAEPADKVK	1244.4	2	2.7102	0.2561
IAVAAQNCYK	1081.3	2	3.1361	0.2441
IAVAHNGELVNAAR	1435.6	2	2.4482	0.11
IAVEAQNKYER	1321.5	2	3.1015	0.3255
IAVEAQNKYERELMLHAADVEALQAAK	3013.4	3	3.7352	0.2492
IAVGSDADLVIWDPDSVK	1901.1	2	3.4308	0.2313
IAVGSDADLVIWDPDSVKTISAK	2401.7	3	4.2101	0.3804
IAVGSDADVVIWDPDKLK	1942.2	2	4.2945	0.3064
IAVSKPSGPQPQADLQALLQSGAQVR	2661.0	3	4.832	0.2574
IAVVAFFPENGVSDFQK	1869.1	2	4.1972	0.413
IAVVGEGR	800.9	2	2.5378	0.1292
IAWPPPTELGSSGSALEEGIK	2140.4	3	4.1809	0.3112
ICHCFSKDEKPVEAIR	1876.2	2	2.7542	0.1081
IDAASPLEKVCLIGCGFSTGYGSAVK	2588.0	3	3.6994	0.278
IDAMHGVVGPYVK	1386.6	2	3.5748	0.2904
IDAMHGVVGPYVKK	1514.8	2	3.901	0.3521
IDASKNEEDEGHSNSSPR	1973.0	3	5.0237	0.3955
IDASKNEEDEGK	1335.4	2	3.9073	0.2942
IDASKSVDEVFDEVVQIFDKEG	2470.7	2	5.0327	0.4682
IDASQTEFEK	1168.2	2	2.7108	0.2315
IDASQTEFEKNVWSFLK	2043.3	2	3.7782	0.3809

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IDATQVEVNPFGETPEGQVVCFDAK	2695.0	3	5.1489	0.4241
IDATSASVLASR	1191.3	2	4.4568	0.4202
IDATSASVLASRFDVSGYPTIK	2299.6	3	5.0893	0.4049
IDAVNAETIR	1102.2	2	2.6351	0.1053
IDDGHRLCSDLMNCLHER	2128.4	3	3.3238	0.1083
IDDIADGAVKPPPNKYPIFFFGTHETAFLGPK	3505.0	3	4.5184	0.3974
IDDIRKPGESEE	1388.5	2	3.0755	0.2253
IDDIVSGHK	984.1	2	2.7893	0.2067
IDDIVSGHKK	1112.3	2	2.6085	0.152
IDDKPVKIDK	1171.4	2	2.589	0.1293
IDDKPVKIDKWDGSAVK	1915.2	3	4.5148	0.4288
IDDLEKNIADLMTQAGVEELESENKIPATQK	3444.8	3	5.1498	0.2743
IDDLEKNIADLMTQAGVEELESENKIPATQKS	3531.9	3	4.9044	0.4596
IDDLIKLHPESKDDKHGSYEDAVHSGALND	3320.5	3	6.3536	0.4035
IDDLQMVLNQTEDHR	1828.0	2	3.9197	0.2289
IDDMSSRIDDLEKNIADLMTQAGVEELESENKIPATQKS	4336.8	3	3.8003	0.2004
IDDPTDSKPEDWDKPEHIPDPDAK	2761.9	3	3.2869	0.12
IDDSKEAMER	1194.3	2	3.3583	0.341
IDDVVNTR	932.0	2	2.563	0.25
IDELPEGAVKPPANKYPIFFFGTHETAFLGPK	3533.0	3	5.5183	0.3454
IDEMPEAAVK	1103.3	2	3.3347	0.2637
IDEPLEGSEDR	1260.3	2	3.8776	0.2979
IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	3832.2	3	5.7828	0.467
IDESSLTGESDHVKK	1645.8	2	4.1298	0.3153
IDEYDYSKPIQGQQK	1813.0	2	4.8495	0.3132
IDFEKEPLGVNAK	1460.7	2	3.9335	0.2153
IDFSKLTSLNVK	1365.6	2	3.8947	0.3228
IDFSSIAVPGTSSPR	1534.7	2	4.4667	0.4111
IDFYFDENPYFENK	1842.0	2	5.287	0.415
IDFYFDENPYFENKVLSKEFHLNESGDPSSK	3698.0	3	3.5862	0.1349
IDGATQSSPAEPK	1301.4	2	3.5657	0.2894
IDGDKDGFVTVDELKDWIK	2194.4	3	5.0416	0.3496
IDGITIHQSLAIIEYLEETRPTPR	2767.1	3	3.4103	0.3207
IDGNLVVRPYTPISSDDDKGFVDLVIK	2977.4	3	6.1011	0.4415
IDHQGKLPVLLLGR	1559.9	2	4.0689	0.2901
IDIDPEETVK	1159.3	2	2.8379	0.1213

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IDIIPNPQER	1195.4	2	2.5226	0.1071
IDILVNNGGMSQR	1417.6	2	3.0979	0.2155
IDINMSGFNETDDLKR	1869.0	2	3.3735	0.3692
IDIPSFDWPIAPFPR	1772.0	2	3.3692	0.3714
IDISNVKIPK	1127.4	2	3.0296	0.2077
IDKAVAFQNPQTHVIENLHAAAYR	2708.0	3	5.8458	0.5102
IDKLMIEMDGTENK	1637.9	2	4.2782	0.2832
IDKTDYMVGSYGPR	1602.8	2	3.8721	0.3689
IDKTDYMVGSYGPRAEEYEFLTPVEEAPK	3336.7	3	3.9841	0.366
IDLPEYQGEPDEISIQK	1975.1	2	3.6059	0.3183
IDLRPVLGEGVPILASFLR	2066.5	3	3.7474	0.2869
IDLSHVTSK	1000.1	2	2.4955	0.2332
IDMNLTDLLGELQR	1631.9	2	2.9226	0.1566
IDNQSQPLGNKVEMEIVSMLEK	2503.9	3	4.4603	0.2795
IDNSQVESGSLEDDWDFLPPK	2392.5	2	5.6938	0.4482
IDNSQVESGSLEDDWDFLPPKK	2520.7	3	4.851	0.4199
IDQIEDLQDQLEDMMEDANEIQEALSR	3193.4	3	5.0013	0.4594
IDQLEGDHQLIQEALIFDNK	2340.6	3	5.8142	0.3896
IDQLEGDHQLIQEALIFDNKHTNYTMEHIR	3624.0	3	5.4981	0.3776
IDQLNRELAEQKATEKQHITLALEK	2921.3	3	5.9836	0.3534
IDQPKETHSIGRD	1496.6	2	2.4995	0.2591
IDQVNQLLELDHQK	1693.9	2	3.3321	0.2558
IDQVNQLLELDHQKR	1850.1	2	3.6949	0.2757
IDQYQGADAVGLEEK	1636.7	2	5.1636	0.404
IDRLTDEGAVHVNDR	1710.8	3	3.8993	0.2711
IDSDISGTLK	1049.2	2	2.5399	0.1162
IDSEGGVSANHTSR	1430.5	2	3.7619	0.4106
IDSGLYLGSGYFTAIQNLR	2089.3	2	2.8919	0.1861
IDSGSEVIVGVNK	1317.5	2	3.3762	0.1685
IDSILEVVQTGR	1330.5	2	3.8188	0.1888
IDSIPHLNNSTPLVDPSVYGYGVQK	2715.0	3	5.6751	0.2879
IDSLLENDRQQTHMLDVMQDHFSR	2930.2	3	5.4253	0.3692
IDSLSAQLSQLQK	1431.6	2	4.1692	0.1789
IDSRLEQYTSAIEGTK	1812.0	2	4.2463	0.3076
IDSYQEPFTHSAPESIPDTFEDAVNILKPSTIIGVAGAGR	4245.7	3	5.3045	0.482
IDTIEIITDR	1189.3	2	4.1275	0.3461

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IDTRNELESYAYSLK	1803.0	2	4.1755	0.3617
IDTRNELESYAYSLKNQIGDKEK	2716.0	3	4.899	0.2307
IDVSVAAGHTDR	1241.3	2	3.0777	0.1467
IDVTAPDVSIEEPEGK	1699.8	2	3.3859	0.2882
IDVYHYEVDIKPDK	1734.9	3	3.2633	0.1878
IDYGEYMDKNNVR	1617.8	2	3.82	0.4206
IDYIAGLDSR	1123.2	2	3.519	0.294
IEADSESQEDIIR	1505.6	2	3.7723	0.1301
IEAIVKNYPEGHK	1498.7	2	4.1202	0.2585
IEANEALVK	987.1	2	3.4027	0.2207
IEASKNELHNLLDKPQLQGIPVLVLGNK	3082.6	3	3.9897	0.2208
IEASKNELHNLLDKPQLQGIPVLVLGNKR	3238.8	3	4.8813	0.3693
IEASLQHEITR	1297.4	2	3.3747	0.2907
IEASRNELHNLLDKPQLQGIPVLVLGNK	3110.6	3	5.9748	0.3484
IEASRNELHNLLDKPQLQGIPVLVLGNKR	3266.8	3	5.6622	0.2531
IEDGNNFGVAVQEK	1520.6	2	3.9458	0.3774
IEDGVPQHLVLVLGGK	1675.0	2	3.9335	0.3721
IEDPSLLNSR	1144.3	2	2.4344	0.2507
IEDVTPIPSDSTR	1430.5	2	4.0091	0.4052
IEEELGDEAR	1161.2	2	4.2862	0.1304
IEEFVYEKLDR	1441.6	2	3.2052	0.3149
IEEGVPQFLVLISSGKSDDEVDDPAVELK	3130.4	3	3.2841	0.1617
IEEGVPQFLVLISSGKSDDEVDDPAVELKQFGVAPFTIAR	4318.8	3	4.1428	0.1988
IEELQLIVNDKSQNLR	1913.2	3	3.8406	0.1655
IEEVPELPLVVEDKVEGYKK	2314.7	2	3.8603	0.3828
IEFSLPDLEGR	1276.4	2	3.0475	0.1559
IEGDPQGVQQAK	1270.4	2	3.1239	0.2689
IEGDPQGVQQAKR	1426.6	2	3.4758	0.4146
IEGEGSVLQAK	1131.3	2	3.1606	0.3204
IEGLDIHFIHVKPPQLPAGHTPK	2546.0	3	4.4223	0.3653
IEGSNKVPVDPATYGQFYGGDSYIILYNYR	3401.7	3	3.6615	0.3105
IEIESFYEGEDFSETLTR	2166.3	2	5.9108	0.5924
IEIKLSDIPEGK	1342.6	2	3.4796	0.1602
IEINFPAEYPFKPPK	1791.1	2	3.8951	0.2131
IEIPVTPTGQSVPSSPSIPGTPTLK	2504.9	3	3.6585	0.1079
IEIQNIFEEAQSLVR	1790.0	2	4.8407	0.3717

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IEKDTEGHLVR	1297.4	2	3.3968	0.2483
IEKLEEYITTSK	1454.6	2	4.443	0.2135
IEKVEHSDLSFSK	1519.7	2	4.8553	0.4109
IELDKSARHLYICDYHKNLIQSVR	2916.4	3	3.4074	0.1613
IELLGSYDPQK	1263.4	2	2.844	0.1056
IELSVWKDDLTTHAVDAVVNAANEDLLHGGGLALALVK	3970.5	3	6.6329	0.5394
IENELKEINTNQEALKR	2043.3	2	6.0218	0.3382
IENFKSGVDADSSYFK	1807.9	2	4.2239	0.3381
IENHEGVR	954.0	1	2.3214	0.1342
IENLSNLHQLQMLELGSNR	2210.5	3	5.3399	0.2953
IENVVLVVPVK	1209.5	2	3.5352	0.2147
IEPADAHVLQK	1221.4	2	2.8518	0.266
IEPELDGSAQVTSHDASTNGLINFIK	2758.0	3	3.8593	0.3558
IEQLSPFPFDLLLK	1661.0	2	4.4505	0.2911
IEQSQHLFQAHK	1466.6	2	3.411	0.2518
IEQSQHLFQAHKEK	1723.9	2	3.5184	0.3909
IEREKEELMER	1462.7	2	2.9767	0.2069
IESDVQEPTEPEDDLDIMLGNK	2488.7	3	3.4111	0.1135
IESEKGKDAFPVAGQK	1704.9	2	4.8837	0.3853
IESILMSLPLTAR	1444.8	2	3.6276	0.2065
IESLSSQLSNLQK	1447.6	2	4.4275	0.3125
IESPEEISLLPK	1355.6	2	3.3314	0.1933
IESVLSSSGK	1007.1	2	3.08	0.197
IESVLSSSGKR	1163.3	2	3.2753	0.2852
IETMLGDVAVAVHPK	1580.9	2	2.4837	0.2201
IETNENNLESAK	1362.4	2	3.6486	0.3361
IETRDGKLVSESSDVLPK	1974.2	3	3.7463	0.1388
IEVEKPFAIAK	1245.5	2	3.5185	0.2374
IEVIEIMTDR	1219.4	2	3.7707	0.314
IEVIKPGDLGVDLTSK	1685.0	2	4.6163	0.3782
IEVQDTSGGTTALRPSASTQALSSSVSSSK	2954.2	3	6.0805	0.4387
IEWLESHQDADIEDFK	1976.1	2	5.7256	0.409
IEWLESHQDADIEDFKAK	2175.3	2	5.5582	0.4306
IEYAKPTR	978.1	2	2.6801	0.1842
IEYDAYRTDLEELNLGPR	2168.3	3	4.769	0.3674
IEYDTFGELKVPNDKYYGAQTVR	2708.0	3	4.9641	0.3674

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IEYQFFEDR	1247.3	2	2.7249	0.2431
IFAPNHVVAK	1096.3	2	2.624	0.1836
IFAQDGEGQR	1121.2	2	3.3077	0.2792
IFAQLDSIIDDR	1406.6	2	2.954	0.2034
IFAYYDVSK	1106.3	2	2.6641	0.2583
IFCCHGGLSPDLQSMEQIR	2135.5	3	3.8771	0.1272
IFCCHGGLSPDLQSMEQIRR	2291.7	3	3.2019	0.1235
IFDAAKAPIQWEER	1674.9	3	3.9634	0.3342
IFDAAKAPIQWEERNVTAIQGPGGK	2698.0	3	3.558	0.1913
IFDANTKPNLNLQVLSNPEFLAEGTAIK	3059.5	3	5.6671	0.3047
IFDANTKPNLNLQVLSNPEFLAEGTAIKDLK	3415.9	3	6.2736	0.4324
IFDANTKPNLNLQVLSNPEFLAEGTAIKDLKNPDR	3898.4	3	6.1157	0.4829
IFDAVGFTFPNR	1384.6	2	3.4869	0.3525
IFDDVSSGVSQLASK	1553.7	2	3.9304	0.3433
IFDEAKTAQEKDSLITPHVSR	2386.6	3	5.618	0.3813
IFDIDEAEEGVKDLKIESDVQEPTEPEDDLDIMLGNK	4191.5	3	4.9457	0.2247
IFDSPEELPKER	1460.6	2	2.5737	0.2114
IFEAFKLTDDVKK	1554.8	2	3.817	0.2856
IFEEDPAVGAIVLTGGDK	1832.0	2	5.135	0.3892
IFFAGTETATK	1186.3	2	3.249	0.2712
IFGGLDMLAEK	1194.4	2	2.7178	0.1518
IFGGLDMLAEKLPNLTHLNLSGNK	2597.0	3	5.4102	0.3058
IFGGVQQLR	1018.2	2	2.8028	0.1535
IFGLLMGTLQK	1221.5	2	3.4379	0.2656
IFGVTTLDIVR	1234.5	2	3.8813	0.2866
IFGYPVGIVGNNGVLFSESAK	2169.5	2	4.8887	0.5042
IFHELTQTDKALFNR	1834.1	2	4.5759	0.4859
IFHERFPFEIVK	1562.8	2	3.2201	0.1976
IFHERFPFELVK	1562.8	2	3.3886	0.2427
IFHIDTNALHVPR	1533.8	2	3.5198	0.3521
IFHTVTTTDDPVIR	1615.8	3	4.3655	0.3858
IFHTVTTTDDPVIRK	1744.0	2	4.8345	0.3175
IFHVNWFR	1119.3	2	2.5859	0.2686
IFILGPSHHVPLSR	1573.9	3	3.5986	0.3325
IFINNEWHDSVSGK	1646.8	2	4.9168	0.4536
IFINNEWHDSVSGKK	1775.0	2	5.0558	0.4224

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IFLLGLADNEAAIVQAESEETKER	2647.9	3	4.519	0.2565
IFLLTNNNLLLADQK	1731.0	2	5.7573	0.3636
IFLLTNNNLLLADQKSGQIKSEVPLVDVTK	3312.8	3	4.9604	0.4031
IFLQDIKKPDCDDWESGLNAMECALHLEK	3363.8	3	5.1807	0.2373
IFLQDIKKPDCDDWESGLNVMECALHLEK	3391.9	3	3.983	0.1855
IFNITDNAAIKPGTPLYAAHFRPGQYVDVTAK	3491.0	3	5.0983	0.2886
IFNLYPR	923.1	2	2.7254	0.1023
IFNTNNLWISLAAVK	1705.0	2	2.6656	0.1721
IFPYEMLMVTNR	1514.8	2	3.4528	0.2203
IFQGNVHNFEK	1333.5	2	3.7697	0.2176
IFQKGESPVDYDGGR	1668.8	2	4.5683	0.4052
IFQNAPTDPTQDFSTQVAK	2109.3	2	5.406	0.4719
IFQTLNGAVDEVVLKFENGK	2222.5	3	3.5419	0.2624
IFQVAQELSGEDMHQFHR	2173.4	3	5.2394	0.4308
IFRDGEEAGAYDGPR	1653.7	3	4.8349	0.3955
IFSGPSSEQFGYAVQQFINPK	2345.6	2	5.4143	0.3622
IFSGSSHQDLSQK	1434.5	2	4.2037	0.2705
IFSGSSHQDLSQKIADRLGLELGK	2600.9	3	4.3518	0.3664
IFSPNVVNLTLVDLPGMTK	2059.5	2	3.1315	0.2103
IFSQHLQNR	1143.3	2	2.7092	0.173
IFTASNVSSVPLPAENVTITAGQR	2473.8	3	4.7866	0.4983
IFTLNLSAPFISQFYK	1890.2	2	3.7742	0.2231
IFTNLYGR	984.1	2	2.505	0.1461
IFTPLLHQIELEKPKPIPYIYGSR	2854.4	3	4.3205	0.3758
IFTSIGEDYDER	1445.5	2	4.1634	0.3968
IFTSIGEDYDERVLPSITTEILK	2641.0	3	5.1334	0.2996
IFTSIGEDYDERVLPSITTEILKSVVAR	3153.6	3	6.0645	0.4391
IFVEESIYDEFVR	1646.8	2	5.2368	0.5038
IFVEESIYDEFVRR	1803.0	2	2.9387	0.1608
IFVGGIKEDTEEHHLR	1881.1	2	4.9613	0.3123
IFVGGIKEDTEEHHLRDYFEQYGK	2912.2	3	4.4273	0.253
IFVGGIKEDTEEYNLR	1884.1	2	5.2744	0.4501
IFVGGIKEDTEEYNLRDYFEK	2566.8	3	4.4512	0.2697
IFVGGIKEDTEEYNLRDYFEKYGK	2915.2	3	5.143	0.3595
IFVGGIKEDTKEHHLR	1880.1	3	3.451	0.3758
IFVGGLNPEATEEK	1504.7	2	4.66	0.3202

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IFVGGLSANTVVEDVKQYFEQFGKVEDAMLMFDKTTNR	4329.9	3	3.6885	0.195
IFVGGLSPDTPEEK	1489.7	2	4.2499	0.3698
IFVGGLSPDTPEEKIR	1759.0	2	4.0746	0.2778
IFVNDDRHVMAK	1445.7	2	3.812	0.3253
IFYPEIEEVQALDDTER	2068.2	2	4.0867	0.378
IFYPETTDIYDRK	1661.8	2	3.414	0.3239
IGAADYQPTEQDILR	1690.8	2	4.5137	0.4412
IGACPSAHKPLLGTEK	1622.9	2	3.9603	0.4069
IGADFLAR	863.0	2	2.8957	0.1976
IGAEVYHNLK	1144.3	2	3.6783	0.2474
IGAEVYHNLKNVIK	1598.9	3	4.4788	0.3679
IGAEVYHNLKNVIKEK	1856.2	2	5.1858	0.3797
IGAHGKPVIFLHPK	1514.8	2	2.9926	0.2459
IGALQGAVDR	1000.1	2	2.9645	0.2411
IGASFLQR	892.0	2	2.941	0.202
IGASTLLSDIER	1275.4	2	3.7543	0.378
IGDEDVGR	860.9	2	2.9962	0.1804
IGDEDVGRVIFGLFGK	1723.0	2	4.7008	0.3594
IGDEDVGRVIFGLFGKTVPK	2148.5	3	4.6918	0.2821
IGDELDSNMELQR	1520.6	2	4.5268	0.3122
IGDEYFTFITDCKDPKACTILLR	2664.1	3	3.673	0.154
IGDFIDVSEGPLIPR	1628.9	2	4.1634	0.4828
IGDLHPQIVNLLK	1460.7	2	2.7351	0.1929
IGDLQAFQGHGAGNLAGLK	1868.1	2	4.8108	0.4082
IGDNLDILTLLK	1328.6	2	4.2835	0.2596
IGDPLLEDTR	1129.2	2	3.8743	0.3201
IGDQEFDSLPALLEFYK	1986.2	2	4.555	0.4307
IGDSLFGAR	936.0	2	2.4782	0.2096
IGDSSQGDNNLQK	1376.4	2	3.9317	0.3511
IGDYVQQHGGVSLVEQLLQDPK	2424.7	3	3.5741	0.1093
IGEAEAAVIEAMGKAEAER	1946.2	3	3.7151	0.2237
IGEEQSAEDAEDGPPELLFIHGGHTAK	2849.0	3	4.947	0.4171
IGEEQSPEDAEDGPPELLFIHGGHTAK	2875.1	3	5.2889	0.4571
IGEHMEEHGIK	1280.4	2	3.2528	0.3242
IGEHTPSALAIMENANVLAR	2108.4	3	5.8284	0.5519
IGEIATGSPVSTELGHVLIEISSTHKK	2805.2	3	4.1183	0.3345

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IGEKYVDMSVK	1269.5	2	2.9205	0.1731
IGEKYVDMSVKTK	1498.8	2	3.4466	0.1959
IGELVGVLVNHFK	1425.7	2	3.2751	0.2683
IGEMPLTDSILCDGLTDAFHNCHMGITAENVAK	3519.0	3	4.7602	0.3113
IGEWELIQESGVPLKPLFGPGYTGIR	2858.3	3	5.0406	0.4046
IGFDAIMR	923.1	2	2.8198	0.1898
IGFEEKDIAANEENRK	1864.0	2	4.6726	0.2883
IGFGSFVEK	984.1	2	2.5762	0.2638
IGFPWSEIR	1105.3	2	3.1755	0.3397
IGGDAATTVNNSTPDFGFGGQK	2155.3	2	5.6233	0.5243
IGGDAATTVNNSTPDFGFGGQKR	2311.5	3	3.2068	0.1381
IGGDAGTSLNSNDYGYGGQK	1975.0	2	5.1594	0.4729
IGGDSGLSSR	949.0	2	2.68	0.2357
IGGDSGLSVR	961.1	2	3.2914	0.2261
IGGGIDVPVPR	1080.3	2	4.2379	0.2748
IGGIFAFK	853.0	2	3.0846	0.2128
IGGIGTVPVGR	1026.2	2	3.8703	0.3425
IGGIGTVPVGRVETGILRPGMVVTFAPVNITTEVK	3580.2	3	3.3038	0.137
IGGIGTVPVGRVETGVLKPGMVVTFAPVNVTTEVK	3524.2	3	6.1509	0.2634
IGGILANELSVDEAALHAAVIAINEAIDR	2960.3	3	5.5879	0.5295
IGGILANELSVDEAALHAAVIAINEAIDRR	3116.5	3	3.825	0.2604
IGGILANELSVDEAALHAAVIAINEAVEK	2932.3	3	5.9317	0.4737
IGGNEGIDVPIPR	1337.5	2	3.5854	0.3379
IGGSTDTGKHIK	1214.4	2	2.7223	0.19
IGGVQQDTILAEGLHFR	1855.1	3	5.1393	0.4988
IGGVTERMPTPVIK	1498.8	2	3.1089	0.1845
IGHFQLMQGK	1159.4	2	3.1276	0.2453
IGHHSTSDDSSAYR	1533.5	2	3.4012	0.3858
IGHIAHLNLR	1144.4	2	2.7375	0.4178
IGHKVESESYR	1305.4	2	2.7232	0.2442
IGHPAPNFK	981.1	1	2.4787	0.319
IGHYILGDTLGVGTFGK	1749.0	3	4.4609	0.441
IGIEIIKR	942.2	2	2.5496	0.1163
IGIFGQDEDVTSK	1409.5	2	3.6592	0.3778
IGIFPPAISISSIPLLPSSVR	2165.6	2	3.4717	0.3786
IGIIDGEYVVNPTRK	1674.9	2	3.6889	0.3252

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IGIIGGTGLDDPEILEGR	1826.0	2	5.1916	0.4711
IGILHENFQTLK	1413.6	2	2.5555	0.1829
IGILHENFQTLKAEDNFEDIITKPPVR	3139.6	3	5.1772	0.3744
IGIMPGHIHK	1103.4	2	2.405	0.1321
IGITNHDEYSLVR	1517.7	2	3.9333	0.3441
IGIVGLPNVGK	1067.3	2	3.3952	0.2967
IGKEMQNA	891.0	2	2.7343	0.1052
IGKENFIEK	1078.2	2	2.5672	0.1499
IGKIEGFEVLK	1233.5	2	2.5223	0.1533
IGKIEGFEVLKK	1361.7	3	4.075	0.2308
IGKPAPDFK	973.2	1	2.4085	0.3315
IGKPAPDFKATAVVDGAFKEVK	2289.7	3	5.3869	0.5284
IGKPHTVPCK	1080.3	2	2.4626	0.1867
IGKVDCTQHYELCSGNQVR	2151.4	2	2.6595	0.1038
IGKVTSEELHYFVQNHFTSAR	2464.7	3	5.8506	0.4457
IGLDDEEKLDLFR	1563.7	2	3.3061	0.2793
IGLENFLLR	1075.3	2	3.3059	0.1703
IGLFGGAGVGK	976.2	2	3.2449	0.173
IGLFGGAGVGKTVLIMELINNVAK	2415.9	3	4.2579	0.1905
IGLFYMDNDLITR	1571.8	2	2.7177	0.1339
IGLIHGHQVIPWGDMASLALLQR	2527.0	3	4.8119	0.3302
IGLINDMVR	1031.3	2	2.6045	0.1182
IGLIQFCLSAPK	1290.6	2	3.6144	0.3184
IGLPHSIK	865.1	2	2.5052	0.1023
IGMSVNAIR	961.2	2	2.4618	0.1639
IGNEGLAADLTDDPDTEEALKEFDFLVTAEDGEGAGEAR	4083.2	3	5.3621	0.391
IGNFIVKKPMVLGHEASGTVEK	2355.8	3	5.916	0.4015
IGNLQTDLSDGLR	1402.5	2	3.4665	0.2849
IGNSGVEEIKGHPFFEGVDWEHIR	2754.0	3	3.7084	0.3553
IGNTGGMLDNILASK	1504.7	2	5.0243	0.4823
IGPALSCGNTVVVKPAEQTPLTALHVASLIK	3129.7	3	5.7616	0.5164
IGPEKIDTLGIYGK	1504.8	2	2.6155	0.2537
IGPIATPDYIQNAPGLPK	1866.2	3	4.0656	0.3858
IGPILDNSTLQSEVKPILEK	2195.5	2	5.5909	0.4728
IGPILDNSTLQSEVKPILEKLTQDQDVDVK	3337.8	3	5.541	0.4171
IGPILDNSTLQSEVKPILEKLTQDQDVDVKYFAQEALTVLSLA	4745.4	3	4.3932	0.2011

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IGPITPLEFYR	1306.5	2	3.6653	0.34
IGPKKPLPDHVSIVEPKDEILPTTPISEQK	3307.8	3	6.5396	0.4764
IGPLGLSPK	882.1	2	2.7817	0.3288
IGPQHQAGSDSLLTGMAFFK	2106.4	2	3.3351	0.3056
IGPSILNSDLANLGAECLR	1957.2	2	2.675	0.2931
IGPYQPNVPVGIDYVIPK	1970.3	3	5.1254	0.4185
IGQETDKTTTR	1250.3	2	3.3617	0.3722
IGQFVFAR	938.1	2	2.8661	0.3481
IGQGYLIKDGK	1192.4	2	3.1927	0.2122
IGQLEEQLEQEAK	1515.6	2	3.7214	0.2475
IGQPTLLLYVDAGPETMTQR	2204.5	2	5.5492	0.5031
IGQQPQQPGAPPQQDYTK	1982.1	2	4.5729	0.3506
IGQSLSSLTSPAEQGVLSEKIDSLQAR	2816.1	3	3.7629	0.2738
IGRIEDVTPIPSDSTR	1756.9	3	3.4784	0.1966
IGRIEDVTPIPSDSTRR	1913.1	2	3.4433	0.3
IGRLEKELENANDLLSATK	2115.4	2	3.7463	0.4188
IGSDVELLLR	1115.3	2	3.4023	0.2304
IGSEGQGFLIAVR	1347.5	2	3.5783	0.2214
IGSFTIQNVFPQSDGDSSK	2028.2	2	3.2238	0.315
IGSLASGNVR	974.1	2	2.7829	0.1374
IGSLDNITHVPGGGNK	1579.7	2	4.009	0.3329
IGSTDNIKYQPK	1364.5	2	3.6446	0.2161
IGSTIDDTISK	1150.3	2	2.9542	0.2896
IGSTIFGER	980.1	2	2.4391	0.2862
IGTADRELIQTSALNFLTPLR	2330.7	2	3.996	0.3117
IGTDIQDNK	1004.1	2	2.6978	0.1398
IGTHNGTFHCDEALACALLR	2143.4	3	3.6361	0.2908
IGTIYEGASNIQLNTIAK	1907.2	3	5.6441	0.3396
IGTLEKEHNVFQNK	1657.9	2	3.983	0.3312
IGVADVDMSR	1063.2	2	3.0528	0.3019
IGVDHVAR	867.0	2	2.9309	0.3077
IGVFSYGSGLAATLYSLK	1848.1	2	3.1398	0.337
IGVHAFQQR	1056.2	2	2.6445	0.378
IGVLDEGKMK	1090.3	2	2.5277	0.191
IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK	3570.0	3	4.0107	0.2326
IGYNPDTVAFVPISGWNGDNMLEPSANMPWFKGWK	3941.4	3	5.1919	0.1913

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IGYPKPALLHSTFFPALQGAQTK	2486.9	3	5.4614	0.5002
IGYSSPLTLSDQSSK	1583.7	2	3.2029	0.2174
IGYSSPQTLADQSSK	1582.7	2	2.5033	0.1557
IHAEEKLDKANEEIAQVR	2094.3	2	6.3226	0.488
IHAEEKPFTCEECGKIITSSSNVAKHK	2988.4	3	3.2628	0.123
IHAGPITK	837.0	1	2.4793	0.2012
IHAGPK	622.7	1	1.8115	0.1191
IHDPQLLTER	1222.4	2	2.4166	0.2782
IHEAAVQELR	1166.3	2	3.2713	0.3203
IHEGCEEPATHNALAK	1720.9	2	4.8386	0.4584
IHEISCGAHSTQCIPVSWR	2125.4	2	3.023	0.1048
IHEMLQPGQDQ	1296.4	2	3.6421	0.2536
IHETNLKK	983.1	1	2.224	0.1188
IHETNLKKQGLLPLTFADPADYNK	2728.1	3	3.5889	0.2756
IHFFLSK	892.1	2	2.4362	0.1912
IHFHNLQGEK	1223.4	3	3.9449	0.2598
IHFNPPLPMMR	1353.7	2	2.4512	0.2228
IHFPEALGHVALR	1460.7	2	3.3755	0.4221
IHFPLATYAPVISAEK	1758.1	2	4.4993	0.5152
IHFRPELPAER	1365.6	2	3.1334	0.2866
IHFSGYDNDRPGNLVYR	2024.2	2	4.45	0.4358
IHGFTVNQVTSVPELFLTAVK	2301.7	2	2.9694	0.2523
IHGSGHVEEPASPLAAYQK	1992.2	3	5.3867	0.5356
IHGVGFK	757.9	1	2.5427	0.1449
IHHATPPQAQPEVK	1553.7	2	2.8001	0.1945
IHHDVNELLSLLR	1559.8	2	3.4839	0.288
IHIMPSLNPDGFEK	1598.8	2	3.8991	0.2939
IHIMPSLNPDGFEKAASQPGELKDWFVGR	3241.7	3	3.4446	0.405
IHIPFISK	955.2	2	2.8456	0.1442
IHLAVTEMASLFPK	1557.9	2	2.5309	0.1979
IHLDEKSFR	1145.3	2	2.6238	0.2482
IHLFDIDVPGKITFQESK	2088.4	2	2.6618	0.1166
IHLNSQFPGTQR	1398.6	2	2.6244	0.1822
IHLPETVEQLRK	1463.7	2	2.5316	0.1115
IHMGSCAENTAK	1262.4	2	2.6037	0.2376
IHMVYSK	878.1	1	2.1544	0.1898

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IHNAENIQPGEQK	1478.6	2	4.1084	0.1386
IHNFGLIQEK	1199.4	2	2.5048	0.167
IHNGESMAYLFR	1438.6	2	2.9156	0.2158
IHNGESMSYLFR	1454.6	2	3.3307	0.3518
IHNHLPEIQK	1229.4	2	2.8356	0.1452
IHNIDIPTTQQVPHIEALLKR	2437.8	3	3.2175	0.1591
IHNLALNCCTQLADLYR	1962.3	2	3.0928	0.197
IHNLTAYLQTLHR	1580.8	2	4.5561	0.4424
IHNNMFDPALIGDKPK	1811.1	3	3.4641	0.1869
IHPQTIIAGWR	1292.5	2	2.8403	0.1733
IHPVDKLTIQGLK	1462.8	2	2.6662	0.2211
IHPVDKLTIQGLKDFTPGKPLK	2446.9	2	5.2425	0.4496
IHQALKEDILEFIK	1698.0	2	4.7483	0.4204
IHQESELHSYLSR	1599.7	2	4.2611	0.4044
IHQIEYAMEAVK	1432.7	2	3.6972	0.2405
IHQIEYAMEAVKQGSATVGLK	2274.6	2	6.5421	0.4899
IHQIGPGMVQQIQSVCMECQGHGER	2767.2	3	4.7186	0.3063
IHQQELEVGISSHQPSFAALNR	2462.7	3	3.4121	0.2347
IHSAPRSGAPAAESKEIVR	1977.2	3	3.4773	0.2006
IHSDHLVASEK	1236.4	2	2.8994	0.3199
IHSDTFASGGER	1277.3	2	2.7994	0.2208
IHSEIVK	826.0	1	2.0187	0.1461
IHSEVVEDTEAVSAVQQLLDDER	2583.7	3	3.4823	0.1697
IHSINLHNFSNSVLETLNEQR	2466.7	3	4.4662	0.3573
IHSITGLPPAMQK	1393.7	2	2.886	0.2547
IHSLSSNKPQRPVFTHENIQGGGEPFQALYNYTPR	3985.4	3	5.3234	0.3947
IHSLTHLDSVTK	1351.5	2	3.4516	0.3299
IHTDFEK	890.0	1	2.2368	0.163
IHTGLSR	783.9	1	1.9167	0.1438
IHTLLKDLQR	1237.5	2	2.6414	0.1988
IHTPMEYKGELASYDMR	2042.3	2	4.5679	0.4708
IHVDFPVILYEV	1444.7	2	2.6109	0.1404
IHVFYIDYGNR	1397.6	2	3.4141	0.3276
IHVFYIDYGNREVLPSTR	2180.5	3	3.9523	0.3033
IHVIDHSGAR	1105.2	2	3.0315	0.2954
IHVLEAQDLIAK	1350.6	2	3.5273	0.344

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IHVLEAQDLIAKDR	1621.9	2	4.82	0.365
IHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIR	3993.6	3	4.803	0.495
IHVQSSSDSSDEPAEKR	1872.9	3	3.4606	0.3048
IHVSDQELQSANASVDDSRLEELK	2684.9	3	5.761	0.498
IHVSDQELQSANASVDDSRLEELKATLPSPDKLPGFK	4037.4	3	5.7853	0.5249
IHVYGYSMAYGPAQHAISTEK	2324.6	2	6.8824	0.5659
IHVYGYSMAYGPAQHAISTEKIK	2565.9	3	3.9403	0.3121
IHYFDPQYFEFEFEA	1983.1	2	3.2965	0.3494
IHYIGQNEPELLVAHAYTR	2225.5	2	5.8844	0.5005
IHYLDTTTLIEPAPR	1741.0	2	3.8959	0.3997
IIAEGANGPTTPEADKIFLER	2243.5	2	4.7094	0.4543
IIAFVGSPVEDNEKDLVK	1974.2	2	4.1186	0.2781
IIAGDKEVVIAQNDK	1613.8	2	3.9013	0.2209
IIAGDKEVVIAQNDKHTGPVR	2261.6	3	5.4497	0.4174
IIALDGDTK	946.1	2	3.0765	0.173
IIALDGDTKNSTFSEIFKK	2128.4	2	3.3248	0.2971
IIAPPERK	924.1	2	2.6281	0.2422
IIAQKIYGADDIELLPEAQHKAEVYTK	3058.5	3	3.9573	0.2096
IIASSPEMNLPTVSALR	1800.1	2	3.1589	0.211
IIATAVCHTDAYTLSGADPEGCFPVILGHEGAGIVESVGEGVTK	4386.9	3	4.7462	0.3182
IIAVDINKDKFAK	1475.8	2	4.3717	0.3779
IICILSHPIK	1137.5	2	2.5525	0.1535
IIDDSEITKEDDALWPPPDR	2326.5	2	2.6456	0.214
IIDEVVNKFLDDLGNAK	1904.2	2	3.7735	0.3136
IIDFGLAR	905.1	2	2.4636	0.182
IIDISDVFRNTEIGFLQDALSKPHGTVK	3115.5	3	4.0973	0.2995
IIDKNGIHDLDNISFPK	1940.2	2	5.0769	0.4716
IIDKNGIHDLDNISFPKQGS	2212.4	3	4.6421	0.3141
IIDKSKRDPTEEIEILLR	2169.5	3	4.5689	0.2783
IIDSLFNTVTDK	1366.5	2	2.5657	0.1661
IIDSLFNTVTDKK	1494.7	2	4.0625	0.3344
IIDTSLTRDPLVIELGQK	2012.3	3	5.9855	0.3482
IIDVVYNASNNELVR	1719.9	3	5.3817	0.4375
IIEDLRAQIFANTVDNAR	2060.3	3	5.2434	0.3875
IIEDQQESLNK	1317.4	2	4.5159	0.2724
IIEDQQESLNKWK	1631.8	2	3.7498	0.1923

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IIEPDNSYISDTLGQVYK	2056.3	2	3.7453	0.3965
IIETLTQQLQAK	1386.6	2	4.4602	0.2474
IIEVVDAIMTTAQSHQR	1913.2	2	2.5563	0.1993
IIFEDDR	908.0	2	2.7917	0.1399
IIGAKDHASIQMNVAEVDKVTGR	2453.8	3	3.4847	0.1521
IIGATDSSGELMFLMK	1714.0	2	4.0896	0.2912
IIGAVDQIQLTQAQLEER	2026.3	3	5.5359	0.4621
IIGFGSALLEEVDPNPANFVGAGIIHTK	2881.3	3	4.015	0.2461
IIGLDQVAGMSETALPGAFK	2019.4	2	5.3988	0.5456
IIGLKPEGVPR	1179.4	2	2.5547	0.1765
IIGNLLYYR	1125.3	2	2.9256	0.1296
IIGVDINKDK	1115.3	2	2.8068	0.3029
IIGVDINKDKFAR	1489.7	2	4.168	0.3323
IIGYTPDLDPETVDDAFAR	2109.3	2	4.1351	0.3963
IIHDFPQFYPLGIVQHD	2040.3	2	4.7975	0.3968
IIHEDGFSGEDVK	1446.5	2	3.887	0.4014
IIHEDGFSGEDVKQYKPVVYSNTIQSLAAIVR	3579.0	3	5.7808	0.433
IIHGQDFDQR	1229.3	2	2.4856	0.1068
IIHTDIKPENILLSVNEQYIR	2509.9	3	4.492	0.3709
IIIDKEYYYTKEEQFK	2111.4	2	4.224	0.4495
IIITGDEDVDQDQALALAIKEAK	2470.8	3	4.2021	0.3497
IIKDFMIQGGDPTGTGR	1807.1	2	4.909	0.4656
IIKDGEQHEDLNEVAKLFNIHED	2707.9	3	5.9801	0.3889
IIKDHLLEESTFAPYIDDLSEEQR	2863.1	3	5.4297	0.4401
IIKPCNHVLSLSFPIR	1838.3	2	3.6658	0.4131
IILDLISESPIK	1341.6	2	4.3172	0.3709
IILDLISESPIKGR	1554.9	2	4.4515	0.3463
IILEAEKMDGAASQGK	1661.9	2	3.9413	0.2195
IILEALR	828.0	2	2.4316	0.1027
IILEALRQAENEPQSAPK	2008.3	2	4.3062	0.2591
IILGGFSQGGALSLYTALTTQQK	2368.7	3	3.311	0.1074
IILHNTMESLLER	1569.9	2	3.0035	0.3093
IILNALVAQQK	1211.5	2	3.6895	0.2572
IILNSHSPAGSAAISQQDFHPK	2319.6	3	4.3347	0.1594
IILPEGAKNIEIDSPYEISR	2258.6	3	4.9418	0.3162
IILPPEKELAMPGEDLKFNLILR	2651.2	3	4.371	0.2779

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IILWDHDLNPEREIEVPDQYGTIR	2923.2	3	4.4985	0.2253
IIMTSSASGIYGNFGQANYSAAK	2352.6	2	5.8156	0.5633
IINADSEDPK	1102.2	2	2.491	0.2062
IINADSEDPKYIINVK	1833.1	2	5.7195	0.3944
IINDDQSLYADVYLEDGLIK	2298.5	2	5.2989	0.4552
IINDDQSLYADVYLEDGLIKQIGENLIVPGGVK	3604.1	3	6.7399	0.5334
IINDLLQSLR	1185.4	2	4.0645	0.2041
IINEPTAAAIAYGLDK	1660.9	2	5.6694	0.3683
IINEPTAAAIAYGLDKK	1789.1	2	4.6982	0.2189
IINEPTAAAIAYGLDKR	1817.1	2	5.1484	0.4013
IINEPTAAAIAYGLDR	1688.9	2	5.6198	0.5394
IINEPTAAAIAYGLDRT	1790.0	2	5.0853	0.4057
IINEVKPTEIYNLGAQSHVK	2254.6	3	5.155	0.2726
IINEVSKPLAHHIPVEK	1925.3	2	4.2504	0.3296
IINNTENLVR	1186.3	2	2.9055	0.185
IIPGFMCQGGDFTR	1542.8	2	2.8161	0.2353
IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK	4000.5	3	4.2259	0.2624
IIQEQDAGLDALSSIISR	1930.1	3	3.5528	0.2907
IIQKDPLR	983.2	2	2.5014	0.1367
IIQLLDDYPK	1218.4	2	3.9164	0.2987
IIRGFCHLCDGQEACCVGLEAGINPTDHLITAYR	3691.2	3	3.7982	0.1057
IIRPLTVYGLEDAPGGHGEVR	2250.5	3	3.839	0.3952
IIRPSETAGR	1100.3	2	2.7881	0.121
IIRVDHAGEYGANR	1571.7	3	3.4941	0.3381
IISAASEGGANVFTVSYFK	1962.2	2	2.9293	0.1913
IISAHGCKVDNSSLTGESEPQTR	2430.6	3	3.6069	0.3164
IISKEGIPGLYR	1346.6	2	3.0374	0.2427
IISKIENHEGVR	1395.6	2	3.7181	0.349
IISLDLPVAEVYKK	1588.9	2	2.9667	0.141
IISNASCTTNCLAPLAK	1721.0	2	4.775	0.4011
IISNASCTTNCLAPLAKVIHDNFGIVEGLMTTVHAITATQK	4299.0	3	5.1101	0.3653
IISNASCTTNCLAPRAKVLHDNFGIVKGLMTTVHAITATQK	4341.1	3	3.8488	0.3318
IISSDRDLLAVVFYGTEKDK	2270.6	3	5.0291	0.2711
IISSDRDLLAVVFYGTEKDKNSVNFK	2960.3	3	3.7365	0.2019
IISSFKNKEDQYDHLDAADMTK	2570.8	3	4.3532	0.3421
IISSIEQKEENK	1418.6	2	4.255	0.3113

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IISSIEQKEENKGGEDK	1905.1	2	5.2292	0.3253
IISSIEQKEENKGGEDKLK	2146.4	3	4.4785	0.1887
IISTLANKNDEIQNFIDTLHHTLK	2780.1	3	4.6167	0.2797
IISTTASKTETPIVSK	1676.9	2	4.4647	0.3887
IISTTNGGQER	1176.3	2	3.4146	0.2532
IITADPKKELENLATSLEHYK	2414.7	3	4.0672	0.2983
IITEGFEAAKEK	1336.5	2	3.4992	0.301
IITGGAPELAVEGNGPVESNAVLTK	2437.7	3	6.3464	0.5227
IITITGTQDQIQNAQYLLQNSVK	2590.9	3	7.2259	0.5213
IITKDFPQYFAVVSR	1785.1	2	3.81	0.3429
IITLAGPTNAIFK	1359.6	2	3.9371	0.2643
IITLEEGDIILTGTPK	1714.0	2	5.433	0.4521
IITLTGPTNAIFK	1389.7	2	3.9721	0.3435
IITMLPTSINAIEAYSGANGILK	2391.8	3	5.7099	0.4363
IITMLPTSINAIEAYSGANGILKK	2520.0	2	3.7545	0.3849
IITVEKHPDADSLYVEK	1958.2	2	4.0834	0.3198
IITVEKHPDADSLYVEKIDVGEAEPR	2925.2	3	6.4293	0.4808
IIVDELKQEVISTSSK	1790.0	2	4.8352	0.4689
IIVGDATEKDASK	1347.5	2	3.0288	0.2534
IIVLGLLPR	994.3	2	2.7649	0.145
IIWELIKEK	1172.4	2	2.943	0.1433
IIWQFIK	948.2	2	2.5397	0.1353
IIYGGSVTGATCK	1270.5	2	3.8024	0.4216
IIYIVHDEVK	1229.4	2	2.9175	0.2236
IIYIVHDEVKDK	1472.7	2	3.6124	0.1728
IIYLNQLLQEDSLNVADLTSLR	2532.9	2	6.4885	0.4795
IKAAVEDPRVLLLDL	1666.0	2	3.6987	0.292
IKAAVPSIK	927.2	2	2.6704	0.1673
IKADIIYPGHGPVIHNAEAK	2144.5	3	4.5374	0.366
IKAESAEAAKK	1146.3	2	3.1099	0.2209
IKAEYEGDGIPTVFVAVAGR	2093.4	3	5.8234	0.5424
IKAIPQLQGYLR	1400.7	2	3.9585	0.3448
IKAKDIVPGDIVEIAVGDKVPADIR	2633.1	3	5.6353	0.4222
IKAPGFAHLAGLDK	1438.7	3	3.3361	0.2946
IKAQDEAFALQDVPLSSVVR	2187.5	2	5.4215	0.4066
IKDAFDRNPELQNLLLDDFFK	2552.9	3	5.7725	0.3717

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IKDEFQLLQAQYHSLK	1962.2	3	4.1826	0.2663
IKDHIQNGK	1053.2	2	2.765	0.1354
IKDHIQNGKLDLTK	1623.9	2	3.6275	0.1574
IKDIAWTEDSKR	1462.6	2	3.6945	0.304
IKDKNELKEICELTGIDQSVLER	2675.1	3	3.95	0.29
IKDLSTIEPLK	1257.5	2	3.144	0.1301
IKDLSTVEALQNLK	1572.8	2	4.9017	0.3118
IKDLSTVEALQNLKNLK	1928.3	2	3.6985	0.3321
IKDMDLWEQQEEER	1850.0	3	4.4717	0.1217
IKDMDLWEQQEEERITTMQLER	2823.2	3	3.9016	0.2162
IKDPDASKPEDWDER	1801.9	2	4.1641	0.3803
IKDRLPLAVVGSNTIIEVNGK	2237.6	3	4.4149	0.3379
IKDSTAASR	949.0	2	2.4504	0.1085
IKDYLLMEEEFIR	1700.0	2	4.605	0.445
IKEALIQQSQEQKEILEK	2156.5	3	4.7231	0.3241
IKEDEDDK	992.0	2	2.4846	0.1589
IKEDEDDKTVLDLAVVLFETATLR	2735.1	3	6.051	0.5186
IKEDNFFQVSK	1355.5	2	2.9458	0.1993
IKEDRPITIKDDK	1571.8	2	2.9935	0.2357
IKEDRPITIKDDKGNLNR	2126.4	3	6.0321	0.3558
IKEIAVTVK	1001.2	2	2.9557	0.1618
IKEINETSSSQLYLLGSYNALPPLHEALLER	3500.9	3	5.051	0.3945
IKEKYIDQEELNK	1650.9	2	4.6087	0.2927
IKELNNTCEPVVTQPKPK	2039.4	3	5.66	0.3446
IKELQNAGDR	1144.3	2	3.0107	0.212
IKELTSTCSPIISKPKPK	1971.4	3	4.8503	0.43
IKELVVTQLGYDTR	1635.9	2	3.9851	0.3053
IKENKPLPPVPIPNLVGIR	2095.6	3	3.7336	0.2875
IKERVEEKEGIPPQQQR	2065.3	3	3.9783	0.1858
IKETPSEQESK	1276.4	2	3.1952	0.1947
IKETVINGLENMGAAFQSMMTGGNIGK	2813.3	3	4.8113	0.3668
IKEVKKENGDKK	1416.6	2	2.5196	0.1265
IKEWVDKYDPGALVIPFSGALELK	2690.1	3	4.1685	0.1924
IKFETNPEDSPADQTLIVQSQPVEVIYDAK	3376.7	3	5.6463	0.4288
IKFPLPHR	1008.2	2	2.5934	0.1918
IKGDAVGRVDEEPTTLPSGEAKPR	2523.8	3	4.4623	0.2635

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IKGEELSEANVR	1345.5	3	3.64	0.2199
IKGEHPGLSIGDVAK	1521.7	2	4.5294	0.5096
IKGEHPGLSIGDVAKK	1649.9	2	4.2294	0.3898
IKGEQEKELSK	1289.5	2	2.7918	0.1411
IKGGADVSGGVSAPDISLGEGHLSVK	2451.7	3	4.1782	0.337
IKGIVEESVTGVHR	1524.7	2	2.4821	0.1824
IKGLPEGFAHPK	1294.5	3	3.6452	0.1734
IKHGDLLFLFPSSLAGPSSEMETSVPPGFK	3190.7	3	5.238	0.3726
IKIGDPLLEDTR	1370.6	3	3.9869	0.2663
IKIIAPPER	1037.3	2	2.7107	0.2753
IKINQIQMK	1116.4	2	2.6971	0.1243
IKIYEFPETDDEEENKLVK	2340.6	3	4.1446	0.2987
IKKDPAQFLQVHGR	1637.9	3	4.3805	0.3274
IKKIEDASNPLLLK	1582.9	2	3.0531	0.1998
IKKKEVFPFPEVSQDELNEINQFLGPVEK	3403.9	3	3.3058	0.1931
IKKLPEYNPR	1258.5	3	3.2187	0.1457
IKKMEEEILLLEDQNSK	2061.4	2	2.4598	0.1031
IKKPEGKPDQK	1268.5	2	3.0449	0.1501
IKKPEGKPDQKFDQK	1787.1	2	3.2613	0.2114
IKKTQDQISNIK	1416.6	2	3.4047	0.1412
IKKTQDQISNIKYHEEFEK	2379.7	3	5.7799	0.4365
IKLDLFSALGDAKR	1547.8	2	2.5536	0.4236
IKLEAERFENLR	1518.7	2	2.8961	0.1854
IKLGHYATQLQK	1400.7	2	2.6989	0.1738
IKLHQEDNDYINASLIK	2015.3	3	3.7811	0.2508
IKLKGTVGEPTYDAEFQHFLR	2450.8	3	4.5281	0.2605
IKLQLWDTAGQER	1558.8	2	3.2057	0.2104
IKLTAEAEELKPFFMK	1896.3	2	4.5391	0.3703
IKLYSESLAR	1180.4	1	3.1139	0.3733
IKNEVDSTLTFR	1423.6	2	3.2048	0.1972
IKNNDPKLEEVNLNNIR	2024.3	2	3.6668	0.3296
IKNVVHELR	1108.3	2	2.6884	0.2101
IKNYILMR	1051.3	2	2.5078	0.1202
IKPAATSHVEGSGGVSAK	1696.9	2	4.0394	0.5582
IKPENSSSASTGGK	1363.5	2	2.7581	0.1967
IKPHLMSQELPEDWDKQPVK	2419.8	3	4.5052	0.4221

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IKPHLMSQELPEDWDKQPVKVLVGK	2916.4	3	5.1252	0.4155
IKPSTLQVENISIGGVLVPLELK	2448.9	2	2.8302	0.1307
IKPVFIEDANFGR	1506.7	2	2.8767	0.2483
IKQEILPEER	1255.4	2	3.0233	0.1043
IKQGLLPSLEDLLFYTIAEGQEK	2607.0	3	3.6674	0.2079
IKQHEGLATFYR	1463.7	3	4.2519	0.3685
IKQHLENDPGSNEDTDIPK	2151.3	2	5.7015	0.4458
IKQHLENDPGSNEDTDIPKGYMDLMPFINK	3461.9	3	4.8053	0.1807
IKQLQNISLAAASGGAK	1670.9	2	3.7518	0.2155
IKREVDDLGPEVGDIKIIPLYSTLPPQQQQR	3548.0	3	3.8095	0.286
IKSDFFELLSNHHLDSQSR	2274.5	3	5.0415	0.3192
IKSDYAQLLEDMQNAFR	2043.3	3	5.9587	0.5011
IKSEHPGLSIGDTAK	1553.7	2	4.0675	0.4176
IKSEHPGLSIGDTAKK	1681.9	3	4.2667	0.4279
IKSESTNHEQQSPQSGK	1886.0	2	3.8722	0.3905
IKSGKQSSTSKLLRDSRGPSVEKLSHRPSDPGKSKGTSHK	4290.8	3	3.3518	0.1102
IKSLTEYLQNVEQK	1693.9	3	3.3913	0.1927
IKSTNPGISIGDVAK	1500.7	2	3.9253	0.2929
IKSVEELLEAELLK	1614.9	2	5.0641	0.3802
IKSVEELLEAELLKVANKEK	2284.7	3	3.7059	0.1174
IKTGPVTLHTQTAIHFAEQIAK	2405.8	3	3.2321	0.2493
IKTLFPLIEAK	1273.6	3	4.0549	0.1595
IKTVDISMILSEAIR	1690.0	2	3.4068	0.2038
IKVAEDEAEAAAAAK	1487.6	2	4.7304	0.4115
IKVAKPVVEMDGDEMTR	1919.3	3	4.2754	0.3339
IKVDEFVTHNLSFDEINK	2149.4	2	6.0426	0.3984
IKVDEFVTHNLSFDEINKAFELMHSGK	3150.6	3	5.0658	0.416
IKVDFVIPK	1059.3	2	3.021	0.1464
IKVDNHLFNK	1228.4	2	2.7061	0.1107
IKVDNHLFNKENLPSR	1925.2	2	4.1384	0.3293
IKVENTEENRR	1388.5	2	2.7758	0.1775
IKVFGPGIEGK	1145.4	2	2.9098	0.2193
IKVFGPGIEGKDVFR	1663.0	2	3.5942	0.2712
IKVGDPAEDFGTFFSAVIDAK	2228.5	3	5.8644	0.5227
IKVGRDYVQK	1206.4	2	2.8525	0.1573
IKVLEEQINEGEQQLK	1899.1	2	3.2585	0.2631

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IKVLEQDKAR	1200.4	2	3.1066	0.1811
IKVSNTLESR	1147.3	2	3.0077	0.2757
IKVSNTLESRLDLIAQQMMPEVR	2673.2	3	3.986	0.1972
IKVVNVELPIEANLVWQLGKDLLNMYIETEGK	3671.3	3	4.0772	0.2798
IKWGDAGAEYVVESTGVFTTMEK	2519.8	2	5.7186	0.4795
IKXGDSGTEYIIESTGVFTTMEK	2520.8	3	3.6381	0.1062
IKYPENFFLLR	1440.7	2	2.7126	0.1768
ILAAALTQHNGDAAASLTVAEQYVSAFSK	2949.3	3	5.7341	0.4079
ILADEALKLGILDKVVNSDPVEEAIR	2822.2	3	5.9717	0.3378
ILADPLDQMKAEAYK	1707.0	2	3.9609	0.3693
ILAEGGGAK	815.9	1	2.069	0.2267
ILAGDKNYITMDELR	1753.0	2	4.4096	0.3989
ILAGSADSEGVAAPR	1414.5	2	4.65	0.4118
ILAIELENLK	1156.4	2	3.9248	0.1717
ILAIGLINEALDEGDAQK	1884.1	2	5.4622	0.411
ILAIGLINEALDEGDAQKTLQALQIPAAK	3019.5	3	4.0931	0.3725
ILALQENFLLQFK	1577.9	2	4.255	0.3768
ILAQATSDLVNAIK	1457.7	2	4.2108	0.3652
ILAQATSDLVNAIKADAEGESDLENSR	2832.0	3	4.1922	0.3186
ILAQATSDLVNAIKADAEGESDLENSRK	2960.2	3	4.0457	0.3011
ILAQITGTEHLKESEADNTKK	2327.6	3	3.5193	0.2826
ILARGENLEHLR	1421.6	3	3.4861	0.221
ILASPVELALVVMK	1483.9	3	3.5063	0.3278
ILASPVELALVVMKDLSQNFPTK	2515.0	2	4.3923	0.3792
ILASTQFEPTAAR	1405.6	2	4.0503	0.4208
ILATPPQEDAPSVDIANIR	2021.3	3	5.8455	0.4736
ILAVGTQTGALR	1200.4	2	3.2329	0.3311
ILCEELGAPANSAVNCVPLEDFGGHHPDPNLTYAADLVETMK	4454.0	3	3.8444	0.2579
ILDAAGANLK	986.1	2	3.4999	0.2392
ILDDDTIITTLENLKR	1874.1	2	5.0183	0.3568
ILDDSDSNLSVVK	1405.5	2	3.4321	0.1863
ILDEIEEHNIK	1353.5	2	3.9602	0.3004
ILDELEKVLDQVETELQR	2171.4	3	4.9246	0.3014
ILDELEKVLDQVETELQRR	2327.6	3	3.3461	0.2657
ILDFSATPDLPDQVLR	1801.0	2	2.6558	0.1633
ILDIDNVDLAMGK	1417.7	2	3.5021	0.3907

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ILDLGITGPEGHVLSRPEEVEAEAVNR	2902.2	3	5.1766	0.4151
ILDLIESGK	988.2	2	2.7422	0.1302
ILDLIESGKK	1116.3	2	3.2885	0.2338
ILDLIESGKKEGAK	1501.8	2	3.9213	0.3181
ILDLQLEFDEK	1363.5	2	2.4551	0.1451
ILDNLMEMK	1107.4	2	3.2259	0.2088
ILDNTSEPQPGEAR	1527.6	2	4.6719	0.3519
ILDPEGLALGAVIASSK	1654.9	2	2.4976	0.1061
ILDPNTGEPAPVLSSPPPADVSTFLAFPSPEK	3292.7	3	4.0476	0.3509
ILDQGEDFPASEMTR	1709.9	2	5.2246	0.5162
ILDQSEAEKAR	1260.4	2	2.8711	0.1338
ILDQSEAEKARKELLELEALSMAVESTGTAK	3362.8	3	4.8158	0.3533
ILDQSEAEKARKELLELEALSMAVESTGTAKAEAESR	4006.4	3	5.8937	0.4265
ILDSFAAAPVPTTTLVLK	1858.2	2	4.3262	0.3517
ILDSGNKKN	989.1	2	2.7637	0.2176
ILDSVGIEADDDRLNK	1773.9	2	4.6685	0.349
ILDSVGIEADDDRLNKVISELNGK	2614.9	3	5.9348	0.4182
ILDSVGIEADDDRLNKVISELNGKNIEDVIAQGIGK	3853.3	3	8.4241	0.4983
ILDVLEEIPK	1169.4	2	4.0402	0.2112
ILDVLEEIPKNAAYR	1745.0	2	3.9163	0.3594
ILDVLEEIPKNAAYRK	1873.2	3	3.6771	0.1209
ILDWHVANTDKK	1440.6	2	3.6395	0.335
ILEDDLKAIIKPQYVDQIPK	2340.7	3	3.8894	0.1071
ILEDNSIPQVK	1256.4	2	2.9597	0.1002
ILEDNSIPQVKDIIFAIK	2057.4	2	3.9775	0.3043
ILEDNSIPQVKDIIFAIKK	2185.6	2	4.1258	0.3019
ILEDQEENPLPAALVQPHTGK	2300.6	3	5.1346	0.404
ILEENKELENALK	1543.7	2	4.5313	0.2889
ILEEVMEKETYKTAK	1813.1	2	3.0607	0.3134
ILEFFGLK	967.2	2	3.0322	0.1837
ILEFFGLKK	1095.4	2	2.922	0.1986
ILEIEDLFSSLK	1407.6	2	3.1349	0.227
ILELDQFKGQQGQK	1632.8	2	4.7038	0.3264
ILELSGSSSEDSEK	1481.5	2	4.7574	0.4037
ILELSGSSSEDSEKVIAGLYQR	2382.6	3	5.2037	0.3575
ILEMGITGPEGHALSRPEELEAEAVFR	2953.3	3	3.9211	0.2497

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ILENEKDLEEAEEYKEAR	2209.4	2	6.2476	0.4474
ILEPGLNILIPVLDR	1676.0	3	4.1846	0.441
ILEQEEEEEQAGKPGEPSKKEEGR	2727.9	3	5.5297	0.4014
ILEQQNSSR	1075.2	2	3.3137	0.2405
ILETTTFFQR	1256.4	2	3.3536	0.3009
ILEVHIDKGMKDGQK	1712.0	2	2.403	0.1126
ILEVHVDKGMK	1269.5	2	3.7221	0.3034
ILEVNHVNVEGATHK	1660.9	2	4.8767	0.3799
ILEVNHVNVEGATHKQVVDLIR	2484.8	3	4.3729	0.3369
ILEVVKDK	944.2	2	2.8553	0.1156
ILEVVKDKAGPHK	1434.7	2	2.801	0.1085
ILEVVKDKAGPHKEIYPYVIQELRPTLNELGISTPEELGLDKV	4846.6	3	4.3506	0.3558
ILEVVNQIQDEER	1585.7	2	4.2504	0.4021
ILFIFIDSDHTDNQR	1835.0	2	4.9466	0.4082
ILFLDPSGKVHPEIINENGNPSYK	2683.0	3	4.1456	0.354
ILFQEFR	953.1	2	2.4344	0.1223
ILFRPVASQLPR	1397.7	2	3.9571	0.3076
ILFSSREEQQDILSK	1794.0	2	2.5801	0.1204
ILGADTSVDLEETGR	1576.7	2	5.6038	0.5048
ILGADTSVDLEETGRVLSIGDGIAR	2558.8	3	4.8365	0.4422
ILGATIENSR	1074.2	2	3.2461	0.215
ILGGHLDAK	924.1	2	2.8265	0.1803
ILGGSVLHLVLALR	1461.8	2	4.4454	0.4456
ILGGVISAISEAAAQYNPEPPPPR	2448.8	3	6.4574	0.4987
ILGILALIDEGETDWK	1787.0	2	3.7322	0.434
ILGIPVIVTEQYPK	1570.9	2	3.5289	0.3483
ILGLAIESQDAGIK	1428.7	2	2.7262	0.2011
ILGSGISSSSVLHGMVFKK	1948.3	2	3.7932	0.3543
ILGTAGTEEGQK	1204.3	2	3.6504	0.3275
ILGTAGTEEGQKIVLQNGAHEVFNHR	2820.1	3	4.9683	0.3586
ILGVDKNASEDEIKK	1659.9	2	4.9422	0.1098
ILGWGVENGTPYWLVANSWNTDWGDNGFFK	3445.7	3	6.0279	0.3831
ILGYINTGKQEGAK	1492.7	2	3.6392	0.2288
ILHENTQTDK	1199.3	2	2.8137	0.2294
ILHENTQTDKALYNR	1817.0	3	3.341	0.1452
ILHGLGFTPAMQR	1441.7	2	3.1818	0.2332

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ILHLLGQEGPK	1205.4	2	3.2282	0.1269
ILHLLTQEALSIHGVK	1773.1	2	5.2678	0.5221
ILHNDPEVEKK	1322.5	2	3.1056	0.2281
ILHQHLGAPEER	1400.6	3	4.0912	0.3552
ILHSYVPEEIRDGNQVR	2026.2	2	3.3767	0.2515
ILHTLLASGEDALDFTQESEPSYISDVGPPGR	3416.7	3	5.6069	0.418
ILHVDNHIGISIAGLTADAR	2087.4	3	5.2067	0.4678
ILHVNGFNGEGGEEDPQAAR	2111.2	3	4.7861	0.2992
ILIAKPIMFR	1202.6	2	2.4366	0.1053
ILIANTGMDTDKIK	1533.8	2	3.9758	0.329
ILIIGESGVGK	1086.3	2	3.362	0.1731
ILIIGGSIANFTNVAATFK	1951.3	2	3.4796	0.2632
ILIIGNSSVGK	1101.3	2	2.6227	0.1361
ILIRPMYSNPPLNGAR	1813.2	2	3.3483	0.2015
ILIRPTAFKPVLPKPR	1847.3	3	3.5128	0.2226
ILISLATGHR	1081.3	2	2.6966	0.1128
ILISLATGHREEGGENLDQAR	2280.5	2	4.1868	0.359
ILISLATGHREEGGENLDQAREDAQEIADTPSGDKTSLETR	4425.7	3	3.4421	0.3055
ILITTVPPNLR	1237.5	2	2.8712	0.1982
ILIVGGGVAGLASAGAAK	1525.8	2	5.3702	0.4843
ILKEDILNYLEK	1491.8	2	4.4121	0.3086
ILKEEQELYQK	1421.6	2	3.3884	0.2604
ILKGEYAVR	1049.2	2	3.2274	0.206
ILKHEGLGAFYK	1376.6	3	3.9893	0.3376
ILKLPSFELLHK	1438.8	3	3.9823	0.3191
ILKPTDENLLK	1284.5	2	2.9814	0.1142
ILKQPSTQSDTYSMLALGNVWLQTLHQPTR	3428.9	3	3.9152	0.2086
ILKRPTSNGVVSSPNSTSRPTLPVK	2637.0	3	4.3087	0.2449
ILLAELEQLK	1170.4	2	4.1909	0.2032
ILLAELEQLKGQGK	1540.8	2	4.5923	0.3863
ILLANFLAQTEALMR	1705.1	2	5.332	0.495
ILLANFLAQTEALMRGK	1890.3	2	3.5933	0.3207
ILLANRNEVFHR	1482.7	2	2.5339	0.1382
ILLDAQHESGR	1239.4	2	2.4645	0.127
ILLDQVEEAVADFDECIR	2079.3	2	3.769	0.2804
ILLELLNQMDGFDQNVNVK	2204.5	2	6.0034	0.4458

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ILLENLGEASSQPSPTQSVQETVR	2584.8	3	6.4682	0.4202
ILLEPYKYLLQLPGK	1789.2	2	2.6781	0.1095
ILLHHAANSVK	1203.4	2	2.7722	0.2947
ILLITEDLKNIGNTFFK	1980.3	2	2.6124	0.1499
ILLLGAGESGK	1058.3	2	3.4056	0.2666
ILLLGEAQVGK	1141.4	2	2.5415	0.1285
ILLLGLDNAGK	1127.4	2	3.2115	0.1406
ILLLGLDNAGKTTLLK	1684.1	2	4.3737	0.278
ILLLNEMEKLEK	1473.8	2	3.9759	0.1933
ILLNPQDKDGSFSVVITGLR	2173.5	2	4.7593	0.4138
ILLNPQDKDGSFSVVITGLRK	2301.7	3	4.9862	0.3324
ILLQGTPVAQMTEDAVDAER	2158.4	2	2.9099	0.194
ILLRNPGNQAAYEHFETMK	2233.5	3	5.0871	0.3433
ILLSHFNWDKEK	1530.8	2	2.9352	0.1996
ILLSQTTGVAIPLHASSLDDVSLASTPK	2836.2	3	4.9488	0.406
ILLSVVSMLAEPNDESGANVDASK	2460.7	2	3.1741	0.1754
ILLTEPPMNPTK	1354.6	2	2.9968	0.1917
ILLTQENPFFR	1378.6	2	3.2065	0.2477
ILMADADGATKFPDVEKLEK	2192.5	3	4.087	0.1917
ILMHHIPEQTTQLLK	1803.2	2	3.2888	0.2847
ILMVGLDAAGK	1088.3	2	3.4623	0.324
ILNDDTALKEYK	1423.6	2	3.3684	0.3252
ILNEDGSPNLDFKPEDQPHFDIKDEF	3061.3	3	3.8964	0.2224
ILNFLMHPKPSGKPLPK	1918.4	2	3.334	0.2056
ILNHVLQHAEPGNAQSVLEAIDTYCEQK	3122.5	3	7.1695	0.4434
ILNNGHAFNVEFDDSQDK	2064.2	2	5.1366	0.4153
ILNNGHAFNVEFDDSQDKAVLK	2475.7	3	5.7137	0.4206
ILNNGHAFNVEFDDSQDKAVLKGGPLDGTYR	3392.7	3	6.0746	0.5029
ILNNSGLPITSAIDLEDAAK	2056.3	2	5.468	0.5804
ILNPEEIEKYVAEIEKEKEENEKKK	3061.4	3	4.0048	0.2708
ILPEIIPILEEGLR	1605.9	3	3.845	0.3079
ILPEYLSNWTMEK	1624.9	2	3.8564	0.3991
ILPNKVDPLVSLMMVEK	1927.4	2	3.4874	0.2834
ILPNKVDPLVSLMMVEKVPDSTYEMIGGLDKQIK	3803.5	3	3.9138	0.2775
ILPSVSHKPFESIDEGHVTHNWDEVDPDPNQLR	3810.1	3	3.4088	0.1773
ILPTLEAVAALGNK	1410.7	2	3.9375	0.4108

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ILPTLEAVAALGNKVVESLR	2094.5	2	4.5755	0.5113
ILPVFDEPPNPTNVEESLKR	2295.6	2	3.693	0.3192
ILQDGGLQVVEK	1299.5	2	4.0142	0.2299
ILQDIASGSHPFSQVLK	1841.1	2	5.5355	0.3956
ILQDIASGSHPFSQVLKEAK	2169.5	2	5.4938	0.4124
ILQDVADEEIAALPR	1653.9	2	3.8998	0.2837
ILQDYKSLQDIIAILGMDELSEEDKLTVSR	3437.9	3	4.5196	0.2182
ILQEAQNLMALTNVDTPLKGGLNTPLHESDFSGVTPQR	4107.6	3	5.0596	0.3103
ILQEDPTNTAAR	1329.4	2	3.8564	0.2235
ILQEGVDPK	999.1	2	3.1469	0.2747
ILQEGVDPKKLDSLTTSFGFPVGAATLVDEVGVDVAK	3818.3	3	6.0294	0.47
ILQEHEQIK	1138.3	2	2.7434	0.1269
ILQEHEQIKK	1266.5	2	3.3567	0.1767
ILQEKLDQPVSAPPSPR	1876.1	2	4.2156	0.3828
ILQETVKELAPR	1397.6	2	3.6304	0.2271
ILQEYITQEGHKLETGAPRPPATVTNAVSWR	3464.9	3	5.3335	0.3994
ILQEYITQQSNKLETGK	1994.2	2	4.8597	0.3601
ILQEYQVQYTPQGDSDNGKENQTVHK	3021.2	3	5.3185	0.2746
ILQHSHGIEEERQDLTTALGLVK	2588.9	3	3.4438	0.2341
ILQMEEEYIQQLCEDIIQLKPDVVITEK	3362.9	3	5.2537	0.3932
ILQNIKVFDFTFSPEEMK	2187.5	2	3.0293	0.2287
ILQNIKVFDFTFSPEEMKQLNALNK	2969.4	3	4.6924	0.342
ILRDIEQYYSTQIDEMPMNVADLI	2872.3	3	3.7585	0.215
ILRDIETFYNTTVEEMPMNVADLI	2829.2	3	4.7397	0.3745
ILREFLGK	976.2	2	2.6443	0.1521
ILRPWQSSETR	1373.5	3	3.2388	0.271
ILSDMRSQYEVMAEQNR	2071.3	3	4.4343	0.3159
ILSDMRSQYEVMAEQNRK	2199.5	3	4.5287	0.3496
ILSDVTHSAVFGVPASK	1729.0	2	4.3933	0.3569
ILSGRPPLGFLNPR	1537.8	2	3.5527	0.2321
ILSGVVTK	817.0	1	1.8647	0.1285
ILSHTEEHKKFE	1498.7	2	2.9811	0.2984
ILSIGGGAGEIDLQILSK	1785.1	2	2.8373	0.3128
ILSIQKDLANIAEVEVSIPAK	2252.6	2	2.5566	0.1781
ILSIQKDLANIAEVEVSIPAKLHNSLIGTK	3216.8	3	5.2516	0.2049
ILSISADIETIGEILK	1716.0	2	5.2553	0.4916

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ILSISADIETIGEILKK	1844.2	2	5.0356	0.5259
ILSLLAASGPTWDQVPPFQWSTSPFSGLLHMGQPDLWK	4210.8	3	4.7191	0.3938
ILSLQNHHIIENNHILYLGR	2398.8	3	5.2447	0.3973
ILSNNPSK	873.0	2	2.4466	0.1304
ILSSDDYGKDLTSVMR	1801.0	2	3.8058	0.5204
ILSTIDRELLKPNASVALHK	2219.6	3	4.1153	0.3589
ILTAERDYLDLTASNNFFVDDYAR	2824.1	3	5.1199	0.3405
ILTDIMWPIIAK	1414.8	1	2.6059	0.2108
ILTDKLKEAETR	1417.6	2	3.823	0.2805
ILTDYGFEGHPFR	1552.7	2	3.2211	0.3524
ILTDYGFEGHPFRK	1680.9	2	3.7991	0.375
ILTEAEIDAHLVALAERD	1980.2	2	5.5089	0.4598
ILTERGYSFTTTAER	1745.9	2	3.743	0.3235
ILTFDQLALDSPK	1461.7	2	3.6407	0.4201
ILTGGADKNVVVFDK	1576.8	2	3.1938	0.2383
ILTHVAEMQGK	1227.5	2	3.205	0.3891
ILTKLLEVSDDPQVLAVAAHDVGEYVR	2952.4	3	3.2767	0.1985
ILTLSQIGR	1001.2	2	2.8152	0.2312
ILTMDGLIEDIKHR	1655.0	2	2.7417	0.3719
ILTPLVSLDTPGK	1354.6	2	3.6086	0.3556
ILTSVDQYLELIGNSLPGTTAK	2334.7	3	4.5548	0.3179
ILTTASSHEFEHTK	1601.7	2	4.2414	0.4114
ILTTASSHEFEHTKK	1729.9	2	4.0185	0.4651
ILTTASSHEFEHTKKDLDGFR	2433.7	3	3.5441	0.3365
ILTTNTWSSELSK	1480.6	2	4.0689	0.4603
ILTTSEDSNAQEIKDIYGLNGQIEHK	2918.2	3	5.8393	0.2453
ILTVEDHYYEGGIGEAVSSAVVGEPGITVTHLAVNR	3755.1	3	6.5169	0.43
ILTVEDHYYEGGIGEAVSSAVVGEPGITVTHLAVNRVPR	4107.6	3	6.6161	0.5184
ILVAHDIHTK	1147.4	2	2.77	0.2515
ILVATNLFGR	1104.3	2	3.5265	0.3514
ILVGNKNDDPER	1370.5	2	2.8937	0.2135
ILVTGGSGLVGK	1101.3	2	2.9363	0.1832
ILVTLLHTLER	1308.6	2	3.0483	0.2489
ILYEGTHLDPERK	1571.8	2	3.212	0.1256
ILYIVASDPYSR	1397.6	2	3.3686	0.3158
ILYKLPGHAGSINEVAFHPDEPIIISASSDKR	3476.9	3	6.061	0.4568

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ILYMTDEVNDPSLTIK	1853.1	2	4.4422	0.4044
ILYSQCGDVMR	1285.5	2	2.5909	0.1646
IMDATNILVSPLVYLYPDIPKEEAFGK	3038.5	3	4.893	0.335
IMDPNIVGSEHYDVAR	1817.0	2	5.3325	0.4514
IMDPYKASYGVEDPEYAVTQLAQTTMR	3079.5	3	3.9378	0.1857
IMEGPAFNFLDAPAVR	1749.0	2	4.8435	0.5024
IMELEDHITQK	1357.6	2	3.8154	0.1699
IMESFKNMVPQQALVIR	2005.4	2	5.4087	0.459
IMGIPEEEQMGLLR	1616.9	2	4.2357	0.429
IMGLDLPDGGHLTHGYMSDVKR	2413.8	3	4.0203	0.3952
IMGPNYTPGKKEDLYLKPIQR	2462.9	3	5.5732	0.3968
IMHFPTWVDLKGEDSVPDTVHHVVVPVNPK	3394.9	3	4.6237	0.3922
IMIPLKISPLQ	1253.6	2	3.0708	0.2003
IMIPLKTSPLQ	1241.6	2	2.8287	0.2273
IMKNEIQDLQTK	1461.7	2	3.9754	0.1171
IMLFTGGPPTQGPGMVVGDELKIPIR	2725.3	3	5.0465	0.4991
IMLFTNEDNPHGNDSAK	1904.1	2	5.4721	0.4875
IMLKGDNITLLQSVSN	1747.1	2	3.9036	0.2986
IMLKNVEDFTGPR	1520.8	2	3.0581	0.2365
IMLLNHPDKGGSPYIAAK	1926.3	3	3.4745	0.2248
IMLPWDPTGK	1158.4	2	2.5334	0.2166
IMMQVHGSK	1031.3	2	2.5968	0.2213
IMNEEDPEKQR	1389.5	2	4.0306	0.2221
IMNHEERFQFPSHVTDVSEEAKDLIQR	3257.6	3	3.6804	0.1646
IMNTFSVMPSPK	1352.6	2	4.0455	0.3115
IMNTFSVVPSPK	1320.6	2	4.6162	0.3403
IMNVIGEPIDER	1386.6	2	4.3972	0.3818
IMNVIGEPIDERGPIK	1782.1	2	4.2321	0.2555
IMNVIGEPIDERGPIKTK	2011.4	2	4.2413	0.3358
IMQEEGQPLKLPDTKR	1884.2	2	4.2166	0.3811
IMQQMSDHRYDK	1552.8	2	2.7162	0.1213
IMQSSSEVGYDAMAGDFVNMVEK	2509.8	2	6.6339	0.5904
IMQSSSEVGYDAMAGDFVNMVEKGIIDPTK	3234.7	3	4.8212	0.3654
IMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVR	3589.1	3	4.8017	0.369
IMQVVDEKLPGLLGNFPGPFEEEMK	2819.3	3	3.224	0.1899
IMSQSQVSK	1008.2	2	2.4595	0.1524

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IMSVIREWGSGSDTLR	1808.1	2	2.773	0.1663
IMVANIEEVLQR	1415.7	3	4.4635	0.1849
IMVANIEEVLQRGEALSALDSK	2387.7	2	5.6324	0.5129
IMVANIEEVLQRGEALSALDSKANNLSSLSK	3302.7	3	4.6966	0.2977
IMVANIEEVLQRGEALSALDSKANNLSSLSKK	3430.9	3	4.9778	0.3565
IMYDLTSKPPGTTEWE	1869.1	2	2.4985	0.2847
IMYLSEAYFR	1293.5	2	3.6824	0.2102
IMYTVFEHTFHVR	1681.0	2	3.7597	0.4894
INAAEIESR	1003.1	2	2.5523	0.1473
INAGMLAQFIDKPVCFVGR	2080.5	2	3.8023	0.3927
INAGMYILSPAVLR	1518.8	2	3.0135	0.1385
INALTAASEAACLIVSVDETIKNPR	2601.0	3	4.4432	0.3749
INASKNQQDDGK	1318.4	2	3.5072	0.1598
INAWNSPTLPIYEPGLK	1914.2	2	4.1596	0.3507
INDRFEFPEQLPLDEFLQK	2379.7	2	3.6828	0.2249
INEAIVAVQAIIADPK	1666.0	2	3.2936	0.4082
INEAKDLLEGQAKK	1557.8	2	3.8997	0.3003
INEGFDLLHSGK	1330.5	2	3.3147	0.2485
INEGFDLLR	1077.2	2	2.8839	0.1643
INEGIGQGDLSELPELHALTAGLK	2476.8	3	4.1572	0.1729
INEGLEHLAK	1124.3	2	3.0439	0.2035
INEILSNALK	1115.3	2	3.0492	0.1096
INEILSNALKRGEIIAK	1883.2	2	3.1213	0.1577
INEKPQVIADYESGR	1719.9	2	4.7736	0.4768
INELTGIKESDTGLAPPALWDLAADKQTLQSEQPLQVAR	4219.7	3	5.9741	0.2896
INEVQTDVGVDTK	1418.5	2	4.5592	0.4045
INFDDNAEFR	1241.3	2	3.0972	0.3472
INFDDNAEFRQK	1497.6	2	3.7542	0.2516
INFDKYHPGYFGK	1586.8	2	4.4897	0.3957
INFDVNGYIVGANIETYLLEK	2386.7	2	4.4151	0.351
INGEVSSISSKFETEPVSK	2039.2	2	4.1479	0.4386
INGKDSIEKEHVEEISELFYDAK	2694.9	3	5.4069	0.4433
INHEGEVNR	1068.1	2	3.0261	0.3231
INHSNQSIKEK	1298.4	2	3.0788	0.2243
INHTFRPQVEK	1369.6	2	2.8222	0.1963
INISEGNCPER	1232.3	2	2.8782	0.1132

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
INKAVSEEQQPALK	1555.8	2	3.6178	0.2129
INKELANIR	1071.3	2	2.9517	0.1463
INKELSDLAR	1159.3	2	3.0154	0.1501
INKESLLPVAK	1212.5	2	3.8371	0.2687
INKLHSEGDQLLAAEHPGR	2086.3	3	6.3159	0.5209
INKLMNESLMLVTALNPHIGYDK	2616.1	2	5.7836	0.472
INKLNSIKDVEQK	1529.8	2	4.909	0.2443
INKYLDEIVKEVEAK	1792.1	3	3.6554	0.2728
INLAEDVLAWEHER	1695.9	2	4.4763	0.3429
INLESEPQEFKPIGTAHNR	2181.4	3	3.9868	0.2409
INLKPSYLVVPQTGFHHEK	2208.5	3	4.311	0.2545
INLKRPPTAGSQFK	1557.8	2	3.6773	0.2707
INLPAPNPDHVGGYK	1592.8	2	2.9902	0.2914
INLQGDIVDR	1143.3	2	2.5709	0.1324
INLRKRRDSLILGGVIGICTILLLLYAFH	3283.0	3	3.4246	0.2235
INLSLSALGNVISALVDGK	1885.2	2	5.4556	0.5038
INLSLSTLGNVISALVDGK	1915.2	2	4.8032	0.5274
INMNGINNSSGMVDAR	1693.9	2	3.2821	0.1755
INMNGVNSSNGVVDPR	1673.8	2	3.5129	0.3067
INNPELLGQYMIDAGTEFGPGTAYGNALIK	3169.6	3	7.4724	0.5785
INNVIDNLIVAPGTFEVQIEEVR	2583.9	3	5.4705	0.3739
INNVNKALDFIASK	1547.8	2	3.9156	0.3008
INNVPAEGENEVNNELANR	2097.2	2	5.443	0.5092
INPDEREEMK	1261.4	2	2.4797	0.1778
INPDGSQSVVEVPYAR	1731.9	3	4.3646	0.355
INQDPQVMLAPLISIALK	1965.4	2	4.8385	0.3581
INQDPQVMLAPLISIALKVSQLQER	2806.3	3	3.6738	0.2528
INQMATAPDSQR	1332.5	2	2.9815	0.2634
INRLPTPIAGLDNIILFLR	2150.6	3	4.1008	0.3051
INSGGKLPNFGFVVFDDSEPVQK	2495.8	2	4.296	0.3715
INSHLPSHIR	1174.3	2	2.4883	0.2101
INSQNQPTGIHREPPPPPFSVNK	2555.8	3	3.999	0.2836
INSTATPDQDRDKIK	1702.8	2	2.6983	0.1324
INSYGYGDHYIHIK	1680.8	2	4.0004	0.3437
INVLAAQYQSLLNSYGEPVDDKSATLLQLITK	3508.0	3	5.2262	0.419
INVNEIFYDLVR	1495.7	2	4.8055	0.3418

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
INVSGLTTK	933.1	2	2.6344	0.1
INVSGLTTKNLDYVATSIHEAVTK	2575.9	3	3.8906	0.1057
INVVNNHQAK	1137.3	2	2.6171	0.1718
INVYYNEAAGNK	1356.5	2	3.382	0.2434
INVYYNEAAGNKYVPR	1872.1	2	4.7048	0.5139
INVYYNEATGGK	1329.4	2	4.5593	0.3748
INVYYNEATGGKYVPR	1845.0	2	4.8241	0.4342
INVYYNEATGNK	1386.5	2	2.8978	0.1954
INVYYNEATGNKYVPR	1902.1	2	4.9847	0.4476
INVYYNESSSQK	1432.5	2	3.8049	0.3456
IPADTFAALKNPNAMLVNLEEPLASTYQDILYQAK	3865.4	3	6.3508	0.4879
IPAEVLILNSIVLPHKELSR	2242.7	3	3.2575	0.2598
IPAFLNVVDIAGLVK	1569.9	2	5.0986	0.3707
IPAYFVTVSDPAVPPGEDPDGR	2300.5	2	4.5006	0.5041
IPDEIIDMVKEEVVAK	1829.1	2	4.6512	0.3388
IPDQLVILDMK	1285.6	2	3.7073	0.3074
IPDQLVILDMKHGVEAK	1907.3	3	3.846	0.2031
IPDWFLNR	1061.2	2	2.9244	0.1915
IPEAPAGPPSDFGLFLSDDDPKK	2414.7	3	3.2598	0.215
IPELLASGMVDNMTK	1619.9	2	3.6802	0.1593
IPEPQKPQLKPPEDIVR	1985.3	3	4.3185	0.3353
IPEQSVLLLHACAHNPTGVDPRPEQWK	3037.4	3	4.2241	0.1619
IPEVHHISQDPLHYSIASVSASQK	2644.9	3	5.6566	0.4191
IPFYGSYTEMDPVIIASEGVEK	2446.8	2	3.0281	0.3228
IPGGATLVFEVELLK	1586.9	2	3.6152	0.4212
IPHEPVINSSNVHVGSR	1843.0	3	3.7108	0.3529
IPHLAIHLQR	1198.4	2	2.6602	0.3392
IPIFSAAGLPHNEIAAQICR	2122.5	3	4.0837	0.3168
IPIHNEDITYDELVLMMQR	2331.7	2	3.2528	0.3211
IPILYGEVEKLEESAVTVMFDKVQFSNK	3215.7	3	4.8905	0.207
IPISLVLR	911.2	2	2.4095	0.2135
IPKEQGFLSFWR	1508.7	2	3.5584	0.3455
IPKEQGVLSFWR	1460.7	3	4.081	0.3251
IPKIQKLLQDFFNGKELNK	2274.7	3	4.1522	0.3044
IPKIQQLVKEFFNGKEPSR	2259.6	3	3.6314	0.2736
IPKNPELVPQNYISDSLAQSVVQHLR	2947.3	3	3.9308	0.2533

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IPKVQKLLQDFFNGRDLNK	2274.7	3	4.0486	0.3453
IPLLSDLTHQISK	1465.7	2	3.9132	0.2969
IPLLSDLTHQISKDYGVYLEDSGHTLR	3072.4	3	6.0947	0.4577
IPLNDLFR	988.2	2	2.9573	0.1511
IPLPGAEMLEEEPLYVNAK	2114.4	2	3.4621	0.3177
IPNFLHLTPVAIKK	1592.0	2	4.2339	0.3257
IPNFWVTTFVNHPQVSALLGEEDEEALHYLTR	3728.1	3	6.0847	0.522
IPNIYAIGDVVAGPMLAHK	1980.4	3	5.3904	0.4858
IPNQFQSDPPAPSDK	1641.8	2	3.3322	0.2673
IPPGDLVFDPDQRGDVVLPFQR	2481.8	3	3.6065	0.2754
IPPYHYIHVLDQNSNVSR	2153.4	2	5.6634	0.5354
IPPYHYIHVLDQNSNVSRVEVGPK	2763.1	3	4.0482	0.3841
IPQNPSPHTHQQQNAPVTVIQSK	2550.8	3	5.0607	0.4279
IPQSTLSEFYPR	1438.6	2	2.8259	0.249
IPRDLYEDELVPLFEK	1977.2	2	3.9432	0.2157
IPSAVGYQPTLATDMGTMQER	2267.6	2	5.5867	0.5489
IPSLFEIVVRPTGQLAEK	1998.4	2	3.1432	0.1941
IPTAGIYGASYVPFAAPATATIATLQK	2695.1	3	5.5209	0.4145
IPTEAPQLELK	1239.4	2	2.8048	0.29
IPTPVIHTK	1006.2	2	2.5039	0.1593
IPTPVIHTKH	1143.4	2	2.6095	0.2613
IPTRPFEEGKK	1302.5	2	2.8988	0.1489
IPVDEEAFVIDFKPR	1776.0	3	4.5314	0.4524
IPVDTYNNILTVLK	1603.9	2	3.3554	0.2466
IPVHPNDHVNK	1270.4	2	3.6012	0.3735
IPVQALLHLR	1160.4	2	3.8194	0.2645
IPVQLQR	854.0	2	2.5923	0.1224
IPVTDEEQTNVPYIYAIGDILEDKVELTPVAIQAGR	3972.4	3	7.3189	0.5186
IPWFQYPIIYDIR	1725.0	2	4.491	0.3858
IPWTAASSQLKEHFAQFGHVR	2411.7	3	3.9006	0.226
IPYAPSGEIPK	1172.4	2	2.7267	0.1737
IPYLPITNFNQNWQDGK	2049.3	2	4.7806	0.4228
IQAAASTPTNATAASDANTGDR	2105.2	3	3.6505	0.2451
IQAAKETLILLLK	1454.8	2	3.5104	0.2046
IQAGDPVAR	927.0	2	2.4495	0.1073
IQAGEGETAVLNQLQEKNHTLQEQVTQLTEK	3479.8	3	4.9512	0.3414

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IQAGEVSQPSKEQLEK	1772.0	2	5.29	0.2593
IQAKPKPKPNQNLSEASGK	2036.3	3	3.3378	0.3262
IQALAEETAQNLKR	1585.8	2	3.3793	0.2725
IQALQQQADEAEDR	1615.7	2	4.7019	0.467
IQALQQQADEAEDRAQGLQR	2269.4	2	4.3507	0.2306
IQASTMAFK	997.2	1	2.4307	0.212
IQDALSTVLQYAEDVLSGK	2051.3	2	6.3115	0.5445
IQDALSTVLQYAEDVLSGKVSADNTVGR	2951.2	3	4.6928	0.4541
IQDKEGIPPDKQR	1524.7	3	4.226	0.2351
IQDLEHHLGLALNEVQAAK	2100.4	3	4.0392	0.2304
IQDLPPVDLSLVNKDENAIYFLGNSLGLQPK	3412.9	3	6.0068	0.3748
IQDVGLVPMGGVMSGAVPAAAAQEAVEEDIPIAK	3335.8	3	3.8975	0.2479
IQDVGLVPMGGVMSGAVPAAAAQEAVEEDIPIAKER	3621.1	3	3.4478	0.2858
IQEAGTEVVK	1074.2	1	1.693	0.1237
IQEAGTEVVKAK	1273.5	2	3.939	0.2648
IQEAKDVYKEHFQDDVFNEK	2483.7	3	5.0835	0.2808
IQEELSALRAEHQQDSEDLFK	2487.7	3	3.202	0.1532
IQEELSALRAEHQQDSEDLFKK	2615.8	3	3.9211	0.1764
IQEENVIPR	1098.2	2	3.136	0.1707
IQEGVESLAGYADIFLR	1882.1	2	5.2609	0.4724
IQEGVFDINNEANGIK	1761.9	2	5.3828	0.442
IQEIIEQLDVTTSEYEK	2039.2	2	6.7781	0.4966
IQEIIEQLDVTTSEYEKEK	2296.5	2	5.3806	0.3904
IQEIIEQLDVTTSEYEKEKLNER	2809.1	3	5.0853	0.3516
IQEKKDEDIAR	1345.5	2	3.1815	0.145
IQELEDLLAK	1172.4	2	2.935	0.1165
IQEPNTFPAILR	1399.6	2	3.2458	0.1908
IQEQVQQTLAR	1314.5	2	3.8585	0.2203
IQESHPELR	1109.2	2	3.1156	0.2197
IQEVADELQK	1173.3	2	3.1296	0.2002
IQEVGEPSKEEK	1373.5	2	3.7366	0.2214
IQEVGEPSKEEKAVAK	1743.0	2	3.9846	0.3277
IQFHNVKPEYLDAYNSLTEAVLPK	2791.2	3	5.8818	0.505
IQFKPDDGISPER	1502.7	3	3.9868	0.3032
IQFKPDDGTTPER	1504.6	2	3.4411	0.2888
IQFKQDDGTGPEK	1463.6	2	4.3542	0.2892

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IQFRLPDGSSFTNQFPSDAPLEEAR	2824.1	3	5.1272	0.3011
IQFTSLYHKEEAPASPLRPLYPQISPLK	3225.7	3	4.7438	0.4188
IQGAQKEPGNK	1170.3	2	2.7386	0.1982
IQGEYKYTQVGPDHNR	1906.0	3	3.7892	0.277
IQGLTVEQAEAVVR	1513.7	2	5.0286	0.445
IQGSEHLYNDHGVIVDYNTTDPLIR	2871.1	3	3.5153	0.1486
IQHALETIHHLK	1440.7	3	3.5968	0.307
IQHAVQLATEPLEK	1577.8	2	3.8069	0.2761
IQHILCTGNLCTKESYDYLK	2343.7	3	3.2612	0.1567
IQHPSNVLHFFNAPLEVTEENFFEICDELGVK	3718.1	3	5.173	0.4606
IQHSITAQDHQPTPDSCIISMVVGQLK	2948.4	3	3.7834	0.287
IQHVVEAVRQEK	1436.6	2	3.4016	0.2013
IQIAPDSGGLPER	1353.5	2	3.2876	0.162
IQIFPVDSAIDTISPLNQK	2100.4	2	4.3213	0.3797
IQIGNTYEGRPIYVLK	1865.2	2	3.999	0.3602
IQIGTQAIERAPSYIEIFGR	2263.6	3	3.5216	0.125
IQIPRPDDPSNQIK	1621.8	2	3.3253	0.1595
IQIWDTAGQER	1317.4	2	2.8323	0.2058
IQKDINELNLPK	1425.7	2	3.7914	0.1835
IQKEALGGQALYPHVLVK	1965.3	3	4.8826	0.4289
IQKETALLQELEDLELGI	2056.3	2	3.0036	0.1376
IQKGDSKKDDEENYLDLFSHK	2510.7	3	5.5701	0.3235
IQKGVFEVKSTNGDTFLGGEDFDQALLR	3086.4	3	4.8333	0.2923
IQKLLQDFFNGKELNK	1936.2	2	3.585	0.2002
IQLGKDNQHQGSYSEGAQMNGIQPEEIGR	3186.4	3	5.7416	0.3597
IQLVEEELDR	1244.4	2	3.6841	0.2869
IQLVEEELDRAQER	1728.9	2	3.3311	0.1519
IQLWDTAGQER	1317.4	2	3.0796	0.1927
IQMSNLMNQAR	1306.5	2	3.4735	0.2247
IQNDAGVR	872.9	2	2.6635	0.1014
IQNGAQGIR	957.1	2	2.8868	0.2128
IQNLEALLQK	1170.4	2	3.2563	0.1906
IQNNDNVGKPK	1227.4	2	3.2751	0.1157
IQPDTIIQVWREDIPVNYMKELELVTK	3272.8	3	3.653	0.1271
IQPEEKPVEVSPAVTK	1752.0	2	2.6685	0.1172
IQPFQNLTLHPASSSLHYSLQLFEGMK	3088.5	3	3.7666	0.2144

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IQQDADSVITVGR	1402.5	2	3.838	0.3321
IQQEIAVQNPLVSER	1724.9	2	4.6102	0.3544
IQQIAEGEKVK	1243.4	2	2.9975	0.1257
IQQIAEGEKVKQVLLAQAEAEKIR	2694.1	3	4.6332	0.3856
IQQIETTLNILDAK	1600.8	2	3.944	0.106
IQQLAISGLK	1071.3	2	2.7971	0.1823
IQQLQEILQDLQK	1597.8	2	3.6692	0.1247
IQQLTALGAAQATAKA	1556.8	2	4.6799	0.4396
IQQLVKEFFNGKEPSR	1921.2	2	4.7773	0.4115
IQQLVQDIASLTLLEISDLNELLK	2711.1	2	3.8814	0.4166
IQQLVQDIASLTLLEISDLNELLKK	2839.3	3	3.988	0.3633
IQQNTFTR	1008.1	2	2.7193	0.2462
IQQQQPPPGEK	1250.4	2	3.0324	0.2128
IQRPPEDSIQPYEK	1700.9	2	4.2547	0.3007
IQRPPEDSIQPYEKIK	1942.2	3	5.0275	0.2392
IQSIPLVIGQFLEAVDQNTAIVGSTTGSNYYVR	3556.0	3	5.226	0.537
IQSLELDKLGTSELLLAK	1972.3	3	4.324	0.2956
IQSLPDLSRLPNVTGSHMHLPFAGDIYSED	3311.7	3	3.9189	0.1924
IQSQNDREK	1118.2	2	2.7076	0.1059
IQSSGGPLQITMK	1360.6	2	2.8813	0.2515
IQSSHNFQLESVNK	1631.8	2	3.4581	0.1453
IQSTVTQPGGK	1116.3	2	2.9154	0.1039
IQTEIIEQEDLIK	1572.8	2	3.2907	0.1886
IQTKEPLPTLPLGR	1563.9	2	2.9219	0.1892
IQTLSQLLLNLQAVIAHQDSYVETQR	2983.4	3	5.4228	0.3318
IQTQPGYANTLR	1362.5	2	4.0402	0.3181
IQTQPGYANTLRDAAPK	1845.0	2	3.5169	0.2733
IQTTTTTQAVQGR	1405.5	2	3.3708	0.3165
IQTYLQSTKPIIDLYEEMGK	2371.7	3	4.9045	0.4396
IQTYLQSTKPIIDLYEEMGKVK	2599.0	3	4.329	0.3498
IQVLGSLVSLEMGK	1474.8	2	4.9556	0.485
IQVLQQQADDAEER	1643.7	2	5.0691	0.427
IQVLQQQADDAEERAER	2000.1	2	4.5584	0.3251
IQVLVEPDHFK	1325.5	2	3.3004	0.1698
IQVNHPAVLR	1147.4	2	2.7821	0.2029
IQVRLGEHNIEVLEGNEQFINAAK	2723.0	3	3.8476	0.1419

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IQVSSEKEAAPDAGAEPITADSDPAYSSK	2936.1	3	5.3816	0.3623
IQVTPPGFQLVFLPFADDK	2133.5	2	4.3857	0.3403
IQVTPPGFQLVFLPFADDKR	2289.7	2	3.7251	0.272
IQVTPPGFQLVFLPFADDKRK	2417.8	2	3.7466	0.364
IQVWHAEHR	1176.3	2	3.231	0.3269
IQVWHEEHR	1234.3	2	3.0514	0.3026
IQVYSRHPAENGK	1499.7	2	3.9433	0.285
IQYAKTDSDIIAK	1466.7	2	3.9515	0.3237
IQYAKTDSDIISK	1482.7	2	4.0426	0.2605
IQYPGIAQSIQSDVQNLLAVLK	2399.8	3	3.7112	0.2152
IQYQLVDISQDNALRDEMR	2308.6	2	3.4439	0.1917
IRAIENIDTLTNLESLFLGK	2261.6	3	4.2248	0.3354
IRAQTEGINISEEALNHLGEIGTK	2594.9	3	5.8683	0.446
IRDAYTHPQFVTDVMKPLQIENIIDQEVQTLSGGELQR	4384.9	3	6.816	0.4566
IRDIDAATEAK	1203.3	2	2.6851	0.2381
IRDPNQGGKDITEEIMSGAR	2188.4	2	4.6056	0.3761
IRDTPEDIVLEAPASGLAFHPAR	2476.8	3	3.4779	0.2466
IRDVINVFHHLR	1519.8	2	2.867	0.2856
IRDVTNNQEK	1217.3	2	2.7065	0.1131
IREDLPNLESSEETEQINKHFHNTLEHLR	3530.8	3	4.4471	0.3607
IREEFPDRIMNTFSVMPSPK	2395.8	3	3.5521	0.2299
IREESGAR	918.0	2	2.6383	0.1069
IREESNTKIDLPAENSNSETIIITGK	2874.2	3	3.8325	0.1129
IREEYPDR	1078.2	2	2.8019	0.1791
IREEYPDRIMNTFSVMPSPK	2411.8	2	3.4099	0.2958
IREEYPDRIMNTFSVVPSPK	2379.7	2	3.9897	0.3243
IREGMAALQSDPWQQELYR	2292.6	2	5.5603	0.5067
IREHVPQLLLLLTAGQSEDSYLQAANALTR	3322.8	3	6.7269	0.4731
IREIADGLCLEVEGK	1645.9	2	3.8105	0.406
IRELEEAMAGER	1404.6	2	4.5357	0.3578
IRELESQISELQEDLESER	2304.5	2	5.9611	0.4243
IRELESQISELQEDLESERASR	2618.8	3	3.9242	0.3058
IRELGSLPQEAFEKYQTLSLK	2451.8	3	4.4838	0.327
IRELQQQIEDLQK	1641.9	2	3.8682	0.2305
IRELTAVVQKR	1313.6	2	3.1085	0.1266
IRETTDFKVDTK	1453.6	2	3.2074	0.2934

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IREYFGGFGEVESIELPMDNK	2431.7	3	4.9881	0.2655
IRFHDFLGDSWGILFSHPR	2301.6	3	5.2469	0.3321
IRFLILPDMLK	1359.7	2	3.5504	0.2008
IRFQESEERPK	1419.6	3	4.0154	0.224
IRGETLGIIGLGR	1355.6	2	3.5009	0.2753
IRGETLGLIGFGR	1389.6	2	2.4398	0.2369
IRGQEKGPGYPQAEALLAEAMLK	2471.9	3	3.799	0.2455
IRGTSYQSPHGIPIDLLDR	2139.4	3	4.6522	0.3623
IRHNEQNLSLADVTQQAGLVK	2335.6	3	3.5225	0.2929
IRIDAMHGVVGPYVKK	1784.2	3	4.2122	0.3588
IRIDSLSAQLSQLQK	1701.0	2	4.6723	0.3059
IRIFDLGR	990.2	2	2.6559	0.2072
IRKPTLDKPSPETFVK	1857.2	2	3.5368	0.2192
IRLEETLEQLAK	1443.7	2	3.8204	0.2435
IRLQAYHTQTTPLIEYYR	2267.6	3	3.8899	0.2711
IRNEKGEIEQER	1501.6	2	3.8316	0.3281
IRNELMQSLNQDSNSNFKDTLLK	2710.0	3	5.9661	0.4475
IRNGENGIHFLLNR	1653.9	3	3.9878	0.2992
IRNPWGEVEWTGR	1600.8	2	2.9168	0.2143
IRPFAVAAVLR	1213.5	2	3.1397	0.2756
IRPTAVTLEHVPK	1461.7	3	4.5334	0.3109
IRPTVQEDGGDVIYKGFEDGIVQLK	2778.1	3	4.0153	0.2026
IRQAEEQIEHLQR	1650.8	2	4.371	0.3547
IRQAETLEQVR	1343.5	2	3.3288	0.1638
IRSIEALLEAGQAR	1527.8	2	3.9947	0.3023
IRSLQEQADAAEER	1616.7	2	2.8686	0.116
IRSQIGNTESELKK	1603.8	2	3.7591	0.3915
IRSQIGNTESELKKLAEENPDLQEAYIAK	3289.6	3	7.4291	0.5265
IRTSTPTGHGASPAKQDELVISAR	2493.8	2	2.6191	0.1149
IRVDVADQAQDKDRDDR	2016.1	3	3.3224	0.2292
IRVESLLVTAISK	1429.7	2	4.0774	0.3976
IRWNDGLDQYRLTPLELK	2231.5	3	3.4464	0.2437
IRYESGDHVAVYPANDSALVNQLGK	2718.0	3	5.7483	0.3536
IRYESLTDPSKLDSGK	1810.0	2	4.1405	0.2954
IRYESLTDPSKLDSGKELHINLIPNKQDR	3381.8	3	4.6135	0.4225
ISAEGGEQVER	1175.2	2	4.153	0.2369

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ISAHQGAQVDSR	1269.3	2	2.7227	0.2061
ISALNIVGDLLR	1284.5	2	3.6051	0.321
ISALQSAGVVVSMSPAQLGTTIYKEFEK	2956.4	3	6.356	0.5059
ISANENSLAVR	1174.3	2	3.1256	0.27
ISAQDAK	732.8	1	1.9325	0.1037
ISASGPESLLGGPGGASAAPAAGSK	2111.3	2	5.0913	0.4378
ISASLLDSR	962.1	2	3.1933	0.2824
ISASSATRELDELMASLSDFKFMAQGK	2935.3	3	3.3097	0.1512
ISATSIFFESMPYK	1621.9	2	3.996	0.3009
ISATSIFFESMPYKLNPK	2074.4	2	4.3454	0.3836
ISAVESQPSR	1074.2	2	3.2688	0.1646
ISAVSVAER	932.1	2	2.5281	0.1526
ISCPEGTNAYR	1211.3	2	3.353	0.3109
ISDAELEAELEKLSLSEGGLVPSSK	2602.9	3	4.1347	0.2268
ISDEDWDIIHR	1399.5	2	3.9805	0.3185
ISDLHRESVDHLTIPSR	1976.2	3	4.3742	0.2973
ISDSEGFKANLSLLR	1650.9	3	3.8367	0.3543
ISDSVLVDIKDTEPLIQTAK	2186.5	2	4.5401	0.2875
ISEDKNPDYR	1237.3	2	2.7437	0.1434
ISEEDELDTK	1179.2	2	3.4572	0.3365
ISEEDELDTKLTR	1549.7	2	4.514	0.321
ISEHVEEAKK	1170.3	2	3.3197	0.2015
ISEIEDAAFLAR	1335.5	2	4.1479	0.3535
ISEKEEVTTR	1192.3	2	3.3401	0.2854
ISEKEEVTTREVSGIK	1806.0	2	4.497	0.3358
ISELDAFLKEPALNEANLSNLK	2430.7	3	4.0551	0.1742
ISELGAGNGGVVFK	1348.5	2	2.5821	0.1396
ISELGAGNGGVVTK	1302.5	2	2.9062	0.2242
ISENYSDKSDIENADESSSSILKPLISPAAER	3467.7	3	5.3891	0.3377
ISEQFTAMFR	1230.4	2	3.8044	0.3737
ISEQSDAK	877.9	2	2.6422	0.1352
ISEQSDAKLK	1119.3	2	2.7512	0.125
ISEQSDAKLKEIVTNFLAGFEA	2411.7	3	4.2481	0.3626
ISEQTYQLSR	1225.3	2	3.5396	0.3256
ISERTPSALAILENANVLAR	2139.4	3	4.8133	0.3155
ISESAKQELIDFK	1508.7	2	3.5547	0.1219

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ISESAKQELIDFKTR	1766.0	3	4.2108	0.3162
ISESGQFSDGLEDR	1540.6	2	4.2027	0.3478
ISESGQFSDGLEDRGLLESSTR	2384.5	3	3.5097	0.2751
ISFAKEPHVEQITR	1655.9	2	3.9907	0.3828
ISFDEYWTLIGGITGPIAK	2082.4	2	2.4111	0.1389
ISFDLAEYTADVDGVGTLR	2043.2	2	2.6179	0.1714
ISFKFDHLR	1163.4	2	3.0782	0.2112
ISFLENNLEQLTK	1549.8	2	4.6617	0.3466
ISFPAIQAAPSFSNSFPQIFR	2326.6	3	5.3647	0.4835
ISFSNIISDMK	1255.5	2	3.767	0.364
ISFYMTNYGEEGTHVGSAAALDNTDLVFGQYR	3528.8	3	4.672	0.3364
ISGASEKDIVHSGLAYTMER	2165.4	2	5.8896	0.5298
ISGDKKLEEIPK	1357.6	2	3.3814	0.1455
ISGETIFVTAPHEATAGIIGVNR	2354.6	2	4.6301	0.3956
ISGGKENTASSK	1179.3	2	3.1998	0.2244
ISGGSVVEMQGDEMTR	1696.9	2	5.0299	0.5088
ISGIKDFSWSPGGNIIAFWVPEDKDIPAR	3217.6	3	3.9042	0.2266
ISGLGLTPEQK	1143.3	2	3.0759	0.1847
ISGLIYEETR	1181.3	2	3.9756	0.3909
ISGLIYEETRGVLK	1578.8	2	4.0969	0.3171
ISGLIYEETRGVLKVFLENVIR	2550.0	3	5.9181	0.4493
ISGLIYEETRGVLKVFLENVIRDAVTYTEHAK	3666.2	3	5.4717	0.5204
ISGLQYSIPDTENQTLNYGK	2242.4	3	3.7303	0.2568
ISGNNKGVSPEPIHLK	1690.9	2	3.2281	0.2442
ISGSILNELIGLVR	1484.8	2	4.6589	0.3555
ISHELDSASSEVN	1388.4	2	2.9716	0.2606
ISHGEVLEWQK	1326.5	2	3.0216	0.1408
ISHLSGSGSGDER	1302.3	2	3.2583	0.2577
ISHLVLPVQPENALKR	1815.2	2	4.6197	0.3776
ISHMVIEEVNFMQNHLEIEK	2441.8	3	3.4142	0.131
ISHYEKEYILSSLR	1739.0	2	3.8194	0.3384
ISIEMHGTLEDQLSHLR	1980.2	3	5.6816	0.4115
ISIEMNGTLEDQLSHLK	1929.2	2	3.7208	0.33
ISIENSEEALTVHAPFPAAHPASR	2545.8	3	4.1056	0.4143
ISINQALQHAFIQEKI	1854.1	3	3.7072	0.2253
ISITEGIER	1018.1	2	2.5167	0.2185

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ISIVEALTLLNNHK	1565.8	2	3.8439	0.3484
ISKEEAMR	964.1	2	2.7227	0.1409
ISKEVLAGRPLFPHVLCHNCAVEFNFGQK	3255.8	3	5.4499	0.413
ISKFDFLVATSQSK	1571.8	2	2.7007	0.2654
ISKFFGKELSTTLNADEAVTR	2328.6	3	3.7873	0.2426
ISKGANPVEIR	1184.4	2	2.7968	0.1346
ISKIENLSNLHQLQMLELGSNR	2538.9	3	6.589	0.4626
ISKLEQQMAK	1176.4	2	3.5413	0.1809
ISLADIAQKLQLDSPEDAEFIVAK	2616.0	3	4.4375	0.2836
ISLAPTDVKELSTKEPGRTLEPQELAR	2980.4	3	3.7767	0.2811
ISLGLPVGAVINCADNTGAK	1914.2	2	4.4207	0.4012
ISLGMPVGPNAHK	1321.6	2	3.2303	0.2944
ISLPLPNFSSLNLR	1571.8	3	4.856	0.4062
ISLPLPNFSSLNLRETNLDSLPLVDTHSK	3222.6	3	3.5906	0.4008
ISLPLPNFSSLNLRETNLDSLPLVDTHSKR	3378.8	3	3.3712	0.1805
ISLSPEYVFSVSTFR	1733.0	2	3.5756	0.3144
ISLVDLAGSER	1160.3	2	3.8428	0.2934
ISMINNPAKEISYENTQISR	2309.6	3	4.5443	0.2878
ISMPDFDLHLK	1316.6	2	2.7792	0.1618
ISMPDVDLHLK	1268.5	3	3.2092	0.3542
ISMPDVDLHLKGPK	1550.8	2	3.7754	0.3237
ISMSHEEEPLGTAGPLALAR	2080.4	2	5.8899	0.3948
ISNDPSPGYNIEQMAK	1764.9	2	3.587	0.3986
ISNDRLGSGDDISVYVIPLIHGNKLS	2784.1	3	4.0456	0.1709
ISNLKEHLASK	1240.4	2	3.7901	0.2219
ISNLPTVK	872.0	2	2.4983	0.1174
ISNLPTVKK	1000.2	2	2.9318	0.146
ISNRPAFMPSEGK	1434.6	2	3.8006	0.3956
ISNSAAYSGSVAPANSALGQTQPSDQDTLVQR	3235.4	3	4.0034	0.1837
ISPDGEEGYPGELK	1491.6	2	3.3268	0.1409
ISPDRVYINYYDMNAANVGWNNSTFA	2997.2	3	5.4428	0.4652
ISPLFGHLDMHSGAQSGPMHGFGFGLPTSR	3140.5	3	4.3014	0.3134
ISQAEEEDQQLLGHLLLVAK	2235.5	2	5.4021	0.419
ISQEIGNLMKEIETLVEEK	2204.5	3	3.4278	0.2676
ISQEKEQQESLALEELELQKK	2501.8	3	5.656	0.3266
ISQKDIEQSIK	1289.5	2	4.9053	0.1706

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ISQKDIEQSIKSETSGSFEDALLAIVK	2938.3	3	6.7587	0.4656
ISQLAAVNR	972.1	2	2.8277	0.1501
ISQLEMAR	948.1	2	3.0879	0.1979
ISQSGDFLR	1023.1	2	2.6657	0.1555
ISQTYQQQYGR	1372.5	2	4.0318	0.4322
ISREECDKYALQSQQR	1955.1	2	5.0331	0.3861
ISRPGDSDDSR	1205.2	2	3.0914	0.207
ISSADPSGAFR	1108.2	2	2.8592	0.2488
ISSDLDGHPVPK	1265.4	2	3.4931	0.3574
ISSEAHREVMK	1287.5	2	2.9015	0.2342
ISSIQATTAAGSGHPTSCCSAAEIMAVLFFHTMR	3499.0	3	3.6811	0.2668
ISSIQSIVPALEIANAHR	1920.2	3	3.9286	0.4138
ISSIQSIVPALEIANAHRKPLVIIAEDVDGEALSTLVLNR	4267.9	3	3.8919	0.3812
ISSLLEEQFQQGK	1507.7	2	4.6631	0.3792
ISSLRNELEHLQYK	1730.9	2	2.5098	0.2071
ISSSDLSLGHVTR	1372.5	2	3.3928	0.2049
ISSSSFSR	870.9	2	2.4168	0.1391
ISSTSVKPKPPPVR	1493.8	2	3.1459	0.3304
ISSVSEVMKESK	1324.5	2	3.5472	0.3119
ISTASGDGR	863.9	2	2.4812	0.1153
ISTASGDGRHYCYPHFTCAVDTENIR	2915.2	3	4.47	0.2659
ISTKPRDPDNELYFAHGLFSAK	2507.8	3	4.7084	0.3822
ISTLKDETGAIFIDRDPTVFAPILNFLR	3164.6	3	4.3973	0.3858
ISTLYYQLGDHELSLSEVR	2224.5	2	4.6492	0.4075
ISTQLDFASK	1110.2	2	2.4069	0.1832
ISTSLPVLDLIDAIQPGSINYDLLK	2700.1	3	3.9433	0.2612
ISTSLPVLDLIDAIQPGSINYDLLKTENLNDDEKLNNAK	4299.8	3	3.6397	0.2264
ISTSVKELENFRNLLQNIH	2256.5	2	3.1373	0.2428
ISTVVSSKEVNK	1291.5	2	2.6841	0.1403
ISTYGLPAGGIQPHPQTK	1866.1	2	3.3198	0.3405
ISVADEAQVQK	1188.3	2	4.1838	0.3403
ISVAGVTSSNVGYLAHAIHQVTK	2353.7	2	5.1953	0.4806
ISVATGALEAAQGSK	1403.6	2	3.4283	0.3883
ISVGSDSDLVIWDPDAVKIVSAK	2415.7	3	3.5705	0.1176
ISVISTGPTLQAR	1343.6	2	3.2869	0.174
ISVIVETVYTHVLHPYPTQITQSEK	2884.3	3	5.8287	0.3966

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ISVMGGEQAANVLATITK	1804.1	2	2.8023	0.1539
ISVMGGEQAANVLATITKDQR	2203.5	3	4.0788	0.4028
ISVNNVLPVFDNLMQQK	1960.3	2	4.8224	0.4211
ISVREPMQTGIK	1359.6	2	3.4409	0.2661
ISVTVSETFDPEEK	1581.7	2	2.9243	0.2612
ISVYSIMGGSTDGLR	1556.8	2	3.9789	0.3723
ISVYYNEASSHK	1398.5	2	3.046	0.3537
ISVYYNEASSHKYVPR	1914.1	2	4.5961	0.4739
ISVYYNEATGGK	1302.4	2	4.002	0.3964
ISVYYNEATGGKYVPR	1818.0	2	5.0332	0.5049
ISYFTFIGTPVQATNMNDFKR	2451.8	2	3.5531	0.297
ISYGPDWKDFYVVEPLAFEGTPEQK	2917.2	2	5.0235	0.4364
ITAAQHSVTGSAVSK	1457.6	2	4.6268	0.4705
ITADLLSNGIDVYPQKEFDEDSEDRLVNEK	3454.7	3	5.1034	0.3429
ITAFVVER	935.1	2	2.671	0.2642
ITAHLVHELR	1189.4	2	3.82	0.3212
ITALEQKEQELQALIQQLSIDLQK	2782.2	3	3.5812	0.1945
ITDLANLSAANHDAAIFPGGFGAAK	2443.7	3	4.7591	0.2048
ITDLKQKVENLFNEK	1820.1	2	4.0643	0.337
ITDLYTDLR	1110.2	2	2.487	0.1393
ITDPQYFLDTPQQAAAILQK	2262.5	2	5.3794	0.4208
ITDSAGHILYSKEDATK	1850.0	2	5.3522	0.4966
ITDSAGHILYSKEDATKGK	2035.2	2	5.4125	0.4765
ITDSEASKPK	1076.2	2	3.0151	0.2157
ITDSPEEIVQK	1259.4	2	3.0321	0.1041
ITDTIGPTETSIAPR	1572.7	2	3.9917	0.2809
ITEADEKNDR	1191.2	2	3.086	0.1828
ITEAPASEKEIVEVKEENIEDATEK	2803.0	3	3.9848	0.3138
ITEAPASEKEIVEVKEENIEDATEKGGEKK	3302.6	3	4.797	0.2169
ITEAVATATEQR	1290.4	2	2.8925	0.1535
ITEDYYVHLIADNLPVATR	2204.5	3	4.9776	0.1873
ITEGDVVVGIASSGLHSNGFSLVR	2415.7	3	4.0333	0.3941
ITEGVPQLLIVLTADR	1739.0	2	3.6723	0.2964
ITEIYEGTSEIQR	1539.7	2	4.2081	0.3582
ITELKEEIEVK	1331.5	2	3.4275	0.1423
ITELQLKLESALTELEQLRK	2356.7	3	5.2481	0.352

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ITELTDENVKFIIENTDLAVANSIR	2820.1	3	4.8029	0.2307
ITELTEAGETKKVNFK	1809.1	2	2.6321	0.1581
ITESEEVVSR	1149.2	2	3.9568	0.3562
ITESEEVVSREVSGIKAAYEAELGDAR	2910.1	3	4.0154	0.1466
ITESEEVVSREVSGIKAAYEAELGDARK	3038.3	3	4.4809	0.2726
ITESVAETAQTIKK	1519.7	2	3.4279	0.4005
ITFHGEGDQEPGLEPGDIIIVLDQK	2722.0	3	4.3849	0.1814
ITFHGEGDQEPGLEPGDIIIVLDQKDHAVFTR	3548.9	3	5.284	0.4103
ITFPKEGDQTSNNIPADIVFVLK	2547.9	3	3.7073	0.1207
ITFTGEADQAPGVEPGDIVLLLQEK	2642.0	3	5.0699	0.4129
ITFTGEADQAPGVEPGDIVLLLQEKEHEVFQR	3567.9	3	4.8728	0.3991
ITGDPYKVQQAK	1348.5	2	3.2757	0.2747
ITGEAFVQFASQELAEK	1869.1	2	4.8321	0.3214
ITGSIADGTDGFVINLGQGTDKLNLHFNPR	3172.5	3	5.7521	0.4573
ITHEVDELTQIIADVSQDPTLPR	2591.9	3	3.4411	0.1845
ITHHADNTLKSFCKWQK	2058.4	2	2.5585	0.1169
ITHLSTLQVGSLNVK	1610.9	2	3.9169	0.3931
ITHNPFGPGQFFDLSIR	1947.2	3	5.0937	0.3995
ITHSPLTICFPEYTGANKYDEAASYIQSK	3249.6	3	4.2805	0.3427
ITHYFIDLNKK	1392.6	2	2.5966	0.1414
ITIADCGQLE	1063.2	2	2.6424	0.269
ITIAIDTSKR	1118.3	2	2.7954	0.1698
ITIKNDPSLPEPK	1452.7	2	2.8717	0.2281
ITITNDKGR	1018.1	1	2.805	0.1738
ITKEAGSVSLR	1161.3	2	2.433	0.2999
ITKFENAFLSHVVSQHQALLGTIR	2711.1	3	6.5876	0.5189
ITKKPIPDEHLILK	1646.0	3	4.806	0.3377
ITKLDQILLNGNNITMLVPGGEGPEV	2737.2	3	4.3176	0.3094
ITKPGSIDSNNQLFAPGGR	1973.2	3	3.5619	0.1166
ITLDNAYMEK	1198.4	2	3.2387	0.2098
ITLDNAYMEKCDENILWLDYKNICKVVEVGSK	3749.3	3	3.6308	0.1303
ITLEDVISHSK	1242.4	2	3.5223	0.2699
ITLKETFLTSPEELYR	1941.2	3	3.2698	0.1284
ITLPVDFVTADKFDENAK	2024.3	2	5.4168	0.501
ITLQDVVSHSK	1227.4	2	3.4074	0.3155
ITLTEIEPSVETTTQEK	1920.1	2	3.6251	0.1017

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ITLTHTLYDVK	1304.5	2	2.8103	0.31
ITLTSDPRLPYK	1404.6	2	2.945	0.2231
ITLTSDPRLPYKVLSVPESTPFTAVLK	2974.5	3	3.9184	0.27
ITLVSAAPGK	957.1	2	2.4245	0.1246
ITMLGIQGDLK	1189.5	2	3.2297	0.1465
ITMQNLNDR	1105.3	2	3.0468	0.2033
ITMQNLNDRLASYLDKVR	2151.5	3	3.2927	0.2083
ITNAGMVSDEELEQMLDSGQSEVFVSNILKDTQVTR	3986.4	3	5.1673	0.3392
ITNLTQQLEQASIVK	1686.9	2	5.1422	0.3804
ITNQVHGLK	1010.2	2	2.6707	0.3038
ITPAHDQNDYEVGQR	1743.8	2	4.3195	0.5097
ITPENLPQILLQLK	1621.0	2	4.1497	0.2971
ITPLEIEVLEETVQTMDTS	2149.4	2	4.5499	0.3577
ITPNLAEFAFSLYR	1642.9	2	4.3878	0.4869
ITPSYVAFTPEGER	1567.7	2	4.0344	0.5214
ITPSYVAFTPEGERLIGDAAK	2236.5	2	4.6754	0.4106
ITPSYVAFTPEGERLIGDAAKNQLTSNPENTVFDAK	3896.3	3	4.4723	0.359
ITPSYVAFTPEGERLIGDAAKNQLTSNPENTVFDAKR	4052.5	3	4.3659	0.3244
ITQDIFQQLLK	1347.6	2	4.0466	0.2533
ITQDIFQQLLKR	1503.8	2	3.7681	0.3544
ITQLVSDQANHVLAR	1665.9	2	4.1979	0.2524
ITQSNAILR	1016.2	2	2.9578	0.2072
ITQVLHFTKDVK	1429.7	2	3.045	0.2802
ITRPLLLLNDKPAGK	1650.0	2	2.4987	0.1084
ITSAPDMEDILTESEIKLDGVR	2433.7	2	3.0964	0.2303
ITSAYLQDIENAYK	1629.8	2	2.863	0.1299
ITSAYLQDIENAYKK	1758.0	2	4.0035	0.305
ITSEAEDLVANFFPK	1681.9	2	3.9323	0.357
ITSEIPQTER	1174.3	2	2.8778	0.1811
ITSFPESEGYSYETSTK	1927.0	2	4.2234	0.4932
ITSGPFEPDLYKSEMEVQDAELK	2627.9	3	3.2568	0.1503
ITSGPFEPDLYKSEMEVQDAELKALLQSSASR	3541.9	3	5.6937	0.5482
ITSIVKDSSAAR	1248.4	2	2.8931	0.2181
ITSPLMEPSSIEK	1432.7	2	3.0866	0.246
ITSQYLGHPR	1172.3	2	3.359	0.2307
ITTGAQDDLRK	1218.3	2	3.1934	0.2793

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
ITTGSSSAGTQSSTSNR	1642.7	2	4.352	0.4842
ITTHFELK	989.1	2	2.659	0.2016
ITTHYTIYPR	1265.4	2	3.363	0.3367
ITTLEAGCFDNLSSSLLVVK	2111.4	3	3.4744	0.193
ITTTVACNMDLSKYPMDTQTCKLQLES	3036.5	3	4.706	0.1281
ITVEDSDKQLLKSPELPSPQAEK	2553.8	3	3.925	0.2418
ITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKER	4814.2	3	3.8391	0.315
ITVLEALRHPIQVSR	1733.1	3	3.6363	0.2258
ITVNEVELLVMK	1388.7	2	3.5057	0.3557
ITVTSEVPFSK	1208.4	2	2.6449	0.2187
ITVTSEVPFSKR	1364.6	2	3.2154	0.2446
ITWSNPPAQGAR	1298.4	2	3.0135	0.1284
IVAAHNK	752.9	1	1.6287	0.1747
IVADKDYSVTANSK	1511.7	2	4.7273	0.4127
IVAELQDKMK	1175.4	2	3.2717	0.2217
IVAERPGTNSTGPAPMAPPR	2020.3	3	4.0691	0.309
IVAERPGTNSTGPAPMAPPRAPGPLSK	2671.1	3	5.6171	0.3976
IVAFADAAVEPIDFPIAPVYAASMVLK	2820.3	3	6.102	0.434
IVAFADAAVEPIDFPIAPVYAASMVLKDVGLK	3332.9	3	3.6016	0.1966
IVAFENAFER	1196.3	2	3.331	0.3303
IVALNAHTFLR	1255.5	2	3.3525	0.3178
IVAPGKGILAADESTGSIAK	1899.2	3	5.2877	0.532
IVAPGKGILAADESTGSIAKR	2055.4	2	5.3717	0.4929
IVAPGKGILAADESVGSMAK	1915.2	3	5.2084	0.4092
IVAPISDSPKPPPQR	1602.9	2	3.8415	0.4608
IVASTLSNPELFEEWTGNVK	2235.5	2	5.4883	0.5294
IVATKPLYVALAQR	1543.9	2	4.2879	0.3699
IVAVIGAVVDVQFDEGLPPILNALEVQGR	3033.5	3	3.5064	0.1826
IVAVTGAEAQK	1087.3	2	3.366	0.3154
IVDDWANDGWGLK	1489.6	2	4.0178	0.3848
IVDDWANDGWGLKK	1617.8	2	3.983	0.3213
IVDGKVVSETNDTK	1505.7	2	4.3058	0.4048
IVDGKVVSETNDTKVL	1717.9	2	4.3254	0.4393
IVDGKVVSETNDTKVLRH	2011.3	3	5.3823	0.471
IVDLIKGQHLSDAFAQVNPLKK	2435.9	3	5.7445	0.5342
IVDLVKELDRDTVFALVNYIFFK	2759.2	3	4.9809	0.3425

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IVDQNTKLAPETK	1457.7	2	3.7376	0.2104
IVDRIDNDGDGFVTTEELK	2137.3	2	4.9287	0.4033
IVDVIGEK	873.0	2	2.7228	0.1612
IVDVIGEKIYKDGER	1735.0	3	3.5637	0.3501
IVEFHHNHIGQTPAESDFQLLEIAR	2903.2	3	4.1957	0.3147
IVEFLQSFDEITAMTGDGVNDAPALK	2783.1	3	3.7231	0.2486
IVEHQNLSK	1068.2	2	2.6521	0.1974
IVEIGDENATLDGTDVLFTGREFFVGLSK	3144.5	3	4.0598	0.2546
IVEIPFNSTNK	1262.4	2	2.5902	0.1004
IVEIPFNSTNKYQLSIHKNPNTSEPQHLLVMK	3722.3	3	4.8302	0.3537
IVEKLEKSTKPIVAAINGSCLGGGLEVAISCQYR	3549.2	3	4.3873	0.1688
IVEKYGYTHLSAGELLR	1950.2	3	4.8928	0.5117
IVEKYGYTHLSAGELLRDER	2350.6	2	4.2226	0.3235
IVEMSTSK	895.1	1	1.7941	0.2585
IVENEKINAEK	1287.4	2	3.421	0.2956
IVENEKINAEKSSK	1589.8	2	3.598	0.3064
IVENIQVFDFK	1352.6	2	3.8458	0.3154
IVENLGILTGPQLFSLNKEELKK	2585.0	3	3.4801	0.151
IVENLQSFNEITAMTGDGVNDAPALKK	2877.2	3	4.5109	0.2403
IVENSDAVTEILNNAELLK	2086.3	2	5.6351	0.4057
IVEPYIAWGYPNLK	1663.9	2	3.9973	0.2795
IVERDGLSEAAAQSR	1602.7	2	4.0112	0.38
IVEVLLMK	945.2	2	2.8705	0.19
IVEVLLMKDR	1216.5	2	3.5035	0.2542
IVEVLLMKDRETNK	1689.0	2	3.5753	0.3157
IVEYEKEMEK	1298.5	2	3.5398	0.2624
IVFEDGNINVNK	1362.5	2	3.1826	0.1073
IVFSGNLFQHQEDSKK	1878.1	2	4.7594	0.3809
IVFSPEEAKAVSSQMIGK	1922.2	3	3.3119	0.3997
IVFTKQPEPVIPVKDATSDLAIIAR	2723.2	3	5.7312	0.3686
IVGDYQQLEER	1350.5	2	2.9381	0.2165
IVGELEQMVSEDVPLDHR	2067.3	2	5.2512	0.4177
IVGGNAAQLAQFDPR	1557.7	2	4.6549	0.3668
IVGHLTHALK	1089.3	2	3.3089	0.3768
IVGPEENLSQAEAR	1513.6	2	4.1749	0.4124
IVGSKPLYVALAQR	1515.8	2	3.7229	0.339

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IVHAFDMEDLGDK	1490.7	2	4.1083	0.4352
IVHSLDYYNTCEYPNEDEMPNRCGIIHVR	3482.9	3	4.0182	0.1361
IVIGMDVAASEFYR	1571.8	2	2.9251	0.2764
IVIGYQSHADTATK	1504.7	2	4.228	0.4972
IVITGDGDIDHDQALAQAIR	2122.3	3	3.9675	0.2797
IVIVPSLNPDGR	1280.5	2	2.6393	0.1024
IVKADEHVIDQGDDGDNFYVIER	2648.8	3	6.5356	0.4907
IVKDLMSK	934.2	2	2.4851	0.1303
IVKDLMSKAEK	1262.5	2	2.9309	0.2441
IVKDSLSDDVVK	1318.5	2	3.0991	0.1474
IVKEAHEPLAVADAK	1591.8	2	2.5414	0.3198
IVKEHNLQVLGLVK	1590.9	2	3.2068	0.2955
IVKEPTSHDNKDICK	1728.0	2	3.1219	0.2924
IVKPNGEKPDEFESGISQALLELEMNSDLK	3332.7	3	6.2968	0.4962
IVKPNGEKPDEFESGISQALLELEMNSDLKAQLR	3801.3	3	6.1568	0.5701
IVKPVKVSAPR	1194.5	2	2.4284	0.2191
IVLADADLDNAVEFAHHGVFYHQGQCCIAASR	3472.9	3	6.4865	0.4099
IVLANDPDADR	1199.3	2	2.7758	0.1665
IVLANDPDADRLAVAEKQDSGEWR	2669.9	3	4.5763	0.3924
IVLDNSVFSEHR	1416.6	2	3.2682	0.2887
IVLDSDAAEYGGHQR	1631.7	2	4.7536	0.4042
IVLEDGTLHVTEGSGR	1683.8	2	4.1487	0.4472
IVLFDTLLEEYSVLNKDIQEDSGMEPR	3155.5	3	4.5444	0.3322
IVLGQEQDSYGGKFDR	1813.0	2	3.8755	0.3257
IVLQNGAHEVFNHR	1634.8	2	4.2868	0.5176
IVNDDQSFYADIYMEDGLIK	2350.6	2	5.6101	0.4684
IVNDDQSFYADIYMEDGLIKQIGDNLIVPGGVK	3642.1	3	5.2334	0.4383
IVNDDQSFYADIYMEDGLIKQIGENLIVPGGVK	3656.1	3	5.9732	0.4654
IVNGEDAVPGSWPWQVSLQDK	2326.5	2	4.6067	0.4295
IVNHPTMLQDPDVREFLEKEELPR	2907.3	3	3.4293	0.3241
IVNHWASPELR	1322.5	2	2.7088	0.2514
IVNLGSSKTDLFYER	1743.0	3	3.3729	0.1098
IVNSAQTGSFK	1152.3	2	3.7356	0.3426
IVNTPFQVLMNSEK	1620.9	2	3.9935	0.3896
IVNTQEQLNHR	1352.5	2	3.4432	0.1757
IVNVSSLAHHLGR	1403.6	2	4.7166	0.447

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IVPAKDLVLLSEIEVAQANDIISSTEISSAEK	3384.8	3	6.1867	0.3911
IVPEWQDYDQEIK	1663.8	2	2.7248	0.3716
IVPNVLLEQGK	1210.4	2	2.5533	0.1675
IVPVEITISLLKR	1481.8	2	2.7022	0.3229
IVQAEGEAEAAK	1216.3	2	4.2057	0.3989
IVQAEGEAEAAKMLGEALSKNPGYIK	2719.1	3	4.7651	0.3192
IVQAEGEAEAAKMLGEALSKNPGYIKLR	2988.5	3	4.0253	0.3056
IVQELPQLLDAR	1395.6	2	2.9002	0.152
IVQISGNSMPR	1202.4	2	3.4726	0.1685
IVQKHPHTGDTK	1361.5	2	3.0871	0.2247
IVQKHPHTGDTKEEK	1747.9	2	3.6347	0.3158
IVQMTEAEVR	1176.4	2	3.6238	0.3303
IVQNSNGYK	1023.1	2	2.9726	0.108
IVQNSNGYKIVTEK	1593.8	2	3.7696	0.2085
IVQTYHVNMAGTNPYTTITPQEINGK	2892.2	3	4.568	0.2452
IVQVVTAEAVAVLKGEQEK	2012.3	2	4.0791	0.4288
IVRSEQEFQEQLESARR	2106.3	3	4.1116	0.1128
IVSAQSLAEDDVE	1376.4	2	3.894	0.3709
IVSDYGKDPSITSILDALDIFLLPVTNPDGYVFSQTK	4044.6	3	4.8658	0.3924
IVSGEAESVEVTPENLQDFVGKPVFTVER	3177.5	3	5.296	0.3788
IVSGIITPIHEQWEK	1751.0	2	4.0976	0.3306
IVSGKDYNVTANSK	1496.6	2	4.9966	0.4314
IVSKIDGDKDGFVTVDELKDWIK	2622.0	3	4.6299	0.3661
IVSLFAEHNDLQYAAPGGLIGVGTK	2571.9	3	5.3156	0.3039
IVSNVPQLEFLNLSSNPLNLSVLER	2797.2	3	3.3681	0.202
IVSQLLTLMDGLK	1431.8	2	4.7687	0.4096
IVSQLLTLMDGLKQR	1716.1	2	4.3433	0.4516
IVSQPQPAR	996.1	2	2.869	0.2889
IVSRPEELREDDVGTGAGLLEIK	2497.8	2	4.7476	0.382
IVSRPEELREDDVGTGAGLLEIKK	2626.0	3	4.5964	0.3265
IVTDRETGSSK	1193.3	2	4.04	0.3325
IVTDRETGSSKGFGFVDFNSEEDAK	2736.9	3	5.275	0.4802
IVTDSDSKTEELR	1493.6	2	3.6081	0.3367
IVTSLGLK	831.0	2	2.5929	0.1142
IVTSTYKDGK	1112.3	2	3.0643	0.2161
IVVAGNNEDVSFSRPADLDLIQSTPFKPLALK	3456.9	3	4.323	0.3457

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IVVAMAK	732.0	1	2.0315	0.148
IVVNLTGR	872.0	2	2.658	0.1474
IVVVTAGVR	914.1	2	2.4986	0.1168
IVYGHLDDPASQEIER	1843.0	3	4.9642	0.4062
IVYGHLDDPASQEIERGK	2028.2	3	4.3679	0.4004
IVYVNEKEGGPNNHLLK	1925.2	2	5.125	0.3724
IVYYLMNIHVQPR	1647.0	2	3.3741	0.3129
IWDKLHEEHINAGR	1718.9	2	2.6898	0.2271
IWDPTPSHTPAGAATPGRGDTPGHATPGHGGATSSAR	3548.7	3	4.3299	0.362
IWDTTQKEHLLK	1512.7	2	2.8488	0.2705
IWDTTQKEHLLKYEYQPFAGK	2596.9	3	5.9216	0.3768
IWHHSFYNELR	1502.7	2	2.7606	0.174
IWHHTFYNELR	1516.7	2	3.9646	0.4387
IWNVHSVLNVLHSLVDKSNINR	2558.9	3	3.3138	0.226
IWQYVYSKDQLQTFSEEHPVLLTEAPLNPR	3604.0	3	4.9261	0.4622
IWQYVYSKDQLQTFSEEHPVLLTEAPLNPSK	3663.1	3	5.4899	0.4365
IYADSLKPNIPYK	1522.8	2	2.6977	0.141
IYAEDPSNNFMPVAGPLVHLSTPR	2627.0	3	6.0676	0.4926
IYALPDDLVEVKPK	1600.9	2	3.403	0.3251
IYCKPHFNQLFK	1538.8	2	3.4209	0.1245
IYDALDVSLIER	1407.6	2	3.6207	0.3648
IYDAQNELSAATHLTSK	1863.0	2	4.6363	0.4666
IYDLNKPEAEPK	1417.6	2	3.8409	0.2707
IYDLNKPEAEPKEISGHTSGIK	2427.7	3	4.091	0.3496
IYDLNKPEAEPKEISGHTSGIKK	2555.9	3	4.1641	0.2852
IYDVEQTR	1024.1	2	2.9279	0.15
IYEDGDDDMKR	1357.4	2	3.1201	0.28
IYEENDRAVFDK	1499.6	2	2.7229	0.1643
IYEENDRAVFDKIVSK	1927.1	3	3.9693	0.2556
IYEKDEEKQR	1338.4	2	3.5387	0.2189
IYELAAGGTAVGTGLNTR	1765.0	2	5.4516	0.4186
IYESHVGISSHEGK	1543.7	2	4.0357	0.4452
IYFGKDIPNMFMDSAGSVSK	2208.5	3	4.788	0.3391
IYFMAGSSR	1032.2	2	3.2456	0.3046
IYGADDIELLPEAQHK	1813.0	2	4.3356	0.4177
IYGADDIELLPEAQHKAEVYTK	2504.8	3	3.4022	0.1583

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IYGISFPDPK	1137.3	2	3.378	0.3198
IYGLGSLALYEK	1327.6	2	4.3883	0.3894
IYHEQEQALQELGNKLSESK	2345.6	3	4.0244	0.2218
IYHPNINSNGSICLDILR	2043.3	2	3.501	0.255
IYHPNVDKLGR	1312.5	2	2.4702	0.1786
IYIDSNNNPER	1335.4	2	3.628	0.3084
IYITDGNMQLTVLTDR	1854.1	2	2.7403	0.1595
IYITLTGVHQVPTENVQVHFTER	2683.0	3	5.8803	0.4765
IYKDGER	881.0	2	2.4011	0.1209
IYKTTTHVPPELGQIMDSETFEK	2666.0	3	3.9075	0.2326
IYKVPSTEAEALASSLMGLFEK	2385.8	2	4.9334	0.4876
IYLDGAPNKDLTQD	1563.7	2	2.9534	0.2371
IYLTADNLVLNLQDESFTR	2226.5	2	6.1132	0.4555
IYLTADNLVLNLQDESFTRGSDSLIK	2927.3	3	3.7167	0.2214
IYLYTLNDNAR	1356.5	2	2.8899	0.1764
IYNDDKNTYIR	1415.5	2	3.0665	0.2205
IYNEIPDINLDVPHSYSVLER	2487.7	3	3.7152	0.2341
IYNHPPHPTMSVDEVLEMLQR	2507.9	3	4.1893	0.1659
IYNLGTGTGYSVLQMVQAMEK	2304.7	2	4.6234	0.2783
IYPEEMIQTGISAIDGMNSIAR	2410.8	3	5.9515	0.4659
IYPHGLVLLDLQSYDGDAQGKEEIDSILNKVEER	3859.2	3	6.3001	0.457
IYPLPDDPSVPAPPR	1634.9	2	3.3878	0.42
IYPLPHMYVIKDLVPDLSNFYAQYK	3029.5	3	3.4193	0.1272
IYPSREEYEAHQDR	1793.9	2	2.7335	0.1301
IYPTFLHLHGK	1326.6	2	2.9678	0.3745
IYQIYEGTSQIQR	1599.8	2	4.8176	0.4508
IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	3152.4	3	5.609	0.4511
IYSALILHDDEVTVTEDKINALIK	2715.1	3	6.6738	0.5245
IYSHDGTDSPPDADEVVIVLNNFKSK	2862.1	3	4.2091	0.3068
IYSHSLLPVLR	1298.6	3	3.4326	0.2815
IYSLSSQPIDHEGIK	1687.9	2	3.8776	0.3392
IYVAELIQQLQQQALSEPAVVQK	2598.0	3	4.947	0.3604
IYVAELIQQLQQQALSEPAVVQKR	2754.2	3	7.1495	0.3573
IYVASVHQDLSDDDIKSVFEAFGK	2684.9	3	6.0216	0.3874
IYVDDGLISLQVK	1463.7	2	4.8321	0.3916
IYVGNASVAQDIPK	1475.7	2	4.8475	0.3883

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
IYVGNASVAQDIPKLQKLGITHVLNAAEGR	3177.6	3	4.7006	0.3217
IYVGNLPPDIR	1257.5	2	3.2677	0.3388
IYVGNLPTDVREKDLEDLFYK	2528.8	3	4.072	0.2649
IYVISLAEPR	1161.4	2	3.1489	0.2675
IYVVDVGSEPR	1234.4	2	3.8993	0.3576
IYVVDVGSEPRAPK	1530.8	2	3.3858	0.136
KAAAEDVNVTFEDQQK	1793.9	2	4.3781	0.404
KAAALEAMKDYTK	1440.7	2	3.2844	0.1954
KAAALEFLNR	1133.3	2	3.7386	0.2567
KAAALEFLNRFEEAK	1738.0	2	4.5063	0.4265
KAAALEFLNRFEEAKR	1894.2	2	3.5486	0.2506
KAAATPAKK	886.1	2	2.9367	0.1351
KAADDTWEPFASGK	1523.6	2	4.9211	0.494
KAADKLIQNLDANHDGR	1880.1	3	4.065	0.3152
KAAEAHVDAHYYEQNEQPTGTCAACITGDNR	3365.6	3	6.0103	0.3294
KAAELEEELKALSDLRADNQR	2400.6	3	3.2801	0.2441
KAAGGATPK	800.9	2	3.1686	0.2359
KAAGGATPKK	929.1	2	3.3626	0.1878
KAAGHPGDPESQQR	1478.6	2	3.3983	0.2714
KAAHSAELEAVLLALAR	1764.1	2	2.8828	0.2634
KAAIISAEGDSK	1190.3	2	3.0695	0.3307
KAAIISAEGDSKAAELIANSLATAGDGLIELR	3170.6	3	4.6499	0.4176
KAALDEAQGVGLDSTGYYDQEIYGGSDSR	3067.2	3	4.9411	0.4467
KAALEAQNALHNIK	1521.7	2	4.4462	0.3437
KAALEAQNALHNMK	1539.8	2	5.0251	0.4172
KAALEEVER	1045.2	2	3.3316	0.1781
KAALEEVERLK	1286.5	2	3.8374	0.1501
KAALSASEGEEVPQDKAPSHVPFLLIGGGTAAFAAAR	3666.1	3	5.4583	0.4781
KAAPGAAGSR	886.0	2	2.5492	0.1632
KAASEYEKEITSLQNSFQLR	2343.6	3	4.0052	0.2361
KAASGEAKPK	987.1	2	3.2343	0.3395
KAASGEAKPKVK	1214.4	2	3.528	0.2384
KAASQPTSLAPEK	1328.5	2	3.1577	0.2196
KAATALKDVVK	1144.4	2	3.6625	0.3389
KAATVHLMQ	999.2	2	2.4143	0.1966
KAAVEALQSQALHATSQQPLRK	2376.7	2	4.9722	0.412

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KAAVTPGKK	900.1	2	3.3076	0.3582
KADAAANQGKK	1102.2	2	2.5457	0.2342
KADEVLEILK	1158.4	2	3.5673	0.2286
KADGVKPQTNSTK	1374.5	2	4.0265	0.2639
KADGYNQPDSK	1223.3	2	3.6135	0.3697
KADIDLTKR	1060.2	2	2.8173	0.1025
KADIGVAMGIAGSDVSK	1619.9	2	5.5135	0.4941
KADQKGVTIIGPATVGGIKPGCFK	2386.8	3	3.3965	0.1889
KADSVANQGTK	1119.2	2	3.3755	0.3258
KADSVANQGTKVEGITNQGK	2046.2	3	5.307	0.4949
KADYQAVDDEIEANLEEFDISEDDIDDGFRR	3634.7	3	5.1782	0.4657
KAEAAASALADADADLEERLK	2159.3	3	3.2732	0.2979
KAEAAVVAVAEKR	1342.6	2	3.6568	0.2793
KAEADPQAIPK	1168.3	2	3.6114	0.2348
KAEAFQLYQEAAQLDMLLEKLPQVAEEISGPLTSANK	4076.6	3	5.7589	0.4024
KAEAGAGSATEFQFR	1570.7	2	5.2971	0.3759
KAEALAQISAAFEDLEQALQQR	2431.7	3	4.2589	0.3687
KAEALAQISAAFEDLEQALQQRK	2559.9	3	4.4744	0.4224
KAEAQIAAK	930.1	2	3.5693	0.2023
KAEDLSSLNGQLQSEVTLLRNEVAQLK	2985.3	3	4.7309	0.2862
KAEEDAALQAK	1174.3	2	3.5546	0.211
KAEEDPEAADSGEPQNKR	1972.0	3	3.6827	0.3052
KAEEEAEAKPK	1230.4	2	2.5648	0.1222
KAEEEKAPATPKTEEKKDSKKEEAPK	2928.2	3	3.7142	0.1271
KAEEIANEMIEAAK	1547.8	2	5.3758	0.4064
KAEEVQAWAQR	1316.4	2	2.7461	0.2968
KAEGAPNQGR	1028.1	2	3.3991	0.1913
KAEGAPNQGRK	1156.3	2	3.0573	0.132
KAEGAQNQGKKAEGAQNQGQKGEGAQNQGK	3041.2	3	3.9591	0.1826
KAEGDAKGDK	1019.1	2	3.2831	0.2196
KAEGDAKGDKAK	1218.3	2	3.7431	0.2636
KAEGEPQEESPLK	1442.6	2	3.9822	0.3268
KAEGSPSEGK	990.0	2	2.5009	0.2191
KAEGSPSEGKK	1118.2	2	3.9219	0.363
KAEGTPNQGK	1030.1	2	2.6954	0.3123
KAEGTPNQGKK	1158.3	2	3.2689	0.2595

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KAEIGIAMGSGTAVAK	1504.8	2	4.7675	0.4356
KAEKEFELR	1150.3	2	2.6712	0.1865
KAEKELESHSSWYAPEALQK	2332.6	3	3.6773	0.2325
KAELEENQR	1117.2	2	2.5378	0.1935
KAELLDNEKPAAVVAPITTGYTVK	2529.9	3	5.0221	0.44
KAEPMQWASLELPAAK	1771.1	2	3.3715	0.2395
KAERDELAGVMIFSTMEPEAPDLDLVEIEQK	3506.0	3	4.3718	0.293
KAESGDKEKDTLK	1449.6	2	4.148	0.2883
KAESVQGGETR	1162.2	2	2.9291	0.2886
KAEVEGKDLPEHAVLK	1764.0	3	5.7273	0.4502
KAEVNTIPGFDGVVKDAEEAVR	2345.6	3	5.7706	0.4896
KAFEEAEKNAPAIIFIDELDAIAPK	2745.1	3	6.7472	0.4586
KAFEEAEKNAPAIIFIDELDAIAPKR	2901.3	3	7.4148	0.4932
KAFLDNGPK	990.1	2	2.497	0.1427
KAFPEHLYQR	1289.5	3	3.5353	0.239
KAFSGYLGTDQSK	1402.5	2	4.4609	0.3983
KAFTEVTQTELQDPHPSR	2085.3	3	3.3186	0.3093
KAFVFPK	837.0	2	2.5812	0.1993
KAGEQQETASR	1205.3	2	3.1785	0.3011
KAGGTGPGEEK	1031.1	2	2.4954	0.1271
KAGIAHLYGIAGSTNVTGDQVK	2201.5	2	5.4568	0.5121
KAGIFQSVK	978.2	2	2.7974	0.2176
KAGKLDPHLVLDQLR	1704.0	2	3.3731	0.2789
KAGLSLKDMDLVEVNEAFAPQYLAVER	3008.4	3	4.8791	0.3996
KAGNFYVPAEPK	1321.5	2	3.2677	0.2288
KAGPAKEQEPMPTVDSHEPR	2205.4	3	4.2881	0.1239
KAGPPPEKR	980.1	2	2.6004	0.1727
KAGQVFLEELGNHK	1570.8	2	4.6829	0.3865
KAGTQIENIDEDFRDGLK	2050.2	3	5.4191	0.4902
KAGTQIENIEEDFRDGLK	2064.2	2	4.4077	0.4402
KAGVDPLVPLR	1165.4	2	3.3929	0.2235
KAHEAALEAR	1096.2	2	3.2543	0.2591
KAHEILPNLVCCSAK	1627.0	2	2.9917	0.1329
KAHGLLAEENR	1238.4	2	2.6092	0.2722
KAHLMEIQVNGGTVAEK	1826.1	2	5.9411	0.4643
KAHQDIHTQLQDVK	1661.8	2	3.9915	0.3759

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KAHQLWLSVEALK	1523.8	2	4.1278	0.2993
KAHSIKDMENTLQLVR	1884.2	2	3.2755	0.279
KAHVLAASVEQATENFLEK	2086.3	2	6.3745	0.3589
KAHVLAASVEQATENFLEKGDK	2386.6	3	5.9048	0.4943
KAIIIFVPVPQLK	1466.9	2	4.2886	0.313
KAILEDMVR	1075.3	2	2.8401	0.1685
KAIQESNDTNK	1248.3	2	3.4821	0.1725
KAIQESNDTNKGK	1433.5	2	3.959	0.2993
KAIVICPTDEDLKDR	1717.0	2	4.2325	0.3964
KAKDDATLSGK	1134.3	2	3.2399	0.3838
KAKDDATLSGKR	1290.5	2	3.7176	0.4074
KAKIDSYQEPFTHSAPESIPDTFEDAVNILKPSTIIGVAGAGR	4573.1	3	3.9053	0.3427
KAKKPAAAAGAK	1112.4	2	3.0924	0.2235
KAKKPAAATVTKK	1342.7	3	3.5196	0.3805
KAKPVKPK	896.2	2	2.4939	0.1278
KAKTATPK	845.0	1	2.0373	0.1007
KALAAAGYDVEK	1236.4	2	4.5377	0.3963
KALAAAGYDVEKNNSR	1707.9	2	5.4351	0.4826
KALDIAENEMPGLMR	1689.0	2	4.003	0.3607
KALDIAENKMPGLMR	1688.1	2	2.5284	0.2257
KALDSNSLENDDLSAPGREPGHFNPESR	3054.2	3	4.7902	0.2842
KALEAQNEIHTK	1382.5	2	3.5752	0.2389
KALEQLNGFELAGRPMK	1903.2	3	3.9846	0.2736
KALEVFPEFAAAHSNLASVLQQQGK	2685.0	3	5.425	0.3562
KALIEVLQPLIAEHQAR	1930.3	3	4.4235	0.327
KALLALNHGLDK	1293.5	2	2.8129	0.1988
KALQDLGLR	1014.2	2	2.9639	0.1648
KALTSFERDSIFSNLTGQLDYQGFEK	2996.3	3	5.9517	0.48
KALXEVLQPLIAEHQAR	1930.3	3	6.0713	0.3476
KAMDFYDPAR	1214.4	2	2.4537	0.1403
KAMDFYDPARHNEFDFISGTR	2518.7	3	3.5311	0.3072
KAMEAVAAQGK	1104.3	2	3.793	0.2371
KAMEAVAAQGKA	1175.4	2	4.331	0.2208
KAMEGAGTDEK	1137.2	2	3.5345	0.3029
KAMEGAGTDEKALIEILATR	2118.4	3	5.2571	0.3444
KAMEGTIDGSLINPTVIVDPFQILVAANK	3056.6	3	4.1804	0.305

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KAMKGFGTDEQAIVDVVANR	2150.4	2	2.913	0.1184
KAMKGLGTDEDAIISVLAYR	2152.5	2	5.1869	0.5662
KANAEELANNLKQEGHNLGLLHGDMDQSER	3333.6	3	4.6904	0.4496
KANDESNEHSDVIDSQELSK	2246.3	3	5.7848	0.502
KANEDELKR	1103.2	2	2.712	0.1229
KANGPNYIQPQKR	1514.7	2	2.5733	0.2032
KANIPIMDTGENPEVPFPR	2126.4	2	5.1988	0.4341
KANLQIDQINTDLNLER	1999.2	2	6.2357	0.3484
KANNSQEPSPQLASSVASTR	2073.2	3	3.6737	0.3562
KANPDLPILIR	1250.5	2	2.642	0.1472
KANVVALVAVAEHSGEFEK	1999.3	3	5.116	0.451
KAPAQKVPAQK	1166.4	2	3.6344	0.3938
KAPDFVFYAPR	1311.5	2	3.2091	0.3436
KAPGFGGFGSSAVSGGSTAAMITETIIETDKPK	3214.6	3	6.544	0.3926
KAPPPLAAALAHEAVSQLLQTDLSEFR	2875.3	3	5.5372	0.4054
KAPPRPGPVPEAAQPFLFTPR	2274.7	2	3.8442	0.2662
KAPSDLYQIILK	1389.7	2	3.6952	0.3046
KAPSEASAQEQR	1302.4	2	3.5367	0.3556
KAPTTDEDKKAAEK	1532.7	2	4.1686	0.3377
KAPVKLESIASVFKDHAEEGTSEDGTKPDEK	3344.6	3	3.3025	0.2599
KAQCPIVER	1044.3	2	2.7249	0.1196
KAQDEGLLSDVVPFKVPGK	2028.3	3	4.8488	0.4122
KAQDEGLLSDVVPFKVPGKDTVTK	2572.9	3	6.92	0.5039
KAQDFHWLTR	1302.5	2	2.9331	0.2129
KAQDIETLKK	1174.4	2	2.7318	0.1889
KAQGHELGASR	1154.3	2	3.6162	0.3537
KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	3283.8	3	5.8015	0.3967
KAQPAQPADEPAEK	1480.6	2	3.9858	0.3705
KAQPAQPADEPAEKADEPMEH	2290.5	3	5.1265	0.4071
KASAFNSWFENAEEDLTDPVR	2427.6	3	3.8394	0.2977
KASDVHEVR	1041.1	2	3.1035	0.2774
KASELPVSEVASILQADLQNGLNK	2525.8	3	4.3977	0.3728
KASFASASAEVGKK	1381.6	2	3.7654	0.3459
KASFEEASNQLINHIEQFLDTNETPYFMK	3446.8	3	4.8978	0.3385
KASGPPKGPSR	1082.2	2	2.5606	0.1793
KASGPPVSELITK	1327.6	2	4.4399	0.427

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KASSRLENLGIPEEELLRQQQELFAK	3028.4	3	4.7812	0.3349
KASSVETKPGASK	1290.4	2	2.8281	0.1345
KASVVTLPVYLNFTR	1709.0	2	2.5074	0.2482
KATATISAKPQITNPK	1669.9	3	3.3567	0.2646
KATDAEADVASLNR	1461.6	2	3.5692	0.2863
KATDAEADVASLNRR	1617.7	2	2.8628	0.2379
KATEGSGSMR	1024.1	2	2.5999	0.1905
KATGAATPK	845.0	2	3.1709	0.2447
KATGAATPKK	973.2	2	2.7922	0.1544
KATGPPVSELITK	1341.6	2	3.5884	0.3324
KATLELTHNWGTEDDATQSYHNGNSDPR	3159.2	3	4.8693	0.3754
KATPGAHTGAIPK	1249.4	2	2.619	0.1182
KATQASQEY	1026.1	2	2.5042	0.1284
KATVDMLQAEGGR	1376.6	2	3.7443	0.3382
KATVNLLGEEK	1202.4	2	3.0767	0.2434
KATVNLLGEEKK	1330.6	3	3.9551	0.2603
KAVAEIEEMCNILK	1591.9	2	5.2927	0.2964
KAVAEIEEMCNILKTEGVTVR	2334.7	3	4.2719	0.1736
KAVAISLPK	927.2	2	2.4876	0.2725
KAVASVAKK	902.1	2	3.5799	0.1063
KAVDEAADALLK	1244.4	2	4.0136	0.3565
KAVEAAQLAEDLKVQLEHVQTR	2477.8	3	5.9487	0.4306
KAVEEPLNAFK	1246.4	2	2.614	0.1489
KAVEEPLNAFKESK	1590.8	2	3.1564	0.1914
KAVEKPPQTEHIEL	1619.8	2	3.2731	0.1959
KAVLASMDNENMHTPDIGGQGTTSEAIQDVIR	3400.7	3	6.9931	0.4355
KAVLFCLSEDKK	1381.7	3	4.653	0.3212
KAVLTPNHVEFSR	1498.7	2	4.161	0.3123
KAVLVALK	842.1	2	2.6302	0.1199
KAVLVALKER	1127.4	2	2.5773	0.1803
KAVPKEDIYSGGGGGGSR	1735.9	2	4.3431	0.3845
KAVTDFTSEVTYDPAGR	1858.0	2	3.6418	0.2909
KAVTHAIPALQPIVHDLFVLR	2339.8	3	4.3475	0.3142
KAVTPAPPIKR	1178.5	2	3.1737	0.29
KAVVEKPAR	998.2	2	2.6738	0.3511
KAVVVCPKDEDYK	1494.7	2	2.8204	0.1863

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KAVVVCPKDEDYKQR	1779.1	3	3.8451	0.3224
KAYADFYR	1034.1	2	2.5362	0.2014
KAYGQALAK	950.1	2	2.88	0.2174
KAYLEPEHTK	1216.4	2	2.8678	0.1722
KAYWQVHLDQVEVASGLTLCK	2389.8	3	4.3258	0.3448
KCEVLCSQSNKPVTLTVEQSR	2350.7	3	4.556	0.204
KDAEAWFTSR	1211.3	2	3.2023	0.2552
KDAENHEAQLK	1283.4	2	3.8617	0.3057
KDAFADAVQR	1121.2	2	2.9101	0.2352
KDAHSNLLAK	1097.3	2	3.3227	0.2203
KDAHSTLLSK	1100.3	2	3.3188	0.2706
KDAHSTLLSKK	1228.4	2	3.2637	0.2488
KDCEVVMMIGLPGAGK	1649.0	2	2.9459	0.2103
KDDEENYLDLFSHK	1753.8	2	5.2501	0.4249
KDDEVQVVR	1088.2	2	3.0808	0.2694
KDDPLTNLNTAFDVAEK	1892.1	2	4.4863	0.4138
KDDPLTNLNTAFDVAEKYLDIPK	2621.9	3	6.4849	0.4893
KDDPTLLSSGR	1189.3	2	2.7595	0.1939
KDDPVTNLNNAFEVAEK	1905.1	3	5.7982	0.4283
KDDPVTNLNNAFEVAEKYLDIPK	2634.9	3	5.0656	0.3586
KDDTDDEIAK	1150.2	2	2.6877	0.1017
KDDTDDEIAKYDGK	1613.7	2	4.6463	0.4274
KDDTDDEIAKYDGKWEVEEMKESK	2890.1	3	5.6425	0.2921
KDDVTSSTGPHK	1272.3	2	3.4863	0.288
KDEEGQKEEDKPR	1588.7	2	3.3221	0.1721
KDEENDSKAPPHELTEEEKQQILHSEEFLSFFDHSTR	4429.7	3	4.7559	0.2671
KDEESGGGSNPFQHLEK	1859.9	3	3.2101	0.1098
KDEKTDTLEDLFPTTK	1882.1	2	5.1605	0.408
KDEKTDTLEDLFPTTKIPNPR	2459.7	3	4.9889	0.3482
KDENKVDGMNAPK	1446.6	2	4.4788	0.2771
KDEPDAFKELGTGNR	1677.8	2	3.8735	0.2961
KDEQEHEFYK	1353.4	2	2.7107	0.1667
KDETNVK	833.9	1	1.7399	0.1108
KDFSSVFQFLR	1374.6	2	3.3167	0.3137
KDFSSVFQFLREEETF	2010.2	2	3.6234	0.3456
KDFVSEQLTSLLVNGVQLPALGENKK	2829.2	3	5.1224	0.363

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KDGADFAK	851.9	1	2.1491	0.1284
KDGLVSLLTTSEGADEPQRLQFPLPTAQR	3169.5	3	4.2784	0.3754
KDGNASGTMLLEALDCILPPTRPTDKPLRLPLQDVYK	4081.8	3	4.6771	0.3455
KDGNASGTTLLEALDCILPPTRPTDK	2728.1	3	4.6229	0.346
KDGNASGTTLLEALDCILPPTRPTDKPLR	3094.5	3	5.6253	0.4205
KDGNASGTTLLEALDCILPPTRPTDKPLRLPLQDVYK	4051.7	3	5.3575	0.4607
KDHPFGFVAVPTK	1443.7	2	2.565	0.1348
KDHRDNLEFFLAGIGR	1889.1	3	4.734	0.3155
KDILLVNDHLLNFVR	1810.1	2	3.4922	0.3418
KDKDPVNK	944.1	2	3.1609	0.184
KDKELYTQNGILHMLDR	2075.4	3	4.5898	0.3404
KDKFSFDLGKGEVIK	1712.0	3	3.2444	0.1383
KDLKDYFSK	1144.3	2	2.7889	0.1687
KDLKDYFTK	1158.3	2	2.8406	0.1707
KDLYANTVLSGGTTMYPGIADR	2344.6	3	6.5531	0.5332
KDLYEPTHGGK	1245.4	2	3.7354	0.2825
KDMMKNASESKLSKDNLKKR	2352.8	3	3.3335	0.1061
KDMSGHYQNALYLGDVSER	2184.4	3	3.3252	0.2162
KDNDFIYHDR	1323.4	2	3.3468	0.1715
KDNDFIYHDRVPDLKDLDPIGK	2614.9	3	4.9133	0.2162
KDPEGLFLQDNIVAEFSVDETGQMSATAK	3142.4	3	5.7271	0.4963
KDPELWGSVLLESNPYR	2004.2	2	2.9341	0.2857
KDPSKNQGGGLSSSGAGEGQGPK	2144.2	2	2.9646	0.2003
KDPSKNQGGGLSSSGAGEGQGPKK	2272.4	3	4.0827	0.269
KDQGELER	975.0	1	2.4451	0.1446
KDQGELERQLLQANPILEAFGNAK	2684.0	3	5.0997	0.3018
KDSDSFK	826.9	1	2.3676	0.1272
KDSETGENIR	1149.2	2	2.8607	0.2509
KDSLSVNEFK	1167.3	2	2.5158	0.1387
KDSLSVNEFKELVTQQLPHLLK	2568.0	3	3.4117	0.2227
KDVDEAYMNK	1213.3	2	3.4318	0.2691
KDVDEAYMNKVELESR	1927.1	2	5.0525	0.4231
KDVDEAYMNKVELESRLEGLTDEINFLR	3328.7	3	3.687	0.1786
KDVKDKETTENENTK	1779.9	2	4.6276	0.3393
KDVKDKETTENENTKFE	2056.2	2	4.3728	0.3988
KDVKDKETTENENTKFEV	2155.3	2	5.0482	0.3791

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KDVKDKETTENENTKFEVR	2311.5	2	5.588	0.4392
KDVKDKETTENENTKFEVRL	2424.6	3	4.8102	0.3574
KDVLTAHPAAPGPVSR	1616.8	2	4.8798	0.4748
KDVSCPIRQVPTGK	1528.8	2	2.6397	0.1
KDVYVQLYLQHLTAR	1848.1	3	5.1725	0.4558
KDWSALSSLAR	1234.4	2	3.3851	0.2823
KEAAENSLVAYK	1323.5	2	3.806	0.3563
KEAEGTEEGGEEEDDEEMDPQTIDSLIELSTK	3555.6	3	6.7382	0.4481
KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	3327.8	3	6.9734	0.3319
KEAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK	3327.8	3	6.4863	0.3719
KEAESSPFVER	1279.4	2	3.5584	0.2962
KEAPPMEKPEVVK	1482.8	2	4.6244	0.3414
KEAVQTAAK	946.1	2	2.5139	0.1867
KEDALLYQSK	1195.3	2	2.696	0.1726
KEDFSEATLK	1168.3	2	2.5332	0.1819
KEDLVFIFWAPESAPLK	1991.3	2	5.4102	0.3122
KEDLYLKPIQR	1403.7	2	3.7355	0.2743
KEDMTYAVR	1113.3	2	2.9095	0.2701
KEDTLAFSEWGSPHAAVPR	2099.3	2	6.3642	0.5542
KEEDSHTTLHETPTTGNHYPSNHQP	2858.9	3	4.512	0.2715
KEEEAVLVGGEWSPSLDGLDPQADPQVLVR	3235.5	3	5.7128	0.4224
KEEEEAEDKEDDEDKDEDEEDEEDKEEDEEEDVPGQAKDEL	4886.7	3	7.041	0.4299
KEEEEEEEEYDEGSNLKK	2215.2	3	5.799	0.2058
KEEEESQPAKK	1303.4	2	2.9261	0.1816
KEEEGSANRRPEDQELESLSAIEAELEK	3188.4	3	5.6382	0.4053
KEEEGSANRRPEDQELESLSAIEAELEKVAHQLQALR	4205.6	3	3.7396	0.1082
KEEEKEELMEWWK	1795.0	2	4.1821	0.1831
KEEELQAALAR	1258.4	2	3.0427	0.1392
KEEELQGALAR	1244.4	2	2.916	0.1264
KEEGEAFAR	1037.1	1	2.7891	0.2215
KEEHLSIEDFTQAFGMTPAAFSALPR	2895.2	3	5.7682	0.399
KEEIIKTLSKEEETK	1806.0	2	5.1158	0.3235
KEELEEELDEAVER	1718.8	2	5.232	0.3522
KEELMFFLWAPELAPLK	2063.5	2	5.337	0.3189
KEEPKLPQQSHSAFGATSSSSGFGK	2593.8	3	5.7842	0.5051
KEEQEVQATLESEEVDLNAGLHGNWTLENAK	3483.7	3	5.9636	0.422

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KEESETANKNDSSK	1567.6	2	2.9618	0.2099
KEETQPPVALKK	1368.6	2	2.5512	0.1021
KEFGGGHIKDELFGTVKDDLSFAGYQK	2988.3	3	3.4591	0.252
KEFLHAQEEVKR	1514.7	2	3.9337	0.3151
KEFSPFGTITSAK	1413.6	2	3.7719	0.3268
KEFTLEFSR	1157.3	2	2.7399	0.2664
KEGDLIAAQAR	1172.3	2	3.5384	0.3183
KEGGLGPLNIPLLADVTR	1864.2	2	6.0386	0.5212
KEGGLGPLNIPLLADVTRR	2020.4	3	3.9046	0.3643
KEGLSFLGGLR	1177.4	2	2.5579	0.1216
KEGNASGVSLLEALDTILPPTRPTDKPLR	3090.5	3	4.4954	0.4171
KEGNASGVSLLEALDTILPPTRPTDKPLRLPLQDVYK	4047.6	3	5.5004	0.5053
KEGPYDVVVLPGGNLGAQNLSESAAVK	2714.0	3	4.1172	0.1596
KEGPYDVVVLPGGNLGAQNLSESAAVKEILKEQENR	3854.3	3	3.6306	0.103
KEGSDGPLATSKPVPAEK	1812.0	3	3.8626	0.3221
KEGTGSTATSSSSTAGAAGK	1756.8	2	5.9061	0.4713
KEHDILSQLQK	1339.5	2	3.3957	0.2716
KEIADYLAAGKDER	1579.7	2	4.1505	0.3495
KEICKFYLQGYCTKGENCIYMHNE	2916.4	3	4.7363	0.1041
KEIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR	3963.3	3	3.8591	0.2883
KEIHTVPDMGK	1255.5	2	4.1518	0.3304
KEKEEEELFPESERPEMLSEQEHMSISGSSAR	3738.0	3	7.0648	0.4219
KEKEPEYTLLTER	1636.8	2	3.1221	0.112
KEKSDVGSSDESAVSIFHELR	2321.5	3	3.382	0.1664
KELDEETER	1149.2	2	2.5297	0.1073
KELEEDFIKSELKK	1737.0	2	5.0908	0.3061
KELENLAAMDLELQK	1746.0	2	2.6766	0.1436
KELQAAGKSPEDLER	1671.8	2	4.6268	0.4296
KELQELSSSIKDLVLK	1831.1	2	2.8065	0.1583
KELSDIAHR	1069.2	2	3.1406	0.3401
KEMTNEEKNIITNLSK	1893.2	2	3.2733	0.3492
KENEEEPQSAPK	1386.4	2	4.0185	0.1877
KENESLTHSTDR	1417.5	2	3.1705	0.2435
KENIKDEK	1004.1	2	2.4592	0.1002
KENISKEEER	1262.4	2	2.9515	0.1993
KENSETTLTR	1179.3	2	2.9992	0.1192

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KENSETVVTGSLDDLVK	1835.0	2	3.1899	0.1567
KEPAVLELEGKK	1341.6	2	3.8173	0.3557
KEPEKPIDREK	1369.5	2	2.4479	0.2335
KEPFTLEAYYSSPQDLPYPDPAIAQFSVQK	3431.8	3	5.4622	0.2874
KEPVGDDESVPENVLSFDDLTADALANLK	3103.3	3	4.6336	0.2518
KEPVQDDSDLDR	1417.5	2	2.8857	0.1447
KEQTADGVAVIPVLQR	1725.0	3	3.4455	0.3079
KEQTPEHGK	1054.1	2	2.4333	0.2533
KERGRRGEGEREK	1587.7	2	2.4921	0.2016
KESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	3343.8	3	4.7939	0.3163
KESKDQLSDDVSK	1479.6	2	4.8376	0.3707
KESKDQLSDDVSKVIAYLK	2167.4	3	5.6284	0.4127
KESKDQLSDDVSKVIAYLKR	2323.6	3	5.2411	0.4491
KESKEETPEVTK	1405.5	2	4.608	0.3109
KESLDVYELDAK	1410.6	2	3.6647	0.4126
KESLQNLLHSSR	1412.6	2	3.1828	0.2854
KESYSIYVYK	1280.5	3	3.7275	0.3811
KESYSVYVYK	1266.4	2	3.6702	0.3897
KETEGDVTSVKDAK	1507.6	2	3.9819	0.3751
KETPPKEVK	1056.2	2	2.9246	0.1028
KETSGTQGIEGHLK	1485.6	2	3.962	0.3975
KETSKDTETVLK	1379.5	2	3.0592	0.1541
KEVEVVEIIQATIIR	1741.1	2	5.3274	0.4242
KEVKGDLENAFLNLVQCIQNKPLYFADR	3267.7	3	5.3332	0.4487
KEVKLPGK	899.1	2	2.499	0.1095
KEVLASPDR	1015.1	2	2.4982	0.125
KEVQDEEK	1005.1	2	2.6453	0.1093
KEVTEEEKTKEEKPEAK	2033.2	3	4.1672	0.3338
KEVVEEAENGR	1260.3	2	3.7273	0.2783
KEWHGPPSQGPSYHDTR	1980.1	3	3.3273	0.2899
KEWSGLLEELAR	1431.6	2	2.4404	0.1571
KEYGGLDVLVNNAGIAFK	1909.2	3	5.1499	0.4221
KFAADAVK	850.0	2	2.7737	0.1683
KFAADAVKLER	1248.5	3	3.6919	0.2534
KFAEAFEAIPR	1279.5	2	3.3597	0.3546
KFAEALGSTEAK	1252.4	2	3.0631	0.2166

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KFAENPKAGDEFVEK	1709.9	2	4.5841	0.2314
KFAPVVAPKPK	1182.5	2	2.9916	0.2496
KFAREEIIPVAAEYDK	1880.1	2	2.9318	0.2263
KFAREEIIPVAAEYDKTGEYPVPLIR	3006.4	3	7.001	0.4944
KFAREEIIPVAAEYDKTGEYPVPLIRR	3162.6	3	4.366	0.2812
KFAYGYIEDLK	1347.5	2	2.6485	0.1746
KFAYLGR	855.0	2	2.6376	0.1157
KFDDENFILK	1269.4	2	3.2237	0.1199
KFDDFQKDLK	1284.4	2	3.6048	0.2256
KFDEALK	851.0	2	2.6324	0.1132
KFDEGRADFPVDEELGLDLGDLSR	2694.9	3	5.9505	0.3991
KFDEGRNNFEGEVTKENLLDFIK	2744.0	3	4.9508	0.2858
KFDKKDEESGGGSNPFQHLEK	2378.5	3	5.742	0.3821
KFDLGQDVIDFTGHALALYR	2280.6	3	7.3536	0.6039
KFDLNSPWEAFPVYR	1870.1	2	4.6026	0.4961
KFDLNSPWEAFPVYRQPPESLK	2650.0	3	3.9123	0.3135
KFDQLLAEEK	1221.4	2	3.2668	0.1784
KFDQLLAEEKAAVLR	1732.0	3	3.7918	0.3339
KFDQLLAEEKTISAK	1722.0	2	5.0642	0.3416
KFDVNTSAVQVLIEHIGNLDR	2369.7	3	6.8139	0.496
KFEDEYSEYLKHNVR	1958.1	2	5.013	0.4846
KFEEDLLLLEDQNSK	1822.0	2	4.4717	0.2497
KFEEEGNPYYSSAR	1677.8	2	4.3834	0.3251
KFEEIPIAHIK	1325.6	2	4.0207	0.2094
KFEEMNAELEENKELAQNR	2323.5	3	3.9816	0.2673
KFEHQLLYNACQLDNPDEQAAQIR	2846.1	3	6.2862	0.3505
KFEHQLLYNACQLDNPDEQAAQIRR	3002.3	3	3.634	0.2051
KFEKPVLTLTEQPKPLTK	2098.5	3	4.645	0.3755
KFERHTLLEYLLGEGNL	2033.3	3	5.1153	0.1278
KFFDANYDGKDYDPVAAR	2093.2	3	5.8332	0.4317
KFFDANYDGKDYNPLLAR	2148.4	3	3.7953	0.2736
KFFKFQVLK	1185.5	2	2.8092	0.1047
KFFLSHPSYR	1282.5	2	2.8396	0.2455
KFGDPVVQSDMK	1351.6	2	3.9136	0.3471
KFGDPVVQSDMKHWPFQVINDGDKPK	3014.4	3	6.1806	0.357
KFGEAIGMGFPVK	1381.7	2	2.438	0.1263

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KFGEAIGMGFPVKVPYR	1897.3	3	4.5205	0.3801
KFGEEIAR	950.1	2	2.5774	0.1416
KFGTINIVHPK	1254.5	2	2.6547	0.1833
KFGVVLDEIKPSSAPELQAVR	2284.6	2	5.8531	0.4337
KFGYVDFESAEDLEK	1777.9	2	5.261	0.4221
KFGYVDFESAEDLEKALELTGLK	2603.9	3	6.3672	0.4599
KFHETVIAALLR	1398.7	2	2.4122	0.2568
KFIAYQFTDTPLQIK	1814.1	2	3.3475	0.262
KFIDIAAAK	977.2	2	2.7374	0.1628
KFIQENIFGICPHMTEDNKDLIQGK	2920.4	3	5.4408	0.4029
KFISDKDASIVGFFDDSFSEAHSEFLK	3068.3	3	7.8276	0.5447
KFIWTNHKFNVTGTPEQYVPYSTTR	3016.4	3	4.4008	0.341
KFKDNTEPGHFQTLLQK	2032.3	3	4.1552	0.3123
KFKGDSR	837.9	1	1.8188	0.1408
KFLALLREEGASPLDFD	1922.2	2	4.0583	0.3537
KFLDAGHK	916.1	2	2.6556	0.1917
KFLDAGHKLNFAVASR	1775.0	2	5.1891	0.445
KFLDGIYVSEK	1299.5	2	3.129	0.2833
KFLDGIYVSEKGTVQQADE	2128.3	2	4.3223	0.3773
KFLDTSHYSTAGSSSVR	1844.0	2	4.5376	0.4041
KFLEEQEITDLK	1493.7	2	4.3665	0.2051
KFLEHLSGAGK	1187.4	2	3.3688	0.3232
KFLPLFDR	1036.3	2	2.4579	0.1503
KFLSDPQVHTVLVER	1769.0	3	5.1496	0.4005
KFLSVLER	992.2	2	2.5685	0.1299
KFMHVLYPR	1191.5	2	2.8235	0.1422
KFMNPFNMPNLYQK	1773.1	2	3.8835	0.3408
KFMQDPMEIFVDDETK	1974.2	2	2.996	0.1348
KFMQDPMEIFVDDETKLTLHGLQQYYVK	3418.9	3	4.9947	0.3128
KFNALFAQGNYSEAAK	1759.9	2	5.9808	0.5175
KFNALKVPVPEDK	1485.8	2	4.0906	0.3207
KFNALKVPVPEDKYTAQVDAEEKEDVK	3092.4	3	6.0509	0.4704
KFNILGTHTK	1159.4	2	2.6774	0.1833
KFNILGTNTK	1136.3	2	2.602	0.1131
KFPEEAAEGGGGAGLVGGR	1759.9	2	2.5061	0.1374
KFPFCDGAHTK	1251.4	3	3.2981	0.2687

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KFPHLAEAQK	1169.4	2	3.1105	0.2403
KFPSGTFEQVSQLVK	1695.9	2	4.8821	0.4357
KFPVFNPATEEELCQVEEGDKEDVDK	2997.2	3	4.7432	0.3491
KFPVFNPATEEELCQVEEGDKEDVDKAVK	3295.6	3	6.4818	0.4783
KFSKEEPVSSGPEEAVGK	1906.1	3	3.2901	0.2472
KFSLAKRLQGDK	1391.6	2	2.4789	0.1779
KFSLDALITHVLPFEK	1859.2	3	5.2195	0.3595
KFSLDALITHVLPFEKINEGFDLLHSGK	3170.6	3	4.1646	0.3847
KFSLDALITNILPFEK	1850.2	2	5.027	0.3687
KFSLDALITNILPFEKINEGFDLLR	2908.4	3	4.9426	0.3043
KFSSFFKSLVIELDK	1789.1	2	2.4556	0.1039
KFSYDLSQCINQMK	1706.0	2	3.7081	0.2415
KFTFGLDWVPK	1338.6	2	3.2202	0.2551
KFTGEQPSISGTFGLK	1697.9	2	2.4573	0.1423
KFTGIKHEWQVNGLDDIKDR	2400.7	3	4.0368	0.3316
KFVADGIFK	1025.2	2	2.7082	0.2156
KFVADGIFKAELNEFLTR	2099.4	2	4.8939	0.4092
KFVEEQHTK	1146.3	2	2.7447	0.1774
KFVETPGQK	1034.2	1	2.4762	0.1997
KFVGGSGQVSER	1251.4	2	3.9172	0.3286
KFVHLLDQSDQDFQEELDLMK	2579.9	3	6.2958	0.4956
KFVHPTLSSK	1144.3	2	2.4425	0.2278
KFVIHPESNNLIIIETDHNAYTEATK	2999.3	3	6.2316	0.3546
KFVIPDFMSFTSHIDELYESAK	2605.9	3	4.8357	0.438
KFVIPDFMSFTSHIDELYESAKK	2734.1	3	3.6095	0.3145
KFVLCPECENPETDLHVNPK	2313.6	3	4.6085	0.3684
KFVMKPPQVVR	1329.7	2	3.0689	0.213
KFYDANYDGKEYDPVEAR	2181.3	3	3.5159	0.3095
KFYGPEGPYGVFAGR	1645.8	3	4.7542	0.4738
KFYPLEIDYGQDEEAVKK	2173.4	2	4.4883	0.4088
KFYPLEIDYGQDEEAVKKLTVNPGTK	2984.3	3	4.7971	0.4078
KGAAFGFNVIATR	1352.6	2	2.7633	0.2042
KGAAPAPPGK	894.1	2	3.2401	0.2325
KGAAYGLAGLVK	1148.4	2	3.1056	0.2694
KGADLNLVDSLGYNALHYSK	2179.4	3	5.2765	0.4225
KGAGDGSDEEVDGKADGAEAKPAE	2304.3	3	4.5179	0.3224

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KGAGSVFR	821.9	2	2.4293	0.1384
KGANLLLSASPDFGDIAVSHVGAVVPTHGFSSFK	3427.9	3	6.1101	0.4726
KGAVAEDGDELR	1260.3	2	3.4791	0.3586
KGAVAEDGDELRTEPEAK	1916.0	2	5.221	0.4047
KGAVQKVSKKLEMHVYSK	2061.5	3	3.4698	0.1311
KGAVTGGEEAK	1047.1	2	2.5681	0.2287
KGDECELLGHSK	1316.5	2	2.472	0.147
KGDEVDGVDEVAK	1361.4	2	3.8988	0.3061
KGDEYIINGQK	1265.4	2	4.1901	0.3547
KGDIFLVR	948.1	2	2.7582	0.1883
KGDIILGGLFPIHFGVAAK	1954.3	2	3.9903	0.3333
KGDIILGGLFPIHFGVAAKDQDLK	2554.0	3	3.2877	0.1033
KGDILTLLNSTNKDWWK	2033.3	3	4.0455	0.3283
KGDIVDIK	888.0	1	2.3953	0.1583
KGDKPWKESGGSVEAPR	1829.0	2	3.7398	0.3802
KGDKTNFPK	1035.2	2	2.4873	0.1697
KGDLDKAIELFQR	1533.8	2	3.6608	0.3556
KGDLLNAHYDGYLAK	1678.9	2	4.8641	0.4911
KGDLSPAELMMLTIGDVIK	2032.5	2	4.3861	0.3988
KGDRTLPVR	1042.2	2	2.7286	0.1316
KGDSSAEELK	1064.1	2	2.8849	0.2678
KGDSSAEELKLATQLTGPVMPVR	2428.8	2	6.5036	0.5082
KGDTAALGGK	918.0	2	2.9453	0.2406
KGDTVYILR	1065.2	2	3.4059	0.2951
KGDVAAAHTCFSGALTHCR	1946.2	2	3.3234	0.1518
KGDVLHMHYTGK	1386.6	2	4.8662	0.3793
KGDVVIVLTGWRPGSGFTNTMR	2392.8	2	4.4258	0.3136
KGEDFVK	822.9	1	2.657	0.1697
KGEDVLGSVR	1060.2	2	2.5687	0.1946
KGEEALFTTR	1152.3	2	3.2389	0.3092
KGEFETGFEK	1172.3	2	3.1714	0.2837
KGEGLPNFDNNNIK	1560.7	2	3.6656	0.2227
KGEHQILVDEKPVPIFLVPTENSIK	2832.3	3	4.5672	0.3113
KGEHQILVDEKPVPIFLVPTENSIKK	2960.5	3	5.2496	0.323
KGEICHLLCKPEYAYGSAGSLPK	2465.9	3	5.4875	0.4109
KGEIFELK	964.1	2	2.6844	0.1538

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KGEITGEVHMPSGK	1470.7	2	3.7567	0.3476
KGEKDIPGLTDTTVPR	1727.9	2	5.2684	0.3968
KGEKNTIVTSYNR	1510.7	2	3.956	0.3695
KGELTQEEKELLEVIGKGTVQEAGTLLSSK	3216.6	3	4.3999	0.232
KGEPGPPDADGPLYLPYK	1915.1	2	3.6884	0.2366
KGEQGGPPPK	995.1	2	2.8564	0.2425
KGESGQSWPR	1132.2	2	3.0329	0.3163
KGESQTDIEITR	1377.5	2	3.2333	0.1938
KGESQTDIEITREEDFTR	2155.3	3	3.6149	0.3358
KGETLSQEEQR	1305.4	2	2.4844	0.1213
KGFIGPGIDVPAPDMSTGER	2045.3	2	5.5734	0.5315
KGFLSGLLDNVK	1291.5	2	3.338	0.1591
KGFLSGLLDNVKQELAK	1861.2	2	3.1062	0.2128
KGFNEGLWEIDNNPK	1761.9	2	4.2115	0.3176
KGFNEGLWEIENNPGVK	1932.1	3	5.0475	0.4465
KGFPHVIYAR	1188.4	2	3.0517	0.2845
KGFSEGLWEIENNPTVK	1949.2	2	5.3309	0.4131
KGGDGIKPPPIIGR	1405.7	2	3.5167	0.2676
KGGGALLHSVKAK	1266.5	2	2.5171	0.1141
KGGGLAGVGGGAH	1038.1	2	2.4879	0.3014
KGGKEFVEAVLELR	1575.8	2	5.1358	0.3922
KGGKEFVEAVLELRK	1704.0	2	4.1755	0.2967
KGGPGSTLSFVGKR	1391.6	2	3.4158	0.3824
KGGPSPGDVEAIKNAIANASTLAEVER	2696.0	3	5.5793	0.4412
KGGPSPGDVEAIKNAIANASTLAEVERLK	2937.3	3	3.8846	0.2762
KGHAVGDIPGVR	1206.4	2	3.5557	0.4036
KGHDAGDHPPITPMK	1601.8	2	3.4257	0.3655
KGHEYTNIK	1090.2	2	2.5318	0.1471
KGHHEAEIKPLAQSHATK	1983.2	3	3.5587	0.1862
KGHYAER	860.9	2	2.4663	0.1819
KGIAFPTSISVNNCVCHFSPLK	2363.8	3	3.646	0.1707
KGIEESLR	932.1	2	2.9698	0.1835
KGIIRPGTAFELLEAQAATGYVIDPIK	2873.3	3	4.467	0.3991
KGINTLVTYDMVPEPK	1806.1	2	3.7922	0.3328
KGIQEAQVELQK	1371.6	2	3.6939	0.1846
KGISDLVLKEYLDNVQLGHILER	2654.1	3	5.6579	0.4549

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KGISLNPEQWSQLK	1628.9	2	4.1778	0.3341
KGISLNPEQWSQLKEQISDIDDAVR	2871.2	3	6.3612	0.4788
KGIVLLEELLPK	1352.7	2	4.3581	0.2552
KGKADAGKDGNNPAK	1471.6	2	4.1949	0.2168
KGKDSLYAQGK	1195.4	2	3.2942	0.2989
KGKDSLYAQGR	1223.4	2	3.9612	0.3554
KGKGDLQPQLDSALQDVNDMYLLLEETEK	3292.7	3	4.5291	0.2727
KGKLPIVNEDDELVAIIAR	2094.4	2	5.0364	0.3742
KGKPAAPGGAGNTGTK	1412.6	2	3.422	0.1794
KGKPNIGQEQPVDDAAEVPQREPEKER	3046.3	3	5.2207	0.3121
KGLDPYNVLAPK	1315.5	2	4.0464	0.2845
KGLEFPMTDLDMLSPIHTPQR	2427.8	3	5.8267	0.3214
KGLEQLLVGGSHLK	1479.7	2	4.1969	0.395
KGLEQLLVGGSHLKENK	1851.1	2	4.189	0.3846
KGLFPFTHVK	1174.4	2	3.0217	0.1107
KGLIAAICAGPTALLAHEIGFGSK	2339.8	3	7.696	0.5913
KGLKEGIPALDNFLDKL	1872.2	3	5.2614	0.356
KGLLGELILLQQQIQEHEEEAR	2575.9	3	3.5433	0.176
KGLPLGSAVSSPVLFSPVGR	1969.3	2	4.6625	0.4914
KGLSFFAFEHSEEYQQAQHK	2412.6	3	3.409	0.1887
KGLTPSQIGVILR	1382.7	3	4.7805	0.3122
KGLVGPELHDR	1221.4	3	3.5002	0.3491
KGLYMANDLK	1153.4	2	2.6769	0.177
KGMWSEGNGSHTIR	1560.7	2	3.2036	0.2995
KGNEQHAFTR	1188.3	2	3.3944	0.3593
KGNFNYIEFTR	1389.5	2	3.2625	0.1008
KGNFYIFDVLDQDGNIVSPSEIQAHLK	3049.4	3	5.719	0.3594
KGNIELASSEPQHFTTTVTR	2217.4	3	4.2403	0.419
KGNKEDYDLSK	1297.4	2	3.5933	0.296
KGNNESYHYAR	1339.4	2	3.3839	0.362
KGNYAER	837.9	2	2.6803	0.2285
KGNYSER	853.9	2	2.439	0.2184
KGPAAPPPTPVKPPR	1510.8	3	3.7162	0.3362
KGPAPELQGVEVALAPEELELDPMAMTQK	3093.6	3	3.4377	0.267
KGPEDTAQLAHAVLAK	1649.9	3	4.7733	0.2987
KGPEFTKDFAPVIVEAFK	2024.3	2	3.3923	0.3376

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KGPELPLVPVKR	1333.6	2	2.6633	0.1304
KGPGLAVQSGDKTK	1386.6	2	3.5523	0.2774
KGPGLYYVDEHGTR	1592.7	2	4.1009	0.4323
KGPGPGGGVSGGK	1055.2	2	2.5165	0.2525
KGPQGYGFNLHSDK	1548.7	2	4.3429	0.3639
KGPQVRDWSHYFKIIEDLRAQIFANTVDNAR	3690.1	3	3.4013	0.2707
KGPSGYGFNLHSDK	1507.6	2	4.4177	0.3755
KGPSSTGASGQAK	1176.3	2	2.5829	0.193
KGPSTVTDLEDTKR	1547.7	2	3.8926	0.3876
KGQAVDYEGSR	1210.3	2	3.623	0.3232
KGQAVDYEGSRTQEEIVAK	2109.3	3	4.46	0.4382
KGQDSIEPVPGQK	1383.5	2	3.3701	0.2255
KGQGGAGAGDDEEED	1435.3	2	4.0228	0.2767
KGQGLTGPTLLPGTPARK	1793.1	2	3.0693	0.2655
KGQGTAATGNQATPK	1430.5	2	3.5984	0.3119
KGQSEEIQK	1047.1	2	2.5312	0.1083
KGQTHTLEDFQR	1460.6	2	3.9833	0.4779
KGRDTLQEANDILNNLKDFDR	2476.7	3	3.593	0.118
KGRPMVISSGMQSMDTMK	1985.4	2	3.9325	0.4128
KGSEHQAIVQHLEK	1604.8	2	3.2206	0.2758
KGSEQESVKEFLAK	1580.8	2	4.0265	0.3405
KGSEVESVKEFLAK	1551.8	2	4.4942	0.3502
KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	3845.3	3	7.5102	0.5905
KGSLESPATDVFGSTEEGEKR	2225.4	3	5.4775	0.4418
KGSLLIDSSTIDPAVSK	1732.0	2	3.2374	0.3872
KGSLLIDSSTIDPAVSKELAK	2173.5	3	4.5099	0.3929
KGSLLIDSSTIDPAVSKELAKEVEK	2659.0	3	5.6721	0.5016
KGSVPLGLATVLQDLLR	1781.1	2	4.1219	0.4492
KGSVSHDTVQPR	1311.4	2	2.4578	0.1329
KGSYNPVTHIYTAQDVK	1922.1	2	4.2228	0.3709
KGSYNPVTHIYTAQDVKEVIEYAR	2783.1	3	4.7267	0.3792
KGTAVFWYNLLR	1468.7	2	3.104	0.244
KGTDDSMTLQSQK	1439.6	2	4.1925	0.2895
KGTDLWLGVDALGLNIYEKDDKLTPK	2904.3	3	4.7764	0.3521
KGTDVPKWISIMTER	1762.1	3	5.0847	0.3852
KGTEVQVDDIKR	1388.6	3	3.6109	0.2085

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KGTVEGFEPADNK	1392.5	2	3.6735	0.2661
KGTVLLADNVICPGAPDFLAHVR	2407.8	2	4.5329	0.4813
KGTVVYGEPITASLGTDGSHYWSK	2554.8	3	3.4889	0.3228
KGVAINFVTEEDKR	1606.8	2	4.212	0.443
KGVAINMVTEEDKR	1590.8	2	4.0845	0.3778
KGVEFPMADLDALSPIHTPQR	2323.7	3	5.7153	0.3786
KGVEGLIDIENPNR	1554.7	2	4.1648	0.3155
KGVEHGPAAIR	1135.3	2	2.4088	0.208
KGVITVKDGK	1045.3	2	3.4307	0.1916
KGVLETFSGTETNKIWPYVYAFLQTK	3022.4	3	4.8131	0.2104
KGVLFGVPGAFTPGCSK	1666.0	2	4.4464	0.4066
KGVNLPGAAVDLPAVSEK	1766.0	2	5.1839	0.4688
KGVNLPGAAVDLPAVSEKDIQDLK	2478.8	3	6.5406	0.4939
KGVNLPGAAVDLPAVSEKDIQDLKFGVEQDVDMVFASFIR	4320.9	3	7.341	0.5689
KGVNLPGAAVDLPAVSEKDIQDLKFGVEQDVDMVFASFIRK	4449.1	3	5.6399	0.4625
KGVQLQTHPNVDKK	1592.8	2	3.2378	0.2356
KGVTSILPVLR	1183.5	2	3.4691	0.2358
KGVVKAEK	859.0	1	2.7512	0.1827
KGWALLHPGR	1135.3	2	2.5455	0.1807
KGWLSLHTGNLDGEDHAAER	2207.3	3	4.3035	0.3549
KGYEEVHVPALKPKPFGSEEQLLPVEK	3050.5	3	5.1598	0.3572
KGYEEVHVPALKPKPFGSEEQLLPVEKLPK	3388.9	3	4.4944	0.3334
KGYEVIYLTEPVDEYCIQALPEFDGKR	3177.6	3	6.6202	0.4921
KGYPEVALHFVKDEK	1761.0	2	3.2825	0.2069
KHAASDVDLEIESLLNQQSTK	2327.5	2	3.4873	0.3553
KHAASDVDLEIESLLNQQSTKEQQSK	2928.2	3	3.5096	0.1875
KHALFPELPK	1180.4	2	2.6131	0.2103
KHALLEADVAAHQDR	1674.8	2	4.6947	0.4747
KHDSGAADLER	1199.3	2	2.6572	0.2755
KHEAFESDLAAHQDR	1754.8	2	5.5888	0.5272
KHEAFESDLAAHQDRVEQIAAIAQELNELDYYDSHNVNTR	4642.9	3	5.0275	0.4235
KHEAFESDLAAHQDRVEQIAAIAQELNELDYYDSPSVNAR	4545.8	3	3.898	0.3527
KHEAFETDFTVHK	1589.7	2	3.6103	0.3459
KHEAFETDFTVHKDR	1861.0	2	5.6075	0.4825
KHEAIETDIAAYEER	1775.9	3	5.3072	0.414
KHEALMSDLSAYGSSIQALR	2178.5	2	4.5559	0.4718

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KHEDFDKAINVQEEK	1831.0	2	4.525	0.3221
KHEEEEAKAER	1356.4	2	3.432	0.3506
KHEGFER	903.0	1	2.0162	0.1167
KHEGFERDLAALGDKVNSLGETAER	2744.0	3	4.5254	0.3969
KHELLEEAR	1125.3	2	2.6834	0.1409
KHFPSVNWLISYSK	1707.0	3	4.5686	0.2058
KHFVCEGCEQLLSGR	1707.0	2	3.7373	0.179
KHFVGYPTNSDFELK	1783.0	2	3.952	0.4164
KHGGPKDEER	1153.2	2	2.8469	0.1868
KHGLEVIYMIEPIDEYCVQQLK	2650.1	2	3.9717	0.3606
KHGTEEQKATYLPQLTTEK	2203.4	3	3.9475	0.3803
KHGVNVQSIADIHPIQVQPGR	2294.6	2	5.2128	0.3723
KHGVVPLATYMR	1372.7	3	3.6201	0.16
KHIEDEKLVR	1267.5	2	2.8448	0.1495
KHIMGQNVADYMR	1563.8	2	3.0781	0.3479
KHINTWVAEK	1226.4	3	3.4595	0.1651
KHIQDAPEEFISELAEYLIKPLNK	2827.2	3	3.8428	0.2758
KHISQISVAEDDDESLLGHLMIVGK	2736.1	3	7.3826	0.5191
KHISQISVAEDDDESLLGHLMIVGKK	2864.3	3	5.82	0.3896
KHISQISVAEDDDESLLGHLMIVGKKCAADLGLNKGYR	4126.7	3	3.765	0.1378
KHKDVAEEIANYRPTLDTLHEQASALPQEHAESPDVR	4197.5	3	3.8416	0.2162
KHLEINPDHPIVETLR	1912.2	2	5.5003	0.3651
KHLEINPDHSIIETLR	1916.2	2	5.3418	0.4457
KHLEINPNHPIVEMLQ	1913.2	2	4.5836	0.265
KHLHSGQEAASPGPAPSLAPGAVVPTSVIAR	3004.4	3	5.0031	0.2908
KHLTSMATSYFGK	1471.7	2	3.459	0.3852
KHLVESTNEMAPLKVWQLQDLSFQTAAR	3242.7	3	5.8244	0.433
KHNLGINNNNILQPVDSK	2019.3	3	3.822	0.3131
KHPDADSLYVEEVDVGEIAPR	2340.5	2	5.7858	0.4961
KHPDASVNFSEFSK	1593.7	2	4.4947	0.4173
KHPDASVNFSEFSKK	1721.9	2	2.9385	0.1914
KHPDSSVNFAEFSKK	1721.9	2	4.2821	0.2115
KHPEVDVLINFASLR	1739.0	3	5.282	0.472
KHPGGGESDASPEAGSGGGGVALKK	2251.4	3	4.4043	0.3073
KHPSSPECLVSAQK	1511.7	2	3.3153	0.2724
KHQILEQAVEDYAETVHQLSK	2467.7	3	4.6039	0.4613

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KHQQLLEEK	1153.3	2	2.8209	0.1038
KHQQLLEEKNILAEQLQAETELFAEAEEMR	3571.0	3	4.5545	0.356
KHSAILASPNPDEK	1507.7	2	4.0961	0.3263
KHSAILASPNPDEKTKEELEELMSDIKK	3182.6	3	3.294	0.2217
KHSELSELNVK	1284.4	2	2.8361	0.2648
KHSGFEDELSEVLENQSSQAELK	2605.8	3	4.8546	0.4051
KHSGFEDELSEVLENQSSQAELKEAVEEPSSK	3562.8	3	5.5261	0.196
KHSLPDLPYDYGALEPHINAQIMQLHHSK	3354.8	3	5.8869	0.486
KHSQFIGYPITLFVEK	1908.2	3	4.9314	0.4138
KHSQFIGYPITLFVEKER	2193.5	3	4.559	0.4375
KHSQFIGYPITLYLEK	1938.3	3	5.1958	0.4704
KHSQFLGYPITLYLEK	1938.3	3	5.0496	0.3846
KHTLSFVDVGTGK	1389.6	2	3.1312	0.3246
KHTLSYVDVGTGK	1405.6	2	4.0114	0.2866
KHVNPVQALSEFK	1497.7	2	3.0125	0.246
KHVTTAEGTPGTTDQEGPPPDGPPEKR	2801.0	3	3.6855	0.2124
KHYGYSLYSAIK	1430.6	2	2.8906	0.1491
KIADDKYNDTFWK	1644.8	2	3.3787	0.2995
KIADDKYNDTFWKEFGTNIK	2434.7	3	5.0128	0.432
KIAEKDDDLKR	1331.5	2	3.6808	0.1589
KIAELEEEQSQGSTTNSDWMK	2412.6	3	5.2824	0.3893
KIAELMPGASGAEVK	1501.8	2	4.4305	0.3204
KIAILHENFTTVKPEDAYEDFIVKPPVR	3271.8	3	5.3924	0.4122
KIAILHENFTTVKPEDAYEDFIVKPPVRK	3399.9	3	4.0233	0.3564
KIANLLKPDKEIVQDGDHMIIR	2548.0	3	7.8363	0.508
KIAQNDHDLGDMSTVADPSVISHLFSHR	3092.4	3	4.3698	0.1726
KIASLSRPVVSLGK	1455.8	2	3.6419	0.2593
KIATEKDFLEAVNK	1606.8	2	4.3848	0.3431
KICALDDNVCMAFAGLTADAR	2199.6	2	4.0013	0.3144
KIDASKSVDEVFDEVVQIFDKEG	2598.8	3	3.4326	0.3182
KIDASQTEFEK	1296.4	2	3.4366	0.2621
KIDASQTEFEKNVWSFLK	2171.4	2	4.4422	0.431
KIDLSHVTSK	1128.3	2	3.2288	0.3246
KIDQEGKIPDETLEK	1743.9	2	5.2423	0.3802
KIDQEGKIPDETLEKLK	1985.3	2	4.8503	0.3181
KIDTHPSPSHSSTVK	1621.8	2	2.7835	0.1337

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KIDTHPSPSHSSTVKDSLIELK	2420.7	3	4.639	0.3077
KIEAEIVR	958.1	2	2.4247	0.1613
KIEALLNLPR	1167.4	2	3.0457	0.1307
KIEDLGAAMEEALILDNK	1974.3	2	5.8208	0.3795
KIEDNNTLVFIVDVK	1748.0	2	3.9499	0.3104
KIEEAMDGSETPQLFTVLPEKR	2519.9	3	4.204	0.3592
KIEEIKDFLLTAR	1576.9	2	5.0534	0.3632
KIEEQLTLEK	1231.4	2	3.8102	0.2041
KIEEVRDAMENEMR	1751.0	2	3.3241	0.2496
KIEFPMPNEEAR	1461.7	2	2.8478	0.2798
KIEFPPPNEEARLDILK	2010.3	2	3.9546	0.2114
KIEFSLPDLEGR	1404.6	2	3.8307	0.2477
KIEFSLPDLEGRTHIFK	2031.3	2	2.6701	0.2787
KIEFVVVGPEAPLAAGIVGNLR	2250.7	3	3.514	0.2907
KIEGKDEKNDNGASGQTSESIKK	2464.6	3	3.3489	0.194
KIEIDNGDELTADFLYEEVHPK	2576.8	3	5.5128	0.3953
KIEIGDGAELTAEFLYDEVHPK	2475.7	3	6.4808	0.4633
KIEISQHAK	1054.2	2	3.036	0.2088
KIENIHIGEK	1181.4	2	3.1311	0.2359
KIENLEALTELEILDISFNLLR	2588.0	2	4.1099	0.4121
KIENVPTGPNNKPK	1536.8	2	3.5226	0.2356
KIEPELDGSAQVTSHDASTNGLINFIK	2886.2	3	6.4805	0.5407
KIEQELTAAK	1131.3	2	3.3436	0.1606
KIEQELTAAKK	1259.5	2	3.7764	0.1864
KIEQVDKEDEITEK	1704.9	2	5.1299	0.266
KIESFGSK	896.0	1	2.2221	0.1889
KIETEVAGLK	1088.3	2	2.4536	0.1017
KIETFLNHYPVESSWIAPELR	2530.9	3	5.2318	0.4199
KIETRDGKLVSESSDVLPK	2102.4	3	4.7893	0.3394
KIEVIKPGDLGVDLTSK	1813.1	2	4.5679	0.3552
KIFDIDEAEEGVKDLK	1850.1	2	4.6636	0.2575
KIFDLQDWTQEDERDKDAAK	2452.6	3	4.5377	0.3143
KIFEYETQR	1214.4	2	2.4283	0.2154
KIFLAQKPAPLLESPFKDR	2199.6	3	4.2421	0.2692
KIFRDEGGK	1050.2	2	2.4544	0.1781
KIFVGGIKEDTEEHHLR	2009.3	3	6.1296	0.405

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KIFVGGIKEDTEEHHLRDYFEQYGK	3040.3	3	4.1219	0.1704
KIFVGGIKEDTEEYNLR	2012.3	3	5.3615	0.3739
KIFVGGIKEDTEEYNLRDYFEK	2695.0	3	4.7549	0.3701
KIFVGGIKEDTEEYNLRDYFEKYGK	3043.4	3	5.3767	0.1894
KIFVGTK	793.0	1	2.5784	0.1137
KIGDEYFTFITDCKDPK	2021.3	2	3.5024	0.3395
KIGDEYFTFITDCKDPKACTILLR	2792.3	3	3.5606	0.1128
KIGDSSVETHR	1229.3	2	2.6696	0.2449
KIGEEEIQKPEEK	1557.7	2	4.204	0.2184
KIGGIFAFK	981.2	2	2.6594	0.2518
KIGILHENFQTLK	1541.8	2	3.3913	0.2239
KIGLDDEEKLDLFR	1691.9	2	4.6044	0.4601
KIGLETVGVK	1044.3	2	2.4288	0.1737
KIGTTPDIILDDLLETDRVTAHF	2584.9	3	4.8856	0.332
KIGYNPATVPFVPISGWHGDNMLEPSPNMPWFK	3729.3	3	3.7319	0.3014
KIGYNPDTVAFVPISGWNGDNMLEPSANMPWFK	3698.2	3	5.7717	0.21
KIGYNPDTVAFVPISGWNGDNMLEPSANMPWFKGWK	4069.6	3	5.368	0.1946
KIHEQGLIAILDVEPQALK	2116.5	2	3.6534	0.3633
KIHESAGLPFFEIFVDAPLNICESR	2834.2	3	5.2033	0.3793
KIHIDLPNEQAR	1434.6	2	4.3683	0.3305
KIHLFDIDVPGK	1382.6	2	4.9338	0.4367
KIHLFDIDVPGKITFQESK	2216.6	2	4.7435	0.4258
KIHPQTIIAGWR	1420.7	3	4.1842	0.1139
KIHSQEEALR	1211.4	2	3.1887	0.2949
KIHTEPQLSAALEYVR	1856.1	3	5.0969	0.426
KIHVTPLIPGK	1203.5	2	2.4023	0.1951
KIIAKGEELLSPLNLEQAAYAR	2428.8	3	4.8708	0.3656
KIIENGENEKTVS	1461.6	2	2.7879	0.1857
KIIFHSGPTNSGK	1386.6	2	3.172	0.1536
KIIKDGEQHEDLNEVAK	1967.2	2	5.0625	0.3586
KIIKDGEQHEDLNEVAKLFNIHED	2836.1	3	5.1741	0.487
KIIKEESDSFKENVKPIKVEVK	2589.0	3	5.374	0.3353
KIILWDHDLNPER	1649.9	2	3.4239	0.3423
KIIPTLEEYQHYK	1662.9	3	3.3232	0.2466
KIITSEAQELGDTTTLEDPSIIAEILSVYQK	3407.8	3	3.9945	0.1285
KIKAAVEDPRVLLLDL	1794.2	2	2.9198	0.1596

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KIKDPDASKPEDWDER	1930.1	2	3.9789	0.374
KIKDRLPLAVVGSNTIIEVNGK	2365.8	3	3.9243	0.2735
KIKEGVEEAAK	1202.4	2	3.5162	0.2063
KIKETVDQVEELRR	1744.0	2	4.1993	0.1969
KIKGEHPGLSIGDVAK	1649.9	2	4.5958	0.3798
KIKVDEFVTHNLSFDEINK	2277.6	2	6.19	0.5117
KIKVDEFVTHNLSFDEINKAFELMHSGK	3278.7	3	6.1322	0.4495
KILAIELENLK	1284.6	2	3.929	0.203
KILATPPQEDAPSVDIANIR	2149.4	3	4.9913	0.5159
KILCEELGAPANSAVNCVPLEDFGGHHPDPNLTYAADLVETMK	4582.2	3	4.1459	0.3045
KILDPNTGEPAPVLSSPPPADVSTFLAFPSPEK	3420.9	3	4.6237	0.3684
KILDSVGIEADDDRLNK	1902.1	2	5.3296	0.3893
KILDSVGIEADDDRLNKVISELNGK	2743.1	3	5.1742	0.353
KILDSVGIEADDDRLNKVISELNGKNIEDVIAQGIGK	3981.5	3	6.2869	0.4039
KILEEENSLAEYHSR	1819.0	3	3.2476	0.2581
KILEVHIDK	1095.3	2	2.6983	0.1679
KILGYINTGKQEGAK	1620.9	2	4.2141	0.3104
KILHVDNHIGISIAGLTADAR	2215.5	3	4.0552	0.329
KILIWSGR	973.2	2	2.5232	0.1548
KILNDLSSDAPGVPR	1582.8	2	2.8895	0.2518
KILQDGGLQVVEK	1427.7	2	3.3223	0.2353
KILSHTEEHK	1222.4	2	2.8518	0.1191
KILTPIIFKEENLR	1715.1	3	3.2827	0.2109
KINELTGIKESDTGLAPPALWDLAADKQTLQSEQPLQVAR	4347.9	3	5.5775	0.2628
KINQLISETEAVVTNELEDGDRQK	2731.0	3	4.5656	0.3077
KINSQNQPTGIHREPPPPPFSVNK	2684.0	3	4.1632	0.1874
KIPAVPNGTAAHGEAEPHGGHSGPELQR	2816.0	3	4.4965	0.4129
KIPGIYVLSLEIGK	1530.9	2	3.1743	0.3393
KIPIVSSLADPLDTPPDSK	1994.3	2	2.4364	0.1048
KIPLVPENLLK	1264.6	2	2.5502	0.1697
KIPNPDFFEDLEPFR	1865.1	2	4.9047	0.4792
KIPSVEDSLGEGSR	1474.6	2	3.0121	0.166
KIQALQQQADEAEDR	1743.9	2	5.7534	0.494
KIQALQQQADEAEDRAQGLQR	2397.6	2	4.644	0.394
KIQASTMAFK	1125.4	2	2.9024	0.2016
KIQFTVPLLEPHLDPEAAEQIR	2545.9	2	6.0089	0.4258

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KIQFTVPLLEPHLDPEAAEQIRR	2702.1	3	4.8135	0.3429
KIQGIEEYKK	1236.4	3	3.7274	0.2224
KIQMSNLMNQAR	1434.7	2	3.0459	0.1373
KIQNDAGVR	1001.1	2	2.6706	0.13
KIQQGLFDVHNEANGIK	1912.1	3	4.7531	0.3216
KIQQNTFTR	1136.3	2	2.672	0.1861
KIQTTTTTQAVQGR	1533.7	2	3.6226	0.3592
KIQVLQQQADDAEER	1771.9	2	5.1477	0.3897
KIQVLQQQADDAEERAER	2128.3	2	4.6329	0.3028
KIREESNTK	1105.2	2	3.1006	0.2489
KIRELESQISELQEDLESER	2432.6	2	2.6707	0.3105
KISASLQSQSPEHLLPVLIQAAQLCR	2832.3	3	4.9366	0.3473
KISEIEDAAFLAR	1463.7	2	3.3511	0.1844
KISELDAFLK	1164.4	2	2.8448	0.1977
KISELDAFLKEPALNEANLSNLK	2558.9	3	7.6065	0.5005
KISELDAFLKEPALNEANLSNLKAPLDIPVPDPVK	3801.4	3	3.6589	0.1856
KISELDAFLKEPALNEANLSNLKAPLDIPVPDPVKEK	4058.7	3	5.8506	0.4211
KISELDAFLKEPALNEANLSNLKAPLDIPVPDPVKEKEKEER	4730.4	3	4.4595	0.2874
KISENSYSLDDLEIGPGQLSSSTFDSEKNESR	3534.7	3	5.905	0.4268
KISGTTALQEALKEK	1617.9	2	4.3282	0.1511
KISIPVDISDSDMMLNIINSSITTK	2737.2	3	4.4453	0.2509
KISKPDLKPFTPEVR	1756.1	2	4.131	0.2568
KISNQFDWALMR	1509.8	2	4.0626	0.3709
KISSDLDGHPVPK	1393.6	2	4.3087	0.4185
KISSIQSIVPALEIANAHR	2048.4	3	6.4923	0.52
KISSPTGSKDLQMVNISLR	2075.4	3	4.8215	0.3721
KISVVSATK	933.1	2	2.6072	0.1006
KITAASK	718.9	1	1.9673	0.1383
KITESVAETAQTIK	1519.7	2	4.7125	0.4003
KITESVAETAQTIKK	1647.9	2	4.9617	0.4728
KITHNPFGPGQFFDLSIR	2075.4	2	5.2035	0.4817
KITIADCGQLE	1191.4	2	2.9586	0.2573
KITIKNDPSLPEPK	1580.9	2	3.5109	0.2619
KIVDQNTK	946.1	1	2.6073	0.177
KIVEGISQPIWLVSDTR	1942.2	2	4.4992	0.4982
KIVNSAQTGSFK	1280.5	2	3.3642	0.2892

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KIWCFGPDGTGPNILTDITK	2177.5	2	5.6084	0.5232
KIYCVACQELDSDVDKDNPALNAQAALSQAR	3351.7	3	6.8066	0.5046
KIYEDGDDDMKR	1485.6	2	4.0454	0.3548
KIYQNIQDGSLDLNAAESGVQHKPSAPQGGR	3280.6	3	5.8671	0.4088
KIYSFTLKPR	1253.5	2	2.7952	0.3129
KKAAAQLLQSQAQQSGAQQTK	2214.5	3	5.1749	0.3032
KKADLHDEEDEQDILLAQDLEDMWEQK	3286.5	3	4.9761	0.366
KKAEEEAEAKPK	1358.5	2	3.7454	0.2431
KKAEPSEVDMNSPK	1560.8	2	3.6938	0.329
KKAESFAQEMFIEQNK	1929.2	2	5.7422	0.3921
KKAQAELASFK	1221.4	2	2.5308	0.1352
KKASLVALPEQTASEEETPPPLLTK	2679.1	3	5.2963	0.381
KKATGSPVSIFVYDVKPGAEEQTQVAK	2879.3	3	4.0841	0.1718
KKAVLFCLSEDKK	1509.8	2	4.4814	0.3283
KKAYADFYR	1162.3	2	2.7788	0.1994
KKDAGAGTEAESLKGNAEAQPLGPEAK	2668.9	3	4.8457	0.3219
KKDALLSALSIQNYHLECNETK	2519.9	3	5.1315	0.2927
KKDASDDLDDLNFFNQK	2014.1	2	5.6369	0.4175
KKDAVLTK	903.1	2	3.4663	0.1496
KKDDDDEEIGGPKEELIPEK	2285.4	3	4.1501	0.2855
KKDDIPEEDKGNVK	1615.8	2	3.412	0.1786
KKDDRIEELEEALR	1744.9	2	3.728	0.2345
KKDEELSSALEK	1377.5	2	4.1633	0.2386
KKDEISVDSLDFNKK	1767.0	2	5.6533	0.4412
KKDESQEGKQQYLQSIEER	2324.5	2	5.4685	0.3882
KKDFDTALK	1066.2	2	3.0542	0.2559
KKDKDDDGGEDDDANCNLICGDEYGPETR	3189.3	3	6.1765	0.4415
KKDLTQTASSTAR	1407.6	2	2.8947	0.2007
KKDPNEPQKPVSAYALFFR	2236.6	3	4.1215	0.2791
KKDQIGKGTQGATAGASSELDASK	2349.5	3	3.2862	0.2576
KKDQVTAQEIFQDNHEDGPTAK	2500.7	3	5.2743	0.4615
KKDQVTAQEIFQDNHEDGPTAKK	2628.8	3	3.6292	0.278
KKDSPEPQVK	1156.3	2	2.6205	0.1084
KKDSQICELK	1192.4	2	2.8735	0.2375
KKDTAASGYGTQNIR	1610.8	2	4.0016	0.3473
KKDVYVPEASRPHQWQTDEEGVR	2756.0	3	3.8403	0.3308

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KKDYEVELLR	1293.5	2	2.7607	0.2091
KKEAISDLQQLWK	1587.8	2	4.5093	0.3412
KKEDALNETR	1204.3	2	3.1423	0.2755
KKEDDMETK	1124.2	2	2.7973	0.18
KKEEEDDDMKELENWAGSM	2285.5	2	4.945	0.4186
KKEEGVIDSSDKEIVAEAER	2233.4	3	5.301	0.3746
KKEEKPNGKIPDHDPAPNVTVLLR	2697.1	3	4.213	0.3228
KKEELASTAEK	1234.4	2	2.76	0.1114
KKEELASTAEKTEQKEPKPLEK	2542.9	3	5.9793	0.3188
KKEEPSQNDISPK	1500.6	2	3.6913	0.241
KKEFEELIDSNHDGIVTAEELESYMDPMNEYNALNEAK	4418.8	3	5.4336	0.4238
KKEGETVEPYK	1308.5	2	3.1372	0.2195
KKEHGSLPQQTTLLDLMDALPSSGPAAQK	3063.5	3	3.763	0.2206
KKEIEELQSQAQALSQEGK	2145.4	2	6.4086	0.4332
KKEIEELQSQAQALSQEGKSTDEVDSK	3007.2	3	5.6621	0.3957
KKEKEFEETMDALQADIDQLEAEKAELK	3281.6	3	7.2798	0.3924
KKELEEEVNNFQK	1635.8	2	5.1045	0.2742
KKELEEIVQPIISK	1655.0	2	5.1218	0.3649
KKELEEIVQPIISKLYGSAGPPPTGEEDTAEKDEL	3813.2	3	5.3544	0.4009
KKELEHVNLSVK	1424.7	2	3.9105	0.2613
KKELQELNELFKPVVAAQK	2213.6	3	5.4236	0.268
KKELVNNLGEIYQK	1676.9	2	4.7997	0.3898
KKEPAITSQNSPEAR	1656.8	3	4.4711	0.3664
KKEPELFQTVAEGLR	1746.0	3	3.9424	0.2947
KKEPEPNFQLLDNPAR	1897.1	2	4.3766	0.3236
KKEPVGDDESVPENVLSFDDLTADALANLK	3231.5	3	6.7654	0.5092
KKEQEPEKVDTEEDGKAEVASEK	2604.8	3	4.7528	0.2327
KKESDLPSAILQTSGVSEFTK	2266.5	3	5.2296	0.4286
KKESILDLSK	1161.4	2	2.5643	0.1541
KKETVSEAPPLLFSDEEEKEAQLGVK	2903.2	3	5.4864	0.3948
KKEVFPFPEVSQDELNEINQFLGPVEK	3162.5	3	6.664	0.4448
KKEVPAVPETLK	1339.6	2	3.7511	0.1841
KKEVPAVPETLKK	1467.8	2	4.2803	0.2643
KKFAENPKAGDEFVEK	1838.1	2	4.9993	0.3464
KKFAYGYIEDLK	1475.7	2	4.0187	0.3135
KKFDDGEDPLDAESQQGGGGNPFHR	2702.8	3	6.0497	0.5359

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KKFEESIHDVAFHPSK	1900.1	2	3.5131	0.3391
KKFQEILER	1191.4	2	2.7128	0.1456
KKGEPGPPDADGPLYLPYK	2043.3	3	5.3695	0.4057
KKGFTTAILTNTWLDDR	1981.2	2	2.5615	0.2604
KKGGPSPGDVEAIK	1383.6	2	3.3355	0.3238
KKGPGAGSALDDGR	1329.4	2	2.8615	0.282
KKGPLVFGEPIAASLGTDGTHYWSK	2661.0	3	6.11	0.5064
KKGPPDADGPLYLPYK	1760.0	2	3.3414	0.205
KKGPSTVTDLEDTKR	1675.9	2	3.1231	0.3429
KKGTVVYGEPITASLGTDGSHYWSK	2683.0	3	6.4425	0.4466
KKGVAVDYLPER	1375.6	2	3.0284	0.1433
KKGVEPSPSPIKPGDIK	1778.1	2	3.233	0.2043
KKHELEMDLESLEAANQSLQADLK	2742.1	3	4.98	0.3462
KKHLEDEL	1012.1	1	2.3402	0.2003
KKIDILLKAVGDTPIMKTKKWAVERTRTIQGLIDFIKK	4398.3	3	3.5325	0.1587
KKIEPEAVLQTR	1412.7	3	4.8546	0.2302
KKILATPPQEDAPSVDIANIR	2277.6	3	5.5108	0.4754
KKKDELDPLLTR	1456.7	2	3.3386	0.2715
KKKEDELWASFLNDVGPK	2105.4	3	5.1095	0.3507
KKKEEGVIDSSDKEIVAEAER	2361.6	2	6.2205	0.4645
KKLDAQVQELHAK	1508.7	2	5.0336	0.3708
KKLDESIYDVAFHSSK	1868.1	3	4.031	0.3885
KKLDSLGLCSVSCALEFIPNSK	2353.8	3	3.6161	0.2723
KKLEEAASR	1032.2	2	2.8319	0.1585
KKLEGELEELKAQMASAGQGKEEAVK	2803.2	3	5.9522	0.4633
KKLEMDLKDLEAHIDSANK	2199.5	3	6.2139	0.4389
KKLEMDLKDLEAHIDSANKNRDEAIK	3026.4	3	4.0904	0.231
KKLEQLYNR	1192.4	2	2.5267	0.1298
KKLGELTGTVK	1174.4	2	3.1103	0.1822
KKLLADQAEAR	1243.4	2	3.6603	0.2094
KKLQLSLADFR	1319.6	2	2.6459	0.1401
KKLVFPVPLDALSL	1540.9	2	3.238	0.3023
KKMDLIDLEDETIDAEVMNSLAVTMDDFR	3359.8	3	5.7011	0.512
KKMQQNIQELEEQLEEEESAR	2590.8	3	6.0591	0.2849
KKNAPPEPVPPPR	1427.7	2	4.1676	0.4084
KKNDIYGED	1082.1	2	2.5891	0.1786

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KKNEELEQLYQDQEVPKPK	2344.6	3	6.1702	0.3724
KKNEGVNWLR	1244.4	2	3.0726	0.1084
KKNGPLEVAGAAVSAGHGLPAK	2073.4	2	6.3425	0.486
KKNLQYYDISAK	1471.7	2	4.0324	0.2982
KKNLSPGAVESDVR	1500.7	2	2.5049	0.2204
KKNPEPWETVDPTVPQK	1994.2	2	4.3821	0.2838
KKNVIQSVLQAIR	1497.8	2	3.7658	0.2057
KKNYPDPVSIIQK	1530.8	2	4.0594	0.1229
KKPFMLDEEGDTQTEETQPSETK	2669.9	3	4.3998	0.2017
KKPFVYTQGQAVLNR	1750.0	3	5.1055	0.3981
KKPIQEPEVPQIDVPNLKPIFGIPLADAVER	3453.0	3	5.2554	0.4373
KKPPVATEGESALNFNLFEK	2220.5	3	5.3711	0.5034
KKPSEEEAAAAAGGPPGGPQVNPIPVTDEVV	3013.3	3	4.3829	0.2722
KKPSLDDLKELMPDVGR	1942.3	2	3.387	0.2245
KKPTPIQLNPAPDGSAVNGTSSAETNLEALQK	3278.6	3	6.9429	0.4292
KKPTPVLLPQSK	1336.6	2	3.1292	0.2851
KKQDFDEDDILKELEELSLEAQGIK	2935.2	3	5.6016	0.399
KKQDPPVTHDLR	1434.6	2	3.0203	0.2537
KKQEALVAR	1043.2	2	3.1865	0.1185
KKQEEEVSTLRK	1475.7	2	3.4204	0.1467
KKQEESSLKQQVEQSSASQTGIK	2549.8	3	4.8857	0.4022
KKQEGIVGSSR	1189.3	2	2.9521	0.169
KKQEQLTPGVVYVR	1645.9	2	4.2323	0.1515
KKQGEDNSTAQDTEELEKEIREDLPVNTSK	3433.6	3	4.6103	0.1228
KKQGIVTPIEAQTR	1569.8	2	3.9747	0.2862
KKQIEELKGQEVSPK	1742.0	2	5.1972	0.2942
KKQLAEQEELER	1501.7	2	4.0558	0.2607
KKQQDVLGFLEANK	1618.9	2	5.279	0.1911
KKQQDVLGFLEANKIGFEEK	2322.6	3	5.3543	0.3774
KKQQDVLGFLEANKIGFEEKDIAANEENRK	3463.8	3	4.9241	0.3065
KKQSDVMR	992.2	2	2.4774	0.1492
KKQVAVAELLENVGQVNEHDGGAQPGPVPK	3110.5	3	6.06	0.3764
KKQYEDALMQLESVLR	1952.3	2	3.9811	0.3446
KKSDLEIELLKR	1472.8	3	4.5158	0.244
KKSEAPSGESR	1176.3	2	2.7721	0.143
KKSEIQTLKEEIEQSLTK	2133.4	3	4.6404	0.2407

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KKSNLELFKEELK	1606.9	2	4.1344	0.2556
KKSPNELVDDLFK	1533.8	2	3.5729	0.3082
KKSPVPVETLKDVK	1568.9	2	3.6685	0.3227
KKTDELPQLVTLPHPNLHGPEILDVPSTVQK	3446.0	3	5.4626	0.3195
KKTDELR	890.0	2	2.6726	0.1154
KKTEAYLPDDKNK	1550.7	2	4.0434	0.2534
KKTVDDVIKEQNR	1573.8	2	4.185	0.3884
KKVDDDLGTIESLEEAK	1891.1	2	5.7155	0.3412
KKVDDDLGTIESLEEAKK	2019.2	3	5.2124	0.3982
KKVDDDLGTIESLEEAKKK	2147.4	2	5.5294	0.3953
KKVEAQLQELQVK	1541.8	2	5.4862	0.2734
KKVEEVLEEEEEEYVVEK	2238.4	3	4.6849	0.2763
KKVETEAK	933.1	2	2.469	0.1128
KKVNPDLQVEVKPSIR	1851.2	3	3.226	0.1877
KKVPVSVNLLSK	1312.6	2	3.4062	0.3005
KKVVDPFSK	1048.3	2	3.0248	0.1846
KKVVDPFSKK	1176.4	2	2.9787	0.1029
KKWDSNVIETFDIAR	1823.0	2	3.8357	0.3852
KKWENPGLGAESHTDSLR	2026.2	2	4.9849	0.3486
KKWNLDELPK	1271.5	2	3.0451	0.1252
KKWNLDELPKFEK	1676.0	2	3.2822	0.3083
KKYDVDTLDMVFLDHWK	2154.5	3	3.4602	0.1897
KKYNDDSDDSYFTSSSSYFDEPVELR	3096.2	3	5.5841	0.4214
KKYPDRVPVIVEK	1571.9	2	3.8563	0.2282
KKYPYWPHQPIENL	1814.1	2	3.0899	0.3079
KLAAAEGLEPK	1127.3	2	2.9796	0.267
KLAADAGTFLSR	1250.4	2	2.6801	0.1615
KLADKTDHKGELPR	1608.8	2	3.7621	0.3689
KLADMYGGGEDD	1271.3	2	2.5213	0.2443
KLADSDQASK	1063.1	2	3.5349	0.3175
KLAEEEDLFDSAHPEEGDLDLASESTAHAQSSK	3558.7	3	6.5592	0.4834
KLAEQFPR	989.2	2	2.5957	0.1647
KLAFAYLEDLHSEFDEQHGK	2378.6	3	5.8324	0.4603
KLAFAYLEDLHSEFDEQHGKK	2506.8	3	3.6046	0.1288
KLAGANPAVITCDELLLGHEK	2193.6	3	4.5479	0.3124
KLAGEKEELLSQIR	1614.9	2	4.0545	0.3143

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KLALQEFSELNER	1577.8	2	3.9148	0.1684
KLALQLHPDRNPDDPQAQEK	2314.5	3	5.5471	0.407
KLALQWHPDNFQNEEEK	2127.3	2	2.6001	0.113
KLANSEPVGTQTAK	1444.6	2	4.4069	0.4174
KLAPEYEK	978.1	1	2.1188	0.1331
KLAQQYYLVYQEPIPTAQLVQR	2651.1	3	5.5728	0.287
KLAQTFSPSIDILK	1561.8	2	3.1351	0.1469
KLAQTLGLEVLGDIPLHLNIR	2314.8	3	5.0156	0.3492
KLASDAGIFFTR	1326.5	2	3.5811	0.3322
KLASLKPAER	1113.3	2	2.8597	0.1025
KLASQGDSISSQLGPIHPPPR	2186.5	2	5.5255	0.4085
KLAVNMVPFPR	1272.6	2	3.8014	0.3293
KLAVNNIAGIEEVNMIKDDGTVIHFNNPK	3195.6	3	5.5124	0.1971
KLCFKENAEQGEVDMESHR	2251.5	3	3.6604	0.2103
KLCQGLFFR	1112.4	2	2.428	0.1103
KLDAGNQLALIEELHKEIR	2191.5	3	5.2018	0.4571
KLDAQVQELHAK	1380.6	2	4.2365	0.3494
KLDDASK	776.9	1	2.2608	0.2181
KLDDFVETGDIR	1408.5	2	3.7842	0.3622
KLDDQSEDEALELEGPLITPGSGSIYSSPGLYSK	3597.9	3	5.9342	0.376
KLDDSYSEAVRQNEELNLLKAQLNETLTK	3364.7	3	4.087	0.1702
KLDEAVAEAHLGK	1381.6	2	5.2456	0.3978
KLDEAVAEAHLGKLNVK	1836.1	2	5.7452	0.4825
KLDEEALLKK	1187.4	2	2.7773	0.1057
KLDEKENLSAK	1275.4	2	2.8072	0.2047
KLDELLGKDHTQVVSLKDKLEFAPK	2853.3	3	6.1286	0.4507
KLDELYGTWR	1281.4	2	3.5146	0.1661
KLDEQYQK	1052.2	2	2.6425	0.1244
KLDGETTDLQDQIAELQAQIDELK	2715.9	3	4.5662	0.1685
KLDGETTDLQDQIAELQAQIDELKLQLAK	3269.6	3	6.4843	0.4281
KLDGETTDLQDQIAELQAQIDELKLQLAKKEEELQGALAR	4495.0	3	6.2407	0.4887
KLDGFPLLR	1059.3	2	2.9464	0.2031
KLDKENLSDER	1347.5	2	2.5532	0.1841
KLDLEAWFPGSGAFR	1694.9	2	4.7877	0.3917
KLDLFANVVHVK	1383.7	2	4.7884	0.2803
KLDLSNVQSK	1132.3	2	2.5788	0.1593

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KLDNKDLFGK	1178.4	2	3.5503	0.2165
KLDNKDLFGKSDPYLEFHK	2295.6	3	3.3624	0.1437
KLDNTTAAVQELGR	1516.7	2	4.1922	0.341
KLDNTTAAVQELGRENQSLQIK	2457.7	3	4.4477	0.2404
KLDPAQSASR	1073.2	2	2.8519	0.2119
KLDPELHLDIK	1321.5	2	3.4064	0.2428
KLDPGSEETQTLVR	1573.7	2	4.1682	0.3872
KLDQEMEQLNHHTTTR	1982.2	2	4.7139	0.3766
KLDREEIKPIR	1397.6	3	3.8424	0.1601
KLDSELTAR	1033.2	2	2.8465	0.164
KLDSLTTSFGFPVGAATLVDEVGVDVAK	2838.2	3	5.2982	0.5545
KLDSLTTSFGFPVGAATLVDEVGVDVAKHVAEDLGK	3688.1	3	4.6289	0.3532
KLDSLTTSFGFPVGAATLVDEVGVDVAKHVAEDLGKVFGER	4276.8	3	6.6542	0.5305
KLDVEEPDSANSSFYSTR	2046.1	2	4.6464	0.3013
KLDVLSNDLVMNMLK	1734.1	2	4.7733	0.3712
KLDVSIEMPEELDISQLR	2116.4	2	6.0129	0.4453
KLDVSVK	789.0	1	2.2532	0.1419
KLDVTIEPSEEPLFPADELYGIVGANLKR	3215.6	3	7.1472	0.4722
KLDYGQHVVAGTPGR	1598.8	2	4.4102	0.4511
KLEAAEDIAYQLSR	1607.8	2	5.549	0.4384
KLEAAEER	946.0	2	3.2003	0.1046
KLEADSLEVK	1132.3	2	2.7104	0.1308
KLEADSLEVKASKEQALQDLQQQR	2757.1	3	3.738	0.2428
KLEAEADKIGLLLAAK	1684.0	2	4.3769	0.3553
KLEAELLQIEER	1471.7	2	4.0308	0.2849
KLEATIIGEWVK	1387.6	2	4.4141	0.3674
KLEDDRNSLQAAK	1488.6	2	3.6744	0.1687
KLEDGPK	786.9	1	2.3592	0.1573
KLEDQLQGGQLEEVILQAEHELNLAR	2975.3	3	8.594	0.5744
KLEDQLQGGQLEEVILQAEHELNLARK	3103.5	3	7.0202	0.4585
KLEDQNEYESR	1411.5	2	3.3791	0.2495
KLEDSTRETQSQLETER	2051.2	2	4.1875	0.2923
KLEDVKNSPTFK	1406.6	2	3.8645	0.3116
KLEDYYKIDEK	1444.6	2	3.3063	0.2308
KLEEDDQAKDI	1304.4	2	3.3628	0.1677
KLEEEEDGKLKKPK	1671.9	3	4.6638	0.2273

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KLEEEGEQFVK	1336.5	2	4.5809	0.2915
KLEEEGEQFVKK	1464.6	2	4.2611	0.3031
KLEEEQIILEDQNCK	1833.1	2	5.5549	0.3031
KLEEERHNLITEMVALNPDFKPPADYKPPATR	3722.2	3	3.6313	0.2012
KLEEHEESLVGR	1426.6	2	3.8448	0.2456
KLEEIESLFDNR	1493.6	2	3.6716	0.1855
KLEEIIHQITNVEALIAR	2091.4	2	3.9887	0.2643
KLEEIPKYKDLLK	1618.0	2	3.5552	0.112
KLEEKEHLLQSNIGTGEKELGLR	2623.0	3	4.8427	0.4167
KLEELEKEEELR	1545.7	2	2.878	0.1687
KLEELELDEQQK	1502.6	2	3.7684	0.1407
KLEELELDEQQKK	1630.8	2	5.1527	0.2155
KLEELELDEQQR	1530.7	2	4.4981	0.2595
KLEELEQKYTYEHDPITK	2265.5	3	3.7791	0.3189
KLEENNHKTEA	1313.4	2	2.765	0.2553
KLEERGFDKAYVVLGQFLVLKKDEDLYR	3373.9	3	3.3423	0.1246
KLEEVVQILGDKFPCTLVAQK	2359.8	3	5.6805	0.5117
KLEGGQQVGMHSK	1399.6	3	3.6654	0.1864
KLEGNSPQGSNQGVK	1543.7	2	4.6492	0.3177
KLEHLITELVHQR	1616.9	2	5.4665	0.4237
KLEHVIK	867.1	2	3.012	0.1254
KLEISSGK	862.0	1	2.4076	0.1563
KLELDILPLQEANAELSEK	2154.4	3	5.0017	0.3996
KLELSDNIISGGLEVLAEK	2029.3	3	6.0964	0.4126
KLELSDNR	975.1	1	2.5465	0.2533
KLELSDNRVSGGLEVLAEK	2058.3	2	3.2723	0.1184
KLELSENR	989.1	2	2.5179	0.1442
KLEMDLKDLEAHIDSANK	2071.3	3	5.1801	0.3703
KLEMDLKDLEAHIDSANKNR	2341.6	3	3.6382	0.2493
KLEMDLKDLEAHIDSANKNRDEAIK	2898.2	3	4.407	0.2329
KLENEVEQR	1145.2	2	3.2503	0.1057
KLENSPLGEALR	1327.5	2	3.1801	0.2342
KLEPVVFEK	1089.3	2	2.6052	0.1406
KLEQCNTELKK	1334.6	2	3.1805	0.1717
KLERPPETPTVDPTVKYER	2256.5	3	5.1168	0.372
KLESTESR	950.0	1	2.5715	0.1863

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KLESVFFHSLSGSK	1566.8	2	3.1566	0.2486
KLETLSLNNNHLR	1552.8	2	4.163	0.4192
KLETTKKPDNVPK	1498.7	2	3.7136	0.2482
KLEVNEAELLR	1314.5	2	3.5758	0.2967
KLEWPLTEVAEGVFETEAPGGYK	2551.8	2	3.5572	0.3018
KLEWPLTEVAEGVFETEAPGGYKFYLQNR	3373.8	3	3.9748	0.3031
KLFDTLNEDLFQK	1611.8	2	4.681	0.3522
KLFEAEEQDLFKDIQSLPR	2307.6	3	5.3934	0.4294
KLFEELVR	1034.2	2	2.4633	0.1609
KLFGQESGPSAEK	1378.5	2	2.896	0.1753
KLFIGGLSFETTDDSLR	1900.1	2	3.9148	0.4046
KLFIGGLSFETTDDSLREHFEK	2570.8	3	5.342	0.401
KLFIGGLSFETTDESLR	1914.1	3	4.5044	0.11
KLFIGGLSFETTEESLR	1928.2	2	5.6026	0.3538
KLFIGGLSFETTEESLRNYYEQWGK	2997.3	3	3.4689	0.1553
KLFLVQLQEK	1246.5	2	3.0272	0.1625
KLFNESHGIFLGLQR	1760.0	2	2.6622	0.1747
KLFNLSKEDDVR	1464.6	2	3.6823	0.2188
KLFVGGIKEDTEEHHLR	2009.3	2	5.6546	0.3397
KLFVGGIKEDTEEHHLRDYFEEYGK	3041.3	3	6.0199	0.2553
KLFVGGIKEDTEEYNLR	2012.3	2	4.8186	0.3585
KLFVGGIKEDTEEYNLRDYFEK	2695.0	3	4.9383	0.2751
KLFVGGLKGDVAEGDLIEHFSQFGTVEK	3022.4	3	5.9355	0.3535
KLFVGMLGK	993.3	2	2.8307	0.1941
KLFYSTFATDDRK	1592.8	3	4.5866	0.425
KLFYSTFATDDRKEGMTAFVEK	2585.9	3	3.2748	0.1753
KLFYSTFATDDRKEGMTAFVEKR	2742.1	3	3.9651	0.2573
KLGDTYPSISNAR	1422.6	2	2.5833	0.2064
KLGDVSPTQIDVSQFGSFKEDTK	2527.8	3	4.8974	0.3827
KLGEMWNNLNDSEKQPYITK	2409.7	3	5.0708	0.3419
KLGEMWNNTAADDKQPYEK	2239.5	3	4.7341	0.3581
KLGEMWNNTAADDKQPYEKK	2367.6	3	3.9718	0.1587
KLGEMWSEQSAK	1394.6	2	2.6395	0.1986
KLGFSHFGNIR	1276.5	2	2.4679	0.2287
KLGGSLADSYLDEGFLLDKK	2170.4	2	5.9474	0.4811
KLGGSQEDQIK	1203.3	2	3.2413	0.1506

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KLGGSQEDQIKNAIDK	1744.9	3	3.4023	0.1334
KLGGSQEDQIKNAIDKLFVLFGAEILK	2976.5	3	3.4707	0.2228
KLGGSQEDQIKNAIDKLFVLFGAEILKKIPGR	3528.1	3	4.1066	0.2247
KLGIDDLVHFDFMDPPAPETLMR	2659.1	3	4.5657	0.193
KLGINSLQELK	1243.5	2	3.3733	0.2382
KLGIPATIVLPESTSLQVVQR	2250.7	2	4.7928	0.3883
KLGLVFDDVVGIVEIINSKDVK	2401.8	3	6.0551	0.4555
KLGMIAGGTGITPMLQLIR	1971.5	2	3.8217	0.3097
KLGNNCVFAPADVTSEKDVQTALALAK	2805.2	3	5.1448	0.3343
KLGPTEGRPQLK	1324.6	2	3.2904	0.1256
KLGSTASLPFIQEHR	1684.9	2	2.7462	0.25
KLHAVVETLVNHR	1516.8	2	2.9005	0.3202
KLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	4053.5	3	7.0689	0.5513
KLHELTVMQDR	1370.6	3	4.2926	0.3168
KLHELTVMQDRR	1526.8	2	2.9701	0.2567
KLHFEDEVTTSPVLGLK	1914.2	2	4.7152	0.4846
KLHGTAQQLLQDSK	1567.8	2	3.6571	0.2362
KLHKFELACLANLCPETAEESK	2475.9	2	3.3736	0.2762
KLHLLSRPQDGEAE	1593.8	2	2.8797	0.2693
KLHNILGVETGGPGGR	1605.8	2	4.1776	0.4
KLHPTDNFAQSSCFGLR	1922.2	2	3.6655	0.282
KLHVSTINLQK	1281.5	2	3.0017	0.135
KLHYNEGLNIK	1329.5	2	3.6906	0.259
KLIAEGPGETVLVAEEEAAR	2083.3	2	3.8871	0.4437
KLIDDYDSTK	1198.3	2	3.0748	0.2992
KLIGTAVPQR	1083.3	2	2.5148	0.2533
KLIHLEIKPAIR	1431.8	3	3.6987	0.2591
KLILDSAR	916.1	2	2.7511	0.1544
KLILSDELKPAHR	1520.8	2	3.6239	0.4173
KLINDYVK	993.2	2	2.8806	0.1182
KLIQDQQEQIQHLK	1750.0	3	4.3681	0.1677
KLISVDTEHSNIYLQNGPDR	2300.5	3	3.3079	0.1572
KLITSEEER	1105.2	2	3.2756	0.243
KLIVDSVKELDSK	1474.7	2	4.4069	0.4409
KLIVQPNTRLEGSDVQLLEYEASAAGLIR	3185.6	3	6.6514	0.3847
KLIYFQLHR	1218.5	3	3.439	0.186

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KLKDVLLQVDDER	1571.8	2	4.5917	0.392
KLKDVLLQVDDERR	1728.0	2	3.6872	0.271
KLKDYAFIHFDER	1682.9	2	3.0118	0.1467
KLKDYAFVHFEDR	1668.9	2	4.237	0.3835
KLKEDKAPQVDVDK	1613.8	2	4.2812	0.3434
KLKEDKAPQVDVDKAVAELK	2225.6	3	6.1877	0.4049
KLKELEVAEGGK	1301.5	2	3.7384	0.1847
KLKELEVAEGGKAELER	1900.2	2	5.8587	0.3902
KLKFPEPQEVVEELKK	1942.3	3	3.9679	0.1262
KLKGTEDELDKYSEALKDAQEK	2539.8	3	3.8144	0.1746
KLKGTEDELDKYSEALKDAQEKLELAEK	3223.6	3	6.8991	0.4607
KLKTEQGGAHFSVSSLAEGSVTSVGSVNPAENFR	3492.8	3	5.6342	0.4371
KLKVEAPQALR	1253.5	2	2.8411	0.2106
KLLAAGQLADALSQFHAAVDGDPDNYIAYYR	3368.7	3	4.0945	0.2806
KLLADQAEAR	1115.3	2	3.3419	0.2722
KLLAQPEKEK	1184.4	2	3.18	0.1298
KLLASLVKR	1028.3	2	2.7159	0.1227
KLLDIVAR	928.2	2	2.6535	0.1433
KLLDLVQQSCNYK	1552.8	2	2.7092	0.1302
KLLEAHEEQNVDSYTESVKEYDSISR	3071.3	3	5.7419	0.4331
KLLEAQSHFR	1229.4	2	3.3108	0.2037
KLLEDRIAEFTTNLTEEEEKSKSLAK	3024.4	3	3.3612	0.1869
KLLEGEEER	1103.2	2	3.231	0.1539
KLLEGEEERLK	1344.5	2	3.0848	0.1115
KLLEGEEERLR	1372.6	2	3.3931	0.1945
KLLEGEESRISLPLPNFSSLNLR	2614.0	3	4.3793	0.2831
KLLEGEESRLESGMQNMSIHTK	2518.9	3	4.937	0.4601
KLLELDPEHQR	1378.6	2	3.3029	0.2094
KLLERLPEVEVPQHL	1801.1	2	4.3623	0.2222
KLLHSFHSELPVLSDSER	2095.3	2	5.1036	0.4563
KLLIIGTTSR	1102.4	2	2.801	0.1721
KLLISDTQHYGVTVPHTTR	2167.5	3	5.2363	0.4039
KLLPDDPYEK	1218.4	2	2.9334	0.1508
KLLSESAQPLKK	1342.6	2	2.9503	0.1906
KLLSKEPSPPIDEVINTPR	2134.5	2	3.853	0.3706
KLLSSSETKR	1149.3	2	2.9093	0.2002

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KLLTEEGQKIGTFER	1750.0	2	3.2391	0.2124
KLLVDAIHNQLTDMEK	1869.2	2	3.2196	0.1678
KLLVGSEDYGR	1237.4	2	3.0376	0.2538
KLMDLSHR	1000.2	2	2.4786	0.1694
KLMEECKR	1037.3	2	2.4017	0.1809
KLMHQAALLGQALQDSR	1881.2	2	5.6902	0.4931
KLMQLQHEK	1155.4	2	2.8995	0.1165
KLMQLQHEKAELEQHLEQEQEFQVNK	3236.6	3	3.5254	0.1381
KLMSDPDSSIIDFYPEDFAIDLNGKK	2960.3	3	4.9449	0.37
KLMVALAK	874.2	2	2.931	0.2333
KLNAFGNAFLNR	1365.6	2	3.0516	0.206
KLNEILQAR	1085.3	2	2.9931	0.1187
KLNELESDLTFK	1437.6	2	2.5838	0.1377
KLNEQSPTR	1073.2	2	2.5524	0.1104
KLNFNGEGEPEELMVDNWRPAQPLK	2913.3	3	5.1285	0.3361
KLNFQVELLLDKLK	1702.1	2	3.6125	0.2092
KLNGLYPFR	1108.3	2	2.7787	0.2507
KLNHQEVVEEDKR	1624.8	2	3.7502	0.2085
KLNKEELPVIPK	1408.7	2	4.1165	0.2109
KLNMDQVLDQILR	1586.9	2	3.7421	0.2722
KLNQALLDLHALGSAR	1721.0	2	5.9971	0.5175
KLNQQAEELQEIHEIQLQEK	2449.7	3	5.0641	0.3336
KLNSPEETAFQTPK	1590.8	2	3.7087	0.2406
KLNTLVQISVIHPVEQSLTR	2276.7	3	3.6922	0.2443
KLNVNAKPFVPNVHAAEFVPSFLR	2696.1	3	5.1311	0.4734
KLNVSSDTVQHGVEGLTYLLTESSK	2707.0	3	5.6006	0.4138
KLNVTEQEK	1089.2	1	2.9767	0.1836
KLNVTEQEKIDK	1445.6	2	4.4845	0.28
KLNVTEQEKIDKLMIEMDGTENK	2708.1	3	6.6302	0.488
KLNVTEQEKIDKLMIEMDGTENKSK	2923.4	3	5.2148	0.4048
KLPDSFFKPPEPK	1530.8	2	3.5278	0.1709
KLPEEEAECYFHSRPK	1964.2	3	3.2659	0.2176
KLPEELGRDQNTVETLQR	2127.3	2	3.6956	0.2268
KLPFAEGLYHFYHNGLAK	2106.4	2	5.214	0.4331
KLPIDVTEGEVISLGLPFGK	2113.5	2	5.6649	0.5055
KLPIQEFHLSR	1368.6	2	3.5556	0.2827

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KLPKNEPQNATGAPGR	1678.9	2	3.5587	0.2296
KLPKNEPQNPGANSAR	1721.9	2	3.5046	0.3504
KLPLTALAQNMQEASTQLEDSLLGK	2701.1	3	5.6635	0.472
KLPPLPSLTSQPHQVLASEPIPFSDLQQVSR	3411.9	3	6.1401	0.4729
KLPSVEGLHAIVVSDR	1721.0	2	4.4166	0.487
KLPSVEGLHAIVVSDRDGVPVIK	2429.8	3	4.8507	0.4545
KLPVESIQIVLEELRK	1895.3	2	4.5063	0.3388
KLQAALEQALER	1370.6	2	3.2198	0.1506
KLQAALISR	1000.2	2	2.4538	0.1447
KLQEQEVFFK	1296.5	2	3.6257	0.2753
KLQEQLEKAEDGSSSK	1777.9	2	5.2167	0.3475
KLQEQLEKAEDGSSSKEGTSV	2251.4	2	6.1206	0.4698
KLQESTQTVQSLHGSSR	1887.0	2	5.4886	0.5348
KLQETQMSTTSKLEEAEHKVQSLQTALEK	3317.7	3	4.318	0.2067
KLQGEVEKYQQLQK	1720.0	2	4.5302	0.3327
KLQGGTPQEPPNPR	1519.7	2	4.1206	0.2223
KLQHDVLK	981.2	2	2.4347	0.1929
KLQIQCVVEDDKVGTDMLEEQITAFEDYVQSMDVAAFNKI	4566.1	3	7.5388	0.543
KLQIVQQEQQLHASNRPALAAK	2472.8	3	3.8379	0.1825
KLQKDLEGLSQR	1415.6	2	3.1366	0.168
KLQKDLEGLSQRHEEK	1939.2	2	4.1411	0.2551
KLQLSGHAMPR	1238.5	2	3.3192	0.2771
KLQNQLQGAIVIERPNVK	2049.4	3	3.852	0.2578
KLQQELEFLEVQEEYIKDEQK	2667.9	3	4.2258	0.3435
KLQQENLKPQEQLTLEPYER	2485.8	3	4.3908	0.3374
KLQQGIPPSGPAGELKFEPHI	2244.6	3	4.8029	0.4369
KLQSNPSLEGVSHVIVDEVHER	2473.7	3	4.2478	0.2639
KLRESXESQLESGMQNMSIHTK	2547.9	2	3.2169	0.2695
KLRETAEADVASLNR	1673.9	3	3.9954	0.2714
KLRETAEADVASLNRR	1830.0	2	3.8672	0.2985
KLSDDNTIGKEEIQQR	1875.0	2	4.6092	0.153
KLSEADNR	933.0	1	2.6046	0.1894
KLSELERPHK	1237.4	2	2.9879	0.1521
KLSELSNSQQSVQTLSLWLIHHR	2706.1	3	4.8908	0.4399
KLSFDFQ	885.0	2	2.745	0.1765
KLSGLNAFDIAEELVK	1748.0	2	3.543	0.3496

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KLSKPSQVSSGQK	1374.6	2	3.2783	0.299
KLSLQERPAGSYLEAQAGPYATGPASHISPR	3254.6	3	6.6438	0.3881
KLSLTLHPDKNKDENAETQFR	2485.7	3	4.9763	0.3319
KLSMYGVDLHHAK	1499.8	2	3.5051	0.2836
KLSQMILDKK	1204.5	3	3.2881	0.124
KLSQRPTVAELLAR	1582.9	2	2.44	0.1148
KLSSAMSAAK	994.2	1	2.5108	0.1588
KLSSWDQAETPGHTPSLR	2011.2	3	3.4682	0.1816
KLSSWVLLMK	1205.5	2	2.6526	0.1487
KLSTIALALGVER	1371.7	2	2.519	0.3134
KLSYAEVCQKPPKEPSSVLVQPLR	2698.2	3	4.0638	0.332
KLTATPTPLGGMTGFHMQTEDR	2390.7	3	4.7841	0.4421
KLTDIINNDHENVK	1653.8	2	4.6437	0.3564
KLTDTSKDEENHEESESLQEDMLGNR	3036.1	3	5.426	0.3568
KLTEIINTQHENVK	1667.9	2	5.582	0.4059
KLTELSMQDEELMKR	1852.2	2	4.9144	0.4242
KLTFLYLANDVIQNSK	1868.2	2	5.4056	0.4185
KLTGIKHELQANCYEEVK	2104.4	2	4.9122	0.3346
KLTGIKHELQANCYEEVKDR	2375.7	3	6.5933	0.4456
KLTGKDVNFEFPEFQL	1913.2	2	4.037	0.2162
KLTGMER	835.0	1	2.2133	0.1651
KLTLLPAVVMHLK	1463.9	2	2.9109	0.1692
KLTPITYPQGLAMAK	1633.0	2	3.4884	0.1045
KLVAIVDPHIK	1233.5	2	4.5402	0.3183
KLVAIVDPHIKVDSGYR	1911.2	2	2.8889	0.2576
KLVEALCAAGHR	1268.5	2	3.7665	0.3062
KLVEGLSALVVDVK	1470.8	2	4.7484	0.4016
KLVESLPQEIK	1284.5	2	3.7375	0.1554
KLVESLPQEIKANVAK	1768.1	2	2.4398	0.1517
KLVGYLDR	964.1	2	3.0332	0.2486
KLVHDKELAAEDEQVFLMK	2244.6	2	4.481	0.3752
KLVIIEGDLER	1285.5	2	4.1287	0.2668
KLVIIEGDLERTEER	1801.0	2	3.9475	0.3748
KLVIIEGDLERTEERAELAESR	2557.8	2	3.87	0.3396
KLVIIESDLER	1315.5	2	3.9787	0.2713
KLVIIESDLERAEER	1801.0	3	3.6294	0.2499

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KLVIIESDLERAEERAELSEGQVR	2771.1	3	4.2808	0.3103
KLVILEGELER	1299.5	2	3.926	0.2208
KLVILEGELERAEER	1785.0	2	3.7716	0.3242
KLVILEGELERAEERAEVSELK	2541.9	3	4.9499	0.3405
KLVINSGNGAVEDR	1472.6	2	3.8061	0.1668
KLVINSGNGAVEDRKPSGLNGEASK	2541.8	3	4.199	0.3275
KLVIPSELGYGER	1461.7	3	3.9968	0.2321
KLVNSVAGCADDALAGLVACNPNLQLLQGHR	3162.6	3	5.2457	0.3878
KLVPLLLEDGGEAPAALEAALEEK	2477.8	3	5.7862	0.5206
KLVPLLLEDGGEAPAALEAALEEKSALEQMR	3293.8	3	6.4409	0.4482
KLVPLLLEDGGEAPAALEAALEEKSALEQMRK	3422.0	3	6.8424	0.4917
KLVSIVADQLEK	1343.6	2	2.6333	0.2643
KLVSQEEMEFIQR	1637.9	2	3.9871	0.3764
KLVTDQNISENWR	1603.8	2	3.9291	0.335
KLVWVPSDK	1072.3	2	2.9004	0.1477
KLYHSEAFTVNFGDTEEAKK	2315.5	3	6.2626	0.4565
KLYLQDNHINR	1414.6	2	2.8829	0.2314
KLYSIAAPAR	1090.3	2	2.554	0.2324
KLYSIILSAPIPEPK	1670.0	2	3.2293	0.2875
KMADLHAVPR	1138.4	2	3.5571	0.3964
KMAVDALEYDESAEDANPAGALEEILENPER	3391.6	3	3.9775	0.1529
KMDADGFLPITLIASFHR	2033.4	3	4.6209	0.3656
KMDAHPPR	952.1	1	1.7722	0.1575
KMDETDASSAVK	1282.4	2	3.7378	0.305
KMDEYVASLHLPSFDAHLTELTDDQAK	3076.4	3	6.0539	0.492
KMDEYVASLHLPTFDAHLTELTDEQAK	3104.4	3	5.8226	0.2647
KMDLIDLEDETIDAEVMNSLAVTMDDFR	3231.6	3	4.9286	0.4525
KMEDSVGCLETAEEVKR	1925.2	2	4.2738	0.3004
KMEEVKEANIR	1347.6	2	3.6716	0.2127
KMEGVTNAVLHEVKR	1712.0	3	4.27	0.429
KMEIDLKDLEAQIEAANK	2060.4	2	6.0108	0.3365
KMEIDLKDLEAQIEAANKARDEVIK	2872.3	3	3.2571	0.1566
KMFESFIESVPLLK	1669.0	2	4.045	0.4012
KMGAPESGLAEYLFDKHTLGDSDNES	2813.0	3	4.7845	0.4139
KMGDHLTNLHR	1322.5	2	3.1761	0.3416
KMGEDMHTIGFGIYEVPEELSGQTNIHLSK	3362.8	3	6.8747	0.3986

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KMGLVDQLVEPLGPGLKPPEER	2403.8	2	7.4462	0.5133
KMIQHAVFK	1102.4	2	2.693	0.1976
KMKPLDGSALYTGSALDFVR	2170.5	3	4.4294	0.3927
KMLKPAFIFDGR	1423.8	2	3.6999	0.2602
KMLLQNYLQNR	1421.7	2	2.8097	0.2004
KMMADEALGSGLVSR	1565.8	2	5.0897	0.368
KMMTGGFFHK	1184.5	2	2.5167	0.1081
KMMTKEELEEEQRTEE	2041.2	3	3.9987	0.191
KMMTKEELEEEQRVQKEQLAAIFK	2938.4	3	4.1012	0.3114
KMNALFEGR	1066.3	2	2.7086	0.2768
KMNDSNSAGAGGPVK	1433.6	2	4.081	0.2819
KMNLGVGAYR	1109.3	2	2.7551	0.2589
KMNLGVGAYRDDNGKPYVLPSVR	2550.9	3	6.0314	0.338
KMNVSPDVNYEELAR	1766.0	2	4.874	0.3596
KMQAHIQDLEEQLDEEEGAR	2370.5	3	5.1251	0.2781
KMQELLQTQDFSK	1596.8	2	4.9127	0.3017
KMQQENMKPQEQLTLEPYER	2521.9	3	4.5939	0.2446
KMQQNIQELEEQLEEEESAR	2462.6	3	5.7403	0.4008
KMSLGQLQSAR	1219.4	2	2.5202	0.1881
KMTFSEHPYNNLR	1637.8	2	2.5517	0.2231
KMTPSYEIR	1125.3	2	2.6625	0.1994
KMVKDQQEAEK	1334.5	2	3.8003	0.1351
KMYESFIESLPFLK	1733.1	2	4.2573	0.2882
KNAALDVEPIHAFR	1581.8	2	2.9637	0.2634
KNAGSLLTR	960.1	2	2.7251	0.2638
KNANKPLLDEIVPVYR	1870.2	3	4.3526	0.433
KNDKEAAGEGPALYEDPPDQK	2273.4	2	4.7884	0.3999
KNEESQEIQK	1233.3	2	2.9848	0.1211
KNELETENR	1133.2	2	2.9215	0.2151
KNELLHLGGR	1137.3	2	2.9107	0.2091
KNFATSLYSMIK	1403.7	2	4.1773	0.283
KNFESLSEAFSVASAAAVLSHNR	2436.7	3	7.2135	0.5541
KNGGLGHMNIALLSDLTK	1883.2	3	5.1333	0.4411
KNGPLEVAGAAVSAGHGLPAK	1945.2	2	4.449	0.4666
KNGQHVASSPIPVVISQSEIGDASR	2577.8	3	5.2452	0.3856
KNHEEEISTLR	1356.5	2	3.728	0.2529

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KNHEEEVK	1013.1	2	2.6709	0.1894
KNHEEEVKGLQAQIASSGLTVEVDAPK	2879.2	3	6.8115	0.5292
KNHEEEVKGLQAQIASSGLTVEVDAPKSQDLAK	3521.9	3	5.7782	0.4578
KNIILEEGKEILVGDVGQTVDDPYATFVK	3192.6	3	6.2098	0.4993
KNILDSKPTANK	1329.5	2	2.6519	0.2211
KNIPEGSHQYELLK	1656.9	2	3.8389	0.2728
KNIQATLHQK	1181.4	2	3.0069	0.1198
KNKDKYVGVSSDSVGGFR	1944.1	2	4.892	0.4635
KNKEEAAEYAK	1281.4	2	3.5173	0.1778
KNKGGVAVKAHQVK	1464.7	2	2.5737	0.1126
KNLEAQHKELEEK	1596.8	2	4.3341	0.2748
KNLHGDGIALWYTR	1644.9	2	2.6329	0.2969
KNLLLEPSLEAK	1355.6	2	2.8021	0.1215
KNLNYLHLDYNFNLKPVK	2234.6	3	3.4017	0.1927
KNLVELAELELK	1399.7	2	2.5256	0.1114
KNNIDTHAR	1069.2	2	3.0565	0.2193
KNNRQPYAVSELAGHQTSAESWGTGR	2846.0	3	5.4678	0.3647
KNPAAYENDK	1150.2	2	2.8621	0.2811
KNPDSQYGELIEK	1521.7	2	4.4209	0.4042
KNPDSQYGELIEKYIKEGK	2240.5	3	4.133	0.3188
KNPEVPVNFAEFSK	1606.8	2	4.3243	0.3382
KNPEVPVNFAEFSKK	1735.0	3	4.8914	0.3859
KNPFGLVPVLENSQGQLIYESAITCEYLDEAYPGKK	4016.5	3	4.5583	0.4491
KNPGVGNGDDEAAELMQQVNVLK	2427.7	2	5.9226	0.5316
KNPLPPSVGVVDKK	1478.8	3	4.0587	0.338
KNPLPPSVGVVDKKEETQPPVALKK	2700.2	3	3.5776	0.2141
KNPQAVLDVLEFYNSK	1866.1	2	3.0613	0.1894
KNPSIAVPIVLKR	1435.8	3	3.4449	0.2381
KNPVKFEGGDRDLEHLSK	2070.3	3	3.5643	0.2827
KNQGVPQIAVLVTHR	1660.9	2	2.7209	0.1043
KNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGK	3711.2	3	4.1087	0.2181
KNQLLLEFSFWNEPVPR	2118.4	2	3.3405	0.1613
KNREELDKYWSQQIEESTTVVTTQSAEVGAAETTLTELRR	4600.0	3	4.2193	0.3342
KNSLISSLEEEVSILNR	1932.2	3	4.329	0.3478
KNSVVEASEAAYK	1396.5	2	3.9027	0.4203
KNSVVEASEAAYKEAFEISK	2201.4	2	6.0044	0.4706

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KNTHENIQLSQSK	1527.7	2	4.3863	0.3372
KNTQVVSDAAYK	1324.5	2	3.8177	0.4001
KNVFIIGATNRPDIIDPAILRPGR	2648.1	3	4.5487	0.3114
KNVLGHMQQGGAPSPFDR	1940.2	2	5.1797	0.4872
KNVLGHMQQGGAPSPFDRNFGTK	2487.8	3	5.2762	0.3343
KNVLGHMQQGGSPTPFDR	1970.2	2	5.0132	0.4786
KNYGVTFPIFHK	1451.7	2	3.9005	0.3836
KNYNWAITR	1166.3	2	2.63	0.2534
KNYVEDIPFLSPTFNPQEVFIR	2655.0	3	4.0568	0.1649
KPAAAAAPGTAEK	1183.3	2	3.6774	0.3114
KPAAAAGAK	784.9	1	3.1634	0.1676
KPAAATVTK	887.1	1	2.6714	0.3109
KPAAATVTKK	1015.2	2	3.4365	0.3151
KPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPR	3273.8	3	5.6232	0.4219
KPAAVLKPSDWEK	1469.7	2	3.973	0.4084
KPADLQNLAPGTHPPFITFNSEVK	2623.0	3	3.2268	0.1424
KPAEDEWGKTPDAMK	1703.9	3	4.6148	0.3605
KPALGFYDTSEENYQALDADFRK	2679.9	3	5.142	0.4003
KPALTAIEGTAHGEPCHFPFLFLDKEYDECTSDGR	3897.3	3	3.3658	0.1885
KPALVAK	726.9	1	2.106	0.1392
KPANDITSQLEINFGDLGR	2089.3	2	4.1173	0.4757
KPATAAGTKK	973.2	2	3.0315	0.3527
KPATSYVR	922.1	1	2.0458	0.2541
KPDPNIKNNAASEGVLASFFNSLLSK	2763.1	3	4.5785	0.3951
KPDQHFKPYLK	1401.6	2	3.6858	0.1616
KPDSMVTNSSTENEA	1610.7	2	4.4824	0.3421
KPDTIEVQQMK	1317.5	2	3.7808	0.2735
KPEASHSFENR	1302.4	2	3.0688	0.2618
KPEDWDEEMDGEWEPPVIQNPEYK	2962.1	3	4.6052	0.3839
KPEDWDERPK	1300.4	2	3.5983	0.2412
KPEEDSSSNQSPAATK	1676.7	2	4.759	0.434
KPEEDSSSNQSPAATKGPGPLGPGAPPPLLFLNK	3400.8	3	5.7796	0.4013
KPEEESPRKDDAK	1529.6	2	2.785	0.1417
KPEENPASK	1000.1	2	2.7807	0.1353
KPEHELFLVYGK	1460.7	2	3.4096	0.266
KPESNAVTK	974.1	2	2.8198	0.227

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KPFNRPQGVQPK	1396.6	2	2.9149	0.1098
KPFPDFVYK	1141.3	2	2.7271	0.1875
KPFPDFVYKR	1297.5	3	3.998	0.3813
KPFPINHGETSDETLLEDAIEVCK	2687.0	3	4.6242	0.3859
KPFPINHGETSDETLLEDAIEVCKK	2815.1	3	4.3666	0.2332
KPFPLVKPLPGEEPLFTIPHTQEAFR	2990.5	3	5.6986	0.4021
KPFSEDVNWGYEK	1599.7	2	3.1057	0.2253
KPFSIEDVEVAPPK	1556.8	2	2.8395	0.1669
KPFSIEDVEVAPPKAYEVR	2175.5	3	3.2853	0.1101
KPFSIEEVEVAPPKAHEVR	2163.5	3	5.2982	0.4548
KPGGEREER	1058.1	2	2.6454	0.178
KPGGFDISLFYR	1400.6	2	2.8753	0.2347
KPGGFDLSLFYR	1400.6	2	3.3931	0.3449
KPGINVASDWSIHLR	1693.9	3	4.0319	0.3024
KPGMFFNPEESELDLTYGNR	2345.6	3	3.8155	0.1919
KPGQSFQEQVEHYR	1733.9	3	4.7191	0.434
KPGSVVAAAAAEAK	1270.5	2	3.3294	0.2687
KPGVIDKFTSDTKPIINK	2002.3	3	4.8923	0.4045
KPGYHAPVALLNDIPQSTEQYDPFAEHRPPK	3517.9	3	6.0383	0.4111
KPHIIIATPGR	1203.5	2	2.745	0.2136
KPHIYYGSLEEK	1464.6	2	2.8279	0.2202
KPHTESLELQVR	1437.6	3	4.2919	0.3979
KPHVVTVAGENR	1307.5	2	2.8239	0.3124
KPIDYTILDDIGHGVK	1785.0	3	4.3865	0.3959
KPIDYTVLDDVGHGVK	1757.0	2	4.9709	0.4977
KPIEDPANDTVDFPKR	1843.0	3	4.3798	0.4408
KPIPDEHLILK	1303.6	2	3.5021	0.2733
KPISTHTVDFTFNK	1635.8	2	4.0139	0.3174
KPITDDDVDR	1174.2	2	3.3436	0.3288
KPKEDEVEASEK	1389.5	2	2.9152	0.1619
KPKPNPNLLFSDVYQEMPAQLR	2587.0	3	4.5655	0.4549
KPKPNPNLLFSDVYQEMPAQLRK	2715.2	3	6.0814	0.5087
KPLEALYGYDYFAR	1706.9	2	2.9708	0.2227
KPLKPCCACPETK	1418.8	2	2.6949	0.118
KPLLEMNDPELLKETTEAR	2228.6	3	3.7372	0.2371
KPLLPYTPGSDVAGVIEAVGDNASAFK	2718.1	2	4.8295	0.5062

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KPLLPYTPGSDVAGVIEAVGDNASAFKK	2846.2	3	5.7507	0.4655
KPLLPYTPGSDVAGVIEAVGDNASAFKKGDR	3174.6	3	3.5626	0.2183
KPLPDHVSIVEPK	1459.7	3	4.3939	0.3441
KPLTSSSAAPQRPISTQR	1926.2	2	4.3971	0.4482
KPLVIIAEDVDGEALSTLVLNR	2366.7	2	7.0155	0.5657
KPLVLCGDLNVAHEEIDLR	2135.5	3	4.3063	0.257
KPLVLCGDLNVAHEEIDLRNPK	2474.9	3	4.6195	0.3488
KPMSLASGLVPAAPPK	1564.9	2	2.5291	0.1834
KPMVLGHEASGTVEK	1583.8	2	4.2406	0.399
KPMVVLGSSALQR	1386.7	2	3.5648	0.2703
KPNEGADGQWK	1230.3	2	3.458	0.2105
KPNIINFDTSLPTSHTYLGADMEEFHGR	3192.5	3	5.1519	0.4103
KPNTVSTSHSGSFAPNNPDLAK	2270.4	3	4.226	0.3733
KPNVAEAGEQFGQLGR	1701.9	2	2.9068	0.1503
KPPARPSAAAAAIAVAAAEEER	2148.4	3	3.631	0.1814
KPPLAQKPSVAPR	1389.7	2	3.4033	0.4336
KPPLLNNADSVQAK	1495.7	2	4.8032	0.3855
KPPMDEKSLEEAR	1530.7	2	3.5242	0.3194
KPPMDEKSLEESR	1546.7	2	3.6796	0.2102
KPPMLQPLALPPGLSVHQALER	2393.9	3	3.9511	0.1908
KPPPSKEELLK	1266.5	2	2.9133	0.1541
KPPPSKEELLKLTETVVTEYLNSGNANEAVNGVR	3699.1	3	3.2655	0.2417
KPPPSPQPTEEDPEHR	1842.0	3	3.4683	0.2067
KPPPVPALPSKLPTFGAPEQLVDLK	2641.1	3	4.0907	0.275
KPPRPGAPGHLGSLASLSSPADSYNEGVK	2891.2	3	4.9883	0.2876
KPPTDEELKETIKK	1656.9	2	2.9944	0.2611
KPPTFGDASVIALELLNSGYEFDEGSIIFNK	3373.8	3	3.3289	0.2113
KPPTGPLPPSKEPLKEK	1844.2	3	3.2558	0.3061
KPQAEKVDVIAGSSK	1557.8	2	3.6932	0.4231
KPQSSSTEPAR	1188.3	2	2.8543	0.1508
KPRPPPALGPEETSASAGLPK	2101.4	3	5.7464	0.4355
KPSDGSPDTKPSR	1372.5	2	4.0652	0.3312
KPSGLNGEASK	1088.2	2	3.1122	0.248
KPSHTSAVSIAGK	1283.5	2	3.8983	0.2818
KPSISITTESLK	1304.5	2	3.3468	0.1898
KPTAIKTEGKPAEVK	1597.9	2	4.4678	0.3259

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KPTFMDEEVQSILTK	1767.0	2	2.5812	0.2124
KPTLDKPSPETFVK	1587.8	2	3.8079	0.2857
KPTSAKPSSTTPR	1358.5	2	3.6627	0.3329
KPTTEEKKPAA	1200.4	2	3.0282	0.231
KPTVTLTYGSSRPSIEIYRPPASR	2678.0	3	3.748	0.1759
KPVAGALDVSFNK	1346.6	2	4.7574	0.3396
KPVEELTEEEKYVR	1749.9	2	4.3487	0.3925
KPVIAAVNGYAFGGGCELAMMCDIIYAGEK	3093.7	3	5.3373	0.3421
KPVIVFVPSR	1142.4	2	2.5072	0.2151
KPVIVFVPSRK	1270.6	2	3.0581	0.2665
KPVSRPATAAAAAAGSR	1582.8	2	2.6238	0.292
KPVTVHSR	924.1	2	2.4967	0.2345
KPVTVSPTTPTSPTEGEAS	1887.0	2	4.9027	0.4946
KPWLAYPHYKPPEK	1755.1	3	4.0491	0.2975
KPYPDDENLVEVK	1546.7	2	4.3801	0.3391
KPYTMDPDHR	1260.4	2	2.4252	0.1728
KQAESASEAAK	1120.2	2	2.926	0.2613
KQAESASEAAKK	1248.4	2	2.9505	0.2687
KQAGPASVPLRTEEEFKK	2016.3	3	4.6495	0.3756
KQALAEHEDELPEHFKPSQLIK	2588.9	3	5.9472	0.3116
KQALQDTLALYK	1392.6	2	2.5911	0.1236
KQAQILASEAEKAEQINQAAGEASAVLAK	2969.3	3	6.9248	0.5617
KQASAIKKEELVAR	1571.8	3	4.0082	0.2988
KQCVDHYNEVK	1363.5	2	2.9329	0.102
KQDAFYKEQLAR	1497.7	2	4.2298	0.2971
KQDASEKDSVPMGSPAFLLSLFDGGTR	2855.2	3	3.6098	0.2444
KQDEPIDLFMIEIMEMK	2111.5	2	3.2145	0.1716
KQDEWIKFDDDKVSIVTPEDILR	2791.1	3	4.8527	0.3664
KQDFDEDDILKELEELSLEAQGIK	2807.1	3	4.7377	0.1907
KQDFPLVK	975.2	2	2.5572	0.1132
KQDGFTHILLSTK	1488.7	2	2.5665	0.1856
KQDIENILHWNVTQHK	2004.2	2	5.0686	0.3209
KQDIGDILQQIMTITDQSLDEAQAR	2832.1	3	4.0915	0.2896
KQEDFMTTMDANEEKINAVVETGR	2758.0	3	3.3135	0.1719
KQEEELTKR	1161.3	2	2.7327	0.1119
KQEELQQLEQQR	1557.7	2	3.2618	0.1574

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KQEEQMETEQQNKDEGKKPEVK	2661.9	3	4.6973	0.2345
KQEESVQKQEAMR	1591.8	2	3.5743	0.2252
KQEIEKPVAVSELFTTLPIVQGK	2556.0	3	4.1454	0.321
KQEIIKTTEQLIEAVNNGDFEAYAK	2854.2	3	5.0594	0.2637
KQEIIKVTEQLIEAINNGDFEAYTK	2896.2	3	4.1708	0.3261
KQELEEICHDLEAR	1713.9	2	4.8596	0.2976
KQELEEICHDLEARVEEEEERCQHLQAEK	3552.9	3	3.8144	0.1498
KQELEEILHDLESR	1739.9	3	5.4013	0.3826
KQELEEILHDLESRVEEEEERNQILQNEK	3608.9	3	4.0847	0.1783
KQELELVVSELEAR	1643.9	3	4.9507	0.3757
KQELLEALTK	1173.4	2	2.7329	0.1736
KQELLEALTKHFQD	1700.9	3	4.2478	0.3584
KQELQPGTAYK	1263.4	2	3.5266	0.1582
KQEQANNPFYIK	1480.6	2	3.0325	0.1174
KQEQLETAR	1103.2	2	2.627	0.1111
KQEVQAWDGEVR	1445.6	2	3.6826	0.1857
KQEWTAIIPNSQLIVIPYPHNVPR	2815.3	3	6.1068	0.3493
KQEYLEVQR	1193.3	2	2.5265	0.1145
KQFEAPTLAEGFSAILEIPFR	2365.7	2	2.824	0.1393
KQFGAQANVIGPWIQTK	1887.2	2	4.3271	0.2971
KQFGHPQIEAR	1311.5	2	2.5316	0.3231
KQGDGGKDLPTEAKK	1572.7	2	2.8849	0.2445
KQGDHYILNGSK	1360.5	2	3.0574	0.1306
KQGEDNSTAQDTEELEKEIREDLPVNTSK	3305.5	3	4.612	0.1827
KQGEVSKAASADSTTEGTPADGFTVLSTK	2885.1	3	6.5418	0.4449
KQGGLGPMNIPLVSDPK	1752.1	2	3.6729	0.3217
KQGGLGPMNIPLVSDPKR	1908.3	3	5.6698	0.4881
KQGKQEAADAALR	1386.5	2	3.2234	0.2266
KQHLEIELK	1138.3	2	2.4952	0.115
KQHPYTFPGGSGTVFAR	1851.1	3	3.5983	0.166
KQHYVLAGASGSPGEEVAIRPSTAPR	2680.0	3	5.1655	0.3861
KQIEELKGQEVSPK	1613.8	2	5.5968	0.3402
KQIQFADDMQEFTK	1729.9	2	4.7274	0.3591
KQIQFADDMQEFTKFPTK	2203.5	3	4.8252	0.403
KQITMEELVR	1247.5	2	2.8767	0.1313
KQIVAGVNYFLDVELGR	1922.2	2	2.618	0.1573

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KQKPQEVPQENGMEDPSISFSKPK	2730.0	3	4.5721	0.3043
KQKPVLEEQVIKESDASKIPGK	2452.8	3	3.5616	0.2661
KQKTEDEVLTSK	1406.6	2	3.3245	0.2384
KQKVEGTEPTTAFNLFVGNLNFNK	2698.0	3	6.0673	0.526
KQLADETLLK	1159.4	2	2.8472	0.1748
KQLADETLLKVDLENR	1886.1	3	4.49	0.3224
KQLIEPVQYDEQGMAFSK	2112.4	3	4.0202	0.2692
KQLKLMEDMDTVIKPRPQVVK	2498.0	2	2.4596	0.1646
KQLLHLAEEK	1209.4	2	2.9059	0.1724
KQLQAIEFNK	1219.4	2	2.7432	0.1155
KQLQDEMLR	1161.4	2	3.0995	0.2032
KQMADTGKLNTLLQR	1718.0	2	3.8784	0.322
KQMVIDVLHPGK	1365.7	3	4.4898	0.3653
KQNAPMTLEEFRK	1592.8	3	4.0625	0.2276
KQNDVFGEAEQ	1265.3	2	3.5498	0.2775
KQNMILSDEAIK	1390.6	2	3.7717	0.2691
KQNNFSLAMK	1181.4	2	2.9643	0.1421
KQNVDQALLNGLELLK	1797.1	2	2.7545	0.2302
KQNVVPTVLALGSDVDMDVLTTLSLGDR	2958.4	3	5.2658	0.5068
KQPALDVLYDVMK	1520.8	2	2.8195	0.2966
KQPPKEPSEVPTPK	1562.8	3	3.4899	0.3029
KQPPVSPGTALVGSQK	1594.8	2	3.2254	0.4099
KQPPVSPGTALVGSQKEPSEVPTPK	2559.9	3	4.5916	0.3926
KQQDVLGFLEANK	1490.7	2	4.1654	0.2189
KQQHNLSAFPK	1298.5	2	2.606	0.1146
KQQISLATQMVR	1403.7	2	2.9968	0.1009
KQQMAEEMVEAAGEDERELAAEMAAAFLNENLPESIFGAPK	4468.0	3	6.0448	0.3651
KQQNQELQEQLR	1542.7	2	4.3429	0.1876
KQQSIAGSADSKPIDVSR	1888.1	2	4.8712	0.4717
KQQTLEAEEAK	1275.4	2	3.6822	0.2335
KQQTTVPQKPR	1311.5	2	2.9355	0.1822
KQSEGLTKEYDR	1454.6	2	3.5083	0.3167
KQSEGLTKEYDRLLEEHAK	2275.5	2	4.4948	0.3835
KQSKPVTTPEEIAQVATISANGDKEIGNIISDAMK	3686.1	3	6.8223	0.489
KQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKK	3814.3	3	3.8826	0.3649
KQSLGELIGTLNAAK	1543.8	2	5.2579	0.3969

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KQSLGELIGTLNAAKVPADTEVVCAPPTAYIDFAR	3661.2	3	4.3889	0.2692
KQSNPLLIHVDTK	1493.7	2	3.9411	0.3664
KQSTDEEVTSLAK	1436.5	2	3.9602	0.3709
KQSVEDILKDHWQK	1755.0	2	4.2078	0.3369
KQTALVELVK	1129.4	2	3.0259	0.2237
KQTDFEHR	1061.1	2	2.6688	0.1972
KQTIDNSQGAYQEAFDISK	2144.3	2	5.7115	0.5006
KQTIDNSQGAYQEAFDISKK	2272.5	2	6.3144	0.4847
KQVAVAELLENVGQVNEHDGGAQPGPVPK	2982.3	3	6.1748	0.4462
KQVEILNRYPHFK	1673.0	2	4.9128	0.3971
KQVEVFRQNLFQEAEEFLYR	2574.9	3	4.1114	0.2611
KQVTPLFIHFR	1386.7	3	3.8102	0.2857
KRDEEEEEASGLKEELIPEKLER	2758.0	3	3.8684	0.2277
KRDHANYEEDENGDITPIK	2245.3	3	3.6889	0.1947
KREDAITQQNTIQNEAVNLLDPGSSYLLQEPPR	3740.1	3	5.6955	0.405
KREDSAPPSSVAR	1400.5	2	2.4435	0.1254
KREEAAAVPAAAPDDLALLK	2050.3	2	5.2183	0.3673
KREEAAAVPAAAPDDLALLKNLR	2433.8	3	3.6794	0.1803
KREEILEEIAK	1358.6	2	2.7501	0.1417
KREEILEEIAKVTEGVLDVIVYASAADKMK	3349.9	3	4.3326	0.2073
KREGELTVAQGR	1344.5	2	3.7164	0.1735
KRELFSNLQEFAGPSGK	1909.1	3	4.431	0.345
KREPLNFGIPDGSTGFSSR	2066.3	2	3.4193	0.2075
KREQSNDIAR	1217.3	2	2.6969	0.1553
KRETEDVPKDK	1345.5	2	2.4365	0.1435
KREYENELAK	1280.4	2	3.1513	0.1839
KRGFGFVTFDDHDPVDKIVLQK	2562.9	3	3.8967	0.3436
KRGWDENVYYTVPLVR	1996.3	2	3.6718	0.4356
KRHQDMFQDLNRKLQHAAEKDK	2738.1	3	3.6431	0.1546
KRIEPLSPELVAAASAVADSLPFDK	2626.0	3	4.2006	0.3866
KRIEPLSPELVAAASAVADSLPFDKQTTK	3084.5	3	3.6987	0.1502
KRIGATQTSTASLKR	1618.9	2	2.7757	0.1629
KRKMSGGSTMSSGGGNTNNSNSKK	2416.6	3	3.6351	0.1453
KRLDKFNEVVSVLK	1676.0	2	3.2939	0.2571
KRLDQVEQELNELR	1771.0	2	2.8545	0.1443
KRLDQVEQELNELRETEGGTVLTATTSELEAINKR	3973.4	3	3.701	0.2211

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KRLEAFLTQK	1234.5	2	2.9847	0.2165
KRLEEAPLVTK	1284.5	2	2.867	0.2438
KRLEEPEEPKVLTPEEQLADKLR	2749.1	3	5.1237	0.4129
KRNEDEDSPNK	1332.4	2	3.6029	0.2645
KRNEDEDSPNKLYTLVTYVPVTTFK	2959.3	3	5.3799	0.5023
KRPAPQQIQQVQQQAVQNR	2246.5	3	5.629	0.3908
KRPASMAVMEGDLVKK	1761.1	3	3.6103	0.2107
KRPEQQDVSSPAK	1470.6	2	3.2571	0.2502
KRPETKPSSDLETSK	1703.9	2	3.6949	0.368
KRPETVATQFK	1305.5	2	3.5463	0.334
KRPLIVFDGSSTSTSIK	1837.1	3	4.2789	0.3767
KRPSWFTQN	1164.3	2	2.4776	0.2213
KRPVGDPFDVKTEQGPQIDQK	2383.6	3	3.9462	0.3303
KRPYDSDNLQHEELLMK	2117.4	3	3.7726	0.2696
KRTEEPDRDER	1431.5	2	2.8389	0.1055
KRVDELQQQVK	1371.6	2	3.6935	0.1566
KRVEGPGSLGLEESGSR	1758.9	2	3.291	0.2381
KRVEISAPSNFEHR	1670.9	2	2.8819	0.133
KSADTLWGIQK	1247.4	2	3.2305	0.2126
KSADTLWGIQKELQF	1765.0	2	3.6907	0.3389
KSAEFLLHMLK	1317.6	2	4.4431	0.297
KSAEIDSDDTGGSAAQK	1680.7	2	4.164	0.3373
KSAGGGPSR	816.9	2	2.7392	0.1614
KSATQFTGR	996.1	2	2.5867	0.2585
KSAVADKHELLSLASSNHLGK	2206.5	3	5.488	0.3873
KSDANASYLR	1125.2	1	2.0167	0.1175
KSDGIYIINLK	1264.5	2	3.6276	0.2354
KSDGKIDVSIEAASGGK	1662.8	2	2.4811	0.2357
KSDIDEIVLVGGSTR	1589.8	2	5.2598	0.4079
KSDIPEKPK	1042.2	2	2.4379	0.1973
KSDLEIELLKR	1344.6	2	3.1919	0.2439
KSDLFQDDLYPDTAGPEAALEAEEWFEGK	3273.5	3	5.2047	0.4273
KSDLFQDDLYPDTAGPEAALEAEEWFEGKNADPILISLK	4338.7	3	3.6533	0.1707
KSDLFQDDLYPDTAGPEAALEAEEWVSGR	3211.4	3	6.1153	0.5627
KSDLFQDDLYPDTAGPEAALEAEEWVSGRDADPILISLR	4305.7	3	3.733	0.1823
KSDLHPTLPAGR	1292.5	2	3.6033	0.2639

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KSDVEAIFSK	1124.3	2	2.8588	0.2294
KSDVEAIFSKYGK	1472.7	3	4.2887	0.3553
KSDVETIFSK	1154.3	2	3.2067	0.2489
KSEAAVPPWVDTNDEETIQQQILALSADKR	3354.7	3	4.1511	0.35
KSEAPSGESR	1048.1	2	2.4324	0.1506
KSEASSEFAK	1084.2	2	2.541	0.2256
KSEDDEKLK	1092.2	2	2.87	0.1332
KSEDDSAVPLAK	1260.4	2	3.9836	0.3583
KSEEEIDFLR	1266.4	2	3.0918	0.2936
KSEESAAPSR	1062.1	2	2.5153	0.2029
KSEHLSVRPQTALEENETQKEVPQDQHLEAPADQSK	4099.4	3	4.4178	0.2236
KSEIEYYAMLAK	1446.7	2	4.5284	0.294
KSEIQTLKEEIEQSLTKR	2161.4	3	4.453	0.3465
KSEMESVLAQLDNYGQQELADLFVNYNVK	3347.7	3	4.6322	0.4258
KSEQLHNVTAFQGK	1587.8	2	3.7256	0.3596
KSESEVEEAAAIIAQRPDNPR	2311.5	2	3.6232	0.3442
KSEVNDKNHEMEEIRK	1987.2	3	3.2771	0.1007
KSFTPDHVVYAR	1420.6	2	3.2758	0.3815
KSGAAAAAVTTETAQHAQGAKPQVQPQK	2776.1	3	7.8993	0.4388
KSGAAAAAVTTETAQHAQGAKPQVQPQKR	2932.2	3	6.2876	0.4417
KSGEKPLLGGSLMEYAILSAIAAMNEPK	2920.4	3	3.8691	0.3015
KSGKDFVTEALQSR	1566.7	2	4.4888	0.3725
KSGKPGPFLLSGSR	1431.7	2	2.4605	0.1086
KSGKPPLQNNEK	1340.5	2	2.8125	0.3047
KSGSFHSSGEK	1151.2	2	2.8023	0.2747
KSGVGNIFIK	1063.3	2	2.6856	0.2604
KSHEAEVLK	1041.2	2	2.4593	0.3255
KSISHYHETLGEALQGVELEFSGLDIK	3002.3	3	4.3607	0.3741
KSLAAAAGKQELAK	1386.6	2	4.7718	0.3182
KSLDQDPVVR	1157.3	2	2.7849	0.1458
KSLEGDLEDLKDQIAQLEASLAAAK	2658.0	3	3.8448	0.1498
KSLEMLELGLSEAQVMMALSNHLNAVESEK	3303.8	3	3.8953	0.1729
KSLETEHKALTSEIALLQSR	2255.6	3	4.2876	0.2609
KSLPEEDVAEIQHAEEFLIKPESK	2768.1	3	5.5644	0.4571
KSLSDSESDDSK	1298.3	2	3.3564	0.3007
KSLTPAVPVESKPDKPSGK	1966.3	2	3.9045	0.3754

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KSNAHYNLQNAFNLAEQHLGLTK	2612.9	3	6.8214	0.4554
KSNFAEALAAHK	1287.4	2	3.7694	0.3471
KSNFSLEDFQHSK	1567.7	2	3.8123	0.384
KSNVKPNSGELDPLYVVEVLLR	2470.8	3	3.6719	0.1346
KSNVSYKNPSLMPK	1593.9	2	2.8133	0.1153
KSPDSDVAATLKK	1360.5	2	2.783	0.1567
KSPENTEGKDGSK	1377.4	2	2.5254	0.1298
KSPSDTEGLVK	1161.3	2	2.4093	0.1142
KSPVAKDVDLEFLAK	1660.9	2	4.5627	0.4728
KSQAQAQVHLQEVK	1594.8	2	4.5312	0.3434
KSQEKPREIMDAAEDYAK	2110.3	2	3.0709	0.3112
KSQGPLEVAEAAVSQSSGLAAK	2129.4	2	5.8398	0.5006
KSQIFSTASDNQPTVTIK	1966.2	2	5.3692	0.4841
KSQTTGFPSLITIFSAPNYLDVYNNK	2920.3	3	3.9194	0.2977
KSRPSSTSSASALYGQPLLLSVPK	2475.8	3	3.3208	0.1824
KSSDSKPGVSSK	1207.3	2	3.2897	0.1894
KSSKGELTTLIHQLQEK	1941.2	2	3.0765	0.1652
KSSTPEEVK	1005.1	2	2.7321	0.1963
KSSTPEEVKK	1133.3	2	3.7386	0.1935
KSTAALEEDAQILK	1517.7	2	3.6846	0.2672
KSTDHPKYSDMIVAAIQAEK	2233.5	3	5.6636	0.496
KSTLRDQINSDHR	1570.7	2	2.4755	0.1184
KSTPKEETVNDPEEAGHR	2025.1	2	4.5337	0.3586
KSTVLQQQYNR	1365.5	2	3.3981	0.2382
KSVEEGKIDGIIDK	1531.7	2	3.2455	0.1238
KSVEVNFTESLLR	1522.7	2	2.4959	0.1244
KSVFEEEVR	1123.2	2	2.6793	0.1691
KSVPSTGGVK	960.1	2	2.8725	0.1925
KSVQPTSEER	1161.2	2	3.0718	0.1351
KSVQYDDVPEYKDR	1742.9	3	3.3398	0.2092
KTAAELLQSQGSQAGGSQTLKR	2260.5	3	6.9039	0.5138
KTAEAGGVTGK	1019.1	2	2.5511	0.1811
KTANDMIHAENMR	1531.7	2	4.7559	0.4461
KTASVLSKDDVAPESGDTTVKKPESK	2719.0	3	6.9916	0.4063
KTCESDTLEALLLTASERPKPLLFK	2805.3	3	3.8785	0.2906
KTDAPQPDVKEEEEEKEEEK	2388.5	3	4.712	0.3924

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KTDAPQPDVKEEEEEKEEEKDKGDEEEEGEEKLEEK	4263.4	3	5.5122	0.3286
KTDDVEAMSSQPALALDER	2077.3	2	3.413	0.3528
KTDFEVFDALMVDSQK	1874.1	2	2.4665	0.1472
KTDGYSGADISIIVR	1595.8	2	2.6644	0.2687
KTDIAAFVKEILGEDS	1736.9	2	3.4805	0.3636
KTDKPRQEDKDDLDVTELTNEDLLDQLVK	3415.7	3	6.1273	0.4214
KTEAAATTR	949.0	2	2.429	0.1302
KTEAAATTRKPESNAVTK	1904.1	3	3.5439	0.307
KTEAPAAPAAQETK	1413.6	2	4.9429	0.3844
KTEELEEESFPER	1623.7	2	4.0876	0.3615
KTEEPPRDFDPALLEFLVCPLSK	2646.1	3	3.5346	0.1509
KTEGDLQGDHQK	1356.4	2	3.6284	0.2223
KTEGKIEELLPGSSIDAETR	2174.4	3	4.0603	0.2603
KTEGTPNQGK	1060.1	2	2.7006	0.165
KTEKEESTEVLK	1421.6	2	3.2652	0.1304
KTEMQEKNPLPSKETIEQEK	2388.7	3	4.3337	0.1838
KTENWLSEWWLK	1620.8	2	2.9189	0.1393
KTEPATGFIDGDLIESFLDISRPK	2651.0	3	6.7105	0.4778
KTERDELLKDLQQSIAR	2044.3	3	5.3193	0.3407
KTESASVQGR	1063.1	2	3.4282	0.2384
KTESIDVMDAVGSNIVVSTR	2122.4	2	4.5859	0.3591
KTETQEKNPLPSK	1500.7	3	4.2291	0.2843
KTETQEKNPLPSKETIEQEK	2358.6	3	5.9338	0.4073
KTETQEKNPLPSKETIEQEKQAGES	2831.0	3	5.1085	0.4086
KTETQEKNTLPTK	1518.7	2	4.0158	0.3414
KTETQEKNTLPTKETIEQEK	2376.6	3	3.8483	0.2654
KTETQEKNTLPTKETIEQEKR	2532.8	3	4.8989	0.3568
KTETQEKNTLPTKETIEQEKRSEIS	2949.2	3	4.5109	0.3608
KTETQTTGAENK	1308.4	2	3.18	0.29
KTEVLMENFR	1267.5	2	2.7109	0.1266
KTEVQAHSPSR	1240.4	2	2.9718	0.1819
KTFDSLIQDALDGLMLEGENIVSAAR	2808.2	2	3.5984	0.3604
KTFNIKNDFTEEEEAQVR	2199.4	3	3.601	0.1715
KTFPTVNPSTGEVICQVAEGDKEDVDK	2908.2	3	5.3315	0.3825
KTFPTVNPSTGEVICQVAEGDKEDVDKAVK	3206.6	3	6.8106	0.4213
KTFPTVNPTTGEVIGHVAEGDR	2326.6	3	3.7913	0.1688

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KTFSHELSDFGLESTAGEIPVVAIR	2705.0	3	5.7635	0.5371
KTFVAGIKEDTEEHHLR	2011.2	2	4.8561	0.2218
KTGEGFYK	930.0	2	2.6808	0.2956
KTGLSSEQTVNVLAQILKR	2086.4	3	3.9338	0.1835
KTGNQHFGYLYGR	1541.7	2	4.2853	0.3367
KTGQAPGYSYTAANK	1557.7	2	4.6527	0.4029
KTGQPMINLYTDR	1537.8	2	2.712	0.2097
KTGSPGSPGAGGVQSTAK	1587.7	2	4.435	0.4806
KTGSYGALAEITASK	1497.7	2	2.9391	0.3279
KTHDASGQLVLISQELLR	2009.3	2	2.4362	0.2344
KTHIQDNHDGTYTVAYVPDVTGR	2588.8	3	5.3205	0.4386
KTHLYTLILNPDNSFEILVDQSVVNSGNLLNDMTPPVNPSR	4568.1	3	5.3865	0.4194
KTHQPSDEVGTSIEHPR	1919.0	2	3.4296	0.2782
KTIPIKYPLKEIVVIHQDPEALKDIK	3030.6	3	4.6536	0.3914
KTIPSWATLSASQLAR	1731.0	2	4.3564	0.4784
KTISPEHVIQALESLGFGSYISEVK	2734.1	3	3.7243	0.1686
KTKEDEKDDKPIR	1602.8	2	4.3413	0.2948
KTKKPKAAESVSKPDVSEEAPGPSK	2596.9	3	3.7155	0.1131
KTKPYIQVDIGGGQTK	1734.0	3	4.7691	0.3529
KTKTENPLILIDEVDKIGR	2183.5	3	5.1262	0.2753
KTLEEAIR	960.1	2	2.5293	0.1282
KTLEEEAKTHEAQIQEMR	2172.4	2	6.0254	0.4849
KTLGHNLLVSELYNQLK	1971.3	3	3.7261	0.3139
KTLLSNLEEAK	1246.4	2	4.4591	0.2832
KTLLSNLEEAKK	1374.6	3	4.7685	0.3193
KTLNNDIMLIK	1303.6	2	3.3663	0.2708
KTLQALEFHTVPFQLLAR	2113.5	2	5.8033	0.4242
KTLSHNLLVSEVYNQLK	1987.3	2	4.9002	0.4259
KTLTTVQGIADDYDKKK	1925.2	2	3.9715	0.373
KTLVEFPQK	1090.3	2	3.002	0.2469
KTNHSSPEAQSK	1314.4	2	2.9803	0.3597
KTPESFLGPNAALVDLDSLVSRPGPTPPGAK	3133.5	3	4.3551	0.2365
KTPPTMEEILKNEK	1658.9	2	3.55	0.2369
KTPQGPPEIYSDTQFPSLQSTAK	2521.8	3	5.2804	0.3507
KTPSKPPAQLSPSVPK	1663.0	2	3.0505	0.2133
KTPVIVTLKENER	1527.8	2	3.5537	0.3995

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KTPWYQ	822.9	2	2.5602	0.1056
KTQDQISNIK	1175.3	2	2.8884	0.1735
KTQEQLALEMAELTAR	1833.1	2	4.6252	0.4214
KTQEQLEVLESLKQELATSQR	2459.7	3	4.9462	0.4484
KTQETLSQAGQK	1319.4	2	4.0896	0.3102
KTQHGVLSQQFVELINK	1970.3	3	5.624	0.3978
KTQKPVFEER	1262.4	2	2.7439	0.1605
KTQNDVLHAENVK	1496.7	2	4.7079	0.3478
KTQQFFDEMADPDLLEESSSLLEPSEMGR	3331.6	3	4.2285	0.3129
KTQVLQPEEK	1200.4	2	2.9741	0.1986
KTSATVGPK	889.0	1	2.3261	0.3174
KTSATVGPKAPSGGK	1386.6	2	4.1001	0.287
KTSETLSQAGQK	1278.4	2	4.219	0.3852
KTSFGSLKDEDR	1383.5	2	3.8131	0.3463
KTSFGSLKDEDRIFTNLYGR	2348.6	2	3.9211	0.2992
KTSLSFLNRPDLPNLAYKK	2206.6	3	4.9663	0.3536
KTSNASRPNFLAPLPHEVTQLR	2477.8	3	4.0968	0.1949
KTSQLLETLNQLSTHTHVVDITR	2636.0	3	6.4715	0.553
KTSYLTELIDR	1339.5	2	3.3411	0.3985
KTTDEELEEMLESGNPAIFTSGIIDSQISK	3284.6	3	6.3859	0.3896
KTTDTASVQNEAK	1393.5	2	4.9346	0.4213
KTTDTASVQNEAKLDEILKEIK	2475.8	3	6.4218	0.4495
KTTHFVEGGDAGNREDQINR	2245.4	2	4.2534	0.1663
KTTPANPVGPSGGMSDDDKIR	2144.4	3	3.5909	0.2899
KTTQSGQMSGEGK	1339.5	2	4.0632	0.4098
KTTTLSGTAPAAGVVPSR	1714.9	2	4.2663	0.4032
KTTVLAMDQVPR	1359.6	2	3.6375	0.4046
KTVAYHEAGHAVAGWYLEHADPLLK	2778.1	3	4.7669	0.4351
KTVGVEPAADGK	1172.3	2	3.7973	0.316
KTVGVEPAADGKGVVVVIK	1867.2	2	5.2163	0.4226
KTVLGTPEVLLGALPGAGGTQR	2136.5	2	3.7322	0.3841
KTVQGPPTSDDIFER	1690.8	2	2.8256	0.3325
KTVTAMDVVYALK	1439.7	2	4.6434	0.424
KTVTAMDVVYALKR	1595.9	2	5.6604	0.4639
KTYRPELIKDGK	1448.7	2	2.628	0.1278
KVACIGAWHPAR	1309.6	2	3.0982	0.1988

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KVADALTNAVAHVDDMPNALSALSDLHAHK	3126.5	3	6.0072	0.4031
KVADGLVK	830.0	1	2.0629	0.1725
KVAGMDVELTVEER	1576.8	2	3.5532	0.2105
KVAHSDKPGSTSTASFR	1776.9	2	4.0908	0.3407
KVAKVEPAVSSVVNSIQVLTSK	2284.7	3	5.1733	0.4289
KVALEMLFTGEPISAQEALLHGLLSK	2797.3	3	5.9348	0.5023
KVAPAPAVVKK	1108.4	2	2.69	0.1658
KVAPQNDSFGTQLPPMHQQQR	2408.7	3	3.3335	0.2569
KVASGVLSPPPAAPPPSSSSVPEAGGPPIKK	2908.3	3	5.5626	0.3962
KVAVATPAKK	1013.3	2	3.3199	0.26
KVAVFFSNTPTR	1367.6	2	3.3218	0.2726
KVAVPYSPAAGVDFELESFSER	2399.6	3	5.1614	0.4835
KVAVVDYVEPSPQGTR	1746.0	2	5.0917	0.364
KVDAGGKVK	902.1	2	2.4607	0.1346
KVDEAIALFQK	1262.5	2	4.3087	0.3126
KVDEQNKDYK	1267.4	2	2.7728	0.1213
KVDGGGTSAASKPK	1303.4	2	3.8093	0.2893
KVDIAGIYPPVTTPFTATAEVDYGKLEENLHK	3519.0	3	4.3853	0.4348
KVDIIADAAYSIFQKPK	1908.2	2	6.3932	0.449
KVDPVSSDKVDPVFPR	1786.0	3	3.6735	0.2726
KVDQPPEAK	1012.1	2	2.4824	0.1857
KVDTTPNQGK	1088.2	2	2.6617	0.1665
KVDTTPNQGKK	1216.4	2	3.4627	0.2508
KVDWLTEK	1019.2	2	2.6046	0.1851
KVEAAHCAACDLFIPMQFGIIQK	2535.0	3	3.7566	0.1096
KVEAPETNIDKTPK	1570.8	2	3.9193	0.2778
KVEAPPAK	840.0	2	2.5387	0.1571
KVEAQLQELQVK	1413.6	2	4.9186	0.2093
KVEAQLQELQVKFNEGER	2146.4	3	4.8817	0.4074
KVEEAAKVTGK	1160.3	2	3.5762	0.2569
KVEEAEPEEFVVEK	1662.8	2	3.8494	0.3236
KVEEDEAGGR	1090.1	2	3.2278	0.2883
KVEEDEAGGRFVAFSGEGQSLR	2369.5	3	4.8876	0.4331
KVEEEGSPGDPDHEASTQGR	2126.1	3	4.193	0.2732
KVEEVVYDLSIR	1450.7	2	3.0854	0.202
KVEGAQNQGK	1059.2	2	3.0599	0.1784

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KVEGAQNQGKK	1187.3	2	3.2127	0.2282
KVEGDIWALQKDVEDFLSPLLGKTPVTQVNEVTGTLR	4098.6	3	6.9625	0.4903
KVEGFDLVQKPSYYVR	1929.2	2	4.333	0.3675
KVEKDTMSDQALEALSASLGTR	2351.6	2	5.8943	0.5197
KVEKVVVSNR	1158.4	2	2.786	0.1738
KVELPVPTHR	1176.4	2	2.907	0.2064
KVENEDMNKDQILLEK	1947.2	2	5.594	0.2791
KVENEDMNKDQILLEKEAELR	2545.9	3	5.9438	0.2609
KVENEDMNKDQILLEKEAELRR	2702.0	3	4.975	0.3885
KVEPPTPQEPGPAK	1475.7	2	3.8194	0.2235
KVEPVPVTKQPTPPSEAAASK	2162.5	3	4.8117	0.3468
KVEQGPPGGIGTAAIRPK	1777.1	3	3.7526	0.2682
KVEQLQQEYTEMK	1654.9	2	4.5233	0.3855
KVESLLDELAFVR	1519.8	2	4.433	0.4151
KVESLQEEIAFLK	1534.8	2	5.5201	0.3516
KVESLQEEIAFLKK	1663.0	3	5.6223	0.4027
KVESTGAVPEFKEEK	1678.9	2	5.4161	0.4164
KVESTKTDSR	1151.3	2	2.6756	0.1893
KVETDHIVAAVGLEPNVELAK	2233.6	2	6.4441	0.5093
KVFDPVPVGVTK	1286.5	2	3.1678	0.2618
KVFIEDVSR	1093.3	2	2.535	0.2618
KVGAENVAIVEPSER	1598.8	2	5.064	0.4029
KVGAENVAIVEPSERHFYQPIWTLVGAGAK	3268.7	3	4.8368	0.3798
KVGALESK	832.0	2	2.7967	0.1609
KVGARRKASGAPAGAR	1553.8	2	2.5454	0.1223
KVGDDIAK	846.0	2	2.7898	0.1886
KVGNPFELDTQQGPQVDKEQFER	2690.9	3	5.4594	0.436
KVGTFFSEVKPAGPTVEQQGEMAR	2594.9	3	5.6353	0.3731
KVGWIFTDLVSEDTR	1767.0	2	2.9799	0.216
KVGYTPDWIFLLR	1608.9	2	4.1675	0.3714
KVHSPQQVDFR	1341.5	2	2.5075	0.1115
KVHVIFNYK	1148.4	2	2.5241	0.2851
KVIDDTNITR	1175.3	2	3.5605	0.3306
KVIDDTNITRLQLETEIEALKEELLFMKK	3463.0	3	4.1465	0.2238
KVIPHFTATADAFKDDR	1933.2	3	4.0056	0.3834
KVIQYLAHVASSHK	1581.8	2	2.8074	0.2364

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KVIQYLAHVASSPK	1541.8	2	4.3411	0.4093
KVIQYLAYVASSHK	1607.9	2	5.2707	0.4691
KVISSANR	875.0	2	2.6776	0.1333
KVITMFVQR	1122.4	2	2.7239	0.1885
KVIVDFSSPNIAK	1418.7	2	2.8495	0.1723
KVKDAQQVEPEGQEKPSPATVR	2422.7	3	4.7938	0.2405
KVLHMDRNPYYGGESASITPLEDLYK	2998.4	3	3.759	0.2143
KVLHMDRNPYYGGESASITPLEDLYKR	3154.5	3	6.3196	0.3107
KVLHMDRNPYYGGESSSITPLEELYK	3028.4	3	4.5858	0.3714
KVLHMDRNPYYGGESSSITPLEELYKR	3184.6	3	6.3642	0.4577
KVLSPYDLTHK	1301.5	2	2.5513	0.1596
KVMLALPSVR	1114.4	2	3.0941	0.1472
KVMSQEIQEQLHK	1598.8	2	3.0535	0.1885
KVMVLDFVTPTPLGTR	1775.1	2	3.8579	0.2727
KVNAEGSVDSVFSQVCTHLDALK	2448.7	3	4.9895	0.3875
KVNDKNPHVALYALEVMESVVK	2484.9	3	3.5333	0.1971
KVNLGVGAYR	1077.3	2	2.8153	0.2725
KVNQQPNTSDKK	1387.5	2	2.9448	0.1509
KVNTGFLMSSYK	1375.6	2	2.6158	0.1038
KVNVTVDYIRPASPATETVPAFSER	2749.1	3	3.6211	0.2984
KVPDKLLDSSTVTHLFK	1929.2	2	4.7089	0.4447
KVPDVLPVLPDLPLPAIQANYRPLPSLELISSFQPK	3967.7	3	3.5954	0.1033
KVPEFQFLIGDEAATHLK	2044.3	3	4.2152	0.3146
KVPGVTAIELDEDTGTFR	1949.2	3	3.2751	0.2609
KVPILVAQEGESSQQLNDSSVIISALK	2855.2	3	5.4889	0.4003
KVPNQYTHLSGLLDIFK	1974.3	2	3.6029	0.3544
KVPQVSTPTLVEVSR	1640.9	2	5.1603	0.4678
KVPTVSRPYSFIEFDTFIQK	2403.8	2	3.2066	0.3143
KVPVPPPKK	990.3	1	1.792	0.1078
KVQAAQSEAK	1060.2	2	2.9587	0.2179
KVQDLEQLIESAR	1529.7	2	4.0482	0.2591
KVQEEFDIDMDAPETER	2053.2	2	5.6684	0.4299
KVQFDGTNSAFKELKFLTPVR	2426.8	2	2.74	0.2058
KVQHQDALQISDVVMASLLR	2252.6	3	3.9413	0.3249
KVQQELSRPGMLEMLLPGQPEAVAR	2779.3	3	5.4353	0.2642
KVQSGNINAAK	1130.3	2	3.6969	0.3375

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KVSDKEKIDQLQEELLHTQLK	2523.9	3	6.8153	0.32
KVSEHSGGR	957.0	2	2.5235	0.1766
KVSEIKDILAQSPAAEPLKNIGNLFEEAEK	3283.7	3	4.2365	0.2218
KVSKQEEASGGPTAPK	1614.8	2	4.6328	0.3527
KVSLAPQANLTELDIYSR	2019.3	3	4.4542	0.4547
KVSNDAKR	918.0	2	2.6651	0.1883
KVSPESNEDISTTVVYR	1925.1	2	5.3065	0.4725
KVSQEILELLNTTTAK	1789.1	2	4.6093	0.4095
KVSQPIEGHAASFAQFK	1846.1	2	4.8703	0.4694
KVSVSATPGHTK	1212.4	2	3.2432	0.323
KVSYSHIQSK	1177.3	2	3.1261	0.3222
KVTAEADSSSPTGILATSESK	2080.2	3	4.5419	0.4171
KVTEENKELANELR	1673.8	2	4.174	0.3264
KVTGEVTDPSGK	1218.3	2	2.4257	0.2616
KVTHAVVTVPAYFNDAQR	2017.3	2	5.4745	0.4844
KVTLSTDKNK	1134.3	2	2.9581	0.1985
KVTQLDLDGPK	1214.4	2	2.9217	0.1803
KVTSVVFHPSQDLVFSASPDATIR	2602.9	3	5.9957	0.5334
KVTTTVHNIIVGK	1410.7	2	3.4168	0.2968
KVVATTQMQAADAR	1490.7	2	2.8358	0.148
KVVDDLLDQITGGDHSR	1869.0	2	2.46	0.1183
KVVDNTTAK	976.1	2	2.9936	0.3074
KVVDNTTAKEFADSLGIPFLETSAK	2683.0	2	5.5893	0.5291
KVVDYSQFQESDDADEDYGR	2367.4	3	5.2226	0.2258
KVVDYTTAK	1025.2	1	2.7774	0.4123
KVVDYTTAKEFADSLGIPFLETSAK	2732.1	3	5.9423	0.5002
KVVEDIEYLK	1236.4	2	2.8588	0.2166
KVVEINHEDLGHDHVSHLDILAVQEGK	3033.3	3	6.1206	0.4713
KVVENEIYSESHR	1590.7	2	3.9557	0.3548
KVVETEDAYK	1182.3	2	3.236	0.2019
KVVGDVAYDEAK	1294.4	2	3.9134	0.4146
KVVGDVAYDEAKER	1579.7	2	4.4259	0.5066
KVVLEAPDETTLKELAETLQQK	2484.8	3	6.1518	0.5415
KVVVCDNGTGFVK	1366.6	2	3.4434	0.3402
KVVVSPTKK	986.2	2	2.8298	0.2716
KVVVVVPNEEDWKK	1669.9	3	3.8322	0.2049

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KVVYENAYGQFIGPHR	1879.1	2	4.8243	0.5276
KVWLDPNETNEIANANSR	2072.2	2	5.6311	0.4587
KWEAAHVAEQQR	1453.6	2	3.7003	0.3826
KWENPGLGAESHTDSLR	1898.0	3	4.915	0.2834
KWGTDEVK	963.1	2	2.5156	0.1025
KWLPELVEHAK	1350.6	2	2.7016	0.2258
KWQDEDGKK	1134.2	2	2.7769	0.2252
KYAAELHLVHWNTK	1711.0	3	3.9505	0.3369
KYAALYQPLFDK	1457.7	2	4.0789	0.3974
KYAALYQPLFDKR	1613.9	3	4.1739	0.3486
KYADALQEIIQER	1577.8	2	3.8522	0.3097
KYAEAVTR	938.1	1	2.7078	0.2465
KYAELLEEHR	1288.4	2	2.8665	0.1282
KYAPTEAQLNAVDALIDSMSLAK	2450.8	2	5.9792	0.549
KYAPTEAQLNAVDALIDSMSLAKKDEK	2951.3	3	4.1132	0.2443
KYAVLYQPLFDKR	1641.9	2	5.261	0.4062
KYDADSSGFISAAELR	1730.9	2	4.8403	0.4952
KYDAFLASESLIK	1485.7	3	4.5368	0.3652
KYDAFLASESLIKQIPR	1980.3	2	5.428	0.4205
KYDASLKELAQLKEQGLLNR	2318.7	2	5.9208	0.4252
KYDEELEER	1211.3	2	2.7765	0.2558
KYDEVLHMVR	1290.5	2	3.2984	0.2658
KYDVDTLDMVFLDHWK	2026.3	3	5.4362	0.4169
KYDVDTLDMVFLDHWKDR	2297.6	3	4.0848	0.2992
KYEAAYGK	930.0	1	2.9791	0.1349
KYEDICPSTHNMDVPNIK	2105.4	3	4.5169	0.4363
KYEDICPSTHNMDVPNIKR	2261.6	3	5.2244	0.4181
KYEEIDNAPEER	1493.6	2	4.4133	0.3467
KYEGGRELSDFISYLQR	2062.3	3	4.722	0.4244
KYEHLLQLLDLAQEK	1842.1	2	5.2632	0.4054
KYEHLLQLLDLAQEKVDVANRLEK	2867.3	3	5.0094	0.3172
KYELGRPAANTK	1348.5	2	3.8979	0.2961
KYEMFAQTLQQSR	1630.9	2	5.0866	0.4499
KYEPPVPTR	1087.3	2	2.6008	0.1987
KYEQEQEKGQEDLKIIEEK	2365.6	3	3.4771	0.114
KYEQGFITDPVVLSPK	1822.1	2	4.8496	0.4492

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KYEQGFITDPVVLSPKDR	2093.4	3	4.8791	0.3734
KYFHAQLQLEQLQEENFR	2322.6	3	4.55	0.2441
KYFSLKPEEKDEK	1641.8	2	4.3605	0.2446
KYGGPPPDSVYSGQQPSVGTEIFVGK	2696.0	3	4.4165	0.3507
KYGGPPPDSVYSGQQPSVGTEIFVGKIPR	3062.4	3	5.7975	0.3523
KYGGPPPDSVYSGVQPGIGTEVFVGK	2636.9	3	3.7659	0.224
KYGGPPPDSVYSGVQPGIGTEVFVGKIPR	3003.4	3	6.3766	0.4301
KYGTDLSR	940.0	1	1.9197	0.1004
KYGYILPDITKDELFK	1944.3	3	4.3863	0.3387
KYHIDLDPHFNDILGQHSR	2306.5	2	3.5457	0.2947
KYIIHKYPSLELER	1790.1	3	4.1179	0.3521
KYILGNPLTPGVTQGPQIDKEQYDK	2804.1	3	6.4942	0.4478
KYILGNPLTPGVTQGPQIDKEQYDKILDLIESGK	3773.3	3	5.1379	0.3904
KYILGNPLTPGVTQGPQIDKEQYDKILDLIESGKK	3901.5	3	5.7882	0.4789
KYKEALLGR	1078.3	2	2.849	0.1354
KYLGQLHYLQSR	1506.7	2	4.0709	0.4122
KYLKPSGNMFPTIGDVHLAPFTDEQLYMEQFTK	3848.4	3	3.7518	0.2232
KYLYEIAR	1056.2	2	2.8419	0.1058
KYMEENDQLK	1298.4	2	2.7255	0.2122
KYMEENDQLKK	1426.6	2	4.1305	0.2964
KYNWSAK	897.0	2	2.6308	0.2868
KYPVAHFIDQTLK	1560.8	2	3.2832	0.2844
KYPYWPHQPIENL	1685.9	2	3.4974	0.2781
KYQILNNEVFAILNK	1808.1	2	2.5375	0.1566
KYRGFTIPEAFR	1485.7	2	2.4536	0.1954
KYRIPADVDPLTITSSLSSDGVLTVNGPR	3073.4	3	4.8179	0.3255
KYRPLFDYFLK	1490.8	2	2.9042	0.2225
KYSIFTEKDEILSDVASR	2102.3	2	3.5994	0.2819
KYSQFINFPIYVWSSK	2008.3	2	5.5658	0.4106
KYTEQITNEK	1254.4	2	3.6439	0.2706
KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	3228.7	3	6.9182	0.5033
KYTMGDAPDYDR	1432.5	2	3.693	0.445
KYTPEQVAMATVTALHR	1917.2	3	5.1465	0.5005
KYVATLGVEVHPLVFHTNR	2181.5	2	5.6751	0.4594
KYVLENHPGTNSNYQMHLLK	2387.7	2	5.1351	0.3401
KYVSQYYPK	1176.3	2	2.8928	0.3406

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
KYVVQNPEQEPLSQFLR	2076.3	3	4.0194	0.168
KYWDVPPPGFEHITPMQYK	2334.7	3	3.597	0.288
KYYFNNPEDGFFK	1669.8	2	2.6614	0.2043
KYYFNNPEDGFFKK	1798.0	2	4.0915	0.3609
KYYGTKDPVPGYSVPAAEHSTITAWGK	2925.2	3	4.4186	0.3284
KYYKVEPLDFGGTQK	1774.0	2	5.1732	0.4436
KYYLDLKENQR	1470.7	2	3.108	0.3132
LAAAEETAVSPR	1215.3	2	4.0945	0.2635
LAAAFAVSR	906.1	2	3.4091	0.3642
LAAAFAVSRLEQDEYALR	2024.3	3	5.7264	0.4346
LAAAILGGVDQIHIKPGAK	1873.2	2	4.7717	0.4641
LAACGPPPVAPPAAVAAVAGGAR	1985.3	2	2.5674	0.2729
LAADAGTFLSR	1122.3	2	3.2983	0.416
LAADDFR	807.9	2	2.526	0.2231
LAADDFRTKFETEQALR	2012.2	2	3.507	0.2423
LAADEDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK	4120.8	3	6.8498	0.4969
LAADEDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4248.9	3	6.6304	0.4292
LAADPSVVNLGQGFPDISPPTYVKEELSK	3073.4	3	4.9099	0.4548
LAADVGK	673.8	1	2.0707	0.1332
LAADVGKAGAEREFR	1590.8	2	2.856	0.252
LAADVGKSGTER	1204.3	2	2.7477	0.2495
LAADVGKSGTEREFR	1636.8	2	2.8618	0.1597
LAAEQELIR	1043.2	2	2.7762	0.1643
LAAESSSSQPPQQR	1486.6	2	2.6936	0.2382
LAAFGQLHK	985.2	2	2.6517	0.1404
LAAIAESGVER	1116.3	2	3.3356	0.3172
LAAIAESGVERQVLLGDQIPK	2208.5	3	4.6094	0.2251
LAAIGEATR	902.0	2	3.0439	0.183
LAALADQWQFLVQK	1631.9	2	2.6963	0.2407
LAALNPESNTAGLDIFAK	1846.1	2	5.403	0.4264
LAALPENPPAIDWAYYK	1933.2	2	4.4273	0.3787
LAALQGRLEGLGSSEADQDGLASTVR	2615.8	3	6.0147	0.5814
LAANAFLAQR	1075.2	2	3.5105	0.2739
LAANDFFR	954.1	2	2.6859	0.2439
LAAQFIPK	888.1	2	2.4034	0.1408
LAAQSQHVGFAR	1285.4	2	2.9823	0.1418

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LAASEAATAISHQAIQILGGMGYVTEMPAER	3188.6	3	3.7919	0.2232
LAASVLDALDPPGPTLDPLDLLPYSETRLDALDSFGSTR	4114.6	3	3.8847	0.3028
LAATNALLNSLEFTK	1606.8	2	5.2985	0.4558
LAATTFISQGIPVYLFSDITPTPFVPFTVSHLK	3610.2	3	4.888	0.3761
LAAVALINAAIQK	1296.6	2	3.6388	0.2645
LAAVDATVNQVLASR	1528.7	2	5.4762	0.5305
LAAVEALNDGELQKAIDLFTDAIK	2559.9	2	3.3032	0.4029
LADAAENFQK	1107.2	2	3.0986	0.3372
LADALQELR	1029.2	2	3.9558	0.291
LADALQELRAQHEDQVEQYKK	2513.7	3	5.6936	0.4099
LADALQELRAQHEDQVEQYKKELEK	3013.3	3	6.6337	0.3573
LADALQELRAQHEDQVEQYKKELEKTYSAK	3563.9	3	3.883	0.2302
LADDLGFEFFEASAK	1660.8	2	5.1601	0.4666
LADDLSTLQEK	1233.4	2	3.9398	0.294
LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	3617.9	3	7.3536	0.4799
LADFGLAR	863.0	2	2.7258	0.2221
LADFGVAGQLTDTQIKR	1834.1	2	4.6988	0.3645
LADFGVLHR	1028.2	2	2.8845	0.2492
LADFGVLHRNELSGALTGLTR	2241.5	3	5.3112	0.4244
LADGGATNQGR	1060.1	2	3.865	0.3494
LADHFGGK	844.9	1	2.1945	0.1821
LADIEQSTGIR	1203.3	2	3.4442	0.2676
LADIQIEQLNR	1313.5	2	2.7634	0.1292
LADKLYNLR	1106.3	2	2.9779	0.1962
LADKVNSSWQR	1304.4	2	3.1381	0.2932
LADKYPVVHIGKR	1496.8	3	5.1142	0.404
LADLASDLLLQYLLQGGAR	2031.3	3	6.1435	0.4697
LADLASDLLLQYLLQGGARQ	2159.5	2	5.4149	0.419
LADLEQEQSSKR	1404.5	2	3.0306	0.2125
LADLIERDRLLLATMESMNGGK	2447.9	3	3.4887	0.1667
LADLTGPIIPK	1138.4	2	3.1505	0.1991
LADMALALESAR	1261.5	2	2.8318	0.1863
LADMYGGGEDD	1143.2	1	2.2291	0.1769
LADPVFIGFCVLQGADCGAK	2025.4	2	3.1094	0.1559
LADQSGLDVIR	1187.3	2	3.2509	0.3429
LADSDQASKVQQQK	1546.7	2	3.5932	0.1442

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LAEAAVAEKR	1058.2	2	2.8382	0.1244
LAEAEETAR	990.0	2	3.0168	0.2639
LAEAFKYFVQGMGYMPSASMTR	2486.9	3	4.8701	0.511
LAEALYIADRK	1263.5	2	3.1416	0.261
LAEAQIEELR	1172.3	2	3.3224	0.2253
LAEDAPNFDGPAAEGQPGQK	2013.1	2	4.4582	0.3935
LAEDILNTMFDTSYSK	1849.1	2	3.2067	0.242
LAEEEDLFDSAHPEEGDLDLASESTAHAQSSK	3430.5	3	6.4452	0.4695
LAEEENKAK	1032.1	2	3.1937	0.1263
LAEEENKAKAEASSGDHPTDTEMKEEQK	3104.3	3	4.8596	0.2953
LAEEKAQASSIPVGSR	1643.8	2	4.7576	0.4264
LAEENPDLQEAYIAK	1704.9	2	5.1026	0.4422
LAEFQTDSQGK	1224.3	2	3.1971	0.158
LAEIQELHQSVR	1423.6	2	3.1639	0.2836
LAEISDVWEEMK	1450.6	2	2.8009	0.2457
LAEISDVWEEMKTTLK	1894.2	2	2.6351	0.262
LAEKEETGMAMR	1366.6	3	3.7755	0.3439
LAEKEKVDLVLLGK	1555.9	2	4.3901	0.4021
LAEKENAR	931.0	2	2.5247	0.1835
LAEKTETVDRLER	1560.7	2	3.1056	0.1495
LAELEEFINGPNNAHIQQVGDR	2465.7	2	5.7559	0.3974
LAELHADLK	1010.2	2	3.0741	0.2526
LAELNSYVPVTAYTGPLVEDFLSGFQVVVLTNTPLEDQLR	4411.0	3	4.1628	0.4132
LAELQEQLKAVHEQLAALSQAPVNKPK	2955.4	3	4.0208	0.2753
LAELSDYRR	1123.2	2	2.5797	0.1099
LAEMPADSGYPAYLGAR	1783.0	2	5.1465	0.5249
LAENFCVCHLATGDMLR	1894.2	2	3.1171	0.2348
LAENIDAQLKR	1271.4	2	3.1052	0.3115
LAENSASSDDLLVAEVGISDYGDKLNMELSEK	3414.7	3	4.3222	0.2861
LAEPQSQGNSQVLLDAPIQLSK	2337.6	2	5.0727	0.4019
LAEPSQMLK	1017.2	2	2.7251	0.1169
LAEQAERYDDMAAAMK	1814.0	2	4.3587	0.3699
LAEQAERYDDMAACMK	1846.1	3	4.1698	0.2427
LAEQAERYDDMASAMK	1830.0	2	4.2717	0.3729
LAEQAERYDEMVESMK	1930.2	3	3.9574	0.2448
LAEQAERYDEMVESMKK	2058.3	3	5.8813	0.3932

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LAEQFVLLNLVYETTDKHLSPDGQYVPR	3247.6	3	4.8909	0.3862
LAERESQEQGLR	1416.5	2	3.4969	0.2152
LAETQEEISAEVAAK	1589.7	2	3.782	0.3598
LAETTDKVK	1005.1	2	2.5857	0.1186
LAETYLHR	1003.1	2	2.583	0.1526
LAEVALAYAK	1049.2	2	3.0925	0.3223
LAEVLEAVMPHLDQTPNPLVSSVFHR	2901.3	3	3.9873	0.2072
LAFHGILLHGLEDR	1591.8	2	3.6538	0.4008
LAFLNVQAAEEALPR	1642.9	2	3.9029	0.382
LAFPSPFGHLSEGFSHSR	1974.2	2	4.6272	0.2274
LAGAPSEDPQFPK	1357.5	2	3.2811	0.1968
LAGAWASEAYSPQGLKPVVSTEAPPIIFATPTK	3399.9	3	5.3838	0.4677
LAGDHIEYYK	1209.3	2	2.8037	0.1917
LAGDPSAGDGAAPR	1255.3	2	3.9914	0.3635
LAGESESNLR	1076.1	2	3.6408	0.2585
LAGESESNLRK	1204.3	2	3.2984	0.2344
LAGGDWFTSR	1110.2	2	3.3058	0.3287
LAGGHGVSASR	1012.1	2	2.6686	0.2504
LAGGNDVGIFVAGIQEGTSAEQEGLQEGDQILK	3345.6	3	4.151	0.325
LAGGNDVGIFVAGIQEGTSAEQEGLQEGDQILKVNTQDFR	4206.5	3	5.3237	0.442
LAGGNDVGIFVAGVLEDSPAAKEGLEEGDQILR	3341.7	3	6.0831	0.4572
LAGGYENVPTVDIHMK	1745.0	2	4.6548	0.4489
LAGHLSEDPRFPK	1467.7	2	3.3172	0.2059
LAGLFNEQR	1048.2	1	3.4911	0.2898
LAGLGLQQLDEGLFSR	1717.9	2	3.0365	0.1373
LAGLHDAILR	1079.3	2	2.6869	0.2358
LAGLSAALLR	985.2	2	3.4946	0.3094
LAGNEQVTR	988.1	2	2.4542	0.1706
LAGPQLVQMFIGDGAK	1645.9	2	4.9366	0.3963
LAGSALTDKHSDKS	1430.5	2	3.7378	0.3031
LAGSLLTQALESHAEGFR	1901.1	3	3.9619	0.4671
LAGTQPLEVLEAVQR	1624.9	2	5.5697	0.4359
LAGTSGSDKGLSGK	1278.4	2	2.8087	0.2355
LAHALLHTQTK	1233.4	2	3.0749	0.2832
LAHEVGWK	940.1	2	2.7686	0.2008
LAHGGQVNLDMEDHRDEDFVKPK	2651.9	3	3.757	0.3801

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LAHLGVQVK	965.2	2	2.6009	0.251
LAHLGVQVKGEDEEENNLEVR	2379.6	3	4.3923	0.2482
LAHQIYQFTDKDKDNVAPR	2260.5	3	3.3165	0.229
LAHQSWALLHEESPLNNFLLSHGPGIR	3038.4	3	3.853	0.1628
LAHVSEPSTCVYALTFETPLVCHPHALLVYPTLPEALQR	4319.0	3	4.1338	0.3289
LAHYNK	745.8	1	1.7636	0.1228
LAHYNKR	902.0	2	2.4319	0.1906
LAIEAGFHHIDSAHVYNNEEQVGLAIR	3005.3	3	3.9879	0.3066
LAIEAGFR	877.0	2	2.5165	0.122
LAIKLPDDQIPK	1351.6	2	2.8428	0.2004
LAILGIHNEVSK	1294.5	2	3.5192	0.2705
LAISEDHVASVK	1269.4	2	2.7073	0.2607
LAKADGIVSK	1002.2	2	2.7291	0.186
LAKDREAAEGLGSHER	1739.9	3	4.7297	0.3448
LAKDSNTILLPSNPGDVTSMVAQAMGVYGALTK	3364.9	3	6.1226	0.4976
LAKELGLETYKVNEVER	1992.3	2	5.2329	0.4532
LAKENAPAIIFIDEIDAIATK	2257.6	2	5.7352	0.5294
LAKENAPAIIFIDEIDAIATKR	2413.8	3	5.3473	0.4978
LAKEQEQAQK	1173.3	2	2.8669	0.1163
LAKHESQQDYSK	1434.5	2	3.2275	0.2443
LAKLSDGVAVLK	1214.5	2	2.9314	0.2671
LAKVDATEESDLAQQYGVR	2094.3	2	6.8147	0.5385
LAKYNQLLR	1119.3	2	3.0774	0.1762
LAKYNQLLRIEEELGSK	2005.3	3	4.0096	0.3265
LALADAGDTVEDANFVEAMADAGILR	2649.9	2	3.668	0.4165
LALDIEIATYR	1278.5	2	3.809	0.3641
LALDIEIATYRK	1406.7	2	2.9852	0.2129
LALDLEIATYR	1278.5	2	3.967	0.3607
LALDMEIHAYR	1332.6	2	2.8744	0.3728
LALDMEIHAYRK	1460.7	2	3.1068	0.2112
LALDMEINAYRK	1437.7	2	3.1824	0.1719
LALEAEVSELRAELSSLQTAR	2287.6	3	6.3911	0.4891
LALEAEVSELRAELSSLQTARQEGEQR	3015.3	3	3.9863	0.2292
LALEGVEKERDFYFGK	1902.1	2	4.1249	0.476
LALELPDVTKEDLAIQKDLEELEVILRD	3222.7	3	4.0217	0.177
LALGDDSPALK	1100.2	2	2.443	0.2185

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LALGDDSPALKEK	1357.5	2	3.1699	0.2873
LALGDDSPALKEKR	1513.7	2	3.6438	0.3268
LALGIPLPELR	1192.5	2	2.4369	0.2639
LALHELKNLTQYSWLLDGFPR	2515.9	3	4.5124	0.4445
LALIGQSLFGQEVYSHLRK	2160.5	2	3.0725	0.2925
LALIQLQISSIK	1327.6	2	3.0168	0.2761
LALKEGHSVLESLR	1552.8	2	2.7474	0.1904
LALLEEAR	915.1	2	2.5512	0.1071
LALLHEGTGPR	1164.3	2	2.9603	0.3016
LALLQEERDKLITEMDR	2074.4	3	3.704	0.2927
LALLVDTVGPR	1154.4	2	4.1474	0.3218
LALQALTEK	987.2	2	2.4527	0.1408
LALQLHPDRNPDDPQAQEK	2186.4	3	4.1985	0.334
LALSQAHSLVQAEAPR	1691.9	2	3.8247	0.3069
LALVTGGEIASTFDHPELVK	2098.4	2	5.3201	0.4908
LAMLEEDLLALKSPSKENIASVLENYHTESK	3474.9	3	5.0514	0.3895
LAMQEFMILPVGAANFR	1909.3	2	5.7407	0.4917
LAMQEFMILPVGAESFR	1940.3	2	4.9244	0.424
LAMSKKEELEEELDEAVER	2249.5	3	3.9698	0.2132
LANEERDAENPDEPKEGVNR	2283.4	3	3.8362	0.1442
LANFGGLAVGLGFGALAEVAK	1976.3	2	2.4104	0.2454
LANFLVHSSNNFGAILSSTNVGSNTY	2729.0	2	4.4936	0.356
LANILFTQELAR	1389.6	2	2.8531	0.2254
LANQAADYFGDAFK	1531.7	2	3.1263	0.2492
LANQFAIYKPVTDFFLQLVDAGK	2600.0	3	5.484	0.4756
LANQFAIYKPVTDFFLQLVDAGKVDDAR	3156.6	3	4.8105	0.447
LANRAPEPTPQQVAQQQ	1877.1	2	4.3625	0.3886
LANRLYGEKTYNFLPEFLVSTQK	2733.1	3	5.6538	0.432
LANSEPVGTQTAK	1316.4	2	2.9051	0.2441
LAPALATGNTVVMK	1386.7	2	3.5667	0.3859
LAPEYEAAATR	1192.3	2	3.5974	0.3316
LAPGTIVEVWK	1213.5	2	2.5919	0.285
LAPGTIVEVWKDSAYPEELSR	2361.6	2	3.5413	0.2352
LAPITSDPTEATAVGAVEASFK	2176.4	2	6.1967	0.5822
LAPITSDPTEATAVGAVEASFKCCSGAIIVLTK	3265.8	3	3.2154	0.1113
LAPPLVTLLSGEPEVQYVALR	2266.7	3	4.7927	0.3491

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LAPRERPPSGTLEKLVSEAKAQLR	2648.1	3	3.2529	0.1175
LAPSRQDIFQEQLAAIPEFLNIGPLFK	3057.5	3	4.141	0.2913
LAPVPFFSLLQYE	1524.8	2	2.6594	0.1121
LAQAAQSSVATITR	1417.6	2	4.6397	0.4969
LAQAEEQLEQETR	1545.6	2	3.2723	0.1303
LAQAHPAGPPTLDPVNDLQLKDMSVVEGGLR	3240.7	3	6.1672	0.4749
LAQALHEMR	1069.3	2	3.0691	0.3132
LAQALHEMREQHDAQVR	2033.3	2	3.7086	0.3672
LAQANGWGVMVSHR	1526.7	3	3.9145	0.3531
LAQATQERTDLYAK	1608.8	2	3.2843	0.3409
LAQAWFNTHR	1244.4	2	3.1735	0.2738
LAQDDLHIMDSLELPTGDPQYLTELAHYRR	3512.9	3	3.4371	0.2532
LAQDFLDSQNLSAYNTR	1957.1	2	6.0152	0.5179
LAQDGAHVVVSSR	1339.5	2	3.4303	0.2948
LAQDPFPLYPGEVLEK	1817.1	2	4.4261	0.3777
LAQDPFPLYPGEVLEKDITPLQVVLPNTALHLK	3671.3	3	4.9864	0.4152
LAQEEAQHR	1082.2	2	3.0235	0.1069
LAQEEESEAKR	1290.4	2	2.8855	0.1974
LAQEGIYTLYPFINSR	1886.1	2	3.2715	0.3195
LAQENEVDFILLGGDLFHENKPSR	2743.0	3	3.4584	0.1855
LAQENEVDFILLGGDLFHENKPSRK	2871.2	3	3.8654	0.2167
LAQENGWGVMVSHR	1584.8	2	3.0662	0.161
LAQEQGGGDNSLLVR	1557.7	2	3.1253	0.1734
LAQFEPSQR	1076.2	2	3.0951	0.2627
LAQGEYIAPEKIENIYMR	2139.5	3	3.501	0.1209
LAQGHTTVDELAR	1411.5	3	4.4852	0.4403
LAQGISQLDRELHLQVVAR	2147.5	3	3.8254	0.3054
LAQGLTHLGK	1038.2	2	3.0681	0.2228
LAQHALAGMQK	1168.4	2	2.9506	0.298
LAQHTLQALQSELDSLRADNIKLFEK	2983.4	3	4.7414	0.3179
LAQIREEK	987.1	2	2.5568	0.1565
LAQKAFEYGVK	1254.5	2	3.0153	0.2696
LAQKKPFTPVK	1257.5	2	2.5692	0.2029
LAQKNPMYQK	1221.5	2	2.948	0.1642
LAQKVPTADLEDVLPLAEDITNILSK	2808.2	3	5.4943	0.4563
LAQLEEAKQASIQHIQNAIDTEK	2579.8	3	4.8527	0.4823

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LAQLEEAKQASIQHIQNAIDTEKSQQALVQKR	3619.0	3	8.8257	0.5715
LAQLQVAYHQLFQEYDNHIK	2459.7	3	4.0666	0.2391
LAQLTLEQILEHLDNLR	2020.3	2	5.054	0.2985
LAQMAILLAEVDKVAR	1742.1	2	2.639	0.187
LAQNILSYLDLK	1391.6	2	3.4074	0.2215
LAQPYVGVFLK	1235.5	2	3.0997	0.2071
LAQQEKQEQVK	1329.5	2	3.4118	0.1586
LAQQEKQEQVKIESLAK	1971.2	2	5.5408	0.3993
LAQQGSDLIVPAGGQR	1610.8	2	3.9361	0.3893
LAQQISDEASR	1218.3	2	2.9998	0.1934
LAQQLTMER	1090.3	2	3.1927	0.2123
LAQQMENRPSVQAALK	1785.1	2	4.0983	0.2583
LAQQQAALLMQQEER	1758.0	3	3.3994	0.1742
LAQQYYLVYQEPIPTAQLVQR	2522.9	2	5.088	0.4617
LAQSAEMYHYQHQR	1762.9	2	4.6227	0.3864
LAQSEYQLLADIIPEHHQK	2234.5	3	3.9314	0.3404
LAQSNGWGVMVSHR	1542.7	2	2.5794	0.1076
LAQTLSTQLFQMVHTQR	2003.3	3	3.6308	0.2855
LAQVQVQKDSK	1244.4	2	2.6659	0.148
LAQYEPPQEEKRAE	1688.8	2	3.3292	0.2431
LAQYESK	838.9	1	2.1538	0.1759
LAQYESKK	967.1	2	2.6547	0.1656
LARDDQIHILK	1322.5	3	3.8074	0.1201
LARDEGWLAEHMLILGITSPAGK	2479.9	3	3.7086	0.1768
LASAAYPDPSK	1120.2	2	2.8229	0.1251
LASALAHNPNSGLHTINLAGNPLEDR	2697.0	3	4.8283	0.4113
LASDHKDIHSSVSR	1552.7	2	3.2851	0.383
LASDLLEWIR	1216.4	2	3.9561	0.2409
LASDSDAESDSR	1253.2	2	3.021	0.4126
LASDTEDNDEALAEILQANDNLTQVINLYK	3335.6	3	4.309	0.2409
LASEAKPAAVAAENEEIGSHIK	2236.5	3	6.7571	0.5461
LASEILMQNWDAAMEDLTR	2208.5	3	4.3278	0.39
LASFSPSPPSPYPTTVGPVESSGLR	2531.8	3	3.3259	0.2943
LASGETVAAFCLTEPSSGSDAASIR	2441.7	2	4.0169	0.3294
LASGVEGSDIPDDGKLIGFAQLSIS	2490.7	2	2.9151	0.1846
LASHLNLAMCHLK	1451.8	3	4.5721	0.4019

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LASIVEQVSVLQNQGR	1742.0	3	4.4656	0.3102
LASKEESSNSSDSK	1469.5	2	3.4035	0.2935
LASLEELKR	1059.2	2	2.9825	0.1287
LASLFPALFSR	1222.5	2	2.9384	0.1593
LASLMNLGMSSSLNQQGAHSALSSASTSSHNLQSIFNIGSR	4206.6	3	5.6299	0.4785
LASQANIAQVLAELKEYATEVDVDFVR	2994.3	3	3.6124	0.3314
LASQGDSISSQLGPIHPPPR	2058.3	3	4.484	0.3766
LASSEGFQKPSASLSQLESQNQLLQER	2977.2	3	5.3177	0.2937
LASTLVHLGEYQAAVDGAR	1972.2	3	5.1115	0.5255
LASVLGSEPSLDSEVTSK	1820.0	2	4.5234	0.4459
LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	2776.1	3	5.9391	0.5591
LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEK	3276.6	3	4.4496	0.4173
LASVSADAEVAR	1189.3	2	3.8283	0.2136
LASYLDK	809.9	1	2.1742	0.119
LASYLDKVR	1065.2	2	3.2039	0.2044
LATALQKLEEAEK	1444.7	2	3.4843	0.1628
LATALQKLEEAEKAADESER	2203.4	2	5.5779	0.4961
LATALQKLEEAEKAADESERGMK	2519.8	2	5.3613	0.4047
LATATFAGIENK	1236.4	2	3.5532	0.3133
LATDKNDPHLCDFIETHYLNEQVK	2845.1	3	5.8788	0.3503
LATFWYYAK	1163.3	2	3.1593	0.2552
LATLETEAAQHQAVVDGLTR	2124.3	3	4.6288	0.2324
LATLGGSQALGLDGEIGNFEVGKEFDAILINPK	3388.8	3	5.8496	0.4341
LATNAAVTVLR	1129.3	2	2.8615	0.2902
LATNTSAPDLK	1131.3	2	3.6176	0.3296
LATNTSAPDLKNVR	1500.7	2	2.9454	0.2462
LATPEDKQDIDKQYVGFATLPNQVHR	2985.3	3	5.2641	0.347
LATPTYGDLNHLVSATMSGVTTSLR	2606.9	3	4.9505	0.425
LATPTYGDLNHLVSATMSGVTTSLRFPGQLNADLR	3719.2	3	4.659	0.3536
LATPTYGDLNHLVSATMSGVTTSLRFPGQLNADLRK	3847.4	3	3.2192	0.2016
LATQLTGPVMPVR	1383.7	2	2.7645	0.1517
LATQSNEITIPVTFESR	1907.1	2	4.3407	0.3909
LAVAGEDAR	902.0	2	2.5677	0.2134
LAVATFAGIENK	1234.4	2	4.498	0.4389
LAVEALSSLDGDLAGR	1587.8	2	5.5573	0.4937
LAVISNFDR	1035.2	2	2.5921	0.1151

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LAVLKEENDKKR	1443.7	3	3.6135	0.2663
LAVLSSSLTHWK	1342.6	2	2.8686	0.264
LAVMSVDLGSESMK	1467.7	2	4.3342	0.4551
LAVNCFVNNNR	1264.4	2	2.5907	0.1122
LAVNMVPFPR	1144.4	2	4.0343	0.3825
LAVNNIAGIEEVNMIKDDGTVIHFNNPK	3067.5	3	5.2318	0.3422
LAVQQVEEAQQLREHQEALHQQR	2770.0	3	4.7876	0.3474
LAVYIDKVR	1077.3	2	3.1653	0.2951
LAVYIDR	850.0	1	1.7407	0.131
LAVYIDRVR	1105.3	2	3.0167	0.1759
LAWMGTWEHLVSTGFNQMR	2265.6	2	2.5904	0.1173
LAWVGDVFTATPAEPRPLTSPLR	2495.9	3	3.8844	0.3826
LAWVSHDSTVSVADASK	1773.9	2	4.1869	0.3999
LAYELYTEALGIDPNNIK	2038.3	2	2.5882	0.1419
LAYINPDLALEEK	1489.7	2	4.2541	0.2746
LAYQDKGVLHNEVK	1614.8	2	4.4911	0.3263
LAYQELQIDR	1249.4	2	3.4561	0.1461
LCDKTTPTGWTLDQCIQTGVDNPGHPFIK	3187.6	3	4.2644	0.2826
LCEAICPAQAITIEAEPR	1929.3	2	5.2448	0.3352
LCLQQGQLCEPLPSLAESR	2086.4	2	3.73	0.1003
LCQPEGIHICDGTEAENTATLTLLEQQGLIR	3368.8	3	5.7098	0.2663
LCYVALDFEQEMATAASSSSLEK	2494.8	2	6.5647	0.4895
LCYYIGATDDAATK	1505.7	2	2.8458	0.1578
LDAAGFWQVWQR	1477.7	2	4.4711	0.439
LDADPSLQR	1015.1	2	2.9412	0.1913
LDADYPLR	963.1	2	2.6826	0.244
LDAEPRPPPTQEAA	1492.6	2	3.7083	0.3763
LDAGNQLALIEELHKEIR	2063.3	3	3.6259	0.1912
LDALQTFIR	1077.3	2	2.572	0.218
LDALSNFHFIPKPPVPEIK	2163.5	3	4.0355	0.3923
LDALVAEEHLTVDAR	1652.8	2	4.2764	0.445
LDAQVQELHAK	1252.4	2	3.4981	0.2771
LDDFDELSEVAQK	1509.6	2	4.2592	0.3361
LDDFVETGDIR	1280.4	2	4.0554	0.4095
LDDLVSTGK	948.1	2	2.542	0.2046
LDDSDREGSVK	1221.3	2	2.8084	0.2093

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LDEEAENLVATVVPTHLAAAVPEVAVYLK	3063.5	2	4.7374	0.4963
LDEEAENLVATVVPTHLAAAVPEVAVYLKESVGNSTR	3894.3	3	4.7195	0.2382
LDELRDEGKASSAK	1519.6	2	4.1974	0.3419
LDEREAGITEK	1261.4	2	2.5614	0.1848
LDEREAGITEKVVFEQTK	2093.3	3	4.1946	0.1727
LDGLVETPTGYIESLPR	1861.1	2	5.1407	0.4367
LDGTEVNGR	961.0	2	2.4322	0.2497
LDGVSSHALSDSSTEFMHQIIDQVLQGGPGK	3255.6	3	5.1643	0.3349
LDHFNFER	1078.2	2	2.5398	0.2991
LDHHPEWFNVYNK	1699.8	3	5.5159	0.3692
LDHKFDLMYAK	1381.6	3	4.6014	0.2756
LDHKFDLMYAKR	1537.8	3	4.0645	0.3793
LDHLAEK	825.9	2	2.4555	0.1638
LDHSTDFFSEAFEHNGRPYSLLVYIPSR	3299.6	3	5.2101	0.5168
LDHYAIIKFPLTTESAMK	2079.4	2	4.2222	0.3715
LDIDPETITWQR	1487.6	2	4.212	0.3004
LDIDSPPITAR	1198.4	2	4.0391	0.3387
LDIKLDSEDKDKEGKPLLK	2185.5	3	4.6509	0.2907
LDILDTAGQEEFGAMR	1767.0	2	3.2225	0.3332
LDINLLDNVVNCLYHGEGAQQR	2485.8	3	3.4124	0.1455
LDKAQIHDLVLVGGSTR	1823.1	2	4.8789	0.4834
LDKDNLSYIEHIFEISR	2093.3	3	4.9648	0.3439
LDKEKAETLASSLQEDLAHTR	2356.6	3	4.0812	0.1632
LDKENALDRAEQAEADKK	2045.2	2	4.5475	0.3495
LDKESYPVFYLFR	1677.9	2	3.6873	0.3146
LDKKKYPYWPHQPIENL	2170.5	2	2.7676	0.1398
LDKLNNQSFGTDLPLVDHQVEEHNIFHNEVK	3632.0	3	5.2975	0.3302
LDKSQIHDIVLVGGSTR	1839.1	3	5.7176	0.4588
LDLAGRDLTDYLMK	1624.9	2	3.2917	0.2252
LDLDLTADSQPPVFK	1659.9	2	4.9401	0.4624
LDLEKKVESLLDELAFVR	2118.5	3	3.331	0.314
LDLERETIELVHTEPTDVAQLPSRVPR	3115.5	3	4.7891	0.2775
LDLERKVESLQEEIAFLKK	2289.7	3	3.3167	0.1757
LDLGEDYPSGK	1194.3	2	3.104	0.3418
LDLHVIPVWQK	1348.6	2	3.2378	0.2298
LDLIAQQMMPEVR	1544.9	2	3.9817	0.3758

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LDLIHESILHK	1318.5	2	2.6654	0.1725
LDLLEDR	874.0	2	2.4992	0.1051
LDLMDEGTDAR	1236.3	2	2.8857	0.1874
LDLNDLAR	930.0	2	2.9971	0.1656
LDLQWVQVLSEGWATPLK	2084.4	2	3.1305	0.1938
LDLSKNKLQQLPADFGR	1944.2	3	3.625	0.2365
LDNNKELAFFANALEEVSIETIEAGFMTK	3246.6	3	4.6896	0.3509
LDNSSSGASVVAIDNKIEQAMDLVK	2605.9	3	4.7045	0.3381
LDNVPHTPSSYIETLPK	1912.1	3	4.7985	0.4301
LDNYDAPDIANIAISNELFEEAFAIFR	3073.4	2	2.5436	0.2725
LDPAALAAQLVPAPVPAAALR	2026.4	2	3.7979	0.3293
LDPGSEETQTLVR	1445.6	2	3.4643	0.3457
LDPHLVLDQLR	1319.5	2	2.7395	0.3971
LDPIQPSDVLSLLDNR	1796.0	2	2.7459	0.172
LDPSIFESLQK	1277.4	2	2.8112	0.2395
LDPTGTFEKEMIGR	1594.8	2	4.4918	0.4631
LDQGGAPLAGTNK	1242.4	2	2.7559	0.2554
LDQGGAPLAGTNKETTIQGLDGLSER	2642.9	3	5.2818	0.4534
LDQIHETK	984.1	2	2.6337	0.1252
LDQLIYIPLPDEK	1557.8	2	4.4975	0.3029
LDQLIYIPLPDEKSR	1801.1	2	3.858	0.1993
LDQPMTEIVSR	1289.5	2	3.8867	0.3172
LDQWLTTMLLR	1390.7	2	4.1681	0.3167
LDRDSLVHSSPHVALSHVDAR	2312.5	3	5.7109	0.4074
LDSDRVSSASSTAER	1581.6	3	3.8538	0.2676
LDSEDKDKEGKPLLK	1715.9	3	4.2175	0.2716
LDSGKELHINLIPNKQDR	2091.4	3	4.7384	0.3371
LDSHFAGLFTHR	1401.6	2	3.031	0.3228
LDSKVNIIPIIAK	1424.8	2	4.0531	0.1375
LDSQKHIDFSLR	1459.6	2	3.4043	0.4097
LDSTQVGDFLGDSAR	1581.7	2	2.7207	0.1163
LDSVIEFSIPDSLLIR	1818.1	2	2.9115	0.1975
LDTGKTFQAVMR	1367.6	2	3.6005	0.3552
LDTGPQSLSGK	1103.2	2	3.229	0.3361
LDTLSAEKDALSGAVR	1646.8	2	4.1752	0.256
LDTSQWPLLLK	1314.6	2	2.8693	0.1203

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LDVATDNFFQNPELYIR	2056.3	2	3.4307	0.4227
LDVGNAEVKLEEENR	1715.8	2	4.7584	0.4267
LDVGNFSWGSECCTR	1674.8	2	2.6146	0.1125
LDVMMETENR	1238.4	2	3.5515	0.3668
LDVPVWDVEATLNFLK	1860.1	2	3.0232	0.3579
LDVTILSPSR	1101.3	2	3.4182	0.2199
LDVTTQTPLTPEQLR	1712.9	2	3.9096	0.3595
LDYDEDASAMLK	1371.5	2	3.8167	0.337
LDYGQHVVAGTPGR	1470.6	2	3.2402	0.145
LDYLSSLK	939.1	2	2.4566	0.1717
LDYNNIPTVVFSHPPIGTVGLTEDEAIHK	3178.5	3	3.7412	0.211
LEAADEGSGDVK	1191.2	2	3.3653	0.2736
LEAALGEAK	902.0	1	2.2668	0.1292
LEAALGEAKKQLQDEMLR	2044.4	2	4.6913	0.4499
LEAATQQNQQLR	1400.5	2	3.4883	0.2307
LEAAYLDLQR	1192.3	2	3.2486	0.3065
LEADLAQLSGEVEEAAQER	2059.2	3	3.5465	0.2744
LEAEEGRNSLSPVQATQKPLVSKK	2610.9	3	4.5174	0.2409
LEAEIATYR	1066.2	2	3.9539	0.311
LEAELAAHEPAIQGVLDTGKK	2191.5	3	3.7016	0.3229
LEAELGNMQGLVEDFKNKYEDEINKR	3084.4	3	4.3766	0.4087
LEAGDKKPDAK	1172.3	2	3.2286	0.2063
LEALDANSR	989.1	2	3.0551	0.253
LEALKTPGTWNHITDQIGMFSFTGLNPK	3118.6	3	5.5354	0.427
LEANHGLLVAR	1193.4	2	3.292	0.2823
LEAPDADELPKGEFDPGQDTYQHPPKDSSGQHVDVSPTSQR	4477.7	3	3.8866	0.23
LEAVSHTSDMHR	1383.5	2	3.8528	0.3923
LEDDAKDNQQK	1304.3	2	3.6645	0.2921
LEDEAAAQALIGGR	1414.5	2	3.0126	0.3071
LEDEFDMFALTR	1487.7	2	3.0652	0.1992
LEDEIDFLAQELAR	1662.8	2	5.1461	0.3245
LEDEIDFLAQELARK	1791.0	2	2.9935	0.164
LEDGTEFDSSLPQNQPFVFSLGTGQVIK	3055.3	2	4.6084	0.3714
LEDLIVKDGLTDVYNK	1836.1	2	4.4257	0.3397
LEDLLQDAQDEKEQLNEYKGHLSGLAK	3086.4	3	5.0583	0.3158
LEDQLQGGQLEEVILQAEHELNLAR	2847.1	3	3.3945	0.1462

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LEDTENWLYEDGEDQPK	2082.1	2	4.9698	0.4483
LEDVKNSPTFK	1278.4	2	2.6369	0.2588
LEDVLPLAFTR	1274.5	2	3.8159	0.3352
LEEAEKAADESER	1477.5	2	4.4698	0.3836
LEEAEKAADESERGMK	1793.9	3	3.603	0.2764
LEEASLLHQFQADADDIDAWMLDILK	3002.3	2	2.6227	0.2123
LEEELDDLLVDLDHQR	1953.1	2	5.5594	0.3264
LEEFMAANNNLELVPESLCRCPK	2622.0	3	4.7401	0.3096
LEEHYELR	1089.2	2	2.488	0.1135
LEEIEADKAPAR	1342.5	2	3.0612	0.2793
LEEKVEHLEEGPMIEQLSK	2239.5	3	4.1493	0.3328
LEELDADKAEMR	1420.6	2	2.842	0.1787
LEELKESILADK	1388.6	2	2.9811	0.1834
LEENNHKTEA	1185.2	2	2.7717	0.1971
LEEPEEPKVLTPEEQLADKLR	2464.8	3	4.5917	0.4117
LEEPTPAPSTSYSPQADSLR	2147.3	2	3.1882	0.3584
LEEQAAQHKADIEER	1767.9	2	4.3795	0.3446
LEEQLENLIEFIR	1646.9	2	3.9961	0.3347
LEETQALLR	1073.2	2	2.8901	0.1085
LEEVKDKDGKPLLPK	1710.0	2	4.3852	0.2905
LEEYKKEQAINR	1521.7	2	4.1553	0.2484
LEEYTGTMMK	1203.4	2	2.8906	0.1241
LEFLYDKLR	1197.4	2	2.9045	0.2653
LEFLYDKLREQTLSPTITSGLHNIAR	3017.4	3	6.4318	0.4253
LEFTAHVLSQKFEK	1677.9	2	4.0121	0.328
LEGDTLIIPR	1127.3	2	2.7624	0.2336
LEGENTQDKNK	1276.3	2	3.2516	0.1119
LEGFHTQISK	1160.3	2	2.5753	0.1044
LEGGEVDLKGPK	1242.4	2	2.6642	0.153
LEGGSGGDSEVQR	1291.3	2	3.8901	0.4162
LEGGSGGDSEVQRTMLELLNQLDGFEATK	3096.4	3	3.5595	0.2266
LEGHKEGIVQTEQIR	1737.9	2	4.3667	0.2838
LEGLGSSEADQDGLASTVR	1906.0	2	5.4649	0.5361
LEGLTDEFEELEFLSTINVGLTSIANLPK	3194.6	2	2.8259	0.2875
LEGLTDEINFLR	1420.6	2	4.6244	0.3889
LEGNSPQGSNQGVK	1415.5	2	3.8875	0.2706

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LEGQEEEEDNR	1348.3	2	3.4272	0.1698
LEGQEEEEDNRDSSM	1768.8	2	4.3477	0.3794
LEGQEEEEDNRDSSMK	1896.9	2	4.3878	0.363
LEGQEEEEDNRDSSMKLS	2097.2	2	4.3441	0.3977
LEGQGDVPTPK	1141.3	2	2.6111	0.135
LEGSDVQLLEYEASAAGLIR	2135.4	2	4.0585	0.3381
LEGTNVQEAQKILNNSGLPITSAIDLEDAAKK	3382.8	3	5.599	0.4314
LEGVLAEVAQHYQDTLIR	2056.3	3	5.2728	0.4434
LEHDVNIQFPDKDDGNQPQDQITITGYEK	3359.6	3	6.604	0.4035
LEHEYIHNFK	1330.5	2	2.8045	0.2192
LEHEYIQNFK	1321.5	2	3.3585	0.2933
LEHLITELVHQR	1488.7	2	3.1863	0.2421
LEHLSVSHNNLTTLHGELSSLPSLR	2756.1	3	6.3134	0.521
LEHPVLHVSWNDAR	1673.9	2	4.0047	0.3941
LEHTHFFSR	1174.3	2	2.8283	0.3737
LEILQIHTK	1095.3	2	3.143	0.1489
LEKDLSFKDTQLKEYEELLASVR	2756.1	3	6.1383	0.45
LEKHELIEFR	1314.5	3	3.3782	0.2664
LEKPAKYDDIK	1320.5	2	2.6094	0.1757
LEKPAKYDDIKK	1448.7	2	3.6082	0.2181
LEKPAKYDDIKKVVK	1775.1	2	3.9314	0.2189
LEKPPKEGVYELATFQMKPGGPALWGDAFK	3306.8	3	4.46	0.3153
LELAQYREVAAFAQFGSDLDAATQQLLSR	3213.5	3	4.0034	0.2189
LELFLPEEYPMAAPK	1749.1	2	3.8254	0.1762
LELGNDWDSATKQLLGLQPISTVSPLHR	3090.5	3	5.7969	0.3158
LELMDIIAENVLSEDR	1861.1	2	3.0257	0.3169
LELQGVKGGVDHAAAFGR	1826.0	2	4.7472	0.4841
LEMDLKDLEAHIDSANKNRDEAIK	2770.1	3	3.4976	0.1112
LENDQIESLR	1217.3	2	3.6457	0.213
LENGEIETIAR	1245.4	2	3.3298	0.2542
LENGELEHIRPK	1435.6	2	3.5381	0.2816
LENHQENSR	1127.1	2	2.6451	0.1547
LENLGIPEEELLR	1525.7	2	2.92	0.1341
LENNDNKPVTNSR	1501.6	2	4.4449	0.3665
LENNENKPVTNSR	1515.6	2	4.3435	0.2879
LENTEDIEEVEQHIQTIK	2169.3	2	4.7782	0.316

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LENVQKFPSPEMIR	1689.0	2	4.4991	0.2916
LENYPIPEPGPNEVLLR	1951.2	2	3.9756	0.3523
LEPKPQPPVAEATPR	1630.9	2	2.5434	0.1696
LEPNAQAQMYR	1321.5	2	2.7759	0.3038
LEPQIASASEYAHR	1572.7	2	3.9193	0.3176
LEPVIMELER	1229.5	2	2.4667	0.1648
LEQDEYALR	1137.2	2	3.0855	0.279
LEQEHTNR	1027.1	2	2.6029	0.2387
LEQEIATYR	1123.2	2	3.9215	0.2736
LEQGLSEHQR	1197.3	2	2.4275	0.1911
LEQGQAIDDLMPAQK	1657.9	2	4.567	0.3933
LEQIAAEQKANPDGK	1612.8	2	4.4321	0.3568
LEQIKKTELGAK	1358.6	2	4.4843	0.1533
LEQKGAEADQIIEYLKQQVSLLKEK	2903.3	3	4.496	0.222
LEQLNQYPDFNNYLIFVLTK	2473.8	3	5.5367	0.4147
LEQPDPGAVAAAAILR	1592.8	2	4.5269	0.4696
LEQQLVHVERPILR	1731.0	2	3.0247	0.2348
LEQQVPVNQVFGQDEMIDVIGVTK	2688.1	3	4.9806	0.4056
LEQVEKELLR	1257.5	2	3.1493	0.125
LEQVSSDEGIGTLAENLLEALR	2358.6	2	4.5287	0.4032
LEQYTSAIEGTK	1340.5	2	3.9134	0.3502
LESADKSDQNNTAEGK	1707.7	2	4.1146	0.4102
LESGMQNMSIHTK	1476.7	2	4.5156	0.3751
LESLEHQLR	1125.3	2	2.9757	0.2279
LESLNIQREKEELEQREAELQK	2714.0	3	3.9719	0.2312
LESLSAATTFEPLEPVKDTDIQGFLKNEKDNALLSAIEESR	4522.0	3	4.6379	0.3638
LESLSYQLSGLQK	1466.7	2	3.8875	0.362
LESNKEGTR	1034.1	2	3.2785	0.2782
LESQHHFQIEK	1396.5	2	3.4148	0.2333
LETADKQSVHIVENEIQASIDQIFSR	2972.3	3	6.7691	0.5066
LETPAPQVPAR	1179.4	2	2.8256	0.2439
LEVAPISDIIAIK	1382.7	2	3.3017	0.2921
LEVAPISDIIAIKSPDTFVR	2185.5	2	5.5787	0.4153
LEVEGAK	745.8	1	2.2325	0.1721
LEVGIQAMEHLIHVLQTDR	2203.6	3	4.3333	0.4304
LEVLDSTK	905.0	1	1.7684	0.1328

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LEVLDSTKSSR	1235.4	2	2.7234	0.1842
LEVNLQAMK	1046.3	2	2.5816	0.2151
LEVQATDREENKQIALGTSK	2231.4	3	4.4902	0.2039
LEVSVDSDQKK	1248.4	2	2.9244	0.2298
LEYHQVIQQMEQK	1674.9	2	3.8989	0.1529
LFADAAAALQGFQTQVLGFIEEGEAAMLGR	3126.5	3	6.0139	0.3888
LFADAGLVCITSFISPFAK	2001.4	2	3.825	0.333
LFAGLVHVK	984.2	2	3.4093	0.2264
LFAQLAGDDMEVSATELMNILNK	2524.9	3	4.3846	0.2954
LFAYPDTHR	1120.2	2	2.65	0.2304
LFDANKDR	979.1	2	2.417	0.1249
LFDDTREAEKVLHYLAIQKPADLAR	2914.3	3	4.3178	0.3372
LFDFQGLQHQVAHVATQLEAAR	2480.8	3	6.0954	0.4741
LFDHPESPTPNPTEPLFLAQAEVYK	2842.2	3	4.9349	0.3628
LFDHPESPTPNPTEPLFLAQAEVYKELR	3240.6	3	6.2613	0.3882
LFDIHKQVLK	1241.5	2	2.8959	0.1397
LFDPINLVFPPGGRNPPSSDELDGIIK	2909.3	3	3.5675	0.1659
LFDPQLKEKPEEESLAAPTWLVHLQQVER	3432.9	3	4.5195	0.263
LFDQAFGLPR	1164.3	2	3.8738	0.3691
LFDSDPITVTVPVEVSR	1875.1	2	5.836	0.5217
LFDSDPITVTVPVEVSRK	2003.3	3	3.3071	0.2694
LFDSTTLEHQK	1319.4	2	3.434	0.2722
LFDYFPKPYPNSEAAR	1916.1	2	3.2952	0.3612
LFEAEAQDLFR	1339.5	2	3.3672	0.2789
LFEAEAQDLFRDIQSLPQK	2249.5	3	4.689	0.305
LFEDTKYTTLIAK	1543.8	2	3.2182	0.2124
LFEETGHEDPITK	1516.6	2	2.6441	0.1897
LFEFAGYDVLR	1330.5	2	3.8905	0.3965
LFEGNALLR	1033.2	2	3.5282	0.2893
LFEKPLDSQSIYQLIEISR	2280.6	3	5.7145	0.4477
LFELEEQDLFRDIQGLPR	2219.5	3	4.6379	0.4333
LFENQLVGPESIAHIGDVMFTGTADGR	2876.2	3	5.1079	0.3951
LFEYKEDSKLDYNNIPTVVFSHPPIGTVGLTEDEAIHK	4318.8	3	5.4626	0.4836
LFFAGEHTIR	1191.4	2	2.462	0.2846
LFFQPHQAGLSK	1373.6	2	3.5492	0.3176
LFGGFNSSDTVTSPQR	1713.8	2	2.7475	0.1376

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LFGGNFAHQASVAR	1475.6	2	4.7593	0.4365
LFGHAQLIQSDDDIGDHQPFANAHDVLAR	3202.4	3	5.621	0.4002
LFGHSSTSALSAILR	1560.8	2	4.6961	0.4837
LFGTSPATEAAPPPPEPVPAAEGPATVQSVEDFVPDDRLDR	4245.6	3	4.5949	0.4346
LFGYEPTIYYPK	1491.7	2	3.095	0.2564
LFHTAPNVPHYAK	1495.7	2	3.4426	0.2963
LFIFHSSLPTAEAPGK	1716.0	2	4.0193	0.3973
LFIFHSSLPTAEAPGKLK	1957.3	2	3.2186	0.4111
LFIGGLNTETNEK	1436.6	2	3.7592	0.2572
LFIGGLNTETNEKALEAVFGK	2252.6	2	4.8351	0.483
LFIGGLNVQTSESGLR	1691.9	2	4.5072	0.4316
LFIGGLPNYLNDDQVKELLTSFGPLK	2893.3	3	5.1228	0.3496
LFIGGLSFETTDDSLR	1771.9	2	4.8298	0.3907
LFIGGLSFETTDDSLREHFEK	2442.7	2	4.2614	0.3712
LFIGGLSFETTDESLR	1786.0	2	5.8061	0.1464
LFIGGLSFETTEESLR	1800.0	2	5.3773	0.432
LFIHESIHDEVVNR	1708.9	2	4.3303	0.4087
LFKEVDGEGKPYYEVR	1930.1	2	4.927	0.3761
LFKNQEDLLSEFGQFLPDANSSVLLSK	3041.4	3	4.168	0.1371
LFKPGQEAVK	1117.3	2	2.5374	0.1173
LFLDRDLMTLPIQNK	1818.2	2	4.0193	0.2246
LFLFHTSLPIAEAPGK	1742.1	2	3.6725	0.4073
LFLFHTSLPIAEAPGKLK	1983.4	3	5.0461	0.3769
LFLNEDDKPHNPMVNAGAIVVTSLIK	2837.3	3	6.4072	0.4609
LFLNETQTQEITEDIPVKTLNMK	2707.1	3	4.1493	0.2083
LFLVQLQEK	1118.4	2	2.9374	0.1292
LFNAIIHR	984.2	2	2.8578	0.1454
LFNDSSPVVLEESWDALNAITK	2449.7	2	3.9244	0.3589
LFNDYGGGSFSFSNLIQAVTR	2294.5	2	4.9323	0.3479
LFNHANQEVQR	1356.5	2	3.1058	0.1904
LFNHLSAVSESIQALGWVAMAPKPGPYVK	3112.6	3	5.8049	0.4773
LFNLSKEDDVR	1336.5	2	2.93	0.2286
LFNLSKEDDVRQYVVR	1982.2	2	3.6646	0.3028
LFNLVHQAYEVLSDPQTR	2131.4	2	4.0694	0.2736
LFNVDRHVGMAVAGLLADAR	2126.5	3	5.5958	0.3639
LFPDIPIGYSGHETGIAISVAAVALGAK	2769.2	3	4.4832	0.4041

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LFPDTPLALDANK	1415.6	2	2.7222	0.1403
LFQCLLHR	1030.3	2	2.5539	0.2016
LFQEDDEIPLYLK	1623.8	2	4.0334	0.1842
LFQEDDEIPLYLKGGVADALLYR	2640.0	2	4.1403	0.3277
LFQENSVLSSLPLNSLSR	2005.3	2	5.4586	0.3157
LFQLMVEHTPDEESIDWTK	2319.6	3	4.327	0.3729
LFQLYPR	937.1	2	2.6645	0.154
LFQPSIQLAR	1173.4	2	3.1179	0.2274
LFQQFGLTK	1082.3	2	3.0239	0.2708
LFQQIYSDGSDEVKR	1785.9	2	4.8803	0.3409
LFQVEYAIEAIK	1424.7	2	4.4096	0.2806
LFQVQGTGANNTK	1378.5	2	4.4437	0.2355
LFRPVAADGQLHTLGDLLK	2065.4	3	4.0603	0.2879
LFRPWLNMDR	1348.6	3	3.4352	0.2309
LFSASEFEDPLVGEDTER	2042.1	2	3.4067	0.2579
LFSGDVVLTAR	1178.4	2	3.0637	0.122
LFSQDHLVIYK	1363.6	2	2.429	0.1498
LFSQGQDVSNKVK	1450.6	2	2.9865	0.1406
LFTAESLIGLKNPEK	1660.9	2	4.2465	0.3474
LFTAESLIGLKNPEKSFPVNSDVGVLK	2904.3	3	5.873	0.4293
LFTEEELAR	1108.2	2	2.9043	0.2536
LFTEEELARYGGEEEDQPIYLAVK	2801.1	3	5.7677	0.3798
LFTESTGVLALEDKELGR	1979.2	2	5.3212	0.4351
LFTTMELMR	1142.4	2	2.4042	0.1736
LFTTTEQDEQGSK	1484.5	2	2.6895	0.1462
LFTVQIPHKR	1239.5	2	3.3453	0.316
LFVDKIR	891.1	1	2.4634	0.1039
LFVDKIREYK	1311.6	2	2.8632	0.2182
LFVGGIKEDTEEHHLR	1881.1	2	4.8958	0.425
LFVGGIKEDTEEHHLRDYFEEYGK	2913.1	3	5.9393	0.2987
LFVGGIKEDTEEYNLR	1884.1	2	4.4918	0.4336
LFVGGIKEDTEEYNLRDYFEK	2566.8	3	4.1439	0.1745
LFVGGLKGDVAEGDLIEHFSQFGTVEK	2894.2	3	4.7028	0.3455
LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	3496.9	3	4.1941	0.2311
LFVGGLNFNTDEQALEDHFSSFGPISEVVVVKDR	3768.1	3	4.61	0.3204
LFVGGLSFDTNEQSLEQVFSK	2346.6	3	6.1294	0.4885

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LFVGMLGKQQGEEDVRRLFQPFGHIEECTVLR	3734.3	3	3.205	0.1124
LFVGNLPADITEDEFK	1809.0	2	4.5102	0.4203
LFVGNLPADITEDEFKR	1965.2	2	4.8213	0.3461
LFVGNLPADITEDEFKRLFAK	2424.8	2	3.1399	0.2538
LFVGNLPPDITEEEMR	1861.1	2	3.7275	0.4052
LFVGNLPTDITEEDFK	1839.0	2	4.8292	0.3991
LFVGNLPTDITEEDFKR	1995.2	2	4.527	0.34
LFVTNDAATILR	1334.5	2	3.8727	0.3532
LFVTNDAATILRELEVQHPAAK	2437.8	3	4.0995	0.3713
LFVVPADEAQAR	1316.5	2	2.836	0.1087
LFVYDPNNPPSSEVLR	1848.0	2	4.7122	0.5145
LFYADHPFIFLVR	1638.9	2	4.3295	0.4535
LFYLALPPTVYEAVTK	1826.2	2	2.8982	0.1916
LFYSTFATDDRK	1464.6	2	3.1139	0.2677
LFYSTFATDDRKEGMTAFVEK	2457.7	3	4.2782	0.2883
LGAAPEEESAYVAGEK	1621.7	2	3.2452	0.1792
LGAAPEEESAYVAGEKR	1777.9	2	4.1926	0.4711
LGAASLGAEDPETQVVLINAVK	2196.5	3	4.3694	0.2556
LGADAVGMSTVPEVIVAR	1786.1	2	4.173	0.47
LGADESEEEGR	1192.2	2	3.0113	0.2608
LGADVTAVEFLGHVGGVGIDMEISKNFQR	3061.5	3	6.4342	0.4999
LGAEVYHTLK	1131.3	2	3.0856	0.2573
LGAGEGGEASVSPEK	1388.5	2	3.1688	0.21
LGAGPDGVEEIKR	1341.5	2	3.4123	0.332
LGAGYGLLSEAELEVVPIIAK	2143.5	2	3.535	0.306
LGAGYPMGPFELLDYVGLDTTK	2358.7	2	5.4938	0.5429
LGAHQLDSYSEDAK	1534.6	2	3.4187	0.2144
LGAMDIDTHKK	1229.4	2	2.4777	0.1358
LGANSLLDLVVFGR	1474.7	2	4.4662	0.3999
LGAPALTSR	886.0	2	2.5225	0.1895
LGAPQQPGPGPPPSR	1456.6	2	3.6126	0.3372
LGAQLADLHLDNK	1408.6	2	3.8642	0.2246
LGAQLADLHLDNKK	1536.8	2	3.733	0.3237
LGAQLADLHLDNKKLGEMR	2123.5	3	3.4819	0.2069
LGAQSVYHLHIHVLGGR	1858.1	2	5.0835	0.4231
LGAVDESLSEETQK	1506.6	2	4.7083	0.4598

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LGDAVEQGVINNTVLGYFIGR	2236.5	3	5.7524	0.3858
LGDHGYDNSLPSMHPFLAAHGPAFHK	2818.1	3	4.7808	0.371
LGDKHATLQK	1111.3	2	2.587	0.1968
LGDKIHGFTVNQVTSVPELFLTAVK	2715.1	3	4.3791	0.4703
LGDKIHGFTVNQVTSVPELFLTAVKLTHDDTGAR	3682.1	3	4.7181	0.2834
LGDLWDYHQHR	1440.5	2	2.7116	0.1883
LGDLYEEEMR	1255.4	2	3.5133	0.3153
LGDPAEYAHLVQAIIENPFLNGEVIR	2880.2	3	6.482	0.4513
LGDPAEYAHLVQAIIENPFLNGEVIRLDGAIR	3506.0	3	3.5657	0.2644
LGDPVYDSTITESMDDMLSKVEAAYLR	3021.4	3	3.8399	0.3203
LGDSHDLQR	1041.1	2	2.9697	0.187
LGDSQLVK	860.0	2	3.2239	0.148
LGDSSGPALKR	1101.2	2	2.9748	0.1686
LGDTPGVSYSDIAAR	1522.6	2	3.9906	0.4138
LGDTYPSISNAR	1294.4	2	3.1757	0.2356
LGDVISIQPCPDVK	1484.7	2	4.066	0.2864
LGDVYVNDAFGTAHR	1635.8	2	4.673	0.4099
LGEDIVITAHVLK	1408.7	2	3.1052	0.2171
LGEDLNKWQALLVQIR	1897.2	2	3.4949	0.2435
LGEEDAGAR	917.9	2	3.1454	0.3103
LGEGEGSMTKEEFAK	1613.8	2	3.28	0.3144
LGEGEGSMTKEEFTK	1643.8	2	3.6033	0.3426
LGEHNIEVLEGNEQFINAAK	2226.4	2	6.3035	0.3362
LGEIVTTIPTIGFNVETVEYK	2324.7	2	4.486	0.4115
LGEKDTSLYRPALEELRR	2147.4	3	3.7587	0.2034
LGEKEETIPPDYRLEEVKDKDGKPLLPK	3238.7	3	3.9527	0.2604
LGELFNPYYDPLQWK	1884.1	3	4.7796	0.3207
LGELILTSESSR	1305.5	2	3.6568	0.2643
LGELLFPSSLAGETLGSFSGLR	2252.6	3	4.4599	0.482
LGELPSWILMR	1315.6	2	3.9491	0.3165
LGELQEKLSELKETVELKSQEAQSLQQQR	3371.7	3	3.8222	0.1563
LGELTMQLHPVADSSPAGAK	2023.3	3	3.4038	0.1593
LGELTMQLHPVADSSPAGAKWTETEIEMLR	3312.8	3	3.8252	0.1541
LGEMWNNTAADDKQPYEK	2111.3	2	4.9328	0.4601
LGEMWNNTAADDKQPYEKK	2239.5	3	4.4009	0.2519
LGEMWSEQSAK	1266.4	2	3.176	0.2848

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LGENMILKR	1074.3	2	2.4346	0.1958
LGENNAELNALAK	1357.5	2	4.0345	0.3288
LGERDDTIPPEYR	1561.7	2	2.8591	0.2925
LGESQTLQQFSR	1394.5	2	3.5235	0.2361
LGESVQDLSSFDEYSSELK	2134.2	2	4.2435	0.2549
LGESVQDLSSFDEYSSELKSGR	2434.6	3	3.7697	0.3169
LGETYKDHENIVIAK	1730.9	3	4.0599	0.3981
LGEVVELLFPPVAR	1539.8	2	2.6108	0.1008
LGEVVNTHGPVEPDKDNIR	2090.3	3	4.6554	0.4219
LGEYEDVSRVEK	1424.5	2	3.1164	0.252
LGFAGLVQEISFGTTK	1668.9	2	3.0871	0.2966
LGFAGLVQEISFGTTKDK	1912.2	2	2.6382	0.178
LGFDVVFNYK	1202.4	2	2.7228	0.1698
LGFEDGSVLK	1065.2	2	3.1663	0.226
LGFEDGSVLKQFLSETEKMSPEDR	2744.0	3	3.77	0.1102
LGFEGGQTPFYIR	1485.7	2	2.5872	0.1642
LGFEGGQTPFYIRIPK	1824.1	2	3.6684	0.3557
LGFFTTYFLPLANTLK	1847.2	2	4.4999	0.4119
LGFGSFVEK	984.1	2	2.6673	0.2731
LGFHLPLEVAYQR	1543.8	3	5.0778	0.3038
LGFISKHELYSR	1450.7	2	2.9739	0.3655
LGFMSAFVK	1000.2	2	3.0379	0.3157
LGFSEVELVQMVVDGVK	1850.2	2	5.4736	0.4443
LGFSNSNPAQDLERVPPGLLALDNMLYFSR	3336.8	3	3.6572	0.1595
LGFVAGVINR	1046.2	2	3.4576	0.2051
LGGAIAAINSIQHNTR	1636.8	2	4.0813	0.3171
LGGEAAHLPHLRPLPESQPSSSPLLQTAPGVK	3286.7	3	3.6689	0.2287
LGGGMPGLGQGPPTDAPAVDTAEQVYISSLALLK	3325.8	3	5.4092	0.4269
LGGHDDLHDDLQEDFHGHSHR	2438.5	3	5.2283	0.4052
LGGHGPSFPLK	1110.3	2	2.8297	0.2936
LGGHGPSFPLKGITEQQKEGLEIVK	2664.1	3	5.2111	0.4008
LGGIGQFLAK	1004.2	2	3.5022	0.2473
LGGKGYKLSPEDYTLK	1770.0	3	4.228	0.3267
LGGNEIVSFLK	1177.4	2	2.4197	0.1867
LGGNPGTNSR	973.0	2	2.5027	0.1369
LGGNVVVSLEGKPL	1382.6	2	3.4791	0.3225

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LGGNYGPTVLVQQEALKR	1944.2	2	2.695	0.213
LGGPEAGLGEYLFER	1608.8	2	4.997	0.4805
LGGPQASLSTK	1059.2	2	2.5259	0.264
LGGSAVISLEGKPL	1341.6	2	5.2217	0.3797
LGGSLADSYLDEGFLLDKK	2042.3	2	4.9573	0.4377
LGGSPFGPAGTGK	1146.3	2	2.7778	0.259
LGGSPTSLGTWGSWIGPDHDKFSAMK	2734.0	3	4.1587	0.4541
LGGSQEDQIK	1075.2	2	2.7699	0.1844
LGGSQEDQIKNAIDKLFVLFGAEILK	2848.3	3	5.2214	0.357
LGGSQEDQIKNAIDKLFVLFGAEILKK	2976.5	3	4.8167	0.3197
LGGVKYDIDLPNKK	1560.8	2	3.8239	0.195
LGHAETDEQLQNIISK	1797.0	2	3.5945	0.3116
LGHASDR	755.8	1	2.1718	0.151
LGHASDRIIALDGDTK	1682.9	2	4.3511	0.4024
LGHELQQAGLK	1194.4	2	2.7429	0.1906
LGHFAPVDAVADQR	1496.7	2	2.8041	0.1745
LGHGLLSGEYSKPVPESGDGERVPEQK	2867.1	3	5.5753	0.4738
LGHGLLSGEYSKPVPESGDGERVPEQKEVQDGIAPR	3833.2	3	5.8847	0.4442
LGHLKKEEAEIQAELER	1994.2	2	2.8787	0.147
LGHPEALSAGTGSPQPPSFTYAQQR	2598.8	3	5.3893	0.4177
LGHQLAEIR	1037.2	2	2.992	0.1248
LGHSFSLVGNK	1159.3	2	3.2384	0.3766
LGHSHLSYLSVR	1369.6	3	4.641	0.4266
LGIEGLSLHNVLK	1393.7	2	4.2318	0.3911
LGIEKTDPTTLTDEEINRFAR	2420.7	3	3.6973	0.2662
LGIHEDSQNR	1169.2	2	2.9178	0.3351
LGIHEDSQNRK	1297.4	2	3.0021	0.2056
LGIHEDSTNR	1142.2	2	3.3157	0.3845
LGIHEDSTNRR	1298.4	2	2.4984	0.1051
LGIHSALLDEKKDQDSK	1898.1	3	3.8842	0.2107
LGILDKVVNSDPVEEAIR	1968.2	2	2.9716	0.1566
LGILTHLYR	1086.3	2	3.2219	0.1278
LGINKTDPSTLTEEEVSK	1962.1	3	3.5007	0.1807
LGINKTDPSTLTEEEVSKFAR	2336.6	3	3.9697	0.2942
LGINSLQELK	1115.3	2	2.997	0.2091
LGINSLQELKQNIAK	1669.9	2	3.5956	0.1762

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LGIPATIVLPESTSLQVVQR	2122.5	3	4.6609	0.4431
LGIQAEPLYR	1160.3	2	2.7484	0.1668
LGIQTDDKGHIIVDEFQNTNVK	2485.7	3	6.2167	0.4384
LGITHVLNAAEGR	1351.5	2	4.119	0.3433
LGIYDADGDGDFDVDDAK	1901.9	2	5.7752	0.5399
LGIYDADGDGDFDVDDAKVLLGLKER	2811.1	3	6.6423	0.5206
LGKADIVQQLLQQGASPNAATTSGYTPLHLSAR	3408.8	3	7.3669	0.5291
LGKDSGLKPFEQVK	1546.8	2	4.7759	0.2834
LGKEIEEYIHKPK	1584.8	3	4.3236	0.178
LGKSEAPETPMEEEAELVLTEK	2431.7	3	4.1966	0.2983
LGKSEVELVQLVIDGVNYLIDCER	2706.1	2	3.1395	0.194
LGLDFPNLPYLIDGTHK	1914.2	3	3.584	0.1769
LGLDYEER	995.1	1	2.2941	0.1534
LGLDYEERVLPSIVNEVLK	2187.5	3	3.6464	0.2361
LGLDYEERVLPSIVNEVLKSVVAK	2672.1	3	5.1349	0.3407
LGLDYSYDLAPR	1383.5	2	3.2655	0.2771
LGLEAKKEENLADWYSQVITK	2436.7	2	2.6455	0.1924
LGLENAEALIR	1199.4	2	3.237	0.2465
LGLGEGAEEK	1003.1	2	2.5427	0.1487
LGLGGNAPVSIPQQSQSVK	1881.1	2	3.4023	0.3746
LGLGHNQIR	1008.2	2	2.7029	0.2174
LGLGIDEDDPTADDTSAAVTEEMPPLEGDDDTSR	3549.6	3	6.691	0.5582
LGLGIDEDDPTADDTSAAVTEEMPPLEGDDDTSRMEEVD	4153.3	3	5.354	0.488
LGLGIDEDEVAAEEPNAAVPDEIPPLEGDEDASR	3534.7	3	4.7938	0.4957
LGLGILNNAFR	1188.4	2	2.6668	0.2842
LGLHYVVYSGLENIKK	1834.2	3	3.622	0.2003
LGLIEWLENTVTLKDLLLNTMSQEEK	3032.5	3	3.7756	0.1653
LGLIPLISDDIVDKLQYSR	2159.5	2	3.2577	0.3182
LGLKEMDNAGQLVFLATEGDHLQLSEEWFYAHIIPFLG	4304.9	3	3.6583	0.1701
LGLKPLEVNAIKK	1423.8	3	3.5978	0.2581
LGLLDNHSSEFNVTR	1702.8	2	3.8449	0.385
LGLLGALMAEDGVR	1415.7	2	2.948	0.3741
LGLLGDSVDIFK	1277.5	2	4.2061	0.3368
LGLLGDSVDIFKGIPFAAPTK	2160.5	2	4.6823	0.4069
LGLLGLANSLAIEGR	1497.8	2	4.5061	0.3922
LGLLGLANSLAIEGRK	1625.9	2	4.4681	0.4555

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LGLMRDDTIYEDEDVKEAIR	2382.6	3	6.1399	0.3956
LGLPGDEVDNKVK	1384.6	2	3.1273	0.3235
LGLPPLTPEQQEALQK	1763.0	3	4.0961	0.1122
LGLQASDIK	945.1	2	3.1309	0.2278
LGLQNDLFSLAR	1347.5	2	3.8341	0.383
LGLQYMELIPK	1305.6	2	2.7397	0.254
LGLSLVVPGGGIK	1210.5	2	3.0885	0.3559
LGLSTLGELKQNLSR	1629.9	3	3.8843	0.4315
LGLSVFTHHR	1167.3	2	2.7865	0.2531
LGLTEIRK	930.1	2	2.5402	0.1056
LGLVFDDVVGIVEIINSK	1931.3	2	3.308	0.2389
LGLVFDDVVGIVEIINSKDVK	2273.7	3	3.4435	0.2753
LGLVGVNLTLDGVK	1398.7	2	4.4213	0.4582
LGMIAGGTGITPMLQLIR	1843.3	2	4.452	0.3766
LGNDFHTNKR	1202.3	2	3.1936	0.2951
LGNDFMGITLASSQAVSNAR	2053.3	2	5.1883	0.4289
LGNFFSPK	910.1	2	2.7191	0.2281
LGNIEFKPESR	1290.5	3	3.4098	0.2819
LGNPTRSEDLLDYGPFR	1951.1	3	3.9066	0.2042
LGNQNVETK	1003.1	2	2.9938	0.2312
LGNSADALESAKR	1332.4	2	3.5898	0.2902
LGNSHQPEKPLVR	1475.7	3	3.3541	0.3307
LGNTISSLFGGGTTPDAK	1736.9	2	4.033	0.349
LGNTSEAHGAAR	1184.2	2	3.6512	0.2564
LGPALATGNVVVMK	1370.7	2	3.5622	0.2891
LGPASAADTGSEAKPGALAEGAAEPEPQR	2749.9	3	4.2616	0.1722
LGPDDPNVAK	1026.1	2	3.2289	0.3076
LGPDDPNVAKTK	1255.4	2	2.6286	0.1734
LGPGGLDDRYSLVSEQLEPAATSTYR	2797.0	3	5.6694	0.285
LGPGGLDPVEVYESLPEELQK	2270.5	2	5.4409	0.5118
LGPLFSLLNENHR	1510.7	2	3.3816	0.3734
LGPLFSLLNENHREK	1768.0	2	2.5854	0.1666
LGPLLDILADSR	1283.5	2	2.4956	0.1046
LGPLLEQEIPQSVPGVQTLLGAGR	2473.9	3	3.412	0.227
LGPLQVAR	854.0	1	1.8907	0.1401
LGPNDQYKFYSVNVDYSK	2138.3	3	3.3007	0.2022

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LGQAEKTELDAHLENLLSK	2110.4	3	6.1017	0.4235
LGQEATVGK	903.0	2	2.9144	0.2875
LGQGLGPIHLSEVR	1476.7	2	2.9827	0.322
LGQHVPTLHPTSEELTIAGMTFTTFDLGGHEQAR	3694.1	3	4.8749	0.3659
LGQHVPTLHPTSEELTIAGMTFTTFDLGGHVQAR	3664.1	3	4.6181	0.3958
LGQHVVGMAPLSVGSLDDEPGGEAETK	2695.0	3	6.4728	0.4843
LGQLEEELEEEQSNSELLNDR	2475.6	2	4.7805	0.3957
LGQLEGLLQAHGDEGCGACGGVQEELGR	2798.1	3	5.5215	0.4115
LGQLNIDISNIK	1328.5	2	2.9412	0.2579
LGQMIVDYENPLKK	1648.9	2	3.2189	0.2883
LGQMVLSGVDTVLGK	1517.8	2	4.6745	0.4014
LGQMVLSGVDTVLGKSEEWADNHLPLTDAELAR	3567.0	3	6.4726	0.4943
LGQSDPAPLQHQMDIYQK	2070.3	2	4.703	0.4804
LGREEPAMSMDANGK	1606.8	2	3.7529	0.2808
LGRLDAVLQR	1141.3	2	2.9066	0.1555
LGRLDQAVLDLQR	1497.7	2	2.7972	0.2056
LGRYNEEERAQQEAEAAQR	2249.3	3	3.5815	0.2815
LGSAADFLLDISETDLSSLTASIK	2468.7	2	5.3439	0.4547
LGSDIKLEDSLWVSLTDQHVQLPMAMTAENLAVK	3755.3	3	4.9445	0.4046
LGSDPQKK	873.0	2	2.551	0.1032
LGSGEPSHSVK	1098.2	2	2.8216	0.305
LGSGGHLHLR	1047.2	2	2.6297	0.3036
LGSGPDGAEEIKR	1329.4	2	3.2451	0.1953
LGSIAIQGAIEK	1200.4	2	4.4022	0.2805
LGSIAIQGAIEKAGIPKEEVKEAYMGNVLQGGEGQAPTR	4012.5	3	7.7184	0.4372
LGSKDVVIK	959.2	2	2.5055	0.1215
LGSLALHNSESLDQEHAK	1950.1	3	3.3222	0.3718
LGSLVDEFK	1008.2	2	2.7266	0.2576
LGSLVDEFKELVYPPDYNPEGK	2510.8	3	4.9083	0.4447
LGSLVDEFKELVYPPDYNPEGKVTK	2839.2	3	4.0364	0.3267
LGSLVDEFKELVYPPDYNPEGKVTKR	2995.4	3	5.4978	0.3808
LGSLVENNER	1131.2	2	3.0694	0.1835
LGSLVENNERVFDHK	1757.9	2	3.8094	0.333
LGSMHSPFR	1032.2	2	3.3067	0.413
LGSPDEEFFHKVR	1561.7	2	3.2366	0.3499
LGSQHSPGR	939.0	2	2.8737	0.2226

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LGSSFTKVQDYLR	1514.7	2	3.1641	0.3758
LGSSGLGSASSIQAAVR	1561.7	2	4.6519	0.4875
LGSSSEIEVPAKTTHVLK	1897.2	2	3.8173	0.3887
LGSTAPQVLSTSSPAQQAENEAK	2315.5	2	5.2179	0.5185
LGSTEVASNVPK	1202.3	2	3.106	0.2776
LGSTIFVANLDFK	1425.7	2	4.0628	0.3155
LGSTVFVANLDYK	1427.6	2	2.4221	0.1277
LGTDDTVMK	980.1	2	2.9521	0.3019
LGTDDTVMKANLHK	1543.8	2	2.9532	0.1555
LGTFEVEDQIEAAR	1578.7	2	3.8897	0.3921
LGTHYQITK	1061.2	2	2.4293	0.279
LGTITPDGADVYSYDEDDMVLDPSLAEHLSHFGIDMLK	4182.6	3	5.0474	0.4402
LGTLSPAFSTR	1150.3	2	3.1429	0.2014
LGTNVESVLQAIIER	1642.9	2	3.0344	0.1664
LGTPQQIAIAR	1168.4	2	2.5735	0.277
LGTPVLQALGDGDFVK	1630.9	2	4.8152	0.4527
LGTQEYLQQLESHMK	1806.0	2	3.0015	0.208
LGTQHPESNSAGNDVFAK	1873.0	2	4.4081	0.4663
LGVAGQWR	887.0	2	2.8722	0.206
LGVFRAESEEGPDVLR	1775.0	2	3.9934	0.3091
LGVIEDHSNR	1140.2	2	3.4289	0.2988
LGVLHPDVITK	1192.4	2	3.1368	0.3064
LGVLHVGQK	951.1	2	2.9843	0.233
LGVLHVGQKLEEQDEFEKIFK	2487.8	3	5.4557	0.4073
LGVNNISGIEEVNMFTNQGTVIHFNNPE	3089.4	3	6.3016	0.16
LGVQDLFNSSK	1208.3	2	3.4739	0.1834
LGVQDLFNSSKADLSGMSGAR	2154.4	3	3.9387	0.3181
LGVQVREELLRAQEAPGQAEPPAAAEVQGAGNENEPR	3883.2	3	3.3396	0.2209
LGVQVVITDPEKLDQIR	1924.2	2	4.7299	0.3729
LGVRPSQGGEAPR	1324.5	2	2.8733	0.2136
LGVTANDVK	917.0	2	2.9627	0.2962
LGVTANDVKNVIIWGNHSSTQYPDVNHAK	3179.5	3	5.9912	0.3902
LGWDPKPGEGHLDALLR	1875.1	3	3.4169	0.2581
LGWVRPDLGELSK	1470.7	2	3.3983	0.1815
LGYAGNTEPQFIIPSCIAIK	2136.5	2	3.412	0.2586
LGYAGNTEPQFIIPSCIAIRESAK	2580.0	3	3.6827	0.188

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LGYAVYETPTAHNGAK	1692.9	2	4.2129	0.3748
LGYFLALTGFR	1258.5	2	3.0946	0.1145
LGYFSVDPDSHQGK	1550.7	2	2.4489	0.2144
LHAATSK	727.8	1	2.3443	0.1734
LHAEAIKR	938.1	2	2.4879	0.2125
LHAEAIKRDPNLFPFEK	2026.3	2	3.6294	0.2455
LHAEFAAERDWEQFHQPR	2268.4	3	3.2279	0.2671
LHAGPEPQALPAFSDLEALSLSTLYSLQK	3098.5	3	4.0889	0.2646
LHAIKEQLIQEGLLDR	1877.2	2	4.0373	0.3125
LHALVVGPGLGR	1189.4	2	3.2505	0.2188
LHALVVGPGLGRDDALLR	1873.2	2	3.4843	0.3501
LHAVLKPFLLR	1307.7	2	2.9165	0.1538
LHAVNAEECNVLQGR	1653.8	2	3.5979	0.2725
LHAVVETLVNHR	1388.6	2	3.21	0.3368
LHAYDQHLNMILGDVEETVTTIEIDEETYEEIYK	4056.4	3	7.0439	0.4809
LHDALDAK	883.0	1	2.7694	0.236
LHDALDAKSKEFAQIIK	1928.2	3	3.6941	0.3477
LHDETLTYLNQGQSYEIR	2181.3	3	5.1545	0.3159
LHDNLIISDLENTVK	1724.9	2	2.7959	0.2381
LHDPEGMGIIPR	1335.6	2	2.5771	0.1702
LHDPQLMGIIPR	1390.7	2	2.4004	0.1638
LHDSISEEGFHYLVFDLVTGGELFEDIVAR	3409.7	3	5.094	0.4681
LHDSLAIER	1054.2	1	3.1142	0.3002
LHDSLAIERK	1182.4	2	3.32	0.1841
LHDSSGSQVGTGFK	1420.5	2	3.7206	0.3784
LHDVEHVLIDVGTGYYVEK	2187.4	2	5.9305	0.5616
LHDVLHSDKK	1192.3	2	3.3059	0.2961
LHDVNSDGFLDEQELEALFTK	2421.6	2	4.8905	0.4662
LHDVNSDGFLDEQELEALFTKELEK	2921.2	3	5.4028	0.4961
LHEADATLKR	1154.3	2	2.9218	0.1994
LHEANNELQK	1196.3	2	2.4753	0.1036
LHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	3925.3	3	7.8874	0.5775
LHEEEPPQNMKPQSGNDKPLSK	2504.8	3	3.2877	0.2117
LHEEINMKEQK	1399.6	2	2.8997	0.1758
LHEENFEITTLR	1502.7	2	2.6451	0.3062
LHEKVNIIPLIAK	1488.8	2	4.3181	0.392

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LHELNQKWEALK	1509.7	2	2.9921	0.1818
LHELTSLLEEKDSLIKR	2025.3	3	4.2503	0.2953
LHEVGRTEPELLVAHAYTR	2192.5	3	4.6916	0.3804
LHEWTKPENLDFIEVNVSLPR	2537.9	3	4.5845	0.3402
LHFEKDADSSER	1434.5	2	3.2628	0.428
LHFFMPGFAPLTAR	1605.9	2	4.0512	0.4718
LHFFMPGFAPLTSR	1621.9	3	4.3162	0.3791
LHFLHSDLALR	1322.5	2	3.1626	0.3166
LHFTIKDPANR	1312.5	2	3.2205	0.3284
LHGELR	724.8	1	1.6777	0.1163
LHGGIDILVSNAAVNPFFGSIMDVTEEVWDKTLDINVK	4159.7	3	4.1801	0.3207
LHGGIDILVSNAAVNPFFGSLMDVTEEVWDKTLDINVK	4159.7	3	4.583	0.2139
LHGGSAPLPQDR	1248.4	2	2.7267	0.2335
LHGGTPANFLDVGGGATVHQVTEAFK	2624.9	3	5.0694	0.4979
LHGHVSAHPDILSLENR	1896.1	2	3.222	0.2694
LHGLNINYNCEICGNYTYR	2261.5	2	3.2723	0.2336
LHGQHLVQQLVLR	1541.8	2	2.9147	0.2315
LHGSPGHAFTLVGR	1449.6	2	3.1784	0.5107
LHGVNINVEASK	1281.4	2	3.0015	0.2578
LHGVRDYAAYNVLDDPELR	2217.4	3	4.4402	0.1795
LHHEFLQQSLR	1408.6	2	2.6069	0.2618
LHHELENVEEKR	1533.7	2	3.3929	0.3462
LHHILQQDAPFGPEDYDQLAPTR	2662.9	3	4.7921	0.3331
LHHQNQQQIQQQQQLQR	2312.5	2	5.761	0.3248
LHHVSSLAWLDEHTLVTTSHDASVK	2785.1	3	5.3382	0.4363
LHIIEVGTPPTGNQPFPK	1946.2	2	4.8332	0.3821
LHIIEVGTPPTGNQPFPKK	2074.4	2	3.5253	0.2633
LHIQNPSFSQINQLVSTIMSASTTTLR	2989.4	3	3.3508	0.1685
LHISPSNMTNQNTNEYLEK	2234.4	3	4.0201	0.1112
LHISQLQHENSILK	1660.9	2	4.4958	0.3949
LHIVQVVCKK	1167.5	2	2.8072	0.1793
LHKNDIAINELMK	1539.8	2	3.6308	0.1854
LHLETDSLALVALGALDTALYAAGSK	2615.0	3	3.4603	0.1674
LHLFPDEYIPEDILK	1843.1	2	3.2485	0.3196
LHLFPDEYIPEDILKNLVEELPQPR	3019.4	3	5.7631	0.4525
LHLGFIEIR	1098.3	2	3.3015	0.1772

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LHLGHTFSLSK	1240.4	2	3.2768	0.2677
LHLGIPEAVFVEDVDSFMK	2147.5	2	4.8668	0.4078
LHLGIPEAVFVEDVDSFMKQPGNETADTVLK	3401.8	3	4.2149	0.2995
LHLGIPEAVFVEDVDSFMKQPGNETADTVLKK	3530.0	3	3.6223	0.2392
LHLGSTPHNLTDANIHELAR	2210.4	3	6.0022	0.5674
LHLGTTQNSLTEADFR	1804.0	2	3.473	0.1292
LHLIAQELPFDR	1452.7	2	2.793	0.1185
LHLIAQELPFDRFSEVK	2043.4	2	4.3716	0.3351
LHLNQNGDHNTK	1391.5	2	3.6304	0.2761
LHLPADDVVSIIEEVEEK	2036.3	3	5.5092	0.3752
LHLPADDVVSIIEEVEEKR	2192.5	2	4.5685	0.4631
LHLPADDVVSIIEEVEEKRK	2320.6	2	3.6665	0.256
LHLQGQTMQDPFGEKR	1886.1	2	4.5965	0.4438
LHLQSTDYGNFLANEASPLTVSVIDDR	2977.2	3	3.9476	0.3334
LHLSGIDANPNALFPPVEFPAPR	2473.8	2	5.7497	0.5006
LHLVALVGTQGR	1264.5	2	3.3096	0.263
LHLVESLLSR	1167.4	2	2.7182	0.2703
LHLYNSLTR	1117.3	2	2.4368	0.2079
LHNAANANQK	1081.2	2	2.7431	0.179
LHNAIEGGTQLSR	1396.5	2	4.1869	0.375
LHNALALIR	1021.2	2	2.6493	0.2671
LHNFHQLSAPQPCFTFSHPNR	2479.8	3	3.3972	0.1057
LHNMIVDLDNVVK	1510.8	2	4.4444	0.4243
LHNMIVDLDNVVKK	1639.0	2	4.6196	0.4479
LHNQQALSSSIEEGLR	1782.9	2	5.0531	0.3422
LHNSLIGTK	983.1	2	2.5213	0.2275
LHNVFNDFLMLSNTQFIENR	2453.8	3	4.4539	0.3223
LHPDKNPNNPNAHGDFLK	2029.2	2	4.0023	0.3881
LHPEDFPEEDKKTYGEIFEK	2452.7	2	4.0741	0.435
LHPESKDDKHGSYEDAVHSGALND	2622.7	3	3.5716	0.2365
LHPVILASIVDSYER	1713.0	2	5.0432	0.5168
LHQAKEQYEALQEETR	1974.1	3	3.6021	0.1926
LHQDLAVQER	1209.3	2	2.6997	0.1102
LHQLAMQQSHFPMTHGNTGFSGIESSSPEVK	3384.7	3	7.288	0.477
LHQLDAEKER	1239.4	2	2.9742	0.164
LHQVYFDAPTCR	1450.6	2	2.7945	0.2147

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LHRPPVIVLQR	1328.6	3	3.3178	0.2821
LHRTELATQEK	1326.5	2	2.4569	0.1352
LHSEFHLSTFK	1346.5	2	2.6616	0.2843
LHSTSQNINLGPSGNPHAKPTDFDFLK	2937.2	3	3.4974	0.1327
LHTAVVSTPPR	1178.4	2	3.0348	0.2788
LHTDDELNWLDHGR	1721.8	3	3.9014	0.2718
LHTDGDKAFVDFLSDEIKEER	2465.7	3	6.3997	0.5997
LHTDGDKAFVDFLSDEIKEERK	2593.8	3	5.2253	0.4683
LHTGSEGQGDSR	1244.3	2	3.2154	0.4221
LHTLEEEKEELAQYQK	1989.2	2	5.1425	0.2587
LHTLSVEHQR	1220.4	2	2.5529	0.3069
LHTNFHIPK	1107.3	2	2.7786	0.197
LHTVGGPGSARPR	1305.5	2	2.7703	0.3583
LHVDVPKDLTKPVVTISDEPDILYKR	2992.5	3	5.8969	0.4691
LHVENEDKK	1112.2	2	2.5796	0.175
LHVSNIPFR	1083.3	2	2.5563	0.1562
LHYCVSCAIHNKVVR	1743.1	2	3.2508	0.2955
LHYCVSCAIHSK	1361.6	2	3.3	0.1741
LIADLGSTSITNLGFR	1678.9	2	5.2978	0.4601
LIAEGNKEELRK	1400.6	2	3.6638	0.1961
LIAFTSEHSHFSLKK	1746.0	2	3.9862	0.2688
LIAHAGSLLNLAK	1321.6	2	2.7407	0.177
LIAHAGSLTNLAK	1309.5	2	3.0003	0.323
LIAHAGSLTNLAKYPASTVQILGAEK	2668.1	3	5.8026	0.4326
LIAINANDPEASK	1356.5	2	3.8568	0.328
LIAINANDPEASKFHDIDDVKK	2454.7	3	4.6537	0.4723
LIALLEVLSQK	1227.5	2	3.9197	0.3627
LIALLEVLSQKK	1355.7	2	3.827	0.2531
LIALLEVLSQKR	1383.7	2	3.8652	0.346
LIALSIDSVEDHLAWSK	1898.1	2	4.6544	0.4708
LIAPVAEEEATVPNNK	1695.9	2	3.8986	0.3738
LIAVDISPVESTGVSHFATYVAAMR	2636.0	3	3.3153	0.2812
LIAVIGDEDTVTGFLLGGIGELNK	2445.8	2	5.0235	0.4095
LIAYQEPADDSSFSLSQEVLR	2369.6	2	4.7149	0.3825
LICCDILDVLDKHLIPAANTGESK	2583.0	3	5.4937	0.3631
LICCDILDVLDKHLIPAANTGESKVFYYK	3283.8	3	5.1765	0.2046

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LIDDEVRILINDAYKR	1947.2	3	4.4501	0.2788
LIDDMVAQAMK	1235.5	2	3.665	0.3776
LIDDMVAQVLK	1245.5	2	4.2346	0.2542
LIDDYDSTK	1070.1	1	2.1144	0.2701
LIDDYDSTKSGLDHK	1707.8	2	3.8526	0.3321
LIDDYDSTKSGLDHKFQDDPDGLHQLDGTPLTAEDIVHK	4351.6	3	4.7158	0.3479
LIDDYGGEDDELAGGPGGGAGGPGGGLYGELPEGTSITVDSKR	4108.3	3	7.0831	0.5262
LIDDYGVEEEPAELPEGTSLTVDNK	2734.9	3	4.5669	0.2158
LIDDYGVEEEPAELPEGTSLTVDNKR	2891.1	3	5.5767	0.3932
LIDIFYPGDQQSVTFGTK	2030.3	2	4.1466	0.4556
LIDLHSPSEIVK	1351.6	2	3.4898	0.3217
LIDLHTNVATAVLEHIK	1888.2	3	5.7632	0.5201
LIDLHTNVATAVLEHIKAR	2115.5	3	4.1176	0.3885
LIDREIISHDTR	1468.6	2	2.9362	0.2057
LIDREIISHDTRR	1624.8	3	3.7116	0.2921
LIDVNHYAKDEVAAR	1714.9	2	4.1052	0.3897
LIDVPDPVPALDLGQQLQLK	2173.5	2	3.0961	0.3457
LIDWGLAEFYHPAQEYNVR	2322.6	2	2.4657	0.1657
LIDYGKLGDTNER	1494.6	2	3.767	0.384
LIEADISKR	1045.2	2	2.6519	0.1768
LIEDFLAR	977.1	2	3.1506	0.1338
LIEDKPR	871.0	1	2.1207	0.1217
LIEEKGAVDALAAALAHISGASSFEPR	2725.1	3	5.1354	0.4062
LIEEKGAVEALAAALAHISGATSVDQR	2722.0	3	5.1256	0.3782
LIEFSPLR	975.2	2	2.6453	0.1945
LIEGVHPGSLVEKLPDSPALAKK	2399.8	2	2.8143	0.1114
LIEKLDIKLDSEDKDKEGKPLLK	2669.1	3	4.5338	0.2219
LIEKNKMSDGKKEELQK	2019.4	3	3.7479	0.1239
LIEKQISQMADDTVAELDRHLAVK	2725.1	3	3.8101	0.2875
LIEKYIAENGTDPINNQPLSEEQLIDIK	3199.6	3	5.327	0.3698
LIELHSPDSR	1167.3	2	2.4653	0.1963
LIELKEHPAHER	1472.7	2	3.5367	0.2517
LIELYKEAGISKDR	1635.9	2	3.869	0.4087
LIENVDPEKAVQLYQQTANVFENEER	3078.3	3	4.4887	0.1858
LIENVDPEKAVQLYQQTANVFENEERLR	3347.7	3	4.7805	0.2964
LIERDPYEHPER	1554.7	3	3.3106	0.2186

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LIESAEELIR	1173.3	2	2.9284	0.1679
LIEVDDER	989.1	2	3.0558	0.2598
LIEVDDERK	1117.2	2	2.9706	0.2145
LIEVDDERKLR	1386.6	2	2.8319	0.2015
LIEYYQQLAQK	1397.6	2	3.1747	0.1547
LIFKPDLTLEEVQAENPKVSR	2427.8	3	4.2872	0.2713
LIFPYVELDLHSYDLGIENR	2407.7	2	4.7906	0.4161
LIFPYVELDLHSYDLGIENRDATNDQVTK	3380.7	3	4.8417	0.3182
LIGDAAKNQLTSNPENTVFDAK	2347.6	2	5.6569	0.3583
LIGDAAKNQLTSNPENTVFDAKR	2503.8	3	4.7877	0.2691
LIGDAAKNQVALNPQNTVFDAKR	2484.8	3	4.2224	0.2233
LIGDAAKNQVAMNPTNTVFDAK	2319.6	2	5.8961	0.4492
LIGDAAKNQVAMNPTNTVFDAKR	2475.8	3	4.202	0.3037
LIGEYGLR	921.1	2	2.8936	0.1446
LIGLSATLPNYEDVATFLR	2094.4	2	3.0951	0.221
LIGNMALLPIR	1211.5	2	2.9878	0.2201
LIGQIVSSITASLR	1458.7	2	4.8713	0.4383
LIHEDGIIRPYDRQESEGSDLLENHIK	3178.5	3	3.9778	0.2701
LIHEQDLEWLQQADVVVAEVTQPSLGVGYELGR	3694.1	3	4.2966	0.2872
LIHPDEDISLEER	1566.7	2	3.0985	0.3495
LIHPDEDISLEERR	1722.9	2	3.6813	0.2476
LIHPSKLNEVEQLLYYLQNR	2471.8	3	4.1606	0.2437
LIHQTNLILQTFK	1569.9	2	4.2619	0.3696
LIKDDFLQQNGYTPYDR	2087.3	2	5.1161	0.4314
LIKDGLIIR	1041.3	2	2.7423	0.2388
LIKEFSIYMTK	1373.7	2	3.5146	0.311
LIKEGDIVKR	1171.4	2	2.9989	0.2603
LIKEPAPDSGLLGLFQGQNSLLH	2448.8	3	7.2303	0.4749
LIKGVIVDKDFSHPQMPK	2053.5	3	3.664	0.2068
LIKLEHAEAK	1152.4	2	2.6946	0.1492
LIKNNASTDYDLSDK	1697.8	2	4.3904	0.3943
LILAANRDEFYSRPSK	1881.1	3	3.2669	0.2813
LILDWVPYINGK	1431.7	2	3.4987	0.2659
LILENHHATIPQK	1514.8	2	2.8592	0.2293
LILEQMQKDPQALSEHLKNPVIAQK	2873.4	3	5.8652	0.5269
LILEQMQKDPQALSEHLKNPVIAQKIQK	3242.8	3	4.0374	0.2611

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LILEVHQFSR	1242.5	2	2.8727	0.2093
LILGLMMPPAHYDAK	1671.1	2	4.3575	0.3951
LILHGTSSQPEHMK	1578.8	2	3.8254	0.3846
LILHGTSSQPEHMKQPR	1960.3	2	5.0809	0.3968
LILKKEDELGDR	1429.6	2	3.0499	0.2107
LILPHVDIQLK	1289.6	2	3.1585	0.2831
LILPVGPAGGNQMLEQYDK	2044.4	2	4.3319	0.4127
LILPVGPAGGNQMLEQYDKLQDGSIK	2786.2	2	3.5619	0.3171
LIMGIGHR	897.1	2	2.5509	0.2801
LIMQYLKENSLHR	1646.0	2	2.9771	0.3661
LINQPLPDLK	1151.4	2	3.3466	0.1856
LINQVLELQHTLEDLSAR	2093.4	2	4.9324	0.4111
LINQVLELQHTLEDLSARVDAVKEENLK	3219.6	3	4.728	0.2959
LINSLYPPGQEPIPK	1666.9	2	3.4327	0.1726
LIPDSIGKDIEK	1328.5	2	2.8052	0.2676
LIPEMDQIFTEVEMTTLEK	2268.6	3	5.3523	0.5143
LIQDQQEQIQHLK	1621.8	2	2.769	0.1245
LIQEAAGRSNLKR	1456.7	2	3.1511	0.1742
LIQEIVDKSGVVR	1456.7	2	3.8861	0.274
LIQESDQHLKDVEK	1682.9	2	4.3275	0.2504
LIQHANVQAHSSLIR	1687.9	2	3.7885	0.4309
LIQHAQIPPEDSEIITNMAHLGVPIVTDSTLR	3511.0	3	4.7843	0.3966
LIQLMEEIMAEKENK	1820.2	2	4.0505	0.2471
LIQNNHYAMEDVATR	1776.0	3	3.6655	0.2513
LIQQPQNASMFVNRPALGILPPENFVEK	3152.7	3	4.8736	0.2906
LIQQQLEKELNTLR	1727.0	2	4.7622	0.2558
LIQSEVALNDLHLTK	1695.0	2	4.2297	0.3655
LIQSHPESAEDLQEK	1724.9	2	5.136	0.3387
LIQVPKGPVEGYEENEEFLR	2347.6	3	4.5035	0.3052
LIRDEGLAVMDK	1360.6	2	2.9904	0.2007
LIRDEGLAVMDKAK	1559.9	2	2.45	0.1543
LIRGPAETEATTD	1374.5	2	2.9685	0.2979
LIRGPGENGDDS	1230.3	2	2.6658	0.239
LISDINKAWERLEK	1716.0	2	3.4936	0.1768
LISEILSESVVPDVR	1656.9	2	2.7225	0.2113
LISELSLLNHKLPAR	1705.0	3	3.3053	0.3516

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LISGDIPGPLQGSGQDMVSILQLVQNLMHGDEDEEPQSPR	4302.8	3	4.8799	0.4356
LISKKEEDVSYLSGQLSEKEAALTK	2768.1	3	5.9085	0.4507
LISLTDENALSGNEELTVK	2047.2	2	5.9426	0.5349
LISQIVSSITASLR	1488.8	2	4.6464	0.5005
LISSDGHEFIVK	1345.5	2	3.3792	0.309
LISSDGHEFIVKR	1501.7	2	3.8972	0.3653
LISWYDNEFGYSNR	1764.9	2	4.8601	0.5339
LISWYDNEFGYSNRVVDLMAHMASKE	3077.4	3	3.8499	0.1794
LISYAQLTGR	1122.3	2	3.2683	0.2729
LITAADTTAEQR	1290.4	2	3.0678	0.3121
LITDLQDQNQK	1316.4	2	2.5575	0.1131
LITEDVQGK	1003.1	2	2.5295	0.137
LITINQQWKPIEELQNVQR	2351.7	3	5.8643	0.432
LITKPSEGTTLRVEDLVK	2000.3	2	2.9138	0.1078
LITLEEEMTK	1207.4	2	3.0923	0.2183
LITLEQGKTLADAEGDVFR	2077.3	3	3.9796	0.1494
LITPAVVSER	1085.3	2	2.8399	0.3619
LITQTFSHHNQLAQK	1767.0	2	4.6301	0.307
LITVNTPDLVLFVGEALVGNEAVDQLVK	2968.4	3	3.7189	0.1152
LIVALMKPSR	1128.5	2	2.9628	0.272
LIVDEAINEDNSVVSLSQPK	2171.4	2	6.2456	0.5022
LIVDVIRFQPGETLTEILETPATSEQEAEHQR	3652.0	3	5.6982	0.3699
LIVENLSSR	1031.2	2	2.9096	0.2545
LIVGLMRPPAYCDAK	1648.0	2	3.4486	0.4432
LIVHNGYCDGR	1247.4	2	2.5726	0.2567
LIVQPNTRLEGSDVQLLEYEASAAGLIR	3057.4	3	4.2271	0.3273
LKAADIDQEVK	1230.4	2	2.8874	0.1816
LKAADIDQEVKER	1515.7	2	2.6212	0.2295
LKAEAELLQQQK	1399.6	2	3.5855	0.1766
LKAEAELLQQQKELAQEQAR	2325.6	2	6.607	0.4211
LKAEAELLQQQKELAQEQARR	2481.8	3	3.4812	0.2501
LKAEATEAAR	1060.2	2	2.8837	0.253
LKAEGSEIR	1003.1	1	2.4479	0.257
LKAELGIPLEEVPPEEINYLTR	2524.9	3	3.5499	0.2451
LKAFLASPEYVNLPINGNGK	2146.5	3	4.533	0.2438
LKAFLASPEYVNLPINGNGKQ	2274.6	3	4.5094	0.2324

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LKAHLEKLEVDLNK	1650.9	2	4.4276	0.3558
LKAIEPNDYTGK	1349.5	2	2.6879	0.1833
LKAIEPNDYTGKVSEEIEDIIK	2505.8	3	3.8378	0.2907
LKAIEPNDYTGKVSEEIEDIIKKGETQTL	3263.6	3	3.9977	0.3245
LKAMDQEITVNPQFVQK	1990.3	2	4.5647	0.4127
LKAQALAIETEAELQR	1785.0	2	5.6174	0.5159
LKASLDRPFTNLESAFYSIVGLSSLGAQVPDAK	3497.0	3	4.4518	0.4416
LKASLDRPFTNLESAFYSIVGLSSLGAQVPDAKK	3625.1	3	5.227	0.3547
LKATDQEK	933.0	2	2.8314	0.1164
LKATVTPSPVK	1141.4	2	3.2795	0.2757
LKATVTPSPVKGK	1326.6	2	3.9872	0.207
LKAVQAQGGESQQEAQR	1829.0	3	4.026	0.1498
LKAYEDQTKPVLEYYQK	2117.4	2	5.2703	0.4431
LKAYEDQTKPVLEYYQKK	2245.6	3	3.6921	0.2748
LKCASLQK	891.1	2	2.6576	0.1519
LKDAVAHCHEAER	1479.6	2	3.5468	0.233
LKDDEVAQLKK	1287.5	2	4.17	0.2609
LKDEDLLPSKYFEVDFPMIVTR	2657.1	3	5.5194	0.4997
LKDELASTK	1005.1	2	3.2656	0.1437
LKDEVLKETVSQRPGATVPTDFATFPSSAFLR	3510.0	3	5.8997	0.4283
LKDHMLIPVSMSELEK	1871.3	2	4.8053	0.3315
LKDIAGEFKEQLQALIPYVLNPSK	2716.2	3	3.9898	0.2308
LKDISSLEFAENK	1494.7	2	2.9042	0.1534
LKDISTLEPLK	1257.5	2	3.2876	0.1343
LKDKEVAFWTNLFAK	1811.1	2	4.4323	0.4333
LKDKNEPVQNLPIQK	1765.0	3	3.2266	0.169
LKDLEALLNSK	1244.5	2	4.128	0.2586
LKDLEALLNSKEAALSTALSEK	2345.7	3	5.9552	0.473
LKDLEALLNSKEAALSTALSEKR	2501.9	3	6.8745	0.5318
LKDLGHPVEEEDELESGDQEDEDDESEDPGKDLDHI	4080.1	3	4.2406	0.2041
LKDLPFIVSHR	1325.6	2	3.1297	0.225
LKDNLGIHYK	1201.4	2	2.6165	0.1564
LKDPANFQYPAESVLAYKEGHLSPDIVAEQK	3459.8	3	4.5755	0.3702
LKDPEKGPVPTFQPFQR	1985.3	2	3.2792	0.2753
LKDQEAKHDEL	1326.4	2	3.0546	0.1427
LKDSAVLDQSAK	1275.4	2	3.3138	0.239

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LKDSEAELQR	1189.3	2	3.4789	0.2361
LKDVLLQVDDER	1443.6	2	3.5942	0.3631
LKDVLLQVDDERR	1599.8	3	3.6813	0.3188
LKDVLLQVDDERRNAEQYKDQADKASTR	3306.6	3	3.9194	0.1866
LKDVQSMDELKDVYNHFLLYYGR	2848.2	3	4.5608	0.3169
LKDWQEGGYTINDKPNPR	2132.3	3	4.1834	0.3402
LKDYAFIHFDER	1554.7	2	4.0833	0.4359
LKDYAFVHFEDR	1540.7	2	4.4752	0.4801
LKEADEMHTLLQLECEK	2031.3	2	5.183	0.4026
LKEAELLEPLMPAIR	1724.1	2	3.671	0.1708
LKEAETRAEFAER	1550.7	2	2.9287	0.2048
LKEAISTSKEQEAK	1562.7	2	4.0243	0.3488
LKEALQPLINR	1295.6	2	3.1812	0.2104
LKECCEKPLLEK	1433.8	2	3.2207	0.1456
LKEDKAPQVDVDKAVAELK	2097.4	3	5.0572	0.3924
LKEEAAMK	920.1	1	2.0261	0.1911
LKEEAAMKAKTE	1349.6	2	3.7889	0.3872
LKEEEEDKK	1148.2	2	3.4202	0.1246
LKEEEEDKKR	1304.4	2	3.3999	0.1122
LKEEENTVGR	1175.3	2	3.1368	0.2264
LKEEIDLLNRDLDDIEDENEQLKQENK	3300.5	3	6.2758	0.3014
LKEELAQKDIR	1343.6	2	3.4131	0.2264
LKEELEEARDIAR	1572.7	2	3.3649	0.1279
LKEELIDAIRQELSK	1786.1	2	4.391	0.3321
LKEELSEVETK	1305.5	2	3.3544	0.1999
LKEEMEGVVKELAENNHILER	2481.8	3	5.0675	0.3365
LKEESRDEESPYATSLYHS	2242.3	3	3.3804	0.2586
LKEEYQSLIR	1279.5	2	3.3315	0.2111
LKEFLEDYDDDRDDPKYYR	2496.6	3	3.9059	0.1995
LKEFMPPGLQELIPFVKPAPIEQEPSKK	3192.8	3	5.0898	0.4263
LKEGDTIIVPGVEGPIVTQIR	2235.6	3	4.5828	0.3788
LKEGDTMMGQQVAK	1536.8	2	4.1578	0.3153
LKEIEHNLSK	1211.4	2	3.0897	0.1429
LKEIVTNFLAGFEA	1552.8	2	4.1215	0.442
LKEIYENMAPGENKR	1793.0	2	4.6046	0.3864
LKEKEDALTRTELETLQK	2146.4	2	4.5481	0.2842

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LKEKEELETGKK	1432.6	3	4.2408	0.1827
LKEKLEDPDPGVQSAAVNVICELAR	2696.1	3	4.0748	0.2082
LKEKYEKDIAAYR	1627.9	2	4.8143	0.3471
LKEKYEKDVADYK	1629.8	2	4.5621	0.3306
LKELDEEHSQELK	1598.7	2	4.5854	0.1692
LKELESQVSGLEK	1460.7	2	4.3524	0.3197
LKELESQVSGLEKEAIELR	2172.5	3	5.4626	0.4793
LKELESQVSGLEKEAIELREAVEQQK	2985.3	3	7.6772	0.4698
LKELESQVSGLEKEAIELREAVEQQKVK	3212.6	3	4.193	0.271
LKELEVAEGGKAELER	1772.0	2	4.15	0.3011
LKELEVAEGGKAELERLQAEAQQLR	2810.2	3	4.8176	0.1855
LKELGATMDGFHR	1475.7	3	3.4051	0.1613
LKELIFEETAR	1349.6	3	3.6366	0.2695
LKELIGATAGK	1101.3	2	3.0936	0.1866
LKELVVPK	926.2	2	2.9796	0.174
LKEMFPIIAQYGDVLVR	1993.4	2	2.4628	0.1876
LKENNIEQIYPVNAISFHNIHNTFATGGSDGFVNIWDPFNK	4664.1	3	5.4291	0.4184
LKENYAAEYANALEK	1727.9	2	5.4341	0.3602
LKEQGQAPITPQQGQALAK	2007.3	3	4.1288	0.4088
LKEQSIFGDHRDEEEETHMK	2459.6	3	3.4476	0.1571
LKEREEFLIPIYHQVAVQFADLHDTPGR	3323.7	3	4.3064	0.3771
LKERLDQPMTEIVSR	1816.1	3	4.1494	0.3193
LKESAEFQTQLEK	1551.7	2	3.5163	0.2642
LKESEEKEVLLK	1445.7	2	3.1345	0.1117
LKESNTTKGELQLKLDELQASDVSVK	2875.2	3	4.525	0.2791
LKESQTQDNITVR	1532.7	2	4.2435	0.3224
LKETAEEEKDDLEER	1834.9	2	5.025	0.4305
LKETAESVLK	1118.3	2	2.728	0.1118
LKETAESVLKKPVVDCVVSVPCFYTDAER	3227.7	3	4.809	0.1825
LKETAESVLKKPVVDCVVSVPCFYTDAERR	3383.9	3	5.4107	0.3702
LKETGYVVERPSTTK	1708.9	2	4.5835	0.393
LKEVFSMAGVVVR	1435.8	2	2.5714	0.1403
LKEVLEYNAIGGK	1434.7	2	3.7607	0.2341
LKEVLEYNAIGGKYNR	1868.1	3	3.4767	0.2608
LKEVVLQVEEER	1471.7	2	3.4941	0.1977
LKEYSSMDAFWQEGR	1848.0	2	2.6649	0.3222

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LKGASLLPGKLPTLVSLFDDEDEEDNLFGGTAAK	3563.0	3	3.7565	0.2
LKGDDLQAIK	1101.3	2	2.7551	0.2033
LKGEATVSFDDPPSAK	1662.8	3	3.309	0.2693
LKGEIDASVPELEGDLRGPQVDVK	2565.9	3	4.3131	0.2616
LKGELESSDQVR	1361.5	3	3.763	0.3012
LKGEMMDLQHGSLFLR	1876.2	3	3.6552	0.2234
LKGFGYAEFEDLDSLLSALSLNEESLGNRR	3345.7	3	5.4975	0.4967
LKGIPVLVGLLDHPKK	1728.2	3	3.2578	0.2535
LKGIVPLAK	939.2	2	2.7187	0.1135
LKGLEAEVLR	1128.3	2	2.7771	0.1921
LKGLEAEVLRLQEELAASDR	2241.5	3	3.3208	0.2152
LKGLGAFVIDSDHLGHR	1836.1	2	5.2738	0.5755
LKGQEDSLASAVDAATEQK	1962.1	2	3.0052	0.2736
LKGSGNLEAIHIIK	1493.8	3	4.296	0.342
LKGSGNLEAIHIIKK	1621.9	2	3.8204	0.2392
LKGTEDELDKYSEALKDAQEKLELAEK	3095.4	3	7.0097	0.4987
LKGTEDELDKYSEALKDAQEKLELAEKK	3223.6	3	4.4938	0.2237
LKGTVGEPTYDAEFQHFLR	2209.4	3	5.4772	0.381
LKHEDTNLASSTIIR	1698.9	2	3.3797	0.2185
LKHEDTNLASSTLLR	1698.9	3	3.3761	0.2949
LKHELTDEELQSLFTNFANVVDK	2692.0	3	4.2115	0.2714
LKHFHPLFEYFDYESR	2129.4	3	4.8584	0.4285
LKHLDFLKQPLATQK	1781.1	2	3.8955	0.3599
LKHMQFPPMYEENSR	1908.2	2	4.0915	0.3245
LKHYGPGWVSMANAGK	1717.0	3	4.5991	0.4203
LKIPKNPELVPQNYISDSLAQSVVQHLR	3188.7	3	3.3721	0.216
LKKDEISVQHIR	1466.7	2	3.6575	0.2817
LKKDEISVQHIREELAELSK	2366.7	3	3.9094	0.3022
LKKDTYIENEK	1381.6	2	3.2301	0.2678
LKKDTYIENEKLISGK	1880.2	3	4.6627	0.2629
LKKEDIYAVEIVGGATR	1863.1	2	5.804	0.4728
LKKEIEELKQELIQAEIQNGVK	2582.0	3	5.6095	0.3361
LKKLEEEQIILEDQNCK	2074.4	2	6.1497	0.3984
LKKTEMQEKNPLPSKETIEQEK	2630.0	3	4.0004	0.2493
LKKTETQEK	1105.3	2	2.722	0.1715
LKKTETQEKNPLPSK	1742.0	2	4.2625	0.3573

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LKKTETQEKNPLPSKETIEQEK	2599.9	3	5.1614	0.3713
LKKTETQEKNPLPSKETIEQEKQAGES	3072.4	3	5.7507	0.396
LKKTETQEKNTLPTKETIEQEK	2617.9	3	4.8316	0.3272
LKKTETQEKNTLPTKETIEQEKR	2774.1	3	5.8054	0.4092
LKLDGLDEDGEKEAR	1688.8	2	4.688	0.4462
LKLDSEQLPLRPK	1537.8	2	3.6955	0.2806
LKLEAELGNMQGLVEDFK	2035.4	2	6.4707	0.4678
LKLEAELGNMQGLVEDFKNK	2277.6	3	6.1039	0.4783
LKLEAELGNMQGLVEDFKNKYEDEINK	3169.6	3	5.5849	0.3743
LKLEAELGNMQGLVEDFKNKYEDEINKR	3325.7	3	6.3363	0.4635
LKLEDFFAR	1139.3	2	3.1752	0.1993
LKLEESYDLEPFLR	1753.0	2	3.5055	0.336
LKLEPHEGLLLR	1418.7	3	3.5072	0.2857
LKLEPHEGLLLRFPYAA	1968.3	2	4.2391	0.4012
LKLGVTANDVKNVIIWGNHSSTQYPDVNHAK	3420.8	3	4.9521	0.3071
LKLHCTPGDGQR	1325.5	2	2.4279	0.1683
LKLPAVVTADLR	1296.6	2	3.2802	0.3712
LKLPSIPLVPVSAQK	1591.0	2	2.9317	0.2176
LKLQHIQAPLSWELVR	1932.3	2	2.4554	0.1461
LKLSEELSGGR	1189.3	2	3.5618	0.2568
LKLSILYPATTGR	1433.7	2	3.3359	0.2908
LKMEDIKEVNQALK	1660.0	2	3.8475	0.2107
LKNAIIIQSFIR	1416.7	2	2.424	0.2124
LKNDNTEAFYK	1343.5	2	3.5561	0.2202
LKNEIPNSHILDQYR	1841.1	2	4.5268	0.2806
LKNGELENIKPK	1383.6	2	3.6017	0.1934
LKNITLDDASAPR	1414.6	3	3.5383	0.2957
LKNKHEAMITDLEER	1828.1	3	5.573	0.532
LKNNKEYLEFR	1454.7	3	3.7253	0.2606
LKNQSESHKQAQENLHDQVQEQK	2747.9	3	5.1265	0.3266
LKNQVTQLKEQVPGFTPR	2084.4	3	3.9964	0.2564
LKNTKIEVLEEELR	1715.0	2	2.6736	0.1345
LKNTLTQTTENLR	1532.7	2	3.2682	0.2042
LKNWEEGGYFNTDKPHPR	2189.4	3	3.9404	0.3217
LKPAFIKPYGTVTAANSSFLTDGASAMLIMAEEK	3575.2	3	6.1558	0.5139
LKPATDKDGKPLLPEPEEKPKPR	2585.0	3	4.2311	0.2905

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LKPDEGGEVPVLNVSYKPQK	2198.5	3	4.2941	0.3575
LKPEGLHQLLAGFEDK	1796.1	2	2.4401	0.3318
LKPGDLVGVNKDSYLILETLPTEYDSR	3037.4	3	3.9123	0.29
LKPGTMIEWGNNWAR	1774.0	2	3.4886	0.2591
LKPGYLEATVDWFR	1695.9	3	4.5452	0.4867
LKPNLGNGADLPNYR	1642.8	2	3.9321	0.3103
LKPPTLIHGQAPSAGLPSQKPK	2266.7	3	4.1539	0.3819
LKPQLLQGVYAMGFNRPSK	2148.6	2	4.4876	0.3778
LKPQYLEELPGQLK	1656.9	2	3.0271	0.1935
LKPTDVGLLAVIANNIITINKDQNVFDSK	3155.6	3	4.5223	0.351
LKPVHGLIFLFK	1412.8	2	2.5496	0.2124
LKPYFLTDGTGTVTPANASGINDGAAAVVLMK	3194.6	3	6.0512	0.5293
LKQAKEEAQAEIEQYR	1935.1	3	5.6053	0.4484
LKQDGDSFR	1066.1	2	2.9838	0.2905
LKQDTYGDIYNFPIHAFDK	2286.5	3	3.4823	0.1897
LKQEEETLSFIR	1493.7	2	2.7648	0.219
LKQEFHYIEEDLYR	1884.1	2	3.8194	0.36
LKQEMGGIVTELIR	1587.9	2	2.9404	0.1925
LKQENTQLVHR	1366.6	2	2.7192	0.1803
LKQETPAVLEDLHK	1621.9	2	2.5001	0.1714
LKQEYFVVAATLQDIIR	2008.3	3	3.7114	0.188
LKQFVFDLHSGK	1419.7	2	4.2478	0.3335
LKQGLYRHPWDDISYVLPEHMSM	2817.2	3	4.2615	0.2097
LKQIEEQTIKAQKELEEQTR	2443.7	3	5.3148	0.3341
LKQIEEQTIKAQKELEEQTRK	2571.9	3	4.1673	0.2112
LKQIEEQTKKAQQELEEQTR	2458.7	3	4.8203	0.196
LKQIEHTLNEK	1353.5	2	3.4135	0.1187
LKQIGALQ	871.1	2	2.7591	0.1142
LKQLAVAHEK	1137.4	2	2.9867	0.1243
LKQLEPGAA	927.1	2	2.484	0.277
LKQLIDKETNDRK	1601.8	2	3.7867	0.3381
LKQMFGNADMNTFPTFK	1991.3	2	4.4429	0.411
LKQMFGNADMNTFPTFKFEDPKFEVIEKPQA	3650.2	3	4.3098	0.2496
LKQQSELQSQVR	1444.6	2	3.9607	0.1916
LKQSADSSSSR	1166.2	2	2.5942	0.25
LKQSAEEQAQAR	1359.5	3	3.749	0.3405

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LKQSLPPGLAVK	1251.5	2	3.045	0.2655
LKQTEITSATQNQLLFHMLK	2345.7	3	3.8626	0.2941
LKQVEDEKNSFR	1493.6	2	3.7748	0.3186
LKQVEDEKNSFREQLEEEEEAK	2708.9	3	4.1563	0.2534
LKQVEDEKNSFREQLEEEEEAKHNLEK	3330.6	3	6.0427	0.4207
LKSDEDEERVHEEL	1728.8	2	3.2962	0.2955
LKSEDEPTR	1075.2	2	3.0076	0.215
LKSELHLLDFQGK	1528.8	2	2.9146	0.1661
LKSENQVLGQYIENLMSASSVFQTTDTKS	3220.6	3	4.8507	0.3518
LKSFNLSALEK	1250.5	2	3.3668	0.3101
LKSIDNGIFVQLVQANSPASLVGLR	2641.1	3	5.6491	0.4106
LKSLEAEILQLQEELASSER	2287.6	2	5.7049	0.3716
LKSMEAEMIQLQEELAAAER	2291.6	2	4.5534	0.38
LKSSELQAIKTELTQIK	1931.3	2	3.8896	0.3166
LKSSLEEESR	1178.3	2	2.7783	0.2339
LKSSVNELTQK	1247.4	2	2.6954	0.1564
LKSVVGNLHR	1123.3	2	2.9119	0.1354
LKTDMYEGLPFFSKL	1790.1	2	3.0774	0.1966
LKTDVDVSLPKVEGDLKGPEIDVKAPK	2892.3	3	4.5874	0.3725
LKTEGNEQMK	1178.3	2	2.6376	0.1323
LKTEKAPKDQVDIAVQELLQLK	2508.9	3	3.9379	0.2433
LKTEQGGAHFSVSSLAEGSVTSVGSVNPAENFR	3364.6	3	5.4084	0.4236
LKTETDKENAEVK	1505.7	2	4.4194	0.2686
LKTETDKENAEVKFKDFLLSLK	2598.0	3	3.7751	0.2728
LKTIEIQATNALDEK	1687.9	2	3.1069	0.1954
LKTLLVNNNR	1185.4	2	2.8286	0.1231
LKTLPDEVLTKEVEELILTESK	2528.9	3	5.3745	0.3654
LKTNHIGHTGYLNTVTVSPDGSLCASGGK	2929.3	3	5.1094	0.3408
LKTNILQYASTRPPTLSPIPHIPR	2715.2	3	3.6285	0.1232
LKTQMLDQEELLASTR	1877.2	2	3.5548	0.3368
LKTSPVEGLSGNPADLEK	1856.1	2	4.9924	0.4241
LKTSTSNVEQYQAMVTSLEESLNKEK	2959.3	3	4.4724	0.3287
LKTVEELLETGLIQVATKEEELNAIR	2941.4	3	6.3426	0.4706
LKTVEELLETGLIQVATKEEELNAIRTENSSLTK	3802.3	3	6.3435	0.4973
LKTVLELQYVLDKLGDDEVR	2347.7	3	5.3706	0.4718
LKTVLSANADHMAQIEGLMDDVDFK	2763.1	3	5.5413	0.3986

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LKTVLSANADHMAQIEGLMDDVDFKAK	2962.4	3	5.166	0.3448
LKVAAHEAEEESDNIAEDFLEGK	2545.7	3	3.57	0.2171
LKVEGYSGTAGDSMAYHNGR	2114.3	3	4.3363	0.3394
LKVESSPSR	1003.1	2	2.5548	0.1568
LKVESSPSRSDYINASPIIEHDPR	2712.0	3	3.2345	0.1292
LKVFDGIPPPYDK	1489.7	2	3.3397	0.2135
LKVFDGIPPPYDKK	1617.9	2	3.9833	0.2246
LKVGLQVVAVK	1154.5	2	2.8498	0.1791
LKVPEWVDTVK	1314.6	2	3.4074	0.2774
LKVPPAINQFTQALDR	1812.1	3	5.8443	0.4241
LKVQEQELTR	1244.4	2	2.9791	0.1525
LKVSELKEELK	1316.6	2	3.9046	0.2152
LKVSELKEELKK	1444.7	2	4.1825	0.2921
LKVTEGGEPYR	1249.4	2	3.0631	0.2218
LKYALTGDEVK	1237.4	2	2.6038	0.1154
LKYALTGDEVKK	1365.6	2	3.9667	0.3202
LKYISLAVLVVQNASLILSIR	2314.8	2	2.4571	0.1654
LKYLAFLR	1024.3	2	2.5209	0.1539
LKYPLEEFVKENQQEEAR	2251.5	3	4.3091	0.1563
LLAAGKVPQR	1053.3	2	2.7514	0.1573
LLAAGQLADALSQFHAAVDGDPDNYIAYYR	3240.5	3	6.5617	0.5641
LLAAGQLADALSQFHAAVDGDPDNYIAYYRR	3396.7	3	4.8793	0.2474
LLAAHCIVGHQHMIPENALEEITK	2669.1	3	3.2992	0.1055
LLAALLEDEGGSGRPLLQAAK	2123.4	2	3.8175	0.391
LLADPTGAFGK	1090.3	2	2.7496	0.2455
LLADPTGAFGKETDLLLDDSLVSIFGNR	2979.3	3	5.7763	0.4607
LLADPTGAFGKETDLLLDDSLVSIFGNRR	3135.5	3	4.736	0.3768
LLADQAEAR	987.1	2	3.5506	0.2776
LLAEGHPDPDAELQR	1661.8	2	3.9794	0.3481
LLAEKEREMAEMR	1606.9	2	2.8768	0.1944
LLAELPASVHALTGVDLSKIPLIK	2500.0	3	3.9489	0.2954
LLAENNEIISNIRDSVINLSESVEDGPK	3070.4	3	5.9338	0.3325
LLAEPVPGIK	1037.3	2	2.6372	0.1288
LLAEPVPGIKAEPDESNAR	2007.2	2	4.4045	0.4549
LLAHVRPPVSK	1217.5	2	2.9528	0.1503
LLAHVTLELQHYHQLLEK	2186.5	3	4.292	0.4114

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLALIYLAHASDVLENAFAPLLDEQYDLATKR	3589.1	3	6.2481	0.5653
LLALYNQGHIKPHIDSVWPFEK	2607.0	2	4.6714	0.41
LLANMVYQYK	1243.5	2	2.9777	0.271
LLAPEAGSHPQQTQKLEEIKENAQDTMR	3164.5	3	4.0482	0.4238
LLASAGQDNVVR	1243.4	2	2.9107	0.279
LLASSDPLAQIAEDKPYAELWMGTHPR	3011.4	3	4.9968	0.4535
LLASTLVHSVK	1168.4	2	3.2536	0.3449
LLASTLVHSVKK	1296.6	2	4.1079	0.3274
LLATEQEDAAVAK	1359.5	2	4.4711	0.3985
LLAVIEEQHK	1180.4	2	2.4656	0.1562
LLAVTGEQAQQAR	1385.6	2	4.1051	0.3641
LLCGLLAER	988.2	2	3.6836	0.1814
LLDAQLATGGIVDPR	1539.8	2	4.2035	0.2025
LLDAQLSTGGIVDPSK	1614.8	2	4.7005	0.4725
LLDAVDTYIPVPAR	1543.8	2	4.0121	0.4642
LLDAVDTYIPVPARDLEKPFLLPVEAVYSVPGR	3655.2	3	6.1024	0.4727
LLDDAMAADKSDEWFAK	1927.1	2	3.9118	0.3581
LLDDNGNIAEELSILK	1758.0	2	4.8745	0.4339
LLDEALKEVDQIELK	1757.0	2	3.7147	0.1824
LLDEEEATDNDLR	1533.6	2	4.3667	0.4104
LLDEEEATDNDLRAK	1732.8	2	4.2513	0.1911
LLDEQFAVLR	1204.4	2	3.1115	0.1212
LLDEVFFSEK	1227.4	2	3.8407	0.2514
LLDFGSLSNLQVTQPTVGMNFK	2410.8	2	5.1778	0.4228
LLDFGSLSNLQVTQPTVGMNFKTPR	2765.2	3	4.3792	0.3435
LLDGEAALPAVVFLHGLFGSK	2155.5	2	4.477	0.4291
LLDIACWIHHK	1349.6	2	3.5994	0.3002
LLDIESQEELEDFPLPTVQR	2372.6	3	4.8706	0.4332
LLDKLVGEFLEVTCINPTFICDHPQIMSPLAK	3587.3	3	5.8056	0.4532
LLDKTTVSHNTK	1357.5	2	3.8205	0.3178
LLDKTTVSHNTKR	1513.7	2	3.9422	0.4023
LLDKVELMLPEK	1428.8	2	2.8323	0.1161
LLDLELTSR	1060.2	2	2.5357	0.1497
LLDMDGIIVEK	1246.5	2	4.0961	0.3034
LLDPEDISVDHPDEK	1722.8	2	3.2753	0.236
LLDPEDVDVPQPDEK	1709.8	2	3.2017	0.2311

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLDPEDVDVPQPDEKSIITYVSSLYDAMPR	3407.8	3	4.7649	0.4394
LLDQIVEK	958.1	2	2.7501	0.2043
LLDSEIKIMK	1190.5	2	3.2524	0.2613
LLDSLPSDTR	1117.2	2	2.4495	0.1353
LLDSSTVTHLFK	1361.6	2	2.9499	0.32
LLDSVEQDFHLEIAK	1758.0	2	4.5878	0.3837
LLDTNPEINQSDSQDSR	1933.0	2	4.8543	0.3968
LLDTVDDMLANDIAR	1675.9	2	3.7856	0.2889
LLDVDNR	844.9	2	2.4824	0.2001
LLDVDNRVVLPIEAPIR	1933.3	3	5.07	0.2148
LLDVVHPAAK	1063.3	2	2.7606	0.3
LLDYSLHKER	1274.5	2	2.7213	0.2415
LLDYTEKPLYENLRDILLQGLK	2649.1	3	4.0177	0.3321
LLDYVPIGPR	1143.4	2	2.4937	0.2677
LLEAAAQSTK	1032.2	2	3.3247	0.2943
LLEAASVSSK	1005.1	2	2.6107	0.2197
LLEAFHNQGPVIKR	1622.9	2	3.7999	0.3835
LLEAHEEQNVDSYTESVKEYDSISR	2943.1	3	5.1064	0.3448
LLEALDEMLTHDIAK	1713.0	2	4.6196	0.3745
LLEAQIASGGVVDPVNSVFLPK	2254.6	2	5.5264	0.5306
LLEAQIASGGVVDPVNSVFLPKDVALAR	2880.3	3	5.4437	0.3463
LLEAQIATGGIIDPEESHRLPVEVAYKR	3106.5	3	5.1871	0.1873
LLEAQIATGGIIDPK	1539.8	2	2.8055	0.1407
LLEAQIATGGIIDPVHSHR	2028.3	3	3.4211	0.189
LLEAQIATGGVIDPVHSHR	2014.3	2	4.2621	0.4219
LLEAQIATGGVIDPVHSHRVPVDVAYR	2914.3	3	5.3207	0.4689
LLEDGEDFNLGDALDSSNSMQTIQK	2741.9	3	6.6992	0.4416
LLEDKNGEVQNLAVK	1670.9	2	5.0321	0.3279
LLEDRIAEFTTNLTEEEEKSK	2496.7	3	4.3251	0.1939
LLEDRIAEFTTNLTEEEEKSKSLAK	2896.2	3	6.1463	0.4779
LLEEANKYEK	1237.4	2	2.6234	0.2191
LLEEHSRIK	1125.3	2	2.4465	0.1398
LLEELEEGQKGVGDGTVSWGLEDDEDMTLTR	3423.7	3	3.6504	0.1671
LLEEQLQHEISNK	1581.8	2	4.3484	0.3085
LLEEQLQHEISNKMEEFK	2246.5	3	4.3001	0.3017
LLEFELAQLTK	1305.5	2	3.4121	0.1299

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLEFNQGKLPFAAAQIGNSFR	2322.7	2	5.5423	0.4975
LLEFQLALKDCEECIQLEPTFIK	2725.2	3	4.5789	0.128
LLEFYDATAHFAK	1526.7	2	3.3129	0.2833
LLEGEDAHLTQYK	1517.7	2	3.6436	0.3362
LLEGEDAHLTQYKK	1645.8	2	3.7777	0.2082
LLEGEDAHLTQYKKEPVTTR	2329.6	3	5.3435	0.4256
LLEGEEER	975.0	2	2.7184	0.1608
LLEGEESR	933.0	2	2.7869	0.1244
LLEGEESRLESGMQNMSIHTK	2390.7	3	6.3118	0.4472
LLEGESEGTREESK	1564.6	2	3.4919	0.242
LLEGGKGGIADSVAK	1415.6	2	3.2001	0.1652
LLEHKEIDGR	1210.4	2	3.0475	0.2419
LLEIDPYLKPYAVDFQR	2081.4	3	4.1251	0.3916
LLEKDTHEKQDTLVALR	2010.3	2	5.711	0.4997
LLEKPKDADNLFEHELGALNMAALLR	2923.4	3	4.0807	0.1762
LLEKSDLHSVLAQK	1581.8	2	3.2137	0.1371
LLELFPVNR	1101.3	2	2.4548	0.174
LLELGPKPEVAQQTR	1679.9	2	3.9318	0.4152
LLELGPKPEVAQQTRK	1808.1	3	3.3741	0.2667
LLELQELVLR	1226.5	2	3.989	0.2023
LLELQYFISR	1282.5	2	2.913	0.3158
LLEMNLMHAPQVADAILGNQMFTHYDR	3130.6	3	7.1302	0.4767
LLENMTEVVRK	1332.6	2	3.2377	0.16
LLEPLVTQVTTLVNTNSKGPSNK	2454.8	2	5.1623	0.4563
LLEPSVGSLFGDDEDDDLFSSAK	2457.6	2	4.9331	0.3977
LLEPVLLLGK	1095.4	2	2.7653	0.1954
LLEPVLLLGKER	1380.7	2	2.9423	0.335
LLEQKTQESQK	1332.5	2	3.0203	0.1866
LLEQKVELAQLQEEWNEHNAK	2550.8	3	4.6114	0.1821
LLEQLQEIGQEKEQLTQELQEAR	2755.0	3	5.6606	0.3335
LLEQWEKDDDIEEGDLPEHKRPSAPVDFSK	3524.8	3	5.813	0.4564
LLEQYKEESK	1267.4	2	3.3636	0.2828
LLEQYKEESKK	1395.6	2	3.8721	0.2252
LLERLPEVEVPQHL	1672.9	3	4.2685	0.2591
LLESDYFR	1043.2	2	2.6758	0.105
LLESEAVNENLRK	1515.7	2	4.0351	0.2657

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLESKEELDSLMTDETIANVPILILGNKIDRPEAISEER	4397.0	3	5.6432	0.5249
LLETELLQEISEIEKR	1944.2	2	4.0629	0.4118
LLETHIHNQGLAAIEK	1788.0	3	4.2593	0.3052
LLETIDQLYLEYAK	1713.0	2	4.6564	0.4482
LLETKWTLLQEQK	1630.9	2	3.2729	0.1609
LLETTDRPDGHQNNLR	1880.0	3	3.7364	0.2105
LLETTEEDKQK	1334.5	2	3.2369	0.2087
LLEVEHPAAK	1107.3	2	3.0754	0.3028
LLEVLSGERLPKPTK	1681.0	2	2.9828	0.2156
LLEVNQQSLLGLTHGEAVQLLR	2432.8	3	5.5192	0.4343
LLEVPVMLTEQYPQGLGPTVPELGTEGLRPLAK	3548.1	3	6.3847	0.4395
LLEVQPQVANSPSSAAQK	1868.1	2	4.4075	0.363
LLEVSDDPQVLAVAAHDVGEYVR	2496.8	3	4.4928	0.4627
LLFEDWTYDDFR	1620.7	2	2.9756	0.2611
LLFEGAGSNPGDK	1305.4	2	3.8244	0.2846
LLFEGAGSNPGDKTLEDRFFEHEVKLNK	3192.5	3	3.6982	0.1248
LLFGHSTEGDILELVDGHFDTK	2444.7	3	5.6911	0.3936
LLFSDGEKVIPR	1374.6	2	2.5462	0.2185
LLFSEDQQGGSLEQLLQR	2062.3	2	5.8205	0.334
LLFTVLGEPLIYSLSFPER	2195.6	2	3.079	0.2605
LLGASELPIVTPALR	1550.9	2	3.3267	0.2274
LLGDLLPEAVR	1196.4	2	2.496	0.1715
LLGELLQDNAK	1214.4	2	4.2093	0.3349
LLGELLQDNAKLVPVLSAK	2022.4	2	4.9799	0.422
LLGEREDVVHVHK	1531.7	3	3.6539	0.2545
LLGFGSALLDNVDPNPENFVGAGIIQTK	2901.3	3	6.61	0.4762
LLGGVTIAQGGVLPNIQAVLLPK	2272.8	2	6.104	0.4452
LLGHEVEDVIIK	1365.6	2	3.2653	0.1907
LLGHWEEAAHDLALACK	1878.1	3	4.6132	0.4168
LLGKVTIAQGGVLPNIQAVLLPK	2343.9	2	5.7479	0.3665
LLGLGVTDFSR	1178.4	2	3.8255	0.2525
LLGLLFPLLAR	1226.6	2	2.9886	0.1011
LLGMGDIEGLIDKVNELKLDDNEALIEK	3099.5	3	4.5445	0.3321
LLGNTFVALSDLR	1419.7	2	4.1617	0.3682
LLGPDAAINLTDPDGALAK	1866.1	2	5.2562	0.4792
LLGPDAAINLTDPDGALAKR	2022.3	2	5.5539	0.5316

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLGPGPAADFSVSVER	1615.8	2	4.2688	0.4376
LLGPNASPDGLIPWTR	1708.0	2	3.4984	0.1964
LLGPSAAADILQLSSSLPLQSR	2238.6	2	6.0245	0.5475
LLGPVLVKQELGEAR	1622.9	2	3.6252	0.2746
LLGQFSEKELAAEK	1563.8	2	3.3565	0.1304
LLGQFTLIGIPPAPR	1593.9	2	3.6525	0.3505
LLGQTDVAVYGVAVPGVEGK	1973.3	2	3.7191	0.3211
LLGRVTIAQGGVLPNIQAVLLPK	2371.9	2	5.9797	0.4037
LLGSDGSPLMDMLQLAEEPVPQAGQELR	2996.4	3	4.0519	0.1842
LLGTIYTAAEEIEAVGGK	1836.1	2	4.9695	0.4498
LLGTQHGEGNSALSPLNPGELLIALHNIDSVK	3309.7	3	4.3066	0.1881
LLHDLQIGEKK	1294.5	2	3.5892	0.3314
LLHDQVGVIQFGPYK	1715.0	2	4.4413	0.3669
LLHDQVGVIQFGPYKQLFLQTYAR	2836.3	3	4.8311	0.4598
LLHDSGLNVVVLEAR	1635.9	2	4.428	0.305
LLHEVQELTTEVEK	1668.9	2	4.3463	0.3054
LLHEVQELTTEVEKIK	1910.2	2	4.8886	0.3993
LLHGMKDDIVPWHTSMQVADR	2450.8	3	3.4539	0.1553
LLHGVMEQLGIAR	1437.7	2	4.0343	0.4207
LLHGVMEQLGIARP	1534.9	2	4.3151	0.393
LLHGVMEQLGIARPR	1691.0	2	4.6135	0.4057
LLHIEELR	1023.2	2	2.4387	0.1563
LLHIEELRELQTK	1622.9	2	4.266	0.2864
LLHIEELRELQTKINEAIVAVQAIIADPK	3269.8	3	4.6727	0.4282
LLHINATALLEYPEYSGPLLPASAVAPGPSALDR	3519.0	3	5.039	0.3541
LLHKYPFILPHQQVDK	1977.3	2	4.2425	0.4
LLHKYPFILPHQQVDKGAIK	2346.8	3	4.2837	0.42
LLHQVVEQLQK	1335.6	2	3.1633	0.2459
LLHSFHSELPVLSDSER	1967.2	2	5.0038	0.5002
LLHTLEGHAMPIR	1488.8	2	3.4941	0.3117
LLHVAVSDVNDDVRR	1708.9	2	4.0148	0.382
LLHYLGHVMVNGPTTPIPVK	2187.6	3	4.675	0.4174
LLIDEAILK	1028.3	2	3.0682	0.1017
LLIEMEQR	1032.2	2	2.6469	0.1363
LLIEMEQRLEQGQAIDDLMPAQK	2671.1	3	3.4481	0.2327
LLIGTLYHR	1086.3	2	2.6841	0.242

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLIHLHPR	999.2	2	2.8509	0.2074
LLIHQSLAGGIIGVK	1519.9	2	3.9938	0.3605
LLIIGDSGVGK	1072.3	2	3.1504	0.1841
LLIIGNSSVGK	1101.3	2	2.7603	0.1013
LLIPGNYKLTASAPGYLAITK	2205.6	3	3.8325	0.2657
LLIQESVWDEAMR	1590.8	2	2.9685	0.3349
LLIQVGHEPMPPTLGTNVLGR	2243.7	2	3.3163	0.2727
LLISHLSGIR	1109.3	2	2.8879	0.1954
LLIVSTTPYSEKDTK	1695.9	2	3.4745	0.3703
LLKDAEALSQR	1244.4	2	3.608	0.3098
LLKDAEALSQRLEEK	1744.0	2	4.1367	0.2756
LLKEEKEELADQVLTLK	2000.3	3	3.525	0.1911
LLKEGEEPTVYSDEEEPKDESAR	2651.8	3	5.5306	0.3778
LLKEGFENESKR	1450.6	2	2.6237	0.1383
LLKEGSSNQR	1132.3	2	2.4697	0.1781
LLKELEQNANHPHR	1699.9	2	3.8538	0.4311
LLKEQEIEDQKNPR	1740.9	2	4.3152	0.2355
LLKFDQLNIQR	1388.6	2	3.3518	0.2123
LLKGIDRYNPENLATLER	2116.4	3	3.7501	0.1582
LLKNQEADQHSAR	1510.6	2	3.9229	0.3414
LLKNQSQYEK	1251.4	2	2.9176	0.1335
LLKPGEEPSEYTDEEDTKDHNKQD	2818.9	3	5.4899	0.4176
LLLATMESMNGGK	1365.6	2	4.8145	0.3809
LLLEFTDTSYEEK	1588.7	2	4.3893	0.4059
LLLEGISSTHAHHLR	1684.9	2	4.6348	0.4809
LLLEGISSTHVNHLR	1689.9	2	3.7359	0.4357
LLLETHLPSK	1151.4	2	2.7328	0.1521
LLLETHLPSKK	1279.6	2	3.3501	0.2901
LLLEVQHASK	1138.3	2	2.6874	0.1968
LLLEYTDSSYEEK	1590.7	2	3.738	0.3085
LLLFDAPDLR	1173.4	2	2.8407	0.2512
LLLFDLIPVVSVAGWPEGAR	2153.6	2	2.4109	0.118
LLLFDYDKVELANMNR	1955.3	2	3.1172	0.3624
LLLFSDGNSQGATPAAIEK	1933.2	2	6.0163	0.4288
LLLFSDGNSQGATPAAIEKAVQEAQR	2716.0	3	5.1586	0.414
LLLGAGAVAYGVR	1260.5	2	4.341	0.4001

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLLGPNGPAVAAAGDLTSEEEEGQSLWSSILSEVSTR	3786.1	3	5.4417	0.4317
LLLHDKDR	1010.2	2	2.6272	0.1126
LLLHYSPQACKNNICLDLSPSHGLDGR	2966.4	3	5.1039	0.3819
LLLIGDSGVGK	1072.3	1	2.5858	0.3146
LLLIGNSSVGK	1101.3	2	2.634	0.1439
LLLINNAGSLGDVSK	1514.7	2	3.8482	0.3669
LLLLAGVDRLDKDLTIGQMQGK	2398.9	3	4.126	0.2967
LLLLESVSGLLQPR	1538.9	2	3.6985	0.2279
LLLLGAGESGK	1058.3	2	3.6913	0.2061
LLLLGAGESGKSTIVK	1586.9	2	3.762	0.3707
LLLNNDNLLR	1198.4	2	3.0801	0.2004
LLLPGELAK	954.2	2	2.8115	0.1536
LLLPGELAKHAVSEGTK	1764.1	2	4.2168	0.474
LLLPGELAKHAVSEGTKAVTK	2163.5	2	4.1536	0.5648
LLLPWLEAR	1111.4	2	2.6359	0.1478
LLLQGLMDSVEAK	1417.7	2	3.9106	0.2838
LLLQLEATK	1029.3	2	2.5977	0.1376
LLLQVESLTTELSAER	1803.0	2	2.8315	0.1147
LLLQVQHASK	1137.4	2	2.9712	0.145
LLLSSETPIEGK	1287.5	2	3.2878	0.2707
LLLVSFDGFR	1167.4	2	3.2145	0.1619
LLLYHLHPFLQR	1550.9	2	3.469	0.2987
LLMHGKEVGSIIGK	1482.8	2	3.7882	0.4332
LLMMAGIDDCYTSAR	1661.0	2	2.4835	0.1158
LLNDEDPVVVTK	1342.5	2	3.7311	0.3451
LLNDEDQVVVNK	1386.5	2	4.0025	0.2409
LLNENSYVPR	1205.3	2	2.7494	0.2792
LLNFPTIVER	1202.4	2	2.8841	0.2043
LLNLDGTCADSYSFVFSR	2009.2	2	4.3367	0.2293
LLNLGLITESQAHTLEDEVAEVLQK	2765.1	3	7.1737	0.5928
LLNLGLITESQAHTLEDEVAEVLQKLISK	3206.7	3	5.2736	0.4599
LLNNGDKWEAEIAANIQADYLYR	2681.9	3	3.5889	0.1201
LLNQEEGEYYNVPIPEGDEEGNMELR	3039.2	3	3.5371	0.2427
LLNQEKSELLVEQGR	1757.0	3	3.4904	0.1171
LLNQPHHGAGIK	1285.5	2	2.4797	0.1167
LLNQQREYEAQQQYR	1968.1	3	3.5958	0.1527

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLNSELADALGGLLNR	1669.9	2	3.1199	0.2432
LLNTFLER	1006.2	2	2.7785	0.2043
LLNYNPEDPPGSEVLR	1814.0	2	3.79	0.2344
LLPDITLLEPVEGEAAEELSR	2295.6	2	4.6253	0.3651
LLPIDGANDLFFQPPPLTPTSK	2382.7	3	3.6498	0.2848
LLPLGATDTAVFDVR	1588.8	2	4.372	0.5388
LLPQLTYLDGYDR	1567.8	2	2.5538	0.239
LLPQLTYLDGYDRDDK	1926.1	2	2.5999	0.256
LLPSAPQTLPDGPLASPAR	1902.2	2	4.1265	0.4195
LLPTHPPDRKLSKNEVLR	2114.5	2	2.4002	0.1291
LLPVLLSTAQEADPEVR	1852.1	2	3.6352	0.2412
LLQAETASNSAR	1261.4	2	4.0638	0.3794
LLQAGFSELKETEKWNIKPESK	2576.9	3	4.4548	0.3272
LLQALVDILNEEN	1484.7	2	4.5034	0.3766
LLQAMEPVHVAR	1364.6	2	2.4552	0.1567
LLQAQGVEVPSKDSLPK	1810.1	2	4.0328	0.3505
LLQAQLQAQKEELQSLMHQPK	2462.9	3	4.8614	0.3537
LLQDFFNGK	1082.2	2	2.9622	0.232
LLQDFFNGKELNK	1566.8	2	4.744	0.2144
LLQDFFNGR	1110.2	2	3.1384	0.2797
LLQDFFNGRDLNK	1580.8	2	3.8471	0.1622
LLQDHPWLLSQNLVVKPDQLIK	2599.1	3	6.7902	0.4906
LLQDHPWLLSQNLVVKPDQLIKR	2755.3	3	5.4995	0.4088
LLQDKNEQAVQSAQTIQQLEDQLQQK	3026.3	3	6.1119	0.4549
LLQDSVDFSLADAINTEFK	2127.3	2	5.8488	0.5905
LLQDSVDFSLADAINTEFKNTR	2498.7	2	4.6382	0.4905
LLQEALEAEERGGTPAFLPSSLSPQSSLPASR	3340.7	3	5.9675	0.3991
LLQEHNNALK	1180.3	2	3.0114	0.1498
LLQEHSGIFGFSVSHTTR	2017.2	3	5.8994	0.5118
LLQGRPPLDFYPPGVHPSGLVPR	2513.9	3	4.546	0.3283
LLQHGINADDKR	1380.5	2	3.3389	0.3343
LLQHHITEQLQDIVDILK	2157.5	2	5.0756	0.3499
LLQIIERYPEETLSLMTK	2178.6	3	4.4423	0.4044
LLQKGIHPTIISESFQK	1940.3	2	3.46	0.162
LLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQR	4491.0	3	5.6648	0.4365
LLQLQEQMR	1159.4	2	3.4817	0.1604

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLQLVEDR	986.1	1	1.6679	0.1679
LLQPGPSEHSK	1193.3	2	2.6239	0.2171
LLQPPAPIMPLDTNWPLLTVSK	2445.9	3	4.045	0.3314
LLQPVIVSPSGTILR	1593.9	2	3.126	0.1687
LLQQEEEIKSLTAEIDR	2016.2	3	4.3084	0.3632
LLQQEEEIKSLTAEIDRLK	2257.6	2	5.0578	0.3943
LLQQGLAQVEAGR	1383.6	2	4.5402	0.3543
LLQQGTAPAQAK	1226.4	2	3.3727	0.3212
LLQQLFLKAPVNTAELTDLLIQQNHIGSVIK	3460.1	3	6.3316	0.3854
LLQQSGAQQFR	1276.4	2	2.9066	0.2118
LLQQVSQIYQSIEFSR	1940.2	2	3.376	0.3802
LLQSIGQAPESISEKELK	1971.2	2	4.2915	0.3604
LLQSLGLK	872.1	2	2.4923	0.2217
LLQSNPVLEAFGNAK	1601.8	2	4.6683	0.4047
LLQTAATAAQQGGQANHPTAAVVTEK	2577.8	3	4.9389	0.2742
LLQTSNITKLEQK	1516.8	2	3.9776	0.2125
LLQVPSSAFADVEVLGPAVTFK	2289.7	3	3.6396	0.1738
LLQYSDALEHLLTTGQGVVLER	2456.8	3	5.9003	0.4659
LLRAEELIQEIQR	1611.9	2	3.256	0.2042
LLRDPADASEAHESSSR	1841.9	3	4.4274	0.3685
LLREDRYMRLKEELQLSDEQLQK	2935.3	3	3.8208	0.1406
LLREEKDELGEQVLGLK	1970.3	3	4.3742	0.3132
LLREELQLLQEQGSYVGEVVR	2459.8	3	5.6965	0.4665
LLRELQEAQNER	1499.7	2	2.5038	0.129
LLRFQSSHHPTDITSLDQYVER	2643.9	3	3.9434	0.1633
LLRGHDQYAYDGKDYIALNEDLR	2740.0	3	5.7533	0.3165
LLRGHNQYAYDGKDYIALNEDLR	2739.0	3	3.9312	0.2535
LLRPDAPAHPR	1243.4	2	2.81	0.2216
LLRSEESVSR	1176.3	2	2.9987	0.2789
LLRSEESVSRLPEEIR	1914.2	2	3.7748	0.1358
LLRVPDGLLSR	1239.5	2	3.3215	0.273
LLRYESSALPSGQLTSLSEYASR	2529.8	3	3.5808	0.2899
LLSATGESEKQFQEAIIVFQEEFK	2773.1	3	3.7161	0.1908
LLSDATVEKDESHAGKVVLR	2168.4	3	5.0184	0.4403
LLSDKLKEAETR	1403.6	2	3.4101	0.2495
LLSDPNYGVHLPAVK	1623.9	2	2.4189	0.1778

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLSDQIALEASLISQIADSLKNTTSDVSR	3090.4	3	3.2886	0.2427
LLSDSLPPSTGTFQEAQSR	2035.2	3	4.1867	0.4833
LLSEEVFDFSSGQITQVK	2028.2	2	3.7607	0.2695
LLSEGADVNAK	1117.2	2	3.0261	0.1112
LLSEIEFLVNHMDLAK	1873.2	2	3.8685	0.2986
LLSEKEVHTK	1184.4	2	2.9862	0.2342
LLSFLKDVYVDSKDPVSSLQVK	2481.9	3	4.715	0.2877
LLSGDTYEAVVTAVDPVADIATLR	2490.8	3	4.6008	0.4075
LLSGVLFHSSPALQPAADHKPGPGA	2468.8	3	4.7107	0.3025
LLSGVLFHSSPALQPAADHKPGPGAR	2625.0	3	4.5974	0.3786
LLSKETSEELLPPPVQTQIK	2251.6	2	4.3495	0.437
LLSKTPELNLDQFHDKTPYTIMFGPDK	3150.6	3	5.4104	0.3912
LLSLLEKDEFK	1335.6	2	3.1648	0.2077
LLSLMDPLLPLSVLSK	1740.2	2	3.9866	0.1913
LLSNPLMGDAVSDWSPMHEAAIHGHQLSLR	3284.7	3	5.0691	0.4315
LLSPFMPFVTEELFQR	1955.3	2	2.5497	0.2324
LLSQHLPQR	1092.3	2	3.19	0.2356
LLSQTMKDHLVR	1441.7	2	3.0082	0.3265
LLSRPQDALEGVVLSPSLEAR	2251.6	2	2.8666	0.1427
LLSTELQAELSR	1360.5	2	3.3343	0.2761
LLTAHGQGYGK	1145.3	2	2.9183	0.2368
LLTEEGQKIGTFER	1621.8	2	3.0992	0.2766
LLTEKDAQIAMMQQR	1777.1	3	3.8386	0.2796
LLTETEDWLYEEGEDQAK	2170.3	2	4.6515	0.4134
LLTHHKDHFTK	1377.6	2	2.7736	0.2884
LLTHNLLSSHVR	1390.6	2	3.6004	0.4325
LLTIGDANGEIQR	1400.6	2	2.5418	0.2057
LLTPITTLTSEQIQK	1687.0	2	3.5826	0.332
LLTPNPGYGTQAGPSPAPPTPPEEEDLR	2903.1	3	4.8511	0.3748
LLTPTHSFLAR	1256.5	2	2.9271	0.2387
LLTQHENIKNEIDNYEEDYQK	2637.8	3	5.0319	0.3569
LLTQMSAGK	949.2	2	2.6534	0.1245
LLTQYILNLGK	1276.5	2	3.4137	0.269
LLTSFLPAQLLR	1372.7	2	4.2784	0.3417
LLTTIGKDLDFEK	1493.7	2	2.9018	0.2675
LLTTILHSDGDLTEQGKISKPDMSR	2757.1	3	3.8941	0.2611

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LLTWDVKDTLLR	1473.7	2	3.3704	0.3277
LLTYNAAR	922.1	2	2.6065	0.1862
LLVEHQAISFMLAEMAMK	2063.5	2	3.1688	0.2332
LLVFSTDAGFHFAGDGK	1783.0	2	2.4821	0.2356
LLVGNDDVHIIAR	1435.7	2	2.4346	0.1584
LLVGNKSDLTTK	1289.5	2	3.2869	0.2608
LLVGVDEKLNPEDIKK	1811.1	3	5.0543	0.3557
LLVLYSGEDDELLQR	1764.0	2	3.0526	0.2702
LLVPYLMEAIR	1318.7	2	4.1664	0.3706
LLVQDKFEVLNYTSIPIFLPEVTIGAHQTDR	3559.1	3	3.8868	0.2743
LLVRPTSSETPSAAELVSAIEELVK	2641.0	3	3.6457	0.1841
LLVSASQDGK	1018.1	2	2.7965	0.1913
LLVSMCQGNRDENQSINHQMAQEDAQR	3117.4	3	6.1634	0.4407
LLVSNLDFGVSDADIQELFAEFGTLKK	2971.4	3	3.6	0.3075
LLVVDPETDEQLQK	1627.8	2	3.7736	0.3515
LLVVDPETDEQLQKLGVQVR	2280.6	3	3.4334	0.2474
LLVVDRETDEFFKK	1740.0	2	3.112	0.1312
LLVVYPWTQR	1275.5	2	2.815	0.1213
LLYAFAEATVPK	1323.6	2	3.4872	0.2103
LLYAVNTHCHADHITGSGLLR	2292.6	3	3.6977	0.2944
LLYDLADQLHAAVGASR	1814.0	2	5.6098	0.3616
LLYLLESTEDPVIIER	1904.2	2	5.1869	0.4403
LLYNNVSNFGR	1297.4	2	3.8784	0.3197
LLYNRPGTVSSLKK	1576.9	2	3.4378	0.177
LMALLGQALK	1058.4	2	3.0635	0.2015
LMASTQPFKDIINNTSLAELEKR	2621.0	3	3.6847	0.1973
LMATLSNTNPSFVR	1551.8	2	4.9907	0.5264
LMDEFKIGELFSK	1557.8	2	2.7947	0.1241
LMDHGQSHPEDIDMYSTR	2133.3	3	4.4519	0.278
LMDHVGTEPSIKEDQVIQLMNAIFSK	2945.4	3	4.6195	0.3393
LMDIKSRLEQEIATYR	1967.3	3	3.5223	0.2781
LMDLLADSREVIRNDGVLLLQALTR	2826.3	3	3.5379	0.205
LMDLLDRHVEDGNVTVQHAALSALR	2775.1	3	4.5879	0.3656
LMEDLDRNKDQEVNFQEYVTFLGALALIYNEALKG	4062.6	3	4.576	0.2261
LMEEIMSEKENK	1481.7	2	4.0946	0.1456
LMELFPANKQSVEHFTK	2020.3	2	3.365	0.397

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LMELHGEGSSSGK	1332.5	2	3.8169	0.3732
LMELHGEGSSSGKATGDETGAK	2163.3	3	5.097	0.3003
LMENMRNDIASHPPVEGSYAPR	2485.8	3	4.4196	0.2864
LMEPIYLVEIQCPEQVVGGIYGVLNR	2934.5	3	4.3021	0.2245
LMEPLKYAEQLPVAQIIHQKPK	2576.1	3	3.5149	0.2017
LMEVMNHVLGK	1271.6	2	3.2168	0.2524
LMFEELR	938.1	2	2.5329	0.179
LMFNSPGFVEYVVDR	1774.0	2	3.0039	0.1446
LMFTAFLPDSTGSFTR	1792.0	2	3.1237	0.386
LMGEDEKPAAK	1189.4	2	2.9685	0.2481
LMGEDEKPAAKENSEGAGAK	2033.2	3	3.7311	0.2188
LMGKDESTSR	1124.3	2	2.4915	0.1354
LMGLEALK	875.1	2	2.4953	0.1462
LMHGILTEQK	1170.4	2	2.6059	0.1056
LMIEMDGTENK	1281.5	2	4.0493	0.2985
LMIEMDGTENKSK	1496.7	2	3.619	0.2146
LMKEILDKKVEK	1474.8	2	3.7323	0.1341
LMKELEEIRK	1289.6	2	2.4177	0.1241
LMKLENSIIPVHK	1522.9	2	2.5486	0.1881
LMLDLNKAK	1046.3	2	2.42	0.1808
LMLLLEVISGER	1373.7	2	4.1809	0.3048
LMLRAADPGPGAELDPAAPPPAR	2284.6	3	3.8388	0.1164
LMMDPLSGQNR	1262.5	2	3.3278	0.2478
LMMDPLTGLNR	1261.5	2	2.4744	0.1432
LMMSELENR	1123.3	2	2.8456	0.1249
LMNDFSAALNNFQAVQR	1940.2	2	3.3383	0.2888
LMNESLMLVTALNPHIGYDK	2260.7	3	5.4209	0.4245
LMNETTAVALAYGIYKQDLPALEEKPR	3036.5	3	5.3705	0.3637
LMNTGKQHTFVETESVR	1978.2	2	4.7591	0.395
LMQDDNRGLEQGIQDNKITANLFR	2791.1	3	5.2279	0.2806
LMQITSLHSLNAFLLPIK	2040.5	3	4.0035	0.3165
LMQLVDHR	1012.2	2	2.8289	0.1555
LMRKNDNGEIEKEK	1704.9	2	2.5599	0.1648
LMSDPDSSIIDFYPEDFAIDLNGKK	2832.1	3	3.894	0.2153
LMSNALSTVTR	1193.4	2	2.734	0.202
LMTDTINEPILLCR	1633.0	2	3.1325	0.3042

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LMTIMDSMNDQELDSTDGAK	2216.5	2	3.7636	0.4494
LMTQAQLEEATR	1391.6	2	3.8529	0.266
LMTTGNNTVR	1107.3	2	2.5543	0.2789
LMVELSKSQDDEIGDGTTGVVVLAGALLEEAEQLLDR	3916.4	3	6.3625	0.4174
LMVHNWEYLGK	1390.6	2	2.83	0.1947
LMVHTVATFNSIK	1461.8	2	3.3813	0.2896
LMVHTVATFNSIKELNER	2103.4	2	4.3955	0.4804
LMYEHELEQLR	1461.7	2	3.074	0.2126
LMYGQEDVPKDVLEYVVFEK	2402.7	3	4.5486	0.3492
LMYNSSNPVLK	1266.5	2	2.6102	0.1085
LNAIYQNNLTK	1292.5	2	3.7758	0.2818
LNAKEIVLK	1028.3	2	2.7368	0.1491
LNATNIELATVQPGQNFHMFTK	2475.8	2	3.8978	0.3056
LNATNIELATVQPGQNFHMFTKEELEEVIK	3445.9	3	4.7154	0.2358
LNATNIELATVQPGQNFHMFTKEELEEVIKDI	3674.1	3	4.4042	0.3588
LNDGHFMPVLGFGTYAPAEVPK	2361.7	2	4.4861	0.4149
LNDGHFMPVLGFGTYAPAEVPKSK	2577.0	3	4.6112	0.4045
LNDGHFMPVLGFGTYAPPEVPR	2415.8	2	5.2113	0.462
LNDGHFMPVLGFGTYAPPEVPRSK	2631.0	3	5.626	0.3404
LNDGSQITYEK	1268.4	2	3.8547	0.2206
LNDHFPLVVWQTGSGTQTNMNVNEVISNR	3272.6	3	5.7195	0.44
LNDHLLLVYTGK	1386.6	2	2.739	0.2518
LNDSNKILVQQTLNILQQLAVAMGPNIK	3078.6	3	3.7644	0.2166
LNDYIFSFDK	1262.4	2	3.3401	0.2681
LNDYLQIETIQALEELAAK	2176.5	2	4.9886	0.3385
LNEAAAGLNQAATELVQASR	2028.2	2	6.2649	0.5385
LNEAKEEFTSGGPLGQK	1806.0	2	5.4137	0.4519
LNEALQAER	1044.1	2	2.7053	0.1806
LNEELKVDEETQEVLENLKDR	2544.8	3	6.7371	0.3793
LNEGVVEFASYGDLKNAIEK	2197.4	2	3.6226	0.2289
LNEHFLNTTDFLDTIK	1922.1	2	5.2538	0.432
LNEHFLNTTDFLDTIKSNLDR	2507.7	3	5.6963	0.537
LNEIDKESQKPFEVK	1805.0	3	3.8178	0.1218
LNEIDKESQKPFEVKGPLPVHTK	2635.0	3	5.2183	0.2472
LNEILQAR	957.1	2	3.2103	0.1117
LNEIVDAANAVISHIDQTALAVYIAMK	2885.3	2	5.7906	0.3766

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LNEKNYELLK	1264.5	3	3.7975	0.1639
LNELESDLTFK	1309.4	2	3.2344	0.1835
LNELGLLPLLLK	1336.7	2	3.252	0.1499
LNELMSQIR	1104.3	2	3.087	0.2562
LNEQHQLILSK	1323.5	2	2.7991	0.1973
LNEQYEHASIHLWDLLEGK	2296.5	3	5.5614	0.4979
LNETTDPDKK	1161.2	2	2.711	0.1332
LNETTETQR	1092.1	2	2.9983	0.3046
LNFAVASR	878.0	2	3.0495	0.2947
LNFEAAWDEVGDEFEKEETFTLSTIK	3050.3	3	3.3366	0.1549
LNFELTDALK	1164.3	2	2.8606	0.2492
LNFGDDIPSALR	1318.5	2	2.4713	0.105
LNFSHGTHEYHAETIK	1885.0	2	5.4546	0.5058
LNFSHGTHEYHAETIKNVR	2254.4	2	5.6122	0.4411
LNGHVVVKDLDIFDR	1741.0	3	4.6844	0.3798
LNGLENRVEVGKDQEFTVDTR	2420.6	3	4.292	0.2143
LNGPQDHSHLLYSTIPR	1949.2	2	2.4107	0.1356
LNGTDPEDVIR	1229.3	2	3.3608	0.2897
LNHKYNPVSLPK	1410.6	3	3.2873	0.2325
LNHLSFAELLKPFSR	1773.1	2	4.132	0.2493
LNHLVDSLQQLR	1436.6	2	3.2982	0.2671
LNHPVTHVDQSSDNIIIETLNHEHYECK	3287.6	3	4.1719	0.1448
LNHQVSEVFNTVAQELLQR	2226.5	3	3.8774	0.2404
LNHVAAGLVSPSLK	1406.7	2	3.6305	0.3088
LNHVAIAVPDLEK	1419.7	2	3.7399	0.3236
LNHVAIAVPDLEKAAAFYK	2071.4	3	3.972	0.2925
LNIISNLDCVNEVIGIR	1886.2	2	3.3679	0.3197
LNINPEDGMADYSDPSYVK	2129.3	2	3.0439	0.2903
LNIPVSQVNPR	1237.4	2	3.1356	0.2991
LNIPYENFYEALEK	1743.9	2	4.0467	0.2859
LNIQPSEADYAVDIR	1704.9	2	4.7035	0.3943
LNITVVQAK	986.2	2	3.0224	0.1173
LNKDIVISVGIYNLVQK	1917.3	2	3.8053	0.1195
LNKDNDTLKDLLK	1530.7	2	5.3285	0.2904
LNKELASSEQNKNHINNELK	2324.5	3	4.9173	0.2348
LNKPFLFDTKPLIVQYEVNFQNGIECGGAYVK	3647.2	3	5.5197	0.4905

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LNLDKMMEQK	1250.5	2	2.9683	0.1892
LNLEAINYMAADGDFK	1786.0	2	5.896	0.4897
LNLEHIATSSAVSK	1470.7	2	3.3016	0.214
LNLGGDFIKESTATTFLR	1984.2	2	4.6821	0.4681
LNLGTVGFYR	1140.3	2	2.7365	0.2387
LNLIHSEISNLAGFEVEAIINPTNADIDLKDDLGNTLEK	4251.7	3	6.0229	0.4464
LNLLDLDYELAEQLDNIAEK	2333.6	2	6.8331	0.3804
LNLNNTVLSK	1116.3	2	3.0307	0.2599
LNLVEAFVEDAELR	1618.8	2	3.8337	0.3396
LNMHMNVQNGK	1286.5	2	2.6828	0.2736
LNMHNLVEPVNKDLEFQLHEPFLLYR	3210.7	3	5.0958	0.3782
LNNLVLFDK	1076.3	2	2.705	0.1995
LNNMNKYDYVLTGYTR	1966.2	2	3.7085	0.3981
LNPHRESDGASDEAEESGSQGKLVEALR	2983.1	3	7.0714	0.4521
LNPNFLVDFGKEPLGPALAHELR	2548.9	3	4.8472	0.4019
LNPVGAKFDPYEHEALFHTPVEGKEPGTVALVSK	3679.1	3	4.6011	0.3913
LNQALLDLHALGSAR	1592.8	2	4.9108	0.4761
LNQDQLDAVSK	1231.3	2	3.2802	0.2939
LNQDQLDAVSKYQEVTNNLEFAK	2668.9	3	4.9919	0.3953
LNQPQPDFTK	1188.3	2	3.3082	0.2312
LNQQLLSKDEQLLHLSSQLEDSYNQVQSFSK	3622.0	3	6.7577	0.2826
LNRLPAAGVGDMVMATVK	1844.2	3	5.5865	0.4023
LNRLPAAGVGDMVMATVKK	1972.4	3	6.3139	0.4105
LNRLTTDFNVIVEALSK	1934.2	3	3.8724	0.1475
LNRPLTLSEK	1171.4	2	3.1259	0.2413
LNRPLTLSEKIVYGHLDDPASQEIER	2995.3	3	6.9238	0.5609
LNRYNYIEGTK	1371.5	2	2.8821	0.1078
LNSDPQFVLAQNVGTTHDLLDICLKR	2912.3	3	4.1507	0.3346
LNSEGKLEQTVSMATTTQPMTQHLHVTYK	3275.7	3	4.4831	0.3003
LNSELQQQLKDVLEER	1943.1	2	3.3872	0.3125
LNSELQQQLKEVHQER	1980.2	3	3.3438	0.1959
LNSGLGQLILKEEMEK	1803.1	2	3.2117	0.2285
LNSGLGQLILKEEMEKESR	2175.5	3	4.2403	0.2811
LNSHMDALHLGSQANR	1764.9	2	2.9277	0.1009
LNSKPQDLTDAYGPPSNFLEIDIFNPQTVGVGR	3605.0	3	5.2798	0.3706
LNSLAIGLR	957.2	2	2.9672	0.224

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LNSNDEDIHTANER	1628.6	2	4.7879	0.4205
LNSNNALIEFLLEGTPEIR	2144.4	2	3.2157	0.1372
LNSNTQVVLLSATMPSDVLEVTK	2460.8	2	4.0447	0.3098
LNSNTQVVLLSATMPSDVLEVTKK	2589.0	3	4.8077	0.2645
LNSVQSSERPLFLVHPIEGSTTVFHSLASR	3310.7	3	6.6021	0.5322
LNSWFQHRPPGASPER	1880.1	3	3.4676	0.2663
LNTAEDAKDVIKEIEDFDSLEALR	2736.0	3	4.8327	0.3599
LNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAAR	3933.3	3	4.7571	0.3571
LNTFGDEVFNDPK	1496.6	2	3.8288	0.377
LNTQEIFDDWAR	1508.6	2	4.5465	0.4574
LNVDEAFEQLVR	1433.6	2	4.2696	0.2173
LNVEAVNTHR	1153.3	2	2.8941	0.1756
LNVFKNDQDTWDYTNPNLSGQGDPGSNPNKR	3493.7	3	5.4863	0.4079
LNVHKVTVLTLQDK	1608.9	2	2.8401	0.3156
LNVHMDSIPHHR	1456.7	2	3.2142	0.3593
LNVTEQEK	961.1	2	2.8387	0.23
LNVTEQEKIDK	1317.5	2	3.2631	0.2056
LNVTEQEKIDKLMIEMDGTENK	2579.9	3	6.3005	0.4049
LNVTEQEKIDKLMIEMDGTENKSK	2795.2	2	4.5733	0.3371
LNVWDIGGQR	1158.3	2	3.1117	0.1084
LNWGEPMHWHLDMYNR	2100.4	2	4.4906	0.3813
LNWLSVDFNNWK	1536.7	2	3.8205	0.2451
LNYSDHDVIK	1204.3	2	3.1949	0.1978
LNYSDHDVIKWVR	1645.8	2	3.1902	0.3197
LNYVFDEGEANT	1372.4	2	2.705	0.1074
LPAAGVGDMVMATVK	1460.8	2	4.0355	0.4404
LPAAGVGDMVMATVKK	1589.0	3	3.6916	0.3367
LPAGAIHFQR	1110.3	2	3.3194	0.3467
LPALTVHVTQPK	1304.6	2	2.9183	0.3279
LPANHPLLTGQR	1317.5	2	3.2608	0.3974
LPASFDAR	877.0	1	2.0827	0.1781
LPATAAEPEAAVISNGEH	1777.9	2	4.1897	0.2637
LPATEKPVLLSK	1296.6	2	3.7612	0.3664
LPAVVQNAHSLVR	1404.6	2	2.4947	0.1742
LPAYLTIQMVR	1305.6	2	3.8537	0.3327
LPDGHELTFPNR	1396.5	2	3.957	0.3354

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LPDGHELTFPNRLGHSHLSYLSVR	2747.1	3	4.0516	0.2041
LPDGSEIPLPPILLGR	1688.0	2	3.7689	0.3248
LPDGSSFTNQFPSDAPLEEAR	2279.4	2	4.9673	0.4629
LPDGTSLTQTFR	1336.5	2	3.1053	0.1969
LPDIFEAQIAGLR	1443.7	2	4.2483	0.4394
LPDLSLDNMIGQSAIAGEEHPR	2364.6	3	3.2077	0.1354
LPDSQQQYNVVKTVKVTEQLRHCSEILK	3285.8	3	4.709	0.1372
LPDTGEGPSR	1029.1	2	2.4169	0.2543
LPEDPLLSGLLDSPALK	1779.1	2	4.5384	0.3626
LPEEHIPFFLHNNR	1764.0	3	4.3569	0.3885
LPEELGRDQNTVETLQR	1999.2	3	3.7087	0.2686
LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR	4095.6	3	6.601	0.6135
LPEFSFEKR	1153.3	2	2.5681	0.1217
LPEGDLGKEIEQK	1456.6	2	2.9618	0.1998
LPEIYIQLQR	1273.5	2	3.6013	0.2508
LPENVVAMSNLSEAVQDADLLVFVIPHQFIHR	3604.1	3	4.1374	0.324
LPESENLQEFWDNLIGGVDMVTDDDRR	3165.4	3	4.5698	0.3074
LPETNLFETEETR	1579.7	2	3.7697	0.346
LPETNLFETEETRK	1707.9	2	4.1714	0.2054
LPEVEVPQHL	1161.3	2	3	0.1371
LPEYTLSQEGGPAHKR	1784.0	2	4.5328	0.4719
LPFAAAQIGNSFR	1392.6	2	3.6664	0.2787
LPFPIIDDR	1086.3	2	3.3816	0.2866
LPFTALGSGQDAALAVLEDR	2045.3	2	3.7498	0.3284
LPFTDGDAQQLQR	1489.6	2	2.7055	0.1864
LPFTPLSYIQGLSHR	1730.0	2	3.1224	0.2681
LPGAIDVIGQTITISR	1654.9	2	2.6734	0.1847
LPGAWDPAAHQGGNGVLLEGELIDVSR	2773.1	3	4.0991	0.2823
LPGDKGLVLMSR	1286.6	2	3.7163	0.3404
LPGHAGSINEVAFHPDEPIIISASSDKR	2959.3	3	5.4953	0.4039
LPGLLGNFPGPFEEEMK	1876.2	2	4.4318	0.3778
LPGPGQALPSAPGVVLGPEDLPVEVLQFHPTSDGILVSAAGTTVK	4434.0	3	5.2042	0.5185
LPGPTGSVVSTGTSFSSSSPGLASAGAAEGK	2766.0	3	5.4635	0.3928
LPGSSSAAAAAAAAAAYNPHHLPLRPILRPR	3119.6	3	3.3544	0.183
LPHIIGGSDLIAHHAR	1708.0	2	4.4267	0.3738
LPHLPGLEDLGIQATPLELK	2155.5	2	5.0169	0.3366

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LPHSVLLEIQKELLDYK	2039.4	2	4.6705	0.3804
LPHVLLLQLGTTFFK	1728.1	2	4.2788	0.3622
LPIFFFGTHETAFLGPK	1923.2	2	4.4373	0.4804
LPIGDVATQYFADR	1566.7	2	4.0495	0.4238
LPILNQPSTQIVANAK	1708.0	2	4.1871	0.3276
LPIPESQVITINPELPVEEAAEDYAK	2867.2	3	5.8782	0.3685
LPIPESQVITINPELPVEEAAEDYAKK	2995.4	3	6.0665	0.3158
LPIPESQVITINPELPVEEAAEDYAKKLR	3264.7	3	4.7056	0.3868
LPKDDVHAK	1023.2	2	2.8091	0.2783
LPKEEDSANLKPSELKK	1927.2	3	4.0925	0.1713
LPLATIVKDLVAQAPLKPK	2016.5	3	4.9292	0.2857
LPLDINPVVHPHGHIFK	1934.3	2	3.8907	0.3427
LPLFGLGR	873.1	2	2.4947	0.1841
LPLHTLTSSTPVVLVR	1734.1	2	3.875	0.4755
LPLIFHLGR	1066.3	2	3.1099	0.2252
LPLLPHEVR	1074.3	2	2.8622	0.2323
LPLQLDDAVRPEAEGEEEGR	2224.4	3	3.5818	0.1552
LPLQLDDAVRPEAEGEEEGRATVNQDTR	3110.3	3	4.16	0.2824
LPLVVEDFVK	1159.4	2	2.4616	0.1337
LPMPNLKDELHHSGWNTCSSCFGDSTK	3006.3	3	4.5915	0.2355
LPNFGFVVFDDSEPVQK	1939.2	2	5.3083	0.4785
LPNFGFVVFDDSEPVQR	1967.2	2	3.6103	0.3983
LPNGLVIASLENYSPVSR	1930.2	2	3.0552	0.2129
LPNLGKHEK	1036.2	2	2.7246	0.2586
LPNLTHLNLSGNK	1421.6	3	3.5996	0.3624
LPPKVESLESLYFTPIPAR	2158.5	3	4.1295	0.3642
LPPLPVTPGMEGAGVVIAVGEGVSDR	2518.9	3	4.4504	0.2889
LPPNTNDEVDEDPTGNK	1855.9	2	3.1827	0.2446
LPPNVVAVPDVVQAAEDADILIFVVPHQFIGK	3413.0	3	4.5759	0.4958
LPPQDFLDRLSSLDNLK	1972.2	2	4.7645	0.3602
LPPQDFLDRLSSLDNLKASVSQVEADLK	3100.5	3	6.6119	0.4831
LPQEPGREQVVEDRPVGGR	2119.3	3	3.2981	0.1179
LPQLMLQSLSTSEELQRQFHLFQLQR	3172.7	3	3.4029	0.1465
LPQLPITNFSR	1286.5	2	2.6367	0.148
LPQPEEGATYEGIQKK	1789.0	2	4.8284	0.4007
LPQPPEGQTYNN	1358.4	2	2.881	0.2029

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LPQTSDDEKKDF	1423.5	2	3.3311	0.3559
LPRPPPPEMPESLK	1588.9	3	3.2493	0.1306
LPRPPPPEMPESLKK	1717.1	3	4.8332	0.3996
LPSDLHPIKVVEGVKELSK	2089.5	3	4.7121	0.3851
LPSDVVTAVR	1057.2	2	3.1019	0.1903
LPSEGPRPAHVVVGDVLQAADVDK	2470.8	3	4.7866	0.3401
LPSEGPRPAHVVVGDVLQAADVDKTVAGQDAVIVLLGTR	3965.5	3	7.3253	0.4874
LPSRPPLPGSGGSQSGAK	1693.9	2	4.7847	0.3812
LPSSPVYEDAASFK	1511.7	2	2.4958	0.1781
LPSVEEAEVPKPLPPASKDEDEDIQSILR	3203.5	3	5.8541	0.4669
LPSVEGLHAIVVSDRDGVPVIK	2301.7	3	4.1341	0.4402
LPTAADLLQIR	1211.4	2	3.6313	0.3413
LPTGYYFGASAGTGDLSDNHDIISMK	2732.0	3	6.3031	0.5544
LPVDYYGIPFAAPTALASR	2023.3	2	4.2977	0.442
LPVNSPMNKGDTEVMK	1761.1	2	5.1534	0.4124
LPVSEGVFVVKDPNGR	1714.0	2	4.4545	0.4248
LPYDVTPEQALAHEEVK	1940.1	2	4.5693	0.4199
LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR	3128.3	3	5.7494	0.3691
LQAANAEDIKSGK	1345.5	2	3.9191	0.405
LQAAVDGPMDKKEE	1531.7	2	4.4234	0.3403
LQAAVEKLLEAISETSSQLEHAK	2496.8	3	5.1996	0.3625
LQAAYAGDKADDIQKR	1763.9	2	5.2824	0.3986
LQAEAPHIVVGTPGR	1545.8	2	4.7873	0.4628
LQAEAQQLR	1057.2	2	2.5425	0.1219
LQAEIDNIKNQR	1442.6	2	4.0659	0.2709
LQAEIEGLKGQR	1342.5	2	3.5652	0.2218
LQAEKADLLGIVSELQLK	1969.3	3	5.3868	0.3589
LQAENDASKEEVKEVLQALEELAVNYDQK	3305.6	3	5.5575	0.4032
LQAGEYVSLGKVEAALK	1777.1	2	4.5022	0.3735
LQAIEHELHELGLLK	1744.0	2	3.3616	0.3697
LQAIEHELHELGLLKDHSLEGR	2538.8	3	7.6319	0.4658
LQAILEDIQVTLFTR	1761.1	2	3.0847	0.204
LQAKDEQGPIR	1255.4	2	2.5709	0.1314
LQAKKEEIIK	1200.5	2	3.0082	0.1063
LQALANEQAAAAHELEK	1808.0	2	5.3534	0.4434
LQALANEQAAAAHELEKMQQSVYVKDDKIR	3399.8	3	3.7722	0.2644

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LQALDTGWNELHK	1525.7	2	4.2522	0.2632
LQALKDTANR	1130.3	2	3.3175	0.2295
LQALQQMDGRNK	1402.6	2	2.4368	0.1664
LQAPQASVTAPSEQTTEFGIHKPHLGK	2874.2	3	3.5431	0.1731
LQAQEHGAER	1139.2	2	2.7349	0.2208
LQAQLNELQAQLSQKEQAAEHYK	2669.9	3	3.819	0.256
LQAQLNELQAQLSQKEQAAEHYKLQMEK	3299.7	3	3.9335	0.2908
LQASNVTNKNDPK	1429.6	2	3.3096	0.1858
LQAVEVVITHLAPGTK	1677.0	2	4.9698	0.4424
LQAVTDDHIR	1168.3	2	3.018	0.3029
LQAYHTQTTPLIEYYR	1998.2	2	5.6821	0.4832
LQAYHTQTTPLIEYYRK	2126.4	2	5.1671	0.3781
LQDAEIAR	916.0	2	2.5563	0.1085
LQDAFSAIGQNADLDLPQIAVVGGQSAGK	2885.2	3	6.5143	0.5522
LQDAYYIFQEMADK	1735.9	2	2.4273	0.1514
LQDEANYHLYGSR	1566.7	2	3.0684	0.2601
LQDEIQNMKEEMAR	1736.0	2	4.838	0.3508
LQDFKLDFGNSQGK	1597.8	2	2.5984	0.138
LQDFKSFLLKDSETSQR	2043.3	3	3.5557	0.2315
LQDFNVGDYIEAVLDR	1868.0	2	5.1496	0.4469
LQDKATVLTTER	1375.6	2	3.6835	0.3177
LQDKLAATQK	1116.3	2	3.2922	0.23
LQDKQEHCSQLESHLK	1924.1	3	3.9486	0.1632
LQDLTLRDLEK	1344.5	2	3.0456	0.1082
LQDMQEIISHYEEELTQLR	2376.6	3	4.5658	0.3519
LQDNVREDLYEAADKWVAAVGK	2491.7	3	5.1396	0.3624
LQDPFSLYR	1139.3	2	2.5461	0.1707
LQDTYNLDTDTISK	1627.7	2	2.9493	0.2414
LQDVFNTVGADIIQLPQIVVVGTQSSGK	2928.3	3	5.8488	0.4895
LQDVHVAEGKK	1224.4	2	3.2076	0.3281
LQDYEEK	925.0	2	2.8649	0.1168
LQDYEEKTK	1154.3	2	2.6768	0.14
LQEAGILSAEELQR	1557.7	2	4.9422	0.3734
LQEAQEREAATASQTR	1789.9	3	3.5701	0.2518
LQEDTDKANK	1162.2	2	3.0117	0.107
LQEEEAKSGHLSR	1484.6	2	3.4483	0.2652

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LQEEITKQSPTLQR	1671.9	2	4.5642	0.2686
LQEELAKLSEK	1288.5	2	3.0858	0.1198
LQEELSQAESTIDELKEQVDAALGAEEMVEMLTDR	3923.3	3	5.1431	0.4479
LQEEMLQREEAENTLQSFR	2352.6	2	4.6152	0.3529
LQEEMLQREEAENTLQSFRQDVDNASLAR	3422.7	3	4.0748	0.3016
LQEESQAASEQLR	1489.6	2	2.4574	0.1827
LQEESQAASEQLRK	1617.7	2	4.3436	0.342
LQEGDKILSVNGQDLK	1758.0	2	5.1985	0.3396
LQEGDKILSVNGQDLKNLLHQDAVDLFR	3180.6	3	3.9672	0.3332
LQEGDLPNAVLLFEAAVQQDPK	2396.7	3	5.2115	0.2914
LQEGYDHSYYFIATFITDHIR	2590.8	3	5.7838	0.532
LQEKEDLQELNDR	1630.7	2	4.8663	0.3179
LQEKEDLQELNDRLAVYIDR	2461.7	3	3.7632	0.2803
LQEKEELRELNDR	1672.8	3	3.5317	0.1147
LQELDAASK	975.1	1	2.258	0.1931
LQELEANPPSDVYLSSR	1919.1	2	3.5096	0.3437
LQENLQQLQHSTNQLAK	1994.2	2	5.0699	0.3988
LQEQEELENYIEHVLLR	2156.4	2	5.6865	0.3458
LQEQEELENYIEHVLLRR	2312.6	3	3.5477	0.1393
LQEQEELENYIEHVLLRRP	2409.7	3	3.8353	0.1713
LQEQLEKAEDGSSSKEGTSV	2123.2	3	5.3709	0.3672
LQESQPGNAVIDK	1399.5	2	2.4372	0.1225
LQETLSAADR	1104.2	2	3.2102	0.2122
LQETSSQSYVEEQK	1656.7	2	2.5643	0.1963
LQEVEVPEDFGPVR	1614.8	2	3.9576	0.2647
LQEVFGHAIK	1142.3	2	3.1898	0.1728
LQEVIETLLSLEK	1515.8	2	4.6457	0.3185
LQEYGSIFTGAQDPGLQR	1981.2	2	3.3904	0.3007
LQFHDVAGDIFHQQCK	1887.1	2	2.489	0.1786
LQFHNVKPECLEAYNK	1934.2	2	3.5976	0.3314
LQGAHLTSILSHEEQMFVNR	2311.6	3	4.6762	0.346
LQGEFQLR	991.1	2	2.7471	0.1333
LQGEGAEVQLTGK	1330.5	2	4.1145	0.2797
LQGEHQGSLIIHPR	1585.8	2	3.497	0.3146
LQGEVEKYQQLQK	1591.8	2	4.624	0.3156
LQGEVVAFDYQSK	1484.6	2	3.7033	0.3305

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LQGGKDFNMPLTISSLK	1850.2	2	3.3992	0.3457
LQGGKDFNVPLSISR	1631.9	2	3.9254	0.3875
LQGGTPQEPPNPR	1391.5	2	3.1008	0.2795
LQGGVLVNEILNHMKR	1822.2	2	3.4303	0.3097
LQGHLLR	837.0	2	2.6564	0.1075
LQGIDLDRTVQQVNQEKQEK	2370.6	3	3.6974	0.1184
LQGPQTSAEVYR	1349.5	2	2.6811	0.2257
LQGVLDSTLNSK	1275.4	2	2.9588	0.2136
LQHAAELIK	1023.2	2	2.53	0.178
LQHAAQMEQK	1184.4	2	2.9926	0.2287
LQHIQAPLSWELVRPHIYGYAVK	2720.2	3	3.9344	0.3814
LQHLENELTHDIITK	1805.0	2	5.1423	0.4062
LQHLQGSALQKPFHASR	1919.2	2	4.9193	0.4778
LQHTLQQVLDQREEVR	1993.2	3	3.9823	0.3616
LQHVEDGVLSMQVASAR	1841.1	2	5.7782	0.4821
LQHVTISQLFAPGDLPELGLEHR	2571.9	3	3.5886	0.2133
LQIEIGKLR	1070.3	2	2.746	0.1812
LQIENEAAKDEVKEVLQALEELAVNYDQK	3331.7	3	5.669	0.3957
LQILHIHTAR	1202.4	2	3.2885	0.2632
LQIQCVVEDDKVGTDMLEEQITAFEDYVQSMDVAAFNKI	4438.0	3	6.816	0.5317
LQIRHEQISDLER	1637.8	2	2.7149	0.1709
LQISHEAAACITGLR	1583.8	2	3.3127	0.2485
LQIWDTAGQER	1317.4	2	2.6685	0.1935
LQIWDTAGQESFR	1551.7	2	4.4225	0.3496
LQKADIEEIKSGR	1487.7	3	3.2009	0.2724
LQKDLEGLSQR	1287.4	2	3.2288	0.2192
LQKDLEGLSQRHEEK	1811.0	2	3.4381	0.2041
LQKEEEIEFLYNENTVR	2155.4	3	3.6933	0.2793
LQKLPAELGPQLLHK	1686.0	3	3.5409	0.2231
LQKPTDSTASSR	1291.4	2	2.8954	0.2551
LQLDSPEDAEFIVAK	1675.9	2	4.1657	0.3207
LQLEETDHQKNLLDEELQR	2352.5	3	5.0738	0.3197
LQLEIDQKKDAENHEAQLK	2251.5	3	4.3438	0.2344
LQLEKVTTEAK	1260.5	2	3.6806	0.1817
LQLETEIEALKEELLFMK	2178.6	2	6.2318	0.4535
LQLETEIEALKEELLFMKK	2306.7	2	5.1218	0.4287

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LQLEYCSLSAASCEPLASVLR	2254.6	2	3.723	0.2478
LQLFIQEVNHAVEETSHQALQNMPK	2906.3	3	6.1361	0.3925
LQLHESQKDYK	1389.5	2	3.0621	0.3241
LQLHESQKDYSK	1476.6	2	3.8263	0.2972
LQLLEEKTDEDEKTILNLENSNK	2718.0	3	5.1504	0.338
LQLLEPFDKWDGKDLEDLQILIK	2771.2	3	5.3268	0.2874
LQLLLLHTR	1107.4	2	2.724	0.1312
LQLLNPEIEAEQILMSPNSYIK	2544.9	2	4.2061	0.2121
LQLLSNLFHGMDK	1516.8	2	2.6774	0.1305
LQLLTGEHRPEDEEELEKELYR	2728.0	3	5.8109	0.3731
LQLLTGEHRPEDEEELEKELYREAR	3084.3	3	3.2333	0.1815
LQLNEKPVQDLNIVLKDNDFLR	2626.0	3	4.0826	0.1274
LQLNIVEMKDENATLDGGDVLFTGR	2750.1	3	5.1161	0.3109
LQLQEQLQAETELCAEAEELR	2445.7	3	5.5253	0.4105
LQLQYTLQELVSK	1563.8	2	4.5788	0.363
LQLSGHAMPR	1110.3	2	2.5665	0.2933
LQLSHDLLGILLLKK	1705.1	2	3.1169	0.2525
LQMEAPHIIVGTPGR	1619.9	2	4.2842	0.433
LQNAHTGLDLTVPQHQEVR	2157.4	3	4.9883	0.2761
LQNAIVNGVLQNTENTSK	1944.1	3	3.2574	0.1347
LQNALNEQRVEFATLQEALAHALTEK	2939.3	3	6.5161	0.4667
LQNALNEQRVEFATLQEALAHALTEKEGKDQELAK	3938.4	3	6.1782	0.5183
LQNEILKDLSDGIHVVK	1922.2	3	5.7095	0.4518
LQNEILKDLSDGIHVVKDAR	2264.6	3	6.5236	0.4032
LQNELDNVSTLLEEAEK	1946.1	2	4.5931	0.39
LQNELDNVSTLLEEAEKK	2074.3	2	3.6125	0.1595
LQNGLQALLISDLSNMEGK	2045.3	2	2.7537	0.1467
LQNGQNGER	1016.1	2	2.9923	0.2811
LQNLDALTNLTVLSMQSNR	2132.4	2	6.0197	0.5521
LQNLEFALNLLR	1444.7	2	4.0916	0.2967
LQNLQLQPGNAK	1324.5	2	4.2693	0.1945
LQNLQLQPGNAKL	1437.7	2	4.3584	0.2196
LQNNNVYTIAK	1278.4	2	3.0529	0.3199
LQNPDLDSEALLALPLPQLVQK	2416.8	3	4.3012	0.2511
LQPHEFQGGTFTISNLGMFGIK	2423.8	3	4.3049	0.3527
LQPHPGLEKKEEEEEEEEYDEGSNLKK	3215.4	3	4.1191	0.3156

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LQPSIIFIDEIDSFLR	1907.2	2	4.1671	0.3373
LQQEDGISFEYHR	1622.7	2	3.7136	0.3407
LQQEETQLEQSIQAGR	1859.0	2	4.2763	0.3211
LQQEGSENERIEELQEQLEQK	2558.7	3	6.4899	0.2305
LQQELDDLLVDLDHQR	1951.1	2	5.8838	0.3727
LQQELDDLTVDLDHQR	1939.1	2	5.1587	0.4351
LQQELEFLEVQEEYIKDEQK	2539.8	3	4.5618	0.226
LQQENSILR	1101.2	2	2.7539	0.1148
LQQENSILRDALNQATSQVESK	2473.7	3	4.6582	0.4521
LQQENSILRDALNQATSQVESKQNAELAK	3228.5	3	6.4874	0.4229
LQQGYNAMGFSQGGQFLR	2003.2	3	5.8488	0.5188
LQQHIQELEAHLEAEEGAR	2202.4	2	6.9499	0.457
LQQHQSMPGTMAEAEDLDGGTLSR	2573.8	2	3.8522	0.3734
LQQLGEAHQAETEVLRR	1979.2	2	4.3912	0.3676
LQQLKDETGELSSADEKR	2048.2	3	4.3887	0.3123
LQQLPADFGR	1145.3	2	2.8053	0.181
LQQLSGSSAISSSDLFGDMDGAHGAGSVSLGNVLPTADIAQFK	4251.6	3	5.9198	0.5273
LQQQHSEQPPLQPSPVMTR	2202.5	3	4.395	0.3357
LQQQLTQAQETLK	1529.7	2	4.7342	0.2619
LQQQQAQQPLQQQQQR	1979.1	3	3.9563	0.2826
LQQTQAQVDEVVDIMR	1874.1	2	5.5916	0.4762
LQQTQNQVDEVVDIMR	1917.1	2	5.0048	0.4789
LQQTYAALNSK	1237.4	2	3.3449	0.293
LQREAEYFELPELVR	1893.1	2	3.2855	0.2845
LQREAEYFELPELVRR	2049.3	3	3.6298	0.2802
LQRELEDATETADAMNR	1964.1	2	4.1873	0.4053
LQRELEDATETADAMNREVSSLK	2607.8	3	3.4193	0.2063
LQRLEAEKQQLEEALNASQEEEGSLAAAKR	3341.6	3	3.5925	0.3062
LQRLEDELNR	1286.4	2	2.9565	0.1694
LQRLEDELNRAK	1485.7	3	3.6944	0.1446
LQSESQKLEIR	1331.5	2	2.9379	0.1302
LQSHSSPEGKEEPEPLSPELEYIPR	2850.1	3	5.9269	0.3948
LQSIGTENTEENRR	1647.7	2	3.0824	0.1632
LQSLTENLTKEHLMLEEELR	2427.8	3	3.7774	0.2242
LQSPEFQSLFTEGLK	1724.9	2	4.1423	0.43
LQSQMSGQQLVEQSHVVLSTLWEPHITQR	3361.8	3	5.242	0.4223

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LQSQVLQAMR	1174.4	2	3.0804	0.3178
LQSQYASSEATISQLRSELAKGPQEVAVYVQELQK	3881.3	3	3.6943	0.1991
LQSRPAAPPAPGPGQLTLR	1928.2	3	4.2711	0.4372
LQSSDGEIFEVDVEIAK	1880.0	2	4.3856	0.4182
LQSSEAEVR	1019.1	2	2.8449	0.2199
LQSSQEPEAPPPRDVALLQGR	2289.5	3	3.5481	0.2051
LQSVLGKVNEIAK	1399.7	2	3.4123	0.2097
LQSVQALTEIQEFISFISK	2182.5	2	4.5303	0.433
LQTEKQELLQK	1358.6	2	3.7765	0.1611
LQTEKQELLQKTEAFAK	2006.3	2	5.6048	0.4222
LQTLVSEQPNKDVVEQMEK	2216.5	2	4.693	0.3193
LQTMKEELDFQK	1510.7	2	4.0219	0.3539
LQTMKEELDFQKNIYSEELR	2515.8	3	3.2846	0.1894
LQTMKEELDFQKNIYSEELRETK	2874.2	3	4.8751	0.3266
LQTSSVLVSGLR	1260.5	2	3.6015	0.2922
LQTSSVLVSGLRGLGVEIAKNIILGGVK	2823.4	3	3.5097	0.2493
LQTYKTAVETAVLLLR	1820.2	2	2.9844	0.2981
LQVEEVHQLSR	1338.5	2	3.4889	0.1456
LQVELDNVTGLLSQSDSK	1947.1	2	6.8806	0.5034
LQVELDNVTGLLSQSDSKSSK	2249.5	2	5.4995	0.3941
LQVEQAPHSSPGAK	1449.6	2	4.2099	0.4431
LQVKEHQHEEIQNVR	1888.1	2	2.4155	0.1577
LQVSQQEDITK	1289.4	2	3.7341	0.2962
LQVTNVLSQPLTQATVK	1841.1	2	5.8911	0.5255
LQVTNVLSQPLTQATVKLEHAK	2419.8	2	4.8986	0.3813
LQVVDQPLPVR	1264.5	2	3.1932	0.3368
LQYLIDLGRVDPSQPIDLTQLVNGR	2825.2	3	6.1452	0.3679
LRAELDEVNKSAK	1473.7	2	3.8576	0.3383
LRAETEQGEQQR	1445.5	2	4.644	0.3408
LRAETEQGEQQRQLLEEELAR	2527.7	3	5.2594	0.276
LRAPDLEYLFEKPR	1748.0	3	4.6205	0.3155
LRAPGALLAAAGLADAATEIVER	2250.6	3	4.294	0.2757
LRAPPNATLEHFYLTSGK	2016.3	3	5.3079	0.4544
LRAPPNATLEHFYLTSGKQPK	2369.7	3	6.1882	0.495
LRAVDFAER	1077.2	2	3.5214	0.2502
LRDDTEAAIR	1160.3	2	3.3024	0.1136

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LRDFLLEHR	1199.4	2	2.441	0.14
LRDHDDAAESLIEQTTALNKR	2397.6	3	5.5716	0.3499
LRDLEDSLAR	1188.3	2	3.4356	0.2547
LRDLHPDLEGQLK	1534.7	2	4.3638	0.3887
LRDLHPDLEGQLKELR	1933.2	3	4.9804	0.3049
LRDNGLLAKPTHGDIIR	1890.2	3	4.99	0.4225
LRDPEVVASELGYVFQAITLTR	2478.8	3	4.5705	0.3841
LRDPLQVHLPLR	1457.7	3	3.3833	0.2369
LRDTEEMLSKKQEFLEK	2125.4	3	3.2529	0.1512
LRDVAALNGLYR	1361.6	2	3.101	0.3289
LREAAEGLR	1015.1	2	2.6671	0.1584
LREAGLAPVPMIIFAK	1727.2	2	3.2499	0.3486
LREAGLVAQHPPAR	1515.7	2	3.5163	0.3043
LREANQQQQFNR	1532.6	2	2.8682	0.1652
LREAQNDLEQVLR	1584.8	2	4.2159	0.1987
LRECLPLIIFLR	1486.9	2	3.4032	0.2871
LREDENAEPVGTTYQK	1851.0	2	5.5731	0.462
LREDGIQKR	1115.3	2	2.8721	0.1189
LREEEQQQHR	1353.4	2	3.1207	0.2463
LREEEVDADAADAAAAEEEDGEFLGMK	2883.0	3	4.1233	0.3312
LREEFSFIPSAALDLLDHMLTLDPSKR	3116.6	3	3.4861	0.2661
LREEIEELKR	1315.5	2	3.7247	0.1258
LREELKPIAFAR	1443.7	2	3.1935	0.2123
LREENKQFKEEDGLR	1892.1	2	4.9134	0.3374
LREFASHLQQLQDALNELTEEHSK	2838.1	3	4.4846	0.269
LREFQESFKNIEK	1668.9	3	3.3936	0.1529
LREKLQEEMLQREEAENTLQSFR	2879.2	3	3.7832	0.3194
LRELNKEMAAEK	1432.7	2	3.6951	0.2998
LRELPLAADALTFAEVSKDPK	2285.6	3	3.7371	0.2291
LREMFGLYGQTTGK	1601.9	2	2.5264	0.1151
LRENELTYYCCK	1535.8	2	3.3027	0.2138
LRENELTYYCCKK	1663.9	2	2.6294	0.1976
LRENKEFLEFR	1481.7	3	4.1541	0.3183
LRENVFQEHQTLK	1642.8	2	3.941	0.305
LRENVFQEHQTLKEKELETGPK	2655.0	3	6.3398	0.4768
LREQEKEEKER	1474.6	2	3.819	0.1437

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LREQGTESR	1076.1	2	2.6526	0.1077
LREQLQLLEEQHR	1692.9	3	4.1686	0.2444
LREQTLSPTITSGLHNIAR	2108.4	3	5.8861	0.4565
LRETAEADVASLNR	1545.7	2	4.014	0.2596
LREVVETPLLHPER	1689.0	3	4.5713	0.3767
LREYEAALNSK	1294.4	2	3.4305	0.1164
LREYEAALNSKDAALATALGDKK	2449.7	3	6.0446	0.4194
LRFDKEGEVR	1249.4	2	2.4142	0.1081
LRFPAEDEFPDLSAHNNHMAK	2440.7	3	6.0006	0.381
LRGGSPLNTGK	1100.3	2	2.9464	0.2296
LRGHGAEGPQEPK	1376.5	2	2.4539	0.1655
LRGIEQAVQSHAVAEEEAR	2094.3	2	6.1009	0.5035
LRGIEQAVQSHAVAEEEARK	2222.4	3	5.1817	0.424
LRGLPFGCTKEEIVQFFSGLEIVPNGITLPVDPEGK	3902.5	3	3.4295	0.1229
LRGTADVTHDLQEMKEESR	2216.4	3	3.8642	0.2059
LRGWEAFLNAPEANR	1744.9	2	3.6927	0.3835
LRGYDYGPHFQGILEASLEGDSGR	2638.8	3	4.0815	0.3505
LRHADLEIR	1123.3	2	2.8282	0.1742
LRHEILLSQSVR	1451.7	2	4.0736	0.334
LRHPLGEAYATK	1356.6	2	3.4786	0.3652
LRIDYER	965.1	2	2.6311	0.126
LRITESEEVVSR	1418.6	2	2.7173	0.2468
LRKDDPLTNLNTAFDVAEK	2161.4	3	4.944	0.466
LRKDDPLTNLNTAFDVAEKYLDIPK	2891.3	3	6.1113	0.5708
LRKDDPVTNLNNAFEVAEK	2174.4	3	4.5557	0.3581
LRKDDPVTNLNNAFEVAEKYLDIPK	2904.3	3	3.9734	0.2717
LRKELEAQLDDAVAEASKER	2272.5	3	4.4905	0.1768
LRKNYVEDIPFLSPTFNPQEVFIR	2924.3	3	3.6587	0.1257
LRLDQPKLDEVTR	1583.8	2	3.5093	0.2568
LRLDTGPQSLSGK	1372.6	2	3.3497	0.3187
LRLEEEQKEEEER	1717.8	2	5.0349	0.289
LRLEHEQASQPTPEK	1763.9	2	3.6305	0.2977
LRLEHEQASQPTPEKAQQNPTLLAELR	3099.4	3	6.8073	0.5126
LRLESEGSPETLTNLRK	1944.2	3	4.8176	0.2956
LRLEVNLQAMK	1315.6	2	2.7858	0.2075
LRLPLDKEPAR	1308.6	3	3.4892	0.1304

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LRLSEELSGGR	1217.4	2	2.538	0.1695
LRNELQTDKPFIPLVEK	2041.4	3	4.159	0.3142
LRNEYGPVLHMPTSK	1743.0	3	3.7	0.2821
LRNGHVGISFVPK	1424.7	3	3.2532	0.1972
LRNILSVVGTDALKK	1628.0	2	2.633	0.1312
LRNVSNLKPVPLIGPK	1746.1	2	3.1117	0.2799
LRNWASGHDLQGK	1482.6	2	3.4144	0.2357
LRPEAQPHPSAGPK	1485.7	2	3.0913	0.2224
LRPEAQPHPSAGPKPAESK	1998.2	2	3.8923	0.3407
LRPESALAQAQK	1312.5	2	3.2842	0.1767
LRPGSIETYEQEK	1550.7	2	3.4447	0.2655
LRPLSYPQTDVFLVCFSVVSPSSFENVKEK	3417.9	3	4.1342	0.2847
LRPLYDIPYMFEAR	1785.1	2	4.1653	0.3386
LRPLYNHPAGPR	1391.6	2	2.7789	0.1272
LRPQTYDLQESNVQLK	1933.2	3	4.7209	0.2313
LRPSPGSLLDTIEDLGDDPALSLR	2551.8	3	4.0799	0.3074
LRPYFEGLSHSSSQTEIGSIHSAR	2660.9	3	4.8542	0.326
LRQEEPQSLQAAVR	1625.8	2	4.5845	0.2305
LRQEFAQHANAFHQWIQETR	2511.7	3	3.7578	0.2987
LRQEIYSSHNQPSTGGR	1931.1	3	3.6527	0.2948
LRQENMELAER	1389.6	2	3.515	0.2453
LRQLAEEDLAQQR	1570.7	2	4.4152	0.2992
LRQNLDALLNQLK	1539.8	2	3.2322	0.2848
LRQPFFQKR	1220.5	2	2.4402	0.1131
LRRPEGASNESERD	1616.7	3	3.664	0.2417
LRSDIAVPIPKDHQVLIK	2043.4	2	3.9522	0.3248
LRSELDVVR	1087.3	2	2.8257	0.1929
LRSELEMVSGNVR	1490.7	2	4.1831	0.3221
LRSENKDIENLRR	1643.8	2	4.0845	0.26
LRSGGTEGLLAEKLEALITQTR	2357.7	3	5.7181	0.412
LRSLESLHSFVAAATK	1731.0	2	3.4013	0.2543
LRSPPEALVQGR	1323.5	2	3.2551	0.2919
LRVAPEEHPVLLTEAPLNPK	2224.6	3	4.9889	0.1709
LRVCEVCSAYLGLHDNDRR	2220.5	3	3.2544	0.1393
LRVDKAAAAAAALQAK	1568.8	3	3.2203	0.2549
LRVDQLKYDVQHLQTALR	2197.5	3	4.4907	0.333

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LRVDYSGGFEPFSVLR	1843.1	2	2.6296	0.1158
LRVHLPSSIYR	1341.6	2	2.5241	0.1703
LSAADEKAVSAAEEVK	1618.8	2	3.6184	0.3176
LSAAVTEAFVR	1164.3	2	3.3051	0.1812
LSAEAEKVLALPEPSPAAPTLRSELELTLGKLEQVR	3858.4	3	3.879	0.2551
LSAEDLVLEGAGLR	1443.6	2	4.4908	0.3649
LSAEEAAHR	984.0	2	2.73	0.1672
LSAEERDQLLPNLR	1654.8	3	4.1752	0.188
LSAEKVEIATLTR	1431.7	2	3.6765	0.2934
LSAIAGSSGNKHPSR	1482.6	2	2.7364	0.2408
LSAIYGGTYMLNKPIEEIIVQNGK	2653.1	3	6.3952	0.4724
LSAIYGGTYMLNKPIEEIIVQNGKVIGVK	3149.7	3	4.8342	0.2921
LSAIYGGTYMLNKPVDDIIMENGK	2644.1	3	5.1351	0.4623
LSAIYGGTYMLNKPVDDIIMENGKVVGVK	3126.7	3	4.2957	0.3805
LSAKEDSIHILNEEYETK	2120.3	3	3.6808	0.3548
LSAKPAPPKPEPK	1360.6	2	3.8534	0.1926
LSAKPAPPKPEPR	1388.6	3	4.2005	0.2838
LSAKPAPPKPEPRPK	1613.9	2	2.9655	0.1077
LSAKPPAKVEAK	1239.5	2	2.6043	0.1303
LSAKPPAKVEAKPK	1464.8	3	3.8649	0.1676
LSAKPPAKVEVKPK	1492.8	2	2.9001	0.183
LSALLQETK	1003.2	2	2.8889	0.1053
LSALLQETKELKNEIK	1858.2	3	3.7645	0.2104
LSAMLVPVTPEVKPK	1610.0	2	3.252	0.2437
LSASLLHSHDTETR	1567.7	2	3.5099	0.4007
LSASSSISSADLFEEPR	1796.9	2	4.3035	0.3352
LSASSTGSTR	967.0	2	2.6945	0.2212
LSATLGGLLQDHGSR	1525.7	2	3.9898	0.394
LSDAGITPLFLTR	1404.6	2	4.3296	0.359
LSDALAVEDDQVAPVPLNVVETSSSVR	2812.1	3	3.8406	0.2786
LSDDNTIGKEEIQQR	1746.9	3	4.1844	0.2725
LSDEHEPEQR	1240.3	2	2.9739	0.2274
LSDETLIDIMTR	1407.6	2	4.3428	0.325
LSDGFNGADLR	1165.2	2	3.7348	0.2686
LSDGVAVLK	902.1	2	3.5435	0.2138
LSDKGLKAELMER	1490.8	3	3.3802	0.2888

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LSDLLAPISEQIK	1427.7	2	4.0897	0.275
LSDLLAPISEQIKEVITFR	2173.5	3	4.1607	0.4407
LSDLQEALDQALNYVR	1849.0	2	2.8149	0.3331
LSDLQKEAEKLESEHPDQAQAILSR	2837.1	3	5.8771	0.4561
LSDPGIPITVLSR	1368.6	2	2.5466	0.1311
LSDQFHDILIR	1357.5	2	3.2606	0.1755
LSDSFSLYPQFMFHLR	1989.3	3	4.1331	0.248
LSDSTLKETLLNGVGYLHEGLSPMER	2861.2	3	4.9084	0.4421
LSDVDANTAIKHEEQSNEDIPIAEQSSK	3070.2	3	4.5476	0.3763
LSDVDRDGMLDDEEFALASHLIEAK	2791.0	3	3.579	0.2921
LSDVTLVPVSCSELEKAGAGLSSLCLVLSTRPHS	3471.0	3	3.5836	0.1987
LSDYLFTLAR	1199.4	2	4.0749	0.32
LSEDSLTKQPEEVFDVLEKLGEGSYGSVFK	3332.7	3	4.1027	0.1043
LSEDYGVLK	1024.1	1	1.7069	0.1444
LSEDYGVLKTDEGIAYR	1930.1	2	5.0382	0.4968
LSEEEILENPDLFLTSEATDYGR	2642.8	2	5.7595	0.3821
LSEEELLDKLEIFFGK	1911.2	2	4.4885	0.4336
LSEEFLTAHPR	1300.4	2	2.5934	0.3046
LSEELSGGR	948.0	2	3.31	0.1881
LSEGEAKEDSLDEEFFHHK	2248.3	3	3.6759	0.1207
LSEGSQPAEEEEDQETPSR	2119.1	2	4.0675	0.4269
LSEHATAPTR	1083.2	2	2.7821	0.3675
LSEHPDIR	967.1	2	2.4351	0.1575
LSEHSSPEEEASPHQR	1820.9	3	6.1775	0.4269
LSEIDVSSEGVK	1263.4	2	3.5272	0.2575
LSEIHHLHPEYVR	1630.8	3	3.9895	0.3551
LSEIMEKGQLVPLETVLDMLRDAMVAK	3031.6	3	4.8706	0.255
LSEIVTLAK	974.2	2	3.0839	0.1675
LSEKHSQNGFIVPPPPEK	2005.3	2	3.9336	0.3786
LSELDDRADALQAGASQFETSAAK	2495.6	3	5.2807	0.2974
LSELEAALQR	1130.3	2	4.4052	0.2525
LSELEFHNSK	1204.3	2	3.1016	0.1155
LSELLPEEVEAEVK	1585.8	2	3.4235	0.1743
LSELQETSEQAQSK	1578.7	2	3.4474	0.2429
LSEMTEAEQQQLIDDHFLFDKPVSPLLTAAGMAR	3804.3	3	7.0285	0.4925
LSENNIQTIFAVTEEFQPVYK	2471.7	3	4.3143	0.3678

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LSENNIQTIFAVTEEFQPVYKELK	2842.2	3	4.1675	0.2753
LSENVIDR	946.0	2	3.0066	0.1306
LSENVVNR	931.0	2	2.7898	0.1456
LSEPKPIFFNLNIAAAKPTPPK	2394.8	3	5.1838	0.3886
LSESQLSFR	1067.2	2	2.7274	0.1939
LSESQLSFRRSPTK	1636.8	2	2.4096	0.1254
LSETSIKDR	1049.2	2	2.4921	0.1019
LSEVVGSGKDGR	1204.3	2	2.6957	0.2398
LSFAHPPSAEVEAIALATLHDR	2346.6	3	5.2855	0.2781
LSFDKDAMVAR	1253.5	2	3.659	0.3599
LSFEDFVTMTASR	1504.7	2	4.266	0.4211
LSFGDTLQVQNIHGAFNALGGADR	2502.7	3	4.461	0.3397
LSFGDTLQVQNIHGAFNALGGADRLTSNPLASHDYILK	4056.5	3	5.5756	0.4064
LSFGLEDEPLETATK	1650.8	2	2.7999	0.1721
LSFLKEPK	962.2	2	2.4312	0.1363
LSFLYLITGNLEK	1511.8	2	3.2856	0.2312
LSFQHDPETSVLVLR	1742.0	3	5.2087	0.3853
LSFSGLRAPVPASELLASGVLSR	2328.7	3	4.5436	0.3473
LSGAEPDDEEYQEFEEMLEHAESAQDFASR	3461.5	3	4.2967	0.2699
LSGAPQASAADVVVVHGR	1734.9	2	4.8985	0.4133
LSGAQADLHIEDGDSIR	1797.9	2	4.8417	0.4352
LSGDVGER	832.9	2	2.4003	0.1055
LSGGDDDAAGQFFPEAAQVAYQMWELSAVAR	3302.6	3	6.5641	0.4863
LSGGGDWHIAYVLLYGPR	1975.2	2	3.7028	0.1682
LSGGIDFNQPLVITR	1630.9	2	4.0426	0.3812
LSGLADQMVAR	1161.4	2	3.6758	0.318
LSGLNAFDIAEELVK	1619.8	2	4.2328	0.2615
LSGPLKEQYAQEHGLNFQR	2216.4	2	5.6698	0.4601
LSGSARPQELVGTFIQQEVGKPEDEASGSFFK	3440.8	3	5.1686	0.3361
LSGSNPYTTVTPQIINSK	1921.1	2	5.5628	0.4512
LSGTEAHVLGLVNHAVAQNEEGDAAYQR	2951.2	3	5.3814	0.4147
LSGTGSAGATIR	1091.2	2	3.381	0.3706
LSGTVGVAAVTAGPGLTNTVTAVK	2185.5	3	4.7684	0.3056
LSGVQYQQHSQALGK	1644.8	2	3.5108	0.257
LSHANSAVVLSAVK	1396.6	2	3.6473	0.3456
LSHEGPGSELPAGALYR	1754.9	2	4.6069	0.4734

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LSHEGPGSELPAGALYRK	1883.1	2	4.8427	0.4
LSHHTSALSVVSSAVPK	1721.0	2	3.9233	0.382
LSHLKPSSEGLAIVTK	1681.0	2	3.5777	0.3682
LSHNGIFTLYSYRDPNTIETLQSFGK	3003.3	3	5.8089	0.4244
LSHSMSPDAQDGH	1382.4	2	3.8434	0.3748
LSIAEVVHQLQEIAAAR	1849.1	3	4.9215	0.4146
LSIIATDHTYR	1290.5	2	2.8756	0.2978
LSILYPATTGR	1192.4	2	2.9872	0.2709
LSINTHPSQKPLSITVR	1892.2	3	3.5904	0.2646
LSIRKEGDGEAK	1303.4	2	2.756	0.1215
LSITGTYDLK	1111.3	2	3.0698	0.2612
LSIVPVRR	940.2	2	2.5119	0.1625
LSKADVER	918.0	1	1.9189	0.1479
LSKAEQDITTLEQSISRLEGQVLR	2716.0	3	4.0515	0.3027
LSKDDIDR	962.0	2	2.8571	0.125
LSKDKDLEIDELQKR	1831.1	3	3.3419	0.1801
LSKDPNIVIAK	1198.4	3	4.4722	0.2833
LSKEDIER	990.1	2	2.7251	0.1014
LSKEETVLATVQALQTASHLSQQADLR	2939.3	3	6.669	0.5107
LSKELDLVSHHVR	1533.8	3	4.5462	0.4172
LSKELGIETYK	1281.5	2	2.7972	0.187
LSKELGIETYKVNVSER	1966.2	2	4.2288	0.2182
LSKELSSTEAQLHDAQELLQEETRAK	2956.2	3	4.8528	0.3227
LSKEYDQLLKEHSELQDRLER	2630.9	3	4.3684	0.2825
LSKLEPEPNTK	1256.4	2	3.8494	0.1092
LSKNGADSEALHVLAFLQELNEK	2527.8	3	5.2089	0.354
LSLDELHRK	1111.3	2	2.5956	0.1677
LSLDKVFR	978.2	2	2.715	0.1226
LSLEEFIR	1007.2	2	2.6664	0.1125
LSLEFGDPASSLFR	1539.7	2	3.6705	0.3993
LSLEGDHSTPPSAYGSVK	1846.0	2	5.3907	0.5169
LSLESEGAGEGAAASPELSALEEAFRR	2748.9	3	4.0005	0.2467
LSLNIDPDAK	1086.2	2	2.9654	0.1626
LSLPQNETVADTTLTK	1731.9	2	3.722	0.4204
LSLQDAVSQGVIDQDMATR	2048.3	2	3.3021	0.2102
LSLSNAISTALPLTQLR	1799.1	2	4.3071	0.3858

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LSLTQSDISHIGSMR	1645.9	2	4.15	0.4904
LSMKEGDPAIYAER	1580.8	2	3.5266	0.2912
LSMKPEPLFR	1218.5	2	2.4224	0.1437
LSMYGVDLHHAK	1371.6	2	2.59	0.2173
LSNHISSLFR	1174.3	2	2.8415	0.3011
LSNHVFNALK	1143.3	2	2.5827	0.2828
LSNIFVIGK	991.2	2	3.5485	0.219
LSNLALVKPEK	1212.5	2	2.6422	0.1134
LSNRPAFMPSEGK	1434.6	2	3.5071	0.2524
LSNRPAFMPSEGR	1462.7	2	3.4867	0.3637
LSNSDSQDIQGR	1320.3	2	3.8816	0.291
LSNTGEYESQR	1284.3	2	3.6355	0.2989
LSNTQGVVSAFSTMMSVHR	2053.4	2	3.9862	0.4173
LSNTSPEFQEMSLLER	1882.1	2	4.7289	0.3569
LSNVSSSGSINLLESPQLATLAEDVTAALAK	3101.5	3	4.2349	0.3937
LSPDAVAQLAFQMAFLR	1879.2	3	4.8371	0.42
LSPEDYTLKVSQAGK	1636.8	2	4.5542	0.3853
LSPEIVELSEPLQVVR	1809.1	2	3.8495	0.3134
LSPEPWTPETGLVTDAFK	1989.2	2	4.0907	0.4139
LSPFMADIR	1050.3	2	2.6436	0.1717
LSPFMADIRDAPQDFHPDRVK	2456.8	3	3.9784	0.3339
LSPGGYFIGTTPNSFELIR	2070.3	2	3.7753	0.3259
LSPISHGNTIALFFR	1673.9	2	3.6742	0.4759
LSPKAEEVATFFAK	1538.8	2	3.3218	0.29
LSPKHPESNTAGMDIFAK	1944.2	2	3.1441	0.3186
LSPLVLEVDPNIQAVR	1764.1	2	5.0965	0.445
LSPNYVVCRDCEVTNDGHTIQVILK	2818.2	3	4.3449	0.1229
LSPPPSQSDQLLAESSSARPQLELHLRPQAAR	3481.9	3	3.3547	0.3352
LSPPSSSAASSYSFSDLNSTR	2162.3	2	3.0246	0.2896
LSPPYSSPQEFAQDVGR	1879.0	2	3.5203	0.3449
LSPQAVNSIAKR	1284.5	2	2.8186	0.2589
LSPQFPNEEDSFHKFVAPEEVLPFTEGDILEK	3691.1	3	5.1482	0.2626
LSQALGNVTVVQK	1357.6	2	3.5011	0.2277
LSQELEYLTEDVKR	1723.9	2	3.8404	0.2975
LSQEQVDNFTLDINTAYAR	2199.4	2	5.7953	0.471
LSQETEALGR	1104.2	2	3.8799	0.1694

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LSQLEGVNVER	1244.4	2	3.3484	0.1463
LSQNNFALGYK	1255.4	2	3.4472	0.2809
LSQPAGGLLDSITNIFGR	1860.1	2	2.4402	0.1183
LSQRFPK	876.0	2	2.4433	0.1225
LSQVLRDLEDESTPIVK	1943.2	2	3.316	0.2063
LSQVSDSVSGQTVVDPK	1746.9	3	3.3062	0.2058
LSQYPNENLHSAVTK	1701.9	2	2.6776	0.1346
LSQYQEPLHLPGVR	1637.9	2	3.0158	0.2701
LSRFDNDRTISFIPPDGDFELMSYR	2993.3	3	3.4467	0.1125
LSRTNEELLWKLQTGDPTSPIK	2527.9	2	2.5769	0.1445
LSSAHNGGSAFGAAGYGGAQPTPPMPTRPVSFHER	3511.8	3	4.0077	0.2615
LSSANGHEER	1100.1	2	3.0702	0.2533
LSSARPGGLGSSSLYGLGASRPR	2247.5	3	4.9127	0.3418
LSSDQNDKAASAAR	1434.5	2	3.8107	0.2367
LSSDQNDKAASAAREELKEAR	2290.4	3	3.4666	0.2115
LSSDVLTLLIK	1202.5	2	3.5918	0.2555
LSSEDKETMEK	1297.4	2	2.7809	0.2377
LSSEMNTSTVNSAR	1497.6	2	4.3473	0.4618
LSSEMNTSTVNSAREELMESR	2372.6	2	3.7722	0.2939
LSSEQFHEAASK	1334.4	2	3.5094	0.3654
LSSEQFHEAASKMESTIKPR	2277.5	3	5.3189	0.3555
LSSETGGMGSS	1013.1	1	1.9502	0.1222
LSSGPEQITLEASSTEGHPGAPSPQHTDQTEAFQK	3664.8	3	5.4217	0.4807
LSSLDNLKASVSQVEADLK	2018.3	3	5.1835	0.3585
LSSLFPFALLQR	1392.7	2	2.9609	0.2062
LSSLIILMPHHVEPLER	1985.4	2	4.7174	0.2368
LSSLPVGPSFLGFR	1477.7	2	2.6863	0.2717
LSSPAVINSR	1044.2	2	2.6837	0.2108
LSSPERDVERDVFLYR	1982.2	2	2.7993	0.1318
LSSQIEKLEHEISHLK	1892.1	2	4.6006	0.3586
LSSQIEKLEHEISHLKK	2020.3	3	4.5299	0.3653
LSSTQQSLAEKETHLTNLRAER	2513.7	3	3.6603	0.2527
LSSVQQILQLSDLWR	1787.1	2	2.8144	0.218
LSSVVTQHDSK	1201.3	2	2.8674	0.2731
LSSVVTQHDSKK	1329.5	2	3.2731	0.3656
LSSWVLLMK	1077.4	2	2.7711	0.214

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LSTDHIPILYR	1328.5	2	2.7516	0.2017
LSTHELTSLLEKELEQSQKEASDLLEQNR	3370.7	3	4.3216	0.416
LSTIALALGVER	1243.5	2	4.0547	0.4057
LSTVASTDILATVLEEMPPFPERESSILAK	3246.7	3	3.3879	0.1395
LSVAAQEAAR	1016.1	2	3.4339	0.2883
LSVDYGKK	910.0	2	2.4787	0.1246
LSVFANGVVTSIQDR	1606.8	2	4.3859	0.3878
LSVGLEDEEDLLEDLDQALKAAHPPSGSHS	3174.4	3	3.8356	0.1777
LSVISVEDPPQR	1340.5	3	3.2426	0.2247
LSVLGAITSVQQR	1372.6	2	3.7975	0.3104
LSVNSHFMK	1063.3	2	2.4658	0.2172
LSVNSVTAGDYSRPLHISTFINELDSGFR	3197.5	3	5.1675	0.4839
LSVSGRDENSVELTMAEGPYK	2283.5	3	3.5676	0.2276
LSVSNMVHTAK	1187.4	2	3.006	0.3634
LSYAGGRPPSYAGSPVHHAAER	2281.5	3	3.3588	0.2855
LSYLLMCLESAVHR	1636.0	2	3.144	0.343
LSYNTASNK	998.1	2	2.6599	0.2532
LTAASVGVQGSGWGWLGFNK	2036.3	3	6.0103	0.5274
LTAASVGVQGSGWGWLGFNKER	2321.6	2	2.9916	0.2885
LTADDEAFLSANAGAILSQFEK	2312.5	3	4.1655	0.1316
LTAEELLNKDFAK	1492.7	2	3.0516	0.2781
LTAFVNTLNGK	1178.4	2	2.5734	0.1647
LTAGLGSLIPEGDAGPDAAGPDAAGPLLPGRPQVK	3280.7	3	3.7764	0.2628
LTAIDILTTCAADIQR	1719.0	2	4.3848	0.362
LTAQVASLTSELTTLNATIQQQDQELAGLK	3187.5	3	4.1588	0.2654
LTAQVASLTSELTTLNATIQQQDQELAGLKQQAK	3643.1	3	6.0755	0.5162
LTASAPGYLAITK	1306.5	2	3.6168	0.3891
LTASAPGYLAITKK	1434.7	2	3.2122	0.4148
LTAVEGSMKENISK	1507.7	2	3.5277	0.3158
LTAYAMTIPFVR	1383.7	2	3.7789	0.39
LTAYLPAMSEDDEDCYGNGAARTGR	2677.9	3	3.2262	0.2107
LTDEDFSPFGSGGGLFSGGK	1976.1	2	3.8412	0.3042
LTDIHGNVLQYHK	1538.7	2	4.0813	0.3738
LTDIHGNVLQYHKDVK	1881.1	2	4.3809	0.4131
LTDKHQSIEEAK	1399.5	2	2.9385	0.1628
LTDKTVIGCSGFHGDCLTLTK	2210.6	2	3.8779	0.3104

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LTDLASQMAEMQLAELRAEIK	2362.8	3	3.8833	0.1863
LTDNIFLEILYSTDPK	1883.1	2	3.1297	0.3171
LTDPGLSSLSALSTQVANLPNTVQHMLLSDALTPQKK	3891.4	3	4.2185	0.434
LTDPIPTTETSIAPR	1612.8	2	3.7417	0.2969
LTDQVMQNPR	1202.4	2	3.2237	0.1638
LTDTLVSK	877.0	2	2.6162	0.1816
LTEAAEQNKEAIR	1473.6	2	3.0751	0.111
LTEAKPVDK	1001.2	2	2.8803	0.2102
LTEAKPVDKVK	1228.5	2	3.7554	0.3071
LTEDEEGNAKLQQR	1631.7	2	4.0341	0.2567
LTEDKADVQSIIGLQR	1787.0	2	5.3631	0.3711
LTEDKKEGLR	1189.3	2	2.4597	0.118
LTEDLEYHELLDR	1646.8	2	3.9603	0.2441
LTEELKEQMK	1249.5	2	3.2896	0.1359
LTEELNKEATVIQDLKTELLQRPGIEDVAVLKK	3736.3	3	6.292	0.3911
LTEKELAEAASK	1290.4	2	3.8345	0.2001
LTELETAVR	1032.2	2	3.5345	0.2383
LTELGTVDPK	1073.2	2	2.9487	0.1102
LTELLENDPSVR	1386.5	2	3.4889	0.159
LTELLKQGQYSPMAIEEQVAVIYAGVR	3008.5	3	3.6674	0.2533
LTELQLRARQLLDQVEQIQKEQDYQR	3243.6	3	4.0407	0.2004
LTELSMQDEELMKR	1724.0	2	3.7765	0.3527
LTEMETLQSQLMAEK	1753.0	2	5.1034	0.381
LTEPQHGLGSQR	1323.4	2	3.0497	0.3929
LTESPCALVASQYGWSGNMER	2300.6	2	2.9554	0.2413
LTESVDVLMPNVGEIVGGSMR	2204.6	2	3.8594	0.2245
LTEVLTDSHVK	1242.4	2	3.4019	0.2785
LTEVPVEPVLTVHPESK	1875.2	2	4.2865	0.3912
LTFASTLSHLR	1246.4	2	2.9358	0.2859
LTFDSSFSPNTGK	1401.5	2	2.7988	0.2201
LTFDSSFSPNTGKK	1529.7	2	3.593	0.2053
LTFDTTFSPNTGK	1429.6	2	4.571	0.4492
LTFDTTFSPNTGKK	1557.7	2	3.0021	0.2366
LTFSGLLNALDGVASTEAR	1936.2	2	5.0357	0.3779
LTFVDFLTYDILDQNR	1974.2	2	3.453	0.2941
LTGFHETSNINDFSAGVANR	2151.3	3	4.1698	0.3064

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LTGIKHELQANCYEEVKDR	2247.5	3	5.7814	0.5192
LTGKDVNFEFPEFQL	1785.0	2	4.1493	0.2091
LTGMPDLTLSFMNPR	1694.0	2	3.1549	0.1925
LTGQLFLGGSIVK	1333.6	2	4.0922	0.3577
LTGTIQNDILKEFMVR	1879.2	2	3.6275	0.3903
LTGVFAPRPSTGPHK	1565.8	2	3.7148	0.2744
LTGVNDKMAEYTNSAGVPSLNAALMHTLQR	3204.6	3	4.6217	0.3032
LTGVSISQVNHKPLR	1649.9	2	3.2573	0.3219
LTHDASNIHTSTPR	1550.7	2	3.5152	0.4407
LTHLHEGLPVK	1244.5	2	3.4116	0.3311
LTHLIDHLKEQEK	1604.8	2	4.0716	0.3075
LTHVDSPLEAPAGPLGQVK	1930.2	2	4.2093	0.22
LTHVLTGK	869.0	1	2.4852	0.2743
LTHVPQGHDGELLCHR	1813.0	3	3.2	0.1749
LTHVTALK	883.1	2	2.4564	0.1091
LTIFDEEVDPDEGLFGPGR	2107.3	2	5.2594	0.4593
LTIGEGQQHHLGGAK	1546.7	2	3.1985	0.2245
LTIGSNLSIR	1074.3	2	2.7636	0.2873
LTISPDYAYGATGHPGIIPPHATLVFDVELLK	3407.9	3	4.0795	0.2865
LTISPDYAYGATGHPGIIPPHATLVFDVELLKLE	3650.2	3	4.2918	0.2397
LTITQFMNHPWINQSMVVPQTPLHTAR	3162.7	3	3.4381	0.1527
LTKDFSALESQLQDTQELLQEENR	2837.0	3	6.0212	0.4291
LTKDFSALESQLQDTQELLQEENRQK	3093.3	2	5.3707	0.3975
LTKDFSALESQLQDTQELLQEENRQKLSLSTK	3723.1	3	5.2704	0.3464
LTKDNNLTTGK	1205.3	2	2.8076	0.2897
LTKEEIVDKYDLFVGSQATDFGEALVR	3045.4	3	5.1879	0.3915
LTKEVTAAR	989.2	2	2.774	0.2344
LTKIEGLQNLVNLR	1611.9	2	3.2724	0.1454
LTKQEEEKQILKQDFETLSQETK	2795.1	3	4.8083	0.2901
LTKVDDQIYSEFRK	1743.0	3	3.645	0.2172
LTLDKLDVK	1045.3	2	2.5163	0.1791
LTLDKLDVRGK	1258.5	2	3.9037	0.235
LTLDKLDVRGKR	1414.7	3	3.8047	0.2927
LTLDTIFVPNTGKK	1547.8	2	3.3836	0.3468
LTLHGLQQYYVK	1463.7	2	2.4795	0.1534
LTLKGGAAVDPDSGLEHSAHVLEK	2445.7	3	4.5086	0.4149

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LTLLHNGEPLYIPVTQEPAPMTEDLLEEQSEVLAK	3920.4	3	6.0482	0.466
LTLQPVDNSTISLQMGTNK	2061.3	2	4.9065	0.3854
LTLQTTSDGVMLDKDLFK	2026.3	2	4.1896	0.2685
LTLQTTSDGVMLDKDLFKK	2154.5	2	3.7795	0.363
LTLSALIDGK	1031.2	2	3.4703	0.2985
LTLSALIDGKNFSAGGHK	1830.1	3	4.1668	0.3498
LTLSALLDGK	1031.2	2	3.0817	0.2439
LTLSALLDGKNVNAGGHK	1809.1	2	5.2578	0.3659
LTLSALLDGKNVNAGGHKLGLGLEFQA	2738.1	3	5.0792	0.4597
LTLSALVDGK	1017.2	2	3.4428	0.3258
LTLSALVDGKSINAGGHK	1782.0	2	3.5348	0.3992
LTLYDIAHTPGVAADLSHIETK	2366.7	3	7.3803	0.5413
LTLYDIAHTPGVAADLSHIETKAAVK	2736.1	3	4.7797	0.3879
LTMQNLNDR	1105.3	2	2.6586	0.19
LTMQNLNDRLASYLDKVR	2151.5	3	4.2499	0.3803
LTMQVSSLQR	1163.4	2	3.4012	0.2324
LTNENLDLKELVEKLEKNER	2428.7	3	4.292	0.3077
LTNSMMMHGR	1178.4	2	3.127	0.3456
LTPEEEEILNK	1315.5	2	3.3259	0.2319
LTPEEEEILNKKR	1599.8	2	3.9938	0.3173
LTPITYPQGLAMAK	1504.8	2	3.4849	0.4512
LTPLPEDNSMNVDQDGDPSDR	2316.4	2	4.284	0.4581
LTPLQLEIQR	1211.4	2	3.1399	0.2863
LTPLSHEVISR	1252.4	2	2.4561	0.2938
LTPTEVKDYLAAIA	1505.7	2	2.8066	0.108
LTQDAVAKANQTK	1388.6	2	3.0442	0.3433
LTQDQDVDVK	1161.2	2	3.19	0.1876
LTQDQDVDVKYFAQEALTVLSLA	2568.9	2	3.0051	0.2361
LTQILSYLR	1107.3	2	3.218	0.2403
LTQLQELDLSNNHLETLPDNLGLSHLR	3085.4	3	4.0691	0.1269
LTQQLEEERIQHQQK	1909.1	2	4.2648	0.2719
LTQYMDGSGMPK	1328.5	2	2.9356	0.1521
LTRDETNYGIPQR	1563.7	3	3.5442	0.3018
LTRPGSSYFNLNPFEVLQIDPEVTDEEIK	3352.7	3	5.284	0.2912
LTRPGSSYFNLNPFEVLQIDPEVTDEEIKK	3480.9	3	4.7532	0.2135
LTRPGSSYFNLNPFEVLQIDPEVTDEEIKKR	3637.1	3	6.0714	0.4264

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LTRSQFLLLTNKFK	1710.1	2	2.5705	0.1303
LTSAIAKQEDVSVQLEALDIMADMLSR	2949.4	3	3.7524	0.2926
LTSAVSSLPELLEK	1487.7	2	3.9116	0.3351
LTSDDVKEQIYK	1439.6	2	4.1402	0.3613
LTSDSTVYDYAGK	1420.5	2	3.1709	0.3016
LTSELDKLTTLYENLSIHNQQLEEEVKDLADKK	3860.3	3	4.2574	0.2817
LTSFIGAIAIGDLVK	1518.8	2	5.9644	0.3457
LTSKEEELKDIQNMNFLLK	2294.7	2	5.8086	0.4166
LTSLAAALDENKDGKVNIDDLVK	2443.7	2	5.2373	0.4047
LTSLVPFVDAFQLER	1736.0	2	4.3572	0.402
LTSNPLASHDYILK	1572.8	2	3.1909	0.3003
LTTDFNVIVEALSK	1550.8	2	4.6422	0.4254
LTTEEVIKELAQIAGRPTEDEDEKEK	2973.2	3	4.499	0.3053
LTTLELLEVR	1187.4	2	4.0445	0.2505
LTTPTYGDLNHLVSATMSGVTTCLR	2653.0	2	4.9024	0.5436
LTTPTYGDLNHLVSATMSGVTTSLR	2637.0	2	4.1396	0.3774
LTTPTYGDLNHLVSATMSGVTTSLRFPGQLNADLR	3749.2	3	3.7945	0.2301
LTTVLNSGFLDEWLTLEDVPSGR	2563.8	2	3.7819	0.4333
LTVADALEPVQFEDGEK	1862.0	2	3.4363	0.3162
LTVDGLEKER	1160.3	2	2.6514	0.2169
LTVEDLEKER	1232.4	2	2.9772	0.3158
LTVEDLEKERDFYFGK	1990.2	2	3.9242	0.3843
LTVEDLEKERDFYFGKLR	2259.5	3	3.8798	0.34
LTVEDPVTVEYITR	1635.8	3	4.6759	0.4423
LTVENSPKQEAGISEGQGTAGEEEEKKK	2975.2	3	5.5084	0.4407
LTVMSLQESGLK	1306.6	2	2.5456	0.1366
LTVNEAVKEGVVGPELHHK	2057.3	2	5.1619	0.466
LTVVDTPGYGDAINCRDCFK	2188.5	2	2.9359	0.2168
LTVYTTLIDVTK	1367.6	2	3.5529	0.2956
LTYEIEDEKR	1296.4	2	2.9097	0.3106
LTYRNPQPQPVDGVFVYPLAEAEVVSGFEAEAAGR	3779.2	3	6.1102	0.4051
LTYTAEVSVPK	1208.4	2	2.4173	0.2647
LVAAPLFELYDNAPGYGPIISSLPQLLSR	3116.6	3	3.9304	0.4217
LVAASQAALGL	1014.2	2	3.9726	0.3178
LVAEFTTSLTNFQK	1599.8	2	4.106	0.3869
LVAENKFGK	1006.2	1	2.4265	0.134

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LVAENKFGKK	1134.4	2	3.6572	0.1963
LVAGEMGQNEPDQGGQR	1786.9	2	5.6054	0.375
LVAIVDPHIK	1105.4	2	3.3386	0.1369
LVAIVDVIDQNR	1355.6	2	4.1127	0.3232
LVALSEPALALLGLGAPPAR	1930.3	2	3.233	0.2643
LVASAYSIAQK	1151.3	2	3.3988	0.3281
LVAVFYTVITPMLNPIIYTLR	2439.0	3	3.5839	0.1355
LVCQGSEGALGHGVGPHQHSGPAPPAAVPPPR	3079.4	3	3.4785	0.2011
LVDISYGGENGFNQAIELSTEVLSNVK	2898.2	3	3.6816	0.2147
LVDKFLEDVK	1206.4	2	2.6001	0.1207
LVDKFLEDVKK	1334.6	2	3.8073	0.2036
LVDKSTELNEEPLMR	1775.0	2	3.1913	0.1906
LVDNEQLNLEDEDIESIDATK	2404.5	2	5.6394	0.389
LVDQNIFSFYLSR	1602.8	2	4.8494	0.4594
LVDQNIFSFYLSRDPDAQPGGELMLGGTDSK	3372.7	3	6.57	0.5014
LVDQNIFSFYLSRDPDAQPGGELMLGGTDSKYYK	3827.2	3	5.6633	0.5006
LVDQSGPPHEPK	1304.4	2	3.3258	0.1776
LVDSKGFDEYMK	1432.6	2	2.8422	0.1235
LVDSKGFDEYMKELGVGIALR	2341.7	3	4.7368	0.3428
LVDSKGFDEYMKELGVGIALRK	2469.9	3	4.616	0.3705
LVDVTTAQV	946.1	2	2.6289	0.1341
LVDYLDVGFDTTR	1514.7	2	4.5272	0.4525
LVEALCAEHQINLIK	1695.0	2	2.6967	0.1857
LVEALPYNTSLVEMK	1708.0	2	3.8285	0.421
LVEARPMIHELLTEGR	1865.2	2	2.906	0.1837
LVEDKPGSR	1001.1	2	2.4696	0.2495
LVEDMENKIR	1247.4	2	2.7215	0.2393
LVEDTKHRPKENLELILTQSVENVGVR	3118.5	3	4.5413	0.2721
LVEGILHAPDAGWGNLVYVVNYPK	2626.0	3	4.2213	0.3448
LVEGILHAPDAGWGNLVYVVNYPKDNK	2983.4	3	6.0303	0.3609
LVEGILHAPDAGWGNLVYVVNYPKDNKR	3139.6	3	4.8563	0.3135
LVEIAQVPK	997.2	2	3.3046	0.2276
LVEIDNGKQR	1172.3	2	3.073	0.2242
LVEIDNGKQREFESR	1821.0	2	3.0567	0.1861
LVEKGETDLIQK	1373.6	2	3.2366	0.1567
LVEKPSPLTLAPHDFANIK	2091.4	3	3.702	0.2279

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LVEKPSPLTLAPHDFANIKANVK	2503.9	3	4.0152	0.4727
LVEPGSPAEK	1027.2	2	2.757	0.2743
LVESLPQEIK	1156.4	2	2.9185	0.2181
LVETLQADSGLLLDALLAR	2012.3	3	4.6837	0.3029
LVEVDSGR	875.0	1	1.6415	0.1099
LVEVDSSRQQEYDFK	1844.0	2	3.4302	0.2372
LVEVIKTPMTSQK	1474.8	2	3.8803	0.2688
LVEVIKTPMTSQKTFESLVDFSK	2629.1	3	4.7788	0.4797
LVEVNGENVEKETHQQVVSR	2295.5	3	5.3627	0.4118
LVEYDIDEVVYDEDSPYQNIK	2547.7	3	5.1492	0.4451
LVFDEYLK	1027.2	2	2.4028	0.163
LVFHTQLAHGSPTGR	1621.8	2	4.3563	0.4848
LVFLGLDNAGK	1147.3	2	3.023	0.1933
LVGAIVYYDGQHNDAR	1791.9	2	3.6376	0.3187
LVGATATSSPPPK	1226.4	2	2.6882	0.2016
LVGEIMQETGTR	1334.5	2	3.2038	0.2536
LVGGKDFEQPLAISR	1630.9	2	4.2855	0.4083
LVGGTTPGK	830.0	2	2.5988	0.1261
LVGILDILDEENRLPQPSDQHFTSAVHQK	3301.7	3	5.8779	0.375
LVGLTGTREEVDQVAR	1743.9	3	3.6352	0.1791
LVGPEEALSPGEAR	1425.6	2	3.5374	0.3515
LVGQGASAVLLDLPNSGGEAQAK	2196.4	3	6.7146	0.5318
LVGQGASAVLLDLPNSGGEAQAKK	2324.6	3	4.4726	0.4113
LVGRPPLPVPAVGIGTVHLHQHEDILAK	2965.5	3	5.8596	0.4881
LVGSDQAPGR	1000.1	2	2.4418	0.2442
LVGSDQAPGRDK	1243.4	2	3.0535	0.2149
LVGSQEELASWGHEYVR	1961.1	2	4.2097	0.3911
LVGVFHTEYGALNR	1576.8	2	4.0668	0.4157
LVGYLDR	836.0	2	2.6625	0.2222
LVHAALAEELGGPVHALAIQAR	2237.6	3	3.584	0.3367
LVHASEQYSK	1162.3	2	2.7155	0.2393
LVHDKELAAEDEQVFLMK	2116.4	3	4.0572	0.2761
LVHHILQDMYK	1397.7	2	3.1605	0.3148
LVHIIGALR	992.2	2	2.4657	0.1849
LVHLQTLVLNGNPLLHAQLR	2250.7	3	5.7438	0.4516
LVHLVESWDLRSGLLHVAIR	2314.7	2	2.69	0.1202

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LVHLWSSDSHQPLWSR	1949.2	2	3.618	0.3195
LVIADTGHHR	1119.3	2	2.4172	0.2035
LVIAGHLLR	992.2	2	2.7889	0.1852
LVIIEGDLERTEERAELAESR	2429.7	3	4.0195	0.2453
LVIKNQQFHK	1255.5	2	2.429	0.1207
LVINGNPITIFQER	1614.9	2	3.4599	0.3998
LVINGNPITIFQERDPSK	2042.3	2	4.344	0.3823
LVINGNPITIFQERDPSKIK	2283.7	2	3.8272	0.2944
LVINSGNGAVEDR	1344.5	2	3.8813	0.3612
LVINSGNGAVEDRKPSGLNGEASK	2413.6	3	3.695	0.3848
LVIPSELGYGER	1333.5	2	2.7144	0.1623
LVIQDKNKYNTPK	1561.8	2	3.2458	0.1256
LVKDVFISAAER	1348.6	2	3.0378	0.3781
LVKDVFISAAERDVYTGDALR	2339.6	2	2.7603	0.1724
LVKELEGVITK	1229.5	2	3.4892	0.2727
LVKGHAYSVTGAEEVESNGSLQK	2404.6	3	4.2253	0.2381
LVKYDEFHDYLER	1727.9	2	2.5763	0.3354
LVLDSVKLEA	1087.3	2	3.2672	0.2266
LVLDTVNEVSR	1245.4	2	3.3298	0.258
LVLEVAQHLGESTVR	1651.9	2	4.9206	0.5395
LVLINTPPGDQEKGEMGLGAVPGR	2449.8	3	3.719	0.3414
LVLLGESAVGK	1086.3	2	2.8848	0.1149
LVLNRNPVNYFAEVEQIAFDPSNMPPGIEASPDK	3774.2	3	5.3379	0.3676
LVLPSLISSR	1085.3	2	2.5123	0.1134
LVLSGEKVLETLQEKGER	2029.3	2	4.6736	0.3614
LVLTNNQLTTLPR	1483.7	2	2.7763	0.2837
LVLTQEQLHQLHSR	1702.9	2	4.416	0.2724
LVLVGDGGTGK	1016.2	1	2.8061	0.2931
LVLVNAIYFK	1180.5	2	3.5456	0.2701
LVLVNAVYFR	1194.5	2	4.0791	0.3578
LVLVSPTSEQYDSLLR	1821.1	2	4.4346	0.4343
LVMAAANR	846.0	2	2.9702	0.1461
LVMAESEKSQKLEER	1778.0	2	3.6854	0.2486
LVMEDGKMDPVAYR	1624.9	2	3.3466	0.4188
LVMEEAPESYK	1296.5	2	3.2213	0.2198
LVNAAGSGR	844.9	1	3.2497	0.2563

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LVNACLAEELPHIHAFEQK	2163.5	2	5.0777	0.3615
LVNELTEKTGKLQQEEVQKK	2343.7	3	3.2003	0.1196
LVNEVTEFAK	1150.3	2	3.775	0.3804
LVNHFVEEFK	1262.4	2	3.4579	0.3119
LVNHFVEEFKR	1418.6	3	4.032	0.4021
LVNHFVEEFKRK	1546.8	2	3.1126	0.2989
LVNLQHLDLLNNK	1534.8	2	4.6826	0.3196
LVNLQHLDLLNNKLVTLPVSFAQLK	2832.4	3	6.0483	0.4452
LVNLYGLLHGLQAAVAQQDTLMEAR	2726.1	3	3.6736	0.212
LVNNADKQQAGR	1314.4	2	3.1757	0.271
LVNNGEKLEFLHK	1541.8	2	3.2292	0.1916
LVNNGEKLEFLHKTPVEEVPAAIAPFQGR	3205.7	3	4.588	0.2508
LVNQQLLADPLVPPQLTIK	2101.5	2	3.3895	0.2271
LVNQQLLADPLVPPQLTIKDFYMTDSISR	3317.8	3	5.3822	0.4597
LVNSVAGCADDALAGLVACNPNLQLLQGHR	3034.5	3	3.4027	0.1963
LVNTSENLSK	1105.2	2	2.9426	0.1832
LVNVSSMGGGAPMER	1505.7	2	4.5281	0.4746
LVPFDHAESTYGLYR	1768.9	2	3.2412	0.4304
LVPGPVFGSKDNFHGLAIFLDTYPNDETTER	3451.8	3	3.6243	0.2541
LVPGRHDIAFVEFENDGQAGAAR	2470.7	3	4.7113	0.2956
LVPKHEEEAFTAFTPAPEDSLASVPYPPLLR	3423.9	3	4.0986	0.2078
LVPLKETIK	1041.3	1	1.9309	0.1211
LVPLKETIKGFQQILAGEYDHLPEQAFYMVGPIEEAVAK	4375.0	3	3.4806	0.172
LVPLLDRPFDETTYEETED	2283.4	2	3.3429	0.2867
LVPLLDTGDIIIDGGNSEYR	2161.4	2	6.4548	0.508
LVPLLLEDGGEAPAALEAALEEK	2349.7	2	6.5366	0.6075
LVPNMTPEVVGEQVTSYLTK	2206.5	3	4.9245	0.4035
LVPNMTPEVVGEQVTSYLTKK	2334.7	2	4.4866	0.3571
LVPRPGSGSSSGSSNSGSQPGSHPGSQSGSGER	3070.1	3	3.9024	0.2575
LVQAAQMLQSDPYSVPARDYLIDGSR	2895.2	3	5.1329	0.4855
LVQAFQFTDK	1197.4	2	3.6087	0.2945
LVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQK	3529.0	3	5.7978	0.4624
LVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYFSK	4388.8	3	5.4524	0.3781
LVQAFQYTDK	1213.4	2	3.0157	0.1087
LVQAFQYTDKHGEVCPAGWKPGSETIIPDPAGK	3542.0	3	5.4791	0.3497
LVQDVANNTNEEAGDGTTTATVLAR	2561.7	2	6.9026	0.6113

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LVQDYGLESEVAQHLAATYGDKAFEVAK	3054.4	3	4.9778	0.3987
LVQEQGSHSK	1113.2	2	3.1761	0.2031
LVQIEYALAAVAGGAPSVGIK	2028.4	3	4.5761	0.3508
LVQNCLWTLR	1246.5	2	2.5041	0.1715
LVQNIIQTAVDQFVR	1745.0	3	3.9909	0.2355
LVQQGLLTPDMLK	1456.8	2	4.3196	0.3682
LVQSPNSYFMDVK	1528.8	2	3.4421	0.3111
LVREIAQDFKTDLR	1705.0	2	5.0386	0.4112
LVREIAQEFKTDLR	1719.0	2	3.4528	0.1187
LVRPEVDVMCTAFHDNEETFLK	2594.9	3	4.4389	0.3135
LVRPEVDVMCTAFHDNEETFLKK	2723.1	2	4.2337	0.4423
LVRPPVQVYGIEGR	1583.9	3	4.4546	0.3304
LVSDDLDSSLANLVGNLGIGNGTTK	2474.7	2	5.176	0.368
LVSDEMVVELIEK	1504.8	2	4.8973	0.4026
LVSDGNINSDR	1190.2	2	3.29	0.3372
LVSDTITQKVEEIDAAILR	2115.4	3	4.6177	0.2199
LVSELDDANLQVENVRDQALILMNAR	2941.3	3	4.0333	0.2605
LVSESSDVLPK	1174.3	2	3.8244	0.2911
LVSGMQHPGSAGGVYETTQHFIDIK	2674.0	3	5.1255	0.437
LVSGWVKPIIIGR	1438.8	3	3.2119	0.1435
LVSHLTAQLNELKEQMTEQR	2369.7	3	4.7096	0.2769
LVSIGAEEIVDGNAK	1515.7	2	4.3068	0.4488
LVSKDGK	746.9	1	1.6721	0.1138
LVSLIGSK	817.0	2	2.5673	0.1504
LVSNHSLHETSSVFVDSLTK	2201.4	2	5.7316	0.5201
LVSPGSANETSSILVESVTR	2047.3	2	4.8027	0.478
LVSQDNFGFDLPAVEAATK	2023.2	2	5.1494	0.4789
LVSQDNFGFDLPAVEAATKKHEAIETDIAAYEER	3780.1	3	5.1376	0.3587
LVSSEQALKELGLAEHQLR	2122.4	3	4.5765	0.3473
LVSSPCCIVTSTYGWTANMER	2319.7	2	3.8003	0.4124
LVSVLQNK	901.1	2	2.9243	0.1955
LVTDLTK	789.9	1	1.9513	0.1162
LVTEFNSQTSAK	1325.4	2	3.5261	0.3068
LVTEMGTYATQSALSSSRPTK	2229.5	2	3.4409	0.2814
LVTENLKEEPMESGKEK	1962.2	3	3.2847	0.2526
LVTLEEFLASTQR	1507.7	2	3.4409	0.2423

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LVTLEEFLASTQRK	1635.9	2	2.5293	0.1797
LVTLEEFLK	1092.3	2	2.6407	0.1395
LVTLKDVEDGAFLLR	1690.0	2	3.4247	0.2128
LVTLPDITSVAK	1257.5	2	2.7411	0.1237
LVTLPVSFAQLK	1316.6	2	3.5084	0.3418
LVTPHGESEQIGVIPSKK	1920.2	3	4.1668	0.2425
LVTSIGDVVNHDPVVGDRLK	2134.4	3	3.4	0.2139
LVTSPCCIVTSTYGWTANMER	2333.7	3	3.8593	0.4107
LVTTGVLK	831.0	1	1.904	0.1326
LVTTVTEIAG	1004.2	1	1.6065	0.2116
LVVHEGSPVTSISAR	1552.8	2	3.5113	0.3854
LVVLDEELEGISPDELKDELPERQPR	3020.3	3	4.1033	0.3662
LVVLGIRPIR	1136.5	2	2.5229	0.1021
LVVLGSGGVGK	986.2	2	2.7032	0.1334
LVVNFESDKLK	1292.5	2	3.5638	0.3341
LVVVGAGGVGK	956.2	2	2.7333	0.1731
LVVWAADRQAALTK	1542.8	2	3.1246	0.1387
LVYLYLMNYAK	1391.7	2	3.6527	0.3017
LWDLTTGTTTR	1265.4	2	2.8161	0.1688
LWEEQLAAAK	1159.3	2	3.0851	0.2242
LWEPLVEEPPADQWKWPI	2234.5	2	3.3827	0.2664
LWFTLDHPPKDWAYSK	2005.3	2	3.4364	0.3424
LWGLTEMFPER	1379.6	2	2.9677	0.2322
LWISNGGLADIFTVFAK	1853.2	2	4.9745	0.4685
LWRVPAEGLEEVLTTPETVLTGHTEK	2907.3	3	4.275	0.3147
LWSNSHRPELVR	1494.7	2	2.6359	0.1028
LYAGSTVK	839.0	1	2.0292	0.1057
LYARDHEDYDPQTVR	1879.0	3	3.2095	0.1467
LYASHSQFIK	1194.4	2	2.863	0.2567
LYAVHQEGNKNVGLDIEAEVPAVK	2594.9	3	4.1885	0.3661
LYDAVLRGPMDSDDSHGSVLR	2304.5	3	4.9942	0.4058
LYDAYELK	1015.1	2	2.8495	0.2002
LYDAYELKHALK	1464.7	2	3.8227	0.337
LYDAYELKHALKGAGTNEK	2122.4	2	4.8209	0.3814
LYDDIDFDIEEFAK	1733.9	2	4.9413	0.3762
LYDIDVAKVNTLIRPDGEKK	2288.6	3	3.975	0.3721

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LYDKIDPEKLSVNSHFMK	2165.5	2	4.5861	0.313
LYDLNHNEIGELIR	1699.9	2	3.7766	0.3652
LYDMQHTPTPIGDETEPTIIER	2557.8	3	3.8321	0.236
LYDNLLEQNLIR	1504.7	2	4.3213	0.1814
LYDNLLEQNLIRVIEPFSR	2333.7	3	3.839	0.1319
LYDRDVASAAPEKAENPAGHGSK	2384.5	3	3.6462	0.2345
LYEALTPVH	1043.2	2	2.6811	0.2798
LYEEGSNKR	1096.2	2	2.4213	0.1526
LYELDGLR	979.1	2	2.6218	0.1117
LYEQLSGK	938.1	1	2.7779	0.1505
LYERGDASKEDIDTAMK	1943.1	2	4.905	0.3877
LYGDESELHFWTVAAHYLHSLSQEK	2962.2	3	3.2044	0.2313
LYGEKTYNFLPEFLVSTQK	2278.6	2	5.0238	0.3762
LYGPSSVSFADDFVR	1660.8	2	4.6662	0.4959
LYGPTNFAPIINHVAR	1784.1	2	3.1883	0.2561
LYGPTNFSPIINHVAR	1800.1	2	3.5399	0.4194
LYGSAGPPPTGEEDTAEKDEL	2177.3	2	5.7279	0.5597
LYGSEAFATDFQDSAAAK	1893.0	2	5.7411	0.5375
LYGSEAFATDFQDSAAAKK	2021.2	2	3.7153	0.2997
LYGSGDQEAWQK	1382.5	2	3.6355	0.2555
LYHEADKTYMLR	1540.8	2	3.2654	0.1989
LYHNEVEIEK	1274.4	2	2.8489	0.1114
LYHNEVEIEKLNKELASK	2158.4	2	4.3363	0.3443
LYHSCADPTGCGTGPDAR	1822.0	3	3.5443	0.27
LYHSEAFTVNFGDTEEAK	2059.2	2	3.5161	0.2084
LYHSEAFTVNFGDTEEAKK	2187.4	2	6.397	0.5237
LYHSEAFTVNFGDTEEAKKQINDYVEKGTQGK	3648.9	3	5.4094	0.426
LYIDSYEKDVAK	1444.6	2	3.5583	0.451
LYIGLAGLATDVQTVAQR	1890.2	3	4.5458	0.4046
LYKDDQLLDDGK	1423.6	2	3.7828	0.3853
LYKDDQLLDDGKTLGECGFTSQTARPQAPATVGLAFR	3985.4	3	5.3978	0.3722
LYKEELEQTYHAK	1652.8	2	4.807	0.3175
LYKEELEQTYHAKLENAR	2236.5	3	5.053	0.3669
LYKENEGKPENER	1606.7	2	3.5751	0.3398
LYKLELEQTYQAK	1627.9	2	4.7249	0.3033
LYKQLDDKDEEINQQSQLVEK	2564.8	3	4.9285	0.2546

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LYKVPDGKPENQFAFNGEFK	2329.6	3	3.2895	0.1523
LYLEDDDPVQAEAYINR	2025.2	2	5.6872	0.5113
LYLINSPVVR	1174.4	2	2.9047	0.1359
LYLVDLAGSEK	1208.4	2	3.7091	0.2759
LYLVDLAGSEKVSK	1522.8	2	4.0367	0.3952
LYLVFPHDSSALSNSFHHLQLFDQDSSNVVSR	3662.0	3	4.1908	0.3628
LYNKDAVIEFLLDKSAEK	2097.4	3	4.5332	0.2889
LYNLDVFQYELYNPMALYGSVPVLLAHNPHR	3649.2	3	6.2935	0.4839
LYNNITFEELGALLEIPAAK	2220.6	2	5.6613	0.4249
LYNNITFEELGALLEIPAAKAEK	2548.9	2	5.0466	0.3744
LYNTHLNK	1003.1	2	2.7012	0.1072
LYNTLDDLLLYINAR	1811.1	3	4.4089	0.1933
LYPAAVDTIVAIMAEGK	1763.1	2	2.5123	0.1784
LYPAVDEQETPLPR	1628.8	2	3.3277	0.3651
LYPEGLAQLAR	1231.4	2	2.9052	0.2406
LYPVLLVKQDGSTIHIR	1953.3	2	2.6925	0.3123
LYQAGEGR	894.0	2	2.8346	0.1855
LYQPEYQEVSTEEQREEISGK	2543.7	2	3.5359	0.1444
LYQQHGAGLFDVTR	1605.8	3	4.1742	0.4169
LYQTDPSGTYHAWK	1667.8	2	4.2411	0.3798
LYQVEYAFK	1161.3	2	2.8584	0.155
LYRPGSVAYVSR	1368.6	2	3.3453	0.359
LYRPPPVLDALGR	1467.7	2	2.8112	0.207
LYSESLAR	939.0	2	2.4649	0.1724
LYSIILSAPIPEPK	1541.9	2	3.311	0.2259
LYSILGTTLKDEGK	1538.8	2	3.8825	0.3856
LYSILGTTLKDEGKLLEAK	2093.4	2	5.3387	0.4052
LYSKDDEPAVK	1265.4	2	2.5069	0.1031
LYSLALHPNAFKR	1530.8	2	2.4678	0.1456
LYSNAYLNDLAGCIK	1658.9	2	4.7297	0.4273
LYSPSQIGAFVLMK	1554.9	2	5.359	0.3974
LYSSSDDVIELTPSNFNR	2058.2	2	5.8569	0.5393
LYSTWIGGSILASLDTFKK	2101.4	2	3.4363	0.4173
LYTDFDEIRQEIENETER	2301.4	3	3.5437	0.2263
LYTGKPNLVNGLQAR	1644.9	2	2.752	0.1292
LYTLVLTDPDAPSR	1561.8	2	4.6108	0.4638

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
LYTLVLTDPDAPSRK	1689.9	2	3.8899	0.2313
LYTLVLTDPDAPSRKDPK	2030.3	3	3.3738	0.3121
LYTNGPLPDKLQQAR	1714.9	2	3.2721	0.1957
LYTVEYLSNMVGGR	1602.8	2	3.4727	0.3271
LYVELHRGEELGGGQDPVQLLSGFPR	2868.2	3	7.1896	0.4199
LYVHEAVK	959.1	2	2.408	0.1424
LYVPHSLWPQIK	1481.8	2	2.5914	0.1644
LYYVCTAPHCGHR	1520.8	2	2.5579	0.1845
MAAADSVQQR	1077.2	2	3.8045	0.3115
MAAAGGGGGGGR	919.0	2	2.633	0.1357
MAAEEEKR	964.1	2	2.6601	0.1858
MAAISESNINLCGSHCGVSIGEDGPSQMALEDLAMFR	3856.4	3	6.0471	0.5145
MAANVENPASADSEAYIEK	2011.2	3	3.6848	0.1715
MAAPIDRVGQTIER	1557.8	2	2.9488	0.2324
MADAIILAIAGGQELLAR	1827.2	3	4.7467	0.2519
MADEAILQER	1176.3	2	2.5784	0.1757
MADFHKEEMDDQDKDK	1983.1	3	4.5284	0.2502
MADGVANVEHILK	1397.6	2	4.0808	0.351
MADKDGDLIATK	1278.5	2	3.1367	0.1718
MADLHAVPR	1010.2	2	3.2444	0.3848
MADSAASLEQQLEQVKLTLLQR	2473.8	3	4.8971	0.3506
MAEAVQNHVK	1127.3	2	3.4687	0.2954
MAEEKLTHK	1087.3	2	3.121	0.227
MAEIGEHVAPSEAANSLEQAQAAAER	2681.9	3	5.1996	0.3414
MAENLGFVGPLK	1276.5	2	3.9767	0.3351
MAENLGFVGPLKSQAADQITK	2219.5	3	3.9727	0.3614
MAETVDTSEMVNGATEQR	1970.1	2	5.0762	0.4396
MAFPLLDMVDLER	1550.9	2	3.1043	0.2551
MAGATPVFIPLR	1273.6	2	3.4295	0.286
MAGDETQPTR	1106.2	2	3.2938	0.24
MAGDPVANVR	1030.2	2	2.5842	0.1485
MAGNEYVGFSNATFQSER	2009.1	2	5.3986	0.4719
MAGTAFDFENMK	1362.6	2	3.5572	0.3341
MAGTAFDFENMKR	1518.7	2	4.128	0.4419
MAHGYGEESEEER	1524.6	2	3.7985	0.4704
MAHGYGEESEEERGLEPGK	2106.2	2	5.7804	0.5049

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MAIQTQQSK	1035.2	2	2.7771	0.1473
MAISDLQGAVGNQIK	1545.8	2	2.42	0.1187
MALDIEIATYR	1296.5	2	4.1664	0.2707
MALDIEIATYRK	1424.7	2	3.408	0.261
MALEVGDYK	1026.2	2	2.9646	0.2537
MALEVGDYKINLK	1494.8	2	3.4519	0.2895
MALIGLGVSHPVLK	1435.8	2	3.9445	0.4828
MALIQMGSVEEAVQALIDLHNHDLGENHHLR	3492.9	3	5.4861	0.2606
MALLMAEMSR	1153.5	2	3.3306	0.2274
MALVLEALPQIAAK	1468.8	2	4.1222	0.3695
MAMLQEEPVIVKPMPGKPNTQNPPR	2804.3	3	3.8059	0.2321
MANRDLLSSVSR	1349.5	2	2.9332	0.1551
MAPALSGANLTSPR	1386.6	2	2.842	0.19
MAPTPIPTRSPSDSSTASTPVAEQIER	2828.1	3	5.8822	0.4299
MAPVPLDDSNRPASLTK	1813.1	2	3.0658	0.3092
MAPYQGPDAVPGALDYK	1794.0	2	4.8826	0.4803
MAPYQGPDAVPGALDYKSFSTALYGESDL	3065.4	3	3.6252	0.137
MAQALEELR	1061.2	2	3.7282	0.1159
MAQALEELRSQHDEQVR	2041.2	3	4.1023	0.2855
MAQEVLTHLKEHPDAWTR	2163.4	3	3.9662	0.3529
MAQFDAKK	939.1	2	2.5895	0.1234
MAQFDAKKFAETQPK	1741.0	3	3.5483	0.2027
MAQLLDLSVDESEAFLSNLVVNK	2536.9	2	4.2069	0.3924
MAQSSSKSPELLAR	1505.7	2	3.6845	0.319
MASEREGSGSSGTGEQKEDQKEEKQ	2713.8	3	4.1982	0.3567
MASGAANVVGPK	1102.3	2	3.5354	0.301
MASGRWAPLGPAWASRRPLQAQIVPK	2846.4	3	3.7314	0.2354
MASNIFGPTEEPQNIPK	1874.1	2	3.6025	0.1145
MASTPHPPGAR	1122.3	2	3.1643	0.4372
MATEVAADALGEEWKGYVVR	2196.5	2	5.235	0.5211
MATHTLITGLEEYVR	1735.0	2	2.5313	0.3088
MATNAAAQNAIK	1204.4	2	2.7235	0.1882
MATNAAAQNAIKK	1332.6	2	3.6014	0.2364
MATNFLAHEK	1162.3	2	2.888	0.3396
MATQASTLYSNNITK	1643.8	2	5.5314	0.4514
MATRPPDRPEGPHTSR	1806.0	2	2.6224	0.1541

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MATYLTGELTATSEDYKLLENMNKLTSLK	3280.8	3	3.93	0.1733
MAVDQDWPSVYPVAAPFKPSAVPLPVR	2939.4	3	5.2533	0.3104
MAVEDHLKTEEELSEEKQILNEMLEVVEQR	3601.0	3	5.6239	0.3867
MAVTFIGNSTAIQELFK	1871.2	2	5.9076	0.4218
MAVTFIGNSTAIQELFKR	2027.4	3	4.713	0.2935
MDAEHPELR	1098.2	2	3.0168	0.2502
MDAILTEAIK	1105.3	2	2.5469	0.1312
MDAPASAAAVR	1060.2	2	2.4153	0.2093
MDAPTSAAVTR	1120.3	2	2.7131	0.1182
MDATANDVPSDR	1292.4	2	4.2625	0.4212
MDATANDVPSPYEVR	1665.8	2	5.2783	0.3332
MDCQECPEGYRVTYTPMAPGSYLISIK	3054.5	3	4.6938	0.2127
MDDKSVPHEEYR	1506.6	2	3.0903	0.146
MDDVINISGHR	1257.4	3	3.8934	0.3333
MDELQLFR	1052.2	2	3.3065	0.2301
MDELQLFRGDTVLLK	1779.1	2	3.7668	0.2417
MDEQKNHHQQQVDSIIKEHEVSIQR	3058.3	3	5.0333	0.3042
MDETDASSAVK	1154.2	2	2.9639	0.283
MDGGSGGLGSGDNAPTTEALFVALGAGVTALSHPLLYVK	3746.2	3	4.9823	0.4246
MDKEETKDWILPSDYDHAEAEAR	2750.9	3	5.2796	0.3352
MDKLEAEKR	1120.3	2	2.5036	0.1182
MDKNASTFEDVTQVSSAYQK	2250.4	2	6.8047	0.484
MDKSAVGHEYQSK	1480.6	2	3.5534	0.3781
MDKSNEELR	1122.2	2	2.4511	0.1114
MDKVEDELKEK	1364.5	2	3.3958	0.2102
MDLAPSKDMGPPKENK	1759.0	2	3.225	0.2726
MDLEKPNYIVPDYMPVVYDKLPQPPSHR	3343.9	3	4.665	0.2325
MDLLPLHMGLHK	1405.8	2	3.3707	0.3287
MDLNSEQAEQLER	1563.7	2	5.0327	0.3317
MDLTAKELTEEKESAFEFLSSA	2477.7	2	4.4339	0.4479
MDPEGSKLLDDAMAADKSDEWFAK	2671.9	3	4.0953	0.2942
MDPMNIWDDIITNR	1735.0	2	3.7465	0.3047
MDQGVGLVLQELR	1458.7	2	3.8184	0.2822
MDQYFNQMEK	1334.5	2	3.8616	0.3776
MDSFDEDLARPSGLLAQER	2151.3	3	3.4958	0.3609
MDSTANEVEAVK	1294.4	2	4.1105	0.3021

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MDSTANEVEAVKVHSFPTLK	2204.5	2	4.8146	0.4924
MDTDLETMDLDQGGEALAPR	2179.4	2	4.4917	0.346
MDYPKQTQVSVLPEGGETPLFK	2465.8	2	5.1613	0.4203
MDYPKQTQVSVLPEGGETPLFKQFFK	3016.5	3	4.5998	0.2893
MEAGLSELSGSVAQTVTQLQTTLASVQELLIQQQQK	3860.3	3	4.0122	0.2047
MEANKENR	992.1	2	2.5878	0.1362
MEATGVLPFVR	1220.5	2	2.6853	0.2048
MEDTEPFSAELLSAMMR	1959.3	2	2.876	0.3098
MEEDPDDVPHGHITSLAVKR	2247.5	3	3.9154	0.2785
MEEEILLLEDQNSK	1691.9	2	3.9464	0.1659
MEEESGAPGVPSGNGAPGPK	1869.0	2	3.8193	0.4002
MEELHNQEMQK	1417.6	2	4.1818	0.2443
MEELHNQEVQKR	1541.7	2	4.2801	0.2797
MEELKEGLR	1105.3	2	2.6595	0.1602
MEELNSEKHR	1273.4	2	2.4757	0.1972
MEEVEAMLLPETLKR	1790.1	2	4.0514	0.3479
MEEVHKEANSVLQWLESKEEVLK	2757.1	3	4.0575	0.1744
MEEVKEANIR	1219.4	2	2.8392	0.1911
MEEVYLPDNINEGQVQVR	2134.4	2	2.9176	0.153
MEGDIDKQR	1092.2	2	2.8531	0.1737
MEGGTENDLR	1122.2	2	2.9419	0.2881
MEIATKDPLNPIKQDVK	1941.3	3	5.2486	0.3459
MEIATKDPLNPIKQDVKK	2069.5	3	4.0315	0.3859
MEIATKEPMNPIKQYVK	2021.4	3	3.4183	0.1319
MEIGLPDEKGR	1245.4	2	3.1508	0.1541
MEIVDHALHALTDEVIIPHSGWER	2770.1	2	2.961	0.185
MEKEYGSLKDSTK	1516.7	3	3.7607	0.3307
MEKGEHSIVYLKPSYAFGSVGK	2428.8	3	6.5635	0.4449
MEKGEHSIVYLKPSYAFGSVGKEK	2686.1	3	3.6555	0.136
MEKYVIESSSHTPELAR	1978.2	3	4.5567	0.3532
MELLAHLLGEK	1254.5	2	3.5211	0.2483
MELLHPLGLDSPIAGFLQK	2080.5	2	4.3833	0.2687
MELQEIQLK	1132.4	2	2.6561	0.1108
MENILSGNPLLNLTGPSQPQANFK	2584.9	3	3.2143	0.1125
MENKPTSSELQK	1392.6	2	3.4067	0.2185
MEPAGSQGVWGLDDFQFLPFIWGSSQLIDHPYLEPR	4135.6	3	4.2185	0.3089

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MEPENKYLPELMAEKDSLDPSFTHAMQLLTAEIEK	4051.6	3	3.5611	0.2502
MEPLNNLQVAVK	1356.6	2	3.2361	0.2291
MEPLWTGFWPAPSLSLGVPLHR	2492.9	3	3.2429	0.143
MESALDQLK	1035.2	2	2.9243	0.1568
MESEEGKEAR	1166.2	2	3.3885	0.2051
MESPIPILPLPTPDAETEKLIR	2461.9	3	3.8399	0.2246
MESQLSASKPTGGLPETAR	1961.2	3	3.6883	0.1727
METKTESSGIETEPTVHHLPLSTEK	2783.1	3	5.3655	0.5008
METTHSFGNPSISVSTQQPPKK	2402.7	3	6.0561	0.4611
MEVGPTMVGDEQSDPELMQHLGASK	2688.0	3	4.0605	0.2977
MEVQEQEEDISSLIR	1807.0	2	2.9319	0.1737
MFADDLHNLNKR	1474.7	2	3.3797	0.3541
MFADYLAHESR	1340.5	2	3.7808	0.4321
MFDKNLQDLVR	1379.6	2	3.5717	0.3031
MFDYTDDPEGPVMPGSHSVER	2367.6	2	4.0752	0.328
MFEELGQR	1010.1	2	2.4079	0.2208
MFEIDYSR	1061.2	2	2.6467	0.1716
MFEIVFEDPKIPGEK	1780.1	2	3.6811	0.3087
MFESFIESVPLLK	1540.8	2	4.4065	0.4341
MFGGPGTASR	981.1	2	2.6394	0.3598
MFGGPGTASRPSSSR	1495.6	2	2.6244	0.2499
MFGIDRDAIAQAVR	1563.8	3	4.1998	0.3526
MFGIPVVVAVNAFKTDTESELDLISR	2853.3	3	5.021	0.3707
MFIGGLSWDTSKK	1470.7	2	3.5653	0.2203
MFIGGLSWDTTK	1356.6	2	2.8877	0.1643
MFIGGLSWDTTKK	1484.7	2	3.8619	0.2483
MFIGGLSWDTTKKDLKDYFSK	2481.9	3	3.6768	0.2911
MFILSDGEGKNGTIELMEPLDEEISGIVEVVGR	3579.1	3	5.0784	0.3741
MFKQFNKLTEDKADVQSIIGLQR	2711.1	3	3.9919	0.295
MFLEGFRLPGEAQK	1623.9	2	2.9977	0.1928
MFLGDNAHLSIINEYLSQSYQK	2572.9	3	4.3	0.2412
MFLLVGAPK	976.3	2	3.0174	0.1393
MFLQYYLNEQGDRVYTLK	2282.6	3	3.8227	0.3639
MFNAENGK	911.0	2	2.6188	0.1424
MFNGEKINYTEGR	1559.7	2	4.2638	0.4763
MFQDIGVSKDLNEQFKK	2028.3	3	3.3173	0.1636

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MFTAGIDLMDMASDILQPK	2098.5	2	5.5981	0.5518
MFTAGIDLMDMASDILQPKGDDVAR	2712.1	3	4.9622	0.4449
MFTNPDNGSPAMTHR	1676.9	2	4.4859	0.4105
MFTQQQPQELAR	1477.7	2	4.4485	0.3762
MFVGGLSWDTSKK	1456.7	2	3.4636	0.3523
MFVGQVPR	934.1	2	2.7708	0.2005
MFVLDEADEMLSR	1556.8	2	4.964	0.3165
MGAGLGHGMDR	1102.3	2	3.6593	0.4107
MGAGLGHGMDRVGSEIER	1873.1	2	3.4615	0.275
MGAGMGFGLER	1126.3	2	3.6348	0.4321
MGANNLER	905.0	2	2.5499	0.118
MGANSLER	878.0	2	2.809	0.2403
MGAPESGLAEYLFDK	1628.8	2	4.0164	0.3787
MGAPESGLAEYLFDKHTLGDSDNES	2684.8	2	4.5072	0.3964
MGATKADFDNTVAIHPTSSEELVTLR	2805.1	2	5.4752	0.5101
MGAVFMDAPVSGGVGAAR	1694.0	2	5.1429	0.5083
MGAYHTIELEPNRQFTLAK	2220.5	2	3.8857	0.2342
MGDEGGESELLGEDLPLEPSVTKAER	2760.0	3	4.1801	0.2457
MGDHLTNLHR	1194.3	2	3.2339	0.2779
MGDNNVIESK	1107.2	2	3.4239	0.3284
MGEDMHTIGFGIYEVPEELSGQTNIHLSK	3234.6	3	4.4113	0.2781
MGESDDSILR	1123.2	2	3.7974	0.3573
MGFPPGAAQALVLQVFK	1775.2	2	2.622	0.2253
MGFPPNIVESAAENMVK	1835.1	2	3.2776	0.3768
MGFTEVTPVTGASLR	1566.8	2	3.5645	0.3884
MGGDIANR	833.9	2	2.4197	0.1055
MGGEAPELALDPVPQDASTK	2027.2	2	5.6437	0.4817
MGGEDDELKGLLGLPEEETELDNLTEFNTAHNKR	3817.1	3	4.8897	0.2569
MGGEEKPIGAGEEK	1432.6	2	3.8695	0.2683
MGGEEKPIGAGEEKQK	1688.9	3	4.6598	0.3715
MGGFHWMQR	1150.4	2	3.2672	0.293
MGGGKGAIDHYVTPVK	1630.9	2	4.4396	0.2282
MGGMEGPFGGGMENMGR	1716.0	2	4.5813	0.4746
MGGSSGALYGLFLTAAAQPLK	2054.4	2	3.646	0.2962
MGHAGAIIAGGK	1083.3	1	3.7259	0.4313
MGHALEEIKK	1156.4	2	2.9129	0.1756

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MGIGGLDKEFSDIFR	1685.9	2	4.6486	0.4254
MGIGGLDKEFSDIFRR	1842.1	3	3.6778	0.3834
MGIVGPEFKDKLLSAER	1891.2	2	3.6499	0.4192
MGIVSDYEKIR	1311.5	2	2.7237	0.2021
MGKIDIDYQK	1211.4	2	2.7132	0.2792
MGKIDIDYQKLHDAFFK	2070.4	2	3.5096	0.2181
MGLAMGGGGGASFDR	1384.6	2	4.0245	0.3912
MGLKDTPTQEDWLVSVLPEGSR	2459.8	2	4.2926	0.3327
MGLLAVLR	873.1	2	2.9771	0.1389
MGLVDQLVEPLGPGLKPPEER	2275.7	3	4.8341	0.3497
MGLVDQLVEPLGPGLKPPEERTIEYLEEVAITFAK	3884.5	3	3.8784	0.1816
MGMTEDDKR	1083.2	2	2.8263	0.3329
MGMYPGVLVPSSR	1394.7	2	3.406	0.4166
MGNGTVVR	834.0	2	2.9861	0.2368
MGNKPHMIQVYR	1474.8	3	3.6196	0.2698
MGNTPDSASDNLGFR	1582.7	2	4.6608	0.4625
MGPAMGPALGAGIER	1428.7	2	3.3579	0.256
MGPFLLNAVR	1118.4	2	3.1553	0.3473
MGPGAASGGERPNLK	1442.6	2	4.4364	0.3478
MGPGATAGGAEK	1047.2	2	3.3363	0.353
MGPGATAGGAEKSNVK	1475.7	2	4.3593	0.4021
MGPGIGAILER	1114.3	2	3.1519	0.1526
MGPLGLDHMASSIER	1614.9	3	4.7852	0.4493
MGPLINRPHLER	1433.7	2	2.5789	0.1749
MGPNIYELR	1093.3	2	3.2726	0.311
MGPPVGGHR	908.1	2	2.7847	0.3685
MGPSGGEGMEPERR	1490.6	2	2.5786	0.1644
MGPVMDR	806.0	2	2.7468	0.1067
MGQMAMGGAMGINNR	1539.9	2	4.6244	0.4348
MGQPSDPTAVVDPQTR	1699.9	2	3.418	0.3072
MGQRPAAGAEVPESVFLHLGR	2223.5	3	5.2271	0.3225
MGRGPGPLQER	1198.4	2	2.533	0.1754
MGVDKIIPVDK	1215.5	2	3.0026	0.2185
MGVDKIIPVDKLVK	1556.0	2	4.1651	0.2712
MGVGKLEMYVLNPVK	1679.1	3	4.3868	0.2601
MGVITVSGLAGLVSAR	1531.8	2	4.3247	0.4467

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MGYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGR	3507.0	3	6.4546	0.5307
MGYMDPR	870.0	2	2.4366	0.2508
MHAAYIRPGGVHQDLPLGLMDDIYQFSK	3174.6	3	4.2888	0.308
MHAPPINMESVHMK	1623.0	3	3.636	0.312
MHDLNTDQENLVGTHDAPIR	2277.5	3	6.1032	0.4714
MHEDINEEWISDKTR	1904.1	2	5.397	0.4307
MHELQSKVEDLQR	1613.8	2	2.541	0.1044
MHEVSFQDKEKEHLTR	2015.2	3	3.3567	0.181
MHFESGSTLKK	1265.5	3	3.565	0.2324
MHGGTGFAGIDSSSPEVK	1777.9	2	5.7175	0.5502
MHITDMKLPHLPGLEDLGIQATPLELK	3012.6	3	3.8262	0.2176
MHLAGKTEQAK	1214.4	2	2.9737	0.2554
MHLGLVIPK	1008.3	2	2.9566	0.2738
MHLSQIQR	1013.2	2	2.6448	0.1115
MHNQIPQVTSDGKR	1611.8	2	4.0464	0.3977
MHQVMSIEEVER	1488.7	2	2.7881	0.2826
MHSPQTSAMLFTVDNEAGK	2065.3	3	4.319	0.4225
MHSPQTSAMLFTVDNEAGKITCLCQVPQNAANR	3578.1	3	5.495	0.3905
MHTTFEHDIQALGTQVR	1985.2	3	5.0735	0.5153
MHVEHER	938.0	2	2.574	0.2845
MHVQLSTSR	1059.2	2	2.9081	0.24
MIAGQVLDINLAAEPK	1684.0	2	5.264	0.338
MIAGQVLDINLAAEPKVNR	2053.4	2	4.1277	0.3408
MIASDSHRPEVK	1370.6	2	3.9817	0.3085
MIDERQQELTHQEHR	1951.1	3	4.0887	0.2842
MIDKNLREDGEK	1448.6	2	3.6298	0.242
MIDLIIPR	971.2	2	2.9288	0.1795
MIDVDSLTDKECDWLNNYHLTCR	2786.1	3	3.8184	0.1402
MIETAQVDER	1192.3	2	3.7187	0.3599
MIINEELMASLDQPTQTVVMHR	2558.0	3	4.2886	0.2026
MIIYRDLISHDEMFSDIYK	2390.8	3	3.5745	0.1647
MIKNEVDMQVLHLLGPK	1966.4	3	4.9509	0.3735
MIKPFFHSLSEK	1464.8	2	4.1655	0.3703
MIKPREGEETLRIEDILEVIEK	2642.1	3	4.2463	0.1278
MILIQDGSQNTNVDKPLR	2043.3	2	5.0198	0.3753
MILKIDDIRKPGESEE	1874.1	2	4.0828	0.2055

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MILLEVNNR	1102.3	2	2.99	0.1314
MILTFEKR	1038.3	2	2.625	0.1952
MIMATNRPDTLDPALLRPGR	2239.7	3	3.2239	0.1975
MIMQDKLEK	1136.4	2	2.8957	0.1579
MIMQDKLEKER	1421.7	2	3.2566	0.1649
MINLSEPDTIDER	1533.7	2	4.2372	0.2159
MINLSVPDTIDER	1503.7	2	3.9911	0.3009
MINTDLSR	950.1	1	2.488	0.2369
MIPCDFLIPVQTQHPIRK	2137.6	2	3.658	0.3074
MIQDGKGDVTITNDGATILK	2091.4	3	5.4583	0.3773
MISDAIPELK	1117.3	2	3.1163	0.1873
MISDLIAGGIQPLQNLSVLK	2111.5	2	5.6722	0.2903
MISEIDKEGTGK	1308.5	2	3.1389	0.1939
MISEIDKEGTGKMNFGDFLTVMTQK	2822.3	3	4.3486	0.3358
MITAKPGKTPIQVLHEYGMK	2243.7	3	3.3814	0.1411
MITSAAGIISLLDEDEPQLKEFALHK	2871.3	3	4.3342	0.3409
MIVDPVEPHGEMK	1482.8	2	3.1198	0.258
MIYASSK	800.0	1	2.4819	0.1184
MIYASSKDAIK	1227.5	2	3.3093	0.3149
MIYASSKDAIKK	1355.6	2	3.1781	0.2385
MKAEFFADVVPAVR	1580.9	2	2.5463	0.1203
MKDKYTPVPDTPILIRAK	2087.5	2	2.6067	0.108
MKDSYIEVLLPLGSEPELR	2190.5	2	2.9954	0.3036
MKEALLSIGK	1090.4	2	3.1795	0.1461
MKEAQLEAEVK	1276.5	2	2.9155	0.1223
MKEEEQAGK	1050.2	2	2.7164	0.1399
MKEEVPTALVEAHVR	1710.0	2	5.4808	0.416
MKEGENNKPR	1203.4	2	3.0543	0.2362
MKEIAEAYLGK	1253.5	1	2.9952	0.16
MKEIAEAYLGYPVTNAVITVPAYFNDSQR	3262.7	2	5.415	0.48
MKELAGMFLSEDENFLLLFR	2404.8	3	5.5392	0.4278
MKELSQDSTGR	1252.4	2	3.6897	0.3077
MKENAEAYLGK	1254.4	2	3.6586	0.1304
MKETAEAYLGKK	1369.6	3	5.0021	0.3784
MKETAENYLGHTAK	1593.8	2	4.7183	0.4252
MKETAVFINISR	1409.7	2	3.5864	0.2523

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MKETIMNQEK	1252.5	2	3.2428	0.1622
MKETLQNVR	1119.3	2	3.0343	0.1014
MKEYGEQIDPSTHR	1691.8	2	4.3093	0.2859
MKEYGEQIDPSTHRK	1820.0	2	3.6928	0.3221
MKFNPFVTSDR	1342.5	2	3.4821	0.2355
MKFQYKEDHPFEYR	1919.2	3	3.5	0.2314
MKFVYKEEHPFEK	1713.0	2	4.7872	0.3166
MKGDYFR	917.1	1	2.4832	0.1861
MKGDYHR	907.0	2	2.6184	0.1512
MKGEAEDILETEK	1493.7	2	4.1379	0.3644
MKGEAEDILETEKSKLQLPR	2316.7	3	4.7327	0.3327
MKGFDVFNALDLMENK	1873.2	2	3.0894	0.2514
MKGNFTLPEVAECFDEITYVELQKEEAQK	3391.8	3	3.4856	0.1516
MKGNVDISAPK	1160.4	2	3.1328	0.2413
MKGTFVER	968.2	2	2.476	0.101
MKGVNSYPSLFIFR	1660.0	2	3.8429	0.3314
MKGYNPAEVGAAGK	1393.6	2	3.3656	0.3394
MKHYEVEILDAK	1476.7	2	4.3412	0.3451
MKKFEEDLLLLEDQNSK	2081.4	3	3.6445	0.2017
MKKFEEDLLLLEDQNSKLSK	2409.8	3	5.3557	0.2922
MKKKEPVGDDESVPENVLSFDDLTADALANLK	3490.9	3	5.8529	0.4163
MKKRVVSIVEADPLPNNAVIHNSWIDPK	3172.7	3	3.2835	0.1053
MKLDYILGLK	1194.5	2	2.9088	0.1469
MKLNISFPATGCQK	1538.9	2	3.9609	0.2156
MKLNTQEIFDDWAR	1768.0	2	4.5331	0.4455
MKLPIFIADAFTAR	1594.9	3	3.9972	0.3479
MKLPQFGISTPGSDLHVNAK	2141.5	3	3.9743	0.2779
MKLSDFNDITNMLLLK	1897.3	2	3.9517	0.1555
MKLTDSVLR	1063.3	2	2.6594	0.1083
MKLTEDPEKQTLPGSK	1803.1	2	3.6066	0.2276
MKNLIPFDQMTIEDLNEAFPETK	2726.1	3	4.0663	0.1249
MKNSCIVCNMGHSNTEIDVTSLR	2553.9	3	3.7812	0.2941
MKNYNKPWEPK	1435.7	2	2.6778	0.1451
MKPILLQGHER	1322.6	2	3.148	0.3044
MKPLMGVIYVPLTDKEK	1963.4	3	4.5706	0.3983
MKPLVVFVLGGPGAGK	1571.0	2	4.7699	0.3965

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MKQDAQVVLYR	1351.6	2	3.5163	0.2869
MKQEEQLQR	1190.4	2	3.1805	0.1645
MKQELEAEYLAIFKK	1842.2	3	4.5619	0.258
MKQELEAEYLAVFKK	1828.2	2	3.9645	0.3432
MKQELSSELSTLLSSLSR	2010.3	2	2.7724	0.2624
MKQEPVKPEEGR	1428.6	2	3.7329	0.3203
MKQEPVKPEEGRDMANR	2016.3	2	4.0171	0.3962
MKQVAEEAAR	1133.3	2	3.3694	0.279
MKQVEELYHSLLELGEK	2047.4	2	5.3458	0.3855
MKRHGRGEIIGIQK	1624.0	2	2.4297	0.1029
MKSEPDKADPFSFEGPEIVDCDGCTIDWK	3261.6	3	4.3679	0.126
MKTATDEAYKDPSNLQGK	1998.2	3	3.2956	0.1389
MKTILSNQTVDIPENVDITLK	2373.8	2	5.6689	0.3729
MKTILSNQTVDIPENVDITLKGR	2587.0	3	6.8466	0.4085
MKTSESSTILVVR	1451.7	2	2.6492	0.1165
MKVELCSFSGYK	1392.7	2	2.8661	0.1468
MKVTNEDFKK	1240.5	2	3.1575	0.2223
MKVVEVLAGHGHLYSR	1797.1	2	4.8733	0.4286
MKVYVPTGFSAFPFELLHTPEK	2540.0	3	3.9108	0.1936
MKYPHLVAGALAASAPVLAVAGLGDSNQFFR	3173.7	3	5.1302	0.4821
MKYPHLVAGALAASAPVLAVAGLGDSNQFFRDVTADFEGQSPK	4449.0	3	4.8927	0.4202
MKYWGVASFLQK	1458.8	2	3.7266	0.1971
MLAAQGVDPGLAR	1299.5	2	3.3268	0.2583
MLAAYLYEVSQLKD	1644.9	2	3.4686	0.3679
MLADLDDLNR	1176.3	2	3.0205	0.1321
MLAEDELRDAVLLVFANK	2048.4	2	5.4373	0.4178
MLAEDELRDAVLLVFANKQDLPNAMNAAEITDK	3661.2	3	4.8484	0.3467
MLAEDELRDAVLLVFANKQDLPNAMNAAEITDKLGLHSLR	4438.1	3	5.9265	0.4963
MLAIYDGFDGFAK	1448.7	2	4.2628	0.2933
MLAPEGALNIHEK	1423.7	2	3.5574	0.2397
MLATLFKDER	1224.5	2	2.9352	0.2247
MLCDTWCIEAAAR	1483.8	2	3.6905	0.1325
MLDAEDIVGTARPDEK	1760.9	2	3.9882	0.3539
MLDAEDIVNTARPDEK	1818.0	2	4.3603	0.3052
MLDAKEQEMTEMRDVMQQQLAEYQELLDVK	3645.2	3	3.6672	0.1924
MLDEAVFQVFKDYISK	1934.2	2	2.7085	0.19

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MLDGIVTDAIEASSIGFNPGHVDIYSASWGPNDDGKTVEGPGR	4447.8	3	4.9467	0.4416
MLDLMLEAVNNIKDAMPK	2047.5	2	4.0008	0.2655
MLDLYSQISSVPIGYSHPALLK	2433.9	3	4.6437	0.4299
MLDMGFEPQIR	1337.6	2	3.7633	0.3415
MLDMKVNPIQGLASK	1646.0	2	3.6655	0.1968
MLDNDSILVDAIRK	1603.9	2	3.8979	0.1552
MLDQPFMTDIIEASSISHMPQLIDIYSASWGPTDNGK	4111.6	3	5.1534	0.3993
MLDQTLIDLNEM	1436.7	2	3.809	0.1983
MLDQTLLDLNEM	1436.7	2	3.8288	0.2391
MLEDRDLFVMR	1425.7	3	3.294	0.2825
MLEENTNILK	1205.4	2	3.5226	0.1644
MLEHLSSLPTQMDYK	1794.1	2	3.3936	0.3143
MLEHLSSLPTQMDYKGQK	2107.4	2	4.8554	0.3668
MLEIDPQKVNINGGAVSLGHPIGMSGAR	2863.3	3	6.305	0.4742
MLEKLPELKPVDKESEVVMKFPDGFEK	3164.7	3	3.8129	0.2563
MLEQLDMR	1036.3	2	2.711	0.2051
MLETKWSLLQQQK	1633.9	2	4.6924	0.2948
MLFKDDYPSSPPK	1525.8	2	3.6621	0.3782
MLGGDEEKDPDAAKKEEERQEALR	2746.0	3	4.4667	0.2857
MLGGEEEKDPDAQKKEEER	2219.4	3	4.7845	0.3375
MLGGEEEKDPDAQKKEEERQEALR	2817.0	3	5.8422	0.3929
MLGQMTDQVADLR	1478.7	2	3.2542	0.2219
MLHDNRNEPTQPR	1608.8	2	2.7553	0.1392
MLHDYIGDKDFK	1482.7	2	3.943	0.2755
MLHDYIGDKDFKK	1610.9	2	4.2524	0.4017
MLHVDPHQR	1133.3	2	2.8142	0.2988
MLINQHTLLFGGDTNPVHPK	2233.6	3	6.3694	0.4108
MLISILTER	1076.3	2	3.0173	0.1994
MLISSIKEKYPSHSFIGEESVAAGEK	2839.2	3	5.2808	0.4212
MLITILGTVKPNANR	1642.0	2	3.5244	0.3002
MLKDEVSK	950.1	2	2.6041	0.1851
MLKMGITGPEGHVLSRPEELEAEAVFR	2998.5	3	3.7364	0.2142
MLKPAFIFDGR	1295.6	2	3.5893	0.3249
MLLADQGQSWKEEVVTVETWQEGSLK	2993.3	3	4.5429	0.2189
MLLDIFDENLHPLSK	1786.1	2	2.6146	0.1852
MLLDPMGGIVMTNDGNAILR	2132.6	2	5.7843	0.365

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MLLDSVLTTHER	1415.6	2	3.8074	0.2942
MLLNLHKK	997.3	2	2.6674	0.1229
MLLVDELRDAVLLLFANKQDLPNAMAISEMTDKLGLQSLR	4488.3	3	4.3161	0.3428
MLMDFEQLQPGDSVIQNASNSGVGQAVIQIAAALGLR	3844.4	3	3.8702	0.2406
MLMHGKEVGSIIGK	1500.9	2	3.5157	0.2177
MLNFNVPHIK	1213.5	2	3.0907	0.122
MLNGLEDSIGLSK	1377.6	2	3.9002	0.3783
MLNIHPSLLPSFK	1497.8	2	2.5145	0.1766
MLPELFQDDEKAISPTSATSSGR	2481.7	3	3.8851	0.1048
MLPTIIADNAGYDSADLVAQLR	2348.7	3	5.5937	0.4217
MLQADPNKVSAR	1330.5	2	3.1387	0.1304
MLQEDELRDAVLLVFANK	2105.4	2	4.9571	0.3168
MLQHAASNK	1000.2	2	3.0315	0.2827
MLQHIDYR	1076.3	2	3.1245	0.2811
MLREPAEPVAAEPK	1538.8	2	3.5247	0.2775
MLSLAEQQLVDCAQDFNNHGCQGGLPSQAFEYILYNK	4147.6	3	5.2669	0.3752
MLSLDFLDDVR	1324.5	2	3.0553	0.2184
MLSLDFLDDVRR	1480.7	2	2.6684	0.1315
MLSQPYLLDPSITLGQYVQPQGVSVVDFVR	3351.9	3	4.1133	0.3122
MLSSSDAITQEFMDLR	1845.1	2	3.4705	0.2844
MLSTFKELFSEK	1460.7	2	2.508	0.2358
MLTAQDMSYDEAR	1531.7	2	4.507	0.3776
MLTFNPHKR	1144.4	2	2.5056	0.1366
MLTKFETK	998.2	2	2.7069	0.2248
MLTNHTFIK	1105.3	2	2.7292	0.3018
MLVDDIGDVTITNDGATILK	2105.4	2	5.7837	0.4859
MLVDVFAPEFR	1324.6	2	3.7795	0.2648
MLVKYPEIINSNQ	1549.8	2	4.8345	0.3342
MLVKYPEIINSNQV	1648.9	2	4.9371	0.367
MLVLDEADEMLNK	1521.8	2	3.3243	0.1967
MLVNENFEEYLR	1557.8	2	4.271	0.3896
MLVSCAKISSRSR	1438.7	2	2.411	0.1859
MLVSGAGDIK	991.2	2	2.8042	0.1808
MLVTFDEELRPLPVSVR	2002.4	3	3.8606	0.2351
MLVVGGIDR	960.2	2	2.4294	0.1239
MLVVGGIDRVYEIGR	1678.0	2	3.1168	0.2153

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK	3798.2	3	7.1393	0.5433
MLWFQGAIPAAIATAK	1690.0	2	3.777	0.3163
MMADEALGSGLVSR	1437.7	2	5.4722	0.4676
MMALDREVQYLLNK	1725.1	2	3.4468	0.1952
MMANGILKVPAINVNDSVTK	2116.5	3	3.6754	0.2662
MMDVLAPHVHGQSLAGAGGGGFLYLLTK	2842.3	3	3.3284	0.2045
MMDYLQGSGETPQTDVR	1929.1	2	5.9377	0.5238
MMEIMTR	912.2	1	2.1896	0.1493
MMEVAAADVK	1065.3	2	3.3676	0.2968
MMEYGTTMVSYQPLGDKVNFFR	2616.0	3	3.9258	0.3112
MMFEKGEPTQTK	1427.7	2	3.8846	0.3449
MMITSQDVLHSWAVPTLGLK	2228.7	3	5.6412	0.5283
MMITSQDVLHSWAVPTLGLKTDAIPGR	2939.4	3	6.6469	0.4809
MMKDLEALMFDR	1500.8	2	4.2191	0.3752
MMLDDIVSR	1080.3	2	3.329	0.2342
MMNGGHYTYSENR	1560.7	2	4.7019	0.4057
MMNGGHYTYSENRVEK	1917.1	3	4.5676	0.3775
MMNGGHYTYSENRVEKDGLILTSR	2773.1	3	4.4052	0.2758
MMRPVSDQVQIK	1432.7	2	3.2701	0.1848
MMTKEELEEEQR	1553.7	2	4.155	0.3656
MMTKEELEEEQRTE	1784.0	2	4.5043	0.2884
MMTKEELEEEQRTEE	1913.1	2	4.9779	0.3955
MMTKEELEEEQRVQKEQLAAIFK	2810.2	3	4.6435	0.4514
MMVANKPDKIQQAK	1602.9	2	3.5944	0.2794
MMVDKDGDVTVTNDGATILSMMDVDHQIAK	3252.7	3	7.113	0.4709
MNCDRVFNVFCLYGNVEK	2152.5	2	3.1025	0.1647
MNDIVKEFEDR	1396.6	2	3.2609	0.2775
MNDSNSAGAGGPVK	1305.4	2	2.89	0.3053
MNEAFGDTK	1013.1	2	2.6968	0.2653
MNEFLENFEK	1301.5	2	3.7611	0.2339
MNEFLENFEKNAHLR	1893.1	3	3.7508	0.2734
MNESDAWFEEKQQQFENLDQQLR	2915.1	3	4.989	0.3654
MNFANVFIGANPLAVDLLEK	2177.6	3	4.5963	0.2757
MNGFIDQIDGIVHFETR	1993.2	3	4.749	0.3767
MNHHPEWFNVYNK	1716.9	3	3.9384	0.2148
MNHQALVR	969.1	2	2.6957	0.2291

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MNIVPIVNTNDAVVPPAEPNSDLQGVNVISVKDNDSLAAR	4188.7	3	3.8224	0.4573
MNKDSKPPGNLK	1329.6	2	3.016	0.1484
MNLAIALTAAR	1145.4	2	4.185	0.3379
MNLASEPQEVLHIGSAHNR	2104.3	2	5.5549	0.5269
MNLASSFVNGFVNAAFGQDK	2118.4	3	5.8766	0.5289
MNLASSFVNGFVNAAFGQDKLLTDDGNKWLYK	3566.0	3	4.0551	0.2394
MNLFQSVTSALDNSLAK	1840.1	2	3.5693	0.3975
MNLFQSVTSALDNSLAKDPTAVIFGEDVAFGGVFR	3719.2	3	4.0101	0.2269
MNLGVGAYRDDNGKPYVLPSVR	2422.7	3	4.6449	0.3121
MNLSAIQDR	1048.2	2	2.9212	0.2126
MNPQSAFFQGK	1255.4	2	2.902	0.1695
MNSIKPDLIQLR	1428.7	2	2.8359	0.141
MNTNPSRGPYHFR	1577.8	2	2.5339	0.2744
MNVDKVIPVEK	1272.5	2	3.177	0.2776
MNVDQAFHELVR	1459.7	2	3.1564	0.24
MNVFDTDLQALSR	1510.7	2	4.9401	0.4572
MNVFDTELKGLSKIER	1881.2	2	5.0567	0.3685
MNVLADALK	975.2	1	2.8857	0.1643
MNVQVTQHR	1113.3	2	3.0415	0.2689
MNYSDAIVWLKEHDVKKEDGTFYEFGEDIPEAPER	4160.5	3	4.3137	0.3409
MPATFIGNSTAIQELFKR	2025.4	2	2.4459	0.1442
MPDLHLKAPK	1150.4	2	3.1337	0.1984
MPDSGPLPETHK	1309.5	2	4.0245	0.3733
MPDSGPLPETHKFGEGVSSPK	2198.4	2	5.0544	0.4529
MPDSGPLPETHKFGEGVSSPKTHLGEALAPLSK	3416.8	3	6.2862	0.5452
MPEDGLSDDKKPFK	1607.8	2	4.4628	0.2856
MPEENFTADHPFLFFIR	2112.4	2	5.1637	0.4307
MPEMNIKAPK	1159.4	2	3.2347	0.1318
MPFPVNHGASSEDTLLK	1844.1	2	4.4947	0.4122
MPFPVNHGASSEDTLLKDAAK	2229.5	2	5.2471	0.4469
MPGAPETAPGDGAGASR	1542.7	2	3.4671	0.3207
MPGGPKPGGGPGLSTPGGHPKPPHR	2371.7	3	3.4021	0.2988
MPGVTPK	729.9	1	1.9755	0.1367
MPILGLGTWK	1116.4	2	2.5537	0.1017
MPLATSTDHGHNLQTVQLLIK	2318.7	3	5.4609	0.4741
MPLIGLGTWK	1116.4	2	2.5743	0.1183

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MPLIGLGTWKSEPGQVK	1842.2	3	3.2986	0.185
MPNVPNTQPAIMKPTEEHPAYTQIAK	2908.3	3	4.3646	0.2816
MPPSHQLDHSK	1277.4	2	2.9478	0.2982
MPQMIVNWQQQQR	1688.0	2	2.7002	0.166
MPSESAAQSLAVALPLQTK	1943.3	2	3.6955	0.2854
MPSHQGAEQQQQQHHVFISQVVTEK	2903.2	3	3.9033	0.2049
MPSHQGAEQQQQQHHVFISQVVTEKEFLSR	3535.9	3	5.4594	0.4402
MPSLPSYK	923.1	1	1.8611	0.2183
MPSSGFAAEGR	1110.2	2	2.9582	0.2954
MPTFSTPGAKGEGPDVHMTLPK	2299.7	3	3.9184	0.161
MPTQSEVDNVFDTGLRDVQPYLYK	2817.1	3	3.7894	0.2789
MPYQEIKNVILEVNEAVLTESMIQNLIK	3261.8	3	3.9518	0.1805
MQAHIQDLEEQLDEEEGAR	2242.4	3	5.5819	0.2588
MQAHIQDLEEQLDEEEGARQK	2498.7	3	4.4661	0.2889
MQAQAMLEGSPQLNMVGLFR	2222.6	3	4.7442	0.3807
MQAQLLELR	1102.3	2	2.8031	0.1639
MQAQMQMQMQGGDGDGGALGHHV	2385.7	3	3.9732	0.2798
MQASIEKGGSLPK	1346.6	2	3.5879	0.2245
MQASIEKGGSLPKVEAK	1774.1	3	4.2012	0.1505
MQAVQEATR	1034.2	2	2.7784	0.2305
MQDIKLPLSK	1173.5	2	2.8821	0.144
MQDLDEDATLTQLATAWVSLATGGEK	2766.0	2	5.4115	0.4495
MQELQEAQNAR	1318.4	2	2.5626	0.2456
MQEVVANLQYDDGSGMKR	2042.3	2	5.0085	0.4491
MQEVYNFNAINNSEIR	1943.1	2	5.0536	0.5056
MQGLEAHKYR	1233.4	2	2.6786	0.3232
MQGQSPPAPTR	1170.3	2	2.6471	0.1386
MQHNLEQQIQAR	1496.7	2	4.2747	0.3546
MQHNVLVAEVTQQLK	1739.0	2	3.4004	0.3196
MQILEDHNKQLESQLHR	2120.4	3	4.6515	0.3395
MQKEITALAPSTMK	1549.9	3	4.9842	0.3664
MQKXKKLEKIGEGTYGTVFK	2299.8	2	2.4086	0.2015
MQLAKKEEELQAALAR	1830.1	3	3.2016	0.1513
MQLEVEKR	1033.2	2	2.7754	0.1993
MQLKPMEINPEMLNK	1817.2	2	4.96	0.2928
MQLKPMEINPEMLNKVLSR	2272.8	3	4.9778	0.2153

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MQLLEIITTEK	1319.6	2	2.8943	0.1648
MQMLEDEDDLAYAETEK	2032.2	2	3.751	0.2812
MQMLEDEDDLAYAETEKK	2160.4	2	4.8566	0.3674
MQNDTAENETTEKEEK	1898.0	2	4.8343	0.3496
MQNHFGAVR	1060.2	2	3.0925	0.2929
MQNHGYENPTYK	1482.6	2	3.9927	0.2609
MQQAEQALQDILRDAQISEGASR	2559.8	3	4.1228	0.2787
MQQNIQELEEQLEEEESAR	2334.5	2	6.652	0.3872
MQQNIQELEEQLEEEESARQK	2590.8	2	5.0232	0.2586
MQQNIQELEEQLEEEESARQKLQLEK	3202.5	3	5.2907	0.2092
MQQNIQELEEQLEEEESARQKLQLEKVTTEAK	3832.2	3	5.7741	0.3101
MQQQLDEYQELLDIK	1895.1	2	5.4442	0.3424
MQQQLDEYQELLDIKLALDMEIHAYRK	3336.8	3	4.4701	0.3045
MQQSVYVKDDK	1341.5	2	2.7332	0.1733
MQQVENGLSEK	1263.4	2	3.6371	0.2491
MQQYDLQGQPYGTR	1685.8	2	4.9818	0.4159
MQTNQTPPTYNK	1423.6	2	3.5425	0.1464
MQVDQEEGHQK	1329.4	2	3.9446	0.1474
MQYAPNTQVEILPQGR	1846.1	2	4.4256	0.3136
MRAEDGENYDIK	1441.5	2	3.5046	0.1172
MRAEDGENYDIKK	1569.7	3	4.9118	0.2458
MRAEDGENYDIKKQAEILQESR	2624.9	3	4.1115	0.2701
MRDVVLSIVNDLTIAESNCPR	2346.7	3	3.8051	0.165
MREDYDSVEQDGDEPGPQR	2224.3	3	5.546	0.3287
MREEFPDRIMNTFSVVPSPK	2381.8	3	3.6815	0.2075
MREESGAR	936.0	2	2.6132	0.1378
MREEYDKIQIADLMEEK	2142.4	3	3.2496	0.1349
MREHLELFWSR	1504.7	2	2.5983	0.1522
MREHVMNEVDTNKDR	1875.1	3	5.1303	0.3597
MREIVHIQAGQCGNQIGAK	2054.4	2	5.5076	0.4115
MREIVHLQAGQCGNQIGAK	2054.4	2	6.0114	0.396
MREQQALSR	1119.3	2	3.1027	0.1101
MRESALEPGPVPEAPAGGPVHAVTVVTLLEK	3153.6	3	3.7119	0.1775
MREWFSETFQK	1489.7	2	2.7834	0.1378
MRHEAPMQMASAQDAR	1831.1	2	3.9983	0.4322
MRIESLSSQLSNLQK	1735.0	2	5.1721	0.2262

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MRLEGQLEALSLEASQALKEK	2345.7	3	4.849	0.3054
MRLESLSYQLSGLQK	1754.0	2	5.271	0.3935
MRPGAYSTGYGGYEEYSGLSDGYGFTTDLFGR	3476.7	3	6.3878	0.536
MRPHIFTLSVPFPTPLEAEIAHGSLAPDAEPHQR	3764.3	3	4.4009	0.3742
MRQSGAFLSTSEGLILQLVGDAVHPQFK	3031.5	3	3.3857	0.2107
MRYVASYLLAALGGNSSPSAK	2157.5	2	4.078	0.4044
MSAEINEIIR	1176.4	2	3.7069	0.1753
MSASDPNSSIFLTDTAK	1786.0	2	6.0703	0.4891
MSATFIGNSTAIQELFKR	2015.3	3	4.4949	0.1622
MSDGKKEELQK	1293.5	2	3.7605	0.2516
MSDGLFLQK	1039.2	2	2.9853	0.2863
MSDSLDTDPSMLGSSK	1671.8	2	5.2175	0.4688
MSEDKPQDYK	1241.4	2	3.3795	0.303
MSEDKPQDYKK	1369.5	2	2.771	0.1714
MSEKDTKEEILK	1451.7	2	3.8021	0.2519
MSESLDTADPAVTGAK	1593.7	2	4.9238	0.4753
MSESLETDPAITAAK	1564.7	2	4.1357	0.354
MSFGEIEEDAYQEDLGFSLGHLGK	2673.9	3	3.442	0.3077
MSGGWELELNGTEAK	1622.8	2	5.0694	0.4076
MSGNGRELGEYGFHEYTEVK	2304.5	3	5.309	0.3711
MSGSGRELGEYGLQAYTEVK	2176.4	3	3.8386	0.2297
MSIASSHGGHPLDVPDHIIAYHR	2511.8	3	4.9748	0.3011
MSIFGHSMGGHGALICALK	1931.3	2	3.5334	0.3605
MSIFGHSMGGHGALICALKNPGK	2327.8	3	3.8191	0.1926
MSKPHLHETEEQPYFR	2030.3	2	3.7317	0.3653
MSLDPADLTHDTTGLTAK	1888.1	2	4.4659	0.4283
MSLDPADLTHDTTGLTAKELEALDEVFTK	3163.5	3	5.8512	0.4309
MSLFYAEATPMLK	1502.8	2	3.4883	0.4355
MSLHNLATVFGPTLLRPSEVESK	2527.9	3	4.1114	0.3821
MSLLQLVEILQSK	1502.8	2	4.25	0.167
MSLPDVDLDLKGPK	1528.8	2	2.4002	0.2145
MSMKEVDEQMLAIQSK	1869.2	2	3.5627	0.1626
MSMKEVDEQMLNVQNK	1925.2	2	5.467	0.4151
MSMKEVDEQMLNVQNKNSSYFVEWIPNNVK	3604.1	3	4.6262	0.4352
MSNYDTDLFVPYFEAIQK	2182.4	2	5.1573	0.513
MSPKPELTEEQKQEIR	1944.2	2	2.7149	0.1303

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MSPYKDILETHLR	1603.9	2	3.4035	0.4461
MSQDDFQSPPIVELR	1763.0	2	2.9573	0.2256
MSQLEVKEKELNK	1576.8	2	3.4538	0.1416
MSQVAPSLSALIGEAVGAR	1858.2	2	4.5394	0.4317
MSSAALIHHYTK	1359.6	2	3.4356	0.3362
MSSEVVDSNPYSR	1471.6	2	4.3961	0.4027
MSSFGDFVALSDVCDVPTAK	2090.4	2	3.5065	0.1004
MSSPEDDSDTKR	1368.4	2	2.6953	0.3111
MSSSDTPLGTVALLQEK	1778.0	2	4.3848	0.4309
MSSSEEESKIDLLDRK	1868.1	3	3.6822	0.2101
MSSTFIGNSTAIQELFK	1875.1	2	4.7263	0.4139
MSSTFIGNSTAIQELFKR	2031.3	2	4.34	0.5149
MSSTIFSTGGKDPLSANHSLKPLPSVPEEK	3156.6	3	5.2243	0.3992
MSSYAFFVQTCR	1440.7	2	3.4796	0.3191
MSTEEIIQR	1107.3	2	2.5275	0.2168
MSTGTFVVSQPLNYR	1700.9	2	4.608	0.4779
MSVEADINGLR	1205.4	2	3.083	0.307
MSVEEQIDR	1107.2	2	2.4554	0.1907
MSVIWDKAVVTGK	1434.7	2	3.8722	0.2932
MSVQPTVSLGGFEITPPVVLR	2228.6	2	5.5562	0.5779
MSVTEGGIKYPETTEGGRPK	2138.4	3	4.414	0.3798
MSYLELMEHPFFTLHK	2024.4	2	3.7809	0.3699
MTAALPKLDLHVIPVWQK	2061.5	3	3.5988	0.29
MTAMDNASK	969.1	2	2.6045	0.1372
MTAMDNASKNASEMIDKLTLTFNR	2704.1	3	5.5282	0.3993
MTATGSGENSTVAEHLIAQHSAIK	2454.7	3	3.526	0.2695
MTDFDRFKVMK	1418.7	2	2.5245	0.1134
MTDIMTEGITIVEDINKR	2080.4	3	3.5469	0.3845
MTDLLEEGITVVENIYK	1968.3	2	2.9976	0.3053
MTDLTSSIPKPLLPVGNKPLIWYPLNLLER	3421.1	3	3.7092	0.2171
MTDQEAIQDLWQWR	1821.0	3	4.7417	0.2915
MTDQEAIQDLWQWRK	1949.2	3	4.2444	0.1443
MTDSFTEQADQVTAEVGK	1958.1	2	4.0916	0.246
MTDSFTEQADQVTAEVGKLLGEEK	2627.9	3	4.0599	0.2686
MTEAQEDGQSTSELIGQFGVGFYSAFLVADK	3327.6	3	3.8119	0.2912
MTEELEALR	1092.2	2	2.5599	0.2409

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MTEEPLMCAYCVTEPGAGSDVAGIKTK	2803.2	3	3.3098	0.114
MTEQHFPHPIQSFSPESMPEPLNGPINILGEGR	3689.1	3	4.6719	0.2744
MTGSEFDFEEMKR	1607.8	2	3.9682	0.4475
MTHNLLLNYGLYR	1608.9	2	4.3718	0.3812
MTIAGTTDTPTDVTHHPIPSEEDINFILNEVR	3565.9	3	5.4187	0.3539
MTILQTYFR	1173.4	2	3.494	0.2343
MTISQQEFGR	1197.3	2	2.9356	0.2629
MTITEQKYEGEYR	1648.8	2	2.9522	0.318
MTKEELNALK	1177.4	2	3.156	0.217
MTKPPVQEMVDELQGPFSYDFSYWAR	3123.5	3	4.8693	0.2334
MTLADDVTLDDLIMAKDDLSGADIK	2681.0	3	4.9006	0.3835
MTLDTLSIYETPSMGLLDKK	2257.7	3	3.8203	0.3441
MTLVASEDYGDTLAAIQGLLK	2210.5	2	7.0012	0.5592
MTNAQIILLIDNAR	1586.9	2	4.4886	0.3101
MTNGFSGADLTEICQR	1743.9	2	3.9943	0.337
MTNTNLAVVFGPNLLWAK	1990.4	2	4.0973	0.42
MTNYDVEHTIK	1351.5	2	3.9026	0.3348
MTNYDVEHTIKK	1479.7	2	4.6643	0.423
MTPGHLLVSVGQFRPEK	1897.2	2	2.6713	0.1503
MTQLVLPGMVER	1374.7	2	2.6197	0.1515
MTQQQENPK	1104.2	2	2.9887	0.2558
MTSGDVLSNRK	1208.4	2	2.413	0.133
MTSSDKDFR	1087.2	2	2.4151	0.1892
MTTQSPLNQSSMNAMGSLSVLSPDRVLPQLISTITASVQNPALR	4657.4	3	3.6026	0.1338
MTTSTDHLKR	1190.4	2	2.8805	0.273
MTVNNLHPR	1082.3	2	2.9364	0.2141
MVADTISRTEK	1251.4	2	2.6407	0.1539
MVEEIGVELVVLDLPDLPEDKLAQSVQK	3108.6	3	4.7126	0.4212
MVEGFFDR	1001.1	2	2.7507	0.22
MVEGFFDRGASIVEDKLVEDLR	2526.9	3	3.9548	0.1304
MVEGFFDRGASIVEDKLVEDLRTR	2784.1	3	3.6511	0.2727
MVEKDQDGGR	1135.2	2	3.2132	0.2878
MVEKDQDGGRK	1263.4	2	2.6947	0.1015
MVFINNIALAQIK	1475.8	2	3.4902	0.135
MVGGIAQIIAAQEEMLR	1831.2	2	4.847	0.4589
MVGGIAQIIAAQEEMLRK	1959.4	2	2.6747	0.1603

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MVGVPAALDMMLTGR	1562.9	2	4.2175	0.4357
MVHFLTHYADK	1362.6	2	2.5652	0.1239
MVHFLTHYADKIESVHFSDQFSGPK	2922.3	3	7.1459	0.5344
MVINHLEK	984.2	2	2.5609	0.161
MVINHLEKLFVTNDAATILR	2299.7	3	5.5115	0.458
MVIPGGIDVHTR	1295.5	2	3.1957	0.3684
MVIPGGIDVNTYLQKPSQGMTAADDFFQGTR	3359.8	3	4.2303	0.3349
MVIPNQPPLTATK	1410.7	2	3.219	0.2153
MVISNPAATHQDIDFLIEEIER	2542.8	3	5.8057	0.4404
MVKDQQEAEK	1206.4	2	2.965	0.1458
MVKEALHER	1113.3	2	2.4904	0.1379
MVLAAAGGVEHQQLLDLAQK	2093.4	2	5.875	0.4791
MVLDHLVIQR	1224.5	2	2.518	0.2709
MVLVDLPGVINTVTSGMAPDTKETIFSISK	3165.7	3	3.4733	0.271
MVLVGDVKDR	1132.4	2	3.0159	0.2862
MVMESGDWLVGGDLQVLEK	2107.4	2	2.8365	0.1671
MVMIQDGPQNTGADKPLR	1972.3	2	4.8213	0.3761
MVMPSWFDLMGLSPDAPEDEAGIKK	2766.2	2	3.8052	0.3775
MVNDAEK	806.9	1	1.8597	0.144
MVNDAEKFAEEDKK	1654.8	2	4.7866	0.2815
MVNDAEKFAEEDKKLK	1896.2	2	4.5639	0.2934
MVNDAEKFAEEDKKLKER	2181.5	3	5.2514	0.3499
MVNHFIAEFK	1236.5	3	3.4952	0.3949
MVNHFIAEFKR	1392.7	2	4.175	0.3755
MVNKAADAVNK	1161.4	2	3.5302	0.2833
MVNPTVFFDIAVDGEPLGR	2078.4	2	3.8402	0.365
MVNSNLASVEELKEIDVEVRK	2403.7	3	3.5894	0.2585
MVPAGMGAGLER	1189.4	2	2.7527	0.2396
MVPVSVQQSLAAYNQR	1792.1	2	5.6416	0.4968
MVQEAEKYKAEDEK	1698.9	2	4.7153	0.2764
MVQEAEKYKAEDEKQR	1983.2	3	5.2099	0.3398
MVQEAEKYKAEDEVQR	1954.2	2	4.6697	0.3682
MVQEAEKYKAEDEVQRER	2239.5	3	4.3315	0.3112
MVQVGVPVMAIR	1300.7	2	2.857	0.1001
MVRELFEMAR	1282.6	2	2.9964	0.2917
MVSDINNGWQHLEQAEK	2000.2	2	5.0665	0.3637

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
MVSDINNGWQHLEQAEKGYEEWLLNEIR	3403.7	3	5.4267	0.3353
MVSHLAEEFKR	1347.6	2	2.7169	0.2789
MVSSYVGENAEFER	1618.7	2	3.6886	0.2602
MVSVLPIFR	1062.4	2	2.592	0.1967
MVTGDNINTAR	1192.3	2	3.3988	0.2763
MVTKNDVMNLLESAGFSR	2013.3	2	3.6675	0.327
MVTLYDNEEVGSESAQGAQSLLTELVLRR	3210.6	3	3.9045	0.2227
MVVDAVMMLDDLLQLK	1835.3	2	4.4173	0.2453
MVVESAYEVIK	1268.5	2	2.9015	0.2358
MVVNEGSDGGQSVYHVHLHVLGGR	2548.8	3	5.6154	0.4809
MVVPAALK	829.1	1	1.6489	0.1504
MVVPGLDGAQIPR	1353.6	2	2.5453	0.3099
MWSIENIAFGSGGGLLQK	1909.2	2	6.0918	0.4
MYAALGDPKAPGLGAFR	1736.0	3	3.8472	0.4323
MYEEHLK	950.1	2	2.4474	0.1834
MYEEHLKR	1106.3	2	2.5916	0.1978
MYESFIESLPFLK	1604.9	2	4.3987	0.3172
MYKEEGLK	998.2	2	2.5308	0.1853
MYKEEGLKAFYK	1507.8	3	4.0185	0.3195
MYKGFQALGDAADIR	1656.9	2	4.1555	0.404
MYKTTPDVIFVFGFR	1822.2	2	3.9239	0.3088
MYPIDFEKDDDSNFHMDFIVAASNLR	3092.4	3	4.41	0.3375
MYQKGQETSTNPIASIFAWTR	2430.7	2	4.9332	0.4329
MYSYVTEELPQLINANFPVDPQR	2726.1	3	6.1058	0.4865
MYVQTVLDVHKK	1461.8	2	2.7074	0.1552
NAAANDKLKK	1073.2	2	3.0037	0.1318
NAADSSVPSAPR	1172.2	2	3.2779	0.3109
NAADSYFSLLQGFINSLDESTQESK	2765.9	3	5.0997	0.4553
NAAGALDLLKELK	1356.6	2	4.028	0.1918
NAAGNFYINDK	1227.3	2	3.2475	0.3308
NAAHALPTTLGALER	1535.7	2	4.1421	0.4164
NAAIAVLEELKKLPPLPAVER	2272.7	3	4.919	0.3329
NAALDVEPIHAFR	1453.6	2	2.6642	0.2119
NAALNTIVTVYNVHGDQVFK	2204.5	2	3.855	0.426
NAAQELATLLLSLPAPASVQQQSK	2479.8	3	3.2785	0.2781
NAAQFLLSTNDKTIK	1664.9	2	3.4939	0.1675

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NAASFKEVSDSLLTSSK	1784.9	3	4.55	0.3976
NAATEDLWESLENASGKPIAAVMNTWTK	3049.4	3	6.3062	0.423
NADELVKQKIHPTSVISGYR	2256.5	3	4.0079	0.2543
NADGKIISLDAK	1245.4	2	3.4449	0.3272
NADGYKLDKQHTFR	1693.8	2	3.8739	0.3417
NADHLLHLK	1061.2	2	2.9769	0.2494
NADLQVLKPEPELVYEDLR	2242.5	3	3.7517	0.3693
NADMSEDMQQDAVDCATQAMEK	2432.6	3	3.4245	0.1999
NADMSEEMQQDSVECATQALEK	2458.6	3	4.9837	0.3067
NADNNSSAFTALSEERDQLLSQVKELSMVTELR	3698.0	3	4.5802	0.2388
NADPAELEQIVLSPAFILAAESLPK	2638.0	3	5.8984	0.4569
NADSEIKHSTPSPTR	1640.7	2	4.0816	0.4674
NADYVQEVKR	1222.3	2	2.5912	0.1794
NAEAVLQSPGLSGK	1371.5	2	4.1244	0.3641
NAEGKRPVELVPPESPLAQLFLER	2691.1	3	4.2507	0.3053
NAEHSLPHYLGALER	1707.9	2	2.5421	0.2029
NAEIGNKDFELDVLEEAYTTEHWLVR	3093.3	3	3.8171	0.2486
NAELKFNFGEEEFKFPPKDGFVALSK	2990.4	3	4.5366	0.2732
NAEPLINLDVNNPDFK	1814.0	2	4.4994	0.4099
NAEQYKDQADK	1310.4	2	3.8258	0.2435
NAEQYKDQADKASTR	1725.8	2	4.7815	0.4608
NAESNAELKGLDVDSLVIEHIQVNK	2737.0	3	3.4706	0.2576
NAESNAELKGLDVDSLVIEHIQVNKAPK	3033.4	3	5.3129	0.464
NAFACFDEEATGTIQEDYLR	2294.4	2	5.978	0.5846
NAFGSTHAEALLK	1359.5	2	3.7992	0.3114
NAFMMLIHADQDR	1562.8	2	3.5938	0.4124
NAGAVIGK	729.8	1	1.9174	0.174
NAGAVIGKGGKNIK	1327.6	2	2.4365	0.1362
NAGEIGEMKDGVPEGAQLQGPVHR	2490.7	3	4.1783	0.3325
NAGIEAQDRR	1130.2	2	2.782	0.1263
NAGLAFIELVNEGR	1503.7	2	3.6436	0.2023
NAGYAVSLR	951.1	2	2.5139	0.2108
NAHSTAIAGLTFLHREPLLVTNGADNALR	3074.4	3	3.3578	0.2015
NAIAKDNDIHSEVSTAELGKR	2269.5	3	5.0826	0.4384
NAIANASTLAEVER	1459.6	2	2.4272	0.2301
NAIDKLFVLFGAEILK	1792.2	2	5.081	0.4738

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NAIDKLFVLFGAEILKK	1920.3	2	3.2456	0.2448
NAIHTFVQSGSHLAAR	1709.9	2	5.1419	0.5133
NAINIEELFQGISR	1604.8	2	4.5943	0.3338
NAINTEMYHEIMR	1622.9	2	3.6244	0.3768
NALDPMSVLLAR	1300.6	2	3.3497	0.2532
NALESYAFNMK	1288.5	2	3.4984	0.2952
NALGAIHHTISVR	1389.6	2	3.302	0.1983
NALGPGLSPELGPLPALR	1773.1	2	5.3425	0.4515
NALKQETEVELYNEFPEPIK	2392.6	2	4.2989	0.2716
NALKQETEVELYNEFPEPIKLDK	2749.1	3	5.9768	0.3858
NALKQETEVELYNEFPEPIKLDKNDR	3134.4	3	5.9737	0.5108
NALKWDKDNLQILR	1728.0	2	3.2309	0.2256
NALPALLIYKGGELIGNFVR	2159.6	2	2.9463	0.1813
NALQQENHIIDGVK	1579.7	2	4.3381	0.3073
NALVSHLDGTTPVCEDIGR	1998.2	2	4.7486	0.4098
NAMGSLASQATK	1179.3	2	4.0533	0.3281
NANAEPAVQR	1070.1	2	3.3813	0.2862
NANELSVLKDEVLEVLEDGR	2243.5	3	3.8771	0.2747
NANFKFTDHLK	1335.5	2	2.5672	0.1051
NANKPLLDEIVPVYRR	1898.2	2	3.1987	0.2948
NAPAIIFIDELDAIAPK	1812.1	2	5.0705	0.4316
NAPAIIFIDELDAIAPKR	1968.3	2	5.254	0.4643
NAPPEPVPPPR	1171.3	1	2.4989	0.191
NAQLNIELEAAHH	1460.6	2	3.8705	0.2698
NAQMAQSPILLLGGAASTLLQNR	2368.7	2	6.1049	0.4702
NAQSNALQER	1131.2	2	3.1795	0.2311
NASDMPETITSR	1322.4	2	2.5999	0.3111
NASEMIDKLTLTFNR	1754.0	3	4.8463	0.48
NASGVVNSSPR	1088.2	2	2.74	0.2469
NASSRPASAISGQNNNHSGNKPDPPPVLR	2984.2	3	3.4244	0.3731
NATNVEQAFMTMAAEIK	1870.1	2	6.0702	0.5425
NATNVEQAFMTMAAEIKK	1998.3	2	2.8514	0.1122
NATNVEQAFMTMAAEIKKR	2154.5	2	3.8536	0.3947
NATNVEQSFMTMAAEIK	1886.1	2	5.6435	0.4757
NATSLQHLLSGAK	1340.5	2	3.0228	0.3727
NAVDAFRVNVIHAR	1582.8	2	2.6743	0.1849

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NAVEEYVYEFR	1419.5	2	3.0525	0.1865
NAVITVPAYFNDSQR	1695.9	2	4.1258	0.3151
NAVPDIQGDSEAVSVR	1657.8	2	2.9778	0.1054
NAVTQEFGPVPDTAR	1602.7	2	4.0133	0.3444
NAVTQFVSSMSASADVLALAK	2111.4	2	6.294	0.4677
NAYAVLYDIILK	1396.7	2	4.5066	0.3416
NAYAVLYDIILKNFEK	1915.2	2	4.7881	0.3065
NAYSHKENLQLNQETEAIKEELLYFK	3154.5	3	6.7732	0.4587
NAYTPQEIVGGIPDSEQLLPELLK	2626.0	3	3.6995	0.2242
NAYTPQEIVGGIPDSEQLLPELLKK	2754.1	3	4.6599	0.3045
NDANPETHAFVTSPEIVTALAIAGTLK	2782.1	3	5.7551	0.4019
NDDDEEEAAR	1164.1	2	3.5913	0.3111
NDEALRQLEAELGAER	1814.9	3	4.6213	0.2966
NDEELNKLLGGVTIAQGGVLPNIQAVLLPK	3115.6	3	6.3305	0.4657
NDEELNKLLGGVTIAQGGVLPNIQAVLLPKK	3243.8	3	4.5104	0.2106
NDEELNKLLGK	1273.4	2	3.45	0.1175
NDEELNKLLGKVTIAQGGVLPNIQAVLLPK	3186.7	3	6.9125	0.4706
NDEELNKLLGRVTIAQGGVLPNIQAVLLPK	3214.7	3	5.8556	0.4569
NDEYENLFNMIVEIPR	1997.2	3	4.4708	0.2268
NDFAIHTLK	1059.2	2	2.7396	0.2139
NDFQLIGIQDGYLSLLQDSGEVR	2581.8	2	6.1756	0.4238
NDFQLIGIQDGYLSLLQDSGEVREDLRLPEGDLGK	3905.3	3	4.387	0.3102
NDFQLIGIQDGYLSLLQDSGEVREDLRLPEGDLGKEIEQK	4533.0	3	3.6249	0.2601
NDFTEEEEAQVR	1467.5	2	3.7156	0.3246
NDGAAILAAVSSIAQK	1529.7	2	5.2622	0.4794
NDGAAILAAVSSIAQKIR	1799.1	2	3.5309	0.1986
NDGALYHNNEEK	1404.4	2	4.0393	0.2796
NDGYLMFQQVPMVEIDGMK	2216.6	2	4.9868	0.3914
NDGYLMFQQVPMVEIDGMKLVQTR	2814.3	3	4.1918	0.2706
NDIASHPPVEGSYAPR	1710.8	2	3.9287	0.387
NDKGDIIVTTK	1204.4	2	2.9765	0.3132
NDKSEEEQSSSSVK	1554.6	2	4.2377	0.3081
NDKSEEEQSSSSVKK	1682.7	2	3.9491	0.2986
NDKSEEEQSSSSVKKDETNVK	2369.4	3	5.3086	0.2235
NDLAVVDVR	1001.1	2	2.7538	0.1753
NDLIVFLADQNAPYFKPK	2094.4	2	4.2781	0.3272

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NDLSPTTVMSEGAR	1478.6	2	3.8346	0.3503
NDLVEALKR	1058.2	2	2.68	0.1008
NDQDTWDYTNPNLSGQGDPGSNPNKR	2891.9	3	4.2667	0.1384
NDSHVLIELHK	1305.5	2	3.3714	0.212
NDTKEDVFVHQTAIK	1745.9	2	4.7888	0.3117
NDTKEDVFVHQTAIKK	1874.1	3	4.9361	0.3819
NDTSGEYKK	1042.1	2	2.6724	0.2341
NDVAHKQLSAFGEYVAEILPK	2330.6	3	4.6062	0.4086
NDVAPTLMSVPR	1300.5	2	3.2619	0.279
NDVLDSLGISPDLLPEDFVR	2215.4	2	4.9359	0.4486
NDVLKQEVQR	1229.4	2	2.4602	0.1232
NDWHGGAIVSALSQTGSLFKPR	2342.6	3	4.4839	0.4781
NDYVAAER	938.0	2	2.8291	0.2575
NEAIQAAHDAVAQEGQCR	1912.0	2	5.2606	0.5135
NEDITEPQSILAAAEK	1729.9	2	4.8685	0.4441
NEDITEPQSILAAAEKAGMSAEQAQGLLEK	3144.5	3	4.3142	0.3457
NEEATKHLETSK	1387.5	2	4.2236	0.3522
NEEDEGHSNSSPR	1458.4	2	3.7572	0.2106
NEEEGNSEEIKAK	1477.5	2	3.6354	0.1978
NEETLREEEEEKKQLSHPANFGPR	2869.1	3	4.2274	0.1504
NEGEDGLEVLSFEFQK	1842.0	2	3.1182	0.1693
NEGSESAPEGQAQQR	1588.6	2	3.9006	0.3437
NEGVATYAAAVLFR	1482.7	2	2.8226	0.2599
NEHLQKENER	1297.4	2	2.6637	0.1129
NEHRPASALVNPLAR	1645.8	3	5.3032	0.34
NEHTYVHSSATIPLDDPTLLFANAGMNQFKPIFLNTIDPSHPMAK	4996.6	3	3.5555	0.2073
NEILTAILASLTAR	1486.7	2	4.5361	0.3615
NEISEMNR	993.1	2	2.4959	0.1225
NEKAPVDFGYVGIDSILEQMR	2382.7	3	3.9486	0.3393
NEKGQYISPFHDIPIYADKDVFHMVVEVPR	3546.0	3	5.5903	0.425
NELESYAYSLK	1317.4	1	3.3559	0.2585
NELESYAYSLKNQIGDKEK	2230.4	2	4.1143	0.4511
NELHNLLDKPQLQGIPVLVLGNK	2554.0	3	5.3469	0.3249
NELHNLLDKPQLQGIPVLVLGNKR	2710.2	3	5.6893	0.3355
NELLHFER	1058.2	2	2.6426	0.1306
NELMYQLEQDHDLQAILQER	2487.7	3	4.6029	0.248

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NELSGALTGLTR	1232.4	2	3.3312	0.2638
NEMGHTPLDYAR	1404.5	2	2.7337	0.3086
NENEEILERPAQLANAR	1968.1	2	3.7584	0.3031
NENTFLDLTVQQIEHLNK	2157.4	2	5.2788	0.4069
NEPIIKVSDHSNR	1509.6	2	3.7685	0.3608
NEPQNATGAPGR	1212.3	2	2.9403	0.3217
NEQDAYAINSYTR	1545.6	2	5.0662	0.4795
NEQESAVHPR	1167.2	2	2.6375	0.137
NESHDYPHR	1155.2	2	2.5641	0.1135
NETSVIDQIGEDLLTWFSGPGEEK	2665.8	2	2.9933	0.3027
NEVQSLNQEMASLLQR	1861.1	2	3.4286	0.2715
NEVSFVIHNLPIIAK	1695.0	2	4.5332	0.4556
NEVSFVIHNLPVLAK	1681.0	2	3.5109	0.4186
NFAALEVLREEEFSPLK	1993.2	2	3.3317	0.2089
NFAALEVLREEEFSPLKNAEPADRDSPR	3202.5	3	3.2847	0.2067
NFATSLYSMIK	1275.5	2	3.5747	0.3138
NFDFEDVFVKIPQAIAQLSK	2310.6	3	4.7407	0.3065
NFDIPKEMTGIWR	1607.9	3	3.2513	0.251
NFDKLSFLYLITGNLEK	2016.3	2	5.3644	0.4894
NFEDVAFDEKK	1342.4	2	3.2571	0.202
NFEHLIPDAPELIHDFLVNEK	2491.8	3	6.5126	0.378
NFELMEAEKTK	1340.5	2	3.7046	0.2608
NFEQVAFDETK	1328.4	2	3.008	0.2799
NFFTRYDYEEVEAEGANK	2183.3	3	4.4678	0.1707
NFGDQPDIR	1062.1	2	2.7289	0.2197
NFGEDMDDER	1228.2	2	2.6286	0.2889
NFGEDMDDERLK	1469.6	2	3.1413	0.2902
NFGEDMDDERLKDLFGK	2030.2	2	4.5155	0.3857
NFGEEVDDESLKELFSQFGK	2319.5	2	5.4415	0.4856
NFGSALGSSGR	1053.1	2	2.9268	0.1488
NFGTDPEVTDLVHNTR	1815.9	2	4.9826	0.4727
NFHIFYQLLEGGEEETLR	2196.4	2	3.4425	0.3277
NFHIFYQLLEGGEEETLRR	2352.6	2	3.7324	0.2458
NFHVFYQLLSGASEELLNK	2210.5	3	6.5416	0.4936
NFHYLLIKDGCRVPAVVFTTLR	2564.0	3	3.329	0.2096
NFHYPPDGYSR	1353.4	2	2.4995	0.2248

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NFIAQGPYENR	1309.4	2	2.7359	0.1464
NFIAQGPYENRTVFETLDIGWQLLR	2982.3	3	3.2921	0.2879
NFILDQTNVSAAAQR	1648.8	3	5.0498	0.3213
NFILDQTNVSAAAQRR	1805.0	2	2.6479	0.1126
NFINNPLAQADWAAK	1673.9	2	4.964	0.4035
NFIVWLEDQK	1292.5	2	3.492	0.1462
NFKENVIRPILK	1471.8	2	3.3984	0.1538
NFLPILFNLYGQPVAAGDTPAPR	2472.8	3	4.0918	0.2797
NFLRDLFLHHK	1440.7	2	2.7376	0.1184
NFLTQDSADLDSIEAVANEVLK	2393.6	2	4.7823	0.3762
NFLTTAIRPHGIFGPR	1798.1	2	2.4599	0.1176
NFPDLDRIVYVNEK	1722.9	2	4.1232	0.2248
NFPDLDRIVYVNEKEGGPNNHLLK	2783.1	3	6.6779	0.4221
NFQEEQINTR	1279.3	2	3.0863	0.1173
NFQNIFPPSATLHLSNIPPSVSEEDLK	2996.3	3	3.5403	0.1745
NFQNIFPPSATLHLSNIPPSVSEEDLKVLFSSNGGVVK	4084.6	3	5.5771	0.3969
NFREEPEHDFSK	1535.6	2	2.8672	0.2306
NFRKPLIVASPK	1370.7	2	3.7841	0.2126
NFRPGTENTPMIAGLGK	1804.1	2	3.855	0.2199
NFSAGGHKVGLGFELEA	1733.9	2	4.0765	0.4235
NFSDNQLQEGK	1280.3	2	4.2101	0.2921
NFSDNQLQEGKNVIGLQMGTNR	2464.7	3	4.7295	0.2985
NFSGAELEGLVR	1292.4	2	3.565	0.2577
NFSGTASTSLLGPPPGLLTPPVATELSQNAR	3095.5	3	4.3976	0.3411
NFSIKEIFDK	1241.4	2	2.5396	0.171
NFSIKEIFDKAISAR	1740.0	2	2.5762	0.18
NFSIVAHVDHGK	1324.5	2	3.2463	0.3342
NFTEVHPDYGSHIQALLDKYNAEKPK	3016.3	3	4.7065	0.3647
NFTGRNDANPETHAFVTSPEIVTALAIAGTLK	3357.7	3	7.0204	0.5279
NFTQGLVEDAPDGSDASQLLHQAEVAQQEFLEVK	3716.0	3	5.7523	0.3976
NFTTEQVTAMLLSK	1583.8	2	4.6549	0.3966
NFVDSPIIVDITK	1461.7	2	2.6297	0.1324
NFVEETVYLLSR	1470.7	2	4.096	0.1708
NFVENFCAITGQSLNHVLCNQDSDLPEGATVPALGLSNK	4118.6	3	4.3877	0.2014
NFVINVVNR	1075.2	2	2.8277	0.2453
NFWVSGLSSTTR	1355.5	2	3.9698	0.3768

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NFYDSPEKIYER	1561.7	2	3.3619	0.3035
NFYELSPHIFALSDEAYR	2173.4	2	5.688	0.516
NFYQEHPDLAR	1390.5	2	3.6318	0.3903
NFYVDGHVPKPH	1410.6	2	3.8375	0.4224
NFYVEHPEVAR	1361.5	2	3.3511	0.4205
NFYVEVPELAK	1309.5	2	2.704	0.1603
NGAGLMVNSR	1019.2	2	2.9009	0.2905
NGALDQQKDELDVR	1601.7	2	4.6878	0.323
NGAPIIMSFPHFYQADER	2094.3	2	5.5459	0.4116
NGAVQTIAQR	1058.2	2	3.4092	0.253
NGDFLPTR	920.0	2	2.4075	0.1832
NGDKGHAGLAGAR	1224.3	2	2.8071	0.1021
NGDLDEVKDYVAK	1466.6	2	3.9854	0.377
NGDLDEVKDYVAKGEDVNR	2137.3	3	5.5988	0.4868
NGDPFVATSIVEAIATVDR	1976.2	2	3.9648	0.3801
NGDTASPKEYTAGR	1467.5	2	2.629	0.1914
NGDTASPKEYTAGREADDIVNWLK	2651.8	2	3.1251	0.2199
NGDVVDKFVGIKDEDQLEAFLK	2480.8	3	5.6381	0.478
NGDVVDKFVGIKDEDQLEAFLKK	2608.9	3	7.6786	0.4832
NGELENIKPK	1142.3	2	2.9804	0.1528
NGENGIHFLLNR	1384.5	2	3.2496	0.307
NGERIEKVEHSDLSFSK	1976.1	3	3.7541	0.1669
NGESSELDLQGIR	1418.5	2	3.7816	0.3341
NGESSELDLQGIRIDSDISGTLK	2448.6	2	4.0797	0.3523
NGETVPIDEQFDKEK	1749.9	2	3.2038	0.2643
NGFLLDGFPR	1136.3	2	3.7146	0.4039
NGFLNLALPFFGFSEPLAAPR	2279.6	2	5.384	0.4395
NGGEDGKGILGR	1173.3	2	2.603	0.1553
NGGHETDAQILELNQQLVDLKLTVDGLEKER	3477.8	3	4.5559	0.332
NGGHFLISIK	1086.3	2	2.845	0.2544
NGGHFVISIK	1072.2	2	2.8427	0.3255
NGGLGHMNIALLSDLTK	1755.0	2	5.4613	0.3958
NGGLITLEELHQQVLK	1793.1	2	3.0762	0.1636
NGGQILIADLR	1170.3	2	2.9302	0.1903
NGGVKPNIIPSYSELIYYFR	2331.7	3	4.2146	0.331
NGHLQSESGAVPK	1324.4	2	2.6996	0.1477

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NGHPEIVQFLLEK	1524.7	2	2.493	0.2423
NGHVGISFVPKETGEHLVHVK	2285.6	3	4.2194	0.356
NGIIKTDKVFEVMLATDR	2051.4	2	2.8029	0.1554
NGKDLGLAFEIPPHMK	1768.1	2	4.3055	0.3086
NGKEVATDVR	1089.2	2	2.9709	0.2201
NGKGSVLPNSDKK	1344.5	2	3.8612	0.2126
NGKPVTTGVSETVFLPR	1803.1	2	4.9783	0.479
NGKPVTTGVSETVFLPREDHLFR	2600.9	2	3.2679	0.1391
NGLHRPVSTDFAQYNSYGDVSGGVR	2697.9	3	6.0666	0.4528
NGLLHGHFTLPFLKDEVK	2066.4	3	4.2992	0.1752
NGLQKYEYVLHPR	1617.8	2	3.1994	0.3347
NGLSFIETSALDSTNVEAAFQTILTEIYR	3205.5	3	3.2905	0.1324
NGLSLAALKK	1015.2	2	2.9709	0.2233
NGLVNSEVHNEDGR	1540.6	2	2.6793	0.1524
NGLWGHALLLASK	1380.6	2	2.7426	0.1997
NGNGGPGPYVGQAGTATLPR	1885.0	2	3.9474	0.3009
NGNLPEFGDAISTASK	1621.7	2	3.8108	0.319
NGPALQEAYVR	1218.3	2	3.0823	0.2642
NGPLEVAGAAVSAGHGLPAK	1817.0	2	5.6172	0.5141
NGPVEGAFSVYSDFLLYK	2007.2	2	5.0231	0.4942
NGQDLGVAFK	1049.2	2	3.1543	0.2916
NGQGFALVYSITAQSTFNDLQDLR	2659.9	3	4.799	0.3619
NGQGFALVYSITAQSTFNDLQDLREQILR	3299.6	3	4.1234	0.275
NGQIDKEAVQK	1230.4	2	2.9095	0.2098
NGQLIQLPVAEIVVGDIAQVK	2205.6	3	5.3008	0.4836
NGQNAAVVHR	1066.2	2	3.038	0.2046
NGQTREHALLAYTLGVK	1872.1	2	4.3666	0.3968
NGQVIGIGAGQQSR	1385.5	2	4.0329	0.438
NGQVVGHVR	966.1	2	2.93	0.2733
NGQYAEASALYGR	1400.5	2	2.7091	0.2572
NGRVEIIANDQGNR	1556.7	2	4.1688	0.32
NGRVEIIANDQGNRITPSYVAFTPEGER	3105.4	3	5.3228	0.4231
NGSEADIDEGLYSR	1526.5	2	4.9266	0.3685
NGSGGGGGGSSGGGETLDDQR	1822.7	2	2.6596	0.1129
NGSGTLDLEEFLR	1451.6	2	2.4511	0.2636
NGSITQIPILTMPNDDITHPIPDLTGYITEGQIYVDR	4113.6	3	6.1222	0.399

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NGSLDSPGKQDTEEDEEEDEKDKGK	2780.8	3	5.6601	0.2973
NGSPAGGDAKELDSK	1446.5	2	2.6233	0.1329
NGSTLKETAIELGYLTAEQFDEWVKPK	3069.4	3	6.5883	0.4552
NGTDKDAEALFK	1309.4	2	2.6976	0.3198
NGTIELMEPLDEEISGIVEVVGR	2500.8	2	3.5211	0.2448
NGTQVHGTITGVDVSMNTHLK	2210.5	3	4.2854	0.3398
NGVAQEPVHLDSPAIKHQFLLTGDTQGR	3030.3	3	3.612	0.2027
NGVELTSLR	989.1	2	3.177	0.2425
NGVGLEFNHLFGYGVLDAGAMVK	2409.7	3	5.667	0.5232
NGVGLEPNINAGGCNFNSFLR	2194.4	3	3.6838	0.1505
NGVHFLQLELINGR	1610.8	2	3.7461	0.3619
NGVKITLPVDFVTADKFDENAK	2422.7	3	5.1964	0.4093
NGVMPSHFSR	1132.3	1	2.7134	0.336
NGVNDIKNHK	1139.2	2	2.6824	0.1967
NGVQAMVEFDSVQSAQR	1867.0	2	5.3859	0.5265
NGWMEQISGK	1150.3	2	3.0853	0.2482
NGYELSPTAAANFTR	1612.7	2	4.7085	0.4364
NGYGFINR	941.0	2	2.7345	0.3242
NGYGFINRNDTKEDVFVHQTAIK	2667.9	3	5.1747	0.3415
NGYGFINRNDTKEDVFVHQTAIKK	2796.1	3	5.7971	0.4274
NHAAPFSK	872.0	1	2.7117	0.2967
NHAHEHFLDLGESK	1634.7	2	4.1356	0.2734
NHAVVCQGCHNAIDPEVQR	2091.3	3	3.2654	0.1792
NHDHQEIAVPVANLK	1685.9	2	4.1849	0.3913
NHEEEISTLR	1228.3	2	3.2349	0.3264
NHEEEVK	884.9	1	2.271	0.2115
NHEEEVKGLQAQIASSGLTVEVDAPK	2751.0	3	6.3801	0.4533
NHEEEVKGLQAQIASSGLTVEVDAPKSQDLAK	3393.7	3	8.4026	0.5365
NHEGDEDDSHVR	1410.3	2	3.9651	0.3561
NHETAFQGMLR	1304.5	2	2.4741	0.2561
NHFSVPLSVYEGDTLLGTASPENEFNIPLGSYR	3625.9	3	4.1835	0.2939
NHGLSDEHVFEVICPSIPGYGFSEASSK	3008.3	3	3.5993	0.2119
NHGVVMPDANKENTLNQLVGAAFGAAGQR	2981.3	3	5.5993	0.4852
NHIHSCFSDVTCFLLPHPGLQVATSPDFDGK	3384.8	3	6.2842	0.3017
NHIIKDQLASK	1267.5	2	3.1436	0.2575
NHIILQENAQHATR	1645.8	2	4.7305	0.4237

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NHILPPMDHSTISLQMGTNK	2235.6	3	3.7865	0.3208
NHIQLVK	852.0	1	2.0629	0.1824
NHLLHVFDEYK	1415.6	2	3.686	0.2874
NHLLHVFDEYKR	1571.8	2	4.9345	0.5018
NHLPQDSQDLVLGGDVPISSIQATIAK	2818.1	3	5.6965	0.2901
NHLPVPNLDPDTYR	1651.8	2	2.8617	0.2332
NHLTQFSPHFK	1356.5	2	3.2748	0.3684
NHLVEIPPNLPSSLVELR	2028.3	3	3.9745	0.2659
NHNEGMVTR	1058.2	1	2.3612	0.2893
NHNSLLSLPQEPYSFSEPAQQAMR	2746.0	3	5.9796	0.4393
NHNSLLSLPQEPYSFSEPAQQAMRK	2874.2	3	4.3194	0.2517
NHPSFYVFNHR	1418.5	2	3.6344	0.3978
NHQDPLAVAYHLIIDNR	1990.2	2	4.1504	0.39
NHQDVAGVFALSSFLNK	1848.1	2	3.1602	0.1981
NHQEEDLTEFLCANHVLK	2141.4	3	4.7909	0.3088
NHQGPLPPVPLHLR	1575.8	2	3.458	0.2553
NHQNLLDSLEQYVK	1701.9	2	4.6472	0.3812
NHQSAAEYNIFEGMELR	2010.2	3	4.4831	0.2098
NHSDSSTSESEVSSVSPLK	1978.0	2	3.1511	0.1243
NHTDSAGTPHVSGGK	1465.5	2	3.062	0.3423
NHTLQEQVTQLTEK	1669.8	2	5.0788	0.4265
NHTLSELLQLR	1324.5	2	3.1617	0.3496
NHVHIANPDFIWK	1591.8	2	3.6823	0.347
NHVQPYIPSILEALMVPTSQGFTEVR	2928.4	3	4.3712	0.2328
NHVSQAIYLLTSR	1502.7	2	2.999	0.3253
NHVVDISESGLITIAGGK	1811.0	2	4.7554	0.4478
NHYNEEMSNLR	1407.5	2	2.8719	0.326
NHYTESISVAK	1249.4	2	2.7411	0.2956
NIANPTAMLLSASNMLR	1818.2	2	5.7306	0.5017
NIAVGKDPLEGQR	1397.6	2	3.3446	0.2154
NIDDGTSDRPYSHALVAGIDR	2273.4	3	3.9558	0.2446
NIDDGTSDRPYSHALVAGIDRYPR	2689.9	3	3.748	0.2143
NIDEAAKHR	1054.1	2	2.4803	0.1866
NIDEHANEDVER	1441.4	2	4.1137	0.4485
NIDEKLTEAAR	1260.4	2	2.8303	0.2218
NIDHMLWLEQPENIATCIALRPYPK	2967.5	3	4.7316	0.3539

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NIDNPALADIYTEHAHQVVVAK	2419.7	2	4.4976	0.2881
NIDQAVTAALETR	1402.5	2	4.0005	0.3479
NIDRTELQTITNDPR	1786.9	3	3.6787	0.1663
NIEDVIAQGIGK	1257.4	2	4.6903	0.3557
NIEEHASADVEK	1342.4	2	3.7086	0.3161
NIEELQQQNQR	1400.5	2	2.539	0.1427
NIEIDSPYEISR	1436.5	2	3.956	0.3166
NIEIDSPYEISRAPDELHYTYLDTFGRPVIVAYKK	4115.6	3	4.2909	0.2864
NIELICQENEGENDPVLQR	2214.4	3	4.0614	0.3609
NIETIINTFHQYSVK	1808.0	2	2.9118	0.2459
NIFLKDQNIFVQK	1607.9	2	3.9951	0.2616
NIGENEGGIDKFSR	1536.6	2	3.5335	0.3914
NIGISAHIDSGKTTLTER	1914.1	2	5.1219	0.4739
NIHKLLDEVFFSEK	1720.0	2	3.8391	0.2749
NIHTNEEDQR	1256.3	2	2.5935	0.1702
NIIGSSPVADFSAIKELDTLNNEIVDLQR	3173.5	3	4.4434	0.4207
NIIGYFEQKDSDNYR	1863.0	2	4.2537	0.402
NIIHGSDSVESAEK	1486.6	2	3.8337	0.3132
NIILEEGKEILVGDVGQTVDDPYATFVK	3064.4	3	7.8746	0.4717
NIIQKFEKVPEGPIPPSTPK	2220.6	3	5.3964	0.322
NIIVFYGSQTGTAEEFANR	2118.3	2	3.9153	0.4692
NIKHSGNITFDEIVNIAR	2042.3	2	5.1031	0.4967
NIKLGIHEDSQNR	1524.7	2	3.9456	0.3297
NILAEQLQAETELFAEAEEMR	2436.7	3	4.1924	0.2411
NILDFPQHVSPSK	1482.7	2	2.4783	0.1393
NILDFPQHVSPSKDIR	1867.1	2	4.1679	0.2273
NILEKHSLDASQGTATGPR	1996.2	2	5.0826	0.4541
NILFVITKPDVYK	1550.9	2	4.2247	0.3384
NILFVITKPDVYKSPASDTYIVFGEAK	3017.5	3	3.4192	0.1505
NILGAQVSEAVPLPEHGVSVVFVNLGNTK	2990.4	3	4.4278	0.333
NILGGTVFR	977.1	2	2.566	0.2771
NILGGTVFREPIICK	1661.0	2	3.954	0.3906
NILHQGQEAILQR	1520.7	2	3.9384	0.315
NILKQGIETPEDQNDLRK	2112.3	3	3.2982	0.1054
NILLTNEQLESAR	1501.7	2	4.6414	0.393
NILLTNEQLESARK	1629.8	2	3.5027	0.2541

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NILSQIVDIDGIWEGTR	1930.2	2	5.2144	0.4322
NILVFGEDGSGK	1236.4	2	2.6021	0.1736
NILVFGEDGSGKTTLMTK	1912.2	2	3.5788	0.31
NINADEAAAMGAVYQAAALSK	2080.3	2	6.153	0.5723
NINENFGPNTEMHLVPILATAIQEELEK	3166.6	3	5.5635	0.3545
NINIGDISIKVPNLPSFK	1970.3	3	3.6462	0.2363
NINIGDLNIKVPNLSQ	1753.0	2	4.5142	0.3572
NINITKDLLDLLVEAK	1813.1	2	5.2901	0.4022
NINPDVLFEVHNYNITTVENFQHFMDR	3308.6	3	3.2978	0.1541
NIPGITLLNVSK	1269.5	2	3.3309	0.3715
NIPGITLLNVSKLNILK	1851.3	2	4.869	0.3938
NIPLLFLQNITGFMVGR	1934.3	2	3.5542	0.3753
NIPLLFLQNITGFMVGREYEAEGIAKDGAK	3296.8	3	3.4717	0.2443
NIPMTLELLQSTR	1516.8	2	2.9982	0.2142
NIPPYFVALVPQEEELDDQK	2345.6	2	3.8515	0.1323
NIPPYFVALVPQEEELDDQKIQVTPPGFQLVFLPFADDKR	4616.2	3	4.5758	0.3125
NIQDTSDLDAIAK	1404.5	2	3.6829	0.2806
NIQDVQSQISK	1260.4	2	3.1294	0.2293
NIQKGDYDVVINDYEKAK	2113.3	3	3.5854	0.1463
NIQVDEANLLTWQGLIVPDNPPYDK	2854.2	3	4.1571	0.1626
NIQVDEANLLTWQGLIVPDNPPYDKGAFR	3285.7	3	4.9643	0.27
NIQVSHQEFSK	1317.4	2	3.5326	0.301
NIRDNEEKDSAFR	1594.7	2	4.0184	0.2731
NIRQEINSPTSTVVVIPSIPHPSLNHGFLAK	3367.8	3	4.4835	0.2143
NISELFYYAQK	1376.5	2	3.8821	0.3863
NISFTVWDVGGQDK	1566.7	2	3.6943	0.2842
NISHYEEQLVK	1360.5	2	3.1719	0.1772
NISRLQAEIEGLKGQR	1813.1	3	4.2675	0.3127
NITLDDASAPR	1173.3	2	2.9842	0.1841
NITLNFGPQHPAAHGVLR	1943.2	2	5.4704	0.4643
NITLPHLESQSLSIQWVYNILDKK	2841.3	3	3.5183	0.2228
NITLSLVANPSHLEAVDPVVQGK	2402.7	3	3.9452	0.2659
NITYLPAGQSVLLQLPQ	1856.2	2	3.8712	0.4006
NIVDHTNEQQK	1326.4	2	3.2567	0.3142
NIVEAAAVR	943.1	2	3.1734	0.2876
NIVEAAAVRDISEASVFDAYVLPK	2578.9	3	4.869	0.3652

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NIVEKIDFDSVSSIMASSQ	2071.3	2	2.6704	0.2221
NIVHNYSEAEIK	1417.5	2	3.4326	0.2481
NIVLSGGSTMFR	1282.5	2	3.4899	0.3133
NIYGNIEDLVVHIK	1627.9	2	4.3933	0.4084
NIYSEELR	1024.1	1	2.6097	0.1355
NIYSEELRETK	1382.5	2	3.0991	0.2867
NIYVLQELDNPGAK	1574.8	2	5.4229	0.274
NIYVLQELDNPGAKR	1730.9	2	4.4309	0.3125
NKAVQLENELENFTK	1778.0	2	4.1907	0.2377
NKDGRLDLNDLAR	1500.6	2	3.0413	0.2101
NKDHPAFAPLYFPMELHR	2184.5	3	5.6616	0.4343
NKDIAFLEAQIYEYVEILGEQR	2642.9	2	3.564	0.2885
NKDQGTYEDYVEGLR	1787.9	2	5.0046	0.4739
NKDQGTYEDYVEGLRVFDKEGNGTVMGAEIR	3492.8	3	5.5662	0.3999
NKDRDDMVR	1149.3	2	2.4921	0.1644
NKDTDISIKPEGVREPDKPAPVEGK	2721.0	3	5.2216	0.3139
NKDTLFQDFKR	1412.6	2	3.036	0.3629
NKDVKGALRTLILGSAAGQSHK	2265.6	2	2.7103	0.1191
NKEDQYDHLDAADMTK	1895.0	2	5.5853	0.3339
NKEEAAEYAK	1153.2	1	2.9822	0.3154
NKEEDLQSTKEERFPAIHK	2300.5	3	3.5116	0.1383
NKEFSQTLENEKNTLLSQISTK	2553.8	3	4.8024	0.3814
NKEGLHNAKEILTR	1623.8	2	3.2645	0.2076
NKEIFLRELISNASDALDKIR	2446.8	3	4.1229	0.316
NKEIMFHVSTK	1334.6	2	3.1511	0.202
NKEPPAPAQQLQPQPVAVQGPEPAR	2649.0	3	3.5067	0.2119
NKEPPAPAQQLQPQPVAVQGPEPARVEK	3005.4	3	3.4395	0.2138
NKEQEDIVVLK	1315.5	2	3.3156	0.1227
NKEQLSDMMMINK	1582.9	2	4.7224	0.3168
NKESKDPADETEAD	1549.5	2	3.5066	0.3092
NKETLGSEAVSSNVIDYGHASK	2307.5	3	5.7016	0.4491
NKEVFIPQDGKK	1403.6	2	3.63	0.2764
NKEVTWEVLEGEVEK	1790.0	2	4.6152	0.4069
NKEVTWEVLEGEVEKEALK	2231.5	2	2.8683	0.243
NKEVTWEVLEGEVEKEALKK	2359.7	3	5.7675	0.3497
NKFDVDAADEK	1252.3	2	3.2282	0.2786

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NKFEEAER	1023.1	2	2.564	0.1494
NKFLIDGFPR	1207.4	2	3.36	0.2655
NKFNQVESDKLR	1478.6	2	3.974	0.2368
NKFVLSGNLHGGSVVASYPFDDSPEHK	2903.2	3	5.1908	0.4041
NKGDSHLNVQVSNFK	1687.8	2	5.2115	0.5005
NKGIIWGEDTLMEYLENPKK	2379.7	3	3.5928	0.2834
NKGVQPLLDAVLEYLPNPSEVQNYAILNKEDDSKEK	4073.5	3	5.0499	0.3346
NKHEAMITDLEER	1586.8	2	4.6069	0.3239
NKHPDEDAVEAEGHEVKR	2061.2	2	4.509	0.4432
NKIAGYVTHLMK	1375.7	2	3.8289	0.2721
NKITITNDQNR	1317.4	2	3.5465	0.2431
NKITLQDVVSHSK	1469.7	2	4.4904	0.4041
NKITLQDVVSHSKK	1597.8	2	4.0268	0.2885
NKITPNLAEFAFSLYR	1885.2	3	5.2426	0.3965
NKITQSNAILR	1258.5	2	2.8717	0.2197
NKIVYPPQLPGEPR	1608.9	2	2.8701	0.2095
NKKQDGAIENR	1273.4	2	2.5779	0.1352
NKLDFLRPYTVPNK	1706.0	2	2.8174	0.1013
NKLDFLRPYTVPNKK	1834.2	2	4.7054	0.2637
NKLDHYAIIKFLLTTESAMK	2337.8	3	4.578	0.2818
NKLDHYAIIKFPLTTESAMK	2321.7	3	6.159	0.5198
NKLDLETLTDILQHQIR	2051.3	3	4.1065	0.1123
NKLQQLPADFGR	1387.6	2	2.6838	0.1651
NKLQSQLLSIEKEVEEYKNFRPDDPAR	3248.6	3	3.9051	0.3265
NKLQSYVDAGTPMYLVIFPEGTR	2601.0	3	3.254	0.2587
NKLVQTAELTK	1245.5	2	2.9415	0.2059
NKLYTDFDEIRQEIENETER	2543.7	3	4.0195	0.307
NKNAAQELATLLLSLPAPASVQQQSK	2722.1	3	3.9263	0.1908
NKPLFFADKLYK	1484.8	2	3.1877	0.2498
NKQELSFYSIPEFDEWKK	2289.5	3	3.7404	0.1956
NKQEVMISDLEER	1591.8	2	4.3988	0.4526
NKQGLETDNKELACEVK	1920.1	2	4.8007	0.3923
NKQKPITPETAEK	1484.7	2	3.8204	0.2295
NKQTYSTEPNNLK	1537.7	2	4.2809	0.2883
NKSEDSTKDDIDLDALAAEIEGAGAAKEQEPQK	3488.7	3	5.6673	0.3858
NKSNEDQSMGNWQIK	1779.9	2	4.6505	0.327

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NKSTESLQANVQR	1475.6	2	4.4436	0.3381
NKTEDLEATSEHFK	1649.7	2	4.4325	0.3684
NKTGAAPIIDVVR	1354.6	2	3.7361	0.2892
NKTKENILEEFSK	1580.8	2	3.9089	0.2983
NKTLIEDEIATILK	1601.9	2	4.1812	0.2726
NKTLVTQNSGVEALIHAILR	2178.5	3	4.6818	0.3552
NKVEDAFYKGELR	1569.7	2	3.876	0.3735
NKVEQLKEELSSK	1532.7	2	3.7989	0.2511
NKVFGLQGVSR	1205.4	2	2.6798	0.1848
NKVRIDQYQGADAVGLEEK	2134.3	3	4.6738	0.1902
NKVSHIDVITAEMAKDFVEDDTTHG	2774.0	3	3.5545	0.3252
NKYEDEINKR	1309.4	2	3.2113	0.2026
NKYEDEINKRTEMENEFVLIKK	2772.1	3	3.4668	0.1072
NKYETEINITK	1353.5	2	2.4905	0.1932
NKYQELINDIAR	1477.6	2	4.0017	0.1878
NKYQIHIPLPPK	1448.7	3	3.4251	0.2365
NLAATLQDIETKR	1473.7	2	2.4901	0.1212
NLAEDRSGINLKDLVQDPSLLGGTISAYK	3089.4	3	4.2518	0.3674
NLANTVTEEILEK	1474.6	2	4.5745	0.3849
NLANTVTEEILEKAFSQFGKLER	2639.0	3	3.6478	0.2113
NLATAYDNFVELVANLK	1896.1	2	5.3927	0.4938
NLATTVTEEILEK	1461.6	2	4.5053	0.2832
NLATTVTEEILEKSFSEFGKLER	2642.9	3	4.6278	0.4102
NLAVSQVVHK	1095.3	2	3.2958	0.2556
NLDAVHDITVAYPHNIPQSEK	2362.6	2	3.43	0.3316
NLDAVHDITVAYPHNIPQSEKHLLQGDFPR	3426.8	3	4.871	0.3432
NLDDGIDDERLR	1431.5	2	2.9913	0.2133
NLDFQDVLDKLADMGIAIR	2148.5	2	5.9126	0.4849
NLDGISHAPNAVK	1336.5	2	2.9216	0.2094
NLDIERPTYTNLNR	1719.9	2	3.504	0.256
NLDKDMYGDDLEAR	1655.8	2	4.3803	0.3096
NLDKEYLPIGGLAEFCK	1911.2	3	4.9243	0.3725
NLDKKDFLGKSDPFLEFFR	2317.6	3	4.7717	0.2736
NLDLDSIIAEVKAQYEEIANR	2405.6	3	4.742	0.3519
NLDLDSIIAEVKAQYEEIAQR	2419.7	3	5.4392	0.3952
NLDPEQMSQVLDAMFEK	1996.3	2	4.9481	0.402

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NLDPFLLFDEFK	1498.7	2	3.2803	0.3263
NLDQEQLSQVLDAMFER	2037.2	3	5.8487	0.5726
NLDQSGTNVAK	1147.2	2	2.95	0.2146
NLDSEKEKELER	1490.6	2	3.3787	0.2969
NLDSLEEDLDFLRDQFTTTEVNMAR	2974.2	3	5.9305	0.5085
NLDTGEEIPLSLAEEKLPTGINPLTLHIMR	3316.8	3	6.0662	0.4163
NLDTVKGSSLHVGSDLLK	1884.1	2	3.7265	0.3871
NLDVQLLDTKR	1315.5	2	2.9558	0.2178
NLDYVATSIHEAVTK	1661.8	2	4.6492	0.4137
NLDYVATSIHEAVTKIQ	1903.1	2	4.4596	0.418
NLEAIVQEIKPTALIGVAAIGGAFSEQILK	3095.6	3	3.7599	0.268
NLEALALDLMEPEQAVDLTLPK	2424.8	2	5.6848	0.4632
NLEALALDLMEPEQAVDLTLPKVEAMNKR	3253.8	3	6.9256	0.5164
NLEAQHKELEEK	1468.6	2	4.0742	0.3274
NLEAYGLDPYSVAAILQQR	2122.4	2	4.3902	0.3241
NLEEGHSSTVAAHYNELQEVGLEKR	2812.0	3	6.1458	0.4577
NLEFQGPLEISR	1403.6	2	2.8078	0.2091
NLEGANQHVSK	1197.3	2	3.2296	0.2105
NLEGYVGFANLPNQVYR	1955.2	2	5.3837	0.4397
NLEGYVGFANLPNQVYRK	2083.3	2	4.9905	0.4807
NLEISIDTLMAK	1348.6	2	3.4163	0.1021
NLENDVNSLKDQLEDLKKR	2272.5	3	4.8953	0.3855
NLEPEWAAAASEVKEQTK	2002.2	2	4.7088	0.398
NLEPKYKELGEK	1448.6	2	2.633	0.1208
NLEQENQNLR	1258.3	2	3.2322	0.1475
NLEQLGGTVTNPGGSGTSSR	1933.0	2	6.3476	0.5525
NLEVLNFFNNQIEELPTQISSLQK	2820.1	3	6.0277	0.3858
NLEWIAGGTWTPSALK	1745.0	2	4.8046	0.4593
NLFAFFDMAYQGFASGDGDKDAWAVR	2901.2	3	4.893	0.3488
NLFFSTNIDDAIKEADLVFISVNTPTK	3014.4	3	4.3867	0.265
NLFFSTNIDDAIKEADLVFISVNTPTKTYGMGK	3652.1	3	3.8189	0.2754
NLFIGHFHTPK	1311.5	2	3.3916	0.274
NLGDVGEKETETEVLLLEHDVPHQPFSQAVLSFLPK	4018.5	3	4.8594	0.2076
NLGFSPGDREENIR	1604.7	2	3.6041	0.2441
NLGIESQVDVMQQATNAILR	2201.5	3	4.9335	0.2957
NLGIGKVSSFEEK	1408.6	2	3.6453	0.3178

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NLGIGKVSSFEEKMISDAIPELK	2506.9	3	4.103	0.2249
NLGLEELGIELDPR	1568.8	2	4.8503	0.3923
NLGLYVK	807.0	1	1.9405	0.131
NLGMTDAFELGK	1296.5	2	3.2716	0.3257
NLGMTDAFELGKADFSGMSQTDLSLSK	2865.2	3	5.0389	0.3217
NLGSIAK	702.8	1	1.7514	0.1794
NLGSINTELQDVQR	1587.7	2	4.9787	0.5034
NLGSLLKPGGFLVIMDALK	1987.4	3	4.2546	0.3812
NLGTALAELR	1058.2	2	3.5175	0.276
NLGTIAK	716.8	1	2.0186	0.1865
NLHALILVNNK	1249.5	2	3.1328	0.2337
NLHGDGIALWYTR	1516.7	2	3.9161	0.435
NLHHELELGVVMGK	1576.8	2	4.0213	0.3987
NLHIPTMENGPELILR	1848.2	3	4.797	0.3051
NLHQSGFSLSGAQIDDNIPR	2170.3	2	6.4328	0.4562
NLHQSGFSLSGTQVDEGVR	2032.2	2	5.7819	0.5359
NLHQSNFSLSGAQIDDNNPR	2228.3	3	6.6238	0.4528
NLHSEISGK	985.1	2	2.4819	0.1456
NLHTHHFPSPLSNNQEVSAFGEDGEGDDLDLWTVR	3936.1	3	6.4903	0.3705
NLHVVFTMNPSSEGLKDR	2045.3	2	5.2053	0.479
NLHYFNSDSFASHPNYPYSDEY	2668.7	2	4.4238	0.3957
NLIDAGVDALR	1157.3	2	3.2743	0.2113
NLIEQLEQDKGMVIAETKR	2216.5	3	4.5234	0.3051
NLIHGSDSVESAR	1385.5	2	2.8991	0.1106
NLIHGSDSVESARR	1541.7	2	3.1034	0.2957
NLIPFDQMTIEDLNEAFPETK	2466.7	2	5.266	0.4087
NLISPDLGVVFLNVPENLK	2082.4	2	3.6799	0.3979
NLIYDNADNKLALVEENGIFELLR	2778.1	3	4.3837	0.1715
NLKASLENSLR	1245.4	2	2.9926	0.1858
NLKASLENSLREVEAR	1830.0	2	3.4638	0.1708
NLKEDGISAAK	1146.3	2	2.8092	0.1107
NLKEDGISAAKDVK	1488.7	2	4.1157	0.2562
NLKHSVDELQK	1311.5	2	2.9426	0.2023
NLKHSVDELQKR	1467.7	2	3.2254	0.3302
NLKLGIHEDSTNR	1497.6	2	3.5555	0.3697
NLKPIKPMQFLGDEETVR	2116.5	3	4.4921	0.3858

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NLKPIKPMQFLGDEETVRK	2244.6	2	4.8405	0.3792
NLKQNLSELEQLNENLKK	2156.4	3	4.3756	0.2222
NLKVTAVPTLLK	1297.6	2	3.4746	0.1722
NLLDEIASR	1031.1	2	3.3627	0.137
NLLDEIASREQEVQK	1772.9	2	3.4689	0.2223
NLLESYHVPELIKDAHLLVESK	2548.9	3	6.0077	0.4629
NLLGELNPSIPLLPDDILSQIR	2431.8	3	4.7178	0.3015
NLLGELNPSIPLLPDDILSQIRK	2560.0	3	3.3103	0.1626
NLLHQDAVDLFR	1441.6	2	2.4632	0.1993
NLLHSLQSSGIGSK	1441.6	2	3.6403	0.3593
NLLHVTDTGVGMTR	1514.7	2	4.1693	0.3871
NLLHVTDTGVGMTREELVK	2113.4	2	5.22	0.3861
NLLHVTDTGVGMTREELVKNLGTIAK	2811.3	3	4.1802	0.4038
NLLLAEVINIIK	1353.7	2	4.557	0.3002
NLLLSGAQLEASR	1372.6	2	4.7094	0.2573
NLLNSVIGR	986.2	2	3.232	0.3473
NLLPATLQLIDTYASFTR	2038.3	2	4.3442	0.3442
NLLQVDLTKR	1200.4	2	2.5098	0.1345
NLLSEHEQLVVTLEDHK	2005.2	3	5.1329	0.3442
NLLSLGHNNIVR	1350.6	2	3.209	0.3116
NLLSVAYK	908.1	2	2.4654	0.2094
NLLSVAYKNVVGAR	1504.8	2	3.8709	0.3348
NLLSVAYKNVVGGR	1490.7	2	2.7874	0.2058
NLLYIYPQSLNFANR	1827.1	2	4.2861	0.3623
NLLYVADSYNHK	1437.6	2	3.6376	0.2868
NLMIETTEDTIKK	1536.8	2	3.5008	0.2199
NLMLSTSEEMIEKEFNNIKPGAVER	2881.3	3	4.3183	0.2904
NLMNAVVQTVK	1217.5	2	3.677	0.2799
NLMQLNLAHNILR	1550.9	2	2.5104	0.2414
NLMTSEIHNTVK	1387.6	2	3.4901	0.1623
NLNGTLHELLR	1280.5	2	3.6256	0.3101
NLNHVSYGR	1060.1	2	2.6351	0.2567
NLNPHSTMDSILGALAPYAVLSSSNVR	2829.2	3	4.7819	0.366
NLNPIFNESFAFDIPTEK	2097.3	2	5.0269	0.2963
NLNPVFNETLR	1317.5	2	2.5819	0.2231
NLNTSALQLEHEHLIK	1861.1	2	4.0319	0.323

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NLNYLHLDYNFNLKPVK	2106.4	2	4.0081	0.3804
NLPFDLTWQK	1262.4	2	3.25	0.2555
NLPGGQQNSSWNFSEDTVISILNTINEVIAENLEAAKK	4146.5	3	5.9467	0.4968
NLPGLVQEGEPFSEEATLFTK	2307.5	3	6.0951	0.4724
NLPIYSEEIVEMYK	1729.0	2	3.5397	0.4306
NLPLADQGSSHHITVK	1717.9	2	4.1304	0.4156
NLPLPPPPPPR	1195.4	2	2.5475	0.1069
NLPQYVSNELLEEAFSVFGQVER	2669.9	3	5.0714	0.4421
NLPSLAEQGASDPPTVASR	1911.1	2	5.8395	0.3345
NLPYKITAEEMYDIFGK	2033.3	2	4.636	0.3675
NLPYKVTQDELKEVFEDAAEIR	2608.9	3	5.0408	0.3534
NLQEAEEWYK	1310.4	2	3.0721	0.2174
NLQEAEEWYKSK	1525.6	2	3.8813	0.1789
NLQEEIDALESRVESIQR	2130.3	3	3.6732	0.2038
NLQEGQVTDPR	1257.3	2	3.551	0.2825
NLQEIQQAGER	1286.4	2	3.8358	0.1515
NLQEQTVQLQSELSR	1773.9	2	5.1842	0.3512
NLQEVLGEEKLKEILKER	2169.5	2	4.6036	0.3709
NLQGISSFR	1022.1	2	2.7606	0.2713
NLQIPPEDLIEMLK	1654.0	2	3.3658	0.3062
NLQLDYVDLYLIHFPVSVKPGEEVIPK	3127.6	3	5.2416	0.3789
NLQLDYVDLYLIHFPVSVKPGEEVIPKDENGK	3671.2	3	5.513	0.426
NLQLLMDRVDEMSQDIVK	2148.5	3	4.6513	0.3942
NLQNLLILTAIK	1354.7	2	4.558	0.2943
NLQNVDMK	962.1	2	2.7747	0.1945
NLQQQYLQINQEITELHPLKAQLQEYQDKTK	3785.2	3	6.3127	0.4019
NLQSEVEGVKNIMTQNVER	2189.4	2	5.4967	0.4175
NLQTVNVDEN	1146.2	2	3.5789	0.1621
NLQYYDISAK	1215.3	2	2.6219	0.1907
NLRDFLLVYNR	1423.6	2	2.8842	0.1808
NLRDIDEVSSLLR	1530.7	2	4.5501	0.3716
NLRNDLLVAADSITNTMSSLVK	2376.7	3	3.6322	0.3236
NLRPGDSQTAAQAR	1485.6	2	2.9968	0.1768
NLSDLIDLVPSLCEDLLSSVDQPLK	2728.1	2	4.2911	0.3308
NLSDSEKELYIQHAK	1775.9	2	4.7783	0.4192
NLSDSEKELYIQHAKEDETR	2406.5	3	4.1069	0.3047

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NLSDVATKQEGLESVLK	1832.0	2	4.9074	0.428
NLSEIENVHGFVSHSHISPIK	2345.6	2	5.098	0.3929
NLSIYDGPEQR	1292.4	2	2.8586	0.3198
NLSLEELQMR	1233.4	2	2.6182	0.2378
NLSLSGHVGFDSLPDQLVNK	2141.4	2	4.7298	0.4687
NLSPGAVESDVR	1244.3	2	2.5323	0.1762
NLSPGAVESDVRGITGVDLFGTTDAVVK	2819.1	3	4.2555	0.3779
NLSPVVSNELLEQAFSQFGPVEK	2533.8	2	5.581	0.4323
NLSPYVSNELLEEAFSQFGPIER	2640.9	2	5.0533	0.5312
NLSQILSDREEIAHNMQSTLDDATDAWGIK	3373.7	3	5.5595	0.415
NLSQILSDREEIAHNMQSTLDDATDAWGIKVER	3758.1	3	5.1617	0.4116
NLSSASQATR	1035.1	2	3.4453	0.1469
NLSSDEATNPISR	1404.5	2	3.0701	0.1806
NLSSNEAISLEEIR	1575.7	2	3.1904	0.1547
NLSSTTDDEAPR	1306.3	2	3.2549	0.3263
NLSTFAVDGK	1052.2	2	2.6088	0.2315
NLSTVMDEIHTVLK	1600.9	2	3.3999	0.4056
NLSTVMDEIHTVLKK	1729.0	2	4.0683	0.4141
NLSVKVPATTSD	1232.4	2	2.6943	0.2276
NLSYHVHK	998.1	2	2.4382	0.137
NLSYQVHR	1017.1	2	2.6509	0.2613
NLTALGLNLVASGGTAK	1600.8	2	5.6722	0.5038
NLTNPNTVIILIGNK	1624.9	2	4.6865	0.3662
NLTQYSWLLDGFPR	1710.9	2	4.9986	0.4126
NLVDFTFVENVVHGHILAAEQLSR	2710.0	3	4.2119	0.4453
NLVDNITGQR	1130.2	2	2.853	0.2117
NLVEKTPALVNAAVTYSKPR	2172.5	3	4.3273	0.3831
NLVELAELELK	1271.5	2	3.3842	0.1739
NLVELAELELKHAK	1607.9	2	4.5328	0.4287
NLVEQHIQDIVVHYTFNK	2198.5	3	5.3571	0.4358
NLVKEEQEKSEK	1461.6	2	3.2537	0.214
NLVLPGIGSFTIIDGNQVSGEDAGNNFFLQR	3294.6	3	5.5465	0.4742
NLVLTGFSHIDLIDLDTIDVSNLNR	2799.1	3	3.7041	0.2676
NLVTEDVMR	1077.2	1	3.1542	0.3113
NLVTEVLGALEAK	1357.6	2	4.8487	0.3341
NLWPFVSDPAPTASSQAAVSAR	2273.5	2	2.6233	0.1031

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NLYKEGDLTHFNQKLEGFTLPR	2621.9	3	4.2004	0.3444
NMADAMR	809.0	1	2.2488	0.15
NMAEQIIQEIYSQIQSK	2024.3	3	6.427	0.4644
NMAEQIIQEIYSQIQSKK	2152.5	2	5.2472	0.2136
NMDAIIVDSEKTGR	1549.7	2	4.3531	0.3472
NMDPLNDNIATLLHQSSDKFVSELWK	3017.4	3	4.4704	0.4088
NMDPLNDNIATLLHQSSDKFVSELWKDVDR	3502.9	3	4.6722	0.4456
NMGGPYGGGNYGPGGSGGSGGYGGR	2191.2	2	6.3382	0.5863
NMGLYGER	940.1	1	2.238	0.1852
NMGYAAK	754.9	1	2.1697	0.2865
NMIHETNEHTLPK	1564.7	2	3.544	0.3711
NMIREQDLQLEELRQQVSTLK	2572.9	3	4.3794	0.2883
NMKDAKDKLESEMEDAYHEHQANLLR	3117.4	3	5.3799	0.419
NMKELTPLQAMMLR	1677.1	2	2.464	0.2256
NMLFSGTNIAAGK	1324.5	2	4.0654	0.285
NMLFSGTNITSGK	1370.6	2	3.9204	0.3439
NMLQFNLQILPK	1459.8	2	4.7396	0.2818
NMMAACDPR	1009.2	2	2.4572	0.1457
NMNKEDEGEITK	1408.5	2	3.9033	0.2192
NMQDLVEDFKNKYEDEINKR	2529.8	3	3.8334	0.1615
NMQDLVEDLKNKYEDEINKR	2495.8	3	3.9144	0.1951
NMQNVEHVPLSLDR	1652.9	2	4.8914	0.3942
NMSVIAHVDHGK	1308.5	2	3.4405	0.319
NMSYQGFTK	1076.2	2	2.4295	0.1976
NMTVADSGTNHDSR	1505.6	2	4.1117	0.3509
NMTVEQLLTGSPTSPTVEPEKPTR	2613.9	3	4.7694	0.3877
NMVPQQALVIR	1269.5	2	2.4048	0.2094
NMVSILSSFESR	1370.6	2	3.9484	0.4033
NNAASEGVLASFFNSLLSK	1970.2	2	5.766	0.48
NNALNQVVLWDK	1414.6	2	3.0757	0.2552
NNASTDYDLSDK	1343.3	2	3.586	0.3038
NNASTDYDLSDKSINPLGGFVHYGEVTNDFVMLK	3763.1	3	3.7376	0.2921
NNEDISIIPPLFTVSVDHR	2167.4	3	4.3712	0.2097
NNEVDLLFLSELQVLHDISSLLSR	2756.1	2	2.7719	0.3489
NNFAVGYR	941.0	2	2.9861	0.3334
NNFEGEVTKENLLDFIK	2011.2	2	4.867	0.4087

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NNFEGEVTKENLLDFIKHNQLPLVIEFTEQTAPK	3958.4	3	5.55	0.3847
NNFTDFTNVR	1228.3	2	3.1279	0.1705
NNGAGYFLEHLAFK	1581.8	2	4.1985	0.4543
NNGVLFENQLLQIGVK	1787.1	2	4.6086	0.2211
NNGVVDKSLFSNVVTK	1721.9	2	4.107	0.4081
NNHHEENISSK	1309.3	2	2.9589	0.284
NNILTDHFQYSR	1508.6	2	2.9958	0.2108
NNIPYFETSAK	1284.4	2	2.823	0.2134
NNIPYFETSAKEAINVEQAFQTIAR	2856.1	3	4.4919	0.4013
NNKEYLEFR	1213.3	2	2.7151	0.1311
NNKGPVKVVVGK	1239.5	2	3.5523	0.2824
NNLAGAEELFAR	1305.4	2	4.5518	0.3759
NNLAGAEELFARKFNALFAQGNYSEAAK	3046.3	3	3.2401	0.1788
NNLFTSSAGYR	1230.3	2	3.4201	0.3259
NNLNPVWRPFK	1385.6	2	3.3415	0.1539
NNLSFIETSALDSTNVEEAFK	2330.5	2	6.6154	0.5783
NNLSFIETSALDSTNVEEAFKNILTEIYR	3333.6	3	3.9602	0.3165
NNLVIFHR	1013.2	2	2.7203	0.1521
NNMQSGVNNTK	1207.3	2	3.0975	0.1887
NNMQSGVNNTKK	1335.5	2	3.7385	0.243
NNNIDAAIENIENMLTSENK	2248.4	2	5.4667	0.4474
NNNLAVTSK	961.1	2	2.6836	0.1849
NNPVHLITEEDLK	1522.7	2	3.7093	0.3352
NNQITNNQR	1102.1	2	3.0931	0.1447
NNQLLHFAFR	1260.4	2	2.5308	0.1811
NNRFSTPEQAAK	1363.5	2	2.8375	0.2298
NNRPSEGPLQTR	1369.5	2	2.7857	0.2624
NNRQPYAVSELAGHQTSAESWGTGR	2717.9	3	6.8626	0.5392
NNSDKDQSLGNWR	1534.6	2	3.6388	0.2276
NNSLQTATENTQAR	1548.6	2	3.4269	0.2006
NNSNDIVNAIMELTM	1679.9	2	2.901	0.2196
NNTEDKLYNLLLLR	1720.0	2	3.1839	0.3238
NNTVGLIQLNRPK	1467.7	2	3.6023	0.3368
NNTVTPGGKPNK	1227.4	2	2.7109	0.1435
NPAMMQEMMR	1239.5	2	3.4276	0.3959
NPAVLSAASFDGR	1305.4	2	3.9355	0.3586

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NPDDITNEEYGEFYK	1834.9	2	5.5099	0.4618
NPDDITNEEYGEFYKSLTNDWEDHLAVK	3344.5	3	4.4378	0.2672
NPDDITQEEYGEFYK	1848.9	2	5.2246	0.5347
NPDNLEELLLNETALGALAR	2167.4	3	4.8193	0.3084
NPDRVLIGGDETPEGQR	1854.0	3	5.4965	0.35
NPDTQWITKPVHK	1564.8	2	4.0442	0.3614
NPEILAIAPVLLDALTDPSR	2119.4	2	4.8318	0.4016
NPEISHLLNNPDIMR	1764.0	2	4.2307	0.4721
NPEISHMLNNPDIMR	1782.0	2	4.8563	0.4295
NPESRIVVPEIKILVK	1835.2	2	2.7727	0.1049
NPFGNAGLLLGEAGK	1458.6	2	3.7048	0.3874
NPFLAAVTTNR	1204.4	2	3.3632	0.2763
NPGFEIIHGLLDR	1481.7	2	3.7497	0.4103
NPGVFLIHGPDEHR	1588.8	2	3.692	0.3827
NPHNDRFVLSK	1327.5	2	2.6324	0.1261
NPKTDKLVNER	1314.5	2	3.0692	0.2394
NPLGSTHPEATLK	1365.5	2	3.8736	0.439
NPLIAGK	712.9	1	2.3097	0.1455
NPLPSKETIEQEK	1513.7	2	3.6666	0.289
NPLPSKETIEQEKQAGES	1986.1	2	3.7745	0.3641
NPNAMLVNLEEPLASTYQDILYQAK	2837.2	2	4.4726	0.3868
NPNGPYPYTLK	1264.4	2	2.711	0.2398
NPNTSEPQHLLVMK	1608.8	2	3.4835	0.3953
NPPENSDSGTGKK	1331.4	2	2.6261	0.1636
NPPGFAFVEFEDPR	1622.8	2	3.5436	0.2813
NPPGFAFVEFEDPRDAADAVR	2321.5	2	3.714	0.3556
NPPGFAFVEFEDPRDAADAVRELDGR	2892.1	2	3.2615	0.2564
NPPGFAFVEFEDPRDAEDAVR	2379.5	2	3.119	0.1762
NPPLAEALLSGDLEKFSR	1958.2	3	3.3269	0.1996
NPPPAIGQFWHVTDLHLDPTYHITDDHTK	3367.7	3	3.8519	0.1992
NPQNSSQSADGLR	1374.4	2	3.7019	0.3283
NPQSTEPVLGGGEPPFHGHR	2114.3	2	4.7763	0.475
NPSDSAVHSPFTK	1387.5	2	3.1776	0.2878
NPSGLTQYIPVLVDSFLPLLK	2315.7	2	3.2261	0.3041
NPSSAAPVQSR	1114.2	2	3.0609	0.2566
NPSTVEAFDLAQSNSEHSR	2090.2	3	4.0365	0.2922

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NPSVIDKQDKD	1259.3	2	2.8254	0.2006
NPTKDGDDAHEAK	1398.4	2	3.2425	0.2292
NPVHNGHALLMQDTHK	1813.0	2	4.8969	0.5064
NPVHNGHALLMQDTR	1703.9	2	4.9515	0.4707
NPVKFEGGDR	1119.2	2	2.8406	0.1631
NPVKFEGGDRDLEHLSK	1942.1	2	4.2356	0.2991
NPVTIFSLATNEMWR	1780.0	2	5.1253	0.4449
NPVWYQALTHGLNEEQR	2056.2	2	5.1646	0.4
NPWSMDENLMHISYEAGILENPK	2690.0	3	4.7803	0.2292
NPWSMDENLMHISYEAGILENPKNQAPPGLYTK	3760.2	3	5.888	0.4908
NPYYGGESASITPLEDLYK	2118.3	2	5.9469	0.4124
NPYYGGESASITPLEDLYKR	2274.5	3	4.2839	0.4137
NPYYGGESSSITPLEELYK	2148.3	2	6.0635	0.5144
NPYYGGESSSITPLEELYKR	2304.5	2	3.2389	0.1041
NQAAIQGRPPYAASAEEVAK	2072.3	3	3.5422	0.2001
NQAHSVLKK	1025.2	2	2.7869	0.1174
NQALKEAGVFVPR	1429.6	2	3.9967	0.3564
NQALNTDNYGHDLASVQALQR	2329.5	3	5.6119	0.4271
NQALTSLAQEAQALKDEMDELR	2475.7	2	3.5888	0.3666
NQALTSLAQEAQALKDEMDELRQSSER	3063.3	3	3.4406	0.2424
NQASHPTATK	1055.1	2	2.4918	0.2147
NQDEESQEAPELLK	1630.7	2	3.4059	0.1095
NQDHYAVLGLGHVR	1579.7	2	4.1706	0.4515
NQDIHVFR	1029.1	2	2.9	0.1562
NQDLALSNLESIPGGYNALRR	2302.5	3	3.5485	0.2772
NQDLAPNSAEQASILSLVTK	2100.3	3	4.8819	0.4615
NQDNLQGWNK	1217.3	2	2.4538	0.1282
NQEADQHSAR	1156.1	2	2.7424	0.1932
NQELLQSQLTEKDSMIENMK	2380.7	2	5.6884	0.3605
NQEQEKVER	1160.2	2	3.1791	0.1937
NQEQLAAELAEFTAK	1663.8	2	4.7493	0.4346
NQEQLLTLASILR	1499.7	2	4.4926	0.4354
NQEQMKPLEEKQEEER	2046.2	2	5.1093	0.3286
NQFLDELMELEIFLAQR	2110.4	2	3.4859	0.1879
NQGACGSCWTFSTTGALESAIAIATGK	2646.9	3	3.642	0.2095
NQGFDVVLVDTAGR	1491.6	2	3.8482	0.2015

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NQGGGLSSSGAGEGQGPK	1588.6	2	4.7207	0.333
NQGGYGGSSSSSSYGSGR	1695.6	2	4.9803	0.5776
NQGIEEALKNR	1272.4	2	2.7038	0.2165
NQHFEVPFIAFYR	1668.9	2	2.8124	0.1165
NQHLVSQQKDPDTEEYRK	2216.4	2	5.6905	0.4639
NQHTLSQPLTDEHLQALFR	2249.5	3	5.3689	0.5071
NQIYIQLSEVDKTKEELTEHIK	2660.0	3	4.4532	0.4432
NQKDDVAQTDLLQIDPNFGSK	2347.5	3	3.5696	0.1293
NQKDDVAQTDLLQIDPNFGSKEDFDSLLQSAK	3581.8	3	5.7131	0.4182
NQKHPESIQGSK	1353.5	2	2.5403	0.2055
NQKVVEEAPSIFLDAETRR	2203.4	2	3.3443	0.1948
NQLDQEVEFLSTSIAQLK	2064.3	2	5.4584	0.5063
NQLHDEVHQWR	1462.6	2	3.6031	0.2227
NQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGK	3583.0	3	5.9982	0.5298
NQLLQKEPDLR	1354.5	2	3.3752	0.2391
NQLLQKEPDLRLENVQK	2066.3	3	4.148	0.2678
NQLLQKEPDLRLENVQKFPSPEMIR	3024.5	3	5.9277	0.4068
NQLNPIGSLQELAIHHGWR	2184.4	2	5.2157	0.4865
NQLTAMSSVLAK	1263.5	2	3.3904	0.2346
NQLTSNPENTVFDAK	1678.8	2	4.6592	0.4166
NQLTSNPENTVFDAKR	1835.0	2	4.4575	0.3971
NQLYESYYLNFISAISR	2082.3	2	2.8176	0.2434
NQNDPLPGR	1011.1	2	2.4684	0.1517
NQNKNKENQELK	1487.6	2	2.438	0.1469
NQNKPFSVPHTK	1397.6	2	3.4332	0.2726
NQQITHANNTVSNFKR	1873.0	3	4.8137	0.4278
NQSESHKQAQENLHDQVQEQK	2506.6	3	3.6875	0.1007
NQSFCPTVNLDKLWTLVSEQTR	2580.9	3	4.0412	0.3824
NQSPVLEPVGR	1196.3	2	2.8213	0.1311
NQSQGYNQWQQGQFWGQKPWSQHYHQGYY	3660.8	3	3.6401	0.2339
NQVALNPQNTVFDAK	1659.8	2	5.3814	0.4195
NQVALNPQNTVFDAKR	1816.0	2	4.5184	0.3984
NQVAMNPTNTIFDAK	1664.9	2	3.5588	0.281
NQVAMNPTNTVFDAK	1650.8	2	5.263	0.486
NQVAMNPTNTVFDAKR	1807.0	2	4.3741	0.4006
NQVEDLLATLEK	1373.5	2	3.8074	0.2629

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NQVTATKADGGTQVIDTK	1848.0	2	5.4324	0.4845
NQWQLSADDLKK	1446.6	2	4.0018	0.2481
NQYDNDVTVWSPQGR	1779.8	2	4.47	0.3723
NQYVPYPHAPGSQR	1614.7	2	3.2432	0.2716
NRAEQWNVNYVETSAK	1910.0	2	3.8834	0.2899
NRAETAAQR	1017.1	2	2.7116	0.2457
NRDASTLQSQK	1248.3	2	2.7835	0.3117
NRDASTLQSQKAEGTGDAK	1978.1	3	3.812	0.349
NRDHDTFLAVR	1344.5	2	3.0945	0.4052
NRDSDKTDTDWR	1509.5	2	3.5052	0.319
NREEDPSLLWQVFGSATGLAR	2347.6	3	3.2821	0.138
NREEEIEQLNEVIEKLQQELANIGQK	3096.4	3	7.1572	0.3251
NREEEWDPEYTPK	1693.8	2	3.7129	0.229
NREELDKYWSQQIEESTTVVTTQSAEVGAAETTLTELRR	4471.8	3	4.5685	0.2411
NREELGFRPEYSASQLK	2025.2	2	3.4782	0.1993
NRELAILLGMLDPAEKDEK	2156.5	3	5.5102	0.3964
NREPLMPSPQFIK	1557.8	2	3.7661	0.3548
NREPVQLETLSIR	1555.8	2	4.1724	0.3899
NRESYEVSLTQK	1454.6	2	3.6182	0.1584
NRETASELLMR	1320.5	2	2.7947	0.1646
NRFSLVPHNYGLVLYENK	2164.5	3	4.3343	0.3995
NRGPPPSWGR	1124.2	2	2.5392	0.1472
NRHEIAVMLLEGGANPDAK	2036.3	2	4.9003	0.4908
NRHGLVPFAFVR	1413.7	2	2.4968	0.2834
NRHPDFLPYDHAR	1638.8	3	3.5843	0.3128
NRHPNFLVVEK	1353.6	3	3.2248	0.133
NRLDYHISVQNMMR	1778.1	2	3.6543	0.3741
NRLENDGATALAEAFR	1748.9	2	3.9742	0.335
NRLPGSQLAVLHIR	1574.9	3	5.0054	0.2845
NRLQQELDDLTVDLDHQR	2209.4	3	7.1433	0.3651
NRNELAETLALLK	1485.7	2	3.6241	0.2236
NRNEQESAVHPR	1437.5	2	4.4234	0.3672
NRNFYELSPHIFALSDEAYR	2443.7	3	4.4328	0.3439
NRNHLLHVFDEYKR	1842.1	3	3.2958	0.1179
NRPEDYQGGR	1192.2	2	3.0551	0.281
NRPEDYQGGRTGEAIVDAALSALR	2560.8	3	3.7084	0.3369

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NRPGSALEKEVESMGAHLNAYSTR	2618.9	3	7.4732	0.4348
NRPLSDEELDAMFPEGYK	2112.3	2	3.6644	0.37
NRPLSDEELDAMFPEGYKVLPPPAGYVPIR	3372.8	3	5.6294	0.3394
NRPNRLIVDEAINEDNSVVSLSQPK	2809.1	3	3.5593	0.2294
NRPPLPAGTNSK	1252.4	2	3.2435	0.3711
NRPSSGSLIQVVTTEGR	1802.0	2	5.2807	0.4854
NRPSVPPPPQPPGVHSAGDSSLTNTAPTASK	3066.3	3	5.6142	0.4076
NRPTSISWDGLDSGK	1633.7	2	4.1757	0.3054
NRPTSISWDGLDSGKLYTLVLTDPDAPSR	3176.5	3	5.9584	0.4815
NRQEVPAFTEPDTTAEVKTPFDLAK	2806.1	3	5.23	0.3994
NRQEYEDIAVK	1365.5	2	2.7331	0.1854
NRSAEEGELAESK	1420.5	2	3.6411	0.2675
NRSNTPILVDGKDVMPEVNK	2227.5	3	3.8277	0.3553
NRSSAVDPEPQVKLEDVLPLAFTR	2683.0	3	4.5563	0.3482
NRTPSDVKELVLDNSR	1844.0	2	3.9727	0.338
NRVPSAGDVEK	1172.3	2	3.0395	0.2308
NRVQNMALYADVGGK	1636.9	2	3.8244	0.2904
NSAQIANLVSEDEAAFLASLER	2349.5	3	5.6171	0.4485
NSCAADDKATEPLPK	1560.7	2	3.6955	0.372
NSCAADDKATEPLPKDCPVSSYNEWDPLEEVIVGR	3850.2	3	5.1439	0.2836
NSDEADLVPAKEANVK	1700.8	2	4.0525	0.2345
NSDIEQSSDSK	1210.2	2	2.5337	0.1985
NSDIEQSSDSKVK	1437.5	2	3.9778	0.2296
NSDLLLLVDTHKK	1496.7	2	4.476	0.3592
NSDMHLLDLESMGK	1590.8	2	3.5369	0.2759
NSDPALGLDDDPDAPAAQLAR	2123.2	2	6.2571	0.5065
NSDRTPLVSVLLEGPPHSGK	2104.4	2	5.264	0.3575
NSDSILEAIQK	1218.3	2	3.8677	0.2792
NSDSLPHR	926.0	2	2.6811	0.1991
NSDVLQSPLDSAARDEL	1830.9	2	3.9137	0.2336
NSEGLHSAR	971.0	2	2.9701	0.299
NSEGWEQNGLYEFFR	1877.0	2	2.5413	0.1473
NSELFDPFDLFDVR	1714.9	2	3.7561	0.3351
NSEPQDEGELFQGVDPR	1918.0	3	4.5664	0.3429
NSETFPTILEEAKELVGR	2034.3	2	3.6229	0.2468
NSEVYQEVQAMFDTLGIPK	2170.4	2	4.9823	0.3538

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NSFGLAPAAPLQVHAPLSPNQTVEISLPLSTVGSVMK	3773.4	3	4.6109	0.3768
NSFGVIPSTPLAIHTPLMPNQSIDVSLPLNTLGPVMK	3901.6	3	5.4431	0.4144
NSFHLLR	887.0	2	2.4576	0.1461
NSFREQLEEEEEAKHNLEK	2360.5	3	4.7969	0.2851
NSFWIHQVTCLGTEPHMANCQVQVAPAR	3139.6	3	3.9442	0.2946
NSGALEKENQMR	1377.5	2	3.4202	0.3294
NSGMPPGAAAIAVLPVTLDTPMNR	2394.8	2	5.9614	0.5344
NSGMPPGAAAIAVLPVTLDTPMNRK	2523.0	2	3.5882	0.3953
NSHLINVLMWELEK	1727.0	2	3.2377	0.2401
NSHNLNQQQR	1239.3	2	3.0701	0.1299
NSHSLYLAGIFR	1378.6	2	3.3642	0.3892
NSILAQVLDQSAR	1415.6	2	4.9397	0.3281
NSILNPINSIR	1241.4	2	2.6168	0.1891
NSILTETLHR	1184.3	2	3.2829	0.2449
NSKNQGIEEALKNR	1601.7	2	3.3049	0.1849
NSKQQLSAEELDAQLDAYNAR	2365.5	3	5.0047	0.3151
NSLDDSAKK	978.0	2	3.1882	0.2367
NSLESYAFNMK	1304.5	2	3.3821	0.2479
NSLFGSVETWPWQVLSK	1979.2	2	4.7606	0.4274
NSLFTGDTLGAGQFSFQRPLLVLVDR	2853.2	3	5.3059	0.4406
NSLHLLMETLNATTPHYVR	2211.5	2	2.6319	0.1017
NSLISSLEEEVSILNR	1804.0	2	4.9904	0.3525
NSLISYLEQIHR	1473.7	2	3.9042	0.3041
NSLKDLPDVQELITQVR	1969.2	3	4.2051	0.2255
NSLKEANHDGDFGITLAELR	2201.4	3	4.3693	0.377
NSLKELWLVIHGR	1565.8	3	4.743	0.4067
NSLLASYIHYVFR	1583.8	2	3.3154	0.179
NSLLHGYR	960.1	2	2.5908	0.2481
NSLLNGSWGSEEK	1421.5	2	4.0033	0.3416
NSLSPVQATQKPLVSK	1698.0	2	3.6304	0.3246
NSLSPVQATQKPLVSKK	1826.1	2	4.0582	0.2828
NSLTSKDPDIKAQYQQR	1993.2	3	3.4581	0.1114
NSLYDMAR	970.1	2	2.5575	0.3364
NSMFHNR	906.0	2	2.6544	0.1987
NSMIALVDNLASK	1376.6	2	3.1228	0.2279
NSMIALVDNLASKEPYYVR	2184.5	3	5.3294	0.4935

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NSMPASSFQQQK	1353.5	2	2.604	0.1812
NSMSETVR	924.0	1	2.7667	0.2844
NSNILEDLETLR	1417.5	2	4.1467	0.3127
NSNLDRHNLQDFINIK	1942.1	2	3.3882	0.1437
NSNLVGAAHEELQQSR	1753.9	2	5.3509	0.4919
NSNPALNDNLEK	1329.4	2	4.0138	0.3247
NSNPALNDNLEKGLLK	1740.9	2	4.3488	0.2008
NSPGSQVASNPR	1214.3	2	3.5186	0.3432
NSPLNKAEVHESYK	1616.8	2	3.6667	0.373
NSPLVSR	772.9	1	2.1705	0.1662
NSPVEAVFSYLTGK	1512.7	2	2.7315	0.2526
NSQEDSEDSEDKDVK	1725.7	2	4.0328	0.3335
NSQGEEVAQR	1118.1	2	2.5593	0.1573
NSQGSEMFGDDDKRK	1714.8	2	2.939	0.1594
NSQLEQENNLLK	1430.5	2	3.7433	0.1799
NSQSFFSGLFGGSSK	1550.7	2	4.5292	0.4966
NSRPEANEALER	1386.5	2	3.3714	0.2745
NSSAVEQDHAK	1186.2	2	3.0756	0.2436
NSSEQELR	963.0	2	2.8103	0.1644
NSSHAGAFVIVTEEAIAK	1845.0	2	2.7409	0.33
NSSLAEFVQSLSQTMGFPQDQIR	2584.8	3	4.8462	0.3142
NSSNKPAVTTK	1147.3	2	2.7524	0.1966
NSSQFFQSYVER	1492.6	2	3.6638	0.3244
NSSVNEGSTYHK	1323.4	2	3.0221	0.2251
NSSYFVEWIPNNVK	1697.9	2	4.5773	0.4196
NSSYVHGGLDSNGKPADAVYGQK	2365.5	3	5.0172	0.4485
NSSYVHGGVDASGKPQEAVYGQNDIHHK	2996.2	3	5.4188	0.3818
NSTFAEEFAHSIR	1509.6	2	2.754	0.3276
NSTFSEIFKK	1201.4	2	2.5294	0.2846
NSTIVFPLPIDMLQGIIGAK	2128.6	2	3.3398	0.2381
NSTPSEPGSGR	1089.1	2	2.4395	0.1052
NSTSSQSQTSTASR	1442.4	2	3.4954	0.4037
NSVLMSGFSHK	1207.4	2	2.6731	0.1321
NSVSNFLHSLER	1403.5	2	2.6854	0.1059
NSVSQISVLSGGK	1276.4	2	3.5686	0.3697
NSVTPDMMEEMYK	1575.8	2	3.1708	0.1938

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NSVTPDMMEEMYKK	1704.0	2	3.0198	0.2337
NSVVEASEAAYK	1268.4	2	3.3514	0.3732
NSVVEASEAAYKEAFEISK	2073.2	2	5.7721	0.5345
NSVVEASEAAYKEAFEISKEQMQPTHPIR	3291.6	3	4.9479	0.3702
NSWGHNFGEEGYIR	1666.7	2	2.5083	0.1186
NSYLEVLLK	1079.3	2	2.9466	0.3438
NSYVAGQYDDAASYQR	1808.8	2	5.0338	0.4613
NTAELQPESGKR	1330.4	2	3.6146	0.2933
NTAKLDRETEELHHDRVTLEVGK	2691.9	3	4.1242	0.2592
NTDEMVELR	1107.2	2	3.5107	0.2218
NTDKNGEELHGGKR	1555.6	2	3.2313	0.277
NTDQASMPDNTAAQK	1592.7	2	5.2914	0.4233
NTDQASMPDNTAAQKVSHLLGINVTDFTR	3146.4	3	5.6965	0.5525
NTDQASMPENTVAQK	1634.8	2	4.0162	0.3196
NTDQATMPDNTAAQK	1606.7	2	3.9644	0.3721
NTDVAQSPEAPK	1257.3	2	3.546	0.2444
NTDVAQSPEAPKQEAPAK	1882.0	2	4.7702	0.4216
NTDVAQSPEAPKQEAPAKK	2010.2	3	4.4166	0.3572
NTDVVATLKK	1089.3	2	2.7157	0.1015
NTDYTELHQQNTDLIYQTGPK	2480.6	3	3.3336	0.2304
NTEAVDLITRLPK	1470.7	2	3.2715	0.1794
NTEDLTEEWLR	1406.5	2	2.904	0.1622
NTEIGFLQDALSKPHGTVK	2056.3	2	3.082	0.2983
NTEKENATVAHLVGALR	1824.0	3	4.1459	0.3327
NTETEESLVKR	1306.4	2	3.0296	0.2971
NTETEQRAPK	1174.2	2	2.663	0.1938
NTEYFNQLKDNSNIILLGDSQGDLR	2869.1	3	4.8046	0.3452
NTFAEVTGLSPGVTYYFK	1995.2	2	4.3242	0.4254
NTGHKIETDLPQIR	1622.8	2	4.145	0.3627
NTGIICTIGPASR	1303.5	2	4.4707	0.3993
NTGTEAPDYLATVDVDPK	1907.0	2	5.3579	0.3959
NTGVISVVTTGLDR	1432.6	2	3.3899	0.3926
NTHATTHNAYDLEVIDIFK	2203.4	2	4.7615	0.4068
NTHATTHNAYDLEVIDIFKIER	2601.9	3	3.278	0.2365
NTHTLLLAGVFR	1342.6	2	3.3438	0.3904
NTIEETGNLAEQAR	1546.6	2	3.1952	0.3513

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NTIQWLENELNR	1530.7	2	4.0761	0.3272
NTIVTSYNR	1068.2	2	2.6909	0.1412
NTKEPPLSLTIHLTSPVVR	2103.5	2	2.9842	0.1222
NTKGGDAPAAGEDA	1274.3	2	3.927	0.3462
NTKIEVLEEELR	1473.7	2	3.5203	0.2887
NTKKEGDLIAAQAR	1515.7	2	4.1977	0.3903
NTKLDDLFLK	1207.4	2	3.072	0.1084
NTKLDDLFLKR	1363.6	3	3.5313	0.2742
NTLFGTFHVAHSSSLDDVDHK	2328.5	3	4.0611	0.3272
NTLFGTFHVAHSSSLDDVDHKILTAK	2855.2	3	3.3006	0.1086
NTLIQFEDFGNHNAFR	1924.1	2	3.316	0.2178
NTLLIAGLQAR	1170.4	2	4.3526	0.2936
NTLNIDKLKIETAQELKNAEIALR	2740.1	3	5.4924	0.4104
NTLPTKETIEQEK	1531.7	2	3.5229	0.1915
NTLPTKETIEQEKR	1687.9	3	3.7703	0.3009
NTLPTKETIEQEKRSEIS	2104.3	3	4.0824	0.3123
NTLSLVNDFIIR	1405.6	2	2.5594	0.2477
NTMSLLAANNLLAGLR	1673.0	2	3.4051	0.2029
NTMSLLAANNLLAGLRGEPMPSELKL	2755.3	3	4.0181	0.1375
NTNGSQFFITTVPTPHLDGKHVVFGQVIK	3183.6	3	5.4629	0.333
NTNSVPETAPAAIPETR	1768.9	3	3.4022	0.2482
NTNSVPETAPAAIPETRR	1925.1	2	2.461	0.2369
NTPFLYDLVMTHALEWPSLTAQWLPDVTRPEGK	3828.3	3	4.6209	0.3972
NTQIDNSWGSEER	1536.5	2	3.7836	0.3579
NTQIIIQEESGIPK	1570.8	2	4.7157	0.368
NTQSNEDLKQEK	1434.5	2	3.407	0.2018
NTSDVISAAK	1006.1	2	2.4639	0.114
NTSQTAAITTK	1136.2	2	2.6066	0.2971
NTTHGSDSVVSASR	1418.5	2	3.4997	0.2331
NTTIPTKQTQTFTTYSDNQPGVLIQVYEGER	3531.8	3	3.8034	0.2925
NTVEIFKFEEAENSLLHLK	2262.5	3	5.747	0.4269
NTVETEREESK	1322.4	2	3.4016	0.1393
NTVHDQEHIMEHLEGVINKPEAEMSPQELQLHYFK	4173.6	3	5.0284	0.2685
NTVSQSISGDPEIDKK	1718.8	2	3.9589	0.1507
NTVTLLEEALDQDRTALQK	2159.4	2	3.7598	0.2333
NTVVATGGYGR	1095.2	2	3.0572	0.3267

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NTVVLFVPQQEAWVVER	2015.3	2	4.7864	0.386
NTVVPTK	758.9	1	2.5492	0.2257
NTYYASIAK	1031.1	1	1.8187	0.112
NVALEKVEELEEHVSHLTEK	2334.6	3	3.2253	0.2172
NVALLSQLYHSPAR	1569.8	2	4.3343	0.4081
NVDGFSPKPVTLLASLFK	1934.3	3	4.3737	0.4908
NVDGVNYASITR	1309.4	2	3.9617	0.3844
NVDKDPAKEDVEK	1487.6	2	3.8345	0.245
NVDKDPAKEDVEKAK	1686.8	3	3.6684	0.2788
NVDLLSDMVQEHDEPILK	2096.3	2	5.4055	0.4407
NVDLSTFYQNR	1357.5	2	3.8136	0.3658
NVDMLSELVQEYDEPILK	2136.4	2	6.0496	0.4916
NVDMLSELVQEYDEPILKHLQDIK	2871.3	3	3.359	0.1039
NVDSNLANLIMNEIVDNGTAVKFDDIAGQDLAK	3519.9	3	4.3937	0.2238
NVDTNQDRLVTLEEFLASTQRK	2578.8	3	3.9852	0.1477
NVDVEFFKR	1154.3	2	2.9128	0.2021
NVDVNVKDEEGRALLHWACDRGHKELVTVLLQHR	3952.5	3	3.386	0.1113
NVDVYDKR	1009.1	2	2.5575	0.1511
NVDYLLIHGTADDNVHFQNSAQIAK	2785.0	3	6.2146	0.5001
NVEAMNFADIER	1409.6	2	4.3527	0.4419
NVEELVIVLKK	1284.6	2	3.1344	0.2417
NVEGQDMLYQSLK	1525.7	2	3.4632	0.3315
NVEPFTSVLSLPYPFASEINK	2353.7	2	5.3366	0.4387
NVESFASMLR	1154.3	2	2.9912	0.3724
NVESYTK	840.9	1	2.1359	0.1261
NVFDEAILAALEPPEPK	1854.1	3	4.8511	0.3536
NVFDEAILAALEPPEPKK	1982.3	2	4.591	0.4039
NVFIAQNVASLQELGGSEK	2005.2	2	2.689	0.1977
NVFIIGATNRPDIIDPAILRPGR	2519.9	3	5.1039	0.4317
NVGHNIYILAHQLAR	1720.0	2	4.154	0.1189
NVGQFSGFPFEK	1357.5	2	3.4628	0.3162
NVHGINFVSPVR	1339.5	2	3.3644	0.3991
NVHMNDNVLHSAFEVGAR	2011.2	3	5.3438	0.5188
NVIAETIKGQTGAILQDTVESLSK	2516.8	3	5.6994	0.4197
NVIFQPVAELK	1258.5	2	2.9875	0.229
NVIFQPVAELKK	1386.7	2	3.04	0.2218

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NVIGLQMGTNR	1203.4	2	3.7248	0.3395
NVIIGPA	683.8	1	1.9154	0.1153
NVIIWGNHSSTQYPDVNHAK	2281.5	2	5.9464	0.4492
NVIKEKYGKDATNVGDEGGFAPNILENKEGLELLK	3805.2	3	7.6612	0.514
NVINTFTQTAHSGR	1546.7	2	4.2176	0.4449
NVIPALELVEPIKK	1563.9	2	2.9876	0.3031
NVIQHLEMELNR	1496.7	2	3.7175	0.4752
NVIQISNDLENLR	1528.7	2	4.2787	0.4272
NVKESAAHDYTLR	1504.6	2	3.3083	0.466
NVKEVLEDFAEDGEK	1722.8	2	3.0933	0.2659
NVKGPVR	769.9	1	1.8374	0.1729
NVKGPVREGDVLTLLESER	2112.4	3	4.3169	0.3187
NVKGPVREGDVLTLLESEREAR	2468.8	3	3.488	0.3879
NVKLNEDKPKETK	1543.7	2	3.602	0.1158
NVKLNEDKPKETKSEETLDEGPPKYTK	3119.4	3	4.6057	0.385
NVKYELQQLEGSSDRILELDQELIKAER	3318.7	3	3.5085	0.1672
NVLAPYAVPSELVLVEEIPR	2209.6	2	4.3371	0.3129
NVLDSSSDFPSSGEGATFTQSHHHLPSR	2999.1	3	3.8664	0.2128
NVLGHMQQGGAPSPFDR	1812.0	3	3.5118	0.19
NVLINKDIR	1085.3	2	2.8726	0.1748
NVLITDFFGSVR	1368.6	2	3.0948	0.2134
NVLIVEDIIDTGK	1429.6	2	4.2125	0.3387
NVLIVEDIIDTGKTMQTLLSLVR	2573.0	3	6.9781	0.5159
NVLLDPQLVPGGGASEMAVAHALTEK	2619.0	2	4.7874	0.4201
NVLLLGEDGAGKTSLIR	1757.0	2	3.8123	0.3664
NVLSDSRPAMAPGSSHLGAPASTTTAADATPSGSLAR	3524.8	3	6.756	0.4553
NVLSLTNKGEVFNELVGK	1962.2	2	5.4692	0.4556
NVLTAILLLLR	1239.6	2	2.6264	0.1825
NVLTESAR	890.0	1	2.3884	0.1721
NVLVGEHNIYK	1286.5	2	2.8965	0.3188
NVMEEGKDFQPSR	1537.7	2	4.007	0.3403
NVMILTNPVAAK	1271.6	2	3.4	0.2697
NVMLLPVGSADDGAHSQNEK	2083.3	2	5.401	0.414
NVMLLPVGSADDGAHSQNEKLNRYNYIEGTK	3435.8	3	3.4999	0.1985
NVMSAFGLTDDQVSGPPSAPAEDR	2462.6	3	4.1597	0.212
NVNAGGHK	796.9	1	1.7991	0.1085

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NVNAGGHKLGLGLEFQA	1725.9	2	4.2209	0.4505
NVNIFKFIIPNVVK	1646.0	2	4.2734	0.348
NVNIQNFHISWK	1500.7	2	3.6132	0.338
NVNNEVHFFENNNFNTIANK	2380.5	3	4.0542	0.3065
NVNNEVHFFENNNFNTIANKLHLQK	3000.3	3	4.7523	0.3547
NVNQSLLELHK	1295.5	2	3.7604	0.2694
NVNTALNTTQIPSSIEDIFNDDR	2578.7	3	4.2842	0.3348
NVNVQNFHISWK	1486.7	2	3.9535	0.3579
NVPVITGSK	915.1	1	2.3079	0.2706
NVPVITGSKDLQNVNITLR	2082.4	2	6.0173	0.5151
NVPVITGSKDLQNVNLTLR	2082.4	2	6.3138	0.5403
NVQAEEMVEFSSGLK	1668.9	2	5.3989	0.4369
NVQDIKNVVLQTLEGHLR	2077.4	3	5.4983	0.366
NVQFVFDAVTDVIIK	1709.0	2	2.9751	0.1423
NVQGIIEILK	1127.4	2	3.2489	0.2209
NVQGILEVSK	1087.3	2	3.0715	0.1725
NVQLQENEIR	1243.4	2	2.8621	0.1065
NVQLSLLTER	1173.3	2	2.7965	0.1743
NVRPDYLK	1005.2	2	2.7218	0.1023
NVSAEQKDENKEAKPR	1844.0	2	3.0438	0.256
NVSEELDRTPPEVSK	1700.8	2	4.1766	0.3483
NVSIGIVGK	887.1	2	2.4055	0.1607
NVSNDPDVIKLQEIPTFQPLLK	2509.9	3	3.9235	0.159
NVSNLKPVPLIGPK	1476.8	2	3.2959	0.2309
NVSSYEK	826.9	1	1.901	0.1519
NVTAIQGPGGK	1042.2	2	3.3059	0.3381
NVTELNEPLSNEER	1644.7	2	4.9743	0.4303
NVTELNEPLSNEERNLLSVAYK	2533.8	2	3.2911	0.116
NVTELNEPLSNEERNLLSVAYKNVVGAR	3130.5	3	5.6694	0.3901
NVTGHYISPFHDIPLK	1839.1	2	4.4482	0.3831
NVTGHYISPFHDIPLKVNSK	2267.6	2	4.8381	0.3566
NVTGHYISPFHDIPLKVNSKEENGIPMKK	3294.8	3	4.0672	0.1595
NVTHIDQALQEAHR	1632.8	2	3.8371	0.3722
NVTKDHIMEIFSTYGK	1884.1	2	5.1199	0.4734
NVTLPAVFKAPIRPDIVNFVHTNLR	2833.3	3	3.5171	0.289
NVTLPAVFKAPIRPDIVNFVHTNLRK	2961.5	3	3.8705	0.3806

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NVTMETE	823.9	1	2.1038	0.1498
NVTVQPDDPISFMQLTAK	2005.3	2	3.5474	0.3692
NVVEELLSGNPHIEKESAR	2122.3	2	2.7036	0.2542
NVVGAR	615.7	1	2.0384	0.1202
NVVGGR	601.7	1	1.9094	0.1173
NVVHQLSVTLEDLYNGATR	2130.3	2	4.2528	0.5416
NVVLPTETEVAPAKDVTLLK	2138.5	2	4.5482	0.3115
NVVLPTETEVAPAKDVTLLKETER	2654.0	2	4.3503	0.472
NVVLQTLEGHLR	1379.6	2	3.4048	0.2925
NVVVVDGVR	957.1	1	2.8521	0.1986
NVVVVDGVRTPFLLSGTSYKDLMPHDLAR	3201.7	3	5.7157	0.4566
NWASGHDLQGK	1213.3	2	2.8116	0.1652
NWDKLVGEIKEEEKNEKLEGDAALNR	3029.3	3	5.1642	0.1936
NWRDPDQTDGLGLSYLSSHIANVER	2845.0	3	7.2632	0.4885
NYAEAK	695.7	1	2.0365	0.1735
NYAGAYREWLEKES	1716.8	2	3.6224	0.4011
NYDESGSPR	1025.0	2	2.6159	0.2407
NYDIGAALDTIQYSK	1672.8	2	3.6915	0.2916
NYDIGAALDTIQYSKHPPPL	2214.5	2	3.2959	0.284
NYDVMKDFEEMR	1577.8	2	4.1245	0.4313
NYDVMKDFEEMRK	1705.9	2	4.2021	0.3539
NYEASVDSLTFSVVTGPAPSQEAGTK	2656.8	3	6.1734	0.5151
NYEEIAKVEK	1223.4	2	3.1772	0.2241
NYEEIAKVEKLKPLEVELR	2301.7	2	4.2889	0.3548
NYEFPHLQNFIK	1550.7	2	3.3485	0.1831
NYEFPHLQNFIKEGVLVEHVK	2541.9	3	3.5792	0.2342
NYFENTDILIYVIDSADR	2162.3	2	3.7663	0.3922
NYGILADATEQVGQHK	1744.9	2	3.0165	0.28
NYGILADATEQVGQHKDAYQVILDGVK	2947.2	3	4.3243	0.2633
NYGILADATEQVGQHKDAYQVILDGVKGGTK	3290.6	3	4.0974	0.3403
NYGSYSTQASAAAATAELLKKQEELNR	2916.1	3	4.1066	0.2095
NYHATTEFLDISQLSFIHDLGPK	2647.9	3	3.2011	0.1682
NYIALDDFVEITKK	1669.9	2	2.9703	0.2045
NYIEMKPHPWFFGK	1795.1	2	4.4158	0.3663
NYILDQTNVYGSAQR	1742.9	2	5.1357	0.5154
NYILSASASALWNDEVDKAEQELR	2723.9	3	4.8077	0.3937

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NYIMDFQVGKEFEEDLTGIDDR	2635.8	3	4.012	0.2616
NYIMDFQVGKEFEEDLTGIDDRK	2764.0	3	5.5767	0.5259
NYIQGINLVQAK	1361.6	2	3.9915	0.3352
NYISQYSEIAIQMMMHMQPK	2444.9	2	4.6429	0.4468
NYIVEDGDIIFFK	1573.8	2	4.674	0.3753
NYKLVAAPLFELYDNAPGYGPIISSLPQLLSR	3522.0	3	4.7968	0.3427
NYKPVVQTTGNAR	1448.6	2	3.087	0.1638
NYKSEEEFIHINNK	1765.9	3	4.5705	0.3395
NYKSEEEFIHINNKLR	2035.2	2	2.9951	0.2483
NYLDWLTSIPWGK	1593.8	2	3.9817	0.2196
NYLGGFALSVAHGR	1462.6	2	3.4764	0.3845
NYLHYSLYDQAEK	1644.8	2	4.1833	0.3179
NYLHYSLYDQAEKLVSK	2072.3	3	4.0525	0.3581
NYLLSLPHK	1085.3	2	2.4355	0.1703
NYLNQHIEHVQK	1523.7	2	2.7935	0.2432
NYLNYGEEGAPGK	1412.5	2	3.9246	0.4275
NYLNYGEEGAPGKWQQQGDLQDTK	2740.9	3	4.2256	0.4387
NYLNYGEEGAPGKWQQQGDLQDTKENR	3140.3	3	5.789	0.4761
NYLNYGEEGAPGKWQQQGDLQDTKENREEAR	3625.8	3	4.185	0.2646
NYMSNPSYNYEIVNR	1865.0	2	5.7605	0.4759
NYNKAVEEEDKMTPEQLAIK	2351.6	2	4.6743	0.2444
NYPATFWVNPQFK	1612.8	2	4.2502	0.4083
NYPEGHKAAAVLPVLDLAQR	2163.5	2	3.9938	0.2957
NYPNTFWMNPQYLIK	1930.2	2	3.3685	0.2758
NYQFDFLRPQHSLFNYFTK	2466.7	3	3.2797	0.2331
NYQQNYQNSESGEKNEGSESAPEGQAQQR	3259.2	3	5.9584	0.459
NYRQLVDTTVELANKVGAAEIISR	2662.0	3	3.4085	0.1386
NYSEGLTMHTHIVSTSNFSETSAFMPVLK	3230.6	3	5.2346	0.3227
NYSVGSRPLKPLSPLR	1785.1	3	3.4206	0.3683
NYSVVFPHDEPLAGR	1701.9	2	2.4122	0.3026
NYTDEAIETDDLTIK	1741.8	2	5.5538	0.4143
NYTDFVHEHNVK	1503.6	2	4.0801	0.4
NYTDNELEKITR	1496.6	2	3.544	0.3179
NYTSVYDKNNLLTNK	1788.0	2	4.2423	0.4723
NYVEDIPFLSPTFNPQEVFIR	2526.8	3	4.7243	0.3967
NYVEELNRHLNATVNNLQAK	2341.6	3	4.4903	0.3202

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
NYVHFAATQVQNR	1548.7	2	2.9177	0.3223
NYYEQWGK	1088.2	1	2.5786	0.2203
PAAPPAPGPGQLTLR	1443.7	2	3.4955	0.2667
PAKYDDLKK	1078.2	2	2.6453	0.2081
PALGARLAECLLLAGDAAGAR	2010.4	2	2.536	0.1351
PANKQEDEVMR	1317.5	2	3.646	0.3378
PANPDEIGNFIDENLK	1786.9	2	3.7129	0.3935
PAPAVGEAEDKENQQATSGPNQPSVR	2678.8	3	5.7943	0.4576
PAPVAQPPAAAPPSAVGSSAAAPR	2139.4	3	3.5277	0.2987
PAQPQEHPFASSR	1452.6	2	3.9692	0.3697
PASPPAPSGSQQGPEEEAAEALLTETVR	2821.0	2	4.5019	0.4582
PAYHSSLMDPDTKLIGNMALLPIR	2655.1	3	5.4816	0.4881
PDYLGADQRK	1163.3	2	3.0368	0.2262
PEEHPVLLTEAPLNPK	1785.0	2	4.738	0.2544
PEEVAIVEELGR	1341.5	2	4.7871	0.3429
PEFLEDPSVLTKDKLKSELVANNVTLPAGEQRK	3668.2	3	5.6655	0.3664
PEHPAQPVLKAEDGIVDAANFEQFLQER	3150.4	3	3.5549	0.139
PENVAPR	782.9	1	2.4241	0.1835
PEPAKSAPAPK	1093.3	2	2.7844	0.2554
PEPTKSAPAPK	1123.3	2	2.7248	0.1893
PESALLGGSEAGER	1373.5	2	4.6272	0.4173
PFLDIQKR	1017.2	2	2.9634	0.1644
PFLELDTNLPANR	1500.7	2	4.3339	0.3896
PFLELDTNLPANRVPAGLEK	2195.5	2	5.7105	0.4337
PFLELDTNLPANRVPAGLEKR	2351.7	3	4.3931	0.3135
PFRLDLLEDR	1274.5	2	2.6152	0.2246
PFVPNVHAAEFVPSFLR	1928.2	3	4.6423	0.2475
PGDIKRGIPNYEFKLGK	1933.2	2	2.8354	0.1165
PGGLLLGDVAPNFEANTTVGR	2099.3	2	6.4271	0.5281
PGGYERGLEPLARRASDTLSAEVR	2601.9	3	3.4151	0.1226
PGHLQEGFGCVVTNRFDQLFDDESDPFEVLK	3540.9	3	4.9131	0.3819
PGIGATHSSR	983.1	2	3.3694	0.3265
PGIVELPTLEELKVDEVK	2009.3	3	4.9617	0.4829
PGIVELPTLEELKVDEVKISSAVLK	2708.2	3	5.6354	0.4074
PGLVDSNPAPPESQEK	1665.8	2	4.4416	0.4161
PGPTPSGTNVGSSGR	1371.4	2	3.2466	0.3461

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
PGVTVKDVNQQEFVR	1716.9	3	5.3459	0.4373
PGYIPNLGECSHYRSKIHLKAGDKLQSPEGKPK	3650.2	3	3.8978	0.1057
PIKVGDAIPAVEVFEGEPGNKVNLAELFK	3082.5	3	6.2494	0.4453
PISQGGIHGR	1022.1	2	2.7476	0.2883
PITEMLPGILSQLGADSLTSLR	2313.7	2	2.9351	0.3227
PKHEFSVDMTCGGCAEAVSR	2125.4	3	5.4539	0.3997
PKKKPTPIQLNPAPDGSAVNGTSSAETNLEALQK	3503.9	3	7.5127	0.5318
PLAGGEPVSLGSLR	1353.5	2	2.4142	0.1096
PLAKDLLHPSPEEEKRK	1988.3	2	4.9156	0.3692
PLFPHVLCHNCAVEFNFGQK	2301.7	3	5.2128	0.451
PLHISTFINELDSGFR	1847.1	2	4.7157	0.5525
PLISVYSEKGESSGK	1581.7	2	4.3765	0.4837
PLSENELLELFEKMMEDMNLNEDKKAPLR	3479.0	3	3.491	0.1703
PLTQVGGDHIK	1165.3	2	3.4799	0.2615
PMFIVNTNVPR	1288.5	2	4.4767	0.4163
PMIHELLTEGR	1296.5	2	4.0943	0.3694
PMPPRPPLPNQQFGVSLQHLQEK	2640.1	3	4.124	0.3753
PMPPRPPLPNQQFGVSLQHLQEKNPEQEPIPIVLR	4026.7	3	6.0029	0.4681
PMTLGYWNIR	1251.5	2	2.4955	0.1122
PNETNEIANANSR	1430.5	2	4.5373	0.4319
PNIVGSEHYDVAR	1457.6	2	4.3114	0.4031
PNIVLFSGSSHQDLSQR	1886.1	3	3.205	0.1465
PNSEPASLLELFNSIATQGELVR	2486.8	3	5.7834	0.5407
PPSVFAEVPQAQPVLVFK	1954.3	2	4.8358	0.5132
PPYTVVYFPVR	1338.6	2	3.8829	0.4143
PQSAVPADTAAAPEVGPVLRPLYMDVQATTPLDPR	3646.1	3	5.2473	0.4715
PQYQTWEEFSR	1471.6	2	3.9189	0.3112
PREDHGRGYFEYIEENKYSR	2546.7	3	3.8056	0.3245
PREEVVQKEQE	1371.5	2	3.3425	0.1689
PRPDPSPEIEGDLQPATHGSR	2257.4	3	5.3693	0.4402
PRPPVYDDGPAGPDAEEAGDETPDVDPELLR	3291.4	3	5.1357	0.4234
PRRHPSTKLSMVGPGSGAETPPSKKAGSQKPTPEGR	3713.2	3	3.6842	0.1577
PSDLRPGDVSSK	1258.4	2	2.6903	0.2769
PSEELEALASLLQELR	1799.0	2	5.4608	0.4241
PSENLGQVLFGER	1446.6	2	2.9268	0.2849
PSGASTGIYEALELR	1564.7	2	4.5218	0.3013

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
PSGGMEALK	890.0	2	2.4257	0.1584
PSGNLVSVLSGAEGSFVSSLVK	2135.4	2	4.8764	0.399
PSHLTNKFEDK	1316.4	2	3.2105	0.1798
PSHLTNKFEDKTVAYTEQK	2237.5	2	6.0188	0.51
PSILPSKDVKPKPIADAK	1905.3	3	3.2664	0.1855
PSKEVEEDEYK	1353.4	2	3.8093	0.2691
PSKGPLQSVQVFGR	1500.7	2	3.2768	0.3129
PSQMEHAMETMMFTFHK	2084.5	2	5.9288	0.4463
PSQVVAETR	987.1	2	3.1741	0.2828
PSSEVIKDANLYISGLPR	1960.2	3	3.6367	0.3115
PSSFFGMDRPPK	1366.6	2	2.9086	0.2463
PSYQEEAVTK	1152.2	2	3.3177	0.2976
PTGAFGKETDLLLDDSLVSIFGNRR	2723.0	3	4.9702	0.3461
PTTQQSPQDEQEK	1516.5	2	4.3675	0.2384
PTTQQSPQDEQEKLLDEAIQAVK	2597.8	3	5.6699	0.4079
PTVRRALSSAGPIPIR	1692.0	3	3.215	0.1271
PTWGNHTPIFR	1326.5	2	3.4957	0.4279
PVDFTGYWK	1113.2	2	2.6115	0.1828
PVDLSKWSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK	4113.5	3	6.0053	0.4908
PVGGLLPLFSSPAGGVLGGGLGGGGGR	2307.6	2	5.1998	0.5105
PVNSPMNKGDTEVMK	1647.9	2	4.3038	0.4209
PVPAPGGGGFSR	1099.2	2	2.4113	0.1342
PVSSAASVYAGAGGSGSR	1581.7	2	6.1547	0.5953
PVTEKDLAEDAPWKK	1727.9	2	4.8515	0.458
PYQYPALTPEQK	1435.6	2	4.1985	0.3429
PYQYPALTPEQKK	1563.8	3	4.9154	0.4046
PYQYPALTPEQKKELSDIAHR	2485.8	3	4.7896	0.4713
QAAAHTDHLRDVLR	1603.8	2	2.5636	0.123
QAAAQEERLADLASDLLLQYLLQGGAR	2915.3	3	5.0855	0.4522
QAAASATQTIAAAQHAASTPK	1996.2	2	5.4447	0.5512
QAADMILLDDNFASIVTGVEEGR	2465.7	2	4.3138	0.4294
QAADMILLDDNFASIVTGVEEGRLIFDNLKK	3437.9	3	3.4128	0.1606
QAAKTEIEKLQMK	1518.8	2	3.1887	0.4211
QAALSAALQQSLQNAESWINR	2300.5	3	4.6103	0.3534
QAAPCVLFFDELDSIAK	1868.1	3	4.4225	0.4206
QAASGLVGQENAR	1301.4	2	3.2852	0.3247

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QAASSLQQASLK	1232.4	2	3.3179	0.2452
QADAYVEKGILDKEEAEAIKR	2377.6	3	5.0185	0.3366
QADFVQTPITGIFGGHIR	1958.2	2	2.5327	0.1471
QADLYISEGLHPR	1499.7	3	3.3272	0.3391
QADNPHVALYQAR	1483.6	2	3.3406	0.3831
QADYVPSDQDLLR	1520.6	2	3.2679	0.1241
QAEATRQAAAQEERLADLASDLLLQYLLQGGAR	3571.9	3	3.3082	0.2071
QAEEIGEKLHR	1310.4	2	2.5175	0.1797
QAEIENPLEDPVTGDYVHK	2155.3	3	3.6621	0.3236
QAEMEGAVQSIQGELSK	1806.0	2	5.1704	0.4115
QAEMLDDLMEK	1323.5	2	3.156	0.2337
QAENEPQSAPK	1199.3	2	2.7671	0.2254
QAEPEEKVPHLIDHQISSGENTR	2615.8	3	4.4738	0.1575
QAEPELDLR	1071.2	2	2.4961	0.1346
QAERLFENQLVGPESIAHIGDVMFTGTADGR	3360.7	3	3.426	0.1315
QAESASEAAKKYMEENDQLKK	2399.6	3	3.2853	0.1518
QAEVANQETKEDLPAENGETKTEESPASDEAGEKEAK	3962.1	3	3.6735	0.1619
QAEVANQETKEDLPAENGETKTEESPASDEAGEKEAKSD	4164.2	3	3.811	0.2219
QAFAKVFNTTPDDLDLHVIYDVSHNIAK	3173.5	3	4.4336	0.3463
QAFDDAIAELDTLNEDSYK	2159.2	2	4.3821	0.4539
QAFDDAIAELDTLNEDSYKDSTLIMQLLR	3330.7	3	4.7242	0.3564
QAFQIGSPWR	1190.3	1	3.0247	0.3176
QAFTPSSTMMEVFLQEK	1975.3	2	3.7068	0.3236
QAGAEALSQAVAR	1272.4	2	2.6878	0.1596
QAGEVTFADAHRPK	1527.7	2	2.972	0.2851
QAGEVTYADAHK	1290.4	2	2.8874	0.3316
QAGEVTYADAHKER	1575.7	2	3.8807	0.3828
QAGEVTYADAHKGR	1503.6	2	3.2656	0.3162
QAGFKESDVGFIPTSGLSGENLITR	2624.9	3	4.8863	0.2382
QAGGFLGPPPPSGK	1310.5	2	3.0363	0.2827
QAGPASVPLR	996.1	2	2.5891	0.2101
QAGPASVPLRTEEEFK	1759.9	2	2.59	0.1033
QAGPASVPLRTEEEFKK	1888.1	2	2.875	0.1537
QAGVFEPTIVK	1189.4	2	2.4063	0.18
QAHILLDCGEDNVCKPKLEVSVDSDQKK	3113.5	3	3.5879	0.1878
QAHLCVLASNCDEPMYVK	2022.4	2	3.3192	0.2669

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QAHVDVK	796.9	1	1.85	0.1175
QAHVDVKFQLPI	1395.6	2	2.8597	0.3254
QAIGWNINIPALLQEK	1809.1	2	2.7915	0.2318
QAIKELPQFATGENLPR	1913.2	2	3.9541	0.2525
QAILGEHPSSFRHDGYGSHGPLLPLPSR	3027.3	3	3.2693	0.2965
QAIPLDENEGIYVQDVK	1932.1	2	4.7859	0.4791
QAIVDKVPSVSSSALVSSLHLLK	2379.8	3	4.0335	0.2804
QAKEEAQAEIEQYR	1693.8	2	3.5254	0.3404
QAKVLENAEGAR	1286.4	2	2.5687	0.1411
QALAEHEDELPEHFKPSQLIK	2460.7	3	3.3748	0.3374
QALAHGLK	838.0	1	1.9476	0.2178
QALDMILDLEPDEELEDNPNQSDLIEQAAEMLYGLIHAR	4454.9	3	4.3684	0.2686
QALHSGQNQLKEMAIPVLEAR	2334.7	3	4.0108	0.3531
QALHSLELHYQAFLR	1827.1	2	3.74	0.3712
QALLKQGQDNLSSVK	1629.8	2	3.6946	0.3134
QALMEQQQR	1132.3	2	2.664	0.1209
QALNEHFQSILQTLEEQVSGER	2557.8	3	3.4386	0.2072
QALNTDYLDSDYQR	1702.8	2	4.0263	0.4035
QALQDLLSEYMGNAGR	1767.0	2	4.6033	0.4275
QALQDLLSEYMGNAGRK	1895.1	3	3.8768	0.2455
QALSYQNADSYHHHTSPQHLLQIR	2846.1	3	4.0784	0.2658
QALVEFEDVLGACNAVNYAADNQIYIAGHPAFVNYSTSQK	4333.7	3	3.5983	0.3371
QALVGQPASLTVTTK	1514.7	2	2.5393	0.2045
QAMLENASDIKLEK	1590.8	2	3.2358	0.3034
QANTGLFNLR	1134.3	2	2.6226	0.2284
QAPAGSPRGLRKGAAPARERRGR	2416.7	3	3.211	0.1363
QAPGLLWDASHQQEQPTSSSHHGGAGAVEIR	3253.4	3	4.1693	0.2886
QAPQTIHLPSGEILDVFDAAER	2408.7	3	4.117	0.3479
QAPQTIHLPSGEILDVFDAAERYQQAGLPLIVLAGK	3861.4	3	3.4427	0.1983
QAQAAVLAVLPR	1237.5	2	3.3444	0.2599
QAQEYEALLNIK	1420.6	2	4.0398	0.3022
QAQIEVVPSASALIIK	1668.0	2	4.4526	0.3001
QAQILASEAEKAEQINQAAGEASAVLAK	2841.1	3	6.9757	0.5083
QAQIPLAAVIKPFATIPSNESPLYLVNHGESGPVR	3716.2	3	5.8592	0.5421
QAQLAQTLQQQEQASQGLR	2127.3	2	4.7848	0.4278
QAQQDRDEMADEVANGNLSK	2220.3	3	4.6206	0.2833

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QAQQERDELADEIANSSGK	2090.2	3	4.8188	0.3964
QAQQERDELADEIANSSGKGALALEEK	2902.1	3	6.2738	0.4174
QAQQERDELADEIANSSGKGALALEEKR	3058.3	3	6.2375	0.5103
QAQVATGGGPGAPPGSQPDYSAAWAEYYR	2954.1	3	4.2445	0.3021
QAQVDLEREKKELEDSLER	2316.5	3	3.2138	0.2983
QARPTYATAMLQSLLK	1793.1	2	3.1611	0.1717
QASAIKKEELVAR	1443.7	2	2.8065	0.2411
QASDTGSNDAHNKK	1473.5	2	2.6042	0.2528
QASEGPLKGILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK	4850.2	3	3.6292	0.275
QASIQHIQNAIDTEK	1696.8	2	3.5249	0.357
QASIQHIQNAIDTEKSQQALVQK	2579.9	3	3.9016	0.3254
QASIQHIQNAIDTEKSQQALVQKR	2736.0	3	3.9848	0.2688
QASPNIVIALAGNK	1396.6	2	3.2359	0.3294
QASPNIVIALSGNK	1412.6	2	2.9654	0.3844
QASPSIVIALAGNK	1369.6	2	3.1797	0.146
QASVADYEETVKK	1468.6	2	3.3867	0.292
QATHDQAVQALKR	1466.6	2	2.6365	0.2614
QATINIGTIGHVAHGK	1617.8	2	3.47	0.2934
QATKDAGQISGLNVLR	1671.9	3	4.3688	0.2822
QATKDAGTIAGLNVLR	1628.9	3	3.9088	0.4179
QATKDAGTIAGLNVMR	1646.9	2	4.2008	0.5211
QATKDAGTITGLNVLR	1658.9	2	2.576	0.1323
QATKDAGVIAGLNVLR	1626.9	3	4.4061	0.3475
QATSTASTFVKPIFSR	1742.0	2	3.2844	0.2318
QATTIIADNIIFLSDQTK	1993.2	2	5.3756	0.5018
QATTIIADNIIFLSDQTKEKE	2379.6	2	4.1844	0.4375
QATVGDINTERPGMLDFTGK	2151.4	2	3.3934	0.3606
QATYGYYLGNPAEFHDSSDHHTFK	2786.9	3	3.6856	0.378
QATYGYYLGNPAEFHDSSDHHTFKK	2915.1	3	3.5301	0.2189
QAVDFLSNEGHIYSTVDDDHFK	2538.7	3	3.5554	0.292
QAVDQIKSQEQLAAELAEYTAK	2435.7	2	4.2805	0.3333
QAVDQISSGFFSPK	1511.7	2	2.9964	0.3172
QAVEMKNDKSEEEQSSSSVK	2241.4	3	3.9328	0.3571
QAVEMKNDKSEEEQSSSSVKKDETNVK	3056.3	3	3.7666	0.1927
QAVEQQIQSHR	1324.4	2	3.0112	0.1825
QAVEQQIQSHRETHQK	1948.1	2	2.9914	0.2697

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QAVITKELIEIISGAAALD	1956.3	2	4.1376	0.2797
QAVQILDELAEKLK	1598.9	2	4.2865	0.2412
QAVQILQQVTVR	1383.6	2	3.1088	0.2543
QAVSASGK	747.8	1	1.9946	0.1368
QAVSMFLGAVEEAKK	1608.9	2	3.3122	0.3582
QAVSMFLGAVEEAKKEGGTVVYGGK	2556.9	3	4.7016	0.4322
QAVTNPNNTFYATK	1569.7	2	4.0949	0.427
QAVTNPNNTFYATKR	1725.9	2	3.7993	0.3954
QAWFIENEEQEYVQTVK	2142.3	3	4.4849	0.2365
QAYVDKLEELMK	1467.7	2	3.8345	0.2762
QDAFYKEQLAR	1369.5	2	2.85	0.17
QDAKDPTSLLGVLQAEADSTSEGLEDAVHSR	3241.4	3	4.3474	0.3204
QDAQDLYEAGEK	1367.4	2	4.2901	0.3676
QDAQDLYEAGEKK	1495.6	2	3.538	0.2982
QDDGSSSASPSVQGAPR	1646.7	2	4.7533	0.471
QDEEKPLHALLHGR	1643.8	3	4.3707	0.4406
QDEHGYISR	1105.1	1	1.7162	0.2389
QDFVQHFSQIVR	1504.7	2	3.2264	0.2092
QDGDPAFLYLLSAPR	1663.9	2	3.0212	0.2567
QDGPGQDK	844.8	1	1.9787	0.1179
QDGPMPKPHSVSLNDTETR	2110.3	3	3.6143	0.3969
QDGPMPKPHSVSLNDTETRK	2238.5	3	3.4517	0.3946
QDHAQQLATAAEER	1568.6	2	3.7096	0.3769
QDHPSSMGVYGQESGGFSGPGENR	2481.6	3	5.5325	0.3842
QDIAFAYQR	1112.2	2	3.183	0.3675
QDILDDSGYVSAYK	1574.7	2	3.6415	0.324
QDKHYGYNSYSVSNSEKDIMAEIYK	2971.2	3	4.8957	0.4347
QDKIYFMAGSSR	1403.6	2	2.4073	0.1027
QDLDRGLELISK	1387.6	2	3.361	0.1214
QDLKGLEETVAKELQTLHNLR	2436.8	3	4.3026	0.4149
QDLLAYLQR	1120.3	2	3.0706	0.2379
QDLLTAAPASEIAEGLNLHTIR	2334.6	3	3.2885	0.2094
QDLPDAMKPHEIQEK	1780.0	2	3.2977	0.2971
QDLPNAMNAAEITDK	1631.8	2	4.1371	0.4026
QDLPNAMNAAEITDKLGLHSLR	2408.7	3	4.7285	0.417
QDLTTLDVTK	1134.3	2	2.5164	0.2263

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QDLTTLDVTKLTPLSHEVISR	2367.7	3	4.8278	0.34
QDMPNAMPVSELTDKLGLQHLR	2494.9	3	3.914	0.3029
QDNKVVIGFVPLAEIMGYSTVLR	2551.0	3	4.2911	0.3231
QDPLLGSSETFNSFLR	1812.0	2	3.9893	0.388
QDRFAGLHFFNPVPVMK	2004.3	3	4.0803	0.4272
QDRPFFLYYASHHTHYPQFSGQSFAER	3318.6	3	5.4098	0.3798
QDVDNASLAR	1089.1	1	2.7764	0.2692
QEAEEAKEALLQASR	1673.8	2	4.4625	0.364
QEAFLLNEDLGDSLDSVEALLK	2420.7	2	5.4012	0.4183
QEAGISEGQGTAGEEEEKKK	2106.2	2	3.681	0.3314
QEALKNDLVEALKR	1627.9	2	3.7852	0.2759
QEAVSMIPPLLLNVRPHHK	2180.6	3	3.6564	0.298
QECDIARAVAR	1232.4	2	3.2215	0.2449
QEDVSVQLEALDIMADMLSR	2264.6	2	4.4354	0.4267
QEEEQDLDGEKGPSSEGPEEEDGEGFSFK	3187.2	3	5.7397	0.3171
QEESEQIKTLNNKFASFIDKVR	2625.9	3	4.3747	0.3222
QEFAQHANAFHQWIQETR	2242.4	2	3.4957	0.3666
QEFEKQDELKR	1450.6	2	2.7025	0.2344
QEGLDGGLPEEVLFGNLDLLPPPGK	2605.9	2	4.0048	0.334
QEGLTFFGTELAPVR	1665.9	2	3.3967	0.253
QEILENKDVVVQHVHFDGLGR	2433.7	3	4.8094	0.4215
QEIQHLFR	1071.2	2	2.6265	0.2397
QEIQHLFREPEK	1554.7	2	2.8699	0.1665
QEIVSLFNAFGR	1381.6	2	3.4657	0.2318
QEKPAEKPAETPVATSPTATDSTSGDSSR	2947.1	3	5.1094	0.4024
QELILSNSEDKSIR	1632.8	2	4.172	0.3521
QELNEPPKQSTSFLVLQEILESEEKGDPNKPSGFR	3973.4	3	3.5239	0.2034
QELQETQERLEAATQQNQQLR	2542.7	3	4.3744	0.2168
QELVTKIDHILDAL	1608.9	2	3.4236	0.2789
QEMQEVQSSR	1222.3	2	3.186	0.2659
QEPERNECFLQHKDDNPNLPR	2580.8	3	4.5513	0.3598
QEPQPQGPPPAAGAVASYDYLVIGGGSGGLASAR	3240.5	3	5.3408	0.3827
QEQVKIESLAK	1273.5	2	2.4259	0.2378
QETESLHGSSGK	1260.3	2	2.4353	0.2612
QETFDAGLQAFQQEGIANITALKDQLLAAK	3234.6	3	6.0288	0.4849
QEYDEAGPSIVHRK	1629.8	2	3.2358	0.3166

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QEYDESGPSIVHR	1517.6	2	3.0118	0.2396
QEYDESGPSIVHRK	1645.8	2	3.3141	0.2825
QFAEENGLLFLEASAK	1768.0	2	2.9604	0.2588
QFAPEYEKIANILKDKDPPIPVAK	2726.2	3	3.888	0.3259
QFAPIHAEAPEFMEMSVEQEILVTGIK	3046.5	3	3.7543	0.2736
QFAPIHAEAPEFMEMSVEQEILVTGIKVVDLLAPYAK	4116.8	3	4.4753	0.4053
QFASQANVVGPWIQTK	1775.0	2	3.9874	0.4082
QFAYQNSWGLTTR	1572.7	2	3.5464	0.2833
QFDHLNHLNPDKFESTDLDMLIK	2772.1	3	4.7945	0.3005
QFDKILELIESGKK	1648.9	2	2.8363	0.1777
QFDSPMPSPFQGGSFTLPLDVMK	2527.9	2	2.6255	0.1418
QFDVNLQVPDR	1331.5	2	2.5376	0.1142
QFEAPTLAEGFSAILEIPFR	2237.5	2	4.6154	0.3888
QFEDEKANWEAQQR	1779.8	2	3.5395	0.3171
QFEGLADKLSFGLEDEPLETATK	2539.8	3	5.3577	0.2349
QFEGLADKLSFGLEDEPLETATKEN	2783.0	3	5.3663	0.2778
QFEHLDPQNQHTFEAR	1998.1	2	2.783	0.2434
QFGAQANVIGPWIQTK	1759.0	2	3.6923	0.2958
QFGFIVLTTSAGIMDHEEAR	2223.5	3	3.8982	0.3255
QFHLTDDDLLR	1373.5	2	2.7771	0.3938
QFIAAQGSSR	1065.2	2	2.5064	0.2852
QFIDSNPNQPLVILEMESGASAK	2489.8	3	5.0521	0.3237
QFILVMNALDNR	1434.7	2	3.9431	0.3187
QFLESSELPR	1206.3	2	2.669	0.2045
QFLLDSGYFSDNILCHFCASMISGLVTTAASMPVDIAK	4068.7	3	3.694	0.1413
QFLPVAFPVGNAFSYYQSNR	2306.6	3	4.239	0.35
QFLQAAEAIDDIPFGITSNSDVFSK	2715.0	2	5.8151	0.5796
QFLQAAEAIDDIPFGITSNSDVFSKYQLDKDGVVLFK	4121.6	3	5.7127	0.3668
QFLQAAEAIDDIPFGITSNSDVFSKYQLDKDGVVLFKK	4249.8	3	5.1219	0.3837
QFLSETEKMSPEDR	1697.8	2	3.9297	0.3414
QFLSETEKMSPEDRAK	1897.1	2	3.0522	0.1548
QFNKLTEDKADVQSIIGLQR	2304.6	3	4.4445	0.2256
QFQDAGHFDAENIKK	1748.9	2	3.448	0.2423
QFSANDKVYTVEK	1529.7	2	3.3578	0.2683
QFSANDKVYTVEKADNFEYSDPVDGSISR	3283.5	3	4.3517	0.2976
QFSSADEAALKEPIIKKFEEEGNPYYSSAR	3406.7	3	3.7189	0.148

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QFVNEWAAEIPGGPEAASAIAEELGYDLLGQIGSLENHYLFK	4550.0	3	3.274	0.1727
QFVPIKVEQIEAGTPGR	1870.1	2	3.7563	0.3799
QFVQSAKEVANSTANLVK	1935.2	3	3.6817	0.2525
QFVTPADVVSGNPK	1459.6	2	3.1822	0.2622
QFYDQALQQAVVDDDANNAK	2254.4	3	5.4786	0.3839
QFYFTQGGNLMSQAR	1748.9	2	3.8902	0.3408
QGAAIGIPYFTAYR	1528.7	2	2.7339	0.1734
QGAFLVNTAR	1077.2	2	2.8022	0.2405
QGAIVAVTGDGVNDSPALK	1813.0	2	6.1445	0.5459
QGAIVAVTGDGVNDSPALKK	1941.2	2	5.2031	0.4833
QGAPGQGGGGGLSHEDTLALLEGLVSR	2577.8	3	4.1952	0.165
QGAPGQGGGGGLSHEDTLALLEGLVSRR	2734.0	3	3.8201	0.4471
QGAPPAAGQGGALVELTPTPGGLALVSPYHTHR	3222.6	3	3.3099	0.2441
QGDMVLEKPYSEATAR	1796.0	2	3.2031	0.332
QGDTGDWIGTFLGHK	1632.8	3	3.2313	0.3881
QGEDNSTAQDTEELEKEIREDLPVNTSK	3177.3	3	3.3271	0.1027
QGEVSKAASADSTTEGTPADGFTVLSTK	2756.9	3	4.9281	0.3305
QGFEPPSFVGWFLGWDDDYWSVDPLDR	3232.5	2	3.7701	0.36
QGFGELLQAVPLADSFR	1849.1	2	4.5444	0.3941
QGGAPDAGQE	929.9	2	2.4365	0.1627
QGGGGGGGSVPGIER	1285.3	2	3.7405	0.4691
QGGLGPIRIPLLSDLTHQISK	2244.6	3	6.1944	0.4548
QGGLGPIRIPLLSDLTHQISKDYGVYLEDSGHTLR	3851.3	3	3.3197	0.2317
QGGLGPMNIPLVSDPK	1623.9	2	4.1104	0.3563
QGGLGPMNIPLVSDPKR	1780.1	2	3.5955	0.4165
QGGPTYYIDTNALR	1569.7	2	3.2008	0.3423
QGHRPLSQSIVEAGSVGQTDLNKR	2578.8	3	5.7461	0.3726
QGIETPEDQNDLR	1515.6	2	2.9831	0.2618
QGIETPEDQNDLRK	1643.7	2	2.9046	0.1538
QGILGAQPQLIFQPHR	1804.1	2	2.7479	0.1755
QGIVPPGLTENELWR	1709.9	2	3.4725	0.3686
QGKLDEAEDDFKK	1523.6	2	3.0605	0.2878
QGKYQDAETLYKEILTR	2057.3	3	3.329	0.1848
QGLLPLTFADPADYNK	1764.0	2	3.2976	0.3611
QGLLPLTFADPADYNKIHPVDKLTIQGLKDFTPGKPLK	4191.9	3	3.5813	0.2646
QGLLPSLEDLLFYTIAEGQEK	2365.7	2	4.632	0.5089

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QGLLPSLEDLLFYTIAEGQEKIPVHK	2940.4	3	3.962	0.4012
QGLNGVPILSEEELSLLDEFYK	2494.8	2	4.082	0.4286
QGLPATSDIKDVDSLMR	1847.1	2	3.2136	0.3735
QGLYDRLPPLPVTPGMEGAGVVIAVGEGVSDR	3251.7	3	6.4916	0.5408
QGLYDRLPPLPVTPGMEGAGVVIAVGEGVSDRK	3379.9	3	5.4003	0.4382
QGLYELSASNFELHVAQGDHFIK	2604.9	3	4.3325	0.4046
QGNAVTLGDYYQGR	1542.6	2	2.5239	0.1987
QGNMTAALQAALK	1317.5	2	3.1328	0.3321
QGPGEPPPRPDLDPELYLSVHDPAGALQAAFR	3412.8	3	4.24	0.2221
QGPISDNYLFTPGK	1537.7	2	3.1992	0.3327
QGPPHINHDDPSLVPNVPYFDLPAGLMAPLVK	3451.0	3	3.46	0.154
QGQDAIPPPDPGEQIFNLPK	2162.4	2	2.8063	0.1409
QGQDNLSSVKETQK	1562.7	2	2.5014	0.1362
QGQDVAPPPNPGDQIFNK	1923.1	2	3.9631	0.2773
QGQDVAPPPNPVPQR	1600.8	2	2.9813	0.2288
QGQETAVAPSLVAPALNKPK	2020.3	2	4.4547	0.3833
QGQNVIGLQMGSNK	1474.7	2	4.0882	0.362
QGQPVLVSGVHKK	1377.6	2	2.7653	0.1187
QGQQQAGGDGKTEQK	1560.6	2	3.3899	0.1887
QGQYSPMAIEEQVAVIYAGVR	2310.6	2	5.2745	0.4567
QGRPVVICDKEDTETIKNTK	2275.6	3	3.4474	0.139
QGRQEALEWLIR	1499.7	2	3.5319	0.248
QGRTLYGFGG	1056.2	1	2.2334	0.2943
QGSGSSQPMEVQEGYGFGSGDDPYSSAEPHVSGVKR	3715.9	3	5.3787	0.5044
QGSLYHEMAIEPLDDIAAVTDILTQR	2901.2	3	3.5597	0.3004
QGSPDQVSPVSEMTSTSLYQDKQEGK	2828.0	3	3.3594	0.2976
QGSSAEQPLGGR	1187.2	2	2.6605	0.3101
QGTFHSQQALEYGTK	1695.8	2	2.8006	0.2737
QGVDDAFYTLVR	1384.5	2	3.3966	0.3565
QGVEDAFYTLVR	1398.5	2	3.3937	0.3364
QGVNNAEKFDYVMQFLNK	2146.4	3	4.2578	0.3403
QGVSHIIVDEVHER	1618.8	2	4.8382	0.1755
QHAFSSHSSGSQSQK	1603.6	2	3.1357	0.3284
QHAQPPKPSSDSSGGR	1636.7	2	2.8163	0.182
QHDQLEAQKLEYHQVIQQMEQK	2753.0	3	3.9881	0.3025
QHEADADLINAGK	1382.5	2	3.1132	0.2636

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QHFISFDTDR	1266.3	2	2.4573	0.1498
QHFISFDTDRSGTVDPQELQK	2449.6	2	2.9854	0.1664
QHFPATPLLDYALEVEK	1972.2	3	4.9893	0.3377
QHFPATPLLDYALEVEKITTSK	2502.8	2	2.8964	0.2554
QHIVNDMNPGNLHLFINAYNSR	2568.9	3	4.9835	0.3713
QHIYKEIVNFSPIAR	1816.1	2	2.6803	0.2383
QHLLTNLVEVDGR	1494.7	2	2.6311	0.1719
QHLNLNNAEQLCR	1553.7	2	2.8615	0.1588
QHLSPAEVEAILQVIQR	1932.2	3	3.3729	0.156
QHLVEVR	881.0	1	1.8611	0.1651
QHLYVDKNTK	1246.4	2	2.4282	0.1363
QHMDITGEENPLNK	1626.8	2	3.555	0.3255
QHNSGPNSKPVVSFIAGLTAPPGR	2432.7	2	2.9281	0.3836
QHPDWEDEELFQHAR	1938.0	2	3.0141	0.3008
QHPQPYIFPDSPGGTSYER	2177.3	3	4.1274	0.31
QHPVPPPAQNQNQVR	1710.9	3	4.2755	0.3097
QHQLYVGVLGSK	1329.5	3	4.5133	0.4031
QHQSDVEALKR	1311.4	2	2.691	0.2853
QHQTRLDIISEDISELQK	2154.4	2	2.7165	0.1628
QHSNSNMVIMLIGNK	1687.0	2	3.439	0.3279
QHSSQDVHVVLK	1377.5	2	2.6315	0.2041
QHVIDGEKTIIQNPTDQQKK	2321.6	3	3.4338	0.2094
QHYIDLKDRPFFPGLVK	2074.4	2	2.8145	0.235
QHYVLAGASGSPGEEVAIRPSTAPR	2551.8	3	3.8175	0.3987
QIAASSQDSVGR	1219.3	2	2.5749	0.2076
QIAEGTSISEMWQNDLQPLLIER	2673.0	3	4.524	0.3333
QIAEGTSISEMWQNDLQPLLIERYPGSPGSYAAR	3780.2	3	4.5194	0.3565
QIANSQDGYVWQVTDMNR	2126.3	2	5.561	0.4821
QIAQLQDFVR	1218.4	2	2.6231	0.2747
QIASLTGLVQSALFK	1576.9	2	3.7082	0.3462
QIATLHAQVADMK	1426.7	2	3.5464	0.4486
QIATLHAQVADMKK	1554.8	2	3.4512	0.3283
QIDNPDYK	993.1	1	2.2442	0.1663
QIEELKGQEVSPK	1485.7	2	4.0454	0.2265
QIEETLAHFHLTK	1567.8	2	2.6856	0.166
QIEIQFAQGDR	1305.4	2	3.4949	0.1802

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QIEKDLEEQSR	1375.5	2	2.8152	0.2348
QIEQEKLASMK	1305.5	2	2.8208	0.1681
QIFHPEQLITGK	1411.6	2	2.6187	0.3286
QIFLGGVDKHTQFWR	1833.1	2	2.9266	0.1564
QIFLGGVDKR	1133.3	2	2.956	0.2297
QIGAFSEGINNLTHMLKEDDMFKDFAAR	3200.6	3	4.258	0.3332
QIGENLIVPGGVK	1324.6	2	2.7925	0.2672
QIGLDQIWDDLRAGIQQVYTRQSMAK	3035.4	3	3.7997	0.1789
QIGNVAALPGIVHR	1445.7	2	3.5434	0.3515
QIGRETGENVLHVR	1608.8	2	3.047	0.2822
QIGSVIRNPEILAIAPVLLDALTDPSR	2873.3	3	5.5758	0.3933
QIGSVIRNPEILAIAPVLLDALTDPSRK	3001.5	3	4.2917	0.2263
QIGVEHVVVYVNK	1484.7	2	3.4702	0.2468
QIHEEALSKFQK	1458.6	2	2.9309	0.1448
QIIEQDKHALLDVTPK	1849.1	2	3.4327	0.2893
QIILEKEETEELKR	1759.0	2	4.2196	0.326
QIIQANPLLEAFGNAK	1728.0	3	5.1348	0.3329
QIIQQNPSLLPALLQQIGR	2131.5	3	4.4216	0.4088
QIITDKDDLVK	1288.5	2	3.1804	0.1152
QIIVDPLSFSEER	1533.7	2	2.5271	0.2206
QIIVVSSPTFLQKSQCR	1935.3	2	2.6515	0.2003
QIKPYTLMSMVANLLYEKR	2299.8	3	3.4946	0.2306
QIKQVEDDIQQLLK	1698.9	2	3.6163	0.2644
QIKQVEDDIQQLLKK	1827.1	2	4.0336	0.3079
QILAPVVKEIMDDKSLNIKTDPVDIYK	3087.6	3	3.4006	0.2522
QILLGPNTGLSGGMPGALPSLPGKI	2389.8	2	4.9903	0.376
QILNFFHHR	1212.4	2	2.848	0.1539
QILVGDIGDTVEDPYTSFVK	2197.4	2	4.4141	0.37
QINDYVEKGTQGK	1480.6	2	3.4724	0.3353
QINQEYLISQVEGHQVSLK	2214.5	3	3.4566	0.2721
QINVGNALEYVSR	1463.6	2	3.3714	0.3923
QINWTVLYR	1193.4	2	2.7493	0.2365
QIPLQSLDLEFGSGFQPR	2033.3	2	4.7447	0.4028
QIPVLQTNNGPSLTGLTTIAAHLVK	2588.0	2	3.9493	0.458
QIPVVGSVLNWFSPVQALQK	2211.6	2	4.3317	0.2856
QIQAAYSILSEVQQAVSQGSSDSQILDLSNR	3337.6	3	5.68	0.4207

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QIQDMLGLTKPAMPMQQAR	2158.6	3	3.3042	0.1227
QIQELVEAIVLPMNHK	1863.2	2	3.3177	0.1641
QIQFADDMQEFTKFPTK	2075.3	2	2.4289	0.1562
QIRVDHAGK	1024.2	2	2.4244	0.1091
QISDVERDVQNFPAATDEKDKFVEK	2910.1	3	3.6932	0.1588
QISRDYGVLLEGSGLALR	1948.2	3	5.4342	0.3421
QISRPSAAGINLMIGSTR	1873.2	3	4.2255	0.4081
QISSLRDEVEAK	1375.5	2	3.4957	0.1904
QITITGTPANISLAQYLINAR	2259.6	2	3.1902	0.2297
QITLNDLPVGR	1226.4	2	2.789	0.1518
QITQSALLAEAR	1301.5	2	3.3117	0.2766
QITVNDLPVGR	1212.4	2	3.413	0.3575
QIVSGSR	746.8	1	1.7515	0.2769
QIVWNGPVGVFEWEAFAR	2106.4	3	5.4955	0.5395
QIYLSENPEETAAR	1621.7	2	3.9662	0.2857
QIYLTDNPEAVAIKLNQTALQAVTPITSFGK	3346.8	3	4.6488	0.3608
QIYPPINVLPSLSR	1597.9	2	3.2611	0.3012
QKAEADKNDKAVKDLVVLLFETALLSSGFSLEDPQTHSNR	4416.9	3	4.3211	0.2985
QKAEADKNDKSVK	1461.6	2	2.4085	0.2006
QKAQVEQELTTLR	1544.7	2	3.2378	0.3934
QKASIHEAWTDGK	1471.6	2	2.6463	0.1858
QKDFLDGVYAFEYYPSTPGR	2354.6	2	4.8174	0.4947
QKDIFAMDDKSENEPIENEAAKYDLK	3043.3	3	4.0535	0.2818
QKDYETATLSEIK	1526.7	2	3.743	0.2981
QKEFDPTITDASLSLPSR	2006.2	2	4.2583	0.362
QKEGESEDLASR	1349.4	2	2.5691	0.2317
QKEVNENFAIDLIAEQPVSEVETR	2760.0	3	4.9956	0.3468
QKEVQMNFLNQLTSVFNPR	2294.6	3	3.6449	0.1346
QKGADFLVTEVENGGSLGSK	2037.2	3	4.4861	0.3843
QKGADFLVTEVENGGSLGSKK	2165.4	2	4.0582	0.3835
QKGYEEEIIHFKK	1649.9	2	2.8826	0.1419
QKHDGTVGLLTYPVLQAADILLYK	2658.1	3	5.0181	0.4084
QKHEIESLYTK	1376.5	2	2.4249	0.1933
QKHGVPPLKLCKNLNR	1846.2	3	3.7763	0.1087
QKHPDKDLEQLVGIANYYALLHQQK	2951.3	3	3.5926	0.3144
QKHSQAVEELAEQLEQTK	2097.3	2	4.1179	0.339

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QKHSQAVEELAEQLEQTKR	2253.5	2	4.6439	0.3353
QKIFQVAQELSGEDMHQFHR	2429.7	3	3.4674	0.2048
QKILDQSEAEK	1289.4	2	2.6804	0.1577
QKISFLENNLEQLTK	1806.1	2	3.4513	0.3964
QKIVELAHSGAR	1309.5	2	2.831	0.2978
QKIVQAEGEAEAAK	1472.6	2	3.6342	0.37
QKIVQAEGEAEAAKMLGEALSKNPGYIK	2975.4	3	4.5918	0.3852
QKKESEAVEWQQK	1618.8	2	2.9619	0.1365
QKKKPKMTDEEIMEKLRTIVSIGDPKKK	3301.0	3	3.2485	0.1202
QKKQEYLEVQR	1449.6	2	2.7134	0.1452
QKLEAQLTENNIVKEELALLDGSNVVFK	3144.6	3	4.8566	0.3565
QKLEAQQGLR	1171.3	2	2.6808	0.1132
QKLEEDAEMK	1221.4	2	2.6043	0.3328
QKLFQEDDEIPLYLK	1880.1	3	4.1186	0.2836
QKLFQEDDEIPLYLKGGVADALLYR	2896.3	3	4.601	0.3439
QKLFQFLQAEPHNSLGK	1986.3	3	3.3551	0.1623
QKLPDGSEIPLPPILLGR	1944.3	3	4.3067	0.3021
QKLQLEKVTTEAK	1516.8	2	3.2644	0.2564
QKLSPDAVAQLAFQMAFLR	2135.5	3	4.0074	0.2984
QKLTAQVEELSK	1374.6	2	2.827	0.2325
QKLTETELKFELLEKDPYALDVPNTAFGR	3367.8	3	4.0324	0.2563
QKNGSSAKPSCPYCCCAVGSK	2119.5	2	2.7426	0.2104
QKPITPETAEKLAR	1582.8	2	2.4722	0.1854
QKPNLGKYDDPPDWQEILTYFR	2725.0	3	3.3732	0.1201
QKPQEVPQENGMEDPSISFSKPK	2601.9	3	3.8031	0.2184
QKQAADAEMEK	1249.4	2	2.4659	0.1518
QKQLEDILVLAK	1398.7	2	2.4827	0.1788
QKQQEAALELEELKK	1786.0	2	3.9253	0.2807
QKSDAEEDGGTVSQEEEDRKPK	2463.5	3	3.4047	0.1747
QKSQQTISQLHSTVHLIEFAR	2452.8	3	3.6983	0.3436
QKTEEELLETTLK	1562.7	2	3.6407	0.376
QKTESTLNALLQR	1502.7	2	3.6448	0.2625
QKTHVHIGEGPSTISNSTIPENATSSGR	2907.1	3	3.9372	0.1788
QKVDDDRKHEIEAAIVR	2023.2	3	3.5438	0.2315
QKVDSLLENLEK	1416.6	2	3.2781	0.2596
QKVDSLLENLEKIEK	1787.0	3	3.4375	0.1673

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QKVDSLLENLEKIEKEQSK	2259.5	2	3.7093	0.343
QKVEGTEPTTAFNLFVGNLNFNK	2569.9	3	5.2808	0.4611
QKVEILNELYQQK	1633.9	2	3.2446	0.153
QKVENLLLEAEKR	1570.8	2	3.2205	0.2128
QKVEQNAAPSHTK	1438.6	2	3.7449	0.3365
QKYTLPLYHAMMGGSEVAQTLAK	2539.0	3	3.8598	0.2166
QLAAENRLTEMETLQSQLMAEK	2535.9	3	4.6045	0.3024
QLAALKQQLVASHLEK	1778.1	2	4.2549	0.4305
QLAALKQQLVASHLEKLLGPDAAINLTDPDGALAK	3625.2	3	3.3422	0.2085
QLADETLLKVDLENR	1758.0	2	3.1485	0.3679
QLADHLGFEFFEASAK	1811.0	2	2.8342	0.3104
QLAEEDLAQQR	1301.4	2	2.8639	0.1115
QLAEFVPLDYSVPIEIPTIK	2273.7	2	4.2347	0.2536
QLAEGTAQQR	1102.2	2	2.6099	0.1999
QLAGEDMEISVK	1320.5	2	2.5785	0.255
QLAGILQVPLEER	1466.7	2	2.7873	0.1934
QLAPIWDKLGETYKDHENIVIAK	2683.1	3	4.7028	0.4311
QLAPLLPSLAPSSAR	1521.8	2	3.1404	0.1876
QLAQIDGTLSTIEFQR	1821.0	3	5.004	0.4
QLAQIDGTLSTIEFQREALENANTNTEVLK	3348.7	3	4.2919	0.468
QLASEDISHITPTQGFNIK	2100.3	2	4.4042	0.438
QLAVYEEFAR	1226.4	2	2.7474	0.1577
QLDDEEVSEFALDGLKQVMAIK	2479.8	3	3.4914	0.1851
QLDDKDEEINQQSQLVEK	2160.3	3	4.1033	0.2018
QLDDLKVELSQLR	1557.8	2	3.4445	0.3884
QLDFNSSKDVAVMQLR	1852.1	2	3.5393	0.3165
QLDMFKTNLEEFASK	1802.0	2	3.4121	0.273
QLDSYKNGFLNLALPFFGFSEPLAAPR	3014.4	3	5.5007	0.4674
QLEAIDQLHLEYAK	1671.9	2	4.1469	0.4189
QLEDGDQPESK	1246.3	2	2.7157	0.1512
QLEDGRTLSDYNIQKESTLHLVLR	2830.1	3	4.6765	0.2544
QLEDLVEELSFSR	1565.7	2	3.7967	0.21
QLEEAEEEAQR	1332.4	2	3.798	0.3252
QLEEAEEEASR	1291.3	2	3.0975	0.2631
QLEEAEEEATR	1305.3	2	3.3176	0.2144
QLEEAEEEATRANASR	1804.9	3	3.2482	0.3232

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QLEEEKNSLQEQQEEEEEARK	2604.7	3	5.0242	0.2095
QLEEEKNSLQEQQEEEEEARKNLEK	3089.2	3	4.6481	0.181
QLEEKEKLLATEQEDAAVAK	2244.5	3	4.8825	0.3759
QLEESVDALSEELVQLR	1959.1	3	4.1071	0.3307
QLEETKALQGQISSQQVAVEK	2315.6	3	3.3029	0.2231
QLEIAHEKLR	1237.4	2	2.674	0.1305
QLEKDFSSMK	1213.4	2	2.6275	0.1176
QLEMILNKPGLK	1384.7	2	3.4209	0.3018
QLEPVYNSLAK	1262.4	2	2.4321	0.1022
QLEQSEKDLVK	1317.5	2	3.2854	0.2232
QLEQTLKQFHIK	1513.8	2	3.3789	0.2487
QLESLPATHIR	1265.4	2	2.7581	0.1263
QLESNKIPELDMTEVVAPFMANIPLLLYPQDGPR	3841.4	3	4.6317	0.2755
QLESTQTESNKK	1393.5	2	3.5191	0.3382
QLETLGQEK	1046.2	1	1.8862	0.1234
QLETLGQEKLKLEAELGNMQGLVEDFK	3062.5	3	3.7829	0.188
QLETLGQEKLKLEAELGNMQGLVEDFKNKYEDEINKR	4352.9	3	3.6226	0.2485
QLETVLDDLDPENALLPAGFR	2327.6	2	2.5913	0.1801
QLEVEPEEPEAENKHKPR	2160.3	2	2.7231	0.3263
QLEVVHTLDGKEYITPAQISK	2370.7	3	4.9054	0.4396
QLFHPEQLITGK	1411.6	2	2.7604	0.2985
QLFHPEQLITGKEDAANNYAR	2416.6	3	4.4084	0.4483
QLFLQTYAR	1140.3	2	2.5813	0.3461
QLFVLAGSAEEGVMTPELAGVIKR	2516.9	3	4.3439	0.3541
QLGAAERDFIHTASISFLTPLR	2444.8	3	4.3011	0.371
QLGDAFADLSLK	1278.4	2	2.8097	0.1921
QLGGSVELVDIGK	1315.5	2	3.2979	0.3943
QLGGSVELVDIGKQKLPDGSEIPLPPILLGR	3240.8	3	4.6952	0.3674
QLGNLGVLGITAPVQYGGSGLGYLEHVLVMEEISR	3672.2	3	3.5904	0.2235
QLGQDLLNSYIENEGK	1822.0	2	3.4659	0.4686
QLGTAYVSATTGAVATALGLK	1994.3	2	4.7764	0.5366
QLGTVQQVISER	1358.5	2	3.0432	0.3598
QLHDDYFYHDEL	1595.6	2	3.2616	0.3686
QLHELAPSIFFYLVDAEQGR	2334.6	2	2.4258	0.1995
QLHEQAMQFGQLLTHLDTTQQMIANSLK	3226.7	3	4.2132	0.2828
QLHQLLPNHVLQK	1568.8	2	3.7019	0.2062

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QLIAELENKNREILQEIQR	2338.6	3	3.3991	0.2526
QLIMANPQMQQLIQR	1813.2	2	3.6188	0.4174
QLIVGVNK	871.1	1	2.545	0.1387
QLIVKEYQAAYGK	1511.7	2	3.6234	0.2804
QLIVPPHLAHGESGAR	1682.9	2	2.9417	0.2388
QLIYNYPEQLFGAAGVMAIEHADFAGVER	3211.6	3	4.9386	0.4322
QLKTAEDYQALNKDIEAQLQHAGLR	2855.2	3	3.5669	0.2776
QLLAEESLPTTPFYFILGK	2168.5	2	4.286	0.1945
QLLAGGIAGAVSR	1213.4	2	4.3163	0.3501
QLLAGLDKVASDLDRQEK	2000.2	3	3.5205	0.3778
QLLDDEEQLTAK	1403.5	2	3.3398	0.2562
QLLDEVEVATEPAGSR	1714.9	2	3.3194	0.173
QLLDLDPEVECLK	1515.8	2	2.7463	0.1048
QLLDQVEQIQK	1342.5	2	3.5478	0.1324
QLLDQVEQIQKEQDYQR	2162.3	2	3.7551	0.2587
QLLGEHLTAILQK	1464.7	2	3.5529	0.2961
QLLGHMEDLEGDAQSVLDAR	2198.4	3	3.7679	0.1207
QLLHLAEEKQTK	1438.7	2	2.7523	0.229
QLLHNFPPDQLTSSGAPFWSGPKR	2682.0	3	3.536	0.3102
QLLLESQSQLDAAK	1544.7	2	4.2575	0.2959
QLLLESQSQLDAAKSEAQKQSDELALVR	3100.4	3	5.3292	0.4626
QLLLQEVENHKK	1479.7	2	2.8911	0.1518
QLLLTADDR	1045.2	2	2.6035	0.1653
QLLLTADDRVNPCIGGVILFHETLYQK	3058.5	3	7.2299	0.4522
QLLQANPILEAFGNAK	1728.0	2	4.9632	0.2974
QLLQANPILESFGNAK	1744.0	3	4.5786	0.3814
QLLQEQESVKQAHLR	1808.0	2	4.0212	0.3502
QLLSDYGPPSLGYTQGTGNSQVPQSK	2723.9	3	4.0161	0.2531
QLLSNPEMMVQIMENPFVQSMLSNPDLMR	3395.0	3	4.0658	0.3253
QLLSPGTALILLEAQAASGFLLDPVR	2695.2	2	4.8524	0.4452
QLLTLSSELSQAR	1446.6	2	4.3164	0.3434
QLLTLSSELSQARDENKR	2089.3	2	3.2908	0.1943
QLMETPANEMTPTR	1619.8	2	3.1281	0.2337
QLNDLWDQIEQAHLELR	2122.3	3	4.1443	0.2816
QLNDVKTTVVYPATEK	1807.0	2	3.2343	0.2896
QLNEINYEDHKLK	1644.8	2	3.4353	0.241

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QLNQFPDFNNYLIFVLTR	2243.5	2	2.7825	0.2458
QLNSTVSSLHSR	1329.4	2	3.4601	0.326
QLNTALPQEFAALTK	1645.9	2	3.1732	0.1787
QLPAMTALQTLHLR	1593.9	2	3.485	0.2464
QLPDKWQHDLFDSGFGGGAGVETGGK	2704.9	3	4.1774	0.3237
QLPFRGDDGIFDDNFIEER	2284.4	3	3.6491	0.2849
QLPFRGDEGIFEESFIEER	2299.5	3	3.6774	0.3056
QLPPTGTPTSKLFIIR	1770.1	2	2.9059	0.1552
QLPQDLGTAYYLTSQAMVDNLALR	2683.0	2	3.5818	0.3905
QLPQDLGTAYYLTSQAMVDNLALRDGQEGITAFLQK	3971.4	3	4.5098	0.3668
QLPTLILFQGGK	1315.6	2	3.0969	0.1562
QLPTSEAVVSAVSEAGASGITEAQAR	2530.7	3	3.8544	0.1906
QLPYYYLSPDRIPNSVAI	2110.4	2	2.7312	0.2172
QLQAETEPIVK	1256.4	2	3.0142	0.1956
QLQALSSELAQARDETKKTQNDVLHAENVK	3366.7	3	6.022	0.4011
QLQEELAEHQVPVEKLQK	2147.4	3	3.9368	0.1588
QLQEERPELSESELTR	1945.1	2	3.1025	0.3136
QLQEETPPGGPLTEALPPAR	2102.3	2	3.0537	0.2131
QLQEYLAQGK	1178.3	2	2.976	0.2579
QLQFLETQLAQVSQHVSDLEEQKK	2828.1	3	4.3398	0.3019
QLQGPEKEPPKPEQVESR	2077.3	3	3.9863	0.2508
QLQIILSKMQDIPIYANVHK	2353.8	3	3.4225	0.147
QLQLAQEAAQK	1228.4	2	2.856	0.2068
QLQLITSLKEQAIGEYEDLRAENQK	2919.2	3	4.5648	0.4735
QLQLQNQELLR	1383.6	2	2.5755	0.147
QLQNIIQATSR	1272.4	2	3.4914	0.2517
QLQQAVTGISNAAQATASDDASQHQGGGGGELAYALNNFDK	4106.3	3	6.2237	0.426
QLQQELEAFRGQLGDVGALDTVWR	2731.0	3	3.563	0.3613
QLQQQREEKEQHGLQLQSEINQLHSK	3158.4	3	3.8991	0.299
QLQSEQPQTAAAR	1428.5	2	4.2831	0.3802
QLQSEQPQTAAARS	1515.6	2	4.511	0.4017
QLQVVPLFGDMQIELAR	1958.3	2	2.7012	0.2479
QLRADMEDLMSSKDDVGKNVHELEK	2889.2	3	3.8274	0.1426
QLRDAQQDAR	1201.3	2	2.7284	0.1089
QLREQVNDLFSR	1505.7	2	2.9165	0.2419
QLREYQELMNVK	1551.8	2	3.8108	0.1619

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QLREYQELMSVK	1524.8	2	3.6717	0.3242
QLRQTMAKFLQEHLAPKAQEIDRSNEFKNLR	3742.3	3	3.3267	0.1119
QLSAFGEYVAEILPK	1665.9	2	3.6577	0.2908
QLSILVHPDKNQDDADRAQK	2292.5	3	3.486	0.2451
QLSLARPQAPALHLR	1672.0	2	3.3207	0.185
QLSLPQQEAQK	1270.4	2	2.8529	0.1578
QLSNPQQEVQNIFK	1673.9	2	4.1358	0.3566
QLSPTEAFPVLVGDMDNSGSLNAQVIHQLGPGLR	3563.0	3	3.966	0.359
QLSQATAAATNHTTDNGVGPEEESVDPNQYYK	3437.5	3	5.9366	0.3879
QLSQQSDGDRDLQEHR	1913.0	3	3.3219	0.2929
QLSSGVSEIR	1076.2	2	2.7246	0.2628
QLSSSGRPTASVIPSGVEWIK	2200.5	2	3.6489	0.2218
QLSVVVPSYNEEK	1492.7	2	3.1902	0.2363
QLTAHLQDVNRELTNQQEASVER	2680.9	3	3.7635	0.2103
QLTEKMESDR	1237.4	2	2.4839	0.1277
QLTEMLPSILNQLGADSLTSLR	2401.8	2	5.4831	0.436
QLTLLGGPTPNTGAALEFVLR	2169.5	2	4.4782	0.4346
QLTVQMMQNPQILAALQER	2213.6	2	5.9532	0.4439
QLTVQMMQNPQILAALQERLDGLVETPTGYIESLPR	4055.7	3	5.6471	0.3704
QLTVTQQSQEEVAR	1617.7	2	4.2409	0.3502
QLVARPDVVEMHDVTAQDPK	2249.5	3	4.5952	0.2638
QLVDTTVELANKVGAAEIISR	2228.5	2	2.7323	0.1925
QLVEKGPQYGTVEK	1576.8	2	2.6768	0.1699
QLVEQVEQIQK	1342.5	2	4.0236	0.1759
QLVFHIGHGDLGSPAVLVSR	2103.4	2	3.9516	0.4278
QLVHELDEAEYR	1502.6	2	3.3167	0.3276
QLVHSFTEGR	1174.3	2	2.9769	0.4111
QLVMNHMHHEDQQVR	1903.1	2	2.6127	0.3005
QLVSEGNIHADKIR	1580.8	2	3.0846	0.4157
QLVSKPLSSSVSNNKR	1745.0	2	4.0963	0.3498
QLWGLLIEETEKR	1615.9	2	3.4095	0.2547
QLYEEEIRELQSQISDTSVVLSMDNSR	3171.4	3	5.6615	0.4967
QLYEFDIKVPLLVR	1734.1	2	4.0524	0.3488
QLYESLMAAHASR	1477.7	2	2.5814	0.1303
QLYHLGVVEAYSGLTK	1779.0	2	3.5978	0.3072
QLYVLGHEAMK	1289.5	2	3.1812	0.2458

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QLYVLGHEAMKR	1445.7	3	3.5496	0.3459
QMADTGKLNTLLQR	1589.8	2	3.721	0.3935
QMAEIAVNAVLTVADMER	1962.3	2	3.1354	0.2855
QMAYENLNDKDQELGEYLAR	2401.6	3	6.2094	0.4811
QMEQISQFLQAAER	1679.9	3	5.0666	0.401
QMFAQMYQK	1175.4	2	2.4443	0.1331
QMFEGEVASLEALR	1580.8	2	4.3125	0.3757
QMFGNADMNTFPTFK	1750.0	2	3.7995	0.3346
QMFGNADMNTFPTFKFEDPKFEVIEKPQA	3408.8	3	3.7968	0.2665
QMGFPLIYVEAEQVEDDRLLR	2522.9	3	3.3388	0.1745
QMIAVADENQNHHLEPEEVLKYSEFFTGSK	3492.8	3	3.3708	0.1717
QMIGYNLATK	1139.4	2	2.42	0.2706
QMKDKQDEEQR	1435.5	2	2.7538	0.2046
QMNDEKTAADYK	1414.5	2	3.0273	0.1924
QMNQTLQDKTNQIDLLQAEISENQAIIQK	3357.7	3	5.1448	0.2836
QMQVLHPAAR	1151.4	2	2.4496	0.1683
QMTEAIGPSTIRDLAVAGPEMQVK	2543.9	3	4.1839	0.2188
QMVIDVLHPGK	1237.5	2	2.9412	0.2303
QMVIDVLHPGKATVPK	1734.1	2	4.5706	0.3316
QMVKEGGIR	1018.2	2	2.5035	0.1784
QNALLFAEEEDGEAGAE	1793.8	2	4.3628	0.3547
QNALLFAEEEDGEAGAED	1908.9	2	5.4042	0.5061
QNCELFEQLGEYK	1601.8	2	4.1646	0.3012
QNCELFEQLGEYKFQNALLVR	2543.9	3	5.1375	0.4352
QNDQVSFASLVEELKK	1836.0	3	4.1314	0.3087
QNFTEPTAIQAQGWPVALSGLDMVGVAQTGSGK	3360.7	3	5.7494	0.55
QNISPDKIPWSALK	1597.8	2	2.7953	0.1443
QNKLEQVEKELLR	1627.9	2	3.7493	0.2952
QNLFQEAEEFLYR	1687.8	2	4.6199	0.2978
QNLFTTWSHHLQQANIQFR	2370.6	3	4.3146	0.3729
QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK	4138.5	3	4.0013	0.2808
QNLLSQSHAYQQFLR	1834.0	3	3.3208	0.1393
QNLSKEELIAELQDCEGLIVR	2401.7	3	3.7592	0.2511
QNLSQFEAQAR	1292.4	2	3.4217	0.3002
QNLSQVPEADSVSFLQELLALR	2458.8	3	4.2243	0.3196
QNNEYQVLLGIK	1419.6	2	3.3377	0.28

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QNPKDIHTLAQLISAYSLVDPEKAK	2781.2	3	3.49	0.31
QNQFYDTQVIKQENESGYER	2477.6	3	3.8281	0.235
QNQLLLERQSLSEEVDR	2058.2	2	2.8168	0.1344
QNRDEVLDNLLAFVCDIRPEIHENYR	3173.5	3	3.7138	0.2592
QNRFEIVYNLLSLR	1766.0	3	4.4501	0.3226
QNSLTQFMSIPSSVIHPAMVR	2344.7	3	3.7356	0.1981
QNVQVFEFQLTAEDMK	1928.2	2	4.5899	0.3703
QNVQVFEFQLTSEEMK	1958.2	2	4.398	0.4295
QNVQVFEFQLTSEEMKAIDGLNR	2698.0	3	3.4945	0.287
QNYHQDSEAAINR	1546.6	2	3.5771	0.3453
QNYVDLVSSLSPSLESSSQVEPGTDR	2796.0	2	2.4559	0.1859
QNYVDLVSSLSPSLESSSQVEPGTDRK	2924.1	3	3.9679	0.2822
QPAENVNQYLTDPK	1617.7	2	3.476	0.3474
QPELPEVIAMLGFR	1600.9	2	2.5775	0.1565
QPPLLGDHPAEYGGPHGGYHSHYHDEGYGPPPPHYEGR	4177.4	3	4.0082	0.3286
QPPPDSSEEAPPATQNFIIPK	2264.5	3	3.9968	0.2017
QQAAYYAQTSPQGMPQHPPAPQGQ	2582.8	3	5.03	0.4541
QQADFVDLSFPTISSTGPNGAIIHYAPVPETNR	3544.9	3	4.4577	0.3863
QQDAQEFFLHLINMVER	2119.4	3	3.9221	0.3858
QQDVLGFLEANK	1362.5	2	2.8103	0.241
QQDVLGFLEANKIGFEEKDIAANEENRK	3207.5	3	4.6564	0.3782
QQEADIQNSKFSYEQLETDLQASR	2830.0	3	3.7941	0.2624
QQEELLAEENQR	1487.6	2	3.2321	0.2165
QQEPVTSTSLVFGK	1521.7	2	2.5218	0.1687
QQEQADSLER	1204.2	2	2.8202	0.2401
QQETAAAETETR	1335.4	2	3.2004	0.3138
QQETAAAETETRTHTLTR	2045.2	2	2.7357	0.1992
QQETHLKQQLALYTEKFEEFQNTLSK	3183.5	3	4.5023	0.3856
QQEVVVAGSSLPTSSK	1617.8	2	4.1702	0.3786
QQFEGYGLEIPDILNASNLK	2250.5	2	4.2141	0.4154
QQFMTTQDASK	1285.4	2	2.4861	0.3317
QQFMTTQDASKDGR	1613.7	2	3.4517	0.3196
QQGVLALRPYLQK	1514.8	2	3.5845	0.2677
QQHLSSLQDYMQR	1634.8	2	2.7632	0.3202
QQHQEQQALQQSTTAK	1855.0	3	4.5671	0.4065
QQHVIETLIGK	1266.5	2	2.5022	0.3145

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QQIAEIEKQTKEQSQLTATQTR	2560.8	3	4.4534	0.293
QQIESEVANLKK	1387.6	2	2.7122	0.121
QQIQSIQQSIER	1458.6	2	3.4196	0.2653
QQKLEQLELEKQKLQEEQENAPEFVK	3185.5	3	4.4274	0.2213
QQLAQYQQQQSQASAPSTSR	2236.3	3	3.7734	0.17
QQLELLEEDKKELELK	1986.3	2	3.586	0.2038
QQLGTAVEMEIAQMLEENSR	2278.6	2	2.4146	0.222
QQLNIHGLLPPSFNSQEIQVLR	2532.9	3	4.7797	0.3183
QQLNNMSFAEIIMGYK	1888.2	2	3.1778	0.2119
QQLQALSEPQPR	1395.5	2	3.4618	0.235
QQLQQVPGLLHR	1417.6	2	2.5306	0.129
QQLSAEELDAQLDAYNAR	2036.1	2	5.7788	0.5001
QQLSEMKSHVEDGDIAGAPASSPEAPPAEQDPVQLK	3759.1	3	5.6695	0.4804
QQLVASHLEKLLGPDAAINLTDPDGALAKR	3156.6	3	5.4324	0.5176
QQLVDKHSTGGVGDK	1569.7	2	2.935	0.2648
QQLVELVAEQADLEQTFNPSDPDCVDRLLQCTR	3776.2	3	5.2183	0.347
QQMAEEMVEAAGEDERELAAEMAAAFLNENLPESIFGAPK	4339.8	3	4.6303	0.3668
QQMLENQMEVR	1406.6	2	3.1711	0.2026
QQNELAELHANLAR	1607.8	2	3.7151	0.2968
QQPDTELEIQQK	1457.6	2	3.0097	0.1217
QQPEVEVTHETLQR	1694.8	2	3.2409	0.3
QQPMALAVALTK	1271.6	2	2.644	0.2613
QQPPDLVEFAVEYFTR	1940.1	3	4.4693	0.4977
QQPPNSFSQQHSETQGAEKPDPESSHSPPR	3316.4	3	4.0266	0.1959
QQPTQFINPETPGYVGFANLPNQVHR	2954.2	3	4.7746	0.4109
QQQEELEAEHGTGDKPAAPR	2192.3	3	3.7819	0.2715
QQQEKGEAEALSR	1474.6	2	2.8658	0.1253
QQQKAQLEQLEVQ	1570.7	2	4.779	0.2466
QQQPLALTQQEQQQPLTLPQQQR	2859.1	3	5.5618	0.3995
QQQQQQNDVVK	1343.4	2	3.1677	0.2591
QQQVEAVELEAK	1372.5	2	2.7834	0.1524
QQQVLPLDPAEPEIR	1733.9	2	2.7815	0.1929
QQREDITQSAQHALR	1781.9	2	5.0438	0.4419
QQRNEVSFVIHNLPVLAK	2093.4	3	4.8855	0.3204
QQSEEDLLLQDFSR	1708.8	2	4.456	0.4518
QQSHFAMMHGGTGFAGIDSSSPEVK	2607.9	2	4.2578	0.3865

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QQSIAGSADSKPIDVSR	1759.9	2	4.0338	0.5137
QQSLETAMSFVAR	1468.7	2	3.4176	0.3588
QQSPGLGRPIWLQIAESAYR	2271.6	3	3.4055	0.2016
QQTHMLDVMQDHFSR	1874.1	3	3.6344	0.4411
QQVAFYGQTLGQAQAHSQEQ	2220.3	3	4.303	0.2509
QQVAPTDDETGKELVLALYDYQEK	2755.0	3	3.9757	0.2526
QQVASLETNDPILGFQATNER	2332.5	2	3.7032	0.314
QRDEKDEHGR	1270.3	2	3.1497	0.1645
QRDSEMGQQSLLFQIDYPEIAEGIMPR	3153.5	3	4.8223	0.2495
QRDYILEGEPGKVSNLQYLHSYLTYIK	3229.6	3	3.6502	0.2197
QREEEIEAQEK	1389.5	2	3.4565	0.1781
QREEELELIDQLRK	1800.0	3	3.9146	0.1391
QREEIKFSHTE	1404.5	2	2.4719	0.2363
QREELGQGLQGVEQK	1699.8	2	4.3609	0.2355
QREELGQGLQGVEQKVQSLQATFGTFESILR	3478.9	3	5.0072	0.333
QREEYQPATPGLGMFVEVKDPEDK	2765.0	3	4.5922	0.3098
QREIEMNR	1076.2	2	2.545	0.1496
QRELAEQELEKQR	1657.8	3	3.7185	0.2262
QREMEEQMR	1237.4	2	2.9653	0.2772
QREPGLGFSFEFTEQQKEFQATAR	2833.1	3	3.8572	0.2259
QREQLDKIQSSHNFQLESVNK	2529.8	3	4.3768	0.3089
QRFDHIFYTGNTAVGK	1855.0	2	3.301	0.2314
QRFPLGGDDEVMSSTLQQFSK	2371.6	3	3.728	0.263
QRGCVHLREIQSLWVEAR	2181.5	3	4.8712	0.1244
QRHELLLGAGSGPGAGQQQATPGALLQAGPPR	3135.5	3	7.0381	0.5444
QRHPFLLLGTTANR	1624.9	3	3.9095	0.3087
QRLDEYKR	1108.2	2	2.9675	0.13
QRMDLVEAFNHSR	1603.8	2	3.5635	0.2147
QRPAAGAPPELHSLR	1600.8	3	3.298	0.1587
QRPEPQVTGTVGLHLGVTPSVIR	2442.8	3	3.6605	0.124
QRPIHLSFDIDAFDPTLAPATGTPVVGGLTYR	3427.9	3	5.388	0.381
QRQEELCLAR	1246.4	2	3.144	0.281
QRQEVCQSYK	1269.4	2	3.142	0.2191
QRQLAEEDAAR	1287.4	2	3.0828	0.2851
QRQPPGTQQSHSSPGEITSSPQGLDNPALLR	3285.5	3	3.8164	0.212
QRRPLRPQVVTDDDGQAPEAK	2377.6	3	3.251	0.2308

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QRRSESPDSRKRRIHRCDFEGCNKVYTK	3453.9	3	3.5896	0.1492
QRSQVEEELFSVR	1607.8	2	3.3041	0.3003
QRVDVEDLGVDFLTIVGHK	2141.4	3	6.2928	0.4124
QRVEAAVGEDLFQEAHEVILK	2382.7	3	7.6348	0.4496
QRVLGPGPHALQLEER	1801.0	2	2.8698	0.108
QRYEDQLKQQQLLNEENLR	2446.7	3	4.5158	0.2956
QRYEILTPNAIPK	1543.8	2	3.4363	0.2424
QRYEILTPNSIPK	1559.8	2	3.6707	0.2357
QSAEKLIEEKGAVEALAAALAHISGATSVDQR	3265.6	3	4.1339	0.3044
QSAERNSNLVGAAHEELQQSR	2325.4	3	3.8189	0.2522
QSDDEVYAPGLDIESSLKQLAER	2564.7	3	4.2425	0.2737
QSDEVGDRDHR	1314.3	2	2.5838	0.1281
QSDVMIVAGTLTNK	1477.7	2	4.5728	0.4018
QSEGLTKEYDRLLEEHAK	2147.3	3	3.4747	0.2427
QSFGAVTPGYDFMAR	1647.8	2	2.9743	0.1038
QSFTMVADTPENLR	1609.8	2	4.391	0.4216
QSGAFLSTSEGLILQLVGDAVHPQFK	2744.1	3	5.0165	0.5122
QSGAFLSTSEGLILQLVGDAVHPQFKEIQK	3242.7	3	3.8881	0.3164
QSHLLLQSSIPDQQLLK	1949.2	2	4.7063	0.419
QSHSESPSLQSK	1315.4	2	2.8682	0.2782
QSHTLPFPPPPALPFYPASAYPR	2552.9	3	6.4528	0.3725
QSIINPDWNFEK	1491.6	2	3.7732	0.2942
QSINTIESLKDVKDAVVQHSQLAAAVENLK	3250.6	3	5.2447	0.4408
QSIWTSTISSHLATK	1660.9	2	4.718	0.4068
QSKPVTTPEEIAQVATISANGDKEIGNIISDAMK	3558.0	3	4.9048	0.4475
QSKPVTTPEEIAQVATISANGDKEIGNIISDAMKK	3686.1	3	3.6457	0.3016
QSLEEQKKLEGELTEEVEMAKR	2605.9	3	3.4728	0.3569
QSLFATKPGGGALVLLEA	1773.1	2	3.2185	0.1845
QSLFFYPSYPDEVR	1748.9	2	4.4642	0.387
QSLGELIGTLNAAK	1415.6	2	4.9219	0.4221
QSLQVIESAMER	1391.6	2	2.7747	0.103
QSMAFSILNTPK	1337.6	2	3.5682	0.2903
QSPEHNLTHPELSVAVEMLSSVALINR	2973.4	3	4.4301	0.1964
QSPENAASPQATNSTQVSQPSGAMTR	2646.8	3	3.8801	0.3093
QSPQLPQAFYPVGHPVDVSFGDLLAAR	2911.3	3	4.0428	0.4875
QSPVAMETASTGVAGVSSAMDHTFSTTSK	2887.2	3	3.8497	0.3789

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QSPVDIDTHTAK	1312.4	2	3.2706	0.2691
QSPVDIDTHTAKYDPSLKPLSVSYDQATSLR	3434.8	3	3.4551	0.2693
QSQADYETR	1098.1	2	2.801	0.2122
QSQEASNHSSHTAQTPGI	1880.9	2	2.5656	0.236
QSQHDKIDASELSFPFHESILK	2557.8	3	3.9457	0.1846
QSRGEPPLPEEDLSKLFKPPQPPAR	2815.2	3	3.4691	0.1458
QSRLEQEEQQRLAELSK	2073.3	3	3.2914	0.1356
QSSATSSFGGLGGGSV	1399.4	2	4.388	0.346
QSSATSSFGGLGGGSVR	1555.6	2	4.654	0.4488
QSSGASSSSFSSSR	1362.3	2	2.7016	0.13
QSSGPGASSGTSGDHGELVVR	1986.0	2	3.1015	0.2696
QSSSSTTSQGGVKR	1410.5	2	2.5338	0.3072
QSSSTNYTNELK	1372.4	2	2.7867	0.255
QSSVAEEVGLLPQQIQAVRDDVESQFPAWISQFLAR	4044.5	3	4.4088	0.3874
QSTSFLVLQEILESEEKGDPNKPSGFR	3037.3	3	3.5184	0.1874
QSTTHLADGPFAVLVDYIR	2104.4	3	3.6522	0.2261
QSVEDILKDHWQK	1626.8	2	2.835	0.2233
QSVENDIHGLR	1268.4	2	2.6388	0.3083
QSVENDIHGLRK	1396.5	2	3.0098	0.3172
QSVFKDFYELEPEK	1759.9	2	2.8866	0.2518
QSVFPFESGKPFK	1498.7	2	3.079	0.2929
QSVHIVENEIQASIDQIFSR	2314.5	3	3.679	0.2161
QSVLEGLSFSR	1223.4	2	3.265	0.3
QSVLNLMTHSVNQGQNIHR	2177.4	3	3.2813	0.1704
QSVYEEKLKQFEER	1814.0	2	3.0771	0.3026
QSYKGSPMEISLPIALSK	1950.3	2	3.0697	0.2519
QTAQQIVSHVQNK	1481.6	2	3.4409	0.3385
QTASVTLQAIAAQNAAVQAVNAHSNILK	2834.2	3	5.5387	0.4612
QTDDLRGEIAVLEATVQNNQDER	2615.8	3	4.6616	0.3439
QTDVGITHFR	1174.3	2	2.5352	0.2805
QTDVLQQLSIQMANAK	1789.0	3	4.3266	0.3248
QTELESLSSELSEVLK	1793.0	2	2.8132	0.1351
QTELFAHFIQPAAQK	1730.0	2	2.7748	0.2728
QTESLESLLSK	1235.4	2	2.8185	0.2219
QTESLESLLSKSQEHEQR	2130.3	2	3.9112	0.4214
QTEVLLQPNPNAR	1480.7	2	3.2777	0.1244

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QTFTHNPLLQPGKDNPPNIPSSSSKPK	2931.3	3	4.6894	0.2999
QTGQWIGMVENFNQALKEIGDVENWAR	3135.5	3	3.5508	0.3176
QTIDNSQGAYQEAFDISK	2016.1	2	5.6105	0.4915
QTIDNSQGAYQEAFDISKK	2144.3	2	4.7777	0.4049
QTIERLEQEHTNR	1654.8	2	2.7541	0.1555
QTIGNSCGTIGLIHAVANNQDKLGFEDGSVLK	3301.7	3	5.4977	0.3746
QTIMETLEQGPAQASPSYVPLFKDIVVPSLNVAK	3673.2	3	4.185	0.2702
QTISEKEVELQHIR	1710.9	3	3.5537	0.2757
QTLENERGELANEVK	1730.9	2	3.9074	0.2957
QTLSTPGTIILGTIPVPK	1837.2	2	3.7059	0.2727
QTMQVDEHARPQTTLEQLQK	2382.6	3	3.6357	0.3161
QTNLENLDQAFSVAER	1836.0	2	3.7356	0.3678
QTNPSAMEVEEDDPVPEIR	2157.3	2	4.5478	0.396
QTNPSAMEVEEDDPVPEIRR	2313.5	2	2.7661	0.2593
QTQIFTTYSDNQPGVLIQVYEGER	2788.0	2	6.9521	0.4669
QTQTFTTYSDNQPGVLIQVYEGER	2776.0	3	6.4815	0.509
QTQVSVLPEGGETPLFK	1831.1	2	4.2663	0.3931
QTSGGPVDASSEYQQELER	2082.1	2	5.5901	0.562
QTSGGPVDASSEYQQELERELFK	2599.7	2	3.2542	0.3643
QTTSNLGHLNKPSIQALIHGLNR	2513.8	3	4.6929	0.3664
QTTVSNSQQAYQEAFEISK	2160.3	2	5.6716	0.5092
QTVAVGVIK	915.1	1	1.86	0.202
QTVVSDTELSIVESSVISLLQEAESKSELSQNISAR	3879.2	3	3.7315	0.3597
QTYFLPVIGLVDAEK	1694.0	2	3.7569	0.3601
QTYSTEPNNLK	1295.4	2	2.7516	0.2615
QVAAVGQEPQVFGR	1486.7	2	3.5168	0.4715
QVAGTMKLELAQYR	1608.9	2	3.1199	0.2886
QVAGTMKLELAQYREVAAFAQFGSDLDAATQQLLSR	3929.4	3	5.305	0.3876
QVAQQEAER	1059.1	2	2.667	0.1542
QVASHVGLHSASIPGILALDLCPSDTNK	2845.2	3	6.0622	0.3792
QVATALQNLQTK	1315.5	2	3.1568	0.2541
QVAVAELLENVGQVNEHDGGAQPGPVPK	2854.1	3	4.7394	0.4027
QVDQLTNDKAR	1288.4	2	2.4327	0.1024
QVDVPTLTGAFGILAAHVPTLQVLRPGLVVVHAEDGTTSK	4109.7	3	4.0063	0.3476
QVEDDIQQLLKK	1457.7	2	2.8579	0.1164
QVEEALHQLHAR	1431.6	2	3.309	0.3438

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QVEGKNPVTIFSLATNEMWR	2321.6	2	3.6966	0.3639
QVEHPLLSGLLYPGLQALDEEYLK	2727.1	3	4.7914	0.4402
QVEHPLLSGLLYPGLQALDEEYLKVDAQFGGIDQR	3914.4	3	3.6379	0.2695
QVEILNRYPHFK	1544.8	2	3.1471	0.3914
QVENAGAIGPSR	1199.3	2	2.6024	0.1839
QVEVDCQQCMLEILDTAGTEQFTAMR	2961.4	2	3.0154	0.1809
QVEVFRQNLFQEAEEFLYR	2446.7	3	3.6366	0.2525
QVEYLVNEKHIYLLPSGR	2159.5	2	4.6717	0.4459
QVFAENKDEIALVLFGTDGTDNPLSGGDQYQNITVHR	4064.4	3	4.7832	0.207
QVFFELNGQLR	1351.5	2	2.7915	0.1299
QVFGEATK	880.0	1	1.9398	0.1159
QVFGEATKQPGITFIAAK	1907.2	2	4.7083	0.4156
QVFGEATKQPGITFIAAKFDGILGMAYPR	3128.6	3	6.3898	0.4913
QVGETSAPGDTLDGTPR	1701.8	2	3.7904	0.268
QVHPDTGISSK	1169.3	1	2.2233	0.361
QVHPDTGISSKAMGIMNSFVNDIFER	2895.3	3	3.6545	0.2655
QVHPFHVYPQPGMQR	1822.1	2	2.9076	0.1251
QVIDVLETDKHFR	1600.8	2	3.4178	0.2481
QVIPGLEQSLLDMCVGEK	1960.3	2	2.7829	0.3071
QVIQGLEALKNEHNSILQSLLETLK	2820.2	3	4.7469	0.3936
QVIQQNPALLPALLQQLGQENPQLLQQISR	3380.9	3	6.7431	0.5359
QVKIDQIEDLQDQLEDMMEDANEIQEALSR	3548.9	3	5.228	0.3409
QVKPYVEEGLHPQIIIR	2020.4	2	3.6557	0.3805
QVLALQSQLADTK	1415.6	2	2.9831	0.2507
QVLDLEDLVFTQGSHFMANKR	2449.8	3	3.302	0.1649
QVLDSKAPKPEDIDEEDDDVPDLVENFDEASKNEAN	4032.2	3	3.5993	0.2028
QVLEELTELPVMVELASDFLDR	2547.9	3	4.5506	0.5081
QVLEGEEIAYK	1279.4	2	2.7125	0.2305
QVLFSADDRVK	1278.4	2	3.0614	0.2248
QVLGQMVIDEELLGDGHSYSPR	2444.7	3	4.2075	0.4897
QVLHGEALAGQAK	1322.5	2	2.9032	0.3027
QVLKYDDFLK	1269.5	2	2.6867	0.1558
QVLLSAAEAAEVILR	1583.9	2	5.0031	0.4647
QVLLSAAEAAEVILRVDNIIK	2266.7	3	3.774	0.2523
QVLLSEPEEAAALYR	1689.9	2	4.2302	0.3589
QVLLYEPQVNSPKDFTEGTLFSVNQEFSLIK	3573.0	3	4.3091	0.2851

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QVLQLQASHR	1180.3	2	3.5093	0.2846
QVLQLQASHRESEEALQK	2095.3	2	4.3458	0.3424
QVLQSTQSPR	1144.3	2	3.051	0.2779
QVLSSLLSGALAGALAK	1599.9	2	3.2306	0.2825
QVMMFSATLSK	1243.5	2	2.5924	0.259
QVMYQQSSGR	1184.3	2	2.417	0.1465
QVNEMKNSMSETVR	1653.9	2	3.4875	0.3298
QVPGGGGGGGSGGGGGSGGGGSGGGR	1844.8	2	4.1374	0.4432
QVPNESFFNFFNPLK	1829.0	2	3.9693	0.2816
QVQFHQGFGDLAVLKPSNK	2114.4	3	3.6826	0.1897
QVQHEESTEGEADHSGYAGELGFR	2634.7	3	4.187	0.3639
QVQHILASASPSGR	1451.6	2	3.5804	0.3211
QVQRPGFFMEPTVFTDVEDYMYLAK	3013.4	3	4.7389	0.2299
QVQSLMVHQR	1226.4	2	3.2955	0.2049
QVQSLTCEVDALK	1434.6	2	3.1612	0.2423
QVQSLTCEVDALKGTNESLER	2321.6	2	4.8746	0.4861
QVQSQAHGLQMR	1383.6	2	3.1462	0.3413
QVQVALETAQR	1243.4	2	3.5084	0.1857
QVREPGQDLVVLPLSITTDFIPSFR	2829.2	3	4.5379	0.3235
QVRPVTEK	957.1	2	2.6239	0.2363
QVRPVTEKLPANHPLLTGQR	2255.6	3	4.9144	0.3684
QVTDAETKPK	1117.2	2	2.622	0.2101
QVTIKPVATAFLPVSAVKTAGSRVINLK	2910.5	3	3.2351	0.1018
QVTITGSAASISLAQYLINAR	2178.5	3	5.3407	0.439
QVTITGSAASISLAQYLINVR	2206.5	3	4.5243	0.4154
QVTQEEGQQLAR	1387.5	2	3.0903	0.1247
QVVAVTGDGTNDGPALK	1642.8	2	4.0306	0.2368
QVVAVTGDGTNDGPALKK	1771.0	2	3.5234	0.3405
QVVEAAQAPIQER	1439.6	2	4.2435	0.3976
QVVEEIFHPERPDSVDIEHMSSGLTDLLK	3322.7	3	4.6914	0.299
QVVNIPSFIVR	1272.5	2	2.9894	0.1947
QVVQTPNTVLSTPFR	1687.9	2	3.0072	0.1768
QVVSASYNSPIGLYSTSNIQDALHGQLR	3020.3	3	3.5745	0.2195
QVVSVVQDEEVGLPFEASPESPPPASPDGVTEIR	3563.9	3	4.8927	0.4213
QVVVEGQEPANFWMALGGK	2061.3	2	3.5095	0.2453
QVYDGFSFIGNTGPYEVSK	2109.3	2	4.3397	0.4773

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
QVYEEEYGSSLEDDVVGDTSGYYQR	2889.9	3	6.0924	0.5991
QVYQIVKPLNPNFCFLQCTSAYPLQPEDVNLR	3740.3	3	5.7032	0.3284
QVYVDKLAELK	1306.5	2	3.1434	0.1943
QWIQISDAVYHMVYEQAK	2210.5	2	2.5531	0.2085
QWYESHYALPLGR	1620.8	2	2.5538	0.1904
QYAGFSTVEESNKFYKDNIK	2369.6	3	3.5594	0.3036
QYAGYDYSQQGR	1436.5	2	3.8562	0.4474
QYALSLANLQMVLEHFQQEEK	2520.8	3	3.4496	0.1761
QYASLTGTQALPPLFSLGYHQSR	2536.8	3	4.9854	0.3927
QYATLDVYNPFETR	1717.9	2	3.3928	0.3252
QYDADLEQILIQWITTQCR	2338.6	2	3.2797	0.2672
QYDGIFYEFR	1338.4	2	3.1242	0.4024
QYEKSENDLKALQSVGQIVGEVLK	2677.0	3	4.4713	0.3941
QYELVVHTDIDAAK	1602.8	2	3.7277	0.2485
QYEQQTYQVIPEVIKNFIQYFHK	2945.3	3	3.8251	0.2798
QYETLAEMVVPR	1436.7	2	2.5136	0.1153
QYKIPDWFLNR	1480.7	3	3.46	0.2523
QYKPVVYSNTIQSLAAIVR	2151.5	2	3.706	0.372
QYLEELQSVQRELEVLSEQYSQK	2828.1	3	3.5142	0.1328
QYLVFHDGDSVVFAGPAGNSVETR	2566.8	3	5.0401	0.2637
QYMEGFNDELEAFKER	2007.2	2	3.1852	0.2718
QYMPWEAALSSLSYFK	1922.2	2	6.0829	0.5032
QYNGVPLDGRPMNIQLVTSQIDAQR	2815.2	3	4.3854	0.3109
QYNSFNFALLEDVQAK	1888.1	2	4.5254	0.4223
QYQHGSVSDTVFDSIPANPALLTYPRPGTSR	3376.7	3	5.1383	0.4428
QYSHHSSVQDAVSQLDSELMDITK	2719.9	3	3.8108	0.2701
QYSIEHVDLGAR	1388.5	2	2.5984	0.2027
QYSLQNWEAR	1295.4	2	2.607	0.2139
QYTSPEEIDAQLQAEK	1851.0	2	3.0992	0.1003
QYTSPEEIDAQLQAEKQK	2107.3	2	3.2647	0.425
QYWDEDLLMK	1341.5	2	2.8101	0.1212
QYYQQPTATAAAVAAAAQPQPSVAETYYQTAPK	3486.8	3	3.816	0.1067
QYYTLLNKAPEYLHR	1910.2	2	4.3979	0.3928
QYYTLLNQAPDMLHR	1864.1	2	4.3591	0.4075
RAAAEVNQDYGLDPK	1647.8	2	3.0442	0.2054
RAAATQPDAK	1029.1	2	3.0021	0.2177

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RAAATQPDAKDTPDEPWAFPAR	2412.6	3	3.5092	0.2099
RAAEDDEDDDVDTKKQK	1979.0	3	4.2587	0.3066
RAAEDDEDDDVDTKKQKTDEDD	2554.5	3	4.456	0.1259
RAAEEAEEAR	1132.2	2	3.1886	0.2486
RAAEEAER	932.0	2	2.745	0.1149
RAAEEEDEADPKR	1516.6	3	3.9456	0.2383
RAAEERQRAR	1243.4	2	2.738	0.1766
RAAELGAR	844.0	2	3.0834	0.1489
RAAGEVLEPANLLAEEKDEDLLFE	2672.9	3	3.9448	0.3198
RAASGYPVKVPLEVQEADEAK	2258.5	3	4.0003	0.1481
RAASGYPVKVPLEVQEADEAKLQQTEAELR	3327.7	3	7.6043	0.5021
RAAVAASSSS	907.0	2	2.5513	0.1812
RAAVIFADTLTLLFEGIAR	2078.4	2	2.5516	0.1328
RADDNATIR	1032.1	2	2.4704	0.2083
RADIKEDKDGK	1275.4	2	2.5858	0.2308
RADLNQGIGEPQSPSR	1725.8	2	4.4471	0.2957
RADPAELR	928.0	2	2.5946	0.1429
RADQLADESLESTR	1591.7	2	3.9393	0.3538
RADQLADESLESTRR	1747.8	3	3.6894	0.2918
RADTFDLQR	1122.2	2	2.6872	0.1092
RADVLAFPSSGFTDLAEIVSR	2252.5	3	5.0517	0.4493
RAEAEKQLQQAQAAGAEQEVEKFTK	2790.0	3	4.2802	0.269
RAEATAASTSR	1121.2	2	3.8293	0.3526
RAEDGIVLDLPLYPAHPQDFHEVEDLIK	3231.6	3	5.3653	0.3249
RAEDGSVIDYELIDQDAR	2066.2	3	5.9936	0.3975
RAEDGSVIDYELIDQDARDLYDAGVK	2928.1	3	5.0969	0.3148
RAEDGSVIDYELIDQDARDLYDAGVKR	3084.3	3	4.4723	0.3653
RAEDGSVIDYELIDQDARDLYDAGVKRK	3212.5	3	3.9711	0.2358
RAEDYPIDLYYLMDLSYSMKDDLENVK	3301.7	3	4.6369	0.3017
RAEFDIHR	1044.1	2	2.9333	0.346
RAEISNAIDQYVTGTIGEDEDLIKWK	2966.2	3	7.2771	0.4408
RAENYGPR	963.0	2	2.8697	0.2248
RAEQDSTTVAAFASSLVSGLNSSASEPAKEPAKK	3436.7	3	5.7486	0.4599
RAESLNGNPLFSK	1433.6	2	2.7701	0.2177
RAEVLALPFKR	1300.6	2	2.9045	0.221
RAEVLGHKTPEPAPR	1658.9	2	4.3539	0.4036

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RAEVNGLAAQGK	1214.4	2	3.3442	0.2262
RAFDSAVAK	965.1	2	2.4023	0.1183
RAFIPLPSAVVQAVFGR	1829.2	2	2.4844	0.1068
RAFQMLR	922.1	2	2.4418	0.1084
RAFSEADMERPLQELGLVPSAVLIVAK	2941.4	3	3.6152	0.1938
RAGAECGLAR	1004.1	2	2.6402	0.1664
RAGDLLEDSPK	1201.3	2	3.1647	0.1548
RAGELTEDEVER	1404.5	2	3.8883	0.3156
RAGKLDPHLVLDQLR	1732.0	2	4.0349	0.3282
RAGLGSGLSLSGLVHPELSR	2007.3	3	4.9687	0.4405
RAIAYATHR	1059.2	2	2.6573	0.218
RAIIPSHLAYGK	1326.6	2	3.3659	0.3343
RAIVHDNKDGTYAVTYIPDK	2277.5	3	4.3235	0.3769
RAIVHDNKDGTYAVTYIPDKTGR	2591.9	3	6.735	0.4824
RAKPEGALQNNDGLYDPDCDESGLFK	2854.1	3	4.7271	0.404
RALAAQLPVLPR	1305.6	2	3.3252	0.3313
RALANSLACQGK	1232.4	2	2.9832	0.1789
RALDDTAR	918.0	2	2.5049	0.1478
RALDIPLVK	1025.3	2	2.7956	0.1275
RALEAEQVEITVGRFR	1875.1	2	2.8525	0.1103
RALELEQER	1144.3	2	3.4777	0.1487
RALEQQVEEMKTQLEELEDELQATEDAK	3305.6	3	6.8224	0.3526
RALEQQVEEMKTQLEELEDELQATEDAKLR	3574.9	3	3.9437	0.2177
RALSSQHQAR	1154.3	2	3.0771	0.2013
RANEFLEVGKK	1291.5	2	2.9792	0.1977
RANEMNISPASLASLYEEDFKQDMAALK	3144.5	3	3.6225	0.1189
RANNTFYGLSAGVFTK	1746.9	2	4.934	0.3645
RAPDQAAEIGSR	1271.4	2	3.351	0.3021
RAPFDLFENK	1237.4	2	2.9705	0.1333
RAPFDLFENKK	1365.6	2	3.3859	0.218
RAPFDLFENR	1265.4	2	3.4655	0.2029
RAPFDLFENRK	1393.6	2	2.4071	0.1298
RAPSSAQYLEEK	1379.5	2	3.0952	0.1202
RAPSSAQYLEEKSDQQKKEELLNAMVAK	3193.6	3	6.4867	0.4087
RAQAEQAALR	1114.2	2	3.3722	0.1901
RAQDFVQWLMNTK	1637.9	2	5.143	0.3501

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RAQDFVQWLMNTKR	1794.1	3	4.5567	0.3648
RAQEEAEAEER	1318.3	2	3.9157	0.3561
RAQEEAEAEERRLQEQEELENYIEHVLLR	3611.9	3	4.946	0.3816
RAQGWQGLKEYDQALADLKK	2319.6	3	3.9744	0.2683
RAQHNEVER	1139.2	2	2.8477	0.2874
RAQLADSFHLQQFFR	1865.1	3	4.2264	0.3174
RAQPFVAAANIDDKR	1672.9	3	5.2122	0.3532
RAQQQAEAER	1187.2	2	2.8947	0.2272
RAQQQLENGFK	1319.5	2	2.8424	0.2707
RAQSELAAHQK	1239.4	3	3.4382	0.1664
RASAYEALEKYPMAYVDYK	2269.6	2	3.1767	0.3448
RASPSKPASAPASR	1383.5	2	4.3983	0.3182
RASRAPSKQRYVQEVMRR	2219.6	3	3.2926	0.1067
RATASEQPLAQEPPASGGSPATTK	2353.5	3	3.9893	0.2373
RATISNPITGDLETVHYR	2044.3	3	4.3866	0.3214
RATLGPTPTTPPQPPDPSQPPPGPMQH	2801.1	3	5.1907	0.3724
RATVVESSEK	1106.2	2	2.8025	0.1825
RAVAGDASESALLK	1388.6	2	3.3794	0.3467
RAVAREESGKPGAHVTVK	1893.1	3	3.3435	0.2198
RAVETTAQSDNK	1320.4	2	3.4155	0.1903
RAVGPSSTQLYMVR	1565.8	2	2.7897	0.246
RAVLAVHPDKAAGQPYEQHAK	2287.6	3	3.7986	0.2546
RAVLQAAR	885.0	2	2.7744	0.1128
RAVPLALALISVSNPR	1678.0	2	2.6755	0.2573
RDAGDKDKEQELSEEDKQLQDELEMLVER	3477.7	3	4.7518	0.2728
RDDDPLNAR	1072.1	2	3.2068	0.2421
RDDGLSAAAR	1032.1	2	2.8411	0.1903
RDDGSWEVIEGYR	1582.7	2	2.9431	0.2167
RDDGTGQLLLPLSDAR	1727.9	2	3.8305	0.401
RDEAGHFLWPGFGENAR	1960.1	2	3.5262	0.307
RDEDKDKVGNVEYFGLGNSPGFPLQYYPYYGK	3718.0	3	5.8176	0.3811
RDEDVSEGSVPNGDSQSGVDSLRK	2534.6	3	3.3385	0.1138
RDELEEGAPSQAMLR	1702.9	2	5.036	0.3048
RDELLAQHAAGALGLPDLVAVLTR	2500.9	3	3.7169	0.1856
RDEQDDDDKGDSKETR	1909.9	2	4.342	0.4888
RDESLKVDEHLAK	1540.7	2	4.8907	0.4275

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RDESLKVDEHLAKQDAQILYK	2500.8	3	3.3095	0.2241
RDFAPPGQQK	1144.3	2	2.8517	0.1077
RDFAPPGQQKR	1300.5	2	3.1053	0.3349
RDFGSFDKFKEK	1504.7	2	3.5806	0.1806
RDFLYARR	1097.3	2	2.4893	0.101
RDFNHINVELSLLGK	1756.0	2	2.5199	0.1463
RDFPEEVAIVEELGR	1759.9	2	5.5325	0.4512
RDFPEEVAIVEELGRR	1916.1	3	6.1408	0.4167
RDFTPAELR	1105.2	2	2.6095	0.1258
RDGGRLSEADIR	1345.4	2	2.554	0.1308
RDGSYGSGR	955.0	2	2.4639	0.1892
RDHALLEEQSK	1326.4	2	4.0094	0.2687
RDHPLPEVAHVK	1398.6	2	3.5762	0.4043
RDIDNLVQR	1129.3	2	2.7438	0.1161
RDKGLVEK	945.1	2	2.5923	0.11
RDLGEELEALKTELEDTLDSTAAQQELR	3175.4	3	7.5261	0.5284
RDLGEELEALRGELEDTLDSTNAQQELR	3202.4	3	4.087	0.33
RDNELIGQTVR	1301.4	2	3.6571	0.3067
RDNYVPEVSALDQEIIEVDPDTK	2646.8	3	4.1036	0.2762
RDNYVPEVSALDQEIIEVDPDTKEMLK	3148.5	3	6.637	0.4023
RDPAGHSQAGAYK	1358.4	2	3.4281	0.3881
RDPFIGEHTEEILEEFGFSR	2409.6	3	4.8478	0.2861
RDPNHSEGSTTLLEGYTSHYPHTK	2728.9	3	5.5237	0.3501
RDPPAYIEEFLQQYNHYK	2312.5	3	4.5107	0.1789
RDQALTEEHAR	1326.4	2	4.4502	0.3586
RDQDNMQAELNR	1490.6	2	4.1156	0.2028
RDSFQEVLR	1150.3	2	2.8042	0.1548
RDSHLTLLNQLLQGLR	1878.2	3	4.4072	0.367
RDTGEKLTVAENEAETKLQAILEDIQVTLFTR	3634.0	3	5.8075	0.2649
RDVDFELIKVEGK	1548.8	3	3.7331	0.2572
RDVQEIFR	1063.2	2	2.8929	0.1115
RDYDDMSPR	1155.2	2	3.0775	0.2098
RDYKVDQEIINIMQDR	2037.3	3	4.397	0.1814
RDYLKEAVTTLK	1437.7	2	3.2047	0.2652
REAEDLQVGQVELGGGPGAGSLQPLALEGSLQ	3177.5	3	5.8996	0.4402
REAEDLQVGQVELGGGPGAGSLQPLALEGSLQK	3305.6	3	9.0021	0.5439

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
REAEDLQVGQVELGGGPGAGSLQPLALEGSLQKR	3461.8	3	7.8412	0.5509
REAESCDCLQGFQLAHSLGGGTGSGMGTLLLSK	3325.7	3	4.58	0.2362
REDEGEPGDEGQLEDEGSQEK	2334.3	3	5.2154	0.3434
REDIFYTSK	1159.3	2	3.0256	0.1174
REDIVDTMVFKPSDVMLVHFR	2536.0	3	4.3146	0.3769
REDKELYTVVQHVK	1745.0	3	3.9372	0.3584
REDLFIVSK	1107.3	2	2.4775	0.1833
REDLLNNAAHAGK	1409.5	3	3.5213	0.3126
REDLVEEIKRR	1443.6	3	3.4451	0.1728
REDLVVAPAGITLK	1482.8	2	4.3346	0.4375
REDLVVAPAGITLKEANEILQR	2436.8	3	5.524	0.4653
REEAAVDAQQQK	1373.5	2	3.9791	0.2896
REEDEPEER	1189.2	2	2.8445	0.1457
REEEEDFIR	1223.3	2	3.2681	0.2397
REEEEFNTGPLSVLTQSVK	2164.4	3	4.4031	0.4
REEEEVLDQGDFYSLLSK	2158.3	2	5.753	0.4555
REEFVQWVELLPDTQTPSWLGLPNNAER	3326.7	3	5.1281	0.2871
REEGAPGDPEAALEDNLAR	2011.1	2	3.5226	0.2899
REELITNWEQIR	1587.8	2	4.7063	0.2811
REELSNVLAAMR	1389.6	2	3.7715	0.2847
REESEAVEAGDPPEELR	1914.0	2	3.0572	0.2453
REGGDGEEQDVGDAGR	1647.6	2	3.9114	0.3913
REHVKR	825.0	1	2.014	0.1142
REKAAGEKVYWTCR	1697.9	2	2.4611	0.1366
REKAEGDVAALNR	1429.6	2	3.7734	0.3845
REKAEGDVAALNRR	1585.8	2	2.7407	0.1309
REKDEKEKAEKQR	1674.8	2	3.6514	0.1589
REKEAEER	1047.1	2	2.7297	0.1269
RELDESLQVAER	1445.6	2	3.9741	0.2947
RELDKAESEIKK	1446.6	2	3.3244	0.2927
RELHGQNPVVTPCNK	1692.9	2	3.5593	0.315
RELLELASR	1087.3	2	2.9437	0.1113
RELVALCRSGRAAALR	1743.1	2	2.6825	0.1016
RENISHNTQDILIPNVLLSQEK	2562.9	3	4.5014	0.2524
RENLSDEDKLNNAK	1646.7	2	4.3669	0.2975
RENPLDSSVEFMQIWR	2008.2	2	4.5024	0.3103

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
REPEEHQVEEEHRK	1832.9	2	3.9934	0.2226
REPHPAEAEK	1164.3	2	2.842	0.2558
REPIPSLEAIYLLSPTEK	2057.4	2	4.2581	0.3795
REPLPSLEAVYLITPSEK	2043.3	2	3.9115	0.3646
REPLSLINVR	1197.4	2	2.433	0.113
REPSSDVHSR	1170.2	2	2.456	0.1903
REPWLLPSQHNDIIR	1875.1	2	4.109	0.2389
REVKKEEGEAFAR	1549.7	2	4.0345	0.3387
RFDAMPFTLR	1254.5	2	2.8937	0.1406
RFDDAVVQSDMK	1411.6	2	3.7624	0.3445
RFDDAVVQSDMKHWPFMVVNDAGRPK	3047.5	3	5.3529	0.492
RFDDPGLMLMGFKPLVLLK	2191.7	3	4.875	0.3884
RFDEAALSIQKEK	1535.7	2	3.776	0.1261
RFDEILEASDGIMVAR	1823.1	2	5.4166	0.4619
RFDGVDVSEVLFGR	1596.8	2	2.5122	0.2202
RFDGYLNQGANNKK	1625.8	2	4.4618	0.298
RFDIYR	870.0	2	2.6297	0.1013
RFDSELSQAHEEAQR	1803.9	3	4.2763	0.3533
RFDSELSQAHEEAQREK	2061.2	3	3.9307	0.3055
RFDVSGYPTLK	1283.5	2	3.7276	0.3671
RFEAEPLPENTNR	1573.7	2	3.9844	0.3027
RFEEALQTIFNR	1524.7	2	4.0392	0.3149
RFEEELAAR	1121.2	2	3.1001	0.1762
RFEELTNLIR	1291.5	2	2.8674	0.1758
RFEKPLEEK	1176.3	2	2.484	0.1202
RFEQAQHMFR	1350.5	2	2.7509	0.254
RFESIPDMLELDHLTVSGDVTFGK	2708.0	3	5.239	0.4376
RFFPYYVYNIIGGLDEEGKGAVYSFDPVGSYQR	3809.2	3	4.1335	0.1758
RFGTVLTEHVAAAELGAR	1899.1	3	3.9118	0.3378
RFGVPIIADGGIQTVGHVVK	2064.4	2	2.7511	0.2392
RFGVPVIADGGIQNVGHIAK	2049.4	2	6.3128	0.4752
RFIPTSIFVKPQGR	1647.0	3	4.2637	0.3164
RFKDPGLVDQLVK	1515.8	2	3.3576	0.1218
RFKGTESISK	1153.3	2	2.6618	0.123
RFKIPGSPPESMGR	1559.8	2	3.1489	0.2135
RFNDGSDEKKK	1324.4	2	2.8977	0.1115

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RFPEEPHVPLEQR	1634.8	2	2.862	0.1254
RFPELESLVPNALDYIR	2033.3	2	3.248	0.2075
RFPGYDSESK	1186.3	2	2.7119	0.1008
RFPGYDSESKEFNAEVHR	2169.3	3	4.149	0.3207
RFPGYDSESKEFNAEVHRK	2297.5	3	4.7855	0.3183
RFPHGIPFLADYVHSLGLK	2168.5	3	6.2441	0.4767
RFPLLINQPHK	1363.6	3	3.3975	0.2214
RFPVAPLIPYPLITK	1726.1	2	3.6736	0.2567
RFPVAPLIPYPLITKEDINAIEMEEDKR	3299.8	3	5.5518	0.2832
RFPVGPPKNDDTPNR	1710.9	3	4.0339	0.2858
RFQGVSLPVHLR	1409.7	3	4.0143	0.263
RFQLLEGPPESMGR	1617.9	2	3.4279	0.2267
RFQSVPAQPGQTSPLLQYFGILLDQGQLNK	3345.8	3	4.7669	0.4081
RFSDFLGLYEK	1375.6	2	2.7543	0.1937
RFSEGTSADR	1126.2	2	3.1566	0.2457
RFSEGVLQSPSQDQEK	1836.0	2	3.0411	0.2784
RFSFSGNTLVSSSADPEGHFETPIWIER	3168.4	3	5.0518	0.4419
RFSMVVQDGIVK	1379.7	2	3.2149	0.2718
RFSTEYELQQLEQFKK	2075.3	3	5.123	0.3608
RFSTEYELQQLEQFKKDNEETGFGSGTR	3326.5	3	7.5999	0.4374
RFTAQGLPDLNHSQVYAVK	2145.4	3	4.5466	0.289
RFVEQVAR	1005.2	2	3.0541	0.2197
RFVNVVPTFGK	1264.5	2	3.5237	0.2787
RFVNVVPTFGKK	1392.7	2	3.5071	0.223
RFYEQMNGPVAGASR	1683.9	2	5.4419	0.4393
RGAAASPEPAR	1083.2	2	2.6014	0.1552
RGAEGILAPQPPPPQQHQERPGAAAIGSAR	3059.4	3	4.9747	0.4764
RGAGMPGQHGQITQQELDTVVK	2351.6	3	4.4453	0.2462
RGAPAAATAPAPTAHK	1488.7	2	3.3859	0.3395
RGAPPSSNIEDFHGLLPK	1936.2	3	4.4859	0.2295
RGDALIEMESEQDVQKALEK	2290.5	3	4.9417	0.2706
RGDDFKKEGK	1180.3	2	2.4817	0.18
RGDDSFGDK	997.0	2	2.4698	0.1799
RGDDSFGDKYR	1316.4	2	3.3018	0.2922
RGDESQFLLQAPGSTELEELTVQVAR	2875.1	3	3.6423	0.1464
RGDFFYHSENPKYPEVGDLR	2427.6	3	4.0245	0.3118

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RGDFIHVMDNSDPNWWK	2118.3	2	2.4328	0.1694
RGDIIGVQGNPGK	1311.5	2	3.7083	0.3289
RGDLHVTLTSAAGTSTVLLAER	2269.5	3	3.7575	0.2039
RGDLPFVVPR	1156.4	2	3.9641	0.2362
RGDPHELR	980.1	2	2.5657	0.1034
RGDQLLSVNGVSVEGEHHEK	2191.3	3	4.0391	0.326
RGDTYELQVR	1237.3	2	3.6692	0.3164
RGDVTFLEDVLNEIQLR	2018.3	2	3.8105	0.2399
RGEAHLAVNDFELAR	1698.9	3	4.9567	0.4854
RGEAPFAQR	1032.1	2	3.087	0.1848
RGEAQLLMNEFESAK	1723.9	2	4.1838	0.3991
RGEAQLLMNEFESAKGDFEK	2300.5	3	4.298	0.296
RGEDLFMCMDIQLVEALCGFQKPISTLDNR	3445.0	3	3.3137	0.1604
RGEEGHDPKEPEQLR	1777.9	2	4.2999	0.3686
RGEEGHDPKEPEQLRK	1906.0	2	3.5896	0.2322
RGEPHVTR	952.1	2	3.1288	0.3137
RGEQADHFTQTPLDPGSQVLVR	2452.7	3	4.5077	0.2742
RGEQLTLPPPPQLGYSITAEDLDLEKK	3010.4	3	4.7673	0.2852
RGERPDYKGEEELR	1734.9	2	4.6068	0.3143
RGESLDNLDSPR	1359.4	2	2.6144	0.1993
RGETESEEFEK	1341.4	2	2.9016	0.1191
RGFAFVTFDDHDSVDKIVIQK	2438.7	3	5.6742	0.3221
RGFAFVTFDDHDTVDKIVVQK	2438.7	3	3.7562	0.2136
RGFCFITFKEEEPVKK	1959.3	3	3.6535	0.2163
RGFCFITYTDEEPVKK	1934.2	3	5.0553	0.3207
RGFGFVTFDDHDPVDK	1853.0	3	3.9693	0.2562
RGFGFVTFDDHDPVDKIVLQK	2434.7	2	4.8024	0.3882
RGFGFVYFQNHDAADKAAVVK	2341.6	3	3.9799	0.2098
RGFIPNIR	973.2	2	2.8911	0.1093
RGFPGYMYTDLATIYER	2054.3	2	2.7957	0.1682
RGFSEEQLR	1122.2	2	3.3006	0.2262
RGFVFITFKEEEPVKK	1955.3	3	3.6324	0.2865
RGFVLQDTVEQLR	1561.8	2	2.5568	0.1815
RGGDGQINEQVEK	1430.5	2	2.8971	0.1175
RGGDGYDGGYGGFDDYGGYNNYGYGNDGFDDR	3437.3	3	5.2786	0.4448
RGGEERVGEEDEEAAEAEAEAEEEAER	2848.8	3	6.0016	0.4024

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RGGETDEFSNVR	1367.4	2	2.6268	0.2615
RGGGGTELGPPAPPRPR	1672.9	3	3.5217	0.3622
RGGGLRLPLLPPESPGPLR	1983.3	3	3.3195	0.2319
RGGPISFSSSR	1151.3	2	3.127	0.2082
RGGPNYQEGLR	1247.3	2	3.4349	0.3245
RGGPPGPPISR	1091.2	2	2.8252	0.1763
RGGTWFAGFGR	1212.3	2	3.6378	0.3736
RGHAVPPTLVPLMNGSATPLPTALGLGGR	2852.4	3	6.1195	0.3777
RGHDDLGDHYLDCGDLSNALK	2315.5	3	3.3956	0.1961
RGHDDLGDHYLDCGDLSNALKCYSR	2825.0	3	3.2437	0.1616
RGHLFLQTDQPIYNPGQR	2141.4	3	4.3991	0.2424
RGHPEAGQ	851.9	2	2.4236	0.1381
RGHREEEQEDLTK	1627.7	2	2.6216	0.2155
RGHREEEQEDLTKDMDEPSPVPNVEEVTLPK	3605.9	3	3.5134	0.1343
RGHVECVNSLIAYGGNIDHK	2183.4	3	4.0487	0.257
RGHVFEESQVAGTPMFVVK	2119.4	2	4.5647	0.4393
RGIEKPPFELPDFIK	1787.1	2	3.2811	0.2022
RGIEKPPFELPDFIKR	1943.3	3	5.217	0.4027
RGIGGIFFDDLDSPSKEEVFR	2385.6	3	3.3662	0.1742
RGIHSAIDASQTPDVVFASILAAFSK	2703.0	3	6.6469	0.5101
RGILTLKYPIEHGIITNWDDMEK	2744.2	3	3.5431	0.1086
RGILTLKYPIEHGIITNWDDMEKIWHHTFYNELR	4241.8	3	4.7389	0.3909
RGIQFLQEQGMLGTSVEDIAQFLHQEER	3261.6	3	5.8167	0.4424
RGLGAGAGAGEESPATSLPR	1855.0	2	7.0395	0.4772
RGLPQLGTLGAGNHYAEIQVVDEIFNEYAAK	3375.7	3	4.7136	0.373
RGLQATQLAR	1114.3	2	3.0104	0.1695
RGLQQITGHGGLR	1393.6	3	3.3931	0.3237
RGLSAQEKAELDQLLSGFGLEDPGSSLK	2947.2	3	4.6984	0.3357
RGPAEESSSWR	1262.3	2	2.9364	0.2493
RGPCIIYNEDNGIIK	1706.0	2	3.6596	0.1951
RGPFELEAFYSDPQGVPYPEAK	2498.7	2	4.4267	0.2957
RGPLAGLGPGSTPR	1336.5	2	3.0251	0.3389
RGPPSDGHEALEKEVQALR	2090.3	3	4.7601	0.1618
RGQAALDR	887.0	2	2.6988	0.222
RGQTCVVHYTGMLEDGKK	2023.3	2	4.7178	0.3785
RGSPLLIGVR	1068.3	2	3.3102	0.2558

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RGTEHSGSTVPSILNR	1711.9	2	4.5993	0.4399
RGTELGGAAGQGGHPPGYTSLASR	2298.5	3	3.446	0.11
RGTGGVDTAATGGVFDISNLDR	2180.3	2	4.7002	0.4011
RGTGGVDTAAVGGVFDVSNADR	2122.2	2	3.2374	0.3259
RGTHTTVSQVQPPPSK	1720.9	3	3.6623	0.4405
RGVAEAAEER	1088.2	2	2.8103	0.1419
RGVFNVQMEPK	1305.5	2	2.5744	0.1305
RGVHKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASR	4235.6	3	6.1992	0.4221
RGVMLAVDAVIAELKK	1714.1	3	6.151	0.2118
RGWDENVYYTVPLVR	1868.1	2	2.6349	0.1048
RHADGSFSDEMNTILDNLAAR	2334.5	3	5.6725	0.4347
RHADGSFSDEMNTILDNLAARDFINWLIQTK	3594.0	3	5.7347	0.4498
RHAEQERDELADEITNSASGK	2357.4	3	5.1882	0.322
RHDAETNITTEK	1415.5	2	3.1077	0.27
RHDEFER	989.0	2	3.006	0.3048
RHDEFERHAEGTFTSDVSSYLEGQAAK	3069.2	3	3.2833	0.2366
RHDEGNLGSLQLEVR	1723.9	2	2.5959	0.1763
RHEAAVPPLAIPSARPEK	1940.2	3	4.3792	0.2487
RHEAFEK	917.0	2	2.6013	0.1327
RHEAFESDLAAHQDR	1782.9	3	3.8549	0.2938
RHEGFAAALGDGKEPEGIFSR	2245.4	3	3.4635	0.2811
RHEILQWVLQTDSQQ	1882.1	3	4.6776	0.3638
RHEMPPHIYAITDTAYR	2072.3	2	4.7871	0.4378
RHEQFIPIAADK	1425.6	2	2.8179	0.1831
RHEVPPHVYAVTEGAYR	1982.2	3	5.0792	0.4078
RHGAEVIDTPVFELK	1711.9	2	2.9531	0.2405
RHILGSIVQSEGSYVESLKR	2259.6	3	6.5997	0.4339
RHPDLSIPELLR	1446.7	2	3.5042	0.3569
RHPDYSVVLLLR	1468.7	3	4.9003	0.4484
RHPYFYAPELLFFAK	1900.2	3	5.512	0.4698
RHPYFYAPELLFFAKR	2056.4	3	4.3676	0.2443
RHQYSDYDYHSSSEK	1902.9	2	4.8106	0.341
RHSQGTFTSDYSK	1514.6	2	3.8903	0.3416
RHVFGESDELIGQK	1615.8	3	5.7386	0.3868
RIALTDNALIAR	1327.6	2	3.4125	0.1934
RIDEINKELNQVMEQLGDAR	2372.6	3	4.9492	0.4139

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RIDITLSSVK	1132.3	2	2.8765	0.2368
RIDTNLNKVSK	1288.5	2	2.6106	0.1008
RIEDIHLLVER	1393.6	2	3.5676	0.2593
RIEELNKTANGNVEAK	1787.0	2	3.0241	0.2128
RIEELQHNLQK	1408.6	2	3.5496	0.2311
RIEEMEDELQKTER	1807.0	3	3.7545	0.1067
RIEESAIDEVVVTNTIPHEVQK	2507.8	3	6.0263	0.4472
RIEGLIER	986.2	2	2.458	0.1162
RIEPADAHVLQK	1377.6	2	3.0775	0.1251
RIEQHYFEDR	1393.5	2	3.0208	0.3114
RIESLIDRDYMER	1696.9	2	3.2376	0.2595
RIEYIEAR	1050.2	2	2.9644	0.2029
RIFDANTKPNLNLQVLSNPEFLAEGTAIK	3215.6	3	5.7977	0.4411
RIFDANTKPNLNLQVLSNPEFLAEGTAIKDLK	3572.1	3	5.6261	0.5082
RIFHTVTTTDDPVIRK	1900.2	3	4.6701	0.2918
RIGFDVVTLSGTR	1421.6	2	2.7382	0.2688
RIGIFGQDEDVTSK	1565.7	2	4.413	0.2775
RIGKENFIEK	1234.4	2	2.5137	0.1482
RIHLELR	937.1	2	2.5247	0.1217
RIHNGESMSYLFR	1610.8	2	3.1846	0.3231
RIIKETQR	1044.2	2	2.6745	0.115
RIIVPHNVSK	1163.4	2	2.5357	0.1271
RIKEDEDDKTVLDLAVVLFETATLR	2891.3	3	5.3485	0.4448
RILELDQFKGQQGQKR	1945.2	2	3.5138	0.3402
RILGLLDAYLK	1275.6	2	2.7702	0.193
RILISLATGHR	1237.5	2	3.4711	0.3439
RILISLATGHREEGGENLDQAR	2436.7	3	3.581	0.272
RILNEDGSPNLDFKPEDQPHFDIKDEF	3217.4	3	5.2369	0.4538
RILSKPIEVQVGGR	1552.8	2	3.7225	0.3403
RILVATNLFGR	1260.5	2	3.7848	0.4054
RIPADTFAALKNPNAMLVNLEEPLASTYQDILYQAK	4021.6	3	6.6571	0.4931
RIPIEDGSGEVVLSRK	1756.0	3	3.8138	0.2908
RIPIHNEDITYDELVLMMQR	2487.9	2	4.15	0.443
RIPIPELEAR	1194.4	2	2.9754	0.2381
RIPLAEWESR	1257.4	2	2.6382	0.2531
RIPQSTLSEFYPR	1594.8	2	2.7056	0.2012

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RIPYAPSGEIPK	1328.5	2	3.3947	0.2516
RIQDLIPVLLR	1336.7	2	3.4609	0.2743
RIQEEMEKER	1348.5	2	2.5554	0.1178
RIQEIIEQLDVTTSEYEK	2195.4	2	5.0918	0.407
RIQEIIEQLDVTTSEYEKEK	2452.7	3	6.6494	0.4156
RIQEIIEQLDVTTSEYEKEKLNER	2965.3	3	5.6682	0.2924
RIQEVGEPSKEEK	1529.7	3	3.3477	0.1639
RIQLQPTSIEKEVFPIMAK	2229.7	3	3.9958	0.2035
RIQLVEEELDR	1400.6	3	3.5533	0.3136
RIQLVEEELDRAQER	1885.1	2	3.8824	0.3333
RIQQLTEEIGR	1343.5	2	3.1437	0.2273
RIQSGLGALSR	1158.3	2	2.9657	0.2807
RIQTYLQSTKPIIDLYEEMGK	2527.9	3	4.8118	0.4153
RISASCQHPTAFEEAIPK	1986.2	2	3.1959	0.1599
RISAVSLANR	1087.3	2	3.4856	0.1762
RISAVSVAER	1088.2	2	3.3963	0.2707
RISEQFTAMFR	1386.6	2	3.4028	0.3809
RISGLIYEETR	1337.5	2	3.6412	0.3111
RISINQALQHAFIQEK	1897.2	2	2.5928	0.2147
RISQTYQQQYGR	1528.7	2	4.4408	0.4299
RITEAEKNER	1246.4	2	3.5817	0.2249
RITKLDQILLNGNNITMLVPGGEGPEV	2893.4	3	4.9753	0.3503
RITYYR	872.0	2	2.5435	0.1629
RIVAVTGAEAQK	1243.4	2	3.4219	0.2015
RIVDDWANDGWGLKK	1774.0	3	4.8265	0.3453
RIVDGKVVSETNDTK	1661.8	2	3.7889	0.4116
RIVISAPSADAPMFVMGVNHFK	2388.8	3	4.1869	0.1833
RIVQNSNGYK	1179.3	2	2.9876	0.2452
RIVSQLLTLMDGLK	1588.0	2	4.4897	0.3829
RIYIPLPEEAAR	1428.7	2	2.8787	0.3316
RKADGYNQPDSK	1379.5	2	3.3447	0.2064
RKADLNTITESSAALQNLIEGSEPILEER	3199.5	3	4.0751	0.1492
RKAEGEPGDEGQLEDKGSQEK	2288.4	3	4.5845	0.2802
RKATGPPVSELITK	1497.8	2	3.272	0.2338
RKAVDEAADALLK	1400.6	3	3.3587	0.2343
RKAVDEAADALLKAKEELEK	2228.5	3	3.6805	0.107

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RKDEISVDSLDFNKK	1795.0	3	4.5225	0.3808
RKDGLALGPGPFVTALEYATDTK	2421.7	3	3.5858	0.2772
RKDLNSDMDSILASLK	1807.1	3	3.6612	0.1312
RKDPEGTPYINHPIGVAR	2021.3	2	4.0531	0.4021
RKDPELWGSVLLESNPYR	2160.4	3	5.1332	0.3116
RKDSAIQQQVANLQMK	1859.1	2	4.9608	0.4278
RKEAEGTEEGGEEEDDEEMDPQTIDSLIELSTK	3711.8	3	6.7334	0.505
RKEDEVEEWQHR	1641.7	2	4.4159	0.3217
RKEEAFR	936.1	2	2.5101	0.1138
RKEEESKFEEMK	1570.7	2	4.3015	0.3196
RKEEESKFEEMKK	1698.9	2	4.4524	0.2956
RKEEIEAQIK	1244.4	2	2.9715	0.1115
RKEELAQSQHAQEQEFVQK	2314.5	3	3.7519	0.3241
RKEFLSELQR	1306.5	3	3.4611	0.1863
RKEGGEGYVPTSYLR	1712.9	2	3.7355	0.2303
RKEIDLLLGQTDDTR	1774.0	2	3.8605	0.3194
RKELEQVCNPIISGLYQGAGGPGPGGFGAQGPK	3284.7	3	6.721	0.3928
RKEMMGRNPKLGAAPNP	1868.2	2	2.4436	0.1143
RKENPIEDDLIFR	1645.8	2	3.7612	0.3383
RKEQEHMINWVEK	1728.0	2	4.9417	0.3399
RKESTDEILGR	1304.4	2	2.798	0.2152
RKETDKNISEAFEDLSK	2011.2	3	3.7369	0.2876
RKEVDMMKEALEK	1607.9	3	3.6829	0.2467
RKEVTDEIVK	1217.4	3	3.446	0.1484
RKEVTDEIVKEFMTPR	1979.3	2	4.5066	0.363
RKEVVVYLDDNQKPPVGEGLNR	2526.8	3	5.2374	0.3446
RKGDEVDGVDEVAK	1517.6	2	4.0936	0.3366
RKGDLDKAIELFQR	1689.9	2	2.9035	0.1516
RKGEEVTPISAIR	1456.7	2	3.8111	0.2476
RKGFNEGLWEIENNPGVK	2088.3	3	3.9947	0.1567
RKGGEADNLDEFLKEFENPEVPREDQQQQHQQR	3997.2	3	3.561	0.1733
RKGKEDEGEEAASPMLQIQR	2273.5	3	5.4022	0.3613
RKGLSEDVSISK	1319.5	2	2.969	0.2351
RKGTDVNVFNTILTTR	1836.1	3	4.5617	0.4617
RKHEDDEPVFEQIENTANPSR	2512.6	3	3.2252	0.235
RKIQALQQQADEAEDR	1900.0	2	4.3019	0.431

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RKIQALQQQADEAEDRAQGLQR	2553.8	3	4.1934	0.1943
RKLDGETTDLQDQIAELQAQIDELKLQLAK	3425.8	3	4.8325	0.3446
RKLDGETTDLQDQIAELQAQIDELKLQLAKKEEELQGALAR	4651.2	3	3.8732	0.2905
RKLDLFANVVHVK	1539.8	3	3.6887	0.2157
RKLEDSTR	1005.1	2	3.0735	0.2038
RKLEGDSTDLSDQIAELQAQIAELK	2773.0	3	6.1056	0.3978
RKLESTESR	1106.2	2	2.8827	0.1458
RKNPAAYENDK	1306.4	2	3.2194	0.3045
RKNQDEESQEAPELLKRPK	2296.5	3	5.2562	0.2732
RKPADLQNLAPGTHPPFITFNSEVK	2779.1	3	4.4816	0.3084
RKPAPAQLNYLLTDEQIMEDLR	2616.0	3	4.1187	0.2412
RKPDTIEVQQMK	1473.7	3	4.3224	0.2968
RKPDYEPVENTDEAQKK	2048.2	2	4.6619	0.3719
RKPIAGGGGFSDK	1290.5	2	2.8137	0.1359
RKPIAGGGGFSDKDLEDIVGGGEYKPDK	2907.2	3	6.336	0.1191
RKPQPDPLQIPHLSLPPVPPR	2383.8	3	3.3921	0.2247
RKPVEGYDISFLITNFHTEQMYK	2818.2	3	4.0084	0.2392
RKPVLPALTINPTIAEGPSPTSEGASEANLVDLQK	3616.1	3	8.3315	0.4823
RKQEELQQLEQQR	1713.9	2	5.2132	0.1992
RKQELAETLANLER	1671.9	2	4.6872	0.3127
RKQNDVFGEAEQ	1421.5	2	2.8709	0.187
RKQQTLEAEEAK	1431.6	2	2.8182	0.1517
RKQYPISLVLAPTR	1643.0	2	3.6502	0.3204
RKRKDIEKLKKIDR	1827.2	2	3.1778	0.1002
RKRMTDPTR	1161.4	2	2.7732	0.1168
RKSDLETSEPKPFLYYPEIK	2441.8	3	4.042	0.322
RKSEPAVGPPR	1194.4	2	2.7643	0.2262
RKSPENTEGK	1146.2	2	3.0313	0.2277
RKTDFFIGGEEGMAEK	1816.0	3	3.5837	0.241
RKTGEAYVQFEEPEMANQALLK	2553.9	3	4.0506	0.1585
RKTPEASAIGLHQDPELGDAALR	2446.7	3	3.6422	0.184
RKTPEELLR	1142.3	2	2.9067	0.1648
RKTVTAMDVVYALK	1595.9	3	3.7568	0.251
RKTVTAMDVVYALKR	1752.1	3	4.9078	0.3716
RKVEKDTMSDQALEALSASLGTR	2507.8	3	4.0374	0.2487
RKVLEEEEQR	1316.4	2	3.0172	0.1425

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RKVPGEGLPLPK	1291.6	2	3.1478	0.2338
RKVSSAEGAAKEEPK	1587.8	2	2.9174	0.1253
RKYEAFLQR	1211.4	2	2.9129	0.1188
RLAAAEETAVSPR	1371.5	2	4.763	0.4147
RLAAVALINAAIQK	1452.8	2	3.9766	0.3372
RLAEDEAFQR	1235.3	2	2.7707	0.1125
RLAEIQELHQSVR	1579.8	2	2.9199	0.2164
RLAISEDHVASVK	1425.6	2	3.3038	0.3192
RLAISEDHVASVKK	1553.8	2	3.1355	0.3029
RLAPEYEAAATR	1348.5	2	4.6866	0.5111
RLAPITSDPTEATAVGAVEASFK	2332.6	2	5.7538	0.4561
RLASSVLR	902.1	2	2.8643	0.1561
RLASTSDIEEKENR	1648.8	3	4.3296	0.2963
RLATLLGLQAPPTR	1507.8	2	2.6143	0.1776
RLDEELEDAEK	1347.4	2	2.7748	0.2106
RLDEELEDAEKNLGESEIR	2246.4	3	3.3589	0.1241
RLDEELEDAEKNLGESEIRDAMMAK	2894.2	3	4.2226	0.3871
RLDEVSR	875.0	2	3.2937	0.1459
RLDEYTQEEIDAFPR	1883.0	2	4.0738	0.4289
RLDGESSELQEQMVEQQQR	2291.4	3	5.1384	0.2915
RLDIDEKPLVVQLNWNKDDR	2467.8	3	4.6557	0.2549
RLDKFAAEHTIFASNTSSLQITSIANATTR	3266.6	3	5.9131	0.5254
RLDKFNEVVSVLK	1547.8	2	3.2957	0.2569
RLDLFQEHMFEVLER	1963.2	3	4.2751	0.3992
RLDLPIER	1012.2	2	2.5188	0.1464
RLDLRDPAALFETHGAEEIR	2310.6	3	3.9863	0.3134
RLDLVHTAALMLDKNNLVK	2165.6	3	5.156	0.2657
RLDPDAIPSPIQVIEDDRNNR	2434.7	3	3.3433	0.1179
RLDQVEQELNELRETEGGTVLTATTSELEAINKR	3845.2	3	4.9356	0.401
RLDTSLGSAR	1076.2	2	2.5934	0.1743
RLDTSSLKLSEYPNVEELR	2250.5	3	3.3223	0.157
RLDVLQAIHTAR	1393.6	2	2.6768	0.2188
RLDVTVQSFGWSDR	1666.8	2	2.7738	0.2023
RLDYESQTAHDNLLTEQIHSLSIEAK	3013.3	3	5.4641	0.3758
RLDYITAEIK	1222.4	2	2.8932	0.2189
RLDYITAEIKR	1378.6	2	3.1504	0.3016

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RLEAAYLDLQR	1348.5	3	4.3218	0.2744
RLEAELAAHEPAIQGVLDTGK	2219.5	2	4.6145	0.5379
RLEAELAAHEPAIQGVLDTGKK	2347.7	2	5.2713	0.5003
RLEAFEHPNVVR	1467.7	2	2.8298	0.2366
RLEALAAEFSSNWQK	1750.9	2	3.2377	0.3651
RLEASDGGLDSAELAAELGMEHQAVVGAVK	3025.3	3	6.9759	0.4402
RLEAYLAR	992.2	2	2.8237	0.1603
RLEDELGGQFLDLSLHDTVTTLILGGHNK	3193.6	3	5.8336	0.4779
RLEDLSESIVNDFAYMK	2031.3	2	5.0665	0.538
RLEDLSESIVNDFAYMKK	2159.4	3	5.1199	0.487
RLEDQLAGLQQELAALALK	2081.4	3	6.057	0.358
RLEEAALR	958.1	2	2.5619	0.1542
RLEEALMADMLAHVEELAR	2198.6	3	4.3908	0.2842
RLEEASLLHQFQADADDIDAWMLDILK	3158.5	3	4.4384	0.2958
RLEEEADRLITYLDQTTQK	2323.5	3	4.17	0.3799
RLEEIPLIK	1111.4	2	2.4993	0.1623
RLEEKDKER	1203.3	2	3.1353	0.1072
RLEEKHEALLK	1366.6	2	3.6594	0.2328
RLEELDLGNNEIYNLPESIGALLHLK	2965.4	3	4.7187	0.2609
RLEEMLRPLVEEGLR	1841.2	2	3.8542	0.3416
RLEEPEEPKVLTPEEQLADKLR	2620.9	3	5.0135	0.3546
RLEEQAAQHK	1210.3	2	2.6851	0.1826
RLEEQAAQHKADIEER	1924.1	3	4.0789	0.3454
RLEESDVLQEAR	1445.6	2	4.2553	0.3318
RLEEWLGR	1059.2	2	2.9044	0.1444
RLEFENQK	1064.2	2	2.5988	0.1671
RLEFLYDKLR	1353.6	3	4.3625	0.2933
RLEFLYDKLREQTLSPTITSGLHNIAR	3173.6	3	3.6152	0.1514
RLEFPSGETIVMHNPK	1856.1	3	5.2331	0.4321
RLEFVAAR	962.1	2	2.927	0.1845
RLEGEDSAR	1033.1	2	2.712	0.1822
RLEGEDSARETPIGLVPK	1968.2	2	3.5483	0.2186
RLEGILGGLGLR	1254.5	2	3.0899	0.3311
RLEGQEEEEDNRDSSMK	2053.1	2	3.8381	0.3553
RLEGTNVTVNVLHPGIVR	1975.3	3	5.4262	0.4384
RLEHQGIR	1009.1	2	2.6622	0.1911

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RLELASNHFLYLPR	1730.0	2	3.3169	0.2367
RLELQLQEVQGR	1469.7	2	4.0559	0.3135
RLEMYGIR	1038.2	2	2.4084	0.114
RLEPVVSDAIYDSK	1592.8	2	3.8374	0.2879
RLEPVVSDAIYDSKAPNASNLK	2388.7	3	5.2509	0.3825
RLEQEKLELSR	1401.6	2	3.9606	0.214
RLEQEVDGVMR	1332.5	2	2.9719	0.2076
RLEQEVNQER	1301.4	2	3.6285	0.1578
RLEQNLSGEEHVQELLKEK	2280.5	3	3.8205	0.2351
RLEQSTLHVHQSQQQALR	2160.4	3	3.4043	0.1272
RLESIATTLVSHK	1455.7	3	3.9753	0.1675
RLESSEAER	1077.1	2	2.7196	0.1924
RLESSGAGGR	990.1	2	3.1018	0.284
RLETYYK	973.1	2	2.4134	0.1243
RLEVLDSTK	1061.2	2	2.7389	0.2159
RLFDFQGLQHQVAHVATQLEAAR	2637.0	3	4.3101	0.3109
RLFEGNALLR	1189.4	2	3.0553	0.2218
RLFEQNVQR	1190.3	2	2.9344	0.1286
RLFIHESIHDEVVNR	1865.1	2	3.6938	0.2344
RLGAPQQPGPGPPPSR	1612.8	2	4.3906	0.3778
RLGAPQQPGPGPPPSRR	1769.0	3	4.6751	0.4177
RLGDSSGPALKR	1257.4	3	3.218	0.2474
RLGELFNPYYDPLQWK	2040.3	2	3.2493	0.2897
RLGELPADHPKGRLLR	1829.1	2	2.6437	0.2485
RLGEPEDCAGIVSFLCSEDASYITGETVVVGGGTPSRL	3887.3	3	7.2008	0.4841
RLGGGLGGTR	944.1	2	3.033	0.292
RLGIFGDTEDVAGK	1478.6	2	3.3705	0.2994
RLGLHYVVYSGLENIKK	1990.3	3	4.0753	0.3145
RLGLSTLGELKQNLSR	1786.1	3	4.1986	0.3907
RLGQHVVGMAPLSVGSLDDEPGGEAETK	2851.1	3	6.3008	0.3682
RLGSLLPVLSPTSLPSPLPATLETPVPAFLK	3213.8	3	5.8434	0.4059
RLGSLVDEFKELVYPPDYNPEGK	2667.0	3	4.8192	0.4291
RLGSLVDEFKELVYPPDYNPEGKVTK	2995.4	3	3.4131	0.1424
RLHAAEGVEPGSQR	1507.6	2	3.7944	0.3825
RLHGLPEQFLYGTATK	1832.1	2	3.6984	0.3891
RLIDLHSPSEIVK	1507.8	2	3.0775	0.2823

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RLIFSTITSK	1166.4	2	2.5881	0.1184
RLKELIGATAGK	1257.5	2	2.7598	0.1797
RLKVPPAINQFTQALDR	1968.3	3	4.2211	0.3162
RLLDQIVEK	1114.3	2	2.4719	0.1044
RLLEDGEDFNLGDALDSSNSMQTIQK	2898.1	3	7.1234	0.4945
RLLEGEESR	1089.2	2	2.4175	0.1971
RLLELGPKPEVAQQTR	1836.1	2	4.6435	0.4435
RLLSRPQDALEGVVLSPSLEAR	2407.8	3	4.8758	0.3825
RLLYMAIDGVAPR	1475.8	2	2.9684	0.2194
RLNAQILSQR	1199.4	2	2.5728	0.1201
RLNKHEENLK	1281.4	2	3.6534	0.2219
RLNMATLR	975.2	2	2.8797	0.1777
RLNQVIFPVSYNDKFYKDVLEVGELAK	3186.6	3	3.3787	0.1118
RLNSKPQDLTDAYGPPSNFLEIDIFNPQTVGVGR	3761.2	3	6.6251	0.4516
RLNSPIGR	913.1	2	2.5288	0.1171
RLNVTPLAR	1040.2	2	3.1944	0.2632
RLPAFTLSHLESHR	1664.9	3	4.8731	0.2551
RLPDAHSDYAR	1301.4	2	3.8214	0.3653
RLPEESGGR	1001.1	2	2.5127	0.1902
RLPENLYNDR	1290.4	2	2.8987	0.192
RLPEYPQVDDLLLR	1728.0	2	2.8239	0.1084
RLPGAIDVIGQTITISR	1811.1	2	2.9171	0.2739
RLPLNFLSGEK	1274.5	2	3.4522	0.2966
RLPNNHIGISFIPR	1634.9	2	4.1387	0.3566
RLPPQQIEK	1109.3	2	2.633	0.1002
RLPSSPASPSPK	1224.4	2	2.7324	0.1502
RLPTHTQLADTSK	1468.6	2	3.932	0.3882
RLPVMMDEALSYLEK	1796.1	2	3.4653	0.2398
RLPVMMDEALSYLEKR	1952.3	3	4.0604	0.2426
RLPVPESITGFAR	1443.7	2	2.6712	0.2355
RLQAEAEEAR	1173.3	2	2.8664	0.2081
RLQALLGDLLDAQK	1554.8	2	3.598	0.1701
RLQEDKEQMAQQLAEETQGFQR	2664.9	3	5.7848	0.493
RLQEENLVITPR	1468.7	2	3.82	0.3021
RLQEETGAK	1032.1	2	3.0357	0.1765
RLQEQEELENYIEHVLLR	2312.6	3	6.9694	0.4307

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RLQEQEELENYIEHVLLRRP	2565.9	3	5.7903	0.4441
RLQGSGVTVNALHPGVAR	1833.1	2	4.329	0.4661
RLQIEDFEAR	1277.4	2	2.738	0.2519
RLQIEESSKPVR	1442.6	3	4.4483	0.3268
RLQLSPWESSVVNR	1671.9	2	4.2785	0.3697
RLQNAHTGLDLTVPQHQEVR	2313.6	3	4.3919	0.3016
RLQQAVLSR	1071.3	2	2.5018	0.1392
RLQQEDGISFEYHR	1778.9	3	4.6881	0.3607
RLQQTQAQVDEVVDIMR	2030.3	3	4.6551	0.3832
RLQQTQNQVDEVVDIMR	2073.3	3	4.2605	0.371
RLQSIGTENTEENR	1647.7	2	4.4676	0.3475
RLQSIGTENTEENRR	1803.9	2	3.5993	0.2639
RLQTQVFK	1020.2	2	2.5452	0.1221
RLQTSSVLVSGLR	1416.7	2	4.4192	0.3928
RLQVEQAPHSSPGAK	1605.8	2	3.939	0.2619
RLSEDYGVLK	1180.3	2	2.5512	0.1129
RLSEDYGVLKTDEGIAYR	2086.3	2	6.2187	0.476
RLSESQLSFR	1223.4	2	2.8702	0.2989
RLSFAVPFR	1093.3	2	2.4786	0.1342
RLSGTEAHVLGLVNHAVAQNEEGDAAYQR	3107.3	3	4.8002	0.2794
RLSLESEGAGEGAAASPELSALEEAFRR	2905.1	3	4.7747	0.3413
RLSLVPDSEQGEAILPR	1881.1	2	3.1705	0.1152
RLSNVSSSGSINLLESPQLATLAEDVTAALAK	3257.6	3	7.5562	0.4246
RLSQPESAEK	1145.2	2	3.008	0.1519
RLSQYPNENLHSAVTK	1858.0	3	4.2675	0.2458
RLSTPAGVQVILR	1410.7	2	3.2657	0.2114
RLTDAFLLLR	1218.5	2	2.581	0.1176
RLTDLDKAQLLEIAK	1728.0	3	4.1332	0.2338
RLTELETAVR	1188.4	2	2.7352	0.2525
RLTEQKGEQQIQK	1586.8	2	3.8069	0.1891
RLTGFHETSNINDFSAGVANR	2307.5	3	5.0708	0.4981
RLTLEDLEDSWDR	1648.8	2	3.673	0.411
RLTPLQLEIQR	1367.6	2	3.3054	0.1369
RLTPTEVKDYLAAIA	1661.9	2	2.839	0.3462
RLTTDKANIKDLSQILK	1958.3	2	2.8292	0.1689
RLTTDKANIKDLSQILKK	2086.5	3	3.6394	0.1747

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RLTVMSLQESGLK	1462.7	2	3.6562	0.3239
RLTVMSLQESGLKVNQPASFAIR	2547.0	3	4.331	0.2751
RLTVSSLQESGLK	1418.6	2	4.0073	0.2625
RLTVSSLQESGLKVNQPASFAVSLNGAK	2903.3	3	5.7636	0.3364
RLVEEVTDDKTLPK	1643.9	3	3.8422	0.2495
RLVEEVTDDKTLPKLER	2042.3	3	3.3029	0.1806
RLVEVDSSR	1061.2	2	2.5013	0.1547
RLVEVDSSRQQEYDFK	2000.2	2	3.2902	0.2758
RLVNAAGSGR	1001.1	2	3.5831	0.3319
RLVPGGGATEIELAK	1511.7	2	2.9086	0.2443
RLVQSPNSYFMDVK	1684.9	2	2.935	0.2649
RLVSDGNINSDR	1346.4	2	3.6077	0.2725
RLVTTGVLK	987.2	2	2.6528	0.1491
RLVVLGFPCNQFGHQENCQNEEILNSLK	3231.7	3	4.1233	0.2855
RLYGSEAFATDFQDSAAAK	2049.2	2	4.9542	0.4786
RLYPPSAEYPDLRK	1705.9	3	3.9846	0.176
RMATEVAADALGEEWKGYVVR	2352.7	3	4.6518	0.2827
RMDAPASAAAVR	1216.4	2	3.4434	0.2318
RMDAPTSAAVTR	1276.4	2	2.7858	0.1585
RMDSFLSSVADMVQSIQVELEAEAEKMR	3201.6	3	4.2908	0.3296
RMEELHNQEMQK	1573.8	2	4.6478	0.3486
RMEELHNQEMQKR	1730.0	2	4.8072	0.3452
RMEELHNQEVQK	1541.7	2	4.1727	0.3412
RMEELHNQEVQKR	1697.9	2	4.716	0.3188
RMEPPASKVPEVPTAPATDAAPK	2361.7	3	5.0683	0.4012
RMFGGPGTASR	1137.3	2	2.7465	0.2236
RMGESDDSILR	1279.4	2	3.1936	0.1985
RMGHAGAIIAGGK	1239.5	2	3.468	0.2378
RMMEVAAADVK	1221.5	2	2.5063	0.164
RMPCAEDYLSVVLNQLCVLHEKTPVSDRVTK	3546.1	3	3.2205	0.1521
RMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITR	4285.9	3	3.341	0.244
RMQNDTAENETTEKEEK	2054.1	3	5.0406	0.3089
RMYEQQRDNLAQQSFNMEQANYTIQSLKDTK	3781.1	3	3.385	0.1211
RNAEQYKDQADK	1466.5	2	3.6599	0.3172
RNDFQLIGIQDGYLSLLQDSGEVR	2738.0	3	6.4583	0.449
RNDFQLIGIQDGYLSLLQDSGEVREDLR	3251.6	3	3.3798	0.2317

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RNDFQLIGIQDGYLSLLQDSGEVREDLRLPEGDLGKEIEQK	4689.2	3	4.0725	0.3594
RNEDEDSPNKLYTLVTYVPVTTFK	2831.1	3	4.674	0.3386
RNEFLGELQKK	1362.6	3	4.1349	0.2501
RNEIDAEPPAKR	1396.5	2	3.3222	0.2408
RNFILDQTNVSAAAQR	1805.0	2	3.4151	0.3331
RNFTSAGDHIIIDGLHAESPDDLVR	2750.0	3	3.5672	0.1564
RNGAAGPHSPDPLLDEQAFGDLTDLPVVPK	3128.4	3	4.5715	0.2872
RNGQGDAPPTPPPTPVDLELEWVLGKMPR	3169.6	3	3.3797	0.1942
RNIPPYFVALVPQEEELDDQKIQVTPPGFQLVFLPFADDKR	4772.4	3	4.8321	0.3251
RNKLDHYAIIKFPLTTESAMK	2477.9	3	3.3421	0.1136
RNLDFQDVLDKLADMGIAIR	2304.7	3	4.798	0.4112
RNLDIERPTYTNLNR	1876.1	2	3.2375	0.1689
RNLGSINTELQDVQR	1743.9	2	3.7746	0.3068
RNPAGSVVMER	1216.4	2	2.876	0.2884
RNPDTQWITKPVHK	1721.0	3	4.1004	0.3372
RNQDLAPNSAEQASILSLVTK	2256.5	2	4.1642	0.3263
RNSDLLLLVDTHKK	1652.9	3	3.6337	0.1847
RNTTGTGR	862.9	2	2.437	0.2084
RPAEAEAHR	1037.1	2	2.5722	0.1471
RPAEDDVPR	1055.1	2	3.2676	0.2177
RPAEDMEEEQAFK	1580.7	2	3.7277	0.3694
RPAEDMEEEQAFKR	1736.9	3	5.8609	0.3916
RPAEDYVPR	1103.2	2	3.5746	0.2965
RPAGDYVPR	1031.2	2	3.2112	0.234
RPAILTYHDVGLNYK	1761.0	2	4.2918	0.4528
RPANQFVPR	1085.2	2	2.9826	0.245
RPASVSSSAAVEHEQR	1711.8	2	4.3234	0.3174
RPAVASARPSILPSK	1550.8	2	2.693	0.2051
RPAVVYIGSAGKPHER	1738.0	3	4.5251	0.3828
RPCFSALEVDETYVPK	1855.1	2	4.1598	0.35
RPDADLKTYFTDK	1570.7	2	4.2048	0.3961
RPDADLKTYFTDKK	1698.9	2	3.3692	0.2167
RPDGFDGLGYR	1253.3	2	2.6952	0.1989
RPDIQYPDATDEDITSHMESEELNGAYK	3226.4	3	7.9082	0.5174
RPDLLTMVVDYR	1478.7	2	4.0111	0.3207
RPDLYGNLGHPLS	1439.6	2	3.0998	0.362

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RPDNTAFK	949.0	2	2.4122	0.1476
RPDPIDWSLK	1227.4	2	3.1232	0.2991
RPDQQLQGEGK	1256.4	2	3.7797	0.326
RPDVVENQPDAASQLNVDASGNLAK	2609.8	3	5.6659	0.3704
RPEAAQLLEDVQAALKPFSVK	2311.7	2	6.9478	0.4228
RPEDQELESLSAIEAELEK	2187.3	3	6.3765	0.5132
RPEDQELESLSAIEAELEKVAHQL	2736.0	3	5.0148	0.4067
RPEDQELESLSAIEAELEKVAHQLQ	2864.1	3	4.9344	0.3002
RPEDQELESLSAIEAELEKVAHQLQAL	3048.4	3	5.6126	0.4545
RPEDQELESLSAIEAELEKVAHQLQALR	3204.5	3	8.2344	0.5653
RPEDQELESLSAIEAELEKVAHQLQALRR	3360.7	3	3.3223	0.2323
RPEEVALGLHHR	1414.6	3	4.1662	0.28
RPEFQTLLTESESEHGER	2146.3	3	5.1164	0.305
RPEGASNESERD	1347.3	2	3.1937	0.3587
RPEGPGAQAPSSPR	1407.5	2	2.6627	0.263
RPEIPTEQSR	1213.3	2	3.14	0.1503
RPEKPVPPPPPIAK	1523.8	2	4.4818	0.3214
RPELEDSTLR	1216.3	2	3.1018	0.313
RPELGVTLTK	1114.3	2	2.4213	0.1874
RPELLTHSTTEVTQPR	1866.1	2	4.4738	0.4718
RPELPDLAPEPR	1390.6	2	3.5834	0.1647
RPENPKPQDGK	1266.4	2	2.7707	0.1817
RPENPKPQDGKETK	1624.8	2	3.9238	0.2502
RPENSLLEETLHFDHAVR	2164.4	3	3.2887	0.2806
RPEQVTWAAQEQELESLREQLEGVNR	3097.3	3	4.1471	0.3538
RPESALLGGSEAGER	1529.6	3	4.9042	0.4344
RPESALLGGSEAGERLLQQGLAQVEAGR	2894.2	3	5.777	0.3945
RPESALLGGSEAGERLLQQGLAQVEAGRR	3050.4	3	3.319	0.3576
RPESFTTPEGPKPR	1599.8	2	2.8809	0.1764
RPETPSSGPLDEEGAVAPVLANGHAPYSR	2976.2	3	3.6931	0.2452
RPEVDGEKYQK	1349.5	2	2.6845	0.2226
RPEVDGVR	928.0	2	2.768	0.1974
RPFAVTTQSFGSNAEGQHSGFGPQPNPEK	3074.3	3	3.6493	0.1167
RPFFPFHSPSR	1375.6	2	2.9093	0.2411
RPFGISALIVGFDFDGTPR	2066.3	2	3.3788	0.3144
RPFPYEIDEILGVR	1705.0	2	3.946	0.3409

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RPGAVATGDIGR	1170.3	2	2.8479	0.2719
RPGGEPSPEGTTGQSYNQYSQR	2397.5	3	5.7335	0.4885
RPGHSLEAER	1152.2	2	2.4859	0.203
RPGIIVAPVLPGAYQQSHSQGYGYMHQTSVSSMR	3705.2	3	6.4302	0.4628
RPGLEGLLAGVDNNLVELEAAR	2307.6	3	4.8667	0.3915
RPGPAGELLLQDIPTGSAPAAQHR	2453.7	2	4.0123	0.2001
RPGSVSSTDQER	1319.4	2	3.1796	0.3485
RPGVSPEGGLSVPGPGAPLEKPGRR	2468.8	3	4.3792	0.3162
RPHDYQPLPGMSENPSVYVPGVVSTVVPDSAHK	3562.0	3	4.9114	0.4327
RPHFPQFSYSASGTA	1653.8	2	3.4572	0.3262
RPHGDIYGINQALGATAK	1883.1	2	4.4731	0.4056
RPHLSIILVGDNPASHTYVR	2246.6	3	3.413	0.1225
RPHLSVILVGENPASHSYVLNK	2431.8	3	4.9926	0.2581
RPHNAIFVNFEDEEVPKQPLEAAAQTWR	3294.6	3	4.803	0.1848
RPISADSAIMNPASK	1558.8	2	4.2877	0.4292
RPKDDQVFEAVGTTDELSSAIGFALELVTEK	3367.7	3	3.2479	0.2269
RPLDAHLALVNQHPIGPFPR	2249.6	3	3.7191	0.2367
RPLDDGVGNQLGALVHQR	1946.2	3	5.8927	0.3774
RPLEAPPER	1065.2	2	2.4315	0.2453
RPLEDGDQPDAK	1341.4	2	2.9515	0.2131
RPLEDGDQPDAKK	1469.6	2	4.2496	0.3436
RPLEQQQPHHIPTSAPVYQQPQQQPVAQSYGGYKEPAAPVSIQR	4937.4	3	5.2721	0.37
RPLFLAPDFDR	1347.5	2	3.0134	0.2728
RPLIDQVVQTALSETQDPEEVSVTVK	2883.2	3	5.9212	0.4451
RPLILQLIFSK	1328.7	2	2.7235	0.1012
RPLILQLVHVSQEDKR	1932.3	2	4.1808	0.3746
RPLILQLVHVSQEDKRK	2060.4	3	3.4632	0.3711
RPLLGLVLTPTR	1336.7	2	3.2997	0.3107
RPLMVLGSQALLTPTSADKLR	2268.7	3	5.0436	0.2817
RPLNSVVLQQGLADR	1666.9	2	4.1354	0.4397
RPLPFAPR	954.2	2	2.517	0.116
RPLQEHVR	1035.2	2	2.9079	0.2562
RPLRPQVVTDDDGQAPEAK	2093.3	2	4.009	0.3775
RPLVLQLVNATTEYAEFLHCK	2446.9	3	3.7079	0.2195
RPMEEDGEEKSPSK	1619.7	3	4.2278	0.3247
RPMEEDGEEKSPSKK	1747.9	2	4.1768	0.316

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RPNKPLFTALVTQCQK	1845.2	2	4.073	0.2875
RPNKQEESESPVERPLKENPPNK	2703.9	3	3.5528	0.1604
RPNPAPGTR	966.1	2	2.6714	0.1637
RPNPDILDHER	1362.5	2	2.6171	0.2011
RPNSVQPGAER	1211.3	2	2.4655	0.1691
RPNVVLLLTDDQDEVLGGMTPLKK	2653.1	3	7.5491	0.4268
RPPASDGLDLSQAAAR	1625.8	2	2.7581	0.1389
RPPENEAPPVPFLHAQR	1956.2	2	4.0919	0.4019
RPPGFSPFR	1061.2	2	2.4744	0.1975
RPPGREAYPGDVFYLHSR	2118.3	3	4.3852	0.3675
RPPGVLHCTTK	1209.4	2	2.532	0.1405
RPPIGYR	859.0	2	2.4656	0.131
RPPPAPAQPPEPEALPTIYVVTPTYAR	2930.3	3	3.5571	0.2169
RPPSAFFLFCSEYRPK	1946.3	3	5.5644	0.3648
RPPSGFFLFCSEFRPK	1916.2	3	4.5566	0.2779
RPPSPIKFDLNEPLHLSFLQNAAK	2734.1	2	3.8013	0.3834
RPPTAGSQFK	1089.2	2	2.7188	0.2075
RPQIDPAVEGFIR	1498.7	2	3.3459	0.4529
RPQPYPYPSKK	1361.6	2	2.7985	0.204
RPQTDQAVEFFIR	1607.8	2	4.4411	0.3415
RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	3225.5	3	5.8257	0.4165
RPRDDYR	978.0	2	2.627	0.2227
RPSAPVDFSK	1104.2	2	2.895	0.1021
RPSENLGQVLFGER	1602.8	2	5.276	0.5092
RPSGNLVSVLSGAEGSFVSSLVK	2291.6	2	5.6866	0.5614
RPSNYPESYFQR	1544.7	2	2.5151	0.2025
RPSPLAHQPVPR	1355.6	3	3.2304	0.3153
RPSSPLIDIKPIEFGVLSAK	2168.6	2	2.4732	0.1399
RPSTSQTVSTPAPVPVIESTEAIEAK	2697.0	3	3.7902	0.2166
RPTEICADPQFIIGGATR	1946.2	2	3.7698	0.3135
RPTELLSNPQFIVDGATR	2015.3	3	4.8809	0.4258
RPTLQAVR	941.1	2	2.4537	0.102
RPTPATLVLTSDQSSPEIDEDRIPNPHLK	3228.6	3	5.0135	0.3514
RPTPNDDTLDEGVGLVHSNIATEHIPSPAK	3182.4	3	6.7825	0.445
RPVDSYDIPKTEEASSGFLPGDR	2537.7	3	5.0114	0.3927
RPVELVPPESPLAQLFLER	2191.6	3	6.1851	0.4481

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RPVFDDKEDVNFDHFQILR	2391.6	3	3.3566	0.1464
RPVGASFSFGGK	1210.4	2	3.8749	0.3551
RPVLFQEYLDIDQMIFNR	2298.6	3	4.5974	0.2911
RPVLLLHPLGGWTK	1587.9	2	4.5609	0.4081
RPVSAMFIFSEEK	1541.8	2	3.0887	0.1433
RPYGVGLLIAGYDDMGPHIFQTCPSANYFDCR	3579.0	3	5.307	0.4035
RQAPHHAADDGVGAAVTEQELLALDTIRPEHVLR	3688.1	3	3.6153	0.2653
RQAQQERDELADEIANSSGK	2246.3	3	3.8354	0.3971
RQAQQERDELADEIANSSGKGALALEEKR	3214.5	3	3.9668	0.307
RQATTIIADNIIFLSDQTK	2149.4	2	2.8611	0.2002
RQAVDVSPLR	1141.3	2	2.5968	0.1799
RQDLEDSLQAQQYFADANEAESWMR	3003.2	3	3.826	0.2593
RQDSEDHSSDMFNYEEYCTANAVTGPCR	3227.4	3	3.947	0.2098
RQDVLYELMQTEVHHVR	2154.4	3	4.3493	0.2975
RQEALPLHQETK	1450.6	2	4.1039	0.3524
RQEEEAGALEAGEEAR	1745.8	2	4.3496	0.1657
RQEEEESVKK	1262.4	2	2.662	0.1186
RQEELNNQLFLYDTHQNLR	2432.6	3	4.4813	0.2896
RQEILSNAGLR	1257.4	2	2.9067	0.2057
RQELDAFLAQALSPK	1687.9	2	3.5404	0.2912
RQELEQVLGIR	1341.5	2	3.3379	0.2937
RQELVTKIDHILDAL	1765.0	2	3.4941	0.321
RQEYLDQQLQK	1449.6	2	3.7037	0.159
RQFASQANVVGPWIQTK	1931.2	3	4.432	0.3174
RQFHLTDDDLLR	1529.7	2	3.8016	0.2791
RQGGLAGSVR	1001.1	2	3.0448	0.2386
RQGGLGPIRIPLLSDLTHQISK	2400.8	3	3.6331	0.3972
RQGTDPISQTK	1231.3	2	2.76	0.179
RQGYGEGFR	1070.1	2	2.6187	0.3143
RQHEAEEGVR	1211.3	2	3.2163	0.237
RQHRPPALLTLYPAPDEDEAVER	2675.0	3	3.2161	0.1379
RQIASEKEEIER	1488.6	2	2.7948	0.1619
RQIQAAYSILSEVQQAVSQGSSDSQILDLSNR	3493.8	3	5.9265	0.3782
RQLEEAEEEAQR	1488.5	2	4.7581	0.2808
RQLEEAEEEAQRANASR	1988.1	2	4.5127	0.3349
RQLEEAEEEATR	1461.5	2	3.9939	0.3069

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RQLEEKEKLLATEQEDAAVAK	2400.7	3	3.9354	0.3013
RQLETLGQEK	1202.3	2	2.8345	0.1488
RQLFHPEQLITGKEDAANNYAR	2572.8	3	5.9331	0.3298
RQLLEGELETLR	1457.7	2	3.0789	0.2632
RQLPVTR	870.0	2	2.6042	0.1772
RQNVAYEYLCHLEEAKR	2123.4	3	3.655	0.1928
RQPAPPR	822.0	2	2.4092	0.1108
RQPEAVHLLDK	1306.5	2	2.4508	0.1543
RQQEELLAEENQR	1643.7	2	5.2396	0.3641
RQQEEMMR	1108.3	2	3.1847	0.1496
RQQEGFKGTFPDAR	1637.8	2	3.7754	0.4392
RQQEGFKPNYMENR	1798.0	2	3.3729	0.2402
RQQETAAAETETR	1491.5	2	4.6732	0.4128
RQQHEQLNEAAQGILTGPGDVSLSTSQVQK	3221.5	3	5.5146	0.2532
RQQLDEQILLLQHSK	1850.1	3	3.7035	0.2329
RQSHLLLQSSIPDQQLLK	2105.4	3	3.6005	0.2315
RQTSGGPVDASSEYQQELER	2238.3	3	5.83	0.4875
RQTSGGPVDASSEYQQELERELFK	2755.9	3	6.57	0.4458
RQTSGGPVDASSEYQQELERELFKLK	2997.3	3	4.7488	0.2499
RQVDQLTNDK	1217.3	2	2.436	0.1023
RQVDQLTNDKAR	1444.6	3	4.402	0.3824
RQVEDLQATFSSIHSFQDLSSSILAQSR	3152.4	3	5.8087	0.4365
RQVKPNATLEK	1284.5	2	2.6448	0.1291
RQVPVEEAR	1084.2	2	2.7307	0.1183
RQVQDESQR	1146.2	2	2.8107	0.1082
RQVQSLTCEVDALKGTNESLER	2477.7	3	5.0423	0.3578
RQVVEAAQAPIQER	1595.8	2	5.0639	0.4029
RQWVEEFFPSVSLGDPTLETLLR	2721.1	3	3.3108	0.2243
RRDELSEEINNLR	1644.8	2	3.5541	0.2561
RRDETMQPAKPSFLEYFEQK	2501.8	3	3.6444	0.169
RRDFTPAELR	1261.4	2	2.5794	0.2695
RREDNLNDSSQQLQDSLR	2175.3	3	4.0673	0.265
RREEGAPGDPEAALEDNLAR	2167.3	2	4.3157	0.3354
RREGLFQRSSRPR	1645.9	2	2.6975	0.1369
RRELEEETNAFNR	1664.8	3	3.8508	0.3568
RREPLPSLEAVYLITPSEK	2199.5	3	3.715	0.2843

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RRFETANLDIPPANASR	1929.1	3	3.6591	0.2472
RRFPEEPHVPLEQR	1791.0	2	3.912	0.1137
RRGEEGHDPKEPEQLR	1934.1	2	4.2709	0.3474
RRGETESEEFEK	1497.5	2	2.4747	0.2117
RRGETESEEFEKLK	1738.9	2	3.7977	0.1027
RRLELQLQEVQGR	1625.9	2	2.758	0.1552
RRPEDQELESLSAIEAELEK	2343.5	3	5.3469	0.4368
RRPEDYDIHNSR	1558.6	2	3.8678	0.3842
RRPEIGTFLR	1245.5	3	3.5539	0.2052
RRPELIPEDLHR	1531.7	3	3.4258	0.1322
RRPEPIIPVTQPR	1559.8	2	3.0199	0.1904
RRPNDPVPIPDKR	1560.8	2	3.0334	0.1385
RRPPLAGLLDALAEAER	1849.1	3	3.8593	0.3028
RRPTPATLVLTSDQSSPEIDEDRIPNPHLK	3384.7	3	4.9499	0.3215
RRRSSSYSPSPVKKKKKKSSKKHKRR	3156.7	3	3.5	0.1763
RRTEEGPTLSYGR	1522.6	2	2.7142	0.2029
RSAPGGGSK	816.9	2	2.7552	0.1643
RSASASHQADIK	1271.4	2	2.4315	0.1556
RSDDMFTFHGPGK	1495.6	2	2.8321	0.1003
RSDSVILNVLYGPDAPTISPLNTSYR	2850.2	3	3.9752	0.1998
RSDSVSASER	1094.1	2	3.0268	0.2022
RSEAEEAITSFNGHKPPGSSEPITVK	2770.0	3	4.1285	0.2567
RSEKDTAAVVSR	1319.5	2	4.135	0.3509
RSELEEQQMHLNVGLR	1940.2	2	4.9657	0.401
RSELEEQQMHLNVGLRK	2068.3	2	3.6529	0.2033
RSELPIAELTGHTR	1580.8	2	3.0719	0.1755
RSENEEFVEVGR	1451.5	2	3.7571	0.2918
RSGQVLEVSGSK	1247.4	2	3.0802	0.2155
RSINQPVAFVR	1287.5	2	3.0512	0.2985
RSKAEELGLPILGVLR	1752.1	3	3.7172	0.276
RSLDSRGETTGSGRAIPIKQSFLLKRSGNSLNK	3576.0	3	3.4648	0.2109
RSLEPLPSSGPDFGGLGEEAEFVEVEPEAK	3174.4	3	5.2151	0.3223
RSLGEGAKEREALRRSNEELR	2457.7	3	3.2005	0.2895
RSNMDNMFESYINNLR	2005.2	3	5.1388	0.3677
RSNMHFTSSSTGGLSSSQSSYSPSNR	2750.9	3	5.1985	0.4178
RSPFLQVFNNSPDESSYYR	2307.5	3	4.1471	0.2722

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RSPHFFQPTNQQFK	1763.0	2	4.7572	0.2735
RSPPIPLAK	979.2	2	2.7045	0.2332
RSPPPSPTTQR	1224.4	2	2.5232	0.1017
RSPSKPLPEVTDEYK	1746.9	2	3.2623	0.1906
RSPSKPLPEVTDEYKNDVK	2203.4	3	5.673	0.4127
RSQAGVSSGAPPGR	1327.4	2	2.917	0.308
RSQIYGSR	967.1	2	2.4483	0.1378
RSTITSR	820.9	2	2.4098	0.1129
RSYDVPPPPMEPDHPFYSNISK	2574.9	3	4.7029	0.3727
RTAEHEAAQQDLQSK	1712.8	2	4.426	0.337
RTAQEVETYR	1253.3	2	2.4585	0.1318
RTAQEVETYRR	1409.5	3	3.2201	0.332
RTCEEHQLCVVAVLPHILDTGAAGR	2690.1	3	3.8255	0.1193
RTDEATFSKIPIGFIPLGETSSLSHTLFAESGNK	3653.1	3	5.0733	0.2736
RTDEEGKDVPDHAVLEMK	2070.3	3	3.802	0.2297
RTDIFGVEETAIGK	1536.7	2	4.3973	0.3811
RTDIFGVEETAIGKK	1664.9	2	4.8671	0.3998
RTDKDTEITCSER	1554.7	2	3.6354	0.1664
RTDLCDHALHISHDEL	1876.0	2	3.6749	0.2578
RTEEGPTLSYGR	1366.5	2	3.8607	0.3129
RTEGVGPGVPGEVEMVK	1742.0	2	2.4058	0.2599
RTEGVGPGVPGEVEMVKGQPFDVGPR	2696.0	3	4.751	0.3484
RTEITIVKPQESAHR	1766.0	2	4.7881	0.4036
RTEMENEFVLIK	1509.8	2	2.7106	0.1217
RTEMENEFVLIKK	1637.9	2	5.5995	0.291
RTEQEEDEELLTESSK	1924.0	2	2.9919	0.2503
RTFEDISEK	1125.2	2	3.1911	0.1733
RTGAIVDVPVGEELLGR	1782.0	2	4.4898	0.3755
RTGFSFPTQEPRPQTQNLGTPGPALSHSR	3166.5	3	3.9988	0.3416
RTGKTSIAIDTIINQK	1760.0	2	4.0863	0.423
RTGPAATTLPDGAAAESLVESSEVAVIGFFK	3093.4	3	4.3209	0.3751
RTGPAATTLPDGAAAESLVESSEVAVIGFFKDVESDSAK	3925.3	3	6.0761	0.5385
RTGPPMGSR	959.1	2	2.5923	0.1896
RTHLPEVFLSK	1327.6	2	3.6468	0.3032
RTHNGESVSYLFSHVPL	1944.1	2	2.5346	0.178
RTIAQDYGVLKADEGISFR	2140.4	2	3.8257	0.3814

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RTIQFVDWCPTGFK	1699.0	2	3.6745	0.4286
RTLEGELHDLR	1339.5	2	2.841	0.283
RTLEGELHDLRGQVAK	1823.0	3	3.4792	0.3364
RTLKIPAMTIAK	1343.7	2	2.4919	0.1847
RTNSTFNQVVLKR	1563.8	2	4.5715	0.3795
RTPDGFDSVPLK	1332.5	2	2.8119	0.2036
RTPFGAYGGLLK	1280.5	2	3.1254	0.1887
RTPFGAYGGLLKDFTATDLSEFAAK	2678.0	3	6.335	0.5136
RTPGRPTSSQSYEQNIK	1950.1	2	2.7815	0.2707
RTPLQHELPAWSERPPTFGTPLLQEAQAK	3300.7	3	5.1892	0.4169
RTPLYDFHLAHGGK	1612.8	2	3.9249	0.3783
RTPMGIVLDALEQQEEGINR	2270.6	3	4.3432	0.3625
RTPMGIVLDALEQQEEGINRLTDYISK	3091.5	3	4.5412	0.2103
RTPMGLLLEALGQEQEAGS	2001.3	2	3.1765	0.2731
RTQAPTKASE	1089.2	2	2.4057	0.2897
RTQAVVSGR	974.1	2	2.463	0.2122
RTQEVLQAVAEK	1372.6	2	3.1029	0.1707
RTVDLSSHLAK	1227.4	2	3.0221	0.2992
RTVQSLEIDLDSMR	1663.9	2	3.7616	0.3877
RTYEEGLKHEANNPQLK	2028.2	2	4.2973	0.4264
RVAAALPGMESTQDR	1602.8	2	3.5991	0.4099
RVAEAHVPNFIFDEFR	1948.2	3	3.9321	0.3252
RVAEELALEQAKK	1485.7	3	3.3053	0.1152
RVAEELALEQAKKESEDQKR	2358.6	3	5.7632	0.4162
RVAGSVTELIQAAEAMK	1775.1	2	4.2278	0.3678
RVAPEEHPVLLTEAPLNPK	2111.4	2	5.0584	0.209
RVASGPSPGEGISPQSAQAPQAPGDNHVVPV	3008.3	3	4.9912	0.3411
RVASGPSPGEGISPQSAQAPQAPGDNHVVPVLR	3277.6	3	5.2668	0.3821
RVATWFNQPAR	1346.5	2	3.1165	0.3334
RVDAENR	859.9	1	1.9633	0.1142
RVDFETFLPMLQAVAK	1866.2	2	2.7613	0.2381
RVDFHDVQDYADNIK	1836.0	2	2.9881	0.1279
RVDFHDVQDYADNIKAQLFETSSK	2828.0	3	4.1414	0.2132
RVDIDEFDENKFVDEQEEAAAAAAEPGPDPSEVDGLLR	4146.3	3	4.6296	0.4153
RVDIIPGFEFDR	1464.7	2	2.4168	0.1684
RVDIQNKR	1029.2	2	2.8724	0.1213

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RVEAAQETVADYQQTIKK	2079.3	3	5.9034	0.4326
RVEDVLGKGWENHVEGQK	2081.3	3	3.7344	0.1482
RVEEDIQQQKATGSEVSQR	2189.3	3	3.8809	0.2519
RVEEGEKEFHVR	1515.7	3	3.3734	0.2572
RVEELGDLAQAHIQQLSEAAGEDDHFLIR	3262.5	3	6.9766	0.4984
RVEHGSGLTR	1112.2	2	3.0139	0.2215
RVEHNQVGEK	1196.3	2	3.2688	0.3371
RVEIMEEESEQ	1379.5	2	2.9107	0.2102
RVEIQMPKPAEAPTAPSPAQTLENSEPAPVSQLQSR	3857.3	3	7.1409	0.5172
RVEISAPSNFEHR	1542.7	3	3.9006	0.3226
RVEPPELPADLQHWISYNEASSQLLR	3050.4	3	5.2338	0.4505
RVEVNGEHATVR	1367.5	3	3.2438	0.3277
RVFITDDFHDMMPK	1753.0	2	3.6857	0.4075
RVFQPSPLASQFELPGDFFNLTAEEIKR	3238.6	3	5.8943	0.3308
RVGGVQSLGGTGALR	1428.6	2	3.8091	0.2772
RVGNGEETPMIGDK	1503.7	2	2.5616	0.1266
RVHELER	939.1	1	1.6787	0.1794
RVHGPLSLLAPLPAAGK	1698.0	2	3.3007	0.2523
RVHLMNPMVPGLTGSK	1738.1	3	3.837	0.3558
RVHPALDTYIK	1313.5	2	2.8994	0.1921
RVHVTQEDFEMAVAK	1761.0	3	5.4426	0.4186
RVIAANNR	914.0	2	2.9169	0.1998
RVIISAPSADAPMFVMGVNHEK	2370.8	2	5.9663	0.4547
RVIISAPSADAPMFVMGVNHEKYDNSLK	3091.6	3	6.443	0.419
RVLDGLHNELQTIGFQIETIGK	2482.8	3	5.2914	0.4324
RVLGLVLLR	1039.3	2	2.9472	0.1987
RVLIAAHGNSLR	1307.5	2	4.1694	0.394
RVLLGETGKEK	1230.4	3	3.8134	0.2577
RVLQALEGLK	1127.4	2	2.7857	0.2557
RVLYPRVVSIAEVGIR	1828.2	2	3.1951	0.1232
RVMVDANEVPIQK	1499.8	2	3.1902	0.161
RVNAIEHVIIPR	1417.7	2	3.9317	0.302
RVNILSDMHLR	1354.6	2	3.4404	0.2845
RVNKEESLQMQVQDILEQNEALK	2744.1	3	3.7005	0.15
RVNQAIWLLCTGAR	1601.9	2	4.6131	0.4569
RVPANYADGVYQALEEPQLPNPR	2598.9	2	4.3036	0.3227

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RVPATTLYAHFEQANIK	1960.2	3	4.601	0.2941
RVPDITECKEEDIMCMYEAEMQWK	2979.4	3	4.2441	0.2985
RVPFSLLR	988.2	2	2.67	0.1166
RVPGSPTNLANR	1282.4	2	3.0871	0.3289
RVPGSSGR	815.9	2	2.4339	0.1164
RVPKVTGDARSAFRPLR	1927.2	2	2.7487	0.1996
RVPPPALSR	993.2	2	2.6156	0.1533
RVPQAKPVAVEEK	1451.7	2	3.6124	0.3047
RVPVLGSLLNLPGIR	1605.0	2	3.675	0.2957
RVQANMGAK	975.2	2	2.5178	0.1042
RVQDPLAELVKIEPK	1736.0	3	4.4134	0.3061
RVQLAEDLKK	1200.4	3	3.6915	0.2401
RVQVAEHPR	1092.2	2	3.0459	0.2523
RVSGHYVTSAAAK	1347.5	2	3.0442	0.2664
RVSHQGYSTEAEFEEPR	2023.1	3	4.6656	0.3975
RVSVWPVAFVGGLRYEAPRVNGAGKVVR	3041.5	3	3.5107	0.1641
RVTNDARENEMDENLEQVSGIIGNLR	2974.2	3	4.1377	0.235
RVTNVGSLLLTPQENESLFTFLGK	2665.0	3	5.3111	0.3104
RVTNVGSLLLTPQENESLFTFLGKK	2793.2	3	3.8332	0.1954
RVVHASGDASYSAGDSGDAAAQPAFTGIK	2808.0	3	6.3432	0.4899
RVVHFAEPGAGTK	1369.6	2	3.7189	0.1791
RVVLVTSGGTK	1117.3	2	2.4197	0.2362
RVVPSDLYPLVLGFLR	1845.2	2	3.9405	0.289
RVYATILNAGTNTDGFKEQGVTFPSGDIQEQLIR	3741.1	3	6.5495	0.5473
RVYGSFLVNPESGYNVSLLYDLENLPASK	3246.6	3	4.0351	0.3467
RWEEVQSYIR	1366.5	2	2.7604	0.1995
RWEVADLQPQLK	1483.7	2	3.3537	0.1289
RWFHPNITGVEAENLLLTR	2267.6	3	5.5022	0.4213
RWHWSSGSLVSYK	1593.8	2	2.9181	0.1334
RWLPAGDALLQMITIHLPSPVTAQK	2758.3	3	5.5569	0.402
RYAGLKPGELPTCESLKDTIAR	2419.8	3	4.1566	0.3548
RYDDPEVQK	1150.2	2	3.0007	0.1838
RYDDPEVQKDIK	1506.6	2	4.0126	0.3474
RYDSNSGGER	1141.1	2	2.8749	0.2064
RYEPIQATPPPPPLPSQYAQPSQPVTSASLHIHSK	3822.3	3	4.9742	0.309
RYEQEHAAIQDK	1488.6	2	3.2599	0.2426

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
RYESHPVCADLQAK	1617.8	2	3.4538	0.2165
RYETLVGTIGKK	1365.6	2	3.0969	0.2163
RYEVPLETPHVHSR	1720.9	3	4.5876	0.4162
RYGGGGYGR	943.0	2	2.8773	0.3253
RYIAGGAGIR	1034.2	2	2.674	0.1016
RYILPDEPAIIVHPNWAAK	2204.6	3	3.9668	0.2682
RYINMLTRPR	1320.6	3	3.3741	0.2499
RYKVPDGKPENEFAFNAEFK	2387.6	3	3.8955	0.3356
RYLSAQKPLLNDGQFR	1907.2	2	4.6998	0.3868
RYNEDLELEDAIHTAILTLK	2358.6	3	6.507	0.4855
RYNGGVGR	879.0	2	2.9624	0.2388
RYNIPHGPVVGSTR	1553.8	2	3.344	0.3597
RYPEEFALR	1181.3	2	2.7188	0.2183
RYPSSISSSPQK	1337.5	2	3.5315	0.1983
RYQEALHLGSQLLR	1684.9	2	3.8216	0.3477
RYQEIEEDRKKAELEGVAVTAPR	2689.0	3	4.6058	0.476
RYTIAALLSPYSYSTTAVVTNPK	2517.9	3	5.5614	0.4906
RYTIAALLSPYSYSTTAVVTNPKE	2647.0	3	6.179	0.5287
RYTLNVLSDLGEGEKVNDEIIIK	2620.0	3	3.3909	0.1883
RYTSLNHLAQAAR	1501.7	2	2.7307	0.2269
SAAASNLSGLSLQEAQQILNVSK	2330.6	3	5.1421	0.4764
SAADDSEAKSNELTR	1594.6	2	4.4837	0.3715
SAADIIALAR	1001.2	2	3.7069	0.2576
SAADLISQAR	1032.1	2	3.701	0.2967
SAADSISESVPVGPK	1444.6	2	3.8644	0.4685
SAAEMYGSSFDLDYDFQR	2103.2	2	6.0007	0.573
SAAEMYGSSFDLDYDFQRDYYDR	2815.9	3	4.3568	0.4389
SAAEMYGSVTEHPSPSPLLSSSFDLDYDFQR	3435.7	3	4.5463	0.2951
SAAETVTK	806.9	1	2.5519	0.1644
SAAETVTKGGIMLPEK	1632.9	3	4.8032	0.2899
SAAETVTKGGIMLPEKSQGK	2033.3	2	4.6105	0.379
SAAILEYLTAEVLELAGNASK	2164.4	3	6.0894	0.3679
SAALQSTQSQEEFKLEDLKKLEPILK	2975.4	3	3.6542	0.1356
SAAMLGNSEDHTALSR	1660.8	2	4.4371	0.3969
SAAPGGGSVAAAAAAMGAALGSMVGLMTYGR	2726.2	3	3.7617	0.339
SAAPSTLDSSSTAPAQLGK	1789.9	2	4.8957	0.4411

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SAAPSTLDSSSTAPAQLGKK	1918.1	2	5.3911	0.4035
SAAQAAAQTNSNAAGK	1461.5	2	5.1237	0.497
SAAREDDSIRPFKVETSDEEIHDLHQR	3182.4	3	3.9729	0.367
SAASVYAGAGGSGSR	1298.3	2	4.3594	0.4422
SAATLITHPFHVITLR	1778.1	3	3.9131	0.3589
SAATSGAGSTTSGVVSGSLGSR	1898.0	2	5.1679	0.5407
SAAYERLENTEDIEEVEQHIQTIK	2847.0	3	4.4355	0.2107
SACGNCYLGDAFR	1377.5	2	2.5747	0.115
SADEPMTTFVVCNECGNR	1974.2	2	2.5434	0.1177
SADFTNFDPR	1170.2	2	3.2784	0.3254
SADFVVEAIGDDVGTLGFSVEGPSQAK	2696.9	2	3.3202	0.283
SADFVVESIGSEVGSLGFAIEGPSQAK	2682.9	3	6.2109	0.4925
SADGVIVSGVKDVDDFFEHER	2322.5	3	5.0212	0.4131
SADIALVAGGSR	1117.2	2	3.6838	0.2684
SADLPAIISTWQELR	1700.9	2	4.1453	0.3858
SADTLWDIQK	1177.3	2	3.0296	0.1445
SADTLWDIQKDLK	1533.7	2	2.8514	0.1131
SADTLWDIQKDLKDL	1762.0	2	2.719	0.1196
SADTLWGIQK	1119.3	1	3.2937	0.3085
SADTLWGIQKELQF	1636.8	2	3.71	0.3571
SADTQSISR	965.0	2	3.0931	0.1337
SADVEKLADELHMPSLPEMMFGDNVLR	3046.5	3	5.4343	0.3522
SADWLGLFAPHHGPPR	1759.0	3	3.658	0.3013
SAEAAAAQAEEDLRASLLAVLSR	2343.6	3	3.2208	0.1576
SAEAAAEATK	949.0	2	3.1185	0.2988
SAEAAAEATKNMEAGAGR	1735.9	2	5.1361	0.4316
SAEAELQSK	963.0	2	2.9076	0.1183
SAEAILKR	888.0	2	2.4588	0.1627
SAEDLDKLRNDGYLMFQQVPMVEIDGMK	3244.7	3	6.2543	0.4659
SAEDLDKLRNDGYLMFQQVPMVEIDGMKLVQTR	3842.4	3	5.0336	0.3183
SAEDSFTGFVR	1216.3	2	3.2798	0.3323
SAEEEAADLPTKPTK	1587.7	2	4.4785	0.3564
SAEETFQLSR	1168.2	2	2.9501	0.2736
SAEFLLHMLK	1189.5	2	3.4927	0.3375
SAEFPDFYDSEEPVSTHQEAENEKDR	3058.1	3	4.3371	0.2829
SAEHTLVDMVQLLFTR	1861.2	2	3.2341	0.2048

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SAEIDSDDTGGSAAQK	1552.5	2	5.6417	0.4618
SAEKEISLWFKPEELVDYK	2312.6	3	4.8269	0.4457
SAELAAALLSIYMERAEDLPLR	2433.8	3	5.1163	0.4307
SAELAAALLSIYMERAEDLPLRK	2562.0	3	4.5674	0.3074
SAEPNALAFAAGETFLVLER	2107.4	2	3.994	0.4051
SAEPSPTVMSTSLGSNLSELDR	2279.5	2	4.5284	0.4876
SAEQQPSEKSTEPK	1546.6	2	3.4287	0.2356
SAESQGRSEILMSLQKVLSGLGGAAASSHRDIYK	3549.0	3	3.3016	0.1533
SAFEEEGKETADITHALSK	2064.2	3	3.2103	0.1358
SAFEEEGKETADITHALSKLTEPASVPIHK	3237.6	3	4.1614	0.1788
SAFLQAFLGR	1110.3	2	3.8718	0.3227
SAFPFSDKLGELSDKIGSTIDDTISK	2773.0	3	3.8694	0.3415
SAFPFSDKLGELSDKIGSTIDDTISKFR	3076.4	3	4.6001	0.4287
SAFSNLFGGEPLSYTR	1746.9	2	4.5729	0.3974
SAGEEEDGPVLTDEQK	1704.7	2	4.57	0.3546
SAGFHPSGSVLAVGTVTGR	1801.0	2	4.5473	0.3995
SAGHHLIPVKENLVDK	1758.0	2	3.8196	0.1671
SAGIKVIMVTGDHPITAK	1839.2	2	4.9274	0.3501
SAGKYDVYLINPQGK	1653.9	2	4.3021	0.3667
SAGLAFSLYQAMAK	1458.7	2	4.3018	0.3874
SAGLAFSLYQAMAKDQAVENILVSPVVVASSLGLVSLGGK	3992.6	3	4.7944	0.3896
SAGLEQPTDPVAR	1341.5	2	3.5129	0.1619
SAGLPSHSSVISQHSK	1622.8	2	3.9572	0.4877
SAGSALYASR	983.1	2	3.4514	0.364
SAGSRIEDGVPQHLVLVLGGK	2133.4	2	4.2192	0.2772
SAGTVELDDQIQANLPDEQVLSEEEIDENFK	3477.6	3	4.8386	0.3107
SAGTVELDDQIQANLPDEQVLSEEEIDENFKALFR	3965.2	3	5.4451	0.3771
SAGVDQNHPR	1081.1	2	3.0539	0.24
SAHAGTYEVR	1091.2	2	3.2329	0.3971
SAHATAPVNIAGSR	1352.5	2	3.6443	0.4853
SAHGYIAAHPSSTK	1427.5	2	3.7607	0.4665
SAHLTNPWNEHKPVK	1759.0	2	3.5947	0.3602
SAHQVAR	768.8	1	1.9006	0.1271
SAHSIAQLQK	1083.2	2	2.6515	0.1941
SAHVNSLAQDETKLK	1641.8	2	4.5331	0.4092
SAIDLEEMASGLNK	1478.7	2	3.709	0.177

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SAIEAELEKVAHQLQALR	2007.3	3	5.276	0.3823
SAINEVVTR	989.1	2	3.3731	0.2096
SAIQANDHHPR	1246.3	2	3.2109	0.2102
SAIRDNNPVVVLENELMYGVPFEFPPEAQSK	3491.9	3	4.9373	0.3633
SAIVHLINYQDDAELATR	2030.2	2	5.2281	0.4416
SAIYGFGDQSNLR	1428.5	2	4.0535	0.4344
SAIYQLEEEYENLLK	1843.0	2	5.5216	0.4398
SAKDSLAWLSLVKEELGDEWLKPELFR	3161.6	3	4.5343	0.2536
SAKGEEVDVAR	1161.2	2	3.6216	0.26
SAKGEEVDVARAER	1517.6	2	2.8094	0.1365
SAKKDKDPVNK	1230.4	2	2.5789	0.1124
SAKPGDDVRER	1230.3	2	2.9356	0.143
SAKPTKPAASDLPVPAEGVR	1992.3	2	5.3424	0.4285
SALALQHRPVVLFGDLAGTAPK	2262.6	3	6.4799	0.5077
SALALVTGAGSGIGR	1330.5	2	4.6663	0.2592
SALDTAAR	804.9	2	2.438	0.1622
SALEDKERDEDDEDGDGDGDGATGK	2597.5	3	5.6417	0.2475
SALENIVFAVTR	1320.5	2	3.7105	0.3643
SALFAQINQGESITHALK	1929.2	2	4.8559	0.4039
SALFAQINQGESITHALKHVSDDMK	2742.1	3	3.9198	0.2081
SALGHALPVAAPGAR	1388.6	2	3.3295	0.2077
SALLPVLHHK	1115.4	2	2.7803	0.2782
SALPYSSFSSDQGLGESSAAPSQPITAVK	2884.1	3	3.8378	0.1008
SALQAIGVEAHQAVMIGDDIVGDVGGAQR	2879.2	3	4.4509	0.3467
SALQSINEWAAQTTDGKLPEVTK	2488.7	3	3.4653	0.3168
SALQSINEWAAQTTDGKLPEVTKDVER	2988.3	3	5.1697	0.3538
SALRDSALNLFNDPMWNQQWYLQDTR	3184.5	3	4.9906	0.4277
SALSGHLETVILGLLK	1652.0	3	5.3953	0.4519
SALSGHLETVILGLLKTPAQYDASELK	2856.3	2	4.8225	0.3309
SALTIQLIQNHFVDEYDPTIEDSYRK	3097.4	3	5.5937	0.3453
SALTVQFVQGIFVEK	1666.9	2	2.6265	0.1117
SALWDSGLDYLHGTGHGVGSFLNVHEGPCGISYK	3575.9	3	3.7148	0.1769
SALYSPSDPLTLLQADTVR	2048.3	3	4.7543	0.4693
SALYYVDLIGGK	1299.5	2	3.3665	0.2918
SAMMYIQELR	1242.5	2	3.2863	0.1755
SAMPFTASPASSTTAR	1583.7	2	3.6717	0.372

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SANAEDAQEFSDVER	1668.7	2	4.5359	0.4051
SANFLDHLYVGIPR	1602.8	2	3.7689	0.2822
SANFLDHLYVGIPRPSGEK	2101.4	3	5.5741	0.4781
SANLVAATLGAILNR	1484.7	3	4.5926	0.3508
SANPAMQLDR	1103.2	2	2.8828	0.1777
SANPAVSKDFSSHDEINNYLQQIDQLKER	3348.6	3	5.3304	0.3683
SANPPHTIQASEEQSSTPAPVKK	2405.6	3	4.8609	0.487
SANPQDHPVIQPNYLSTETDIEDFR	2888.1	3	4.7431	0.3806
SANSELGGIWSVGQR	1561.7	2	4.3423	0.4004
SANSNPAMAPR	1116.2	2	3.2479	0.217
SANTQVVR	875.0	1	1.7819	0.1098
SAPELKTGISDVFAKNDLAVVDVR	2545.9	3	5.6492	0.4746
SAPEPKKPEENPASK	1609.8	2	3.5906	0.3116
SAPGGGSKVPQKK	1241.4	2	2.6197	0.1857
SAPLIADQAVLQLLPK	1678.0	2	5.0208	0.3331
SAPSIPKENFSCLTR	1650.9	2	2.6012	0.1485
SAPYEFPEESPIEQLEER	2151.3	2	4.4971	0.4117
SAQAAPEPR	927.0	2	2.4035	0.1612
SAQPASAEPR	1014.1	2	3.0335	0.2868
SAQPIEKFVTDIDELGKDLLLK	2473.8	3	3.6543	0.1802
SAQPLPLKIEELALAK	1722.1	2	3.1721	0.3606
SASASHQADIK	1115.2	2	2.741	0.2393
SASHAVPASK	955.1	2	2.8104	0.3962
SASHAVPASKK	1083.2	2	2.5038	0.1942
SASIKDIKK	990.2	2	2.7366	0.1477
SASLHLPK	853.0	2	2.9215	0.1766
SASLISQAEHSLKENDHAR	2094.2	3	4.3019	0.406
SASPDDDLGSSNWEAADLGNEER	2436.4	2	5.1852	0.5676
SASSGAEGDVSSEREP	1565.5	2	4.3055	0.3666
SASSLHETK	960.0	2	2.5609	0.2002
SASSTNLKDILADLIPKEQAR	2271.6	3	5.3511	0.4082
SASYKPVFVTEITDDLHFYVQDVETGTQLEK	3561.9	3	5.9357	0.4573
SATDGNTSTTPPTSAK	1536.6	2	3.1531	0.3899
SATDVKVTADMVKEALEEAEKAQVAAEK	2963.3	3	4.1392	0.2159
SATEHVQGHLGK	1264.4	2	2.9759	0.2472
SATEQSGTGIR	1107.2	2	2.9183	0.2591

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SATEYKNEEYQR	1518.6	2	2.5551	0.285
SATGKEVLQNLGPK	1442.6	2	3.8347	0.2315
SATKVTADVINAAEK	1518.7	2	4.2992	0.33
SATKVTADVINAAEKLQVVGR	2171.5	3	4.3908	0.1753
SATLASIDAELQK	1347.5	2	3.1957	0.2567
SATSSSVSNVVITK	1380.5	2	2.4653	0.1159
SATVTRLEDLLQDAQDEKEQLNEYKGHLSGLAK	3702.0	3	5.1278	0.3493
SATYVNTEGR	1098.1	2	3.176	0.4432
SAVADKHELLSLASSNHLGK	2078.3	3	6.2336	0.5197
SAVEAERLVAGK	1230.4	2	3.5676	0.2199
SAVEAQNEVTENPK	1516.6	2	4.6105	0.2524
SAVEAQNEVTENPKQK	1772.9	2	5.5606	0.3946
SAVGNAAHTSDR	1186.2	2	3.5682	0.4104
SAVLISSKPGCFIAGADINMLAACKTLQEVTQLSQEAQR	4094.7	3	4.7659	0.2511
SAVLQEAR	874.0	1	2.4248	0.1401
SAVLSEPVLFLKPSTAYAPEGSPILMPAYTR	3307.8	3	6.2237	0.4235
SAVNTEEEKK	1135.2	2	2.5124	0.2526
SAVPPGADKKAEAGAGSATEFQFR	2393.6	2	4.8354	0.2912
SAVRPASLNLNR	1298.5	2	2.9927	0.2527
SAVTTVVNPK	1016.2	2	3.2535	0.2634
SAVTTVVNPKYEGK	1493.7	2	3.2189	0.2661
SAWLSGYENPVVSR	1565.7	2	4.4352	0.4342
SAYDSTMETMNYAQIR	1882.1	2	5.2421	0.4435
SAYEFSETESMLK	1522.7	2	3.9297	0.456
SAYFAEK	815.9	1	1.9544	0.2293
SAYGGLTSPGLSYSLGSSFGSGAGSSSFSR	2833.0	2	5.2346	0.3166
SAYGGPVGAGIR	1105.2	2	3.1827	0.453
SAYKIVSGEAESVEVTPENLQDFVGKPVFTVER	3627.0	3	4.7308	0.2167
SAYQTIDSAEAPADPFAVPEGR	2293.4	2	4.9528	0.4654
SCREAEGLAHPGDTGAR	1727.8	2	2.5054	0.1784
SDAEEDGGTVSQEEEDRKPK	2207.2	3	3.3079	0.2649
SDALETLGFLNHYQMK	1868.1	2	4.4388	0.4312
SDALETLGFLNHYQMKNPNGPYPYTLK	3113.5	3	4.1901	0.1643
SDALNSAIDK	1034.1	2	2.762	0.1314
SDALNSAIDKMTK	1394.6	2	3.4294	0.2397
SDDELLDDFFHDQSTATSQAGTLSSIPTALTR	3441.6	3	4.5548	0.3432

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SDDEVDDPAVELK	1432.5	2	3.8369	0.2559
SDDKVTLEER	1192.3	2	3.1676	0.1643
SDEDKDKEGEALEVK	1692.8	2	4.5515	0.2666
SDEDKDKEGEALEVKENSGYLK	2484.6	3	5.2158	0.3129
SDEKAAVAGK	976.1	1	2.6368	0.1532
SDEKAAVAGKKPVVGK	1584.8	2	4.1997	0.3363
SDEKAAVAGKKPVVGKK	1713.0	2	5.1632	0.4157
SDEMNVK	822.9	2	3.0025	0.2122
SDFGKFVLSSGK	1272.4	2	3.7108	0.282
SDFQVNLNNASR	1365.4	2	4.2326	0.2368
SDFYDIVLVATPLNR	1724.0	2	4.3182	0.3681
SDGIYIINLK	1136.3	2	3.0367	0.1547
SDGSLEDGDDVHR	1402.4	2	2.7513	0.1309
SDGTETSTNLHQK	1418.4	2	3.3994	0.2916
SDHLIQTDTVNLHR	1649.8	2	3.1795	0.2109
SDIAVPIPK	940.1	2	3.1201	0.195
SDIAVPIPKDHQVLIK	1774.1	2	3.1879	0.1934
SDIDEIVLVGGSTR	1461.6	2	3.8288	0.3768
SDIGEVILVGGMTR	1447.7	2	4.3228	0.3248
SDILGHLR	911.0	2	2.4814	0.2355
SDKDLETQVIQLNEQVHSLK	2325.6	3	5.0721	0.3931
SDKKPDREEIQMSNMGSNTK	2296.5	3	3.4198	0.178
SDKMNIFGGFR	1272.5	2	3.3693	0.3299
SDKNNEFIVIHNGIITNYK	2220.5	3	3.8709	0.3405
SDKNNEFIVIHNGIITNYKDLK	2576.9	3	5.0693	0.3755
SDKNNEFIVIHNGIITNYKDLKK	2705.1	3	5.8641	0.4509
SDKSPDLAPTPAPQSTPR	1866.0	2	4.5334	0.4581
SDKVPDNKNTHTLLLAGVFR	2226.5	3	3.8409	0.4447
SDKWIDIHNPATNEVIGR	2066.3	3	3.4096	0.1758
SDLAVPSELALLK	1356.6	2	3.2343	0.2493
SDLLLSGRDWNTLIVGK	1888.2	3	3.2704	0.1439
SDLQMAVLSFEKDDDHNGHIDFITAASNLR	3361.6	3	6.2729	0.4423
SDLYSSGR	884.9	2	2.6999	0.1997
SDMLKDIIKEYTDVYPEIIER	2571.9	3	4.8996	0.42
SDPFLEFFR	1158.3	2	3.2293	0.3229
SDPIQEIRDLAEITTLDR	2086.3	3	3.9945	0.258

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SDPLLIGIPTSENPFK	1729.0	2	3.1656	0.2651
SDPLLIGIPTSENPFKDKK	2100.4	2	3.6649	0.2956
SDPNRETDDTLVLSFVGQTR	2251.4	3	3.7888	0.1304
SDPPQEAAQFTSQVIILNHPGQISAGYSPVIDCHTAHIACK	4346.9	3	4.7355	0.3867
SDQVNGVLVLSLLDK	1600.8	2	4.4955	0.3334
SDRIEPLTFYLDPQWQLALNPSER	2890.2	3	4.2658	0.2176
SDRPELTGAK	1074.2	2	2.9887	0.2822
SDRQQFLGHMR	1375.5	2	2.5329	0.2072
SDSDKSSSQVPPILQETDKSK	2277.4	3	4.169	0.3071
SDSFENPVLQQHFR	1704.8	2	3.8451	0.4935
SDSHGPKEDGGFRHSEAFEALQQK	2658.8	3	4.0209	0.313
SDSHPSDALTR	1186.2	2	2.5774	0.2426
SDSKALDLLDR	1233.4	2	2.5417	0.194
SDSRAQAVSEDAGGNEGR	1806.8	2	2.9	0.1627
SDTSFMFQR	1119.2	2	3.3155	0.2871
SDTSGDYEITLLK	1442.6	2	3.646	0.2946
SDTSGHFER	1036.0	2	2.7741	0.2075
SDVAAKGQDEESLSSSKR	1895.0	2	3.6183	0.222
SDVDLYQVR	1095.2	2	2.8004	0.1844
SDVEAIFSKYGK	1344.5	2	3.3089	0.2111
SDVLELTDDNFESR	1640.7	2	5.4639	0.4604
SDVLVEYQGEGR	1352.4	2	4.2704	0.3197
SDVQIHVPTFTFR	1547.7	3	3.5463	0.354
SDVYCEVCEFLVK	1534.8	2	2.7498	0.1245
SDYAQLLEDMQNAFR	1802.0	2	4.7496	0.3604
SDYDGIGNR	997.0	2	2.4135	0.1072
SDYINASPIIEHDPR	1727.9	2	3.7584	0.3804
SDYLNTFEFMDK	1510.6	2	3.5338	0.3674
SDYLNTFEFMDKLGENLK	2165.4	2	4.2375	0.3723
SDYLNTFEFMDKLGENLKIK	2406.7	3	3.9996	0.3155
SEAANGNLDFVLSFLK	1725.9	2	2.475	0.1325
SEADSDKNATILELR	1662.8	2	3.3014	0.3268
SEAEEAITSFNGHKPPGSSEPITVK	2613.8	3	4.7652	0.3905
SEAHLTELLEEICDR	1758.9	2	4.8871	0.3699
SEALAVDGAGKPGAEEAQDPEGK	2227.3	3	5.2287	0.4211
SEALPTDLPAPSAPDLTEPK	2050.3	2	3.9335	0.3168

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SEAQKQSDELALVR	1574.7	2	4.0662	0.3092
SEASAFGASHHVAYFEASAK	2068.2	3	4.297	0.2831
SEASLHPVLMSEAPWNTR	2026.3	2	4.3898	0.4467
SEAVVEYVFSGSR	1430.5	2	4.1396	0.4567
SEDFGVNEDLADSDAR	1740.7	2	3.6671	0.2078
SEDFSLPAYMDR	1431.6	2	3.8588	0.3584
SEDLLDYGPFR	1312.4	2	3.6256	0.3217
SEDPDQQYLILNTAR	1763.9	3	4.6129	0.3242
SEDPLFVLEHSLPIDTQYYLEQQLAKPLLR	3558.0	3	4.1052	0.3952
SEDQDLQGLKDKPLK	1714.9	2	2.8891	0.2347
SEDTLKALEDFLASLR	1809.0	3	4.0979	0.2737
SEDYVDIVQGNR	1395.5	2	3.5568	0.3162
SEEAHAEDSVMDHHFR	1898.0	2	4.6572	0.4451
SEEDLFLQVYEDLIQELAK	2283.5	2	3.0553	0.2152
SEEEQSSSSVKKDETNVK	2012.1	2	4.5559	0.2907
SEEERTTEAEKNER	1708.7	2	3.5173	0.1436
SEEERVTETQKNER	1735.8	3	3.8336	0.2746
SEEHADSKEHAK	1368.4	2	2.5313	0.239
SEEMQTVQQEQLLQETQALQQSFLSEKDSLLQR	3895.3	3	6.1956	0.4328
SEENTKEEKPDSK	1521.6	2	3.2163	0.236
SEEQLKEEGIEYK	1582.7	3	4.3908	0.3508
SEESYKDSTLIMQLLR	1914.2	2	5.0834	0.4356
SEETLDEGPPK	1202.3	2	3.1219	0.2001
SEETLDEGPPKYTK	1594.7	2	3.8078	0.2972
SEETSKNQIK	1164.2	2	2.805	0.1094
SEEWADNHLPLTDAELAR	2068.2	3	4.7726	0.3267
SEFEQNLSEK	1211.3	2	2.7525	0.1497
SEFGSVDGPLPHPR	1495.6	2	2.5304	0.3763
SEFVVPDLELPSWLTTGNYR	2324.6	2	5.0173	0.4533
SEGEDKPQSEGKPASQAKPESQPR	2568.7	3	4.874	0.3541
SEGEFKQTSSFLV	1459.6	2	3.6016	0.169
SEGEGEAASADDGSLNTSGAGPK	2108.1	2	4.1533	0.3753
SEGEGKPQGEGKPASQAKPESQPR	2480.6	3	4.9421	0.3885
SEGETIMSSSMGK	1344.5	2	3.6589	0.3805
SEGGLSAAPAR	1016.1	2	3.0374	0.123
SEGSHHITSTPGVPK	1534.7	2	3.5843	0.2849

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SEGSMSTDKR	1098.2	2	2.4857	0.2738
SEHKLSTDHIPILYR	1810.0	2	4.1805	0.4464
SEHKVWSPLVTEEGKR	1883.1	3	4.6108	0.3434
SEHPGLSIGDTAK	1312.4	2	3.054	0.3058
SEHPGLSIGDTAKK	1440.6	2	3.1873	0.3046
SEHQKLEENIDNIKR	1854.0	2	4.4369	0.3657
SEHSHSTTLPR	1252.3	2	2.7131	0.2673
SEHTQTVSQLTSQNEVLR	2058.2	3	3.5144	0.1785
SEIDLFNIR	1107.2	2	3.0079	0.2322
SEIDLFNIRK	1235.4	2	3.1139	0.1933
SEIDLLDIR	1074.2	2	3.2163	0.2202
SEIDLLNIR	1073.2	2	3.2548	0.1054
SEIDLVQIK	1045.2	2	2.7802	0.1636
SEIIPMFSNLASDEQDSVR	2139.3	2	3.5604	0.3385
SEIQAEQDRK	1204.3	2	2.6702	0.1192
SEISENTDASGK	1238.2	2	2.4316	0.1036
SEIVGVSRAGTTSR	1420.6	2	2.4973	0.1353
SEKELNHLAVDEASGVVYLGAVNALYQLDAK	3318.7	3	4.7161	0.2341
SEKFAFQAEVNR	1426.6	2	3.2874	0.3359
SEKGVIQVYDLGQDGQGMSR	2168.4	3	3.959	0.3254
SELALCLGLK	1047.3	2	2.5854	0.1596
SELASAVLEAVENNTLSIEPVGLQPIR	2851.2	3	4.5677	0.314
SELASAVLEAVENNTLSIEPVGLQPIRFVK	3225.7	3	4.0291	0.1518
SELDMLDIR	1092.2	2	3.3828	0.2697
SELELTLGKLEQVR	1615.9	2	3.2687	0.2412
SELEMVSGNVR	1221.4	2	3.215	0.1161
SELERESK	978.0	2	2.681	0.1367
SELGKLSLDKVFR	1492.7	2	3.6315	0.3761
SELGNQSPSTSSR	1350.4	2	3.8666	0.3936
SELHIENLNMEADPGQYR	2117.3	2	3.5736	0.4177
SELLVEQYLPLTEEELEKEAK	2491.8	3	3.3391	0.1719
SELSGNFEKTILALMK	1782.1	2	3.3964	0.2145
SELVAMLEEEELRK	1676.9	2	3.8095	0.2714
SELVANNVTLPAGEQRK	1827.0	2	4.1271	0.3277
SEMESVLAQLDNYGQQELADLFVNYNVK	3219.5	3	3.8131	0.2017
SEMTPEELQKREEEEFNTGPLSVLTQSVK	3337.7	3	5.2616	0.4269

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SENAVVDGPFLVEK	1504.7	2	3.215	0.1941
SENESEAAR	993.0	2	2.5306	0.1864
SENGLEFTSSGSANTETTKVTGSLETK	2776.9	3	4.0417	0.3114
SENLDNPIQTVSLGQSLFFHFPPLLR	2971.4	3	4.1523	0.3257
SEPALAPADFVAPLAPLPIPSNLFVPTPDAEEPQLPDGTGR	4209.7	3	3.7342	0.2462
SEPDDSDPFSFDGPEIMGCTGCQIDWKK	3106.4	3	3.2423	0.2393
SEPHSLSSEALMR	1444.6	2	3.2122	0.3792
SEPIPESNDGPVK	1369.5	2	3.1682	0.2332
SEPNQTENDALEPEDLSQAAEQDEMR	2948.0	3	5.0851	0.419
SEPPVSEQLDVAGR	1484.6	2	2.7892	0.4561
SEPQNLGGAAGR	1157.2	2	2.8849	0.3237
SEPVKEESSELEQPFAQDTSSVGPDR	2850.0	3	3.8424	0.2536
SEPVKEESSELEQPFAQDTSSVGPDRK	2978.1	3	6.0585	0.4319
SEQAVAQLEEEKKHLEFLGQLR	2583.9	3	4.726	0.3144
SEQAVAQLEEEKQHLLFMSQIR	2615.9	3	4.8973	0.3699
SEQDQAENEGEDSAVLMER	2138.2	2	6.6001	0.4678
SEQFINLR	1007.1	2	2.885	0.209
SEQSSMLELLR	1293.5	2	3.171	0.2468
SEQSVAQLEEEKKHLEFMNQLK	2647.0	3	3.6588	0.2283
SEQSVAQLEEEKKHLEFMNQLKK	2775.1	3	4.0646	0.1834
SESAEELKKR	1177.3	2	2.9065	0.1505
SESELIDELSEDFDR	1784.8	2	4.5673	0.4898
SESEVEEAAAIIAQRPDNPR	2183.3	3	3.8405	0.3572
SESLKDVLER	1176.3	2	2.642	0.1315
SESPEEPEQLR	1301.3	2	2.9905	0.1115
SESPEEPEQLRK	1429.5	2	3.1194	0.1309
SESPKEPEQLR	1300.4	2	2.52	0.1285
SESPKEPEQLRK	1428.6	2	3.0337	0.1058
SESRVPPPSDAPLPFDR	1868.0	3	3.7479	0.2772
SESTAAAEHK	1031.1	2	2.4728	0.2276
SETAPAAPAAPAPAEKTPVK	1905.1	2	3.2179	0.3513
SETDLLDIR	1062.2	2	2.5306	0.1318
SETEDSILHQLFIVR	1788.0	2	3.4179	0.274
SETHAAGHSQEK	1282.3	2	3.7292	0.4744
SETITEEELVGLMNK	1693.9	2	3.835	0.2535
SETSGSFEDALLAIVK	1667.8	2	5.1058	0.4899

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SETYKYLYGR	1280.4	2	2.5759	0.2965
SEVAAENHLR	1126.2	2	2.9341	0.2273
SEVAKDFEPER	1307.4	2	3.1447	0.2814
SEVATLTAAGK	1048.2	2	2.4266	0.1127
SEVATLTAAGKEVMLVGIGDKIR	2359.8	3	3.6492	0.1406
SEVEEQKEQR	1262.3	2	2.9096	0.1897
SEVELAAALSDKR	1389.5	2	3.2352	0.257
SEVELAAALSDKRGLESDVAELR	2459.7	3	4.2089	0.2197
SEVPGAAAEGSGGSGVGIGDR	1830.9	2	5.2295	0.5163
SEVQQPVHPKPLSPDSR	1902.1	3	3.9725	0.3823
SEVTDLRR	976.1	2	2.6129	0.1237
SEWGSLLEELVAEGK	1647.8	2	4.4977	0.3646
SEWSDLLSDLQK	1421.5	2	4.4255	0.301
SEYDRGVNTFSPEGR	1714.8	3	3.6932	0.305
SEYMEGNVR	1085.2	2	2.418	0.2152
SEYNDQLTR	1126.2	2	2.5464	0.1877
SFAHFDVQSMLFDLNEAAANR	2384.6	3	3.3328	0.1139
SFAHLLPSPEPSPEGSYVGQHSQGLGGHYADSYLKR	3871.2	3	4.5336	0.3042
SFANEEGEAQKFR	1513.6	2	2.9478	0.1719
SFAVGMFK	887.1	2	2.7435	0.1884
SFAVGMFKGQLTTDQVFPYPSVLNEEQTQFLK	3652.1	3	4.7208	0.2821
SFDALNFVTMLKMVWISK	2131.6	2	3.1761	0.1727
SFDDPIVQTER	1307.4	2	3.5567	0.33
SFDELGEIIQSVYEDLVANGVIVPAQEVPPPTVPMDYSWAR	4534.1	3	3.7226	0.2263
SFDFEIETK	1116.2	2	2.7323	0.2309
SFDFIHLDPFGTSVNYLDSAFR	2549.8	3	3.9759	0.2618
SFDKLLKDLPELALDTPR	2072.4	2	3.4761	0.2663
SFDLISHNR	1089.2	2	2.4631	0.2615
SFDSASQVPNPAAAAIPR	1800.0	2	3.797	0.3782
SFDSNAFTLLLR	1384.6	2	4.3306	0.4429
SFEADAFQDLLATYGPLDNVR	2343.5	2	5.4343	0.4751
SFEDIHHYR	1204.3	2	3.125	0.2504
SFEDRVGTIK	1152.3	2	2.4427	0.1679
SFEEKVENLKSK	1438.6	2	3.5567	0.1136
SFEGRELLVIELSDNPGVHEPGEPEFK	3026.3	3	4.4199	0.2515
SFENGIGKELHEQLVALDK	2128.4	3	4.601	0.4327

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SFENGIGKELHEQLVALDKQNK	2498.8	2	5.89	0.5266
SFENKPPAHIAASHLSEPAKPAHSQNQSNFSSYSSK	3883.2	3	5.814	0.3877
SFENSLGINVPR	1333.5	2	3.4151	0.3642
SFEVEEVETPNSTPPR	1818.9	2	4.2419	0.2501
SFEWLSQMR	1184.3	2	3.1192	0.2699
SFFHQHYLGGQEPTPSNIR	2216.4	2	4.81	0.4148
SFFLQPGEQLEQGIQDVYVLSEQQGLLLR	3336.7	3	6.1529	0.5343
SFFQAATEHLLPMGTALPLLEAQAATHTLVDPITGQR	3948.5	3	4.4726	0.3226
SFFSEIISSISDVK	1559.7	2	4.3534	0.4121
SFFSFLGEAFDGAR	1551.7	2	4.5374	0.4783
SFFWNVAPGAESAVASFVTQLAAAEALQK	3012.4	3	3.8944	0.2748
SFFWNVAPGAESAVASFVTQLAAAEALQKAPDVTTLPR	3963.4	3	3.5878	0.1229
SFGIEDKDKQIITFFSPLTILVGPNGAGK	3094.5	3	3.3806	0.1378
SFGTRPLSSGFSPEEAQQQDEEFEK	2831.9	3	3.2844	0.1976
SFHSFYQLLQGGSEQMLR	2129.4	2	6.121	0.5337
SFIKDYPVVSIEDPFDQDDWGAWQK	2987.2	3	6.3424	0.3957
SFITTDVNPYYDSFVR	1925.1	2	4.5724	0.391
SFKNQIATHEK	1303.4	2	3.6733	0.2745
SFLEDTTPARDEK	1509.6	2	3.4488	0.2291
SFLEEVLASGLHSR	1545.7	2	4.4875	0.4132
SFLEFAEDVIQVPR	1650.9	2	3.4961	0.2678
SFLENLKVNTENLLQVENTGK	2391.7	3	4.2052	0.3311
SFLHIGK	802.0	2	2.4892	0.1088
SFLINFIHTLENQR	1733.0	2	2.7657	0.1304
SFLIWVNEEDHTR	1646.8	2	3.4062	0.3297
SFLLKDSETSQR	1411.5	2	3.3613	0.1754
SFLNAHHR	982.1	2	2.4055	0.3111
SFLPEKSGYPDIGFPLFPLSK	2340.7	3	4.0477	0.3177
SFLRLAKISFDVLIKKALA	2134.6	2	3.0078	0.1196
SFLSQGQVLK	1107.3	2	2.687	0.1553
SFLSQGQVLKLEAK	1548.8	2	3.8921	0.1702
SFLVASVLPGPDGNINSPTR	2042.3	2	2.8217	0.1696
SFLYEIVSNKR	1356.6	2	2.7858	0.2707
SFMALSQDIQK	1268.5	2	3.2427	0.1988
SFMHVNTNANFYK	1573.8	2	3.6807	0.3647
SFMHVNTNANFYKDSGITYLGIK	2622.0	3	6.0238	0.5201

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SFNALQEEKQDLSKEIESLKVSISQLTR	3222.6	3	4.6772	0.3308
SFNVDLLAGK	1064.2	2	2.8188	0.1589
SFPDFPTPGVVFR	1466.7	2	3.3249	0.4175
SFPDQFSTGEPPALDEVPEVR	2318.5	2	4.1909	0.4667
SFPKDDPSKPVHLTAFLGYK	2248.6	3	4.0776	0.3862
SFPLHFDENSFFAGDKK	1987.2	2	3.6592	0.3717
SFQGPVLIGSSHGGVNIEDVAAESPEAIIKEPIDIEEGIKK	4275.8	3	4.2763	0.2904
SFQGPVLIGSSHGGVNIEDVAAETPEAIIKEPIDIEEGIKK	4289.8	3	5.7928	0.4955
SFQQSSLSR	1040.1	2	2.5883	0.225
SFSASQADPLSDPDQ	1565.6	2	4.3517	0.3707
SFSASQADPLSDPDQM	1696.8	2	4.9789	0.5049
SFSASQADPLSDPDQMN	1810.9	2	4.8402	0.5272
SFSASQADPLSDPDQMNE	1940.0	2	5.27	0.4845
SFSASQADPLSDPDQMNED	2055.1	2	6.2114	0.5148
SFSASQADPLSDPDQMNEDK	2183.3	2	5.2824	0.3568
SFSASQADPLSDPDQMNEDKR	2339.4	2	4.556	0.4931
SFSASQADPLSDPDQMNEDKRHSQGTFTSDYSK	3678.8	3	3.8088	0.2763
SFSERFPEDGPELEEILTQLATADAR	2923.1	3	5.0478	0.3407
SFSGGQLASGPDPAFPR	1691.8	2	4.6574	0.3809
SFSHGATLAQHR	1312.4	2	2.8046	0.2228
SFSKESDDPMAYIHFTAEGEVTFK	2738.0	3	4.1499	0.3071
SFSNIISTLNPTAK	1493.7	2	3.9731	0.1889
SFSQPEAGGSHHK	1369.4	2	3.2194	0.2892
SFSTASAITPSVSR	1411.5	2	3.5819	0.4686
SFTETMSSLSPGKPWQTK	2013.3	2	2.9377	0.1845
SFTKDAHALIYKDLPFETLEVEAK	2767.1	3	3.5275	0.186
SFTPDHVVYAR	1292.4	2	2.8313	0.232
SFTPHQQAHIPNSIMTILEASGK	2508.8	3	4.5713	0.4235
SFTPHQQAHIPNSIMTILEASGKQEPEAK	3191.6	3	3.3778	0.1754
SFTPVFLGSALK	1267.5	2	3.136	0.3465
SFTSEDDLVKLQILNLGAK	2092.4	3	4.3324	0.2809
SFTSSSPSSPSR	1227.3	2	2.7755	0.2928
SFVDKVGESNNMV	1426.6	2	3.2755	0.2658
SFVEFILEPLYK	1485.7	2	3.4343	0.2635
SFVELSGAER	1095.2	2	2.699	0.1438
SFVLNLGK	878.1	2	2.5235	0.1348

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SFVVTSVVAFPTDSK	1584.8	2	3.3938	0.326
SFVWHALDYADELPKPEQLAIR	2599.9	3	3.9743	0.2556
SFYDLSAISLDGEKVDFNTFR	2425.6	3	3.8164	0.2315
SFYPEEVSSMVLTK	1617.8	2	4.6627	0.462
SFYSGAVVSHHETALGLPR	2029.2	3	3.9713	0.4192
SGAAQGLAEVMAGLGVEK	1688.9	2	3.7385	0.3415
SGAAQGLAEVMAGLGVEKLEK	2059.4	3	3.9304	0.37
SGAEAQTPEDSPNR	1459.5	2	3.4118	0.2048
SGAEDQTPKDVPNKSGAEK	1959.1	3	3.3321	0.2522
SGAEEQGPIDGPSK	1372.4	2	3.0291	0.1432
SGAEEQTSKDSPNK	1478.5	2	4.0245	0.3637
SGAEVEAGDAAER	1262.3	2	3.1212	0.1829
SGAFGHLFRPDNFIFGQSGAGNNWAK	2797.0	3	6.827	0.4886
SGAHVDFYDK	1139.2	2	2.4502	0.1951
SGAHVVVTGPPNAGK	1391.6	2	2.4581	0.3199
SGAPAAESK	817.9	2	2.9426	0.3177
SGAPAAESKEIVR	1315.5	2	3.5286	0.4147
SGAQASSTPLSPTR	1360.5	2	4.3982	0.3359
SGASGPENFQVGSMPPAQQQITSGQMHR	2929.2	3	6.3407	0.4495
SGATAGAAGGR	875.9	2	3.651	0.4131
SGAVQGAGSLGPGSPVR	1497.6	2	3.3869	0.3845
SGAYLIPLLER	1232.5	2	2.7646	0.1601
SGDAAIVDMVPGKPMCVESFSDYPPLGR	2940.4	3	3.8235	0.395
SGDAPLTVNELGTAYVSATTGAVATALGLNALTK	3249.6	3	6.1311	0.5128
SGDGLSGTQKEAALR	1490.6	2	3.0635	0.1451
SGDGVVTVDDLR	1233.3	2	3.267	0.1441
SGDIVMIQSEHTGAIDVLSADLESADLLGDHRK	3494.8	3	4.9791	0.3086
SGDLGDMEPLKGTTPLMQKI	2132.5	3	4.9502	0.3951
SGDSEVYQLGDVSQK	1612.7	2	5.3504	0.4298
SGDSEVYQLGDVSQKTTWHR	2294.4	3	4.1604	0.2416
SGDTLLLLHHGDFSAEEVFHR	2381.6	3	5.9467	0.4093
SGDWKGYTGK	1099.2	2	2.6848	0.1306
SGDWVCPNPSCGNMNFAR	1956.2	2	2.9109	0.1512
SGDYALER	911.0	2	2.7789	0.2894
SGEADLGPARR	1129.2	2	2.5033	0.1149
SGEATDGARPQALPEPMQESK	2200.4	2	5.0029	0.4016

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SGEEGMPDLAHVMR	1529.7	2	3.5278	0.3845
SGEHDFGAAFDGDGDR	1653.6	2	4.5597	0.4332
SGEHDFGAAFDGDGDRNMILGK	2310.4	3	5.0997	0.4503
SGEILYR	837.9	2	2.6346	0.1788
SGEKITVTPSSK	1234.4	2	3.0264	0.2374
SGEKPLLGGSLMEYAILSAIAAMNEPK	2792.3	3	4.6135	0.5093
SGELAQEYDKR	1296.4	2	2.8725	0.2419
SGELEQEEER	1206.2	2	3.7292	0.2666
SGELEQEEERLSKEWEDS	2181.2	3	5.0461	0.3352
SGELEQEEERLSKEWEDSKR	2465.6	3	5.7141	0.3198
SGENFKLLYDLADQLHAAVGASR	2476.7	3	7.0482	0.5003
SGERPVTAGEEDEQVPDSIDAR	2358.4	3	4.5657	0.2005
SGESVKVHQLDVAIPLHLK	2071.4	2	4.1728	0.3439
SGETEDTFIADLVVGLCTGQIK	2297.6	2	6.394	0.5301
SGETEDTFIADLVVGLCTGQIKTGAPCR	2883.2	3	5.049	0.3908
SGETEDTFIADLVVGLCTGQIKTGAPCRSER	3255.6	3	4.5673	0.3226
SGEVLVNVKEHSR	1454.6	2	4.2458	0.3303
SGFEGMFIR	1044.2	2	2.7803	0.2882
SGFEPASLKEEVGEEAIVELVENGK	2661.9	3	3.3098	0.1486
SGFEPASLKEEVGEEAIVELVENGKK	2790.1	3	6.5162	0.4682
SGFSLDNGELR	1195.3	2	2.8486	0.3483
SGFSSISVSR	1027.1	2	2.8315	0.202
SGFTPLHIAAHYGNINVATLLLNR	2594.0	3	4.1135	0.2822
SGGASHSELIHNLR	1478.6	2	4.1827	0.3941
SGGASHSELIHNLRK	1606.8	2	4.1235	0.337
SGGELDIVVTSNKEVK	1675.9	2	4.4635	0.3857
SGGGGDIHQGFQSLLTEVNK	2045.2	3	5.5892	0.4718
SGGGGDIHQGFQSLLTEVNKTGTQYLLR	2978.3	3	6.7891	0.4361
SGGGGGGGGSSWGGR	1193.2	2	3.9283	0.3531
SGGGGYSQNR	983.0	2	3.4074	0.3034
SGGGYGGDR	825.8	2	2.8398	0.2686
SGGIETIANEYSDR	1512.6	2	3.9089	0.4009
SGGLGGSHALLLLR	1351.6	2	3.6455	0.3204
SGGMERPFVLAR	1320.5	2	2.6465	0.1814
SGGMSNELNNIISR	1492.6	2	4.2127	0.3593
SGGNSYGSGGASYNPGSHGGYGGGSGGGSSYQGK	3014.0	3	3.4823	0.1684

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SGGPHGAGVLGLHLEGPFISR	2059.3	2	5.8237	0.5216
SGGTALHVAAAK	1083.2	2	3.0634	0.3252
SGGTEGLLAEKLEALITQTR	2088.3	3	4.9379	0.3857
SGGTVVENGVHK	1184.3	2	2.9363	0.1935
SGHEQVVEMLLDR	1513.7	2	3.9393	0.3667
SGHFEQAIKEGEDMIAEEHFGSEK	2706.9	3	6.7936	0.6098
SGHIQDYQITASSIFR	1824.0	2	5.1137	0.4753
SGHIQTLLR	1025.2	2	2.5754	0.1166
SGHKPDNIK	996.1	2	2.5204	0.1588
SGHKPDNIKGNLEFR	1712.9	2	3.6277	0.2541
SGILAAESIFNQLTSENLQSK	2251.5	2	6.279	0.5103
SGIPIVTSPYQIHFTK	1789.1	2	4.3394	0.4624
SGKAPILIATDVASR	1499.7	2	4.2297	0.451
SGKDFVTEALQSR	1438.6	2	3.6381	0.3476
SGKDLTKR	905.0	2	2.6505	0.1901
SGKGFYIYQEGVK	1476.7	2	3.8479	0.3899
SGKGPILMELQTYR	1593.9	2	3.1471	0.2623
SGKKLEDGPK	1059.2	2	2.8064	0.2433
SGKKLEDNPK	1116.3	2	3.043	0.1509
SGKLKVPEWVDTVK	1586.9	2	3.4787	0.2556
SGKNQFNR	951.0	2	2.5486	0.1905
SGKNSQEDSEDSEDKDVK	1998.0	2	5.192	0.3531
SGKPAELLK	943.1	1	2.5606	0.2403
SGKPAELLKMFGIDRDAIAQAVRGLITKA	3071.6	3	3.3485	0.2096
SGKTELAEPIAIRPTSETVMYPAYAK	2825.2	3	5.0791	0.4364
SGKWEGLVYAPPGKEK	1747.0	2	3.649	0.2771
SGKYDLDFK	1073.2	2	2.9447	0.1951
SGKYDLDFKSPDDPSR	1827.9	3	4.9384	0.5334
SGKYDLDFKSPDDPSRYISPDQLADLYK	3235.5	3	5.7087	0.4451
SGLAIVSQHDLDQLQADAINAFGESLQKK	3098.4	3	7.693	0.4228
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHK	3300.5	3	5.8011	0.4561
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAAR	3712.0	3	4.9143	0.3957
SGLEELVLSEMNSPSR	1748.9	2	3.5135	0.2831
SGLGELILPENEPGSSIMPGK	2126.4	2	4.6409	0.3782
SGLGPADLALLGLSAER	1640.9	2	4.1753	0.4269
SGLIFYR	856.0	2	2.6075	0.2463

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SGLIHVGDELR	1196.3	2	2.6324	0.2477
SGLKKQELLEALTK	1558.8	3	4.7458	0.269
SGLKKQELLEALTKHFQD	2086.4	2	3.3178	0.2846
SGLLDKWK	947.1	2	2.5392	0.1651
SGLNIAHFK	987.1	2	3.2475	0.1572
SGLPPSEEQPTSQR	1513.6	2	3.0424	0.297
SGLSSPIYIDLR	1321.5	2	2.967	0.1899
SGLTADSKLHGK	1214.4	2	2.9896	0.3078
SGLTGLVIGGLYPVFLAIPVNGGLAAR	2627.1	3	3.8143	0.1848
SGMFWLR	897.1	2	2.9785	0.1845
SGMFWLRF	1044.3	2	2.5512	0.2215
SGMNVAR	734.8	1	1.6106	0.1555
SGMSHEEDQLIPNLYR	1890.1	2	4.2541	0.4058
SGNALFHASTLHR	1411.6	2	3.7842	0.3618
SGNFGGSR	781.8	1	1.7937	0.2755
SGNFNFGAYHTLEEISQEMDNLVAEHPGLVSK	3535.8	3	5.4522	0.4767
SGNIINMSSVASSVK	1494.7	2	5.1102	0.4586
SGNIVAGIANESK	1260.4	2	4.1447	0.3633
SGNLTEDDKHNNAK	1543.6	2	4.4858	0.4252
SGNLVSVLTQAEGAFVASLIK	2105.4	3	5.4002	0.4924
SGNYTVLQVVEALGSSLENPEPR	2460.7	3	5.5821	0.4319
SGPASTFNDRVFASELNAGIIKTDQNYEK	3174.4	3	3.9444	0.1499
SGPEPLQEGPGPK	1293.4	2	3.3803	0.2364
SGPFGQIFRPDNFVFGQSGAGNNWAK	2800.0	3	7.9069	0.4756
SGPFGQLFRPDNFIFGQTGAGNNWAK	2828.1	3	3.2742	0.1803
SGPGGGLVEEGELIEVVHLPLEGAQAFADDPDIPK	3557.9	3	6.0415	0.4934
SGPGLIGLGIK	1012.2	2	4.0925	0.247
SGPGSQLNTK	989.1	2	2.6584	0.2495
SGPKPFSAPKPQTSPSPK	1839.1	2	4.8123	0.3559
SGPLFNFDVHDDVR	1618.7	2	3.2774	0.3045
SGPLISDAELDAFLTEQYLQTTNIK	2769.1	3	3.9516	0.1779
SGPNIYELR	1049.2	2	2.8858	0.1951
SGPVILADEIKNPAMEKLELVR	2423.9	3	4.2818	0.3109
SGQAKETIPLQETSLYTQDR	2266.5	2	5.5925	0.4284
SGQEQIEDRDTMDFSGLSLIK	2370.6	3	5.3401	0.4329
SGQGAFGNMCR	1128.3	2	2.8897	0.3286

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SGQHHIFSFFAFK	1553.7	2	3.8391	0.4082
SGQKPVLDVHAELDR	1664.8	2	3.6906	0.3755
SGQLGIQEEDLR	1345.4	2	4.0844	0.279
SGQLGIQEEDLRK	1473.6	2	3.9634	0.3441
SGQLGIQEEDLRKESK	1818.0	2	4.0276	0.3305
SGQLGIQEEDLRKESKDQLSDDVSK	2806.0	3	5.4853	0.4755
SGQNNSVFTLYELTNGEDTEDEEFHGLDEATLLR	3846.0	3	6.8698	0.559
SGQRKPATSYVR	1350.5	2	2.4923	0.1855
SGQSALYDALFSSQSPK	1786.9	2	3.0803	0.3041
SGQVLEVSGSK	1091.2	2	3.4604	0.3501
SGQVLEVSGSKAVVQVFEGTSGIDAK	2593.9	3	3.474	0.2325
SGRPVDLSKVPSPLTDEEGDFILIHHEDLR	3373.7	3	4.8867	0.3676
SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLFK	4058.5	3	6.2561	0.4916
SGSAHEYSSSPDDAIFQSLAR	2226.3	2	6.1517	0.5327
SGSDEVQVGQQR	1290.3	2	4.0858	0.3143
SGSEAQTTKDSTSK	1427.5	2	3.2527	0.3907
SGSGTMNLGGSLTR	1338.5	2	3.903	0.3802
SGSHTVAVMNVGAPAAGMNAAVR	2169.5	2	3.5164	0.1983
SGSISYTELQQALSQMGYNLSPQFTQLLVSR	3448.8	3	4.8668	0.3964
SGSKFPVFNMSYNPAENAVLLCTR	2647.0	3	4.9542	0.2713
SGSLEFSIAGQPNDFFPVQVSFVSKK	2817.1	3	4.2955	0.424
SGSLSLTQFADMISLK	1699.0	2	4.5749	0.3986
SGSMDPSGAHPSVR	1385.5	2	4.2551	0.397
SGSSFVHQASFK	1282.4	2	2.5572	0.2572
SGSYSYLEER	1191.2	2	2.58	0.2457
SGTDGAIALTGVDEAYTLEEFQHLLPK	2877.2	3	3.8184	0.109
SGTGATATVSPKEILNLTSELLQK	2459.8	3	4.0657	0.158
SGTIFDNFLITNDEAYAEEFGNETWGVTK	3270.5	3	5.6918	0.4622
SGTQDIQPGPLFNNNADGVATDITSTR	2790.9	3	4.6421	0.3451
SGTQSDKVTLK	1164.3	2	3.304	0.135
SGTRVDHQTGPIVWGEPGTNGQHAFYQLIHQGTK	3719.0	3	4.4951	0.3416
SGTSEFLNK	983.1	2	2.8845	0.2225
SGTSTPTTPGSTAITPGTPPSYSSR	2409.5	2	5.1375	0.4759
SGTTWVSQILDMIYQGGDLEK	2342.6	2	3.8152	0.2443
SGTVDPQELQK	1202.3	2	2.9826	0.2503
SGTYSRKPLLPYTPGSDVAGVIEAVGDNASAFK	3369.7	3	6.7336	0.4678

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SGVAYIAAPSGSAADKVVIEACDELGIILAHTNLR	3527.0	3	3.9799	0.198
SGVDADSSYFK	1176.2	2	3.2506	0.2017
SGVEVLFNELEIPVEEYSFGR	2414.7	3	6.3193	0.5614
SGVGNIFIK	935.1	2	2.5379	0.1919
SGVISDTELQQALSNGTWTPFNPVTVR	2919.2	3	3.9596	0.1587
SGVLQALLGR	1014.2	2	3.3191	0.1719
SGVNSELVKR	1089.2	2	2.4817	0.201
SGVPVLAVSLALEGK	1440.7	2	4.2424	0.3951
SGVSDHWALDDHHALHLTR	2168.3	3	3.2626	0.2614
SGVSLAALK	846.0	2	3.0767	0.1901
SGVSLAALKK	974.2	2	3.6126	0.2531
SGVSLAALKKALAAAGYDVEKNNSR	2534.9	3	4.1504	0.3278
SGVYQHVTGEMMGGHAIR	1931.2	2	5.7136	0.5289
SGYDYSELDPEMEMAYEGQYDAYRDQFR	3430.6	3	3.5328	0.2985
SGYFDER	873.9	2	2.4169	0.1883
SGYHQSASEHGLVVIAPDTSPR	2309.5	3	6.2652	0.4514
SGYITIGYR	1030.2	2	2.8977	0.286
SGYLAGDKLLPQR	1418.6	3	3.6054	0.2954
SGYLLPDTK	994.1	2	3.4088	0.261
SGYLLPDTKAYGDRIER	1955.2	2	3.0541	0.2919
SGYLSSER	898.9	2	2.5471	0.2479
SGYPDIGFPLFPLSK	1638.9	2	3.4078	0.162
SGYRIDFYFDENPYFENK	2305.4	2	3.1606	0.2526
SHAQKNENAR	1155.2	2	3.1412	0.2539
SHATTEPEQTEPEQREPTPYPDER	2825.9	3	3.6086	0.2747
SHCIAEVENDEMPADLPSLAADFVESK	2919.2	3	4.9004	0.2289
SHDAIIDDLNRK	1397.5	2	3.5885	0.3442
SHDDGNIDLESDSFLKFDSEPSAVALELPTR	3406.6	3	6.407	0.4773
SHDGKLLASADDFGK	1561.7	2	4.6992	0.4324
SHDGKTPQLPR	1236.4	2	3.0996	0.3937
SHDPEEAIRHDVIVSIVTAAK	2288.5	3	3.8349	0.3755
SHDTTSNTLAQLLAK	1600.8	2	3.7038	0.4147
SHEAEVLK	913.0	1	1.8647	0.1022
SHEAEVLKQLAEKR	1638.9	2	4.6454	0.5114
SHEDPRVVAAVR	1336.5	2	2.5918	0.1781
SHEETDSTKEEAAK	1562.6	2	4.5379	0.3944

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SHEGETAYIR	1163.2	2	3.1285	0.3299
SHEGETSYIR	1179.2	2	2.5454	0.2236
SHENEAEALRGEIQSLKEENNR	2554.7	3	4.3129	0.3132
SHESYAK	821.9	1	1.7677	0.1152
SHEVKAEGYEVAHGGR	1726.8	3	3.6	0.3877
SHFEQWGTLTDCVVMRDPNTKR	2621.9	3	3.2209	0.1032
SHFGRDLMTDLKSEISGDLAR	2349.6	3	4.3773	0.3082
SHFNPLSLEELGSNTGIQVFNQIVK	2773.1	3	5.5187	0.4409
SHFVAASLSNQK	1289.4	2	3.8157	0.4349
SHFVLIAGEPLREPVIQHGPFVMNTNEEISQAILDFR	4206.8	3	5.626	0.4306
SHGGIDVK	812.9	1	2.2525	0.1808
SHGLESVPVLPGSGEAGVSFDLPAQADTLHSANK	3389.7	3	5.2866	0.432
SHGLFGLNENQLR	1485.6	2	3.4018	0.2519
SHGLLVQQALPK	1291.5	2	3.9478	0.3745
SHGQDYLVGNKLSR	1574.7	2	4.3482	0.4843
SHGSQETDEEFDAR	1608.6	2	5.1629	0.519
SHGVLGLYR	1002.2	2	2.7137	0.2241
SHHAASTTTAPTPAAR	1577.7	2	4.5503	0.5067
SHHYVLEPVFASALLK	1812.1	2	3.3217	0.1046
SHHYVLEPVFASALLKR	1968.3	2	2.9974	0.1287
SHIDKANFNNEK	1417.5	2	3.4997	0.299
SHIGVVPQDTVLFNDTIADNIR	2425.7	3	3.7491	0.2282
SHIMAAK	757.9	1	2.2776	0.2372
SHIQQLRVEEDVASDLVMKVDALLSAQPK	3221.7	3	4.4842	0.2395
SHIQSLPDLSLLPNVTGGLAPLPSAGDLFSTD	3234.6	3	4.2898	0.4392
SHKAESSELVR	1243.4	2	2.7235	0.2944
SHLEVPLEENVNRR	1692.9	2	3.1641	0.2296
SHLGNVHDQDN	1236.2	2	3.3267	0.3135
SHLIDKGMLTSTTEDE	1777.9	2	4.0734	0.3604
SHLKITDSAGHILYSKEDATK	2315.6	3	4.5029	0.4008
SHLLNCCPHDVLSGTR	1753.0	3	3.7701	0.3725
SHLMYAVREEVEVLKEQIKELIEK	2915.4	3	3.8634	0.1852
SHLVGVKPFEADR	1455.6	2	3.0739	0.2375
SHLVHGSSPGVMGTSVATSASK	2098.3	3	3.3669	0.2397
SHMAEESKNEYAAQLQR	1993.1	3	3.835	0.2673
SHMDDLNSENAKLDAELIQYREDLNQVITIK	3618.0	3	5.5679	0.2828

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SHMMDVQGSTQDSAIKDFVLK	2338.6	2	6.4274	0.5105
SHNVAAGSYEAPLPPGSFHGDFAYGTYR	2970.2	3	4.7982	0.405
SHPEPQTPKDSPSK	1535.6	2	2.8122	0.2887
SHPETLTHTASPHPGGAEEGDR	2284.3	3	3.4188	0.3059
SHPLDPIDTVDFER	1641.8	2	3.2533	0.2589
SHPPLHEYADLNQLTQGDQEK	2421.6	3	3.639	0.109
SHPSLQSEQIGIVK	1523.7	2	2.8552	0.1511
SHQDFSR	876.9	1	2.2166	0.1583
SHQGVVIASDWLVGGK	1653.9	2	3.0477	0.2379
SHQKPPQGMEIK	1380.6	2	2.8199	0.1612
SHQLIHAASLK	1205.4	2	3.1658	0.3088
SHQWFGASVR	1175.3	2	2.5905	0.2556
SHRDPYATSVGHLIEK	1811.0	2	4.4242	0.3642
SHREEMEAR	1145.2	2	2.8411	0.1824
SHRTEMDWVLK	1402.6	2	2.7189	0.1743
SHSAHFFEFLTK	1451.6	2	3.8913	0.4844
SHSDNSPNAFK	1204.2	2	3.2409	0.2549
SHSDNSPNAFKDASSPVPPPHVPPPVPPLRPR	3395.8	3	4.6029	0.354
SHSGGIPGSLSGGISHNSMEVTK	2240.4	3	4.0403	0.3476
SHSGMVK	745.9	1	2.2278	0.1533
SHSIFLINIK	1172.4	2	2.7422	0.2465
SHSIFLINVK	1158.4	2	2.993	0.2785
SHSIFLINVKQENTQTEQK	2245.5	3	3.8467	0.2404
SHSLAQPPEFDSGVETFSIHAEKPK	2740.0	3	3.5904	0.314
SHSLSQHTATSSK	1371.4	2	3.5282	0.427
SHSMETMVGGQK	1292.5	2	2.5676	0.2481
SHSPSASQSGSQLR	1429.5	2	3.5286	0.2905
SHSPSSPDPDTPSPVGDSR	1922.9	2	4.604	0.46
SHSQASLAGPGPVDPSNR	1777.9	2	3.9326	0.389
SHSSESLGILKDYPHSAFTLEK	2447.7	3	3.3454	0.1196
SHSSPASLQLGTGAGAAGSPAQQHAHLR	2695.9	3	4.1555	0.4201
SHSTEPGLVLTLGQGDVGQLGLGENVMER	2995.3	3	5.499	0.3962
SHSYLRAIQAGYSQDDECIPMMTPSDITSTIR	3589.0	3	3.8156	0.1704
SHTALLR	797.9	1	1.6274	0.1449
SHTDIKVPDFSEYR	1694.8	2	4.4326	0.3627
SHTDQLVLIFAGK	1429.6	2	2.5665	0.2752

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SHTEEDCTEELFDFLHAR	2180.3	3	6.1381	0.4987
SHTFPELAYRK	1349.5	2	2.745	0.2372
SHTLLSPSPKPK	1292.5	2	2.6763	0.1792
SHTSEGAHLDITPNSGAAGNSAGPK	2377.5	3	7.1854	0.4899
SHTSLKDELSDVSQGGSK	1876.0	2	5.2919	0.479
SHVAGQMLHGGGSR	1394.5	2	4.0245	0.4243
SHVEDGDIAGAPASSPEAPPAEQDPVQLK	2914.1	3	4.8555	0.1353
SHVLQQTQR	1097.2	2	2.8307	0.263
SHVVREDLNPR	1322.5	2	3.1723	0.2782
SHYEEGPGK	1004.0	2	2.8512	0.1808
SHYEEGPGKNLPFSVENK	2033.2	2	5.2472	0.3998
SHYKVGENADSQIK	1576.7	2	4.2126	0.3897
SIAADHKDLIHDVSFDFHGR	2281.5	3	4.2893	0.3204
SIAAHLDNQVPVESPR	1733.9	2	4.6007	0.4601
SIAFPSIGSGR	1092.2	1	3.2084	0.2893
SIATLAITTLLK	1245.5	2	4.3258	0.2725
SIATLMTDEIFHDVAYK	1955.2	2	3.5373	0.3389
SIATTLIDDTSSEVLDELYR	2242.4	3	4.3593	0.2934
SIDDLEEKVAHAKEENLSMHQMLDQTLLELNNM	3841.3	3	4.8021	0.2984
SIDGSIVLPLAR	1241.5	2	2.5937	0.1982
SIDLKDKYK	1110.3	2	3.0208	0.207
SIDNGIFVQLVQANSPASLVGLR	2399.7	3	5.0421	0.3689
SIDQFANLVLHQTVER	1871.1	2	2.9738	0.3292
SIDSEKEAK	1007.1	2	3.1965	0.1395
SIEALLEAGQAR	1258.4	2	3.3552	0.221
SIEAVHEDIR	1169.3	2	3.1947	0.1468
SIEDFAHSSFQMALSK	1799.0	2	5.0903	0.4162
SIEEQLGTEIKPIPSNIDK	2112.4	2	5.0581	0.391
SIEQLEKELLNGQK	1629.8	2	3.3554	0.2598
SIEQLEKELLNGQKLQGPETAR	2482.8	3	5.5652	0.3677
SIEQSIEQEEGLNR	1632.7	2	3.3609	0.2207
SIFDFSALKELLSGPNR	1895.1	2	5.3946	0.4221
SIFDFSALKELLSGPNRLK	2136.5	2	3.3433	0.2547
SIFDHIKLPQASK	1484.7	2	3.2871	0.2253
SIFEYEPGKSSILQHERPASLYQSSIDR	3239.5	3	4.091	0.2
SIFEYEPGKSSILQHERPPPLPTTPTPVPR	3372.8	3	4.3495	0.1261

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SIFHQLANLPTDPPTIHK	2030.3	3	3.6076	0.2531
SIFKPFIFVDDVK	1555.8	2	4.2543	0.3374
SIFKPFIFVDDVKLVPK	1993.4	3	6.1602	0.5118
SIFPIHPSFR	1201.4	2	2.4863	0.1898
SIFQHIQSAQSQR	1530.7	2	4.2275	0.411
SIFSGIGSTAEPVSQSTTSDYQWDVSR	2907.1	3	4.0442	0.3224
SIFYVPDMKPSMFDVSR	2020.4	2	4.0636	0.4085
SIGEAIQYLHSINIAHR	1923.2	2	4.7605	0.43
SIGTANRPMGAGEALR	1601.8	2	3.7815	0.2768
SIGTANRPMGAGEALRR	1758.0	3	3.3511	0.2133
SIGTGGIQDLKER	1374.5	2	3.1793	0.2256
SIGVSNFNHR	1131.2	2	2.9931	0.2403
SIHANFSSGVGTTAASSK	1722.8	2	2.8542	0.3608
SIHDALCVIR	1127.3	2	3.0809	0.3695
SIHEIPREELR	1379.5	2	2.4576	0.1526
SIIFANYIAR	1168.4	2	2.9898	0.2695
SIIGMGTGAGAYILTR	1581.9	2	3.1776	0.1478
SIIKDYFHR	1179.4	2	3.1225	0.2179
SIIMRENFIPTIVNFSAEEISDAIREK	3124.6	3	5.8028	0.407
SIIQSAQQDSIKK	1446.6	2	2.6232	0.1605
SIISETSNKIDAEIASLK	1920.2	2	3.8989	0.1809
SIISMFDRENK	1340.5	2	3.7953	0.257
SIITYVSSLYDAMPR	1717.0	2	3.8325	0.3248
SIKADDKLIAEEGVDSLNVK	2145.4	3	5.6482	0.4259
SIKDTICNQDER	1422.5	2	2.6808	0.1833
SIKENASAGVER	1261.4	2	3.2256	0.3567
SILADDFLDFYLEYFPELK	2339.6	2	3.1787	0.2265
SILAETEGMLR	1220.4	2	3.5533	0.3365
SILAETEGMLRDLQK	1705.0	2	4.5931	0.3434
SILDQSISSFMR	1384.6	2	3.9032	0.3057
SILEKDPSIHQAR	1494.7	2	3.6909	0.3148
SILFVPTSAPR	1188.4	2	3.5748	0.3235
SILGTLTVEQIYQDRDQFAK	2326.6	3	3.2489	0.2332
SILHYIADKHNLFGK	1757.0	2	3.0813	0.2335
SILLQSLIEGMEDR	1604.9	2	4.8283	0.304
SILLSGTVLPSAQR	1442.7	2	3.6535	0.2713

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SILYDERSVHKVEPITK	2015.3	3	3.6644	0.317
SINAGGHKVGLALELEA	1679.9	2	4.1113	0.3906
SINDNIAIFTEVQK	1592.8	2	3.8904	0.3316
SINDNIAIFTEVQKR	1749.0	2	4.1929	0.3364
SINGELYAPLQHVSAVLPGGAADR	2436.7	3	3.2487	0.1866
SINPDEAVAYGAAVQAAILMGDK	2305.6	3	4.9653	0.4088
SINPDEAVAYGAAVQAAILSGDK	2261.5	2	5.6378	0.4476
SINPLGGFVHYGEVTNDFVMLK	2438.8	3	4.6398	0.3277
SINQPVAFVR	1131.3	2	3.1794	0.2304
SINQQSGAHVELQR	1567.7	2	3.5846	0.312
SIPAYLAETLYYAMK	1735.0	2	4.4842	0.4803
SIPDGSEKGDFIALDLGGSSFR	2269.5	2	3.779	0.3806
SIPHITSDRLLIK	1493.8	2	3.0746	0.1154
SIPLDEGEDEAQR	1459.5	2	3.1983	0.4455
SIQAALDSAYKELTDLHK	2004.2	3	3.6232	0.3412
SIQAALDSAYKELTDLHKANAAKDSEAQEAALSR	3617.9	3	6.1687	0.5128
SIQADGLVWGSSK	1348.5	2	4.9211	0.4555
SIQEELQQLR	1244.4	2	3.5373	0.1026
SIQEIQELDKDDESLR	1919.0	2	5.2044	0.3988
SIQEIQELDKDDESLRK	2047.2	2	5.3495	0.3397
SIQEIQELDKDDESLRKYKEALLGR	2978.3	3	4.8789	0.4011
SIQFVDWCPTGFK	1528.8	2	4.2995	0.4221
SIQLDGLVWGASK	1374.6	2	4.506	0.3591
SIQMLTLLR	1075.4	2	2.9533	0.1801
SIQQGFCFNILCVGETGIGK	2115.5	2	2.7334	0.1326
SIRDTPAKNAQK	1329.5	2	3.3575	0.2069
SIRNEDKILTIEVK	1658.9	3	4.569	0.2277
SIRPDNMSEYSK	1427.6	2	3.1348	0.1864
SIRPGLSPYR	1146.3	2	2.8245	0.2096
SISFHPSGDFILVGTQHPTLR	2310.6	3	4.8467	0.3336
SISGPSVGVMEMR	1350.6	2	2.6471	0.2059
SISHYHETLGEALQGVELEFSGLDIK	2874.2	3	5.0917	0.4487
SISLYYTGEK	1161.3	2	2.4934	0.1847
SISLYYTGEKGQNQDYR	2023.1	2	4.3153	0.3474
SISQEQEKR	1105.2	2	2.7957	0.1369
SISQHYSKPR	1203.3	2	2.9172	0.2446

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SISTSLPVLDLIDAIAPNAVR	2166.5	3	4.7371	0.5166
SISVIDSPGILSGEK	1502.7	2	2.5084	0.1373
SITDAHPPGTAILHIK	1671.9	2	2.6517	0.135
SITHDIEEK	1072.2	2	2.69	0.146
SITHDIEEKGVR	1384.5	2	3.2686	0.2501
SITHFGRPPFEPFFNSLQEVHPQVR	2968.3	3	5.6244	0.511
SITNDSAVLSLFQSINGMHPQLLELLNQLDER	3598.0	3	5.5374	0.4268
SITPNEKQPEHLGLDQYIIKR	2480.8	3	3.7557	0.2325
SITVTQDEGIRPSTTMEGLAK	2235.5	2	4.5647	0.2869
SIVDAYVLLNLGDSVTTDHISPAGNIAR	2913.2	3	4.3655	0.3837
SIVDFVKDHGNIK	1472.7	2	3.852	0.3877
SIVDKEGVPR	1100.3	2	3.0002	0.2127
SIVDLYTGNAEEDADTK	1841.9	2	5.3759	0.502
SIVDYKPNLDLLEQQHQLIQEALIFDNK	3326.7	3	5.1167	0.4391
SIVEEIEDLVAR	1373.5	2	4.5148	0.2682
SIVEGIIEEEEEDEEGSESISKR	2594.7	3	3.3618	0.1333
SIVEHVASKLNIPATNVFANR	2281.6	3	3.8214	0.1008
SIVIRPLEPQPAPHLAR	1895.2	3	4.6061	0.3388
SIVPQGGSHSLR	1238.4	2	2.7782	0.2803
SIVPTMHYQDSLPR	1644.9	2	3.2204	0.336
SIVSELAGLLSAMEYVQK	1939.3	2	4.3494	0.4052
SIVVIHPDTGR	1194.4	2	2.7712	0.3266
SIWAFGPDATGPNILVDDTLPSEVDKALLGSVK	3427.8	3	3.21	0.1743
SIYDDISSPGLGSTPLTSR	1967.1	2	5.3483	0.4932
SIYFQPPSFYVSAQDLPHIENGGVAVLTGKK	3364.8	3	3.5415	0.1392
SIYGEKFEDENFILK	1833.0	2	5.348	0.4063
SIYGERFPDENFK	1602.7	2	3.7056	0.2547
SIYGERFPDENFKLK	1844.1	2	3.4359	0.1984
SIYGSRFPDENFTLK	1775.0	2	4.3147	0.2829
SIYYITGESK	1161.3	2	3.2313	0.3004
SIYYITGESKEQVANSAFVER	2392.6	3	5.9774	0.5569
SKAAWEAGKFGNEVIPVTVTVK	2332.7	2	5.5133	0.4717
SKADYTSHLR	1178.3	2	2.8325	0.1065
SKAEELGLPILGVLR	1595.9	3	4.4447	0.3758
SKAEEVVSFVK	1223.4	2	2.5977	0.1148
SKAELMEISEDKTK	1609.8	2	4.9299	0.4425

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SKAGLAYHLR	1116.3	2	2.4934	0.1534
SKAMTGVEQWPYR	1553.8	2	2.7497	0.1944
SKCEELSGLHGQLQEAR	1886.1	2	5.126	0.4286
SKDDQVTVIGAGVTLHEALAAAELLK	2651.0	3	7.0263	0.502
SKDDQVTVIGAGVTLHEALAAAELLKK	2779.2	3	7.9431	0.5736
SKDDQVTVIGAGVTLHEALAAAELLKKEK	3036.5	3	4.1383	0.283
SKDHFGLEGDEESTMLEDSVSPK	2538.7	3	5.1375	0.3741
SKDHFGLEGDEESTMLEDSVSPKK	2666.9	3	3.8332	0.2398
SKDIALHLNPR	1264.5	2	3.0366	0.3063
SKDIVLVAYSALGSHR	1717.0	3	5.7194	0.4573
SKDIVLVAYSALGSQR	1708.0	2	5.9082	0.5566
SKDKEEGKEER	1335.4	2	3.5086	0.2783
SKDKLDQVSSEIK	1477.6	2	4.2031	0.268
SKDKLDQVSSEIKEK	1734.9	2	5.0199	0.4319
SKDLAEVGEGGGHSQAR	1698.8	2	5.1593	0.4574
SKDQDDQKPGPSER	1587.6	2	4.5796	0.3457
SKDQFEFALTAVAEEVNAILK	2324.6	3	5.2641	0.4587
SKDSATAQAWFSAIHSNVNDLLTR	2633.9	3	4.7735	0.3525
SKDTVSEDTIR	1251.3	2	3.0031	0.2701
SKDVNGPEPLNSR	1413.5	2	3.9715	0.3253
SKDYEFMWNPHLGYILTCPSNLGTGLR	3114.5	3	5.3079	0.3156
SKEAEAAFLNVYKR	1626.8	2	2.4031	0.2216
SKEAYEKDEQINLLKEELDQQNK	2794.0	3	4.1716	0.1544
SKEEAFDAICQLVAGKEPANVGVTK	2605.9	3	5.3993	0.4558
SKEEDKHLK	1114.2	2	2.7122	0.1748
SKEEELKALEDRLESESAAK	2263.4	3	4.0476	0.3395
SKEFAQIIK	1064.3	2	2.8741	0.1795
SKEFQLFSSPHGK	1492.7	2	3.6123	0.3942
SKEGKEAGSEPAPEQESTEATPAE	2460.5	3	3.2403	0.2148
SKEIENGHIFTVNDQFTSK	2195.4	3	4.3372	0.3558
SKEISQFLNR	1222.4	2	2.6864	0.1578
SKELDNFCNPIIYKPKPK	2135.5	2	4.8748	0.4062
SKENHADLGIFVK	1458.6	2	2.9782	0.2536
SKENISLLEK	1161.3	2	2.9323	0.1623
SKENISLLEKEREDLYAK	2166.4	2	4.5475	0.3976
SKENVLYK	981.1	2	2.5756	0.1271

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SKEPQLIAFYHK	1461.7	3	3.7404	0.1954
SKEQAELEAAR	1232.3	2	3.5462	0.2319
SKESDEPHHSK	1281.3	2	2.6199	0.1431
SKESVPEFPLSPPK	1542.8	2	3.7827	0.3407
SKETQEELNK	1206.3	2	3.4949	0.1428
SKEVDKLIR	1088.3	2	2.5587	0.1121
SKFADLSEAANR	1309.4	2	3.2921	0.2861
SKFALITWIGENVSGLQR	2020.3	2	5.9895	0.4746
SKFKDLEDK	1110.2	2	3.0501	0.2339
SKFVESDADEELLFNIPFTGNVK	2600.9	3	3.7503	0.2005
SKFVLVKFDTQYPYGEKQDEFKR	2854.2	3	4.256	0.2966
SKGAVAIADAIR	1172.4	2	3.268	0.2856
SKGEGRPPEKPSSNLLEEAAAKPK	2521.8	3	4.4835	0.29
SKGGIEIVKEK	1188.4	2	3.2006	0.2245
SKGGVVGIK	845.0	1	2.012	0.1297
SKGGVVGIKVDK	1187.4	2	4.0742	0.3854
SKGGVVGIKVDKGVVPLAGTNGETTTQGLDGLSER	3441.8	3	7.2943	0.5217
SKGHGFITPADGGPDIFLHISDVEGEYVPVEGDEVTYK	4077.4	3	6.8965	0.5491
SKGIAYIEFK	1156.4	2	2.7391	0.2597
SKGIYQSLEGAVQAGQLK	1878.1	2	5.213	0.3987
SKGLAPDLPEDLYHLIK	1910.2	3	5.2457	0.4448
SKGLAPDLPEDLYHLIKK	2038.4	3	4.2251	0.3011
SKGPSAAGEQEPDKESGASVDEVAR	2502.6	3	5.3714	0.4844
SKGPSAGEQEPDKESGASVDEVAR	2431.5	3	5.2731	0.4045
SKGQENDHVHEK	1408.5	2	3.6023	0.3355
SKGQESFKKQEK	1424.6	2	3.4735	0.1134
SKHEEEAVQK	1185.3	2	2.9875	0.1794
SKHQTTSTSKPASFQQPLGSNQALGQAMSSAAAYR	3639.0	3	4.0702	0.1733
SKHSEQDELMADISKR	1875.1	2	4.3625	0.3922
SKIEDYFPEFAR	1502.7	2	3.9609	0.3885
SKIGSTDNIKYQPK	1579.8	2	3.0364	0.2924
SKINVNEIFYDLVR	1711.0	2	4.8066	0.4321
SKISVNDFIIK	1264.5	2	2.8863	0.2038
SKITVTSEVPFSKR	1579.8	2	3.1024	0.1769
SKKDQGELER	1190.3	2	3.5443	0.2029
SKKDQGELERQLLQANPILEAFGNAK	2899.3	3	3.9603	0.2454

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SKKEQVPSGAELER	1558.7	2	3.9083	0.35
SKKNEIMVAPDKDYFLIVIQNPTE	2794.2	2	2.9572	0.318
SKKPAGGVDFDET	1351.4	2	2.9677	0.2725
SKKVEEAEPEEFVVEK	1878.1	2	4.8463	0.3469
SKLAAAILGGVDQIHIKPGAK	2088.5	2	4.4005	0.3222
SKLANILFTR	1163.4	2	2.6905	0.143
SKLDAEVSKWDDSGNDIIVLAK	2404.7	3	5.389	0.3642
SKLDKAEDQHLVEMEDTLNKLQEAEIK	3156.5	3	3.6175	0.1724
SKLDSLASDHQK	1329.4	2	3.8298	0.3303
SKLEDIANAALAASAVTQVAK	2072.3	2	5.4868	0.4854
SKLESELANFGPR	1448.6	2	3.3695	0.2124
SKLETLPKEDLIK	1514.8	2	3.173	0.1253
SKLGESQTLQQFSR	1609.8	2	3.8274	0.25
SKLHEMEGAVK	1229.4	2	2.6853	0.1475
SKLILFPR	974.2	2	2.8964	0.2264
SKLNHNAAFMQIPMGLEGNFK	2348.7	2	4.7241	0.4302
SKLPKPVQDLIK	1366.7	2	2.6762	0.1439
SKLQSQLLSLEK	1374.6	2	3.4214	0.2216
SKLQSQLLSLEKEVEEYKNFRPDDPTR	3251.6	3	3.544	0.2719
SKLSQLHESR	1185.3	2	3.0048	0.2905
SKLSQTEDR	1064.1	2	3.0693	0.2271
SKLTFSCLGGSDNFK	1604.8	2	4.307	0.4216
SKLVEVIEEVNK	1387.6	2	3.9884	0.3361
SKLVEVIEEVNKVK	1614.9	2	3.5705	0.3499
SKLVEVIEEVNKVKQEK	2000.3	2	4.9647	0.4177
SKPDLESSLESLVFDLR	1936.2	2	4.3639	0.4844
SKPELPPGLSPEATAPVTPSRPEGGEPGLSK	3084.4	3	4.0133	0.3152
SKPGAAMVEMADGYAVDR	1869.1	2	5.0923	0.5466
SKPIIAEPEIHGAQPLDGVTGFLVLMSEGLYK	3412.0	3	3.7332	0.3286
SKPIPIMPASPQKGHAVNLLDVPVPVAR	2933.5	3	4.0136	0.2686
SKPLAASPKPAGLKESSDK	1912.2	2	3.5543	0.2403
SKPLAASPKPAGLKESSDKVSR	2254.6	3	3.938	0.4588
SKPQIAALKEETEEEVQDTRL	2415.6	3	3.6268	0.3295
SKPVFSESLSD	1196.3	2	2.6024	0.2674
SKQEALKNDLVEALK	1686.9	2	4.4175	0.2628
SKQEALKNDLVEALKR	1843.1	2	5.1615	0.4

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SKQLEDELVSLQK	1517.7	2	4.3844	0.3029
SKQLEDELVSLQKK	1645.9	2	4.7512	0.2697
SKRDPTEEIEILLR	1699.9	3	4.6233	0.3323
SKREQEVTELKK	1475.7	2	3.5597	0.1294
SKSDPIMLLK	1132.4	2	2.6442	0.1182
SKSEEAHAEDSVMDHHFR	2113.2	3	6.1732	0.4573
SKSLESQVENLQK	1490.6	2	2.7819	0.1115
SKTADVTSLFGGEDTSR	1771.9	2	3.4654	0.3588
SKTAVYKVPPFTFHVK	1850.2	2	2.4601	0.197
SKTDGSQKTESSTEGKEQEEK	2314.4	3	3.4652	0.2855
SKTFNPGAGLPTDKK	1561.8	2	3.7301	0.3194
SKTHAVLVALK	1167.4	2	3.1	0.3665
SKTIVQLKPR	1170.4	2	2.7609	0.2338
SKTKEQILEEFSK	1567.8	2	3.9759	0.3356
SKTVTSFYNQSAIDAAAEKPSVR	2471.7	3	3.3307	0.2118
SKVDEAVAVLQAHHAK	1703.9	2	5.4861	0.5133
SKVDEAVAVLQAHQAK	1694.9	2	4.5623	0.4568
SKVDKGSAEEEKIDALLSSSQIR	2491.7	3	3.3412	0.153
SKVEILEAEVMQLR	1645.9	2	2.7405	0.1068
SKVELIAYFEK	1327.6	2	3.579	0.3442
SKVGGTKPAGGDFGEVLNSAANASATTTEPLPEKTQESL	3862.2	3	5.8537	0.3621
SKVTLLEGDHVR	1354.5	2	4.0206	0.3385
SKVYEDPALSAIFLHNNYNYILK	2714.1	3	3.3426	0.1654
SKYEALQTFAR	1314.5	2	2.7967	0.2483
SKYHPDEVGK	1160.3	2	3.4503	0.2561
SKYHPDEVGKR	1316.4	2	2.7815	0.1755
SKYTTPSGEVR	1225.3	2	3.1679	0.2902
SLAAAAGK	688.8	1	2.1795	0.115
SLAAAAGKQELAK	1258.4	2	4.2405	0.344
SLAAALAQHSVPLQLELR	1918.2	2	4.2183	0.3953
SLAAEEEAAR	1047.1	2	2.8355	0.1857
SLAALSQIAYQR	1321.5	2	3.6364	0.3556
SLADELALVDVLEDK	1630.8	2	4.194	0.3837
SLADELALVDVLEDKLK	1872.1	2	4.9131	0.3583
SLADELALVDVLEDKLKGEMMDLQHGSLFLQTPK	3786.4	3	6.1519	0.444
SLADIAREEASNFR	1579.7	3	3.6517	0.3628

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SLADIGKTVSSASR	1392.5	2	3.2134	0.3808
SLAEDFAEQPIKDAVITVPVFFNQAER	3036.4	2	4.0807	0.257
SLAEDFAEQPIKDAVITVPVFFNQAERR	3192.6	3	5.2266	0.476
SLAEEQYQDFEAR	1586.6	2	3.3297	0.1886
SLAEGNLLYQPQLDTLK	1904.2	2	3.9839	0.2244
SLAEIVKKDDFVLDSEYLVTLLVVVPK	3034.6	3	3.7568	0.1227
SLAGSSGPGASSGTSGDHGELVVR	2186.3	2	5.5886	0.508
SLAHLALNDVSLQALPGDVGNLANLVTLELRENLLK	3826.4	3	5.3856	0.4252
SLAHLETLSHSFILSLK	1897.2	2	4.023	0.3361
SLAMEMVLTGDR	1323.6	2	3.3308	0.2888
SLAMEMVLTGDRISAQDAK	2037.3	2	5.1851	0.3888
SLAMLGSSEDNTALSR	1652.8	2	4.6028	0.4246
SLAQAEAEKQKEEAER	1817.9	2	4.9311	0.4243
SLAQAEAEKQKEEAEREAR	2174.3	3	4.6203	0.2918
SLAQHIPGPGGIEGVK	1560.8	2	2.9273	0.1534
SLAQHIPGPGGIEGVKGAASGVVGELAR	2629.0	3	4.5973	0.4057
SLASDITDEQKK	1335.4	2	3.0157	0.3141
SLATTRPTVNADDLLK	1715.9	2	3.4948	0.1753
SLAVLTYDHSR	1262.4	2	2.694	0.1242
SLAVSGLGVIGR	1129.3	2	3.9534	0.4093
SLAYLTAATHGLDEEAESLKETFDPEKETIPDIDPNAK	4161.5	3	4.5212	0.3407
SLDADEFRQGLAK	1450.6	2	3.3324	0.2597
SLDAQSVYVATDSESYVPELQQLFK	2819.1	3	3.9961	0.2501
SLDDGKVSR	977.1	2	2.4063	0.1565
SLDDVIKR	946.1	2	2.6686	0.2421
SLDDVIKRANNTFYGLSAGVFTK	2517.8	2	3.4908	0.2688
SLDEISQPAQELKR	1614.8	2	3.9507	0.3499
SLDFLIELLHKDQLDETVNVEPLTK	2911.3	3	5.3875	0.3564
SLDIQVPNFPADETK	1674.8	2	3.2596	0.1311
SLDIQVPNFPADETKGFHQVPFAPIVFIER	3413.9	3	4.9146	0.3499
SLDKDPLLLSGTHVMEGSGR	2113.4	3	3.2196	0.2685
SLDKDPMLLSGTHVMEGSGR	2131.4	3	3.4504	0.1242
SLDLDGIIAEVK	1273.5	2	4.7879	0.3349
SLDLDGIIAEVKAQYEEMAK	2224.5	2	4.7867	0.3344
SLDLDISKTNVNGGAIALGHPLGGSGSR	2708.0	3	7.1966	0.5758
SLDLFNCEVTNLNDYR	1917.1	2	4.7402	0.4191

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SLDMDSIIAEVK	1321.5	2	4.8027	0.3562
SLDMDSIIAEVKAQYEDIANR	2382.6	3	5.6961	0.5051
SLDMDSIIAEVKAQYEDIANRSR	2625.9	3	3.3189	0.1269
SLDNFFAKR	1098.2	2	2.4456	0.1417
SLDNNYSTPNER	1410.4	2	2.9596	0.2049
SLDPENSETELER	1519.6	2	4.5643	0.3839
SLDVRQEELGAVVDKEMAATSAAIEDAVR	3075.4	3	5.8579	0.4133
SLDWQIDVDLLNK	1559.7	2	2.9487	0.2357
SLEAASEK	834.9	1	1.8731	0.1385
SLEAASEKYSEKEDKYEEEIK	2506.7	3	5.6912	0.3494
SLEAASEKYSEKEDKYEEEIKLLSDK	3063.3	3	4.6007	0.2632
SLEAASEKYSEKEDKYEEEIKLLSDKLK	3304.6	3	5.088	0.3747
SLEAASEKYSEKEDKYEEEIKLLSDKLKEAETR	3891.2	3	4.9475	0.3837
SLEADLMQLQEDLAAAER	2004.2	2	3.5094	0.2428
SLEAEGFQVTYLPVQK	1810.0	2	4.0992	0.3338
SLEAEILQLQEELASSER	2046.2	2	5.8274	0.4951
SLEAIELGLGEAQVILALSSHLGAVESEKQK	3221.6	3	3.4402	0.2704
SLEAQVAHADQQLR	1566.7	2	4.5299	0.41
SLEAQVAHADQQLRDLGK	1980.2	3	4.112	0.3983
SLEAQVAHADQQLRDLGKFQVATDALK	2954.3	3	5.042	0.3128
SLEDALRQTASVTLQAIAAQNAAVQAVNAHSNILK	3619.0	3	7.0968	0.5509
SLEDALSSDTSGHFR	1622.7	2	4.4206	0.4842
SLEDALSSDTSGHFRR	1778.9	2	2.8982	0.176
SLEDDIRSDTSFMFQR	1948.1	3	4.7607	0.3494
SLEDLKLK	946.1	2	2.5424	0.1305
SLEDLQDEYDFK	1502.6	2	2.957	0.252
SLEDQVEMLR	1220.4	2	3.7545	0.3136
SLEDVTAEYIHKAEHEK	2000.2	2	3.3106	0.2903
SLEEAEAYSR	1155.2	2	2.5456	0.2922
SLEEFNDVYLVTHLMGADLNNIVK	2736.1	3	3.6533	0.1063
SLEEIYLFSLPIKESEIIDFFLGASLKDEVLK	3688.3	3	5.1863	0.145
SLEEKNESLTEHPR	1669.8	2	3.5545	0.3463
SLEELPVDIILASVG	1555.8	2	2.7095	0.2678
SLEELRLEDYQANR	1736.9	3	4.0212	0.2691
SLEENLATAKHDLLR	1710.9	2	3.7046	0.1951
SLEGDLEDLKDQIAQLEASLAAAK	2529.8	3	6.172	0.4098

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SLEGDLEDLKDQIAQLEASLAAAKK	2658.0	3	6.4646	0.4297
SLEIEEKINK	1203.4	2	2.9951	0.106
SLELYRELDLNSVLLK	1906.2	3	5.6266	0.3347
SLENYHFVDEHGK	1575.7	2	3.4507	0.3684
SLENYHFVDEHGKDQGINIR	2372.5	3	5.5988	0.4986
SLEQYDQVLDGAHGASLTDLANLSEGVSLAER	3360.6	3	6.2104	0.502
SLERAEAGDNLGALVR	1671.8	2	3.2295	0.1388
SLERPMSSASMASDFR	1773.0	2	3.4015	0.3331
SLERPMSSASMASDFRK	1901.2	3	4.9963	0.2889
SLESLDTSLFAK	1311.5	2	4.0877	0.3075
SLESLHSFVAAATK	1461.6	2	3.8901	0.3659
SLESQVENLQK	1275.4	2	2.8599	0.196
SLETEHKALTSEIALLQSR	2127.4	2	5.8373	0.4405
SLETEILESLK	1262.4	2	2.9253	0.2611
SLETENAGLR	1090.2	2	3.4261	0.2734
SLETVYLER	1110.2	2	2.7875	0.2507
SLETVYLERNPLQK	1690.9	2	3.4425	0.2511
SLETVYLERNPLQKDPQYR	2350.6	3	4.3335	0.268
SLEVTFTPVIEDIGK	1648.9	2	3.0695	0.2736
SLFDDKAVEIEELTYIIKQDINSLNK	3040.4	3	4.7051	0.2945
SLFDYFLTDLK	1362.6	2	3.2798	0.2338
SLFFPDEAINKHPR	1671.9	2	3.1348	0.2515
SLFGHTVGGAAGVVSR	1515.7	2	4.3232	0.3847
SLFNRAEGPPEPSR	1557.7	2	2.8158	0.1712
SLFSSIGEVESAK	1354.5	2	3.6369	0.2938
SLFVQELLLSTLVR	1618.9	2	3.822	0.2739
SLGAEHVITEEELR	1583.7	2	3.7924	0.3094
SLGAEPLEVDLK	1271.4	2	3.288	0.2245
SLGALTGPQLLSLAQSPAGSHVLDAILTSPSVTR	3359.8	3	3.3252	0.2087
SLGDDISSETSGDFR	1586.6	2	4.5861	0.3822
SLGDDISSETSGDFRK	1714.8	2	4.0753	0.3336
SLGEIPIVESEIKK	1542.8	2	3.2711	0.2531
SLGEIPIVESEIKKEAGELKPEEEITVGPVQK	3477.9	3	6.0106	0.4561
SLGELGLEHFQAPLVR	1767.0	2	4.0983	0.359
SLGETQLVLYGDVEELKR	2050.3	2	4.879	0.4124
SLGHSRGEADLFDSGDIFSTGTGSQSVER	3014.1	3	5.3534	0.4101

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SLGKGSAPPGPVPEGSIR	1706.9	3	3.7378	0.3563
SLGLFGLQVPEEYGGLGFSNTMYSR	2724.0	3	3.7832	0.1984
SLGLSLSGGDQEDAGR	1562.6	2	3.0368	0.1733
SLGLVDRNNEPLTHAMYNLASLR	2585.9	3	4.1163	0.3059
SLGNVIDPLDVIYGISLQGLHNQLLNSNLDPSEVEK	3906.3	3	7.8744	0.5211
SLGNVIDPLDVIYGISLQGLHNQLLNSNLDPSEVEKAK	4105.6	3	4.5776	0.3962
SLGNVIDPLDVIYGISLQGLHNQLLNSNLDPSEVEKAKEGQK	4548.1	3	4.6223	0.3421
SLGNVIHPDVVVNGGQDQSKEPPYGADVLR	3162.5	3	6.6314	0.4087
SLGPAAPIIDSPYGDPIDPEDAPESITR	2895.1	3	3.804	0.1012
SLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMAR	4072.5	3	4.7283	0.2996
SLGSAGPSGTLPR	1200.3	2	2.7236	0.2654
SLGSLASLHPRPGEGPGHSASAAGAQAR	2640.9	3	3.4937	0.1465
SLGSMKEENNHLQEELER	2144.3	3	3.5976	0.2617
SLGSSDLKF	954.1	2	2.6033	0.1679
SLGSVQAPSYGAR	1293.4	2	3.552	0.3038
SLGSVQAPSYGARPVSSAASVYAGAGGSGSR	2856.1	3	4.4644	0.4547
SLGSVSPSSSGFSSPHSGSTISIPFPNVLPDFSK	3408.7	3	4.0512	0.2755
SLGTADVHFER	1232.3	2	3.049	0.3418
SLGTDLMNEMR	1267.5	2	3.086	0.3452
SLGVGYAAVDNPIFYKPNTAMLLGDAK	2827.2	3	3.8311	0.3107
SLGVGYAAVDNPIFYKPNTAMLLGDAKK	2955.4	3	4.9281	0.3261
SLGVHLSFIR	1129.3	2	3.6423	0.2726
SLGYAYVNFQQPADAER	1930.1	2	5.7544	0.4582
SLGYAYVNFQQPADAERALDTMNFDVIK	3178.5	3	4.8572	0.4378
SLHDAIMIVR	1155.4	2	3.2094	0.2845
SLHDALCVLAQTVK	1498.8	2	3.9584	0.4464
SLHDPDGLVATYISEVHEHDGHLYLGSFR	3266.5	3	5.9117	0.5114
SLHLVIQNDQGHTSVLHSYPESVGR	2775.0	3	4.7318	0.4126
SLHQAIEGDTSGDFLK	1718.8	2	5.0917	0.3769
SLHQQSTQLSSSLTSVK	1832.0	2	4.5945	0.4396
SLHSAHSLASR	1166.3	2	2.5669	0.2795
SLHSATTIGNK	1129.2	2	3.1124	0.3159
SLHSELMCPICLDMLK	1834.3	2	2.8044	0.1182
SLHSIINPPIAK	1290.5	2	2.6115	0.1333
SLHTLFGDK	1018.1	2	2.7474	0.318
SLHTLFGDKLCTVATLR	1876.2	3	5.0551	0.4245

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SLIDMYSEVLDVLSDYDASYNTQDHLPR	3261.5	3	4.3198	0.2752
SLIGVDKFLGQATVALDEVFGAGR	2464.8	3	3.4387	0.1641
SLIPSYIRDSAAAVVVYDITNVNSFQQTTK	3302.7	3	4.6881	0.3207
SLIVGLK	729.9	1	1.8106	0.1142
SLKADLQKLKDELASTK	1889.2	2	4.3078	0.4522
SLKAGNASKDEIDSAVK	1733.9	2	4.1108	0.3649
SLKDEDVLQK	1175.3	2	3.0933	0.1735
SLKDEDVLQKLPVGTTATLYFR	2495.9	3	4.5722	0.272
SLKDFSSSKR	1155.3	2	2.7099	0.1837
SLKDMEESIR	1208.4	2	3.466	0.2886
SLKELQEMDKDDESLIK	2022.3	2	5.2742	0.3893
SLKLNTAEDAKDVIKEIEDFDSLEALR	3064.4	3	4.7554	0.3724
SLKLNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEAAR	4261.7	3	3.458	0.1789
SLKNLQLDYVDLYLIHFPVSVKPGEEVIPK	3456.0	3	5.8266	0.3435
SLKSQVAEAK	1061.2	2	2.7237	0.1643
SLKSTQDEINQAR	1490.6	2	4.2746	0.3816
SLLASLHTSR	1085.2	2	3.2265	0.1776
SLLATMKTELQK	1363.6	2	3.3945	0.2528
SLLDASEEAIKK	1304.5	2	2.6404	0.2582
SLLDEHHISYVIDEDVKSGR	2313.5	3	5.425	0.3466
SLLDIISDPDAGTPEDK	1786.9	2	4.2109	0.3342
SLLEGQEDHYNNLSAS	1777.8	2	4.6905	0.4062
SLLEGQEDHYNNLSASK	1906.0	2	5.4706	0.4863
SLLEGQEDHYNNLSASKV	2005.1	2	4.5278	0.4697
SLLEGQEDHYNNLSASKVL	2118.3	2	4.9631	0.3584
SLLEILNSAADILINSSEADEDGIRDEK	3032.3	3	3.8744	0.1947
SLLEKELESVGIR	1473.7	2	3.2856	0.2754
SLLELGGNNAIIAFEDADLSLVVPSALFAAVGTAGQR	3702.2	3	4.2003	0.3168
SLLEQYHLGLDQK	1544.7	2	3.4194	0.1781
SLLEQYHLGLDQKR	1700.9	2	3.5766	0.294
SLLGDSAPTLHLNK	1466.7	2	3.9846	0.3078
SLLGEVEQNLQAAK	1500.7	2	4.2633	0.387
SLLGKDVLFLK	1233.5	2	3.4598	0.2689
SLLGKDVLFLKDCVGPEVEK	2190.6	2	5.6045	0.4728
SLLGKDVLFLKDCVGPEVEKACANPAAGSVILLENLR	3884.6	3	7.5242	0.34
SLLGVKENNKK	1230.4	2	2.5602	0.1575

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SLLHGDFHAFSAGPGLFSYIR	2293.6	3	5.7451	0.4943
SLLKTYEQVLENLESK	1895.1	2	4.4781	0.3315
SLLKTYEQVLENLESKR	2051.3	2	4.6429	0.4309
SLLLSVNAR	973.2	2	2.7585	0.1081
SLLQALNEVK	1115.3	2	3.255	0.2059
SLLQALNEVKGR	1328.5	2	3.3094	0.2364
SLLSAEEAAK	1019.1	2	3.1408	0.2385
SLLSGLLIKDPNKR	1554.9	2	3.3125	0.206
SLLSHEFQDETDTEEETLYSSKH	2726.8	3	4.2632	0.2786
SLLSIPNTDYIQLLSEIAK	2119.4	2	2.6536	0.2323
SLLSLPEKEDKKEK	1644.9	2	3.4935	0.1626
SLLSMLSDLQIYQDSFEQR	2274.5	2	5.1479	0.365
SLLSNLDEVKK	1246.4	2	3.1148	0.2334
SLLSNLDEVKKER	1531.7	2	3.0588	0.2517
SLLSQEKEELQMSLLK	1877.2	2	3.6532	0.3107
SLLSSASATVGHGLTAVK	1699.9	2	4.6919	0.4631
SLLSSASATVGHGLTAVKEK	1957.2	3	3.268	0.319
SLLSVFEEDAGTLTDYTNQLLQAMQR	2945.3	2	3.674	0.3789
SLLTEADAGHTEFTDEVYQNESR	2613.7	2	2.8616	0.1377
SLLTIQEVDEFLLR	1676.9	2	4.9332	0.3823
SLLVIPNTLAVNAAQDSTDLVAK	2354.7	2	5.5779	0.5225
SLLVNPEGPTLMR	1427.7	2	3.6242	0.2785
SLLVTELGSSR	1162.3	2	3.8519	0.3092
SLMPYFLLTQAVR	1539.9	2	3.8727	0.4165
SLNADVPEQLITPLVSLGHISMLAPDQFASPMK	3522.1	3	4.2824	0.2547
SLNDITAK	862.0	1	1.8006	0.1228
SLNDITAKER	1147.3	2	3.2521	0.2258
SLNESKIEIER	1318.5	2	2.5683	0.1331
SLNIKTDPVDIYK	1506.7	2	3.739	0.2928
SLNILTAFQK	1135.3	2	4.0628	0.3091
SLNVESNFITGVGILALIDALRDNETLAELKIDNQR	3957.4	3	5.4821	0.4012
SLPEETVDFMVQHTSFK	1996.2	2	2.8648	0.2801
SLPEIDGLSKETVLSSWMAK	2192.5	2	3.6367	0.3573
SLPELDRDKSDSDTEGLLFSR	2381.5	3	3.4407	0.1724
SLPFGAQSTQR	1192.3	2	3.0489	0.2995
SLPHLPGTPRPTSSLPPGSVK	2126.4	2	2.9689	0.1099

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SLPIVFDEFVDMDFGTGAVK	2188.5	2	5.582	0.5984
SLPIYSPEKVEEYR	1710.9	2	3.4701	0.3085
SLPIYSPEKVEEYRNR	1981.2	2	4.1304	0.1925
SLPLLLSQAGVR	1254.5	2	3.7126	0.3529
SLPLQPGMVITIEPGIYIPEDDKDAPEKFR	3370.9	3	3.5614	0.3526
SLPNEEIVQKIEEVLSGVLDTELR	2712.0	3	3.7075	0.3513
SLPSDLAFNGDLAK	1448.6	2	3.3175	0.2823
SLPVEEQPKQIIVTR	1738.0	2	3.5457	0.3298
SLQAKDEDKDEDEKEK	1908.0	3	3.9414	0.1923
SLQALGEVIEAELR	1528.7	2	4.8999	0.2861
SLQDASRGDPAHAGLAELGHR	2159.3	3	4.514	0.4377
SLQDIIAILGMDELSEEDKLTVSR	2677.0	2	5.4533	0.5553
SLQEANAEKVTQEIVTER	2046.2	2	4.9135	0.2943
SLQEEHVAVAQLR	1480.7	2	2.8627	0.3195
SLQEEHVAVAQLREEAER	2095.3	2	3.2589	0.2443
SLQELFLAHILSPWGAEVK	2139.5	2	5.2119	0.3606
SLQELFLAHILSPWGAEVKAEPVEVVAPR	3187.7	3	7.8529	0.5259
SLQENEEEEIGNLELAWDMLDLAK	2791.0	3	4.6067	0.4023
SLQENIAYGLTQKPTMEEITAAAVK	2708.1	3	4.7694	0.2088
SLQEQADAAEER	1347.4	2	4.7839	0.3269
SLQEQADAAEERAGTLQR	1974.1	2	4.2093	0.3393
SLQETIQSLKLTNQELLR	2115.4	2	3.7171	0.326
SLQMYLER	1040.2	2	2.5517	0.1832
SLQPSVLMQLK	1244.5	2	2.6331	0.1171
SLQPVVEDVSLSWHLPPGLSAK	2360.7	2	3.559	0.3658
SLQQLAEERSQLLGSAHEVQR	2380.6	3	5.2175	0.3826
SLQQSWELLATHENHLNQDDTVPESSR	3136.3	3	3.3541	0.2399
SLQQTSGPATAK	1189.3	2	3.4286	0.2726
SLQSQLQNKESEVLEGAER	2146.3	3	3.5383	0.2666
SLQSVAEER	1019.1	2	2.8188	0.1885
SLQTLKDRLESLEHQLR	2067.3	3	3.66	0.2518
SLRDLTPEHLPLLR	1660.9	3	3.5955	0.358
SLREAQAALAEAQEDLESER	2217.3	2	3.1657	0.242
SLREAQAALAEAQEDLESERVAR	2543.7	3	3.708	0.2094
SLREHMGNVVEALIALTN	1968.3	2	2.4971	0.1476
SLRGSDALSETSSVSHIEDLEKVER	2745.9	3	5.7107	0.4587

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SLRPDPNFDALISK	1573.8	2	3.5689	0.2082
SLRVDIAEGR	1116.3	2	3.3826	0.1327
SLRVPAHISLLHVEQEVAGDDTPALQSVLESDSVR	3770.2	3	5.1299	0.389
SLSALGNVISALAEGSTYVPYR	2269.5	2	4.4863	0.3633
SLSALGNVISALAEGSTYVPYRDSK	2599.9	2	4.1164	0.3432
SLSALGNVISALAEGTK	1631.9	2	4.8751	0.3452
SLSDSESDDSK	1170.1	2	2.8684	0.3497
SLSDSESDDSKSK	1385.4	2	2.9597	0.2153
SLSDTVEKLKDEVLKETVSQRPGATVPTDFATFPSSAFLR	4369.9	3	4.3459	0.3102
SLSEDTDGTEEDPQAELAIIHGQMAYILQLQGR	3630.9	3	6.5541	0.4665
SLSEGHPTAQHEK	1421.5	2	3.6454	0.3675
SLSELESLKLPAESNEK	1875.1	2	4.3161	0.3609
SLSELESLKLPAESNEKIK	2116.4	2	3.9901	0.3407
SLSHIDPDVLYPSLNVTSFDSVVPEKLDDLVPK	3641.1	3	3.7518	0.2019
SLSHLPLHSSK	1206.4	2	3.1198	0.2975
SLSHLPLHSSKEDAYDGVTSENMR	2674.9	3	4.2015	0.3536
SLSIEIGHEVKTQNK	1683.9	2	3.0192	0.2553
SLSLGGHVGFDSLPDQLVSK	2057.3	3	4.131	0.3637
SLSLSLADSGHLPDVHGFNSYGSHR	2654.8	3	4.3502	0.362
SLSNTKPTVNEHDLLK	1797.0	2	4.0863	0.3064
SLSNVIAHEISHSWTGNLVTNK	2408.7	3	4.3619	0.4515
SLSQIHEAAVR	1211.4	2	3.6284	0.246
SLSQSFENLLDEPAYGLIQAG	2253.5	3	4.9063	0.2204
SLSSAINASTGNYLLESVNKLFGEK	2643.9	2	4.3257	0.3415
SLSSELKKPQAHLPVHTEK	2130.4	3	3.3557	0.1612
SLSSQASKLGEQMADLHLYNQK	2449.7	3	4.19	0.3027
SLSSSLDDTEVK	1281.3	2	2.4427	0.1966
SLSSSLDDTEVKK	1409.5	2	4.0074	0.3353
SLSSSPQAQPPRPAELSDEEVAELFQR	2970.2	3	3.8991	0.3276
SLSTAPVVQPLSIQDLVR	1924.2	2	2.7746	0.3069
SLSVLSSSTIIANPDIPEAYK	2206.5	2	2.9998	0.2089
SLTELFVKENHELR	1715.9	2	3.0747	0.2764
SLTELQELEAVYER	1680.8	2	3.8598	0.1464
SLTEYLQNVEQK	1452.6	2	3.7781	0.2687
SLTMSGHVGFESLPDQLVNR	2188.5	2	4.5616	0.4726
SLTNDWEDHLAVK	1528.6	2	4.4144	0.3981

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SLTNDWEDHLAVKHFSVEGQLEFR	2859.1	3	3.9455	0.1707
SLTPAVPVESKPDKPSGK	1838.1	2	3.9418	0.4675
SLTTLGLVISALADQSAGK	1846.1	2	5.7648	0.4522
SLTTLGLVISSLADQAAGK	1846.1	2	4.7702	0.2612
SLTTLGLVISSLADQAAGKGK	2031.3	2	2.6479	0.1121
SLVDLTAVDVPTR	1386.6	2	3.3067	0.2689
SLVDYENANK	1153.2	2	2.8934	0.2648
SLVESVSSSPNK	1234.3	2	2.4702	0.1179
SLVESVSSSPNKESNEEEQVWHFLGK	2948.1	3	5.8568	0.4026
SLVEYSQDVLAHPVSEEHLPDVSLIGEFSDPAELGK	3909.3	3	4.8876	0.3228
SLVIELDKELYGPDNHLVEWHR	2664.0	3	4.4822	0.3251
SLVLDTKDLTIEK	1475.7	2	3.485	0.2691
SLVPAAELLESR	1285.5	2	2.9483	0.3219
SLVSDKTSISEK	1294.4	2	2.8559	0.3284
SLVSKGTLVQTK	1261.5	2	3.3133	0.2563
SLVSVTKEGLELPEDEEEKKK	2388.7	3	4.7402	0.3052
SLVSVTKEGLELPEDEEEKKKMEESK	2993.3	3	6.2562	0.4444
SLVSVTKEGLELPEDEEEKKKMEESKAK	3192.6	3	5.4438	0.3941
SLYASSPGGVYATR	1429.6	2	4.6157	0.3607
SLYDEVAAQGEVVR	1536.7	2	4.5683	0.3891
SLYDEVAAQGEVVRK	1664.8	2	4.3607	0.3838
SLYGKDLIADLK	1336.6	2	2.9553	0.2206
SLYGKDLIADLKYELTGK	2028.3	2	6.2063	0.494
SLYGKDLIADLKYELTGKFER	2460.8	3	6.0888	0.4674
SLYHDISGDTSGDYR	1686.7	2	3.8752	0.3644
SLYHDISGDTSGDYRK	1814.9	2	4.6	0.4179
SLYNVNGLK	1008.2	2	2.466	0.1799
SLYQSAGVAPESFEYIEAHGTGTK	2543.7	2	4.4774	0.4567
SLYQSAGVAPESFEYIEAHGTGTKVGDPQELNGITR	3824.1	3	4.5525	0.2773
SLYSEKEVFIR	1371.6	2	3.1389	0.2748
SLYSFIKGDTSGDYR	1709.8	2	2.9272	0.3307
SLYVAEYHSEPVEDEKP	1993.1	2	5.1315	0.3808
SLYYYIQQDTK	1422.6	2	4.2889	0.2953
SLYYYIQQDTKGDYQK	2014.2	2	4.8797	0.4277
SMAASGNLGHTPFVDEL	1746.9	2	3.909	0.3138
SMAEDTINAAVK	1250.4	2	4.1915	0.2921

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SMAEDTINAAVKTHNLK	1844.1	2	3.9644	0.3555
SMASGGGVPTDEEQATGLER	1993.1	3	4.5577	0.386
SMDFEEAER	1114.2	2	3.1	0.3287
SMDFEEAERSEPTQALELTEDDIKEDGIVPLR	3664.9	3	5.6206	0.3462
SMDNMTVRVPETVADAR	1893.1	3	4.1497	0.2075
SMEAEMIQLQEELAAAER	2050.3	3	5.5545	0.4232
SMEMLVEHQAHDILT	1755.0	2	3.8304	0.3547
SMENEDKEETVAK	1510.6	2	4.0468	0.3427
SMFAGDKK	884.0	2	2.4757	0.1105
SMFAGVPTMR	1097.3	2	2.6817	0.212
SMGFIGHYLDQK	1396.6	2	3.3504	0.284
SMGFIGHYLDQKR	1552.8	2	3.2876	0.3207
SMGSQEDDSGNKPSSYS	1776.8	2	4.1586	0.4145
SMIASTAITVHYLDLSLNPSGEVTR	2677.0	2	3.6402	0.2827
SMIGEPTNFVHTAHVGSGDLFSGMNSVSSIQNQMQSK	3925.3	3	3.664	0.1942
SMKFVDGLMIHSGDPVNYYVDTAVR	2816.2	3	4.1822	0.3873
SMKGLGTDDNTLIR	1521.7	2	4.0299	0.3853
SMKLPQEQSQLPNPSEASTTFPESHLR	3041.3	3	3.973	0.2277
SMLEVNYPMENGIVR	1753.0	2	5.0458	0.298
SMLQATAEANNLAAAASAK	1834.0	2	5.9412	0.4554
SMLRPLELSLPSQTSYSENEILKK	2765.2	3	3.7187	0.1068
SMMGGGLAEIPGLSINFAK	1894.2	2	4.3802	0.3843
SMMQDREDQSILCTGESGAGKTENTKK	2946.2	3	5.493	0.2153
SMMQSLSQNPDLAAQMMLNNPLFAGNPQLQEQMR	3836.4	3	5.7128	0.4598
SMNINLWSEITELLYK	1955.3	2	2.9079	0.2015
SMPEQTGEK	1007.1	1	1.7235	0.1308
SMPESLDSPTSGRPGVTSLTTAAAFKPVGSTGVIK	3448.9	3	5.0143	0.4394
SMPIRKDDEVQVVR	1672.9	2	3.8212	0.2799
SMPVLGSVSSVTK	1292.5	2	2.7758	0.2696
SMQNHAAVFR	1161.3	2	3.5355	0.3889
SMQVVPLDKQITIIDSPSFIVSPLNSSSALALR	3529.1	3	6.5563	0.4835
SMSDVSAEDVQNLR	1551.7	2	3.2339	0.1977
SMSGHPEAAQMVR	1401.6	2	3.71	0.3811
SMTEAEQQQLIDDHFLFDKPVSPLLLASGMAR	3590.1	3	6.3316	0.4766
SMTLLNTMDR	1182.4	2	2.9408	0.2039
SMTLLNTMDRILYESQR	2072.4	2	3.3244	0.2283

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SMVEDITGLR	1121.3	2	2.7285	0.2486
SMVEEGTGLR	1079.2	2	3.1356	0.181
SMVNTKPEKTEEDSEEVREQK	2494.7	3	4.6591	0.2183
SMVPVQVQLDVPVVK	1639.0	2	4.3729	0.4163
SMYEEEINETR	1401.5	2	3.4402	0.2894
SNAFAEKNGLQKYEYVLHPR	2365.6	3	3.4288	0.1492
SNAHYNLQNAFNLAEQHLGLTK	2484.7	3	7.1345	0.5241
SNAQGIDLNR	1088.2	2	3.904	0.2943
SNAQRQDIAFAYQR	1668.8	2	4.1203	0.389
SNASLTNNQNLIQSLKEDLNKVR	2600.9	3	3.6869	0.1918
SNCKPSTFAYPAPLEVPKEK	2207.5	3	3.3714	0.2205
SNDPQMVAENFVPPLLDAVLIDYQR	2846.2	3	3.671	0.2556
SNDPVATAFAEMLK	1494.7	2	2.9321	0.2962
SNDPVAYALAEMLKENK	1894.1	2	2.6311	0.2892
SNEAASKELASK	1235.3	2	2.7394	0.2358
SNEDQSMGNWQIK	1537.6	2	3.194	0.1822
SNEEGSEEKGPEVR	1547.6	2	3.8585	0.3517
SNEGKLEGLTDEFEELEFLSTINVGLTSIANLPK	3710.1	3	4.5817	0.252
SNEILTAIIQGMR	1446.7	2	3.4876	0.3174
SNELGDVGVHCVLQGLQTPSCK	2285.6	2	2.7546	0.2077
SNETNGYLDSAQAGPAAGPGAPGTAAGR	2559.6	3	5.0459	0.3831
SNFAEALAAHK	1159.3	2	3.687	0.4467
SNFEPFFMMIATPAPHSPWTAAPQYQK	3096.5	3	3.9046	0.2511
SNFLNCYVSGFHPSDIEVDLLK	2498.8	2	4.629	0.4704
SNFSLAILNVGAPAAGMNAAVR	2145.5	3	5.7866	0.4295
SNFSNSADDIKSK	1413.5	2	3.3072	0.2854
SNGHIYDNR	1076.1	2	2.7181	0.1332
SNGKETVVGR	1047.1	2	2.64	0.1606
SNGWILPTVYQGMYNATTR	2173.4	3	5.3963	0.4046
SNGYEEAYSVFKK	1522.6	2	3.2768	0.2388
SNHDKNVIPDEVLQTLLDHYSHK	2703.9	3	5.6021	0.4262
SNIDALLSRLEQIAAEQK	2000.2	3	5.5637	0.3638
SNIDALLSRLEQIAAEQKANPDGK	2582.9	3	4.6325	0.1815
SNILLLGPTGSGK	1257.5	2	3.2141	0.1136
SNKDGGNQEVEIAR	1517.6	2	3.5465	0.3062
SNKEIMEHIR	1257.4	2	2.8715	0.191

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SNLAYDIVQLPTGLTGIK	1904.2	2	4.8833	0.4387
SNLELFKEELK	1350.5	2	2.518	0.1252
SNLFEDATSALVTGQSYENMVTEIMSMGYER	3475.8	3	3.3319	0.1577
SNLGSVVLQLK	1158.4	2	3.3131	0.3558
SNLISGSVMYIEEK	1570.8	2	3.3618	0.132
SNLLTQDNGILTFSNLSPGQYYFKPMMK	3209.7	3	5.3424	0.3481
SNLMDAISFVLGEK	1524.8	2	2.8542	0.121
SNLVDNTNQVEVLQR	1729.9	2	4.0912	0.3024
SNLVDNTNQVEVLQRDPNSPLYSVK	2831.1	3	4.3755	0.354
SNLVGMGVIPLEYLPGENADALGLTGQER	3015.4	3	3.8811	0.3962
SNMDNMFESYINNLR	1849.0	2	5.2651	0.4813
SNMGHPEPASGLAALAK	1651.9	2	3.2449	0.1256
SNNHENVSLAK	1213.3	2	3.426	0.2374
SNNTSKPSHSVDAHTAEVNCLSFNPYSEFILATGSADK	4041.3	3	5.8037	0.3963
SNNVEMDWVLK	1335.5	2	3.5815	0.2488
SNNVEMDWVLKHTGPNSPDTANDGFVR	3002.2	3	3.8551	0.1901
SNPEDQILYQTER	1593.7	2	4.3734	0.4356
SNPEIQDFMR	1237.4	2	2.9208	0.2908
SNPGHYLGHLIGHEGPGSLLSELK	2513.8	3	4.9628	0.4742
SNPSAVAGNETPGASTK	1588.7	2	4.2403	0.4427
SNPSENEEKEAQSQLIK	1932.0	2	5.2028	0.3331
SNPSENEEKEAQSQLIKSDEMQR	2678.8	3	4.2743	0.3967
SNPSVLQGLLR	1184.4	2	2.9168	0.3306
SNQLFNGHGGHIMPPTQSQFGEMGGK	2758.0	3	3.5817	0.1664
SNQNGKDSKPSSTPR	1603.7	2	4.8335	0.3152
SNQQLENDLNLMDIK	1776.0	2	5.2431	0.4388
SNQQLVDIIEK	1287.4	2	3.2795	0.1911
SNRDELELELAENRK	1817.0	2	2.9784	0.1451
SNRIEEQNDKISELIER	2074.2	3	4.616	0.2223
SNSEDKLNSK	1122.2	2	2.8076	0.2126
SNSFNSTFEHHLPPSPLEHGTPFQR	2865.1	3	3.7521	0.2574
SNSVEMDWVLK	1308.5	2	3.2134	0.1338
SNSVEMDWVLKHTGPNSPDTANDGFVR	2975.2	3	6.2485	0.3403
SNTAGSQSQVETEA	1409.4	2	4.2204	0.3967
SNTENLSQHFR	1333.4	2	3.4567	0.2264
SNTKLTEELAVANNR	1660.8	3	3.5049	0.1171

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SNTLPISLQSIR	1329.5	2	3.4438	0.2948
SNTPILVDGKDVMPEVNK	1957.2	2	4.8164	0.4964
SNTPILVDGKDVMPEVNKVLDK	2412.8	2	4.6868	0.4485
SNTPILVDGKDVMPEVNKVLDKMK	2672.2	3	4.3066	0.1185
SNTSPEELGPLANQLTSDYGR	2250.4	3	4.8289	0.4886
SNTTSKPSHLVDAHTAEVNCLSFNPYSEFILATGSADK	4054.4	3	5.832	0.3842
SNVKPNSGELDPLYVVEVLLR	2342.7	3	5.1778	0.1866
SNVSDAVAQSTR	1235.3	2	4.7275	0.4459
SNVTAVHK	856.0	2	2.6906	0.2143
SNYFEVPLPYFEYFK	1944.2	2	4.1799	0.3367
SNYLLNTTIAGVEEADVVLLVGTNPR	2760.1	3	3.279	0.2096
SNYNFEKPFLWLAR	1786.0	3	4.6376	0.3807
SNYNLPMHK	1104.3	2	2.9214	0.1773
SPADPTDLGGQTSPR	1499.6	2	4.257	0.457
SPAFVQLAPLSSK	1345.6	2	2.6671	0.1299
SPAGLQVLNDYLADK	1604.8	2	5.421	0.4217
SPAGSIVHELNPNFQPPKRPFK	2461.8	3	4.3318	0.3321
SPAHLSLIR	994.2	2	2.8865	0.3081
SPAISWVNNLEVDSR	1687.8	2	3.2677	0.23
SPAKPVQTITPHGK	1461.7	2	3.4708	0.3602
SPAPPLLHVAALGQK	1499.8	2	4.0804	0.3815
SPAPSSDFADAITELEDAFSR	2227.3	2	4.3892	0.4746
SPAQILIR	898.1	2	2.9434	0.2176
SPAQILLR	898.1	2	3.0709	0.2276
SPASDTYIVFGEAK	1485.6	2	4.4815	0.4382
SPASDTYIVFGEAKIEDLSQQAQLAAAEKFK	3357.7	3	3.9401	0.2969
SPAVATSTAAPPPPSSPLPSK	1961.2	2	4.3475	0.4442
SPCIVLADADLDNAVEFAHHGVFYHQGQCCIAASR	3760.2	3	5.2139	0.3991
SPDEAYAIAK	1065.2	2	3.1219	0.2971
SPDFTNENPLETR	1520.6	2	4.3514	0.4434
SPDLLMYQGPPDTAEIIK	1989.3	2	2.8551	0.2289
SPDPGIVPQEAPVGNSLSELSEENFDGK	2914.1	3	4.3928	0.4613
SPDPGIVPQEAPVGNSLSELSEENFDGKFANLTPSR	3801.1	3	4.4073	0.2487
SPEDSSPDAAR	1132.1	2	2.9803	0.2155
SPEEGAETPVYLALLPPDAEGPHGQFVSEK	3166.4	3	5.3491	0.3908
SPELAAQPSTYLAVAEELADVSGK	2447.7	3	3.955	0.2185

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SPENTEGKDGSK	1249.3	2	2.7598	0.2964
SPEQQLSATQK	1217.3	2	3.1998	0.1834
SPEYLSLFIDDKLKK	1797.1	3	4.4284	0.3441
SPFEQHIK	986.1	2	2.5254	0.1473
SPFEVQVGPEAGMQK	1604.8	2	5.1309	0.341
SPFSVAVSPSLDLSK	1534.7	2	4.5716	0.3366
SPFTVGVAAPLDLSK	1502.7	2	4.5302	0.3364
SPFVVQVGEACNPNACR	1792.0	2	3.5407	0.163
SPGAAGLTSR	917.0	2	2.5418	0.1621
SPGADLLQVLTK	1242.4	2	4.4582	0.4234
SPGDTAKDALFASQEKFFQELFDSELASQATAEFEK	3985.3	3	5.3766	0.4606
SPGETSKPRPFAGGGYR	1764.9	2	3.1876	0.2559
SPGGHSDGASPR	1125.1	2	2.5216	0.2285
SPGIISQASAPR	1184.3	2	3.0913	0.1743
SPGLGGGEGGSHGVIQDLSILHQHVQQQPAQHHR	3563.8	3	4.2799	0.3032
SPGPPALKHPATK	1301.5	2	2.7861	0.2677
SPGSQGVR	787.8	1	1.8861	0.1065
SPGSVSTHHSSPR	1336.4	2	3.4649	0.3445
SPGVVISDDEPGYDLDLFCIPNHYAEDLER	3380.6	3	4.8964	0.2612
SPHPSSALHFPTTSILPQTASTYFPHTAIR	3264.6	3	4.3217	0.2527
SPIAEAVFR	990.1	2	2.9286	0.2848
SPIAEAVFRK	1118.3	2	3.054	0.2484
SPIIFIGTGEHIDDFEPFK	2163.4	2	4.7642	0.4106
SPIIFIGTGEHIDDFEPFKTQPFISK	2965.3	3	4.9586	0.3457
SPILLGSLAHQIYR	1568.8	2	4.5379	0.3907
SPILVATAVAAR	1169.4	2	2.7354	0.1934
SPINVESLLDGLNSLVLDLDFPALRK	2840.3	3	4.2717	0.4494
SPISVPGGSALISNLGK	1597.8	2	2.7611	0.3615
SPITGNDLSPPVSFNLMFK	2065.4	2	5.361	0.4552
SPKDLVVICKVFNPQLPFKPHGSR	2708.2	3	3.3056	0.114
SPKDNVDDPTGNFR	1562.6	2	4.3711	0.4887
SPKDPSQLNSK	1201.3	2	2.7708	0.1473
SPLELQMQEGEHTIR	1769.0	2	3.6775	0.3186
SPLGEVAIRDIVQFVPFR	2044.4	3	5.3451	0.4127
SPLLAGGSPPQPVVPAHKDK	1996.3	3	4.0808	0.2931
SPLLQLPHIEEDNLR	1775.0	2	3.5482	0.3235

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SPLMSEFQSQISSNPELAAIFESIQK	2883.2	3	3.8311	0.2393
SPLQSQPHSR	1137.2	2	3.291	0.1671
SPLVLEVDPNIQAVR	1650.9	2	5.04	0.4689
SPNELVDDLFKGAKEHGAVAVER	2482.7	3	4.9369	0.3702
SPPEKTQADLLAFLHSQVDKAEVNAGVK	2994.3	3	3.3496	0.1475
SPPFFENLTLDLQPPK	1844.1	2	2.987	0.2349
SPPGQVTEAVK	1113.2	2	3.1546	0.3198
SPPIPLAKVDATAETDLAK	1938.2	2	2.5927	0.2186
SPPSYSVLYPSSDPK	1624.8	2	4.4393	0.3248
SPPTVLVICGPGNNGGDGLVCAR	2197.5	2	3.3917	0.1722
SPPYTAFLGNLPYDVTEESIKEFFR	2922.2	3	4.7824	0.3871
SPQDLASTSR	1062.1	2	2.659	0.2835
SPQLILVNMASFPECTAAAIK	2205.6	2	2.5775	0.1666
SPQMVSAIVR	1088.3	2	3.1769	0.2323
SPQSLSAAIAAMQK	1403.6	2	4.8636	0.3079
SPSAQLMEQVAQLK	1530.8	2	4.7979	0.3421
SPSDSSTASTPVAEQIER	1862.9	2	4.9101	0.4775
SPSEEPPEEEIPKEDGILVLSR	2451.7	3	4.1704	0.2538
SPSELFAQHIVTIVHHVK	2043.4	3	6.1682	0.458
SPSGGAAGPLLTPSQSLDGSR	1956.1	2	5.2057	0.506
SPSKENIASVLENYHTESK	2134.3	2	4.8448	0.4061
SPSKPLPEVTDEYKNDVK	2047.3	2	3.8277	0.409
SPSLQSETVHYKR	1532.7	2	2.5331	0.1784
SPSQKKPVSK	1086.3	2	2.8898	0.2065
SPSSSSVGGR	920.9	2	2.5841	0.3247
SPSTLLPK	843.0	2	2.4377	0.1811
SPSWQRPNQGVPSTGR	1754.9	3	3.2777	0.1692
SPTADAKPAPK	1083.2	2	2.8607	0.1837
SPTDWALFTYEGNSNDIR	2087.2	2	2.571	0.2009
SPTKAPHLQLIEGK	1519.8	2	3.8183	0.3201
SPVAKDVDLEFLAK	1532.8	2	4.2767	0.3429
SPVAVQSTK	917.0	2	2.8086	0.2982
SPVDVLQIFR	1174.4	2	3.416	0.3019
SPVESTTEPPAVR	1370.5	2	3.5724	0.3459
SPVEVAQDVLAAVGK	1483.7	2	4.2298	0.3798
SPVEVAQDVLAAVGKK	1611.9	2	4.736	0.4488

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SPVKVTLSEGPHHVALFK	1947.3	2	5.3502	0.4775
SPVLDTKPK	985.2	2	2.4248	0.1273
SPVYLDLAYLPSGSSAHLVDEEFFQR	2942.2	3	3.5689	0.1821
SPWSNKYDPPLEDGAMPSAR	2219.4	3	4.3793	0.3704
SPYGGGRPGR	1004.1	2	2.6441	0.1094
SPYLYPLYGLGELPQGFAR	2142.4	2	5.9956	0.4983
SPYQEFTDHLVK	1464.6	2	3.8685	0.3496
SPYQLVLQHSR	1328.5	2	2.8012	0.1058
SPYSYSTTAVVTNPK	1615.8	2	4.5294	0.4776
SPYTVTVGQACNPSACR	1755.0	2	3.0496	0.1914
SQAADQITK	962.0	2	2.5783	0.1358
SQAEDVRVEGSFPVTMLPGDGVGPELMHAVK	3254.7	3	5.4525	0.4164
SQAEPLSGNKEPLADTSSNQQK	2330.5	3	4.65	0.2731
SQAIHQLK	925.1	2	2.8218	0.1527
SQAPGQPGASQWGSR	1514.6	2	3.2002	0.2349
SQAPLESSLDSLGDVFLDSGRK	2322.5	2	2.7385	0.259
SQAVEKPPSEKPR	1453.6	2	3.4666	0.3184
SQAYADYIGFILTLNEGVK	2103.4	2	3.6521	0.3739
SQDAEVGDGTTSVTLLAAEFLK	2253.4	2	6.4743	0.569
SQDDEIGDGTTGVVVLAGALLEEAEQLLDR	3115.3	3	6.5187	0.4662
SQDFGNLFSFPSYSQK	1853.0	2	3.9309	0.2899
SQDPQEDKKEEK	1461.5	2	2.7228	0.2269
SQDPTPPSAPQEATEGSK	1827.9	2	2.7658	0.2437
SQEAQSLQQQR	1303.4	2	2.9026	0.146
SQEDLNEPIKR	1329.4	2	3.1721	0.1699
SQEEPKDTFEHDPSESIDEFNK	2609.7	3	4.7315	0.3753
SQEESEEGEEDATSEVD	1870.7	2	5.5282	0.4849
SQEETPGHR	1041.1	2	2.9121	0.3037
SQEGRPVQVIGALIGK	1652.9	2	2.936	0.177
SQEIDDHQHEMSVLQNAHQQK	2503.7	3	5.7854	0.3242
SQELSGPASNGGISQTNTYDAQYER	2674.7	3	6.3628	0.4293
SQEMVHLVNK	1185.4	2	3.9865	0.2739
SQEMVHLVNKESSETPDQFMTADETR	3011.2	3	6.7566	0.4835
SQEPLPDDDEEFELPEFVEPFLK	2750.9	3	4.8184	0.3555
SQEQEVLER	1118.2	2	2.8541	0.1003
SQEQLAAELAEYTAK	1652.8	2	5.3976	0.4477

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SQESGEEAGSQENHPQESK	2059.0	2	5.1996	0.5256
SQESGYYDR	1105.1	2	2.571	0.1508
SQESNVSIQKENLELKEHIRQNEEELSR	3368.6	3	4.4275	0.3549
SQETECTYFSTPLLLGK	1918.2	2	5.6612	0.4819
SQEVEDKTKEYELLSDELNQK	2526.7	3	5.2052	0.261
SQEVEDKTR	1092.1	2	2.7853	0.2044
SQFEAQKIWYEHR	1722.9	2	4.5851	0.3558
SQFFEQGSSDSVVPDLPVPTISAPSR	2749.0	3	4.5334	0.3288
SQFSDKPVQDR	1307.4	2	3.2915	0.3425
SQFTITPGSEQIR	1464.6	2	4.1759	0.3245
SQGAALDKYAK	1152.3	2	3.6345	0.3424
SQGADKDLAAK	1104.2	2	2.7992	0.1959
SQGEKEMYTLGITNFPIPGEPGFPLNAIYAK	3384.8	3	4.3294	0.1641
SQGGEPTYNVAVGR	1435.5	2	4.5122	0.3912
SQGGVQPIPSQGGK	1340.5	2	3.6188	0.2027
SQGLSQLYHNQSQGLLSQLQGQSK	2630.9	3	3.3287	0.2367
SQGPLEVAEAAVSQSSGLAAK	2001.2	2	5.9605	0.5794
SQGQDVTSSVYFMK	1577.7	2	2.8456	0.3554
SQHERDPWYSWDQPGLR	2158.3	3	3.4968	0.2621
SQHKEELGAVR	1254.4	2	2.4355	0.2833
SQHPYVLTEDTLK	1531.7	2	3.5653	0.4188
SQHSGNAQVTQTK	1386.5	2	3.8846	0.4142
SQIDDLYSTIKV	1382.5	2	3.7327	0.17
SQIEQLKQQNYQQASSFPPHEELLK	2972.3	3	4.5234	0.4138
SQIFSTASDNQPTVTIK	1838.0	2	5.7426	0.4818
SQIGNTESELKK	1334.5	2	2.9175	0.1027
SQIGNTESELKKLAEENPDLQEAYIAK	3020.3	3	5.9801	0.4218
SQIHDIVLVGGSTR	1482.7	2	4.5995	0.4657
SQILKHPSLAR	1250.5	2	3.0533	0.1405
SQKADSPSIDYAELLQHFEK	2307.5	2	3.5933	0.4407
SQKADSPSIDYAELLQHFEKVQNK	2777.0	3	3.973	0.1048
SQKEINDMK	1093.2	2	2.4591	0.1225
SQKELPTEPPYTAYVGNLPFNTVQGDIDAIFK	3554.9	3	5.1994	0.4419
SQKELPTEPPYTAYVGNLPFNTVQGDIDAIFKDLSIR	4139.6	3	6.34	0.5068
SQKLGDSESVSK	1265.4	2	3.141	0.2976
SQKPVMVK	917.2	2	2.421	0.1007

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SQKVDTLPYVPEPIKVAIAENLLDVIK	2994.5	3	3.6006	0.2392
SQLDIIIHSLK	1267.5	2	3.0855	0.2805
SQLDIIIHSLKK	1395.7	2	4.1626	0.3201
SQLDLFDDVGTFASGPPK	1895.1	2	5.755	0.5007
SQLEAIFLR	1077.3	2	2.9942	0.2466
SQLEEKENKKFPVFK	1852.1	2	4.2216	0.3684
SQLEESISQLR	1290.4	2	3.9302	0.3408
SQLGAHHTTPVGDGAAGTR	1833.9	2	5.5284	0.5077
SQLLGSAHEVQR	1325.5	2	3.7219	0.3082
SQLLKDPQVLFAGYK	1708.0	2	2.831	0.1177
SQLLKDPQVLFAGYKVPHPLEHK	2646.1	3	5.4051	0.3502
SQLNSQSVEITK	1334.5	2	4.1623	0.3111
SQLNSQSVEITKLQTEKQELLQK	2674.0	3	4.4997	0.1396
SQLPTLEQDGGTQNPVSSPGMSQELR	2758.0	3	4.8515	0.4113
SQLVYQSR	981.1	2	2.4728	0.2974
SQMAAVEPERTPLQR	1713.9	2	3.4295	0.2616
SQMDGLIPGVEPR	1399.6	2	3.3433	0.1072
SQNIVTDSSSLSAEAIR	1778.9	2	3.6707	0.2855
SQNKEDYAGLKEEFR	1814.9	3	3.9306	0.2343
SQNKEDYAGLKEEFRK	1943.1	2	5.26	0.4171
SQNQQYLVR	1136.2	2	2.951	0.1925
SQNVMAAASIANIVK	1517.8	2	5.8408	0.4761
SQPAILLLTAAR	1254.5	2	3.4327	0.2911
SQPAILLLTAARDAEEALR	2039.3	2	3.3154	0.1275
SQPERDWVLNEFR	1676.8	2	2.4353	0.4009
SQPHSLATETR	1227.3	2	2.4325	0.1636
SQPLQNVSTVLQKPNPLYNQNTDMVQK	3086.5	3	3.3686	0.1454
SQPVYIQYSNHR	1492.6	2	3.5924	0.4314
SQQHHGLAADLGK	1362.5	2	3.3824	0.3696
SQQLIEWVKDTYSPDEHLWATLQR	2945.2	3	4.2683	0.2446
SQQSEVTR	935.0	2	2.5264	0.1272
SQQTISQLHSTVHLIEFAR	2196.5	3	4.4334	0.3412
SQREDEEEEEGENYQK	1999.9	2	5.0822	0.4467
SQREDEEEEEGENYQKGER	2342.3	3	6.4295	0.3961
SQRPEESEPLEK	1429.5	2	3.373	0.1848
SQSAAVTPSSTTSSTR	1568.6	2	3.8229	0.3276

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SQSGGYSDR	956.9	2	2.8319	0.3219
SQSHLPYFTPKPPQDSAVIK	2241.5	3	3.504	0.2603
SQSLTNAFNLPEPAPPRPSLSQDEVKAETIR	3394.7	3	5.0056	0.4354
SQSSDTEQQSPTSGGGK	1681.7	2	5.5149	0.4666
SQSSHSYDDSTLPLIDR	1922.0	2	5.4174	0.4606
SQSSHSYDDSTLPLIDRNQK	2292.4	3	4.2916	0.3248
SQSSNDTFPTAMHIAAAIEVHEVLLPGLQK	3206.6	3	5.3356	0.4803
SQTDKDYYQLQAILEAERR	2328.5	3	3.3334	0.1705
SQTEAVTFLANHDDSR	1791.9	2	3.649	0.3784
SQTGVGELTTQNTR	1492.6	2	3.9608	0.4338
SQTHSLPAPESPEPAAPPRPQTPENGPEASD	3193.3	3	5.0106	0.3223
SQTHSLPAPESPEPAAPPRPQTPENGPEASDPSEELEALASLLQELR	4973.3	3	5.4558	0.5316
SQTTGFPSLITIFSAPNYLDVYNNK	2792.1	3	3.6696	0.2128
SQVDHVIWPDGKR	1537.7	3	4.1564	0.279
SQVDKLTLTSR	1248.4	2	3.1556	0.2317
SQVEEELFSVR	1323.4	2	3.5966	0.3597
SQVFSTAADGQTQVEIK	1810.0	2	5.3896	0.5057
SQVMDEATALQLR	1462.7	2	4.4969	0.3762
SQVMDEATALQLREGLTSIEEVTKNLQK	3133.5	3	4.8812	0.2778
SQVTNYLGIEWMR	1597.8	2	4.3789	0.4472
SQVVAGTNYFIK	1327.5	2	3.3663	0.3011
SQWSPALTISK	1218.4	2	2.7607	0.2044
SQYAHYFDLSLVNNGVDETLKK	2542.8	3	3.5638	0.22
SQYEVMAEQNR	1355.5	2	4.3314	0.4723
SQYEVMAEQNRK	1483.6	2	3.1435	0.2409
SQYSGQLHEVR	1304.4	2	2.8088	0.2856
SRAEAALEEESR	1348.4	2	3.2314	0.2247
SRAEAESMYQIKYEELQSLAGK	2532.8	3	5.8287	0.4683
SRAEAESMYQIKYEELQSLAGKHGDDLR	3226.5	3	4.9301	0.4808
SRAEAESMYQIKYEELQSLAGKHGDDLRR	3382.7	3	3.507	0.1778
SRANEEYGLR	1195.3	2	2.9057	0.2163
SRDESASETSTPSEHSAAPSPQVEVR	2742.8	3	4.5824	0.374
SRDEWDKLAR	1276.4	2	2.6674	0.1016
SRDLIKDKIEPSAK	1600.8	2	2.8243	0.1408
SRDLLVQQASQCLSK	1676.9	2	4.1793	0.4461
SRDNGPDGMEPEGVIESNWNEIVDSFDDMNLSESLLR	4169.4	3	6.3844	0.4479

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SRDSDESGDKTTR	1454.4	2	2.8027	0.1275
SRDVAQLGDVVHGVESLVELLGWTEEMRDLVQR	3738.2	3	4.454	0.2854
SREAIDSPVSFLALHNQIR	2154.4	3	4.7702	0.3355
SREDLSAQPVQTK	1459.6	2	4.2262	0.2803
SREDLSAQPVQTKFPAYER	2223.4	3	3.3645	0.1443
SREEAAAGTIPGALNIPVSELESALQMEPAAFQALYSAEKPK	4387.9	3	5.5727	0.4887
SREEDDVTKDIVLR	1675.8	2	4.7004	0.3428
SREHGIAMR	1057.2	2	2.4382	0.1598
SREIFLSQPILLELEAPLK	2197.6	2	4.8981	0.3985
SREQILDQLKNEILTSGNIPPNYQYIFQPISASAK	3978.5	3	4.8657	0.4326
SREVLELGQVLDTGKR	1801.0	3	5.1324	0.2401
SREYQLNDSAAYYLNDLER	2321.4	2	5.6103	0.3717
SREYQLNDSAK	1311.4	2	3.8095	0.2584
SREYQLNDSASYYLNDLDRISQSNYIPTQQDVLR	4067.3	3	3.8448	0.1553
SRFDLEKYNQLKDAIAQAEMDLKR	2884.3	3	5.3983	0.4228
SRFEYPPPPVSLGSSSHTAR	2173.4	3	5.2096	0.3846
SRGELDLQLQEYQHSLER	2202.4	3	3.5452	0.167
SRGFGFVLFK	1158.4	2	2.8344	0.1671
SRGFGFVTFADPASVDKVLGQPHHELDSK	3143.5	3	4.2105	0.2402
SRGPPRPRPAPAVGEAEDKENQQATSGPNQPSVR	3582.8	3	4.0178	0.1256
SRKESYSIYVYK	1523.7	3	3.6493	0.3175
SRKESYSVYVYK	1509.7	2	4.6012	0.4689
SRLDQELKLIGEYGLR	1891.2	2	4.5693	0.4525
SRLEQEIATYR	1366.5	2	4.1008	0.3034
SRLGDLYEEEMR	1498.6	2	3.2547	0.3461
SRLNATASLEQER	1475.6	2	4.0681	0.3176
SRNPDFLLHIIQR	1609.9	3	3.5339	0.1361
SRNTDEMVELR	1350.5	2	3.175	0.313
SRPAGGSAVPSSGR	1286.4	2	2.7237	0.2815
SRPAHSLPPGEDGRVEPYVDFAEFYR	2993.2	3	3.2837	0.1463
SRPAPSPESIKR	1325.5	2	2.8199	0.1917
SRPFTVAASFQSTSVK	1713.9	2	4.9146	0.4438
SRPQGLTEAEQR	1372.5	2	2.5742	0.1362
SRPTSFADELAAR	1421.5	2	2.4551	0.2228
SRPVDPSVPFDSK	1431.6	2	3.2972	0.2773
SRQELEQHSVDTASTSDAVTFITYVQSLK	3242.5	3	7.4598	0.5596

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SRQELEQHSVDTASTSDAVTFITYVQSLKR	3398.7	3	6.7507	0.4452
SRQPSYVPAPLRK	1499.7	2	2.6248	0.1023
SRSEVDLTR	1063.1	2	2.7198	0.146
SRSGALEPPTSAPPTLALVPGGAAAR	2445.8	3	3.6186	0.1398
SRSGEGEVSGLMR	1365.5	2	2.9942	0.2727
SRSVIEQGGIQTVDQLIKELPELLQR	2951.4	3	5.7037	0.3325
SRTLTAVHDAILEDLVFPSEIVGKR	2768.2	3	4.4977	0.3366
SRTPSASNDDQQE	1435.4	2	3.5084	0.3552
SRVEQEQEAK	1204.3	2	2.912	0.1363
SRVVGNPFDSKTEQGPQVDETQFK	2694.9	3	4.3919	0.4295
SRYDSIDSYLSK	1434.5	2	2.9333	0.2449
SSAEYSVHK	1008.1	2	2.6615	0.1719
SSAFGTLNWFTK	1359.5	2	2.4013	0.1312
SSAIVEIFSK	1081.2	2	2.7528	0.1891
SSALQWLTPEQTSGKEHPYLFSQCQAIHCR	3447.8	3	5.1538	0.2322
SSALREEVQSLREEAEK	1962.1	2	2.7359	0.1636
SSANVEEAFFTLAR	1542.7	2	4.4524	0.2992
SSAPAQEEEEDPLAYYENHTSQIEIVR	3107.2	3	3.68	0.2162
SSAQDPQAVLGALGR	1470.6	2	4.9072	0.4022
SSASAPDVDDPEAFPALA	1760.8	2	2.9654	0.2227
SSASFSTTAVSAR	1272.3	2	2.8465	0.266
SSASSWSEEPVQSNMDISTGHMILSYMEDHLK	3598.9	3	4.3519	0.2623
SSAVDPEPQVK	1157.3	2	3.0059	0.2723
SSAVDPEPQVKLEDVLPLAFTR	2412.7	2	4.9693	0.4888
SSAYESLMEIVK	1357.6	2	3.5844	0.3116
SSDDGFPQIR	1122.2	2	2.8291	0.2206
SSDEEGSQDESLDSK	1613.5	2	4.562	0.3439
SSDPDYLAAVDKWLGVLLPK	2188.5	2	3.2283	0.1885
SSDRLDEAAQR	1248.3	2	2.4704	0.1408
SSEEDKKEEEVK	1437.5	2	3.1556	0.1566
SSEEDKKEEEVKK	1565.7	3	4.133	0.2673
SSEEEKRVTVIK	1405.6	2	3.4808	0.1744
SSEEEKRVTVIKAPHYPGIGPVDESGIPTAIR	3434.8	3	4.5382	0.2699
SSEFFEMLEK	1247.4	2	3.5481	0.2212
SSEHVHSQGR	1124.1	2	3.0111	0.3062
SSEIEQAVQSLDR	1462.5	2	3.1741	0.189

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SSEIEQAVQSLDRNGVDLLMK	2333.6	2	3.9536	0.3595
SSEKVFVSLPTELEDLIPEVEEFYKK	3057.4	3	4.1187	0.1891
SSELRPGEFVVAIGSPFSLQNTVTTGIVSTTQR	3480.9	3	4.9144	0.4241
SSEMGIENVILGMPHR	1771.1	2	2.6257	0.115
SSEMNVLIPTEGGDFNEFPVPEQFK	2813.1	2	4.0819	0.4114
SSEMNVLIPTEGGDFNEFPVPEQFKTLWNGQK	3641.0	3	3.734	0.18
SSENGHIHSTSLQHIK	1775.9	2	3.6103	0.2167
SSENPNEVFR	1179.2	2	2.8088	0.1206
SSEPEHQEALQPVNLSELESIVTERPQFSR	3438.7	3	4.5011	0.3232
SSEPVQHEESIRKPSPEPR	2190.4	2	2.6728	0.1163
SSEQILATLKGHTK	1513.7	2	3.075	0.2772
SSESDHFSYVQLR	1555.6	2	3.2018	0.214
SSFADISNLLQIEPR	1690.9	2	4.2268	0.2097
SSFDEMLPGTHFQR	1652.8	2	3.5597	0.319
SSFDQMVSGTSFQR	1577.7	2	4.0681	0.3624
SSFDWLTGSSTDPLVDHTSPSSDSLLFAHK	3236.4	3	4.1654	0.3089
SSFDWLTGSSTDPLVDHTSPSSDSLLFAHKR	3392.6	3	6.2685	0.5394
SSFFIEPQKPVFPETR	1910.2	3	3.4147	0.2792
SSFHSDPQHWLSR	1584.7	2	2.9188	0.2733
SSFREEDNTYR	1404.4	2	2.4924	0.24
SSFSHYSGLK	1113.2	2	3.2289	0.3317
SSFSHYSGLKHEDK	1622.7	2	3.268	0.1611
SSFSQHAR	920.0	2	2.4394	0.1161
SSFYPDGGDQETAK	1502.5	2	2.7981	0.3134
SSFYVNGLTLGGQK	1471.6	2	4.8158	0.3833
SSGATPVSGPPPPSASSTPAGQPTAVSR	2549.7	3	4.1094	0.3186
SSGFGLEFNSFQHQLR	1855.0	3	3.3172	0.3078
SSGFLSNLLGGH	1189.3	2	2.6364	0.1912
SSGFPVHLLPDIAEPGSVAGR	2107.4	3	3.9459	0.2589
SSGGAYPNIPLSSPLPGVPKPVFATVDGQEKFETK	3617.1	3	4.8824	0.3013
SSGGGYSGDR	942.9	2	2.8627	0.1528
SSGGREDLESSGLQR	1578.6	2	4.4515	0.3578
SSGGSEHSTEGSVSLGDGQLNR	2162.2	3	3.6066	0.1617
SSGIVSLGVGDR	1147.3	2	3.0056	0.1441
SSGLESSEAR	1023.0	2	2.8163	0.1813
SSGLPNIPVQTISR	1469.7	2	3.4184	0.2548

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SSGLTAVWVAR	1147.3	2	2.8225	0.1327
SSGMPTDQESLSSGDAVLQR	2066.2	2	2.5973	0.142
SSGMTLDNISR	1181.3	2	2.4137	0.1522
SSGNSSSSGSGSGSTSAGSSSPGAR	2104.0	2	6.1729	0.5949
SSGPPATFPSSK	1163.3	2	3.2887	0.3525
SSGPPPPSGSSGSEAAAGAGAAAPASQHPATGTGAVQTEAMK	3705.9	3	5.3912	0.3296
SSGPTSLFAVTVAPPGAR	1715.9	3	3.3059	0.2981
SSGPYGGGGQYFAKPR	1629.8	2	3.8999	0.4414
SSGSPYGGGYGSGGGSGGYGSR	1911.9	2	5.2369	0.5742
SSGTASSVAFTPLQGLEIVNPQAAEKK	2732.0	3	3.3922	0.2572
SSGVAPAASPAAPSPGSSGGGGFFSSLSNAVK	2808.0	3	5.1272	0.4545
SSGVPVDGFYTEEVR	1642.7	2	2.9918	0.2564
SSHLKGQAVPASK	1310.5	2	3.5077	0.3603
SSHLPTEVIEKPPAVPVSFEFSDAKDENER	3356.6	3	6.9119	0.5232
SSHSNAYFYGFFK	1555.7	2	3.9846	0.465
SSHSNQTNHKPSPDQIIQPLLELDQNR	3098.3	3	4.7016	0.2799
SSHVTIDTLKGVK	1385.6	2	3.0067	0.3284
SSHYDELLAAEAR	1462.5	2	3.8059	0.3328
SSIAGLLLK	902.1	2	2.8918	0.1643
SSIDSEPALVLGPLK	1526.8	2	3.943	0.4609
SSIFDADEEKSK	1356.4	2	2.6187	0.2025
SSIHISNLEPELR	1495.7	2	2.9455	0.2106
SSIHNFMTHPEFR	1603.8	2	3.565	0.2831
SSILLDVKPWDDETDMAKLEECVR	2794.2	3	5.4295	0.246
SSILQHERPASLYQSSIDR	2188.4	3	4.31	0.3609
SSILQHERPPPLPTTPTPVPR	2321.7	3	5.5224	0.4711
SSIMAFAIGNK	1139.4	2	2.9539	0.1688
SSKAVVHGILMGVPVPFPIPEPDGCKSGINCPIQK	3617.3	3	5.0965	0.3164
SSKDVPLTIKDPAVGFLETISPGYSIHTYLWR	3593.1	3	5.2451	0.3649
SSKEESLPKPK	1230.4	2	2.6385	0.1613
SSKELDFLREENHK	1732.9	2	3.3247	0.1915
SSKELLLQPVTISR	1571.8	2	4.2383	0.3469
SSKGELTTLIHQLQEK	1813.0	2	4.5309	0.445
SSKGELTTLIHQLQEKDK	2056.3	2	4.2869	0.3648
SSKGELTTLIHQLQEKDKLLAAVKEDAAATK	3338.8	3	6.8216	0.4286
SSLDNIEMAYAR	1370.5	2	3.5903	0.1515

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SSLGAPAISAASFLQDLIHR	2055.3	2	4.3721	0.4923
SSLGPVGLDKMLVDDIGDVTITNDGATILK	3059.5	3	4.455	0.2753
SSLGSHQLPR	1082.2	2	2.6272	0.1883
SSLHYKPTPDLR	1414.6	3	3.5168	0.2062
SSLLAENQVLMER	1490.7	2	2.6657	0.3084
SSLLDDLLTESEDMAQR	1924.1	2	3.2897	0.3295
SSLRGLAGEIVGEVR	1543.8	2	2.6792	0.2365
SSLSSAQADFNQLAELDR	1953.1	2	5.4866	0.4842
SSLSVPYVIVPLKTGLQEVEVK	2386.8	3	3.2297	0.4205
SSLTQHSWQSLKDR	1673.8	2	3.4023	0.1041
SSLVSALLGEMEKLEGK	1792.1	2	4.3998	0.435
SSMNVDEAFSSLAR	1514.6	2	2.9067	0.3195
SSNADAEEKLDR	1335.4	2	3.1012	0.3077
SSNLLDLKNPFFR	1551.8	2	3.2753	0.2471
SSPEPVALTESETEYVIR	2008.2	2	4.8464	0.461
SSPEQPIGQGR	1156.2	2	2.5752	0.1078
SSPGLYTSPGQDSLQPTAVSPPYGGDISPVSPSR	3403.7	3	4.4974	0.3281
SSPHGSLGSVVNSLSGLKLDNILSGPK	2665.0	3	3.3813	0.2654
SSPLDNKLNVEDVDSTK	1862.0	2	4.8325	0.5148
SSPLDNKLNVEDVDSTKNRK	2260.4	3	4.1094	0.3371
SSPQFGVTLLTYELLQR	1953.2	2	3.5744	0.3024
SSPSFSSLHYQDAGNYVCETALQEVEGLK	3161.4	3	4.2764	0.2398
SSPSHTISRPIPMPIR	1777.1	2	3.2231	0.1749
SSPSKHQPPPIR	1331.5	2	2.5338	0.205
SSPTDKHTLVK	1213.4	2	2.7411	0.2248
SSPVDLVTATDQKVEK	1717.9	2	4.4375	0.4082
SSPVVIDASTAIDAPSNLR	1914.1	3	4.1872	0.2899
SSPVVNDGVVR	1129.2	2	2.837	0.183
SSPYPTDVAR	1093.2	2	2.677	0.2507
SSQEQGELQGR	1219.2	2	3.5196	0.1367
SSQESGEEAGSQENHPQESK	2146.1	2	4.5808	0.4442
SSQFLAPK	878.0	2	2.738	0.155
SSQGGSLPSEEK	1206.2	2	3.6581	0.3336
SSQHKQDLTEK	1301.4	2	3.4047	0.2159
SSQIGAVVSHQSSVIPDREYLR	2429.7	3	4.6216	0.4603
SSQPLASK	817.9	2	2.5425	0.168

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SSQPLASKQEK	1203.3	2	2.6489	0.3012
SSQPLASKQEKDGTEKR	1890.0	2	4.2014	0.3331
SSQSEALLNITNNGIHFAPLQTFTDEEMMIK	3481.9	3	4.5026	0.2247
SSQSSSQQFSGIGR	1456.5	2	4.2158	0.4401
SSQTSGTNEQSSAIVSAR	1810.9	2	5.2077	0.4604
SSRLEEDDGDVAMSDAQDGPR	2251.3	3	3.8653	0.105
SSRLPDIFEAQIAGLR	1774.0	3	4.997	0.3622
SSRPEFDWQDPLVLEEQLTTDEILIR	3131.4	3	3.6742	0.1787
SSRPEFDWQDPLVLEEQLTTDEILIRDTFR	3651.0	3	3.5696	0.2597
SSSADFGTFNTSQSHQTASAVSK	2346.4	2	5.3777	0.5415
SSSAGGQGSYVPLLR	1479.6	2	2.6882	0.2472
SSSFSDTLEESSPIAAIFDTENLEK	2718.9	3	3.351	0.138
SSSGAEHPEPK	1126.2	2	3.0971	0.1746
SSSGLLEWESK	1223.3	2	3.5576	0.3541
SSSGLLEWESKSDALETLGFLNHYQMK	3072.4	3	4.9319	0.3214
SSSILKGMELSVLDSLNAR	2021.3	3	4.3649	0.2683
SSSMAAGLER	1009.1	2	2.6585	0.1118
SSSNLALALYR	1195.4	2	2.7512	0.1366
SSSPELVTHLK	1198.4	2	2.6808	0.2032
SSSPELVTHLKWDDPYYDIAR	2493.7	3	4.1617	0.2836
SSSPSEILQELGKGSTHPQPGVSPPAAPAAPGPK	3278.6	3	5.1951	0.3529
SSSQTSGSLVSK	1168.2	2	2.9105	0.2838
SSSSGGYGGGYGGVLTASDGLLAGNEK	2462.6	2	5.4463	0.4217
SSSSGHYVSWVK	1324.4	2	2.5746	0.183
SSSSLLASPGHISVKEPTPSIASDISLPIATQELR	3591.0	3	6.2847	0.5259
SSSSQTLTQFDSNIAPADPDTAIVHPVPIR	3166.4	3	4.6227	0.2579
SSSVGSSSSYPISPAVSR	1755.9	2	4.8487	0.4214
SSSVTSIDKESR	1296.4	2	2.7145	0.1326
SSTFNSQEPHNILPLASSQIR	2327.5	3	4.1208	0.2274
SSTPLPTISSSAENTR	1648.8	2	3.2309	0.2879
SSTSEGLLLKIDPLLPKEVKNEESEKEDA	3200.5	3	4.0375	0.2613
SSTTSMTSVPKPLK	1464.7	2	3.2715	0.3285
SSTVGLVTLNDMK	1365.6	2	2.6113	0.2194
SSTVTEAPIAVVTSR	1518.7	2	2.8807	0.1128
SSVAADVISLLLNGDGGVGR	1901.1	3	5.43	0.3397
SSVLENFVGR	1108.2	2	2.7418	0.2401

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SSVLENFVGRDFLPR	1737.0	3	3.6573	0.3528
SSVNSHMTQSTDSR	1537.6	2	3.8798	0.4088
SSVSGIVATVFGATGFLGR	1827.1	2	5.0226	0.5019
SSVSHSVLSEMQVIEQETPVSAK	2473.7	3	3.5077	0.1241
SSVSSRSIFK	1098.2	2	2.5819	0.2714
SSVVGGFVSHYLLEK	1622.8	2	3.6358	0.2774
SSWWTHVEMGPPDPILGVTEAFKR	2742.1	3	5.8835	0.5455
SSYEKLQSSLESEVSVLASK	2172.4	2	3.0467	0.2224
SSYPVMGFEFQVR	1547.8	2	2.708	0.3545
SSYYMIGEQK	1206.4	2	2.635	0.1996
SSYYVVSGNDPAAEEPSR	1929.0	2	5.1321	0.3713
SSYYVVSGNDPAAEEPSRAVLDALLEGK	2939.2	3	4.7682	0.4061
STAEGEAFIQALPGSGTTPLLR	2217.5	2	4.7955	0.3696
STAGDTHLGGEDFDNR	1692.7	2	4.5894	0.4525
STAGDTHLGGEDFDNRMVNHFIAEFK	2910.1	3	4.0274	0.2792
STAISLFYELSENDLNFIK	2205.4	3	6.1325	0.3849
STAISLFYELSENDLNFIKQSK	2548.8	2	4.7112	0.424
STANKYQVFFFGTHETAFLGPK	2491.8	3	5.6736	0.437
STANKYQVFFFGTHETAFLGPKDLFPYEESKEK	3858.3	3	3.6932	0.2777
STANNVEIHIPVPNDADSPK	2119.3	3	3.7275	0.1947
STAPSAAASASASAAASSPAGGGAEALELLEHCGVCR	3330.6	3	5.5919	0.4733
STAQQELDGKPASPTPVIVASHTANKEEK	3035.3	3	6.3996	0.4256
STAYEDYYYHPPPR	1759.9	2	4.0977	0.4502
STDFAPIKEDFGQEKKTDDVEAMSSQPALALDER	3771.1	3	6.2248	0.5058
STDHPKYSDMIVAAIQAEK	2105.4	3	5.6255	0.3422
STDHPKYSDMIVAAIQAEKNR	2375.6	3	6.5116	0.5374
STDLNESR	921.9	2	2.5498	0.1165
STDTFNYATYHTLEEIYDFLDLLVAENPHLVSK	3861.2	3	3.7423	0.2721
STDTTKTHPTIK	1330.5	2	3.1083	0.3322
STDYGIFQINSR	1401.5	2	3.7617	0.1744
STEEARKELQAAGK	1518.7	2	3.6457	0.2591
STEEARKELQAAGKSPEDLER	2345.5	3	5.0023	0.379
STEEPTAPASPQPPNDSR	1881.9	2	3.6259	0.4176
STEEVKPIDENLGQTGK	1846.0	3	3.3627	0.2678
STESLQANVQR	1233.3	2	2.6861	0.2824
STFAGHGR	832.9	2	2.5565	0.3128

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
STFETEHAGQR	1263.3	2	3.1945	0.3634
STFVLDEFKR	1242.4	2	3.1651	0.313
STFVLDEFKRK	1370.6	2	2.9347	0.2242
STGDIAGTVVPETNKEPR	1872.0	2	4.0432	0.3728
STGEAFVQFASQEIAEK	1843.0	2	5.4524	0.4949
STGEAFVQFASQEIAEKALKK	2283.6	3	3.2837	0.2538
STGEALVQGLMGAAVTLK	1747.1	2	5.0144	0.4351
STGEPLGHVPAR	1221.3	2	3.4602	0.4121
STGFTNLGAEGSVFPK	1612.8	2	4.8858	0.3658
STGGAPTFNVTVTK	1380.5	2	3.6187	0.4188
STGGAPTFNVTVTKTDK	1724.9	2	3.9608	0.4132
STGKENKITITNDKGR	1762.9	2	4.2961	0.2424
STGKGIVEFASKPAAR	1619.8	2	2.6107	0.1178
STGLNAVPSQILEGQWAAR	1999.2	2	4.5357	0.4084
STGNFLTLTQAIDKFSADGMR	2274.5	3	4.2548	0.4466
STGPAPAGSTR	1002.1	2	2.4456	0.1846
STGVALSIAVGLLEGTFPNTGAR	2232.5	2	3.6509	0.2646
STGYDPVKLFTK	1356.5	2	3.1707	0.3079
STGYSSQPGAK	1083.1	2	2.4203	0.2726
STHEFLHEVPAASEEIFK	2072.3	2	5.1703	0.4588
STHGLAILGPENPK	1434.6	2	4.6209	0.2791
STHQAAIVSK	1042.2	2	2.6439	0.196
STHTLDLSR	1030.1	1	2.6036	0.2351
STHTLDLSRELSEALGQIFDSQR	2604.8	3	4.4313	0.3616
STHVPVGEDQVQHMELVQDLAQGFNKK	3036.4	3	3.4523	0.2273
STIETALKMEK	1251.5	2	2.5384	0.2669
STIGGQIMYLTGMVDKR	1871.2	2	3.5734	0.3751
STIGVEFATR	1081.2	2	2.8125	0.2748
STIIGESISR	1063.2	2	2.4098	0.1358
STISTELALALR	1275.5	2	3.8276	0.2989
STKDELASLKEQLEEKESEVKR	2577.8	3	4.612	0.3966
STKHWELTAEGEEIAR	1858.0	2	2.7776	0.2502
STKPIVAAINGSCLGGGLEVAISCQYR	2709.1	3	4.0751	0.3065
STLADYSAQKDLEPESDRSAQPLPLKIEELALAK	3729.1	3	5.0807	0.4047
STLEPVEK	903.0	1	1.8486	0.1441
STLEQKPSKPAAPQVPPKKPTPPTK	2654.1	3	4.0974	0.3071

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
STLINSLFLTDLYPER	1883.1	2	5.2181	0.4147
STLINSLFLTDLYSPEYPGPSHR	2608.9	3	4.8394	0.4581
STLITDGSTPINLFNTAFGLLGMGPEGQPLGR	3276.7	3	5.2637	0.6044
STLITDGSTPINLFNTAFGLLGMGPEGQPLGRR	3432.9	3	5.2107	0.44
STLLFGQR	922.1	2	2.8593	0.1753
STLLLLLTGK	1059.3	2	3.4284	0.2099
STLLLYQSPTTGLFPTK	1868.2	2	2.6193	0.1994
STLMDTLFNTKFESDPATHNEPGVR	2809.1	3	4.5978	0.3978
STLNEIYFGK	1172.3	1	3.2414	0.3233
STLNEIYFGKTKDIVNGLR	2169.5	3	4.184	0.266
STLNELVDYITISR	1624.8	2	4.1908	0.3877
STLNPQWNESFTFK	1699.8	2	3.4616	0.2524
STLPDADREREAILAIHKEAQR	2520.8	3	3.2117	0.2046
STLQTLPEIVAK	1300.5	2	3.0457	0.1842
STLQTMESDIYTEVR	1773.9	2	4.5372	0.4585
STLVLHDLLK	1139.4	2	2.9734	0.2585
STLVLHDLLKHTPVDHPDYPLLQDALR	3108.5	3	3.9191	0.1815
STMLELEKQGLEAMEEILTSSEPLDPAEVGDLFYDCVDTEIK	4691.2	3	5.0103	0.3704
STMVGTPYWMAPEVVTR	1926.2	2	3.3374	0.3638
STNGDTFLGGEDFDQALLR	2057.2	2	6.3334	0.5737
STNIAAAASEPHS	1256.3	2	3.2428	0.1079
STNLLAAETASLEEQLQGWGEVMLMADK	3037.4	3	3.7436	0.2096
STNLLAAETASLEEQLQGWGEVMLMADKVLR	3405.9	3	4.2132	0.3066
STNLNCSVIADVRHDGSEPCVDVLFGDGHR	3214.5	3	3.214	0.1555
STNPGISIGDVAK	1259.4	2	3.1203	0.2715
STNVVYQAHHVSR	1498.6	2	4.7798	0.5059
STPAAVGAMEDKSAEHKR	1886.1	2	3.1782	0.2704
STPAEDDSRDSQVK	1535.6	2	3.3162	0.3109
STPAEDDSRDSQVKSEVQQPVHPKPLSPDSR	3418.6	3	5.2851	0.4513
STPAITLESPDIKYPLR	1902.2	2	4.5169	0.5039
STPEYFAER	1100.2	2	2.5484	0.3434
STPKEETVNDPEEAGHR	1897.0	2	4.4818	0.46
STPTAEAEEAGIGDTPSLEDEAAGHVTQAR	3012.1	3	5.8868	0.2134
STQAATQVVLNVPETR	1714.9	2	3.9518	0.4369
STQAPLIIRPDSGNPLDTVLK	2236.6	2	4.4249	0.4441
STQAPLIIRPDSGNPLDTVLKVLEILGK	2989.5	2	4.0475	0.3636

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
STQAPLIIRPDSGNPLDTVLKVLEILGKK	3117.7	3	4.0579	0.2908
STQDEINQAR	1162.2	2	3.4093	0.2546
STQGVTLTDLQEAEKTIGR	2048.2	3	3.3965	0.1588
STQTAEDKEEPLHSIISSTESVQGSTSK	2978.1	3	4.9164	0.315
STRFEEFLQR	1313.4	2	3.0547	0.2266
STSAPQMSPGSSDNQSSSPQPAQQK	2533.6	3	4.9409	0.4495
STSATDTHHVEMAR	1543.6	2	2.4653	0.1521
STSESFIQHIVSLVHHVK	2049.3	2	3.7401	0.329
STSHKPDEIYGMIER	1764.0	3	3.7792	0.2387
STSQGSINSPVYSR	1483.6	2	4.0171	0.3814
STTALHQENNK	1243.3	2	2.8327	0.213
STTELGENLQELRDLTQEMEVHAEKLK	3143.5	3	4.9429	0.3999
STTLDAGNIKLAFNSLLEKAEAR	2463.8	3	3.4526	0.1437
STTLEKEVPVIFIHPLNTGLFR	2512.9	3	4.3147	0.1886
STTNELKSEK	1137.2	2	2.6657	0.1644
STTRAEVDLVVQDLK	1674.9	2	3.8268	0.2021
STTRAEVDLVVQDLKQAVAQLEDQA	2729.0	3	4.5077	0.3506
STTSDIPHMLNQVESK	1788.0	2	4.2935	0.3161
STTTGHLIYK	1121.3	2	3.0757	0.406
STTTSDMIAEVGAAFSK	1716.9	2	3.8007	0.4554
STTTSDMIAEVGAAFSKLFET	2207.4	2	2.6038	0.1315
STTYSLESPKDPVLPAR	1862.1	2	4.1687	0.3777
STVAALLQNLYQPTGGQLLLDGKPLPQYEHR	3422.9	3	4.7501	0.2864
STVASMMHR	1020.2	2	2.7519	0.1947
STVAVNMNDLGSQPHEDREPVDPTTK	2839.0	3	5.1279	0.4032
STVDAEAVHK	1057.1	2	2.5804	0.2131
STVEGIQASVK	1119.3	2	2.6166	0.2376
STVLQQQYNR	1237.3	2	3.2292	0.1501
STVLTPMFVETQASQGTLQTR	2296.6	2	5.9002	0.4575
STVPTDFSSAKIEVSQLLK	2051.3	2	3.9035	0.3136
STVRDIDPQNDLTFLR	1891.1	3	4.0903	0.2917
STWLILHHK	1135.3	2	2.8608	0.1843
STYIKSPPFFENLTLDLQPPK	2436.8	2	2.5961	0.2203
STYNHLSSWLTDAR	1651.8	2	3.8431	0.3804
STYPRPHEYLSPADLPK	1972.2	2	3.7584	0.29
SVAADFIQQGIR	1305.5	2	2.5339	0.1316

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SVAAIHPSLEIPMLIPK	1817.2	3	3.4968	0.2729
SVADGQESTPPTPAPTSGIVGALMEVMQK	2900.3	3	3.7951	0.1716
SVADGQESTPPTPAPTSGIVGALMEVMQKR	3056.5	3	3.7602	0.2462
SVAGKEDNTDTDQEKKEEK	2152.2	3	5.0644	0.238
SVAQQASLTEQR	1318.4	2	3.2834	0.2418
SVASFSIYSPHTGIQEYQDGVPK	2511.7	3	3.5549	0.2064
SVDEVFDEVVQIFDK	1769.9	2	4.8633	0.4443
SVDEVFDEVVQIFDKEG	1956.1	2	5.2517	0.4234
SVDFDSLTVR	1139.2	2	2.4378	0.2099
SVDIHDSIQPR	1267.4	2	2.6208	0.2322
SVDKKVESAKESLK	1548.8	3	3.6228	0.1162
SVDNRPQAPLVSASAVNEEVSK	2298.5	3	3.3685	0.167
SVDNRPQAPLVSASAVNEEVSKIK	2539.8	3	3.9336	0.2573
SVDPDSPAEASGLR	1401.5	2	2.9265	0.1599
SVDPTLALSVYLR	1434.7	2	4.1895	0.393
SVEAAAELSAK	1076.2	2	3.989	0.3665
SVEAAAELSAKDLK	1432.6	2	4.0923	0.3589
SVEAILEESTEKLK	1576.8	2	4.3619	0.2782
SVEDAQDVSLALTQR	1632.8	2	5.2574	0.3969
SVEDRFDQQKNDYDQLQK	2257.4	3	4.0434	0.3018
SVEEELHQR	1127.2	2	2.4589	0.1653
SVEEGKIDGIIDK	1403.6	2	3.6287	0.187
SVEEGKIDGIIDKTIIGDFQK	2306.6	3	4.7007	0.4199
SVEEGKIDGIIDKTIIGDFQKEQK	2692.0	3	6.215	0.4104
SVEEISTLVQK	1233.4	2	2.6614	0.1841
SVEELLEAELLK	1373.6	2	3.9505	0.2445
SVEELLEAELLKVANKEK	2043.3	3	3.2541	0.1649
SVEEPTQPGGTGLSDSR	1717.8	2	4.5117	0.4436
SVEHDKASK	1001.1	2	2.561	0.178
SVEITTDNILEGR	1447.6	2	2.6175	0.2624
SVELDNDDGGGSAAQK	1563.6	2	4.9624	0.337
SVEMHHEALSEVLPGDNVGFNVK	2509.8	2	3.6906	0.1248
SVENLATATTTLTSLAQLLGK	2133.4	2	3.2104	0.1583
SVETDSSTVEHVR	1446.5	2	2.6377	0.2843
SVETLKEMIK	1178.4	2	3.4454	0.1664
SVETLKEMIKSGMNVAR	1894.3	2	4.9137	0.4576

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SVEVNFTESLLR	1394.6	2	3.5107	0.4075
SVEVQGETETIIATK	1605.8	2	3.627	0.3329
SVFALTNGIYPHK	1447.7	2	3.4496	0.346
SVFALTNGIYPHKLVF	1807.1	2	3.6615	0.4095
SVFDIPIFTEEFLNHSK	2024.3	2	3.5082	0.3034
SVFGGLVNYFK	1231.4	2	3.4316	0.3485
SVFILGASGETGR	1294.4	2	3.4934	0.2928
SVFKPFIFGVGVAQAPQVLSPTFGAQDPVR	3161.6	3	6.8856	0.508
SVFKPFIFVPHISQLLDTSSPTFELEDLVK	3436.0	3	4.9906	0.394
SVFVGNIPYEATEEQLKDIFSEVGPVVSFR	3358.7	3	3.7449	0.2889
SVGATNMNEHSSR	1390.5	2	3.2787	0.357
SVGDGETVEFDVVEGEK	1796.9	2	5.0964	0.4753
SVGDGETVEFDVVEGEKGAEAANVTGPDGVPVEGSR	3561.7	3	4.6155	0.4134
SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK	3474.7	3	4.9488	0.2563
SVGELPSTVESLQK	1474.6	2	4.2928	0.3682
SVGELPSTVESLQKVQEQVHTLLSQDQAQAAR	3478.8	3	7.4197	0.5179
SVGGSGGGSFGDNLVTR	1567.6	2	4.5993	0.4259
SVGGSGGGSFGDNLVTRS	1654.7	2	4.7666	0.4049
SVGMIAGGTGITPMLQVIR	1902.3	2	5.272	0.4142
SVGNTIDPVILFQK	1531.8	2	3.6202	0.3475
SVGPDFGKK	935.1	2	2.4414	0.1023
SVGRDEREDITHTYK	1806.9	2	2.5654	0.2236
SVGRDEREDITHTYKYPEGSSEER	2841.9	3	5.2696	0.3012
SVGRDEREDITHTYKYPEGSSEEREAFTR	3446.6	3	3.8283	0.2737
SVGYKPDFVGFEIPDKFVVGYALDYNEYFR	3536.9	3	3.7716	0.2091
SVGYPHPDWIWR	1513.7	2	2.8525	0.2163
SVHELEK	841.9	1	1.9003	0.1195
SVHFPGQAVGTR	1256.4	2	2.4833	0.2393
SVHKVEPITK	1138.3	2	3.0881	0.3114
SVHNGAPAPVSGEKDVVFLLDGSEGVR	2738.0	3	5.3199	0.5278
SVHPYEVAEVIALPVEQGNFPYLQWVR	3142.6	3	6.7258	0.4194
SVHSFAADSEELKQK	1676.8	2	5.2434	0.3861
SVHSLISDFKDPPTAK	1743.0	2	4.1459	0.4687
SVIDYQTHFR	1266.4	2	2.8673	0.2585
SVIEICQEVIKQSNVQILVPPAR	2565.0	3	3.2385	0.1393
SVIEQGGIQTVDQLIK	1729.0	2	4.8836	0.3887

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SVIEQGGIQTVDQLIKELPELLQR	2708.1	3	5.4979	0.4055
SVIGHLQTKGS	1127.3	2	2.5984	0.2155
SVINLLFAAYTGDVSALR	1911.2	2	4.3782	0.3964
SVISHSVTSDMQTIEQESPIMAKPR	2773.1	3	6.0473	0.4592
SVKDLVILLYETALLSSGFSLEDPQTHANR	3318.7	3	3.2963	0.2356
SVKEAEDNIREMLMAR	1893.2	2	2.8165	0.2463
SVKEDSNLTLQEK	1491.6	2	3.9528	0.2852
SVKEDSNLTLQEKK	1619.8	3	3.7629	0.1494
SVKEYVDPNNIFGNR	1752.9	2	3.6291	0.3173
SVKGLVAVITGGASGLGLATAER	2128.5	2	6.4924	0.5306
SVKKPAPPPAPPQATK	1614.9	2	2.4822	0.1581
SVKNQAHSVLKKTLQDQTLVQIFK	2755.2	3	3.7503	0.1552
SVLAETEGILQK	1288.5	2	3.8478	0.3317
SVLALTHEGR	1083.2	2	3.0794	0.2672
SVLAVENLLTLDR	1443.7	2	3.8741	0.2043
SVLDKTKHSVESMITTLDPGMAPYIK	2863.3	3	3.9448	0.2866
SVLEDMEDSVLAVMPPDIAAEAQALRR	2928.3	3	4.2873	0.3124
SVLEKTSVSEK	1207.4	2	2.7636	0.1748
SVLELIPELNEKEEAYNSLMK	2450.8	2	3.4397	0.1456
SVLGEADQKGSLVAPDRLR	2012.3	2	3.4885	0.1345
SVLGQLGITK	1016.2	2	3.449	0.3402
SVLLCGIEAQACILNTTLDLLDR	2475.9	2	3.7974	0.1315
SVLLLAYKPMEGNFEEIAR	2181.5	3	4.1925	0.349
SVLNKESHSPFGLDSFNSTAK	2266.5	3	3.9195	0.1639
SVLRPAVLQAPQPK	1504.8	2	3.1766	0.2186
SVLTGGLDALEFIGK	1520.8	2	3.8071	0.3135
SVLVDFLIGSGLK	1348.6	2	3.8626	0.3876
SVLWWLPVEK	1257.5	2	2.8717	0.1262
SVMLYAAEMIPK	1353.7	2	3.0588	0.1826
SVMTEEYKVPDGMVGFIIGR	2229.6	2	5.3116	0.5038
SVNDQPSGNLPFLKPDDIQYFDKLLVDVDESTLSPEEQKER	4708.1	3	4.611	0.3006
SVNESLNNLFITEEDYQALR	2356.5	2	6.3035	0.5148
SVNEVMEWMNNVMNAQAK	2096.4	2	3.4942	0.1502
SVNFSLTPNEIK	1349.5	2	2.8827	0.2157
SVNGLAFYDWDNTELIR	2014.2	2	4.597	0.4534
SVNGQIESLISPDGSR	1659.8	2	3.7379	0.2164

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SVNPYLQGQR	1162.3	2	2.9262	0.1713
SVNSAGLHTVQR	1269.4	2	3.4306	0.2609
SVNVKPLVTHR	1250.5	2	3.0691	0.2602
SVPEVDPAATMPR	1370.6	2	2.5976	0.1574
SVPHFSDEDKDPE	1502.5	2	3.6871	0.3138
SVPLATAPMAEQR	1371.6	2	3.517	0.4119
SVPLATAPMAEQRTESTPITAVKQPEK	2882.3	3	3.9703	0.2072
SVPRGEAAGAVQELAR	1611.8	2	4.2751	0.3549
SVPTSTVFYPSDGVATEK	1886.0	2	4.5541	0.5186
SVPTSTVFYPSDGVATEKAVELAANTK	2784.1	2	3.818	0.3317
SVPTWLKLTSDDVKEQIYK	2251.6	2	4.4363	0.4521
SVPVSAGGEGETSPYSLEASPLGQLMNMLSHPVIR	3613.1	3	5.3784	0.5128
SVQALIKDFQGTPTFTYK	2045.3	2	3.9187	0.3875
SVQATTENKELK	1348.5	2	3.581	0.2445
SVQLAIEITTNSQEAAAKHEAQRLEQEAR	3223.5	3	4.0289	0.3048
SVQNHNNKSVNESLNNLFITEEDYQALR	3278.5	3	5.5084	0.4736
SVQPQSHKPQPTR	1490.6	2	2.8461	0.2181
SVQSHKDLILQCLDDKDESIR	2443.7	3	3.9565	0.2259
SVQTFADK	896.0	1	2.2289	0.2128
SVQTFADKSKQEALKNDLVEALK	2563.9	3	6.0543	0.4506
SVQTFADKSKQEALKNDLVEALKR	2720.1	3	6.6682	0.4603
SVQTFADKSKQEALKNDLVEALKRK	2848.2	3	4.1976	0.1513
SVQTTLQTDEVK	1349.5	2	3.1243	0.2725
SVREFLEKNYTDEAIETDDLTIK	2731.0	3	3.4542	0.2724
SVRPNLQDKR	1213.4	3	3.8022	0.2506
SVSDDSEKNMISK	1440.6	2	3.4291	0.3116
SVSDNDIRKYEMFAQTLQQSR	2517.8	3	4.4801	0.3144
SVSDYDGK	870.9	1	1.9559	0.1922
SVSDYDGKLSNFK	1460.6	2	3.5099	0.3378
SVSHGSNHTQKPDEQR	1807.9	2	4.3365	0.293
SVSHQTVQQLVLEKEQALADLNSVEK	2895.2	3	5.8985	0.4746
SVSLTGAPESVQK	1303.4	2	3.66	0.2632
SVSQGFCFNILCVGETGLGK	2060.4	2	2.8275	0.1066
SVSSNVASVSPIPAGSK	1587.8	2	4.7255	0.4128
SVSTPSEAGSQDSGDGAVGSR	1951.9	2	4.6971	0.4858
SVSTPSEAGSQDSGDLGPLTR	2062.1	2	4.2653	0.3704

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SVSYPSLLSHITSSLMNHPVIPMANK	2825.3	3	3.2596	0.2521
SVTDSIRDEYAFLQK	1772.9	3	3.3157	0.1608
SVTEQGAELSNEER	1549.6	2	5.4914	0.3748
SVTEQGAELSNEERNLLSVAYK	2438.6	2	4.2715	0.3575
SVTEQGAELSNEERNLLSVAYKNVVGAR	3035.3	3	6.1549	0.3472
SVTGTDVDIVFSK	1368.5	2	3.0593	0.3408
SVTHFDSLAVIDIPGADTLDKLFDHAVSK	3113.5	3	5.5565	0.2871
SVTLEDGKTFIPGQGNNAYVFPGVALGVIAGGIR	3419.9	3	4.6847	0.378
SVTLKDLDVALPIIENYKDR	2303.6	3	4.4711	0.2622
SVTNEDVTQEELGGAK	1677.7	2	4.8036	0.3228
SVTTKKPPLAQKPSVAPR	1906.3	3	4.4537	0.3794
SVTVVEDDEDEDGDDLLHHHHVSGS	2744.7	2	4.8078	0.4747
SVTVVEDDEDEDGDDLLHHHHVSGSR	2900.9	3	5.5609	0.4638
SVVEFLQGYIGVPHGGFPEPFR	2433.7	2	4.3922	0.5044
SVVLMSHLGRPDGVPMPDK	2036.4	2	4.1623	0.2917
SVVLMSHLGRPDGVPMPDKYSLEPVAVELK	3265.8	3	6.9399	0.4255
SVVPGGGAVEAALSIYLENYATSMGSR	2701.0	2	3.5708	0.3772
SVVSGSINTVLGSR	1376.5	2	3.5535	0.2635
SVVTGGVQSVMGSR	1364.6	2	3.7828	0.376
SVYDDQPNAHKK	1402.5	2	2.4614	0.1032
SVYENDVLEQLKQALYGDKKPR	2594.9	3	4.1787	0.4067
SVYGGEFIQQLK	1369.5	2	3.4672	0.2872
SWDIFFR	971.1	2	2.4303	0.2046
SWDTGSPSSANAGYCASLTSCSGFK	2485.6	3	3.2835	0.1069
SWDTGSPSSANAGYCASLTSCSGFKK	2613.8	3	4.0592	0.3023
SWEQKLEEMR	1336.5	2	2.5022	0.2068
SWGIGAPSSVNPGYCVSLTSSTGFQK	2631.9	3	5.3781	0.4275
SWHDIEKDNAR	1371.4	2	2.6737	0.1989
SWHDVQVSSAYKK	1535.7	2	2.4587	0.273
SWHDVQVSSAYVK	1506.6	2	3.7921	0.4021
SWMHTAGVVDANTAAQSGVGLAR	2300.5	3	3.3495	0.1741
SWNETLTSR	1094.2	2	2.8255	0.2386
SWPFNLEEIKDLLPEMR	2118.4	2	3.4306	0.2699
SWSHYTVPAGMTVIQWVSDFSER	2685.0	3	3.6252	0.1621
SWTAADMAAQTTK	1382.5	2	4.4099	0.3933
SWTAADTAAQITQR	1520.6	3	4.3557	0.2532

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SWVNQMESQTGEASKLPYDVTPEQALAHEEVK	3603.9	3	6.6952	0.4773
SYAEIIFGKCGRIGQR	1799.1	2	2.8502	0.1496
SYAVSSSVLHGIEPR	1602.8	2	3.8298	0.4557
SYAVVGVPPDIMGIGPAYAIPVALQK	2628.1	3	3.5548	0.1649
SYCAEIAHNVSSK	1409.6	2	2.5372	0.15
SYDFFRHDNEEAMKIR	2059.3	3	3.5748	0.3015
SYDQVHSGK	1021.1	2	2.4384	0.1896
SYDSLHRPK	1103.2	2	2.8013	0.2313
SYDVPPPPMEPDHPFYSNISK	2418.7	2	4.1168	0.3776
SYDYDLIIIGGGSGGLAAAK	1942.2	2	3.8303	0.3095
SYEALVQHVIEDHER	1826.0	3	3.6319	0.4644
SYEAQDPEIASLSGK	1595.7	2	4.2129	0.3449
SYEAYVLNIVR	1327.5	2	3.7199	0.3036
SYEKEKASLPGVKK	1564.8	2	2.985	0.1455
SYELAGGDLAGLLEALSDMGLEEGVR	2666.9	2	5.0916	0.4601
SYELPDGQVITIGNER	1791.9	3	4.9494	0.4761
SYELPDGQVITIGNERFR	2095.3	2	3.0013	0.2192
SYETLVDFDNHLDDIRNDWTNPEINK	3165.3	3	3.4578	0.1445
SYFSEEGIGYNIIR	1648.8	2	4.1341	0.1185
SYFSSFTDDIISQPMLK	1980.2	2	3.5602	0.2883
SYGPAPGAGHVQEESNLSLQALESR	2598.8	3	5.49	0.4171
SYGPAPGAGHVQEESNLSLQALESRQDDILKR	3467.7	3	3.8961	0.2512
SYHEEFNPPKEPMKDDITGEPLIR	2844.1	3	5.9355	0.4326
SYHEEFNPPKEPMKDDITGEPLIRR	3000.3	3	5.2224	0.4072
SYIQSLPQTPR	1290.5	2	3.1392	0.2008
SYIYSGSHDGHINYWDSETGENDSFAGK	3138.2	3	6.0499	0.4974
SYKVSTSGPR	1082.2	2	2.5604	0.3335
SYLEKQDFDQMLQEIQEVKTPEELETFMLK	3692.2	3	4.0875	0.2022
SYLENPAFMLLDLK	1655.0	2	5.0931	0.4344
SYLFNIMDTPGHVNFSDEVTAGLR	2685.0	3	4.1283	0.3652
SYLNMDAIMEAIKK	1628.0	2	3.6082	0.4446
SYLTEQVNQDLPK	1535.7	2	3.7942	0.3508
SYLTEQVNQDLPKEVLAELEALER	2789.1	3	6.5152	0.5531
SYLTEQVNQDLPKEVLAELEALERR	2945.3	3	4.9653	0.3265
SYLTPVRDEESESQR	1796.9	2	3.2125	0.2191
SYLYFTQFK	1197.4	2	2.7538	0.2602

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
SYLYQLQQEAPHPR	1730.9	2	2.4601	0.1776
SYNDELQFLEK	1386.5	2	3.907	0.292
SYNDELQFLEKINK	1741.9	2	3.7174	0.1669
SYPGSQLDILIDQGKDDQFLLDGQLLPDNFIAACTEK	4083.5	3	5.2262	0.3675
SYQDPSNAQFLESIR	1755.9	2	4.9784	0.4312
SYQEELDKLR	1281.4	2	2.5489	0.1299
SYQFGIIGNDR	1270.4	2	3.5315	0.3069
SYQFWDTQPVPK	1496.6	2	3.7574	0.3247
SYREHIEQQIQTYQR	1980.1	3	4.0967	0.2161
SYSFDEIRK	1145.2	2	2.6899	0.2879
SYSFHQSQHR	1277.3	2	2.6871	0.306
SYSMIVNNLLKPISVEGSSK	2167.5	2	2.9895	0.3779
SYSPYDMLESIR	1461.6	2	3.7222	0.4387
SYSPYDMLESIRK	1589.8	2	3.2258	0.3365
SYSSGGEDGYVR	1277.3	2	3.2876	0.2861
SYSSTLTDMGR	1218.3	2	2.9954	0.3231
SYSVEKSPQDEGLHLLKPLSIPK	2566.9	3	3.6078	0.1121
SYSVGASGSSSR	1145.2	2	2.6145	0.2445
SYTITGLQPGTDYK	1544.7	2	3.473	0.3493
SYVDPSTDER	1169.2	2	2.4233	0.2211
SYVKLPSASAQS	1238.4	2	3.1426	0.2833
SYVSEKDVTSAK	1314.4	2	2.9897	0.3278
SYVTTSTR	915.0	2	2.4297	0.1893
SYVYAEEPNIDIHNFVGTFTR	2473.7	3	3.6243	0.2502
TAAAAAEHSQR	1113.2	2	2.9768	0.1659
TAAAAAEHSQRELDTVTLEDIKEHVK	2864.1	3	6.4568	0.3555
TAAALAPASLTSAR	1301.5	2	3.3168	0.2727
TAAANAAAGAAENAFR	1477.6	2	3.6468	0.2924
TAAANAAAGAAENAFRAP	1645.8	2	4.2085	0.3125
TAAAVAAQSGILDR	1344.5	2	4.6144	0.4474
TAADELEAFLGGGAPGGR	1689.8	2	3.8547	0.3877
TAADVVSPGANSVDSR	1546.6	2	3.4159	0.275
TAAESFK	753.8	1	1.6491	0.1499
TAAFLLPILSQIYSDGPGEALR	2333.7	3	6.4629	0.5451
TAAFLLPILSQIYTDGPGEALK	2319.7	3	5.9188	0.4558
TAAGLMHTFNAHAATDITGFGILGHAQNLAK	3151.5	3	7.4634	0.4635

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TAAGLMHTFNAHAATDITGFGILGHSQNLAK	3167.5	3	4.9502	0.3196
TAAKGEAAAERPGEAAVASSPSK	2157.3	3	6.3428	0.4678
TAAKGEAAAERPGEAAVASSPSKANGQENGHVK	3192.4	3	4.6235	0.2316
TAAMLSSAESFSK	1330.5	2	4.2784	0.3816
TAASGAAGDKDTK	1193.2	2	3.1016	0.3949
TAASGIPYHSEVPVSLKEAVCEVALDYKK	3106.5	3	3.216	0.2114
TAASGVEANSRPLDHAQPPSSLVIDKESEVYK	3397.7	3	6.3036	0.3551
TAATLATHELR	1184.3	2	3.1182	0.2821
TAAVANSMNYLTK	1384.6	2	4.6795	0.4323
TAAYGHFGR	980.1	2	2.6399	0.3744
TAAYVNAIEK	1080.2	2	3.2761	0.2368
TAAYVNAIEKVFK	1454.7	2	4.1056	0.3579
TADDGCLENTPDTAEFSR	1943.0	2	5.4673	0.4672
TADDPSLSLIK	1160.3	2	3.0306	0.2449
TADGIVSHLK	1041.2	2	3.1547	0.3333
TADGIVSHLKK	1169.4	2	3.4614	0.3414
TADKHKDVIINQEGEYIK	2102.3	2	4.7489	0.4494
TADLAPHPEEK	1208.3	2	2.6415	0.2049
TADMDVGQIGFHR	1447.6	2	3.4501	0.4187
TADRQYMEGFNDELEAFKER	2450.6	3	4.7286	0.3448
TAEDAKDFFK	1172.3	2	2.4064	0.1193
TAEDYQALNKDIEAQLQHAGLR	2485.7	3	3.9051	0.2294
TAEELMNFSKGEENLMDAQVK	2385.7	3	5.4305	0.4055
TAEFAPFVVFIAAPTITPGLNEDESLQR	3035.4	3	4.9968	0.4262
TAEFQVAR	922.0	2	2.7708	0.2762
TAEFVPYVVFIEAPDFETLR	2344.6	3	3.8205	0.1764
TAEGQALSEAR	1133.2	2	3.4006	0.1876
TAEHEAAQQDLQSK	1556.6	2	4.6615	0.3572
TAEHFQEAMEESK	1537.6	2	3.9696	0.393
TAEHFQEAMEESKTHFR	2079.2	2	4.9986	0.4559
TAEKTDKEEEGKVEVKDQQSK	2407.6	3	3.8402	0.2037
TAELLSHHQVEIKQEFPR	2163.4	3	3.8864	0.3066
TAELSPFIVFIAPTDQGTQTEALQQLQK	3076.4	2	2.6282	0.1063
TAELSPFIVFIAPTDQGTQTEALQQLQKDSEAIR	3748.1	3	3.7238	0.2879
TAENATSGETLEENEAGD	1838.8	2	5.2941	0.4862
TAEVLANK	846.0	2	2.6112	0.2065

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TAFDDAIAELDTLNEDSYK	2132.2	2	5.4758	0.5015
TAFDDAIAELDTLNEDSYKDSTLIMQLLR	3303.6	3	6.3819	0.5062
TAFDEAIAELDTLNEDSYK	2146.3	2	5.3251	0.5198
TAFDEAIAELDTLNEDSYKDSTLIMQLLR	3317.7	3	4.0644	0.2869
TAFDEAIAELDTLNEESYK	2160.3	2	5.4833	0.4924
TAFDEAIAELDTLNEESYKDSTLIMQLLR	3331.7	3	6.5301	0.5946
TAFDEAIAELDTLSEESYK	2133.3	2	5.74	0.5094
TAFDEAIAELDTLSEESYKDSTLIMQLLR	3304.7	3	6.2892	0.5441
TAFHQEQGHQLLK	1537.7	2	4.2035	0.3331
TAFHQEQGHQLLKK	1665.9	2	4.2329	0.2877
TAFPSLPDTDDHKTDNTGTLPEDVAFR	2962.1	3	3.2663	0.2975
TAGDHPGR	810.8	2	2.4262	0.173
TAGPLESSETEEASQLK	1777.9	2	3.5542	0.3496
TAGPLESSETEEASQLKER	2063.2	2	5.5604	0.435
TAGVKVETTEDLVAK	1561.8	2	4	0.3456
TAGYPNVNIHNFTTSWR	1979.1	2	3.2758	0.3921
TAGYYPNPPLVLSSDETLISK	2266.5	3	5.7498	0.316
TAHETDKSEGGK	1260.3	2	3.3774	0.4232
TAHETDKSEGGKR	1416.5	2	3.3851	0.4062
TAHSSLALFRDDTGVK	1718.9	2	4.9019	0.3983
TAHYGMLFDEYQGLSHLEALEILSNESESK	3413.7	3	3.5674	0.2086
TAIGALKLNIGDLQVTKETIEDVEEMLNNLPGVTSVHSR	4207.8	3	5.4487	0.3712
TAIKEQLDSSNSTIAILQTEKDKLELEITDSK	3563.9	3	4.8768	0.3344
TAIKEQLDSSNSTIAILQTEKDKLELEITDSKK	3692.1	3	5.29	0.3003
TAKDVVENGETADQTLSLMEQLRGEALK	3048.4	3	5.6062	0.4121
TAKEQGIHSLEVLITR	1796.1	2	3.3112	0.3867
TALAEAELEYNPEHVSR	1930.1	2	5.3108	0.5122
TALALAIAQELGSK	1386.6	2	3.714	0.1925
TALAMGADR	906.0	2	2.5298	0.2037
TALAMGADRGIHVEVPPAEAER	2291.6	3	3.7145	0.188
TALDAFGR	850.9	2	2.8811	0.2296
TALDKIEEMEMTNSHLAK	2062.4	3	4.1898	0.1262
TALFEEISR	1066.2	2	2.8963	0.2289
TALGVAELTVTDLFR	1606.8	2	4.4612	0.4507
TALHLATEMEELGLVTHLVTK	2307.7	3	4.6313	0.2772
TALHVAAAEGHVEVVK	1631.9	2	5.1679	0.5005

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TALIHDGLAR	1067.2	1	2.5992	0.3326
TALINSTGEEVAMR	1492.7	2	4.121	0.4185
TALINSTGEEVAMRK	1620.9	2	3.9975	0.3582
TALLDAAGVASLLTTAEVVVTEIPK	2483.9	2	2.5904	0.2824
TALLDAAGVASLLTTAEVVVTEIPKEEK	2870.3	3	5.3541	0.4346
TALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGAMGGMGGGMGGGM	4380.1	3	5.5958	0.3795
TALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGAMGGMGGGMGGGMF	4527.2	3	5.6941	0.4459
TALLPSDSVFAEER	1535.7	2	3.0462	0.1948
TALPAAELGLYSLVLSGALAYAGR	2378.8	2	3.8757	0.3252
TALPAQSAATLPAR	1368.6	2	4.3806	0.4318
TALPTSGSSAGELELLAGEVPAR	2227.5	2	4.7068	0.3802
TALPTSGSSAGELELLAGEVPARSPGAFDMSGVR	3332.7	3	3.4827	0.3247
TALQEEIKSKVDQIQEIVTGNPTVIK	2883.3	3	4.0366	0.23
TALQKEITTR	1161.3	2	3.0261	0.3589
TALTYYLDITNPPR	1638.8	2	4.436	0.3987
TALVANTSNMPVAAR	1516.7	2	5.1162	0.4462
TALVERDDFSSGTSSR	1728.8	2	3.3743	0.1107
TALYNYIFAK	1204.4	2	2.4741	0.1646
TAMKYNLGLDLR	1395.7	3	4.216	0.2332
TAMNVNDLFLAIAK	1521.8	2	3.0525	0.1411
TAMNVNEIFMAIAK	1553.9	2	4.6769	0.3868
TAMSTPHVAEPAENEQDEQDENGAEASADLR	3314.4	3	6.35	0.4177
TANDAVELHIKNVQPSDQGHYK	2465.7	3	3.5819	0.1376
TANDMIHAENMR	1403.6	2	3.6842	0.344
TANKDHLVTAYNHLFETK	2103.3	2	5.6519	0.4424
TANKDHLVTAYNHLFETKR	2259.5	2	5.0449	0.482
TANLYDVETSELVHSLTGHDQELTHCCTHPTQR	3738.0	3	4.4833	0.2716
TAPAVVYIEILDRHPFLGR	2168.5	2	3.4086	0.3845
TAPFDSRFPNQNQTR	1779.9	2	3.2919	0.2778
TAPSTNSSAPAVVGNPGVTEVSPEFLAALPPAIQEEVLAQQR	4245.7	3	4.2434	0.3179
TAPTSTIAPGVVMASSPALPTQPAEEAAR	2823.2	3	4.7639	0.3394
TAPYVVTGSVDQTVK	1565.7	2	4.2999	0.3097
TAQALSSGSGSQETK	1452.5	2	4.7673	0.4847
TAQEKDSLITPHVSR	1682.9	2	4.1878	0.4018
TAQNLSIFLGSFR	1454.7	2	3.3248	0.2651
TAQSGALRDVSEELSR	1719.8	3	3.4922	0.2727

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TASDFITK	883.0	1	2.1535	0.1468
TASDFITKMDYPK	1517.7	2	3.1066	0.1691
TASFSESRADEVAPAKK	1794.9	2	3.8259	0.2082
TASGSSVTSLDGTR	1339.4	2	3.5976	0.4159
TASIKPEVALLDTQDMENMSDDDGWEFVNLGDQQSFGIK	4346.7	3	4.1575	0.2532
TASNVEEAFINTAK	1495.6	2	5.0163	0.4319
TASNVEEAFINTAKEIYEK	2158.4	2	4.8367	0.4626
TASNVEEAFINTAKEIYEKIQEGVFDINNEANGIK	3901.2	3	4.2632	0.2771
TASPNRAGKGVIEQTEK	1787.0	2	2.901	0.2246
TASTNNIAQAR	1147.2	2	3.3601	0.3115
TASTPTPPQTGGGLEPQANGETPQVAVIVRPDDR	3458.7	3	5.0112	0.4133
TATADDKKLQFSLK	1566.8	2	3.7545	0.1817
TATADDKKLQFSLKK	1695.0	2	4.4556	0.2849
TATADDKKLQSSLKK	1634.9	2	4.3309	0.3528
TATALLESPLSATVEDALQSFLK	2406.7	2	4.2268	0.3979
TATANGFQMVTSGVQSK	1727.9	2	5.2601	0.4397
TATEKPGPAEAAR	1299.4	2	2.8935	0.2194
TATESFASDPILYRPVAVALDTK	2466.8	2	4.7759	0.4598
TATESFASDPILYRPVAVALDTKGPEIR	3019.4	3	6.564	0.5646
TATFAQALQFVPETQVSLLDNGLR	2620.9	3	6.196	0.5034
TATGLTHIIETR	1313.5	2	2.8341	0.2308
TATGLTHIIETRK	1441.7	2	3.0575	0.2697
TATLRHDADGQATLLNLLLR	2193.5	2	3.7061	0.3504
TATPEIVDNKDGTVTVR	1817.0	2	3.8625	0.3968
TATPQQAQEVHEK	1467.6	2	3.9306	0.3373
TATPQQAQEVHEKLR	1736.9	2	4.8425	0.4663
TATSLAEGLSLVVSPDSIHSVAPENEGR	2838.1	3	3.9613	0.2751
TATVGGAMMGSTHIYDMSTVMSR	2405.8	3	4.6195	0.4482
TATVYPEPQNKEAFVR	1851.1	2	3.247	0.3883
TAVAHRPGAFK	1155.3	2	3.2488	0.3458
TAVAHRPGAFKAELSK	1683.9	2	3.9653	0.3685
TAVAPSAVNLADPR	1382.5	2	3.2979	0.1877
TAVDGPDLEMLTGQER	1732.9	2	4.1361	0.3628
TAVDSLVAYSVK	1253.4	2	3.2784	0.4051
TAVDSLVAYSVKIETNENNLESAK	2596.8	3	3.5506	0.2414
TAVEHATDEDILAK	1513.6	2	4.7791	0.4419

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TAVETAVLLLR	1186.4	2	3.996	0.2669
TAVFGFETSEAK	1287.4	2	2.6945	0.1392
TAVFGFETSEAKGPDGMALPRPR	2435.7	3	4.0658	0.2431
TAVIDHHNYDISDLGQHTLIVADTENLLK	3247.6	3	7.0285	0.5081
TAVIDHHNYDISDLGQHTLIVADTENLLKAPTIVGK	3914.4	3	6.435	0.5236
TAVLDFIEDYLKR	1583.8	2	4.0173	0.4057
TAVPSPVEAAAASDPAAAR	1752.9	2	3.3167	0.3688
TAVSSELRTEVEENQK	1820.9	2	4.1266	0.1117
TAVSSELRTEVEENQKYFK	2259.5	2	4.0682	0.2609
TAVTTVPSMGIGLVK	1474.8	2	3.7158	0.3286
TAVVVGTITDDVR	1346.5	2	2.9814	0.2156
TAVVVGTITDDVRVQEVPK	2027.3	2	4.475	0.2638
TAVVVGTITDDVRVQEVPKLK	2268.6	2	4.5243	0.2667
TAYFSLDTR	1074.2	2	2.8106	0.3284
TAYGPNGMNK	1053.2	2	2.6364	0.2513
TCEEHQLCVVAVLPHILDTGAAGR	2533.9	3	4.7727	0.2075
TCFVDCLIEQTHPEIR	1905.2	2	3.2403	0.1853
TCVADESAENCDKSLHTLFGDK	2384.6	3	3.6695	0.2402
TCVADESAENCDKSLHTLFGDKLCTVATLR	3242.7	3	5.0849	0.3634
TDAASKPFAEVR	1292.4	2	2.8203	0.2415
TDAAVEMKR	1021.2	2	2.9177	0.2611
TDADSESDNSDNNTIFVQGLGEGVSTDQVGEFFK	3624.7	3	6.3179	0.4956
TDADSESDNSDNNTIFVQGLGEGVSTDQVGEFFKQIGIIK	4277.5	3	6.3299	0.5619
TDAGGEDAILQTR	1347.4	2	3.2968	0.2692
TDAISEEKLREIFGLYGQTTGK	2457.7	3	4.3089	0.3877
TDAPQPDVKEEEEEKEEEKDKGDEEEEGEEKLEEK	4135.2	3	4.8461	0.3791
TDASSASSFLDSDELER	1830.8	2	4.7843	0.1975
TDASSASSFLDSDELERTGIDLGTTGR	2802.9	3	5.3921	0.4841
TDAVDSVVR	962.0	2	3.0714	0.1166
TDDEVVQR	962.0	2	3.1622	0.1695
TDDEVVQREEEAIQLDGLNASQIR	2729.9	3	5.3509	0.3539
TDDGCLENTPDTAEFSR	1871.9	2	5.0843	0.4254
TDDYLDQPCLETVNR	1782.9	2	4.5974	0.359
TDDYLDQPCYETINR	1847.0	2	3.9319	0.3679
TDEEGKDVPDHAVLEMK	1914.1	3	3.7096	0.3106
TDEFQLHTNVNDGTEFGGSIYQK	2601.7	3	4.7387	0.264

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TDEGERKCGGPGCGGLVTVAHNAWQK	2672.0	3	3.9132	0.1053
TDEGIAYR	925.0	2	3.129	0.1697
TDEKVDESGPPAPSKPR	1810.9	3	4.1104	0.4496
TDESGPHSHR	1123.1	2	2.5884	0.2942
TDFKEEPEPGFKR	1580.7	2	2.9751	0.1617
TDGALLVNAMFFKPHWDEK	2220.5	3	3.9422	0.3108
TDGKVFQFLNAK	1368.6	3	3.9693	0.3234
TDGSQKTESSTEGKEQEEK	2099.1	3	4.5316	0.3061
TDIARTEYLSNADER	1754.8	3	4.0702	0.2256
TDIFGVEETAIGKK	1508.7	2	2.4546	0.1291
TDITYPAGFMDVISIDK	1887.1	2	2.4129	0.1418
TDITYPAGFMDVISIDKTGENFR	2591.9	2	3.8353	0.3877
TDKAEVVNGYEAK	1424.5	2	3.5458	0.3222
TDKSSASAPDVDDPEAFPALA	2105.2	2	4.3356	0.4164
TDKTLVLLMGK	1219.5	3	3.8441	0.3544
TDKTMTELEIDMNQR	1826.0	2	3.6915	0.2867
TDKVFEVMLATDR	1525.8	2	3.4304	0.2949
TDLAAVPASR	1001.1	2	2.8029	0.1468
TDLADKR	818.9	2	2.5884	0.1104
TDLEKDIISDTSGDFR	1812.9	2	4.6486	0.4314
TDLEKDIISDTSGDFRK	1941.1	3	5.8574	0.4739
TDLEMQIEGLKEELAYLK	2124.4	2	5.1381	0.3535
TDLEMQIEGLKEELAYLKK	2252.6	2	5.7378	0.4745
TDLEMQIEGLKEELAYLKKNHEEEISTLR	3461.9	3	6.3518	0.4684
TDLEMQIEGLKEELAYLRK	2280.6	3	5.1052	0.3897
TDLKGDDLEEGVTSEEFDKFLEER	2802.9	3	4.9382	0.5308
TDLKQGLNGVPILSEEELSLLDEFYK	2952.3	3	3.9566	0.1174
TDLLLEPYNK	1206.4	2	3.3728	0.1773
TDLNPDNLQGGDDLDPNYVLSSR	2519.6	2	4.8921	0.4856
TDMDQIITSK	1152.3	2	3.3798	0.2609
TDMDQIITSKEHLASK	1818.0	2	2.7931	0.2557
TDMIQALGGVEGILEHTLFK	2173.5	2	4.7537	0.4481
TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHKTPASPVVHIR	4041.1	3	4.8442	0.4435
TDPHLCDFLETHFLDEEVK	2289.5	2	4.5833	0.3943
TDPSILGGMIVR	1259.5	2	3.2779	0.3218
TDQAQKAEGAGDAK	1390.4	2	4.1601	0.3626

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TDQVIQSLIALVNDPQPEHPLR	2484.8	2	5.6673	0.4093
TDQVIQSLIALVNDPQPEHPLRADLAEEYSK	3491.8	3	7.0239	0.2288
TDQVIQSLIALVNDPQPEHPLRADLAEEYSKDR	3763.1	3	4.5984	0.1551
TDSSPNQAR	976.0	2	2.5086	0.1309
TDTESELDLISR	1379.5	2	3.6187	0.2439
TDTGRGNGPLPLGGSGLMEEMSALLAR	2702.1	3	6.0758	0.3962
TDTGVSLQTYDDLLAK	1740.9	2	4.2979	0.3077
TDTLEDLFPTTK	1381.5	2	3.8526	0.3496
TDTLEDLFPTTKIPNPR	1959.2	3	4.1881	0.3512
TDTSHHDQDHPTFNK	1780.8	2	3.4774	0.4102
TDVAESEKEGLLTR	1548.7	2	3.7346	0.3577
TDVNKIEEFLEEK	1594.7	2	2.6216	0.1685
TDVNKIEEFLEEVLCPPK	2104.4	2	2.9909	0.2087
TDYNASVSVPDSSGPER	1781.8	2	4.8596	0.5121
TDYVASSIQR	1140.2	2	3.932	0.4573
TEADAEKTFEEK	1398.5	2	3.0936	0.2317
TEADAEKTFEEKQGTEIDGR	2255.3	3	3.7013	0.1968
TEAHKEIHSQQVK	1535.7	3	4.1262	0.4054
TEAPSATGQASSLLGGR	1603.7	2	3.8059	0.3837
TEAVASSLYDILAR	1509.7	2	3.2776	0.2381
TEDGKIYQR	1110.2	2	2.9157	0.2633
TEDGKVEKHYLFYDGESVSGK	2389.6	3	4.5502	0.3977
TEDKNSAGHKPSSNR	1628.7	2	2.5344	0.1433
TEDSGLQTQVIAAATQCALSTSQLVACTK	2940.3	3	3.251	0.1847
TEDSIRDYEDGMEVDTTPTVAGQFEDADVDH	3459.5	3	5.2624	0.2936
TEEDLKKGHQK	1313.4	2	3.1732	0.2786
TEEGPTLSYGR	1210.3	2	3.1656	0.2508
TEEIHENVISPSDLSDIKGSVLHSR	2764.0	3	5.2926	0.3665
TEELAQAYDAFTLAPASTSR	2143.3	2	2.4619	0.1262
TEELNREVAGHTEQLQMSR	2229.4	3	5.1792	0.4301
TEEQGIPRPLHPPPPPPVQPPQHPR	2800.2	3	4.3852	0.314
TEEREQQLQSTLQQAQGFHSEIEDFLLELTR	3706.0	3	4.1618	0.3013
TEETLFEIQGIDPIASAIQNLK	2431.7	3	3.4658	0.1775
TEFLSFMNTELAAFTK	1851.1	2	5.4349	0.4771
TEGAEKKQQMAR	1377.6	2	3.2285	0.2031
TEGDEEAEEEQEENLEASGDYK	2502.4	2	5.5223	0.4321

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TEGLSVLSQAMAVIK	1547.8	2	2.4045	0.2675
TEGNIDDSLIGGNASAEGPEGEGTESTVITGVDIVMNHHLQETSFTK	4860.2	3	5.406	0.3934
TEHINIHQLR	1261.4	2	2.966	0.2842
TEIDKPSQMQVTDVQDNSISVK	2463.7	3	4.1115	0.1968
TEILSLEKPLLLHTGMGR	2009.4	3	4.3009	0.3348
TEIQQQSALSLLNGTFDFQNDFLR	2787.0	3	5.2524	0.3221
TEISEMNR	980.1	2	2.6073	0.2255
TEKEESTEVLK	1293.4	2	2.6512	0.203
TEKETIQKDLDAK	1519.7	2	4.0423	0.3022
TEKHESQKDYVK	1492.6	2	3.9436	0.3367
TEKQLEAIDQLHLEYAK	2030.3	3	3.3234	0.2032
TEKYEHKSEVK	1378.5	2	3.478	0.2417
TEKYVDTPFGKPSDALILGK	2180.5	3	3.5742	0.1792
TELADKVTK	1005.1	2	2.848	0.1423
TELADKVTKLQVELDNVTGLLSQSDSK	2933.3	3	5.5276	0.4503
TELDAHLENLLSK	1483.6	2	2.478	0.2938
TELENKLQQQLTQAAQELAAEKEK	2743.0	3	5.6366	0.4446
TELHGQLISVEK	1354.5	2	3.0293	0.3154
TELHLNHLAENNVFGIVPLAKPEEK	2814.2	3	4.5858	0.2959
TELISVSEVHPSR	1454.6	2	3.0803	0.1575
TELLPGDRDNLAIQTR	1813.0	2	4.0212	0.2748
TELLQRPGIEDVAVLKK	1910.2	3	3.8681	0.2459
TELPQFVSYFQQR	1643.8	2	3.6006	0.3563
TELRPGETLNVNFLLR	1873.1	3	5.2768	0.4095
TELSPSFINPNPLEWFASEEPTEESEKPLTQSGGAPPPPGGK	4451.8	3	4.1919	0.2279
TELTPAYF	942.0	1	1.6583	0.2025
TEMDWVLK	1022.2	2	2.5023	0.1997
TEMEDLMSSKDDVGK	1685.9	2	4.064	0.4244
TEMEDLMSSKDDVGKSVHELEK	2508.8	3	4.7919	0.3473
TEMSEVLTEILR	1421.6	2	3.2144	0.2363
TENLLGSYFPK	1269.4	2	3.8466	0.2697
TENNDHINLK	1198.3	2	3.3316	0.2809
TENPGDASDLQGR	1360.4	2	2.9123	0.121
TENPLILIDEVDKIGR	1826.1	2	3.1612	0.2155
TENVFVDEPLIHATTYIPLMDNADSSPVVDKR	3589.0	3	4.8835	0.3254
TEPMAWNETADLGLDIGAQGEPLGYRQDDPSYR	3667.9	3	3.7009	0.289

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TEPTAQQNLALQLAEK	1756.0	2	4.2385	0.3909
TEPTAQQNLALQLAEKLGSLVENNER	2868.1	3	4.3116	0.3691
TEPVPDQDELDQLSK	1714.8	2	3.4002	0.3963
TEQGPQVDETQFK	1507.6	2	3.979	0.3938
TEQGPQVDETQFKK	1635.8	2	3.423	0.3916
TEQKEPKPLEK	1327.5	2	3.3626	0.1731
TEQTEDLKR	1120.2	2	2.5316	0.1602
TERPVNSAALSPNYDHVVLGGGQEAMDVTTTSTR	3575.9	3	7.4325	0.3097
TESSTEGKEQEEK	1482.5	2	3.3396	0.2963
TESTLNALLQR	1246.4	2	3.0281	0.1294
TESTPITAVKQPEK	1529.7	2	3.5172	0.3021
TESTPITAVKQPEKVAATRQEIFQEQLAAVPEFR	3815.3	3	5.7958	0.4352
TETEKQHMNTIK	1460.6	2	2.8607	0.2611
TETIRPASVYTK	1366.5	2	2.854	0.2053
TETQEKNPLPSK	1372.5	2	3.6616	0.2599
TETQEKNPLPSKETIEQEK	2230.4	3	4.9658	0.4051
TETQEKNPLPSKETIEQEKQAGES	2702.9	3	5.165	0.3883
TETQEKNTLPTK	1390.5	2	3.4697	0.2111
TETQEKNTLPTKETIEQEK	2248.4	3	3.7026	0.2205
TETQEKNTLPTKETIEQEKR	2404.6	3	5.452	0.4388
TETQEKNTLPTKETIEQEKRSEIS	2821.0	3	5.7825	0.3369
TETVEEPMEEEEAAKEEKEESDDEAAVEEEEEEKKPK	4311.4	3	5.9431	0.2291
TEVALAKDMESPTKLDVTLAK	2261.6	3	3.7983	0.2388
TEWLDGK	848.9	2	2.4007	0.1399
TEWLDGKHVVFGK	1516.7	2	4.1066	0.419
TEYLSNADER	1198.2	2	2.8275	0.2994
TEYQATHGSR	1150.2	2	2.8837	0.3464
TFAGNTPLHLAAGLGYPTLTR	2172.5	3	5.3044	0.4082
TFAPEEISAMVLTK	1537.8	2	4.9184	0.3874
TFDEIASGFR	1143.2	2	3	0.4295
TFDMHSLESSLIDIMR	1896.2	2	3.3282	0.3667
TFDQLTPDESKER	1566.7	2	3.7752	0.4063
TFDQLTPEESKER	1580.7	2	3.534	0.2929
TFDSIVMDPK	1153.3	2	3.3511	0.3704
TFEEKLTPLLSVR	1533.8	2	4.2091	0.3239
TFEELKKHEDSAIPR	1801.0	2	3.7023	0.4203

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TFEGIDPK	907.0	2	2.7177	0.2471
TFEGVDPQTTSMR	1469.6	2	3.0758	0.3467
TFEHVTSEIGAEEAEEVGVEHLLR	2682.9	3	6.1109	0.53
TFEINPR	877.0	1	2.6086	0.159
TFEMSDFIVDTR	1461.6	2	3.459	0.3203
TFESLVDFSK	1173.3	2	3.9004	0.3425
TFFIHFQQQ	1196.3	2	2.6484	0.1765
TFFLEALR	997.2	2	3.0695	0.2215
TFFPEEISSMVLTK	1629.9	2	3.2559	0.3109
TFFSFPAVVAPFK	1458.7	2	4.0576	0.4703
TFGETHPFTK	1165.3	2	3.0554	0.3295
TFHETLDCCGSSTLTALTTSVLK	2429.8	2	4.9425	0.4085
TFHFNTVEEVHSR	1603.7	2	4.6137	0.4705
TFHGAGLVVPVDKNDVGYRELPETDADLKR	3313.7	3	4.873	0.2822
TFHHVYSGKDLIAQAR	1844.1	3	3.745	0.3122
TFHIFYQLLSGAGEHLK	1962.2	2	5.2571	0.3818
TFHIFYYLLSGAGEHLK	1997.3	2	6.1581	0.4698
TFIAIKPDGVQR	1345.6	2	3.1425	0.2045
TFIGPGGNMPGYLRPETAQGIFLNFK	2827.3	3	3.6842	0.2781
TFIGPGGNMPGYLRPETAQGIFLNFKR	2983.4	3	3.2725	0.215
TFIIGELHPDDRPK	1638.8	2	4.3196	0.3422
TFKEFLLSLDDSVDETEAVKR	2443.7	3	5.6552	0.4638
TFKIPDKQYVLTALAAR	1936.3	3	3.5802	0.203
TFLEGFRLPGEAQK	1593.8	2	3.3409	0.2075
TFLETSTDTAVTNEWEKR	2129.3	2	2.8463	0.2994
TFLLEYHNR	1193.3	2	2.8243	0.2304
TFLQDLAR	964.1	2	2.5085	0.1093
TFLRPSPEDEAIYGPNTK	2036.2	2	4.3068	0.3877
TFLTLSLQDMASR	1483.7	2	4.1823	0.3853
TFLVWVNEEDHLR	1658.8	2	4.1063	0.3624
TFNIKNDFTEEEEAQVR	2071.2	3	4.1467	0.2964
TFNIKNDFTEEEEAQVRK	2199.4	3	3.7043	0.223
TFNKLAEFGAEFK	1502.7	2	2.615	0.2088
TFNLEKQNHTPR	1485.6	2	3.2437	0.4026
TFNLPLLMLGGGGYTIR	1824.2	2	4.5611	0.4347
TFNLTAGSLESTEPIYVYK	2134.4	2	5.502	0.6133

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TFNQVEIKPEMIGHYLGEFSITYKPVK	3170.7	3	6.2435	0.4619
TFNTSTGGLLLPSDTK	1652.8	2	4.3816	0.3625
TFNTSTGGLLLPSDTKR	1809.0	2	4.3795	0.4804
TFNVDMYEEIHR	1554.7	2	3.2609	0.3477
TFPNHYSIVTGLYEESHGIVANSMYDAVTK	3345.7	3	5.162	0.4452
TFPNHYSIVTGLYEESHGIVANSMYDAVTKK	3473.9	3	4.0155	0.2638
TFPTINIEPDIKR	1544.8	2	3.1863	0.3413
TFQLQLLSPSSSIVPAFNTGTITQVIK	2892.3	3	6.6989	0.4078
TFRLNEIDKESQKPFEVKGPLPVHTK	3039.5	3	3.7296	0.2291
TFRPPYYHR	1237.4	3	3.7927	0.3466
TFSFAIPLIEK	1266.5	2	2.4085	0.2437
TFSFAIPLIEKLHGELQDR	2215.5	2	2.5317	0.1175
TFSGQTHGFVHR	1374.5	2	3.4985	0.5139
TFSHELSDFGLESTAGEIPVVAIR	2576.8	2	5.4011	0.4479
TFSQSSHLVQHR	1427.6	2	3.5413	0.3353
TFSVWYVPEVTGTHK	1752.0	2	2.5455	0.1288
TFSYAGFEMQPK	1406.6	2	3.61	0.4399
TFTAWCNSHLR	1336.5	2	2.735	0.2831
TFTDCFNCLPIAAIVDEK	2001.3	2	3.5011	0.1068
TFTDHMLMVEWNDKGWGQPR	2449.8	3	5.3082	0.352
TFTEMDSHEEK	1354.4	2	2.6319	0.2557
TFTEMDSHEEKVFR	1756.9	2	4.3328	0.4561
TFTGEHVVALMPEVGSLQHAR	2280.6	3	3.4904	0.2755
TFTTQETITNAETAK	1656.8	2	4.4963	0.4611
TFTTQETITNAETAKEWFLQAAK	2630.9	2	3.9905	0.4086
TFTTQETITNAETAKEWFLQAAKDPSAVAK	3299.6	3	6.0789	0.4859
TFVAGIKEDTEEHHLR	1883.1	2	4.2633	0.3002
TFVEESIYNEFLER	1776.9	2	3.2972	0.2656
TFVHVVPAKPEGTFK	1657.9	3	3.8759	0.4171
TFVNITPAEVGVLVGK	1644.9	2	5.5268	0.4566
TFVNITPAEVGVLVGKDR	1916.2	2	4.728	0.4205
TFVQEDIYDEFVER	1790.9	2	5.103	0.4882
TFYGLHQDFPSVVLVGLGK	2078.4	2	5.0999	0.5171
TFYGLHQDFPSVVLVGLGKK	2206.6	3	5.7366	0.509
TFYNQAIMSSK	1290.5	2	2.5614	0.3281
TGAAPIIDVVR	1112.3	2	2.8135	0.3364

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TGAEGAVLDEAK	1161.2	2	3.1157	0.2679
TGAEGAVLDEAKNINK	1630.8	2	4.2568	0.2818
TGAFSIPVIQIVYETLKDQQEGK	2565.9	2	3.4009	0.3107
TGAFSIPVIQIVYETLKDQQEGKK	2694.1	2	2.8985	0.1725
TGAHLELSLAK	1140.3	2	2.8749	0.2859
TGAIVDVPVGEELLGR	1625.8	3	5.1518	0.5087
TGAIVDVPVGEELLGRVVDALGNAIDGK	2779.1	3	3.8669	0.2782
TGAIVDVPVGEELLGRVVDALGNAIDGKGPIGSK	3318.8	3	6.1581	0.5763
TGAIVDVPVGEELLGRVVDALGNAIDGKGPIGSKTR	3576.1	3	4.0597	0.2561
TGALEGPEVDGFVK	1419.6	2	3.6063	0.2786
TGALEGPEVDGFVKDMMELVQPSISGVDLDK	3278.7	3	4.6256	0.2574
TGALEGPEVDGFVKDMMELVQPSISGVDLDKFR	3582.1	3	6.4175	0.5017
TGALLLQGFIQDR	1432.6	2	4.3155	0.3513
TGAQELLR	888.0	2	2.9218	0.2055
TGASFQQAQEEFSQGIFSSR	2206.3	3	4.4994	0.4343
TGDDYIAIGADEEELGSQIEEAIYQEIR	3129.3	3	5.4315	0.511
TGDEEMLKDK	1166.3	2	2.7618	0.263
TGDFQLHTNVNDGTEFGGSIYQK	2529.7	3	6.0543	0.5542
TGDLLEVQQPVDLGALR	1825.1	2	5.3115	0.3984
TGDPNMGDSAVPTHWEPYTTENSGYLEITKK	3440.7	3	4.4198	0.264
TGDTGMLPANYVEAI	1552.7	2	2.5591	0.1245
TGEAIVDAALSALR	1387.6	2	4.7973	0.3399
TGEAQIHAHLVRPYVGIHLR	2268.6	3	3.5214	0.3303
TGEAYVQFEEPEMANQALLK	2269.5	2	3.6983	0.2659
TGEEDKKINEELESQYQQSMDSK	2717.9	3	5.5385	0.4435
TGEEKYVEESK	1299.4	2	3.3161	0.3005
TGEGFYKYK	1093.2	2	2.8667	0.3368
TGEKPNGSVEPER	1400.5	2	4.5354	0.2502
TGEKPNGSVEPERELDLPVDLDDISEADLDHPDLFQNR	4277.5	3	4.9149	0.3802
TGEMSGPVFTDSGIHIILR	2031.3	3	4.7914	0.3779
TGEMSGPVFTDSGIHIILRTE	2261.5	2	3.8886	0.3318
TGENVEDAFLEAAK	1494.6	2	4.0031	0.3226
TGENVEDAFLEAAKK	1622.8	2	4.6226	0.3898
TGEVLDTK	862.9	1	2.625	0.1482
TGEVVVTSKK	1048.2	2	2.776	0.1765
TGFAVIHDAAR	1158.3	2	3.1795	0.3187

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TGFGFTNVTAHQKWKFSR	2113.4	2	2.8908	0.1192
TGFLEIDEHMR	1348.5	2	3.0169	0.2454
TGGADQSLQQGEGSK	1463.5	2	4.1556	0.4373
TGGADQSLQQGEGSKK	1591.7	2	3.9728	0.3187
TGGAFSNALSSLNVLRPGEIPDAAFIHAAR	3054.4	3	4.3955	0.2749
TGGFGAAPVFGSPPTFGGSPGFGGVPAFGSAPAFTSPLGSTGGK	3958.3	3	3.3886	0.2355
TGGKEAASGTTPQK	1333.4	2	3.6249	0.3425
TGGLEIDSDFGGFR	1471.6	2	3.8761	0.2597
TGGMAFHSYFMEAIAPPLLQELKK	2681.2	3	4.0041	0.1349
TGGTVSDQALLFGDDDAGEGPSSLIR	2579.7	2	3.2312	0.2949
TGGVQTVTLIPGDGIGPEISAAVMK	2412.8	3	5.2679	0.3936
TGHIAAGTSTNGIK	1328.5	2	3.3735	0.4237
TGHIAAGTSTNGIKFK	1603.8	3	3.2388	0.1944
TGHSLLHTLYGR	1355.5	2	3.8685	0.4062
TGIDLGTTGR	991.1	2	2.8936	0.1625
TGIKNGVHFLQLELINGR	2010.3	3	3.4995	0.1355
TGISDVFAK	938.1	2	2.7916	0.1664
TGISDVFAKNDLAVVDVR	1920.2	2	5.2466	0.4557
TGISHGHTVYVVHDGFEGLAK	2225.4	3	5.6007	0.5481
TGIYEEK	839.9	1	1.7748	0.1459
TGIYEEKHAK	1176.3	2	2.698	0.2636
TGKGQPSNKEDVDDLVSQLR	2187.4	3	3.7425	0.2235
TGKIPVTDEEQTNVPYIYAIGDILEDKVELTPVAIQAGR	4258.8	3	6.3255	0.5183
TGKLQQEEVQK	1288.4	2	2.5022	0.1369
TGKLQQEEVQKK	1416.6	3	4.5985	0.2982
TGKPLSVELGPGIMGAIFDGIQRPLSDISSQTQSIYIPR	4144.7	3	6.6156	0.4989
TGKPMINLYTDKDTGKPK	2008.3	3	4.0635	0.2707
TGKQEEAFTLAQEVAALEPTDDNSLQALTILYR	3638.0	3	5.1154	0.2735
TGKSIEQLEKELLNGQK	1916.2	2	5.0505	0.2965
TGKSIEQLEKELLNGQKLQGPETAR	2769.1	3	4.5174	0.2677
TGKTIEELEKEMLNGQKLQGPQTSAEVYR	3279.7	3	5.4182	0.4193
TGLEDPERYLFVDR	1710.9	3	3.3119	0.2184
TGLIDYNQLALTAR	1549.8	2	4.1934	0.3871
TGLIKGSGTAEVELK	1503.7	2	3.0314	0.1975
TGLIKGSGTAEVELKK	1631.9	2	4.3885	0.3766
TGLKELEFLK	1178.4	2	2.4697	0.1381

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TGLLATLTR	946.1	2	2.6681	0.1911
TGLQAGLTIDEFAPR	1589.8	2	2.7119	0.2185
TGLSQLHNALNDVKDIQQSLADVSKDWR	3153.5	3	4.0463	0.3246
TGLVEFAR	893.0	2	2.8386	0.2405
TGLYNYYDDEKEK	1638.7	2	3.5877	0.224
TGMILLAGEITSR	1362.6	2	3.235	0.348
TGNFQVTELGR	1222.3	2	2.6686	0.3176
TGNKYNVYPTYDFACPIVDSIEGVTHALR	3245.6	3	4.7133	0.3069
TGNQHFGYLYGR	1413.5	2	3.6252	0.3364
TGNSEKETALPSTK	1463.6	2	4.4892	0.4283
TGPAATTLPDGAAAESLVESSEVAVIGFFK	2937.2	3	5.8147	0.5026
TGPAATTLPDGAAAESLVESSEVAVIGFFKDVESDSAK	3769.1	3	3.7486	0.3345
TGPDPASAPGR	1026.1	2	2.4859	0.2176
TGPNLHGLFGR	1169.3	2	3.2754	0.4128
TGPNLHGLFGRK	1297.5	2	3.2743	0.3307
TGPSGHNIR	939.0	2	2.4553	0.3106
TGPVTLHTQTAIHFAEQIAK	2164.4	2	4.2446	0.2613
TGQAAELGGLLK	1158.3	2	3.0702	0.2525
TGQAAELGGLLKYVRPFLNSISK	2463.9	3	3.284	0.2642
TGQAPGYSYTAANK	1429.5	2	4.4042	0.3829
TGQEIPVNVR	1113.2	2	3.3432	0.2974
TGQEVVFVAEPDNK	1533.7	2	3.6857	0.201
TGQEVVFVAEPDNKNVYK	2038.2	2	3.0574	0.1187
TGQEYKPGNPPAEIGQNISSNSSASILESK	3105.3	3	5.3152	0.3558
TGQIKEVER	1060.2	2	2.8727	0.1634
TGQPMIHIYLDKETGKPK	2057.4	2	5.0755	0.4206
TGQPMINLYTDR	1409.6	2	2.4998	0.2023
TGQPMINLYTDRETGK	1825.0	2	4.0993	0.3752
TGRLPEAAFLAR	1302.5	3	4.2158	0.2399
TGSAVAPVHPPNR	1303.5	2	3.2826	0.1984
TGSESSQTGTSTTSSR	1574.5	2	4.2571	0.427
TGSGGVASSSESNR	1296.3	2	3.1515	0.4476
TGSHSEPQAR	1070.1	2	2.5252	0.1293
TGSNISGASSDISLDEQYKHQLEETKK	2967.1	3	3.5871	0.1611
TGSPGSPGAGGVQSTAK	1459.5	2	3.6663	0.3514
TGSPGSPGAGGVQSTAKK	1587.7	2	2.9746	0.3523

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TGSQGQCTQVR	1165.3	2	3.6488	0.2812
TGSSAQEAASGVALGEAPDHSYESLR	2591.7	2	5.2878	0.4557
TGSSAQEAASGVALGEAPDHSYESLRVTSAQK	3206.4	3	6.1464	0.3917
TGSSAQEEASGVALGEAPDHSYESLR	2649.7	3	5.6232	0.364
TGTAEMSSILEER	1424.6	2	3.7962	0.3769
TGTAYTFFTPNNIK	1575.7	2	4.151	0.4066
TGTAYTFFTPNNIKQVSDLISVLR	2687.0	3	3.4056	0.2273
TGTDKTLVKEVVQNFAK	1879.1	3	4.0526	0.3674
TGTITTFEHAHNMR	1616.8	2	4.3945	0.4892
TGTQYLLR	952.1	2	2.6203	0.2807
TGTYRQLFHPEQLITGKEDAANNYAR	2995.3	3	4.8699	0.2918
TGVAVNKPAEFTVDAK	1647.9	2	4.1153	0.2958
TGVELGKPTHFTVNAK	1699.9	2	4.2998	0.3718
TGVHHYSGNNIELGTACGK	1959.1	2	5.1687	0.4578
TGVIEHEHPVNK	1360.5	2	3.2741	0.1951
TGVKDASDQNFDYMFK	1867.0	2	3.1035	0.145
TGVVKEGDQIVGATIYFDNLQSGEVTQLLNTMGHHTVGLK	4272.8	3	3.4798	0.2624
TGYESGEYEMLGEGLGVKETPQQK	2631.9	3	4.8442	0.3508
TGYSDPEPESPPAPGR	1657.7	2	3.2171	0.1664
TGYSMVQENGQR	1370.5	2	3.5951	0.3785
TGYTLDVTTGQR	1312.4	2	3.2686	0.3034
TGYTLDVTTGQRK	1440.6	2	3.3889	0.1381
TGYTPDEKLR	1180.3	2	2.6396	0.1948
TGYTQASQNIR	1239.3	2	2.8583	0.184
THAAEDIVYTLQLEDR	1875.0	2	3.1092	0.1854
THAVLVALKR	1108.4	2	3.6186	0.366
THDMFVADNGKPVPLDEESHK	2367.6	3	3.4775	0.1747
THEDIEAQIR	1212.3	2	3.3172	0.3278
THEDIEAQIREIQGK	1767.9	2	4.3642	0.377
THEDIEAQIREIQGKK	1896.1	2	4.6388	0.357
THETFHEEEEDMDSYQDRDLER	2812.8	3	3.4903	0.3041
THETLSHAGQK	1209.3	2	2.5576	0.2481
THFEYEKESPYGLSFNKGEVFR	2665.9	3	4.8615	0.4817
THFGGGK	703.8	1	1.7447	0.1162
THFGGGKTTGFGMIYDSLDYAK	2367.6	2	5.2081	0.5177
THFTVR	760.9	1	1.6042	0.1504

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
THGSFILPHISTAR	1537.7	2	2.5153	0.2219
THHILIDLR	1118.3	2	3.0925	0.3032
THIDTVINALKTER	1611.8	2	3.3397	0.3562
THIETVINALKTER	1625.9	2	4.3402	0.4016
THILLFLPK	1082.4	2	3.089	0.2866
THINIVVIGHVDSGK	1589.8	2	5.3146	0.5402
THINIVVIGHVDSGKSTTTGHLIYK	2692.1	3	6.0073	0.3312
THINTVIIGHVDSGK	1591.8	2	2.6409	0.2842
THINYGVKGDVAVVR	1628.9	2	2.478	0.118
THLGEALAPLSK	1237.4	2	3.6348	0.483
THLLSRLPIPESQVITINPELPVEEAAEDYAK	3575.0	3	5.326	0.3267
THLPEVFLSK	1171.4	2	2.4163	0.1075
THLPGFVEQAEALK	1540.7	2	4.3404	0.4866
THLPGFVEQAEALKAK	1740.0	3	4.347	0.4429
THLPTIESAIHSVLR	1674.9	2	3.592	0.4148
THLRDMIILPEMVGSMVGVYNGK	2562.1	3	3.4157	0.2383
THLSALVHHSVIPPDRPPGASAGLTK	2660.0	3	3.3106	0.1209
THLSLSHNPEQK	1391.5	2	3.8829	0.2417
THLTEDTPKVNADIEKVNQNQAK	2594.8	3	5.8917	0.514
THLYGSLLYYLQIAQRPDEPDTLEAAK	3107.5	3	3.5261	0.2138
THLYTLILNPDNSFEILVDQSVVNSGNLLNDMTPPVNPSR	4440.0	3	4.7327	0.3818
THMADENKNEYAAQLQNFNGEQHK	2819.0	3	4.7129	0.2261
THMQDLKDVTNNVHYENYR	2378.6	2	6.2777	0.4755
THMQNIKDITSSIHFEAYR	2292.6	2	4.7956	0.4632
THMTHHAVSDHEATLR	1844.0	3	4.655	0.4495
THMVVANTMEDFQK	1651.9	2	4.4494	0.3949
THNDIIHNENMR	1494.6	2	4.6617	0.4722
THNGESVSYLFSHVPL	1788.0	2	4.2549	0.482
THNLEPYFESFINNLR	1995.2	2	3.0887	0.3284
THNVHVEIEQR	1362.5	2	3.6318	0.3572
THPHFVIPYR	1267.5	2	2.722	0.3218
THPQWYPAR	1156.3	2	2.6215	0.3645
THPSGRDPETPIIVVK	1747.0	2	3.6238	0.2103
THPSVVPGSIAFSLPQR	1794.0	3	3.49	0.2733
THPSVVPGSIAFSLPQRK	1922.2	2	3.468	0.3858
THSDQFLVAFKEVGR	1734.9	2	4.5066	0.431

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
THSDSKPYGPMSVGLDFSLPGMEHVYGIPEHADNLR	3956.4	3	5.0657	0.4622
THSQGGYGSQGYK	1370.4	2	3.4532	0.3434
THSTSSSLGSGESPFSR	1724.8	2	4.4076	0.4563
THTDSSEKELEPEAAEEALENGPK	2612.7	3	4.731	0.255
THTDVGLLEYQHHSR	1793.9	2	5.0623	0.4719
THTGEKKFACPECPK	1676.9	2	2.6138	0.1172
THTGERPNACADCGK	1560.7	2	2.6961	0.1015
THTQDAVPLTLGQEFSGYVQQVK	2547.8	3	4.9044	0.4393
THTQDAVPLTLGQEFSGYVQQVKYAMTR	3170.5	3	4.5116	0.3789
THTQGQAFSLSVFHHWQIVPGDPLDK	2947.3	3	3.6502	0.3384
THTSQAILQPVLAAEDFTIFK	2331.7	3	4.3781	0.4022
THTTMSGVAHR	1198.3	2	2.9427	0.4043
THTTSASAR	932.0	1	1.84	0.2433
THVADFAPEVAWVTR	1699.9	2	4.3408	0.5045
THVEKEDGEAR	1271.3	2	3.5515	0.356
THVGSYK	791.9	1	1.9877	0.1549
THVHIGEGPSTISNSTIPENATSSGR	2650.8	3	4.5463	0.2203
THYIVGYNLPSYEYLYNLGDQYALK	2999.3	3	5.3234	0.494
THYPAQQGEYQTHQPVYHK	2313.5	2	4.2283	0.3562
THYQADIER	1133.2	2	2.735	0.2158
THYSELTTLTSQYIK	1786.0	2	3.8498	0.4977
TIADHCPDSACKQDLLAYLQR	2362.7	3	3.5493	0.2693
TIAECLADELINAAK	1575.8	2	4.9508	0.3769
TIAEIFGNPNYLR	1508.7	2	4.1775	0.3471
TIAFLLPMFR	1209.5	2	3.1666	0.1473
TIAIIAEGIPEALTR	1568.8	2	5.4516	0.4878
TIAIIAEGIPEALTRK	1697.0	2	4.152	0.337
TIALNGVEDVRTVLEHYALEDDPLAAFK	3101.5	3	3.2125	0.173
TIALNGVEDVRTVLEHYALEDDPLAAFKQR	3385.8	3	3.9475	0.232
TIAMDGTEGLVR	1263.4	2	3.8341	0.4038
TIAMDGTEGLVRGQK	1576.8	2	3.418	0.3134
TIAMDGTEGLVRGQKVLDSGAPIKIPVGPETLGR	3478.0	3	5.2294	0.3743
TIAPALVSK	900.1	1	1.9585	0.3261
TIAQDYGVLK	1108.3	2	2.9814	0.3115
TIAQDYGVLKADEGISFR	1984.2	2	5.178	0.5529
TIAQGNLSNTDVQAAK	1631.8	2	4.9231	0.4941

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TIAQVLVHLHR	1287.5	2	3.6857	0.3397
TIARQTARCACRKGQIAGTTRAR	2490.9	3	3.2951	0.2223
TIAVDFASEDIYDKIK	1829.0	2	5.412	0.4384
TIAVLLDDILQR	1370.6	2	4.3246	0.3302
TIAYENK	838.9	1	1.6955	0.1154
TIDDLEDKLK	1190.3	2	3.0136	0.2454
TIDDLEDKLKCTKEEHLCTQR	2519.8	3	3.7674	0.1164
TIDDLEEKLAQAK	1474.6	2	4.0698	0.2628
TIDDLEEKLAQAKEENVGLHQTLDQTLNELNCI	3740.1	3	3.5028	0.1103
TIDDRIVHELNTTVPTASFAGK	2386.6	3	4.7446	0.2611
TIDGILLLIER	1256.5	2	3.25	0.2298
TIDLGAAAHYTGDKASPDQNASTHTPQSSVK	3170.4	3	6.6187	0.401
TIDPELLGK	986.1	1	2.0461	0.1429
TIDQIHKEAEMEEHREHIK	2374.6	3	3.6698	0.153
TIDWVAFAEIIPQNQK	1874.1	2	4.8243	0.2885
TIEAEAAHGTVTR	1356.5	2	3.8084	0.4399
TIEEQLDEEHLESHKK	1966.1	2	4.5337	0.3462
TIEKFEKEAAEMGK	1611.8	2	4.1696	0.3961
TIEQIHKEAK	1197.4	2	2.8026	0.1185
TIESANQQTDKLKELYGQVLYR	2598.9	3	3.5333	0.1831
TIESILEPVAQQISHLVIMHEEGEVDGK	3103.5	3	4.1112	0.3173
TIEVLQLQDQGSK	1459.6	2	2.4691	0.2133
TIEYLEEVAITFAK	1627.9	2	4.2143	0.4087
TIEYLQPNPASR	1389.5	2	3.964	0.3253
TIFAYFTGSK	1135.3	2	3.0389	0.3632
TIFAYFTGSKDAGGK	1563.7	2	2.7349	0.2783
TIFQGIAAK	949.1	1	1.8373	0.1466
TIFSALENDPLFAR	1594.8	2	3.6229	0.3143
TIFTGHTAVVEDVSWHLLHESLFGSVADDQK	3440.8	3	4.8848	0.3761
TIGGGDDSFNTFFSETGAGK	2009.1	2	5.9811	0.5827
TIGGGDDSFNTFFSETGAGKHVPR	2498.6	2	4.1554	0.4697
TIGGGDDSFTTFFCETGAGK	2012.1	2	4.7943	0.4966
TIGNNGDQSHK	1171.2	2	2.8943	0.1866
TIGTGLVTNTLAMTEEEK	1909.1	2	4.4727	0.4554
TIGTGLVTNTLAMTEEEKNIK	2264.6	2	4.4094	0.3202
TIGTGLVTNTLAMTEEEKNIKWG	2507.8	2	3.5622	0.2801

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TIGTKPVAHIDQFTADMLGSAELAEEVNLNGSGK	3515.9	3	3.9876	0.1974
TIGVITKLDLMDEGTDARDVLENK	2648.0	3	4.4452	0.3266
TIHSYQGQIISHEK	1641.8	2	4.3638	0.4142
TIHSYQGQIISHEKK	1770.0	2	4.6463	0.3487
TIIGSFNGALAAVPVQDLGSTVIK	2372.7	2	4.3054	0.3874
TIIGSFNGALAAVPVQDLGSTVIKEVLKR	2998.5	3	4.8838	0.3902
TIISYIDEQFER	1514.7	2	3.5298	0.2809
TIKDLQEEVSNLYNNIR	2050.3	2	3.8533	0.3175
TIKDVFHNHGIHATTIQPEFASVGSK	2836.2	3	4.707	0.3802
TIKVWQLGSSSPNFTLEGHEK	2359.6	3	5.7054	0.3649
TILKAPGIILLDEATSALDTSNER	2542.9	3	4.264	0.2635
TILKDATLTALDR	1431.7	2	4.0047	0.3798
TILKDATLTALDRGQQQVFK	2247.6	2	5.379	0.4778
TILLSTTDPADFAVAEALEK	2106.4	2	3.8647	0.2605
TILNHVLHVVK	1273.6	2	3.5368	0.3459
TILSNQTVDIPENVDITLK	2114.4	2	5.5188	0.4905
TILSNQTVDIPENVDITLKGR	2327.6	3	4.0132	0.3138
TIMKENTELVQK	1434.7	2	3.3347	0.1835
TINEVENQILTR	1430.6	2	4.0593	0.3443
TINLYPLTNYTFGTK	1747.0	2	3.8816	0.2109
TIPGKQQLLIGAYAK	1601.9	2	2.8329	0.1799
TIPIDGNFFTYTR	1545.7	1	2.8336	0.1678
TIPIKYPLKEIVVIHQDPEALKDIK	2902.5	3	5.0783	0.3186
TIPSWATLSASQLAR	1602.8	2	4.6103	0.4847
TIPYSDKLFEMVLGPAAYNVPLPK	2665.1	2	4.5596	0.4075
TIPYSDKLFEMVLGPAAYNVPLPKK	2793.3	3	4.8867	0.3917
TIQDKNKEIER	1374.5	2	3.0637	0.2196
TIQFVDWCPTGFK	1542.8	2	3.9246	0.3698
TIQNSSVSPTSSSSSSSSTGETQTQSSSR	2893.9	3	3.7676	0.246
TIQTAESLGVPYEQWK	1851.0	2	5.0665	0.3985
TIQVDNTDAEGR	1319.4	2	3.7366	0.4044
TIRDIIALNPLYR	1558.9	3	4.2566	0.2197
TIRNDNSSR	1063.1	2	2.5971	0.1368
TIRPMDMETIEASVMK	1853.2	2	4.1108	0.418
TIRYPDPLIK	1216.5	3	3.6972	0.1604
TISAQNMDILQNPLMIK	1931.3	2	4.4604	0.3081

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TISAVGEQLLPTVEHLQLELDQLKSELSSWR	3522.0	3	4.2489	0.3427
TISHESGEHSAQGK	1468.5	2	3.5261	0.3735
TISHVIIGLK	1081.3	2	2.6625	0.2507
TISQTSAPVWDESASFLIR	2109.3	2	3.4646	0.2789
TISSLEEIVEKQGDTIEYLKR	2452.7	3	3.8526	0.3194
TISSSLAVVDLIDAIQPGCINYDLVK	2749.2	3	3.297	0.1296
TISTSDPAEVLVK	1360.5	2	2.9355	0.2358
TITDVINIGIGGSDLGPLMVTEALKPYSSGGPR	3330.8	3	5.329	0.4403
TITFEQFQEALEELAK	1898.1	3	5.409	0.4714
TITGFQTHTTPVLLAHGER	2080.3	3	5.0815	0.5151
TITLEVELSDTIDNVK	1791.0	2	4.1566	0.2025
TITLEVELSDTIDNVKAK	1990.2	2	3.6189	0.2041
TITLEVEPSDTIENVK	1789.0	2	5.3666	0.4344
TITSAHTSSTSTSLESDSASPGVSDHGR	2776.8	3	6.1506	0.4486
TITSSYYR	991.1	1	2.108	0.1174
TITVALADGGRPDNTGR	1714.9	2	2.8418	0.1292
TIVAINKDPEAPIFQVADYGIVADLFK	2949.4	3	6.3863	0.5386
TIVEEVQDGKVISSR	1660.9	2	4.6121	0.3703
TIVHESERLEALK	1525.7	2	3.5153	0.3523
TIVITSHPGQIVK	1393.7	2	4.0231	0.3578
TIYAGNALCTVKCDEK	1730.0	2	3.3257	0.2107
TKAGDLRDTGIFLDLMHLK	2145.5	3	6.2018	0.3623
TKALLADAQLMLDHLK	1782.1	3	4.9756	0.3206
TKAPDDLVAPVVK	1353.6	2	2.7054	0.1724
TKAQYEQTLAELHR	1688.9	2	2.4107	0.25
TKDDIIICEIGDVFK	1710.0	2	3.1402	0.1493
TKDDLEQLTTEIK	1534.7	2	3.4712	0.1531
TKDEIITTTVPEDIMSNRGNDLLLK	2818.2	3	4.5097	0.1557
TKDEYLINSQTTEHIVK	2020.2	2	5.309	0.4418
TKDGHEVR	942.0	2	2.5089	0.1702
TKDGVREVFEMATR	1639.9	3	3.5166	0.315
TKDGVVEITGK	1147.3	2	3.4893	0.2766
TKDGVVEITGKHEER	1698.9	2	4.6925	0.4751
TKDGVVEITGKHEERQDEHGYISR	2785.0	3	4.4725	0.3852
TKDIEDVFYK	1258.4	2	4.0228	0.311
TKDLPVTEAVFSALVTGHAR	2113.4	2	5.879	0.5124

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TKDSGSISLQETR	1422.5	2	3.291	0.2464
TKDSLVLNNITR	1374.6	2	2.695	0.109
TKDVEILHLR	1224.4	2	2.9272	0.2748
TKEAGMQPQLQIR	1500.7	2	3.8287	0.2695
TKEAVLLLKK	1143.4	2	3.0173	0.2534
TKEDEKDDKPIR	1474.6	2	3.645	0.3137
TKEEALELINGYIQK	1750.0	2	4.9015	0.3817
TKEELEAEKR	1233.4	2	3.7958	0.1855
TKEELEELMSDIKK	1693.9	3	5.3287	0.3489
TKEEVAGTLEAVQTIQSITQALQK	2587.9	3	4.0667	0.1246
TKEEVEAAKAAALLAK	1643.9	2	5.016	0.397
TKEGVLYVGSK	1181.4	2	2.6888	0.1792
TKEGVVHGVATVAEK	1525.7	2	4.5766	0.4634
TKEIEAIHAILR	1394.6	2	3.6386	0.285
TKELTSELKENFIR	1708.9	2	4.3473	0.3879
TKENDAHLVEVNLNNIK	1952.2	3	4.285	0.2778
TKENILEEFSK	1338.5	2	3.7	0.2258
TKEQASHLGGAVFSGAGNIAAATGLVK	2556.9	3	5.1134	0.4293
TKEQIENLLR	1244.4	2	2.7936	0.1003
TKEQILEEFSK	1352.5	2	3.5003	0.1765
TKEQILEEFSKVTEGLTDVILYHQPDDK	3277.6	3	5.3237	0.3985
TKETPPTAHLILPEQHMSLAQQK	2600.0	3	3.7578	0.1726
TKEVIFSVEDGSVK	1538.7	2	3.2858	0.1946
TKEVIQEWNLTNIKR	1873.1	2	4.075	0.3363
TKEVYELLDSPGK	1479.7	2	4.3165	0.3301
TKEVYELLDSPGKVLLQSK	2148.5	3	3.8342	0.1329
TKEVYELLDSPGKVLLQSKDQITAGNAAR	3146.5	3	6.4576	0.4206
TKFFGTFPGNYVK	1506.7	2	3.8062	0.3626
TKFSMVLPEVEAALAEIPGVR	2258.7	2	3.2462	0.3309
TKGDSDEEVIQDGVR	1648.7	2	4.2581	0.2599
TKGEPAPPPGK	1079.2	2	2.6212	0.1934
TKGFHTTIDIGVK	1417.6	2	4.0165	0.367
TKGTSSFGK	913.0	1	1.9154	0.2022
TKGVDEVTIVNILTNR	1773.0	2	5.2857	0.4264
TKHDVKFPLDSTGSELK	1903.1	2	4.1329	0.3388
TKHEEILQNLQK	1481.7	2	3.2285	0.2161

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TKHIEEENLIDEDFQNLK	2216.4	2	5.9155	0.4492
TKHKLDVTSVEDYK	1663.9	2	4.3153	0.4241
TKIEGLDIHFIHVKPPQLPAGHTPK	2775.2	3	4.9507	0.3027
TKIYHPNIDEK	1358.5	2	2.9435	0.1905
TKKDDSHSAEDSEDEKEDHKNVR	2700.7	3	4.0585	0.3261
TKKFDELLHLASR	1558.8	2	3.4629	0.3936
TKKQELSEAEQATR	1619.8	2	4.0437	0.3247
TKLDDLALLEDLEKQR	1901.2	3	4.2859	0.3432
TKLEAQAYTAYLSGMLR	1917.2	2	5.0444	0.4434
TKLEEALSPEVLELRNESGGHAVPPGSETHFR	3488.8	3	4.6905	0.3257
TKLHQLSGSDQLESTAHSR	2096.2	2	6.2748	0.4932
TKLLHQTGLSLYSTSHGFYEEEVKK	2897.2	3	5.5139	0.4955
TKNALDPMSVLLAR	1529.8	2	3.9797	0.2071
TKNFDKLSFLYLITGNLEK	2245.6	3	4.8369	0.3364
TKPADMVIEAYGHGQR	1774.0	2	5.196	0.4932
TKPFPWGDGNHTLFHNPHVNPLPTGYEDE	3318.6	3	4.4729	0.3072
TKPIWTRNPDDITNEEYGEFYK	2717.9	3	4.8724	0.4595
TKPIWTRNPDDITQEEYGEFYK	2732.0	3	4.7656	0.385
TKPLATTQPAK	1156.4	2	3.1571	0.3713
TKPQDMISAGGESVAGITAISGKPGDK	2616.9	3	4.3879	0.2553
TKPQDMISAGGESVAGITAISGKPGDKKK	2873.3	3	4.8313	0.35
TKPSDEEMLFIYGHYK	1959.2	2	5.0383	0.3946
TKPVTGNLRPEEALQALTIYEGK	2529.9	2	4.1687	0.4296
TKPYIQVDIGGGQTK	1605.8	3	4.678	0.3618
TKQFAPIHAEAPEFMEMSVEQEILVTGIK	3275.8	3	4.8757	0.1905
TKQFIDSNPNQPLVILEMESGASAK	2719.1	3	5.2005	0.3305
TKQGVAEAAGK	1060.2	2	2.6356	0.2345
TKQQIEEQR	1160.3	2	3.1291	0.2323
TKQTMHGILER	1314.5	2	3.5516	0.2772
TKSENGLEFTSSGSANTETTK	2190.3	3	3.8311	0.381
TKSENGLEFTSSGSANTETTKVTGSLETK	3006.2	3	5.7646	0.4338
TKSQGGEPTYNVAVGR	1664.8	2	4.409	0.3569
TKSTGGAPTFNVTVTK	1609.8	2	3.9791	0.3947
TKTEAQKELLDTELDLHKR	2269.5	3	4.0665	0.103
TKTEISEMNR	1209.4	2	3.3121	0.2457
TKTENPLILIDEVDKIGR	2055.4	3	6.1391	0.3994

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TKTENSGEALAK	1249.4	2	3.1061	0.2723
TKTETITGFQVDAVPANGQTPIQR	2573.8	2	2.6727	0.1088
TKTYSEDNFEELQYFPNFYALLK	2862.1	3	4.5058	0.3905
TKVEAFQTTISK	1353.5	2	3.8754	0.304
TKVEATKNETSAPFK	1651.8	2	4.8927	0.4882
TKVEEVNRQQSAQLEQLVKELQLKEDAR	3311.7	3	3.9338	0.139
TKVENGEGTIPVESSDIVPTWDGIR	2700.9	3	4.834	0.2461
TKVHAELADVLTEAVVDSILAIK	2436.8	3	6.4583	0.5263
TKVHAELADVLTEAVVDSILAIKK	2565.0	3	4.1592	0.3152
TKVMQEEIFGPILPIVPVK	2139.6	2	3.1383	0.3143
TKVMQEEIFGPILPIVPVKNVDEAINFINER	3555.1	3	5.1567	0.4289
TKYNANKTPDKLQQAALPLLSNAECK	2861.3	3	5.3972	0.3855
TKYNLDLTNLNQPLLDVDHTSSR	2658.9	3	3.7535	0.1705
TKYWELIYEDSMDLIAK	2119.4	2	5.0815	0.5028
TLAAEMQELR	1162.3	2	2.816	0.2169
TLADVLVQEVIKQNMENKFPGLEK	2745.2	3	4.4112	0.39
TLAEEQHKNQLLQEELEALQLQLR	2876.2	3	6.0131	0.2767
TLAEIAKAELDGTILK	1687.0	2	4.6461	0.359
TLAEIAKVELDNMPLR	1814.1	3	5.7225	0.3811
TLAEIAKVELDNMPLRGK	1999.4	3	5.2381	0.3926
TLAEINANRADAEEEAATR	2046.1	3	4.5415	0.3499
TLAEINANRADAEEEAATRIPA	2327.5	2	4.1763	0.2661
TLAESALQLLYTAK	1522.8	2	4.3053	0.3842
TLAFTSVDLTNK	1310.5	2	4.0107	0.4212
TLAFTSVDLTNKATGK	1667.9	2	4.1252	0.2973
TLAGDVHIVR	1081.3	2	3.0032	0.3201
TLAGDVHIVRGDFDENLNYPEQK	2631.8	3	5.1793	0.4799
TLAGLPLLVAYKEDEIPVLKDELIHELK	3161.7	3	5.7835	0.4669
TLAHFRPIEDNEK	1570.7	2	3.8858	0.2919
TLAIELAPR	984.2	2	3.5192	0.1862
TLAKDEALKR	1145.3	2	2.4772	0.1883
TLALKLQEQEQLLKEGFQK	2245.6	2	3.9414	0.3601
TLALLVLAHSSDVLENVFSSLTDDKYDVAMNR	3539.0	3	4.9041	0.3791
TLAMDTILANAR	1290.5	2	4.0502	0.3096
TLAPGLFFSLMASR	1511.8	2	3.7289	0.4281
TLAPLLASLLSPGSVLVLSAR	2079.5	3	5.3372	0.3467

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TLAQLNPESSLFIIASK	1833.1	3	5.4731	0.4469
TLATDILMGVLKEVVR	1759.1	2	4.0742	0.3168
TLATGYQYSFPELGAALKEIVA	2343.7	2	4.1033	0.4186
TLATLSENNMEAK	1422.6	2	3.983	0.4131
TLAVITKLDLMDAGTDAMDVLMGR	2552.0	3	4.1814	0.2677
TLAYLLPAIVHINHQPYLER	2362.8	2	4.1479	0.317
TLDDGFFPFIILDAINDR	2083.3	2	2.6685	0.1434
TLDFDALSVGQR	1322.4	2	3.5345	0.3534
TLDGGLNVIQLETAVGAAIK	1984.3	3	6.0044	0.467
TLDGGLNVIQLETAVGAAIKSFENSLGINVPR	3298.7	3	7.1498	0.4996
TLDLIDEAYGLDFYILK	2003.3	2	4.1247	0.4036
TLDLPIYVTR	1191.4	2	3.3802	0.1944
TLDNDILLIK	1158.4	2	4.1722	0.3217
TLDSVTELASEVSQLNTIKEHLEEEIKHHQK	3587.9	3	3.7559	0.2198
TLDSWRDEFLIQASPR	1935.1	3	4.0022	0.2218
TLDTFLRSEEEKQHR	1890.0	2	2.836	0.1209
TLDVFNIILAR	1275.5	2	3.879	0.2886
TLEAEFNSPSPPTPEPGEGPR	2210.3	2	5.2446	0.4401
TLEDGKKEAAASGLPLMVIIHK	2322.8	2	4.2331	0.4104
TLEDIDLGPTEK	1331.5	2	4.0028	0.3497
TLEEAIRSDTSGHFQR	1848.0	3	3.8897	0.3088
TLEEDEEELFK	1382.5	2	3.6295	0.2642
TLEEEAKTHEAQIQEMR	2044.2	3	5.5842	0.4965
TLEEEAKTHEAQIQEMRQK	2300.5	3	4.0786	0.2611
TLEEGHDFIQEFPGSPAFAALTSIAQK	2906.2	3	4.9908	0.3194
TLEFKPYVIFIKPPSIER	2178.6	3	4.3803	0.2276
TLEGELHDLR	1183.3	2	3.594	0.3164
TLEGELHDLRGQVAK	1666.9	2	4.6085	0.3576
TLEGELHDLRGQVAKLEAALGEAK	2549.9	3	6.5677	0.5291
TLEGELHDLRGQVAKLEAALGEAKK	2678.0	3	4.5508	0.3224
TLEGELHDLRGQVAKLEAALGEAKKQLQDEMLR	3692.2	3	5.4316	0.3912
TLEGERNQIYIQLSEVDKTKEELTEHIK	3345.7	3	4.7642	0.3182
TLEHLEHTYLPQVSHYR	2124.3	3	3.3148	0.3271
TLEKNQEILDDTAK	1618.8	2	3.9246	0.2982
TLEKNQEILDDTAKNLR	2002.2	3	4.2269	0.2626
TLELQGLINDLQR	1513.7	2	3.6666	0.283

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TLENELDELDPDNALLPAGLR	2309.5	2	5.1472	0.3883
TLEQHDDIVTHYK	1599.7	3	3.3141	0.2492
TLEQTGHVSSENKYQDILNEIAKDIR	3003.3	3	6.1949	0.4486
TLESNLFDDNIDIFADLTVKPK	2509.8	2	2.7902	0.1967
TLESSIQGLR	1104.2	2	3.0996	0.2344
TLESVDPLGGLNTIDILTAIR	2212.5	3	5.55	0.518
TLETESHGLDR	1258.3	2	2.7297	0.1797
TLETLLLPTANISDVDPAHAQHYQDVLYHAK	3475.9	3	3.8615	0.2005
TLETVPLER	1058.2	2	2.9517	0.1602
TLEVEIEPGVRDGMEYPFIGEGEPHVDGEPGDLR	3741.1	3	5.1157	0.3669
TLFANIVLSGGSTLFK	1669.0	2	3.7972	0.3591
TLFGFLGKIDELR	1509.8	2	3.7454	0.351
TLFGRDLLDDLKSELTGK	2022.3	3	3.8161	0.143
TLFGRDLLDDLKSELTGKFEK	2426.8	3	5.7582	0.4896
TLFSFLGEIEELR	1554.8	2	3.7802	0.2996
TLFSNIVLSGGSTLFK	1685.0	2	5.6487	0.4831
TLFSNIVLSGGSTLFKGFGDR	2217.5	2	4.3656	0.3387
TLFVSGLPLDIKPR	1556.9	2	2.7909	0.1778
TLGDFAAEYAK	1186.3	2	2.8615	0.1901
TLGGLEMELR	1119.3	2	2.7953	0.3447
TLGHNLLVSELYNQLK	1843.1	2	2.8938	0.191
TLGILGLGR	900.1	2	2.5003	0.1274
TLGKDHPAVAATLNNLAVLYGK	2267.6	2	5.3583	0.5158
TLGKDNSK	863.0	2	2.4956	0.1281
TLGLTQHVQACETTVELLFDSVIHLGCKPYLDSQR	3917.5	3	3.647	0.1914
TLGLYGKDQQEAALVDMVNDGVEDLR	2851.1	2	5.226	0.461
TLGQLQPDELSPK	1426.6	2	3.691	0.1715
TLGTMIAGDTSGDYR	1558.7	2	3.0652	0.2436
TLHEVSLQESIR	1412.6	2	2.7423	0.3122
TLHEWLQQHGIPGLQGVDTR	2286.5	2	3.2212	0.3609
TLHLQTGNLLNWGR	1623.8	2	4.0526	0.4087
TLHNLVIQYASQGR	1600.8	2	4.4299	0.3491
TLHPAVHAGILAR	1356.6	2	3.0911	0.4669
TLHPDLGTDKDKEQWK	1912.1	2	3.6096	0.3616
TLHPDLGTDKDKEQWKEVHK	2405.7	3	3.2346	0.237
TLHSDDEGTVLDDSR	1660.7	2	5.1957	0.4649

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TLHSTFQPNISQGK	1558.7	2	3.412	0.3629
TLHWDTDPSVLQLHSDSDLGR	2393.6	3	3.4109	0.3478
TLHWDTDPSVLQLHSDSDLGRGPIK	2789.1	3	3.4798	0.3264
TLIEFLLR	1005.2	2	3.0612	0.2144
TLIEKTNEER	1233.4	2	3.2313	0.2706
TLIEKTNEERK	1361.5	2	2.6955	0.1062
TLIENGEKITSLHR	1611.8	2	2.9191	0.2
TLIGHVPDQR	1136.3	2	2.854	0.2965
TLIGHVPDQREIISFGSGYGGNSLLGK	2817.1	3	5.4532	0.4232
TLIGHVPDQREIISFGSGYGGNSLLGKK	2945.3	3	4.707	0.4342
TLINAEDPPMVVVR	1554.8	2	4.1604	0.4763
TLKELGLVDGQELAVADVTTPQTVLFK	2887.3	3	4.4174	0.2701
TLKGHTDSVQDISFDHSGK	2073.2	2	5.0001	0.4213
TLKIQDVGLVPMGGVMSGAVPAAAAQEAVEEDIPIAK	3678.3	3	6.1303	0.4283
TLKKDEDIPLFPVQTK	1873.2	2	3.1475	0.1679
TLKLTTPTYGDLNHLVSATMSGVTTCLR	2995.5	3	6.2774	0.4728
TLLEEKVKLEEQLKETVEK	2287.6	3	4.0377	0.2691
TLLEGPDPAELLLMGSYLGKPGPPQPAPAPEGQDLR	3727.2	3	3.6876	0.2332
TLLEGSGLESIISIIHSSLAEPR	2423.7	2	4.9142	0.3688
TLLEKELQEVIALTSQELEESREK	2817.1	3	4.379	0.2918
TLLENTAITIGR	1302.5	2	3.6237	0.2729
TLLFTFNVPGSGNTYPK	1857.1	2	3.9266	0.4514
TLLHHAVSTGSK	1251.4	2	3.1011	0.3619
TLLLNIFQDTK	1306.5	2	4.0067	0.3092
TLLPHDPTADVFVTPAEEKPIEIQWVKPEPK	3527.0	3	3.3319	0.1725
TLLPLLLESSTESVAEISSNSLER	2589.9	3	4.9893	0.4568
TLLQKPHVDITDPEKPHQPK	2322.6	3	5.3415	0.4311
TLLSDPTYRELIEQLR	1948.2	3	3.3834	0.1959
TLLSNLEEAK	1118.3	2	3.1382	0.2437
TLLSNLEEAKK	1246.4	2	3.3581	0.2027
TLLVADPR	885.0	2	2.6371	0.2027
TLLWTELFR	1179.4	2	3.3567	0.2967
TLMAQSIYGGR	1197.4	2	2.7909	0.3279
TLMELLNQMDGFDTLHR	2035.3	2	5.1594	0.4327
TLMNLGGLAVAR	1216.5	2	4.1765	0.3192
TLMNLGGLAVARDDGLFSGDPNWFPK	2793.1	3	6.3647	0.4215

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TLMNLGGLAVARDDGLFSGDPNWFPKK	2921.3	3	3.2262	0.2016
TLMNTIMQLR	1221.5	2	2.6703	0.2638
TLNAGAYSK	925.0	2	2.6607	0.1309
TLNDELEIIEGMK	1505.7	2	4.5899	0.4404
TLNDELEIIEGMKFDR	1924.2	2	4.5718	0.3837
TLNDKTENQK	1191.3	2	3.0413	0.2488
TLNEEKRKEEESKFEEMK	2285.5	3	4.2965	0.2142
TLNETELTELQSQISDTSVVLSMDNSR	3012.3	3	5.5687	0.429
TLNEWSSQINPDLVR	1772.9	2	4.6084	0.2765
TLNKNVFTSAEELER	1751.9	2	3.2973	0.2626
TLNLAGNLLESLSGLHK	1781.0	2	4.437	0.3583
TLNMDMFTWEPR	1541.8	2	4.0212	0.363
TLNMTTSPEEK	1251.4	2	2.9448	0.2486
TLNQLGTPQDSPELR	1669.8	2	4.1906	0.31
TLNQPDSQLQLTTGNGLFLSEGLK	2575.9	2	5.3515	0.4503
TLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKK	3891.4	3	3.7524	0.2532
TLNQQLTNHIR	1338.5	2	3.2378	0.3246
TLNVESNFISGAGILR	1691.9	2	4.6769	0.3888
TLPDEVLTKEVEELILTESK	2287.6	3	3.5939	0.2062
TLPETLDPAEYNISPETR	2047.2	2	4.3656	0.4463
TLPEYTGYRPFLDPSISPEFVVASEQFFSTMVPPGVYMR	4458.1	3	4.5717	0.4098
TLPLTGSTFHDQIAMLSHR	2126.4	2	5.0035	0.4209
TLPQAEALDR	1114.2	2	2.4275	0.3467
TLPQAEALDRAYQIDTVINLNVPFEVIK	3172.6	3	3.4417	0.1067
TLPQAEALDRAYQIDTVINLNVPFEVIKQR	3456.9	3	5.0707	0.2349
TLPTLQELHLSDNLLGDAGLQLLCEGLLDPQCR	3591.1	3	6.7858	0.3513
TLPTLQELHLSDNLLGDAGLQLLCEGLLDPQCRLEK	3961.6	3	5.1308	0.3039
TLPYLVSNVIELLDVDPNDQEEDGANIDLDSQR	3701.9	3	3.8133	0.1319
TLPYLVSNVIELLDVDPNDQEEDGANIDLDSQRK	3830.1	3	4.4606	0.3341
TLQALEFHTVPFQLLAR	1985.3	2	6.0477	0.3907
TLQALQIPAAK	1154.4	2	3.4108	0.3587
TLQALQIPAAKLEGVLAEVAQHYQDTLIR	3191.7	3	6.0377	0.4625
TLQEDLVKDVLSNAHIQNELER	2565.8	3	5.3106	0.3806
TLQEEVMEAMGIK	1479.7	2	3.4799	0.225
TLQELEELQNDSEAIDQLALESPEVQDLQLER	3698.0	3	3.7335	0.1655
TLQEQLENGPNTQLAR	1813.0	2	5.4484	0.3652

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TLQEQSGAMNIR	1348.5	2	3.0764	0.1823
TLQEVLTMEYR	1383.6	2	3.1435	0.1879
TLQEVTQLSQEAQR	1631.8	3	4.7688	0.297
TLQEVTQLSQEAQRIVEKLEK	2471.8	3	3.5601	0.202
TLQGLEIELQSQLSMK	1819.1	2	5.9944	0.4238
TLQGTVSQAQER	1318.4	2	3.7496	0.3623
TLQIFNIEMK	1237.5	2	3.5253	0.2151
TLQKLDEYLNSPLPDEIDENSMEDIKFSTR	3542.9	3	5.9565	0.3693
TLQLALDLVSSR	1316.5	2	3.6355	0.2632
TLQNTPSLHSR	1254.4	2	3.0612	0.2449
TLQNTSSEGSR	1180.2	2	2.9699	0.1571
TLQQNAESRFN	1308.4	2	3.0822	0.2923
TLQTEQEANTEGQKK	1705.8	2	4.7837	0.3653
TLQYKLLEPVLLLGKER	2014.4	3	5.4896	0.3929
TLRDIETFYNTSIEEMPLNVADLI	2799.1	2	3.9319	0.2998
TLREQGVEEHETLLLR	1924.1	3	4.2974	0.36
TLRKDQVELVENMVTVGK	2060.4	2	2.4176	0.1838
TLRLAGTQPLEVLEAVQR	1995.3	3	4.348	0.3024
TLRVEEVEDAISQTSQTLQLLIEHDPVSQR	3436.8	3	3.5286	0.1883
TLSAISSSTDPTSYDGFGPFMPGFDIIPYNDLPALER	3994.4	3	3.3409	0.1587
TLSDYNIQK	1082.2	2	2.4322	0.155
TLSDYNIQKESTLHLVLR	2131.4	3	5.193	0.3298
TLSEKETEAR	1164.2	2	3.5064	0.2136
TLSFGSDLNYATR	1445.6	2	3.3616	0.4842
TLSFGSDLNYATREDAPIGPHLQSMPSEQIR	3432.8	3	5.2465	0.3657
TLSGFSSTSVLPHTGYIYHSDIVQSLPPDLR	3389.8	3	3.8801	0.3532
TLSGFSSTSVLPHTGYIYHSDIVQSLPPDLRR	3545.9	3	4.6986	0.4363
TLSGTPEESKR	1205.3	2	2.5239	0.1349
TLSGTPEVHSNKR	1426.6	2	2.8944	0.3405
TLSHPQQMALLDQTK	1712.0	2	4.2037	0.38
TLSKDDVNYK	1183.3	2	3.1077	0.224
TLSKEEETK	1065.2	2	2.9268	0.208
TLSKEEETKK	1193.3	2	3.2263	0.2435
TLSLDEVYLIDSGAQYKDGTTDVTR	2762.0	3	4.8945	0.4159
TLSSPTEPVKR	1215.4	2	2.7628	0.2223
TLSSSTQASIEIDSLYEGIDFYTSITR	2999.2	2	2.8697	0.2627

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TLSSVQNEVQEALQR	1702.8	3	4.5949	0.2351
TLSTIATSTDAASVVHSTDLVVEAIVENLK	3086.4	3	7.1498	0.6093
TLSTIATSTDAASVVHSTDLVVEAIVENLKVK	3313.7	3	6.2598	0.5411
TLSTIATSTDAASVVHSTDLVVEAIVENLKVKNELFK	3945.5	3	5.3282	0.433
TLSTIATSTDAASVVHSTDLVVEAIVENLKVKNELFKR	4101.7	3	3.2222	0.201
TLSYLLPAIVHINHQPFLER	2362.8	2	4.2772	0.4115
TLTAAAVSGAQPILSK	1528.8	2	4.1895	0.305
TLTAAAVSGAQPILSKLEPQIASASEYAHR	3082.5	3	5.908	0.4463
TLTAIAVILTNFHDGRPLPIER	2448.8	3	3.9437	0.4083
TLTAVHDAILEDLVFPSEIVGK	2368.7	3	5.3956	0.5616
TLTAVHDAILEDLVFPSEIVGKR	2524.9	3	6.5927	0.5448
TLTEGDSPGSQ	1092.1	2	2.4442	0.249
TLTEINIAFLPYESQVYSLDSADSFQSFYSPHK	3800.1	3	4.2919	0.1723
TLTELILDAQEHVK	1610.8	2	3.687	0.3653
TLTGKEIEIDIEPTDKVER	2187.4	2	5.6048	0.3467
TLTGKTITLEVEPSDTIENVKAK	2488.8	3	5.5124	0.3386
TLTGLINVGSIDCQQYHSFCAQENVQRYPEIR	3685.1	3	4.0372	0.2148
TLTGTAALTVQSQEDNLR	1919.1	3	4.8149	0.4195
TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	3003.4	3	4.9275	0.3881
TLTIVDTGIGMTK	1350.6	2	4.6827	0.4452
TLTIVDTGIGMTKADLINNLGTIAK	2575.0	3	6.729	0.451
TLTLVDTGIGMTK	1350.6	2	4.4896	0.4578
TLTLVDTGIGMTKADLINNLGTIAK	2575.0	3	7.2696	0.5016
TLTLVDTGIGMTKADLINNLGTIAKSGTK	2948.4	3	3.7446	0.2651
TLTPAGDLQETFSGMDQVR	2067.3	2	4.2219	0.3778
TLTPIIQEYFEHGDTNEVAEMLRDLNLGEMK	3609.0	3	3.8843	0.3223
TLTPISAAYAR	1164.3	2	2.518	0.3083
TLTSDVANLANEKEELNNKLKDVQEQLSR	3301.6	3	4.0847	0.2621
TLTTVQGIADDYDK	1540.7	2	3.3082	0.3015
TLTTVQGIADDYDKKK	1797.0	2	3.9799	0.2933
TLVDIAKSQDAEVGDGTTSVTLLAAEFLK	2994.3	3	4.1863	0.3309
TLVGKNFEQVAFDETKNVFVK	2414.7	3	5.4655	0.5681
TLVGVGASLGLR	1143.4	2	3.2865	0.276
TLVLIGAQGVGR	1184.4	2	3.1289	0.2989
TLVLLDNLNVR	1270.5	2	3.6758	0.3132
TLVLLGAHGVGR	1193.4	2	2.9548	0.2577

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TLVLLMGK	875.2	2	2.7543	0.1739
TLVLSNLSYSATEETLQEVFEK	2502.8	3	5.8242	0.5197
TLVNKEEPPKELPAAEPVLSPLEGTK	2788.2	3	4.6502	0.4011
TLVNPANVTFK	1204.4	2	2.7564	0.2082
TLVQQLKEQNEALNR	1785.0	3	3.5237	0.2148
TLVSTVGSMVFNEGEAQR	1926.1	3	5.4363	0.4298
TLVSVTKEGLELPEDEEEKKKQEEK	2917.2	3	6.7958	0.3568
TLVSVTKEGLELPEDEEEKKKQEEKK	3045.4	3	4.7938	0.2801
TLVTLGKEDLSIK	1417.7	2	2.8971	0.2206
TLVTQNSGVEALIHAILR	1936.2	2	4.8361	0.4646
TLVVHEKADDLGK	1425.6	2	4.2192	0.4136
TLVVHEKADDLGKGGNEESTK	2228.4	2	6.3037	0.4328
TLVVHEKADDLGKGGNEESTKTGNAGSR	2872.1	3	6.8625	0.4277
TLVWSEKEQVEK	1476.7	2	3.3625	0.209
TLWTVLDAIDQMWLPVVR	2157.6	3	5.7317	0.3495
TLYGFGG	714.8	1	1.9449	0.2707
TLYLQSVTSIEER	1539.7	2	3.8532	0.412
TLYNNQPIDFLK	1466.7	2	2.836	0.2209
TLYNNQPIDFLKK	1594.8	2	3.7285	0.2694
TLYVEEVVPNVIEPSFGLGR	2219.5	3	5.0732	0.3988
TLYVGNLSR	1023.2	2	2.7613	0.2376
TLYVHWTDAGQLTPALLHSR	2280.6	3	4.6604	0.1339
TMADSSYNLEVQNILSFLK	2174.5	2	4.5122	0.3414
TMATMGDTLASR	1255.4	2	2.6383	0.3376
TMAVLQIEAEKAELR	1703.0	2	4.2374	0.4027
TMDASER	809.9	1	1.8138	0.16
TMGYSVTAPEDTRR	1584.7	2	2.6828	0.1314
TMIELSDNENPWTIFLETVDPELAASGATLPK	3504.9	3	3.9261	0.2527
TMIQQQGGSIVNVGSIVGLK	2030.4	2	4.7745	0.3199
TMIQSPSGVILQEAADVHAR	2124.4	3	3.4409	0.2167
TMKHTTDLDASK	1348.5	2	3.1009	0.3559
TMLDSLWAAGQELQAWK	1949.2	2	4.1197	0.3737
TMLDSLWAAGQELQAWKSPGADLLQVLTK	3172.6	3	6.1321	0.3784
TMLEDLGMDDEGDDDPVPLPNVNAAILK	2999.3	3	3.7123	0.1186
TMLEDLGMDDEGDDDPVPLPNVNAAILKK	3127.5	3	4.0201	0.3869
TMLELINQLDGFDPR	1763.0	2	3.8389	0.3764

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TMLELLNQLDGFDSR	1753.0	2	5.046	0.4444
TMLELLNQLDGFDSRGDVK	2152.4	2	4.2965	0.3068
TMLELLNQLDGFEATK	1824.1	2	5.4521	0.442
TMLELLNQLDGFEATKNIK	2179.5	2	3.3139	0.2001
TMLELLNQLDGFQPNTQVK	2190.5	2	5.7884	0.3335
TMLESAGGLIQTAR	1448.7	2	4.7922	0.2756
TMLITHMQDLQEVTQDLHYENFR	2864.2	3	5.7648	0.5169
TMNISPEQPQH	1282.4	2	3.063	0.1753
TMNIYFPKKEAVTFDQANPTQILGK	2856.3	3	5.0614	0.3849
TMQGSEVVNVLK	1305.5	2	3.5289	0.1854
TMQNTNDVETAR	1380.5	2	3.5297	0.246
TMQNTSDLDTAR	1353.4	2	3.4499	0.2919
TMQTLLSLVR	1162.4	2	2.7819	0.2285
TMSEVGGSVEDLIAK	1536.7	2	3.5663	0.3684
TMSEVGGSVEDLIAKGPVSK	2005.3	2	4.4185	0.4758
TMSIVSYNHLGNNDGENLSAPLQFR	2779.0	3	5.0438	0.3701
TMTQKDVEDMFSR	1588.8	2	3.9976	0.3691
TMVGFGPEDDHFVAELTYNYGVGDYK	2926.2	3	4.5621	0.4084
TMYVLPFSMGPVGSPLSR	1940.3	2	5.7066	0.5677
TNADTDGMVK	1052.1	2	2.5345	0.3409
TNADTDGMVKILGQK	1591.8	2	3.1488	0.2508
TNANAEKTDEEEKEDR	1879.9	2	4.4738	0.377
TNDPFIQEVALVTLGNNAAYSFNQNAIR	3082.4	3	5.5357	0.29
TNDPFIQEVALVTLGNNAAYSFNQNAIRELGGVPIIAK	4060.6	3	4.0123	0.2209
TNEAQAIETAR	1204.3	1	4.0986	0.3388
TNEERKTLLSNLEEAK	1876.1	3	3.3401	0.2279
TNEGVIEFR	1065.2	2	3.0737	0.3076
TNEIVEEQYTPQSLATLESVFQELGK	2955.2	3	7.184	0.5847
TNEIVEEQYTPQSLATLESVFQELGKLTGPNNQKR	3964.3	3	5.2815	0.386
TNEKVELQELNDR	1588.7	2	4.3813	0.341
TNEKVELQELNDRFANYIDKVR	2696.0	3	4.5087	0.434
TNENKYQGRDDEASNLVGEEK	2397.5	3	4.0802	0.3394
TNEQMHQLVAAYK	1533.7	2	4.1603	0.449
TNEQMHQLVAAYKDAYER	2168.4	3	5.1478	0.4446
TNEQMHQLVAAYKDAYERDLEADIIGDTSGHFQK	3896.2	3	5.531	0.4752
TNFDNDIALVR	1278.4	2	2.9075	0.2245

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TNFFIQLVRPGVAQPEDTVQFR	2563.9	3	4.1001	0.2265
TNGKEPELLEPIPYEFMA	2079.4	2	4.381	0.3841
TNHIGHTGYLNTVTVSPDGSLCASGGK	2687.9	3	5.835	0.3874
TNHQGIYVLQDNK	1530.7	2	2.5199	0.1168
TNHSNIMDDPFIREHIEELLR	2580.9	3	3.2313	0.2794
TNIAFLQNVLNNQQFLAGTVDTQFIDENPELFQLRPAQNR	4620.1	3	5.6231	0.2624
TNISDEESEQATEMLVHNAQNLMQSVK	3048.3	3	5.0805	0.2486
TNISDEESEQATEMLVHNAQNLMQSVKETVR	3533.8	3	5.1487	0.4384
TNKDEKDILR	1232.4	2	2.8396	0.1139
TNLAVHEDKNRVPYVK	1884.1	2	3.7553	0.3671
TNLDESDVQPVKEQLAQAMFDHIPVGVGSK	3254.6	3	5.5184	0.4705
TNLIVNYLPQNMTQDELR	2163.4	2	5.3286	0.4105
TNLKAEAETLVSR	1432.6	2	3.8545	0.2648
TNLLLQAHLSR	1266.5	2	2.5597	0.1773
TNLSVHEDKNR	1313.4	2	2.8663	0.194
TNLSVHEDKNRVPYVK	1900.1	2	4.2992	0.445
TNLTSQSSTTNLPGSPGSPGSPGSPGSPGSVPK	3039.2	3	3.3783	0.1299
TNLYQDDAVTGEAAGLALGLVMLGSK	2608.9	2	4.5236	0.3999
TNNLETGPSTR	1190.2	2	3.529	0.1865
TNNVSEHEDTDKYR	1708.7	2	4.4214	0.4378
TNPEVHNYQPQYHPNIHPSQPR	2654.8	3	3.9319	0.217
TNPPLIQEKPAK	1336.6	2	2.4827	0.1113
TNQELQEINR	1245.3	2	3.6944	0.3291
TNQELQEINRVYK	1635.8	2	3.5475	0.195
TNQELQEINRVYKEMYK	2187.5	2	4.5578	0.2843
TNQIGTVNDR	1118.2	2	2.9951	0.236
TNQLLQDIKLLENVTQEQNELLK	2726.1	3	4.781	0.3277
TNQRGAEILADTFKDYAVSTVPVADGLHLK	3231.6	3	5.0816	0.5042
TNRLAELEEFINGPNNAHIQQVGDR	2837.1	3	6.5295	0.4349
TNRPPLSLSR	1141.3	2	2.649	0.2595
TNSGGGDGPHISSK	1314.3	2	3.4078	0.2701
TNSHVKEELEHPGVEHFKEEDKLK	2861.1	3	3.8425	0.2445
TNSTFNQVVLK	1251.4	2	3.1437	0.2789
TNSTFNQVVLKR	1407.6	2	2.7506	0.2847
TNTVKVPKPIK	1225.5	2	2.6064	0.2164
TNVIQSLLAR	1115.3	2	3.298	0.2901

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TNVLGHLQQGGAPTPFDR	1909.1	2	4.15	0.4024
TNVLGHLQQGGAPTPFDRNYGTK	2472.7	3	3.3337	0.2075
TNVLYELAQYASEPSEQELLR	2454.7	3	4.906	0.4509
TNVLYELAQYASEPSEQELLRK	2582.8	3	5.4801	0.3899
TNVNGGAIALGHPLGGSGSR	1836.0	2	5.2546	0.5432
TNVVTMPTAHPR	1324.5	2	3.6476	0.3207
TPAAAAAMNLASPR	1342.6	2	3.1689	0.3136
TPAFAESVTEGDVR	1479.6	2	4.1062	0.3966
TPAGNFVTLEEGKGDLEEYGQDLLHTVFK	3209.5	3	6.951	0.5727
TPAGNFVTLEEGKGDLEEYGQDLLHTVFKNGK	3508.8	3	5.529	0.4416
TPAGNFVTLEEGKGDLEEYGQDLLHTVFKNGKVTK	3837.2	3	4.0829	0.2563
TPAIPFASYGLHHTSLLKR	2110.4	2	3.0837	0.2488
TPALIALR	855.1	2	2.5731	0.2062
TPALIVYGDQDPMGQTSFEHLK	2448.7	3	5.3987	0.3613
TPALIVYGDQDPMGQTSFEHLKQLPNHR	3194.6	3	5.0556	0.3619
TPALVFEHVNNTDFK	1732.9	2	2.4991	0.2189
TPALVNAAVTYSKPR	1588.8	2	4.4107	0.4495
TPANEKVEIQK	1257.4	2	3.2155	0.246
TPAQFDADELR	1263.3	2	3.5325	0.3432
TPAQFDADELRAAMK	1664.9	2	3.6483	0.3691
TPAQYDASELK	1223.3	2	3.8869	0.495
TPAQYDASELKASMK	1640.8	2	4.6862	0.4506
TPASPVVHIR	1077.3	2	2.5094	0.2123
TPAVEGLTEAEEEELRAELTKVEEEIVTLR	3385.7	3	6.643	0.5546
TPDFESTGLYSAMPR	1672.8	2	4.4802	0.5047
TPDGFDSVPLKTSSGGLDMDL	2153.4	2	4.3504	0.3792
TPDGGHSSQEIK	1256.3	2	2.7055	0.2458
TPDGNKSPAPKPSDLRPGDVSSK	2351.6	3	3.7882	0.2306
TPDGTENGDFLALDLGGTNFR	2211.3	2	3.2299	0.4212
TPDKVNHAVLAVGYGEK	1799.0	2	5.3375	0.4987
TPDRVSEADIQR	1387.5	3	4.4512	0.3248
TPDSGHVSQEPK	1282.3	2	2.9973	0.2643
TPDVLKK	801.0	2	2.5294	0.1158
TPEAPAHSEKPR	1320.4	2	3.219	0.2969
TPEASPEPK	956.0	2	3.1153	0.2339
TPEEGGYSYDISEK	1575.6	2	4.0463	0.4387

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TPEEYPESAK	1151.2	2	3.0007	0.2765
TPEEYPESAKVYEK	1670.8	2	4.1252	0.3467
TPELNLDQFHDK	1457.6	2	3.9376	0.3316
TPELNLDQFHDKTPYTIMFGPDK	2709.0	3	5.3416	0.4662
TPESFLGPNAALVDLDSLVSRPGPTPPGAK	3005.4	3	4.3424	0.2795
TPETLLPFAEAEAFLKK	1906.2	3	5.1939	0.4437
TPFAGVDDFFIPPTNLIINHIR	2498.9	3	4.1508	0.2798
TPFGAYGGLLK	1124.3	2	3.2546	0.3526
TPFGAYGGLLKDFTATDLSEFAAK	2521.8	2	6.1537	0.4304
TPFGSAKPLDYVEIHKVNK	2144.5	2	2.6912	0.1492
TPFHTSLHQGTSK	1441.6	2	2.6701	0.1563
TPFLLSGTSYK	1214.4	2	3.4371	0.216
TPFLLSGTSYKDLMPHDLAR	2263.6	3	5.7086	0.4907
TPFLLVGTQIDLR	1473.7	2	2.7836	0.1556
TPFLLVGTQIDLRDDPSTIEK	2359.7	2	4.6016	0.32
TPFLLVGTQIDLRDDPSTIEKLAK	2672.1	3	4.9402	0.2162
TPGDQILNFTILQIFPFTYESKR	2730.1	3	3.913	0.22
TPGKEAVAMESYAK	1482.7	2	4.3376	0.4073
TPGPGAQSALR	1055.2	2	3.02	0.3093
TPGRAGTEALPDGLSVEDILNLLGMESAANQK	3269.6	3	3.5133	0.251
TPGTGSLAAAVETASGR	1546.7	2	4.0231	0.254
TPGYVVTPHTMNLLK	1672.0	2	3.8532	0.363
TPHYGSQTPLHDGSR	1653.7	2	2.7482	0.4097
TPIAAGHPSMNLLLR	1591.9	2	3.6907	0.3766
TPIATR	658.8	1	1.7591	0.1161
TPIGSFLGSLSLLPATK	1703.0	2	5.4372	0.515
TPIGSFLGSLSLLPATKLGSIAIQGAIEK	2884.4	3	4.4712	0.2629
TPIKKPGDGR	1069.2	2	2.4233	0.1845
TPIQVLHEYGMK	1416.7	2	3.1661	0.2284
TPKDESANQEEPEAR	1701.7	2	4.3257	0.362
TPKEAIEGTYIDKK	1593.8	2	4.2656	0.1977
TPKEKEEFAVPENSSVQQFKEEISKR	3066.4	3	4.7063	0.3349
TPKGPSSVEDIKAK	1457.7	2	3.1359	0.1152
TPLAVELEVLDGHDPDPGR	2031.2	3	4.5174	0.4038
TPLEQEIFNLLHK	1582.8	2	2.8523	0.2288
TPLFDQIIDMLR	1462.7	2	3.6535	0.4013

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TPLFDQIIDMLRVEQVK	2046.4	2	4.0534	0.3512
TPLHEIALSIK	1222.5	2	2.9392	0.2362
TPLLLMLGQEDR	1386.6	2	4.0272	0.3806
TPLPSAPVLPELTAIPLTAYGPMAAAAAAAAVVR	3273.9	3	5.6963	0.4242
TPLQGILQLGQELKPK	1764.1	3	4.9667	0.4378
TPLSEAEFEEIMNR	1666.8	2	4.4109	0.3618
TPLVSVLLEGPPHSGK	1631.9	2	2.9035	0.3216
TPLYDFHLAHGGK	1456.6	2	3.2577	0.3194
TPLYLQPDAYGSLDR	1709.9	2	3.8035	0.2873
TPMGIVLDALEQQEEGINR	2114.4	2	6.3126	0.4677
TPMGIVLDALEQQEEGINRLTDYISK	2935.3	3	4.664	0.3534
TPMGLLLEALGQEQEAGS	1845.1	2	3.4244	0.3048
TPMTSQK	792.9	1	1.8806	0.1009
TPMTSQKTFESLVDFSK	1947.2	3	4.8671	0.5254
TPQAPASANLVGPR	1379.5	2	2.7255	0.1464
TPQSVTAKQPPEIDKKNEK	2139.4	3	3.3016	0.1705
TPSAAYLWVGTGASEAEK	1839.0	2	6.1969	0.4957
TPSAAYLWVGTGASEAEKTGAQELLR	2708.0	3	6.6929	0.4211
TPSALAILENANVLAR	1653.9	2	5.2854	0.3743
TPSDVKELVLDNSR	1573.7	2	4.2016	0.3978
TPSKQPGSIGSR	1215.3	2	2.8811	0.1103
TPSNELYKPLR	1318.5	2	3.4084	0.281
TPSSDVLVFDYTK	1472.6	2	3.7337	0.3906
TPSTMENDSSNLDPSQAPSLAQPLVFSNSK	3164.4	3	4.4651	0.2717
TPTAPAVNLAGAR	1239.4	2	2.7266	0.3793
TPTEALASFDYIVR	1583.8	2	5.2758	0.3616
TPTHEMFVGFTPSPVAQPHPSAGLNVDFESVFGNK	3744.1	3	4.3399	0.2766
TPTLASTPIPPTPQAPSPAVDAEIR	2528.8	3	4.1069	0.326
TPTPVHYRPHGAK	1461.7	2	2.8342	0.3385
TPTQTNGSNVPFKPR	1644.8	2	3.5191	0.2348
TPTSSGKPSAK	1061.2	2	2.5597	0.2343
TPVEEVPAAIAPFQGR	1682.9	2	2.8044	0.2594
TPVEPEVAIHR	1248.4	3	4.0826	0.2603
TPVGFIGLGNMGNPMAK	1705.0	2	4.3572	0.4519
TPVIDADKPVSSQLR	1626.8	2	4.9036	0.4658
TPVLFDIYEIK	1338.6	2	3.2152	0.1162

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TPVLFDIYEIKEAIK	1780.1	2	5.0722	0.4658
TPVPSDIDISR	1200.3	2	2.4158	0.1437
TPVQMMYLR	1139.4	2	2.5152	0.2215
TPVSEDMLGR	1105.2	2	3.4595	0.357
TPVSITEHPK	1109.3	2	2.553	0.2897
TPVTDPATGAVK	1157.3	2	3.3094	0.3095
TPVTDPATGAVKEK	1414.6	3	4.4129	0.3884
TPVTQVNEVTGTLR	1515.7	2	2.8227	0.31
TPVVTGTGPNFSLGELQGHLAYDLNPASTGLR	3284.6	3	4.4449	0.3883
TPVVTGTGPNFSLGELQGHLAYDLNPASTGLRR	3440.8	3	3.8294	0.3067
TPYHVNLLLAGYDEHEGPALYYMDYLAALAK	3514.0	3	4.5599	0.1902
TPYTDVNIVTIR	1392.6	2	2.8249	0.2855
TPYTIMFGPDK	1270.5	2	2.8375	0.2562
TPYTMSYGDSLYYNNAYGALDAYYKR	3062.3	3	4.2644	0.4521
TPYTPNSQYQMLLDPTNPSAGTAK	2596.9	2	3.3009	0.101
TPYVTTTVSAHSAK	1463.6	2	2.8	0.2513
TQADLDSLVRECPGIEPVCVDLGDWEATER	3318.6	3	3.934	0.1785
TQAPAVATT	859.9	1	1.7055	0.1973
TQAYQDQKPGTSGLR	1650.8	3	4.2772	0.3829
TQDASGPELILPASIEFR	1945.2	2	4.9043	0.4324
TQDGETALQLAIR	1416.6	2	3.1442	0.2056
TQDPAKAPNTPDILEIEFK	2128.4	3	4.6313	0.363
TQDPAKAPNTPDILEIEFKK	2256.5	3	4.294	0.3059
TQDQDENVALEACEFWLTLAEQPICKDVLVR	3579.0	3	3.9663	0.1684
TQDQISNIKYHEEFEK	2010.1	2	5.3996	0.4675
TQDQISNIKYHEEFEKSR	2253.4	2	5.0897	0.4394
TQDTINRIQDLLAEGTITGVIDDR	2658.9	3	4.289	0.2294
TQDTINRIQDLLAEGTITGVIDDRGK	2844.1	3	4.2389	0.3479
TQEEGEERAESEQEAYLRED	2399.4	3	4.5088	0.2711
TQEEIVAK	918.0	2	2.5649	0.1737
TQEELKELQAER	1474.6	2	3.4947	0.1113
TQEERAQLLQPTLEINPR	2137.4	3	4.5035	0.1614
TQEHFTHNTVR	1370.5	2	2.8689	0.2052
TQEHIEESR	1129.2	2	3.2429	0.2777
TQEKEQIKTLNNK	1574.8	2	4.4242	0.1103
TQEKEQIKTLNNKFASFIDK	2383.7	3	5.3869	0.1251

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TQEKEQIKTLNNKFASFIDKVR	2639.0	3	5.4477	0.2365
TQEKEQIKTLNNKFASFTDKIR	2641.0	3	4.2542	0.2378
TQEQISNVKYHEDFEKTK	2225.4	2	4.7325	0.3694
TQEQLALEMAELTAR	1704.9	2	3.4575	0.1994
TQEQNIQHLNHSLSHKEQLLQEFR	2959.2	3	6.3638	0.4521
TQESGDQDPQEAQK	1561.5	2	4.6104	0.3682
TQETLSQAGQK	1191.3	2	3.8481	0.3251
TQETPSAQMEGFLNR	1709.9	2	4.0868	0.413
TQFGEKIHNFGLIQEK	1890.1	2	3.5866	0.2719
TQGAVEAAK	875.0	2	2.6474	0.1719
TQGAVEAAKVGALASLIR	1756.0	3	4.1807	0.2692
TQGELFLLLDSR	1392.6	2	2.9496	0.2095
TQGFLALFSGDTGEIKSEVR	2156.4	2	4.2068	0.3701
TQGTKIASDGLK	1219.4	2	3.0256	0.2275
TQHFVSAK	918.0	1	2.2439	0.1204
TQHHVEALVEHQNGK	1727.9	2	4.6313	0.4595
TQHIQQPR	1008.1	2	2.6329	0.2127
TQIALSPNNHEVHIYK	1865.1	2	4.8229	0.3561
TQIALSPNNHEVHIYKK	1993.3	2	4.3602	0.4547
TQIAPGSQTVLGIGPGPADLIDKVTGHLK	2885.3	3	4.407	0.3384
TQIDHYVGIAR	1273.4	2	3.3772	0.3093
TQILAASYELHK	1374.6	2	3.1968	0.1881
TQIQSQESDLKSQEDDLNR	2235.3	3	3.4238	0.2065
TQKEIEQEAAVELSQLRDPQHDLDR	2950.2	3	4.3324	0.1683
TQKEIEQEAAVELSQLRDPQHDLDRVK	3177.5	3	4.1797	0.129
TQKKAEVEGKDLPEHAVLK	2121.4	3	5.8612	0.4581
TQKLQQELEAANQSLAELRDQR	2570.8	3	3.6464	0.2633
TQKPGESGINIVTADFVELGDFISTVIK	2980.4	2	2.6998	0.2319
TQLASWSDPTEETGPVAGILDTETLEKVSITEAMHR	3915.3	3	4.3326	0.1865
TQLEELEDELQATEDAK	1963.0	2	6.3832	0.5321
TQLEQLPEHIKEPIWETLSEEKEESKS	3239.5	3	4.8604	0.4071
TQLEWTEAILEDEQTQR	2091.2	2	6.3417	0.4523
TQLKGSELEITLTR	1589.8	2	3.8327	0.3071
TQLLQDVQDENKLFK	1820.0	2	4.6343	0.2811
TQLNDSLKEIHQK	1554.7	2	3.8514	0.3373
TQLPYEYYSLPFCQPSK	2065.3	2	3.0115	0.197

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TQLVSNLKK	1031.2	2	2.5812	0.1265
TQLYDKQREEYQPATPGLGMFVEVKDPEDK	3513.9	3	5.2167	0.2955
TQLYDKQREEYQPATPGLGMFVEVKDPEDKVILAR	4066.6	3	5.022	0.317
TQLYEYLQNR	1328.5	2	2.6744	0.1595
TQMLDQEELLASTR	1635.8	2	2.6787	0.2218
TQNDVDIADVAYYFEK	1892.0	2	5.6415	0.4625
TQNDVDIADVAYYFEKDVK	2234.4	3	4.0113	0.1794
TQNDVDIADVAYYFEKDVKGESLFHSK	3120.4	3	3.3987	0.1601
TQNDVLHAENVK	1368.5	2	2.7235	0.1809
TQNPMVTGTSVLGVK	1532.8	2	2.9295	0.134
TQNVLGEK	889.0	1	2.1231	0.1983
TQPAVATAATAAEK	1330.5	2	3.012	0.359
TQPDGTSVPGEPASPISQR	1925.0	2	3.4436	0.3716
TQPHHSTPTK	1134.2	2	2.4941	0.2466
TQPMTAQAASYR	1325.5	2	2.748	0.2348
TQPSSQPLQSGQVLPSATPTPSAPPTSQQELQAK	3488.8	3	5.0403	0.4295
TQPVEATDDAFWDQFWADTATSVQDVFALVPAAEIR	4013.3	3	4.4382	0.3125
TQPYDVYDQVEFDVPVGSR	2215.4	3	3.8453	0.1839
TQQAAQANITLQEQIEAIHK	2236.5	3	3.7214	0.3188
TQQMLHGLQR	1212.4	2	2.8101	0.1416
TQSNLPTSLEGLSNLADVDLSCNDLTRVPECLYTLPSLR	4250.8	3	4.9727	0.2973
TQSSASLAASYAAQQHPQAAASYR	2466.6	3	4.7825	0.4291
TQSSLVPALTDFVR	1534.7	2	3.6682	0.3801
TQSVEITKTDTEGK	1537.7	2	4.0488	0.3121
TQSVEITKTDTEGKIK	1779.0	2	4.2302	0.3721
TQTAIASEDMPNTLTEAEK	2051.2	2	5.2978	0.433
TQTAISVVEEDLK	1433.6	2	3.9964	0.2544
TQTAISVVEEDLKLLQLK	2029.4	2	4.3199	0.381
TQTSDPAMLPTMIGLLAEAGVR	2273.7	3	5.093	0.4091
TQTVTISDNANAVKSEIPTKDVPIVHTETK	3238.6	3	5.8631	0.4175
TQVAGGQLSFK	1136.3	2	2.4115	0.2301
TQVYKPPALKK	1273.5	2	2.517	0.2227
TQYACPPFDLTECSFKDGAGNSFDLSSLSR	3258.5	3	4.4366	0.4167
TRAEAEAAAVHGAR	1410.5	2	4.0591	0.326
TRDDEPVCGRPLGIR	1684.9	3	3.2862	0.3265
TRDELEVIHLIEEHR	1890.1	2	4.9952	0.3962

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TRDMGGYSTTTDFIK	1693.9	2	4.856	0.4189
TREEECHFYAGGQVYPGEASR	2387.5	3	6.0596	0.3995
TREEFLTLIR	1278.5	2	3.1948	0.1322
TREEIQEVR	1160.3	2	3.4687	0.1604
TREGNDLYHEMIESGVINLK	2319.6	3	6.2911	0.378
TREGNDLYHEMIESGVINLKDATSK	2822.1	3	7.4636	0.4519
TRELETLQQTVEELQAQVHSMDGAK	2843.1	3	6.7488	0.3145
TREYFYYVDHQGQLFLDDSK	2525.7	3	3.3973	0.2747
TRFPPEPNGILHIGHAK	1885.2	3	4.368	0.4143
TRFVASKPLEEEEMEVPVLPK	2429.8	3	3.9269	0.3394
TRIEGLLAAFPK	1316.6	2	3.4427	0.1615
TRKPLEALYGYDYFAR	1964.2	3	3.8201	0.3073
TRLEEKVEHLEEGPMIEQLSK	2496.8	3	4.0198	0.1546
TRLEQEIATYR	1380.5	2	3.1073	0.1803
TRLQQELDDLLVDLDHQR	2208.4	2	3.1689	0.3517
TRNEMTAEEK	1209.3	2	2.7179	0.1116
TRNTMSLLAANNLLAGLR	1930.3	2	4.6461	0.4182
TRPEVGEMLR	1188.4	2	2.6494	0.2177
TRPLEFAAIGDYLDTFALK	2142.4	2	2.6174	0.2207
TRPLKAENPYLFLR	1719.0	2	3.2774	0.3132
TRPVVAAGAVGLAQR	1466.7	2	3.8044	0.4305
TRQGVDDAFYTLVR	1641.8	2	3.7673	0.2755
TRRDEPTGEVLSLVGKLEGTR	2314.6	3	3.8214	0.2378
TRREAEDLQVGQVELGGGPGAGSLQPLALEGSLQ	3434.8	3	6.8006	0.4685
TRREAEDLQVGQVELGGGPGAGSLQPLALEGSLQK	3562.9	3	5.7526	0.4043
TRRPNVVLLLTDDQDEVLGGMTPLKK	2910.4	3	6.1402	0.5349
TRTFNTSTGGLLLPSDTKR	2066.3	3	3.6283	0.1005
TRTFYGLHQDFPSVVLVGLGKK	2463.9	3	3.3678	0.193
TSAADLVTETDHLVEDLIISELR	2541.8	3	4.4538	0.2907
TSAADLVTETDHLVEDLIISELRER	2827.1	3	4.3208	0.3093
TSAALSTVGSAISR	1321.5	2	4.2518	0.3888
TSADGNEKKIEMVR	1578.8	2	4.0069	0.3173
TSAEAPSHHLQQQQQQR	2103.2	2	5.3171	0.3719
TSAGHEEGATR	1116.1	2	3.2042	0.38
TSAGSYSSPPPAPYSAPQAPALSVTGPITANSEQIAR	3644.0	3	6.6751	0.4927
TSAGTTDPEEATR	1336.3	2	2.9427	0.3426

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TSAHYEENK	1079.1	2	2.5191	0.1838
TSAKEEDAFHFVSYVPVNGR	2254.4	3	3.5111	0.2395
TSASIILR	861.0	2	3.0274	0.1399
TSASPFFLAVGYHKPHIPFR	2273.6	2	3.0399	0.2975
TSATKGTGLDEAMEWLVETLK	2281.6	2	3.7043	0.2035
TSATWLALSR	1106.3	2	3.5022	0.4034
TSDDEVFKYLAK	1416.6	2	2.7985	0.2663
TSDIFGSPVTATSR	1439.6	2	4.5743	0.4055
TSDKIQEYPQMLIEFLK	2084.4	2	3.504	0.202
TSDLIVLGLPWK	1342.6	2	3.5417	0.2454
TSDSDQQAYLVQR	1511.6	2	3.769	0.3091
TSDVGGYYYEK	1282.3	2	2.6366	0.1443
TSDVGGYYYEKIER	1680.8	2	3.2693	0.2759
TSDVSSYLEGQAAK	1456.5	2	4.5801	0.4116
TSDVVVAGEFDQGSDEENIQVLK	2480.6	2	6.4395	0.4403
TSEAPKKDEEK	1262.3	2	2.6319	0.1401
TSEEEKKLLVYEALEYAKR	2300.6	3	5.018	0.4667
TSEFMPYVVFIAAPELETLR	2314.7	2	5.1593	0.4498
TSEGSAGSAGLGGGGAGAGAGVGAGGGGGSGASSGGGAGGLQPSSR	3476.5	3	7.5935	0.5311
TSEGVTNEKGTDSQAMEEEKPEGHV	2690.8	3	5.8598	0.5005
TSEIEGANQLLELFDLFR	2096.3	2	3.9216	0.2349
TSEQKKEPEPKDEVLQQK	2142.4	3	3.7598	0.2073
TSESGELHGLTTEEEFVEGIYK	2456.6	3	6.4834	0.4912
TSESGELHGLTTEEEFVEGIYKVEIDTK	3142.4	3	6.5803	0.5676
TSETLSQAGQK	1150.2	2	3.9034	0.3272
TSEVDLAKPLVK	1300.5	2	3.1574	0.2813
TSEVQDLQDEVQRENTNLQK	2375.5	3	4.0169	0.3693
TSFFQALGITTK	1314.5	2	4.5209	0.3909
TSFHALTSILK	1218.4	2	2.4204	0.2544
TSFIQYLLEQEVPGSR	1868.1	3	3.6274	0.2055
TSFLDDAFRK	1200.3	2	2.8794	0.2691
TSFQNLIEGFEALLK	1711.0	2	4.0131	0.3207
TSFTPVGDVFELNFMNVK	2046.3	2	5.6089	0.553
TSGHDHPDVATMLNILALVYR	2324.6	3	3.9066	0.3793
TSGHDHPDVATMLNILALVYRDQNK	2810.1	3	4.0538	0.2353
TSGHVDKFADFMVK	1582.8	2	4.3014	0.4245

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TSGHVDKFADFMVKDVK	1925.2	2	4.4589	0.4028
TSGPASGHALR	1054.1	2	2.6427	0.2625
TSGTEPADFALPSSR	1536.6	2	3.7333	0.4317
TSGTLISFIYPAQNPELLNK	2207.5	3	5.0724	0.4267
TSHGEVISVPHK	1291.4	3	3.7958	0.3865
TSHGHLIFPK	1137.3	2	2.6212	0.1966
TSHILSLQK	1027.2	2	2.7397	0.2288
TSIAIDTIINQK	1317.5	2	4.3446	0.3176
TSIAIDTIINQKR	1473.7	2	3.5995	0.305
TSIDAYDNFDNISLAQR	1944.0	2	5.6873	0.4426
TSIDAYDNFDNISLAQRLEKHELIEFR	3239.5	3	4.2161	0.3563
TSIEDQDELSSLLQVPLVAGTVNR	2585.8	3	5.1208	0.3783
TSIVQAAAGGVPGGGSNNGKTPVCHQCHK	2777.1	3	3.4017	0.154
TSKAEELLAEEK	1348.5	2	3.6651	0.2949
TSKDTSASAVAVGLK	1435.6	2	4.1058	0.3623
TSKETDVVNFDDIASSENLLHLTANRPK	3116.4	3	5.6947	0.4848
TSLAGDTSNSSSPASTGAK	1739.8	2	4.2244	0.4772
TSLALDESLFR	1252.4	2	3.4202	0.1891
TSLHLLMETLNATTPHYVR	2198.5	3	5.206	0.3659
TSLLDNMIGVGDMVLLEPLNEETFINNLK	3234.7	3	4.2757	0.2204
TSLLDNMIGVGDMVLLEPLNEETFINNLKK	3362.9	3	4.7181	0.2381
TSLLDNMIGVGDMVLLEPLNEETFINNLKKR	3519.1	3	4.3053	0.2397
TSLPHFHHPETSRPDSNIYK	2364.6	3	3.5209	0.3022
TSLVATPGIDKLTEK	1573.8	2	3.9843	0.4261
TSMESLIHHFK	1330.5	2	3.5301	0.356
TSMNAHSLSEEADSLKHQLDVVIAEK	2854.1	3	4.5338	0.3539
TSMNVNEIFMAIAK	1569.9	2	4.1141	0.3205
TSMTEEYRVPDGMVGLIIGR	2225.6	3	5.3262	0.386
TSNASRPNFLAPLPHEVTQLR	2349.6	3	4.1117	0.2827
TSNEVQYDQR	1240.3	2	2.9304	0.1083
TSNEVTVETDKK	1351.4	2	3.1523	0.2517
TSNHAIVLAQLITK	1509.8	2	3.9415	0.3455
TSNLNEELGQVK	1332.4	2	3.0431	0.1168
TSPADGKPR	929.0	2	2.4878	0.1201
TSPADHGGSVGSESGGSAVDSVAGEHSVSGR	2841.9	3	7.1863	0.4658
TSPDHPTSLPEPDYSEFQSHPYHR	2825.9	3	3.4503	0.143

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TSPGRVDLPGSSTTLTK	1717.9	2	4.3786	0.3723
TSPHGILDILVHER	1587.8	2	2.7488	0.337
TSPKPAVVETVTTAKPQQIQALMDEVTK	3012.5	3	4.4749	0.4208
TSPVADAAGWVDVDKETLQHR	2296.5	2	5.7971	0.4958
TSPVADAAGWVDVDKETLQHRR	2452.7	3	3.5463	0.267
TSQENISFETMYDVLSTKPVLNK	2646.0	3	4.8194	0.4707
TSQLLETLNQLSTHTHVVDITR	2507.8	3	5.2358	0.519
TSQQLQLIDEQDSYIQSR	2153.3	2	4.6642	0.3985
TSQQNVYNPSEGSTWNPFDDDNFSKLTAEELLNKDFAK	4352.6	3	4.384	0.3006
TSQTVATFLDELAQK	1652.8	2	4.5388	0.3973
TSQTVATFLDELAQKLKPLGEQER	2704.0	3	3.9255	0.2867
TSREEIFSQNR	1367.5	2	2.6855	0.1481
TSRPENAIIYNNNEDFQVGQAK	2509.7	3	5.9885	0.5585
TSSAETPTIPLGSAVEAIK	1873.1	2	4.2063	0.3548
TSSAQVEGGVHSLHSYEK	1917.0	2	4.6379	0.512
TSSESIYSRPGSSIPGSPGHTIYAK	2580.8	3	3.7678	0.1844
TSSGTKPSVKPTSATK	1577.8	2	3.5689	0.3678
TSSIHQLIAPASYSPIQPHSLIK	2489.9	3	4.8187	0.3114
TSSISGPLSPAYTGQVPYNYNQLEGR	2801.0	2	4.6199	0.3822
TSSPHKEESPKK	1355.5	2	2.9981	0.1538
TSSSETEEKKPEKPLILQSLGPK	2527.9	3	4.5052	0.2807
TSTSAVPNLFVPLNTNPK	1901.2	2	3.6241	0.3918
TSTSSSSVQAR	1111.1	2	2.7301	0.3274
TSTTAEKTDEEEKEDR	1869.9	2	4.2951	0.3365
TSTTGVATTQSPTPR	1505.6	2	3.8184	0.5129
TSTVDLPIENQLLWQIDR	2142.4	2	3.5553	0.2083
TSTVDLPIENQLLWQIDREMLNLYIENEGK	3577.0	3	4.6222	0.4553
TSVIQGIHTDHNTLK	1664.8	2	4.3613	0.3037
TSVLEMIAQAR	1219.4	2	4.0856	0.2626
TSVPENHAQSR	1226.3	2	2.4181	0.1637
TSVPKEVVDYIIFGTVIQEVK	2365.8	3	4.668	0.3905
TSVPKEVVDYIIFGTVIQEVKTSNVAR	2994.4	3	5.3174	0.4352
TSVQTEDDQLIAGQSAR	1819.9	2	4.8897	0.3769
TSVTDVKFAPK	1193.4	2	2.5419	0.1143
TSYAQHQQVR	1218.3	2	3.1552	0.3078
TSYEEFTHKDGVWNLQNEVTKER	2812.0	3	5.0826	0.4481

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TSYFPNPYNQEK	1488.6	2	3.3504	0.4402
TTAAMWALQTVEK	1450.7	2	2.7312	0.1841
TTAAMWALQTVEKER	1736.0	2	2.8343	0.283
TTAQVLIR	902.1	2	2.5083	0.1289
TTARDQDLEPGAPSMGAK	1846.0	2	4.4041	0.3305
TTDEELEEMLESGNPAIFTSGIIDSQISK	3156.4	2	3.5771	0.2385
TTDGVYEGVAIGGDRYPGSTFMDHVLR	2915.2	3	4.4958	0.3719
TTDGYLLR	939.0	2	3.1493	0.1809
TTDIFQTVDLWEGK	1653.8	2	4.172	0.3484
TTDMAPSKETEMALAK	1725.0	2	4.2733	0.3724
TTEAEKNER	1078.1	2	2.5892	0.1043
TTEAEPKPLEEPKHETK	1965.2	3	3.3313	0.3264
TTEALKSEEK	1136.2	2	2.922	0.232
TTEEALHASHGFMWYT	1882.0	2	2.6405	0.2428
TTEETSKPKDD	1251.3	2	2.8954	0.2292
TTELPAADPFALAPFPSK	1874.1	2	4.3565	0.34
TTELQDELSHLR	1442.6	2	3.2501	0.3208
TTFEDLIQR	1123.2	2	3.2012	0.2469
TTFHEASR	949.0	1	1.9754	0.207
TTGFGMIYDSLDYAK	1682.9	2	4.0832	0.1373
TTGFTFVVDR	1143.3	2	2.6215	0.2687
TTGIVETHFTFK	1381.6	2	2.8909	0.2967
TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	3198.6	3	5.0611	0.3184
TTGIVMDSGDGVTHIVPIYEGYALPHAILR	3197.7	2	2.7392	0.1581
TTGIVMDSGDGVTHTVPIYEGYALPHAILR	3185.6	3	7.0868	0.5453
TTGKPIEASIR	1173.3	2	2.6704	0.3064
TTGKPIEASIRGELSGDFEKLMLAVVK	2891.4	3	3.4912	0.1906
TTGMGAIYGMAQTTVDR	1774.0	2	2.9402	0.1729
TTGNATVDHLSK	1244.3	2	3.4797	0.3796
TTGVVLDSGDGVTHAVPIYEGFAMPHSIMR	3159.6	3	5.2777	0.3937
TTHFVEGGDAGNREDQINR	2117.2	2	4.9117	0.3459
TTHHLVYPESFR	1487.6	2	3.1674	0.3176
TTHLIAKEEMIHNLQ	1779.1	2	3.8038	0.2921
TTHTGQVLGSLVHVK	1577.8	2	4.9101	0.3646
TTHYTPLACGSNPLKR	1760.0	3	3.3547	0.2381
TTIAGVVYKDGIVLGADTR	1950.2	2	4.7226	0.4807

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TTIEAIHGLMSQVIK	1642.0	2	3.855	0.3367
TTIEAIHGLMSQVIKDK	1885.2	2	3.2708	0.283
TTIEAIHGLMSQVIKDKLFNQINIS	2815.3	3	3.6456	0.1803
TTIHEMFLSTLDPK	1633.9	2	2.7918	0.2673
TTIHQLTMQKEEDTSGYR	2139.3	2	5.0237	0.4609
TTIMAVQFDGGVVLGADSR	1938.2	2	4.6722	0.3438
TTISVAHLLAAR	1253.5	2	3.2712	0.2929
TTITMAHLLAAR	1299.6	2	3.5612	0.3583
TTITMAHLLAAREDLSK	1872.2	2	4.3661	0.3221
TTITTTTTSSSGLGSPMIVGSPR	2253.5	2	5.7758	0.5215
TTKAPTEPGKYPCGEFCPR	2083.4	2	2.5989	0.1201
TTKNEEENEKEKELQLEYLLGAFESLGK	3271.6	3	4.8069	0.2498
TTKSPSDSGYSYETIGK	1821.9	2	4.439	0.3698
TTLKFIWNQKRAHIAKSTLSQKNK	2843.3	3	3.5911	0.1485
TTLKREDKSPIAPEELALVHNLR	2632.0	3	3.7636	0.1807
TTLPGVVNGANNPAIR	1594.8	2	3.6781	0.2847
TTLPTFQSPEFSVTR	1711.9	2	3.2231	0.2909
TTLTAAITK	920.1	2	2.7382	0.1679
TTLTSDESVKDHTTAGR	1819.9	2	4.6963	0.4276
TTNFAGILSQGLR	1378.6	2	4.6238	0.3964
TTNIQGINLLFSSR	1564.8	2	4.334	0.3292
TTPDVIFVFGFR	1399.6	2	3.8844	0.4699
TTPLQTHSIIISDQVPSDQDAHQYLR	2965.2	3	4.8713	0.3467
TTPSVVAFTADGER	1451.6	2	4.085	0.5115
TTPSYVAFTDTER	1488.6	2	3.6273	0.4411
TTPSYVAFTDTERLIGDAAKNQVALNPQNTVFDAK	3798.2	3	3.6408	0.2685
TTPSYVAFTDTERLIGDAAKNQVALNPQNTVFDAKR	3954.4	3	5.0812	0.4451
TTPSYVAFTDTERLIGDAAKNQVAMNPTNTVFDAK	3789.2	3	4.5936	0.282
TTPTFFPKDILTLR	1650.9	2	2.7564	0.3498
TTQETIDKTANQASDTFSGIGKK	2442.6	3	5.1356	0.4202
TTQIINITMTK	1264.5	2	2.7581	0.1549
TTQVPQFILDDFIQNDR	2051.2	2	4.9881	0.4043
TTQVTQFILDNYIER	1842.0	2	2.763	0.114
TTRTPEEGGYSYDISEK	1934.0	3	3.2308	0.1556
TTSAKETQSIEK	1323.4	2	3.0397	0.275
TTSGYAGGLSSAYGGLTSPGLSYSLGSSFGSGAGSSSFSR	3727.9	3	8.25	0.2819

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TTSHGRVGATAAVYSAAILEYLTAEVLELAGNASK	3536.9	3	4.9109	0.3291
TTSHGRVGATAAVYSAAILEYLTAEVLELAGNASKDLK	3893.4	3	4.4149	0.3006
TTTAAAVASTGPSSR	1378.5	2	3.2702	0.1516
TTTGNKVFGALKGAVDGGLSIPHSTK	2557.9	3	4.5298	0.3532
TTTGNKVFGALKGAVDGGLSIPHSTKR	2714.1	3	3.8035	0.2652
TTTGSYIANR	1084.2	2	2.8752	0.3328
TTTLSGTAPAAGVVPSR	1586.8	2	4.215	0.4108
TTTTNTQVEGDDEAAFLER	2099.2	2	4.936	0.4416
TTVEPTPGKGPK	1212.4	2	2.7046	0.1905
TTVKDLSELGSVR	1405.6	2	2.9627	0.3155
TTVKESATEEK	1223.3	2	2.7315	0.2245
TTVKESATEEKLTPVLLAK	2059.4	2	5.7814	0.3763
TTYDSSLSSYTVPLEKDNSEEFRQR	2954.1	3	4.3848	0.2797
TTYGGAAAAVRQSKLRNTPYQAPVRR	2834.2	3	3.2176	0.1304
TTYLEDLPPPPEYELAPSKLEEEVDDVFLIR	3620.0	3	3.2494	0.2842
TTYLVLDEADR	1296.4	2	3.4076	0.2403
TTYLVLDEADRMLDMGFEPQIR	2615.0	2	2.7197	0.1205
TVAATNMNEESSR	1410.5	2	3.4243	0.3946
TVAEGHGDTLYVGTTR	1677.8	2	4.7487	0.5666
TVAEKVDAVR	1088.2	2	3.1139	0.2417
TVAELEAEKAATITPFRK	1976.3	3	5.0865	0.3834
TVAGGAWTYNTTSAVTVK	1828.0	2	4.6893	0.4657
TVAGIIVEPIQSEGGDNHASDDFFR	2675.8	3	3.342	0.1806
TVAIHSDVDASSVHVK	1665.8	2	4.7324	0.4615
TVAIPSGENQINQIALNPTGTFLYAASGNAVR	3289.6	3	6.4786	0.3976
TVAPMPPAQDHKR	1448.7	2	2.4402	0.1981
TVASPGVTVEEAVEQIDIGGVTLLR	2554.9	3	5.9144	0.3845
TVATPLNQVANPNSAIFGGAR	2099.3	2	3.1519	0.1666
TVATPLNQVANPNSAIFGGARPREEVVQKEQE	3451.8	3	3.4253	0.2668
TVAVITSDGR	1019.1	2	3.042	0.2646
TVAYHEAGHAVAGWYLEHADPLLK	2649.9	3	5.1003	0.3627
TVAYTEQK	940.0	1	2.0647	0.1022
TVDFTQDSNYLLTGGQDK	2003.1	2	4.1776	0.3648
TVDLKPDWGK	1159.3	2	2.7701	0.2276
TVDLSSHLAK	1071.2	2	2.8951	0.241
TVDLSSHLAKVTAEVVLAHLGGGSTSR	2707.0	3	6.6503	0.4689

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TVDNFVALATGEK	1365.5	2	3.8276	0.4023
TVDNFVALATGEKGFGYK	1918.1	2	4.9093	0.4529
TVEAEAAHGTVTR	1342.4	2	3.7024	0.4393
TVEEIEACMAGCDKAFTPFSGPK	2432.8	3	4.5357	0.2906
TVEELLETGLIQVATKEEELNAIR	2700.0	3	5.9855	0.3972
TVEEVLGHFGVNESTGLSLEQVK	2473.7	2	5.1074	0.4319
TVEEVLGHFGVNESTGLSLEQVKK	2601.9	3	4.9307	0.4415
TVEEVTVERNEK	1433.5	2	3.0714	0.205
TVEINNTDAEGR	1319.4	2	3.0769	0.226
TVEIPDPVEAGEEVK	1612.8	2	3.2594	0.3126
TVEIPDPVEAGEEVKVR	1868.1	2	4.179	0.4406
TVEKELTYEK	1240.4	2	2.6394	0.1769
TVENIKDPLFR	1332.5	2	3.153	0.1554
TVENLEKYVVKDGKLPLLLSR	2415.9	3	4.6267	0.2422
TVENVTVFGTASASK	1511.7	2	5.1358	0.4402
TVENVTVFGTASASKHEALKENGVTHPIDYHTTDYVDEIKK	4547.0	3	3.8519	0.207
TVEPFSELGLGEGPQLQILEEMKPLESLALEEASGPVSQSQK	4498.0	3	4.6719	0.4352
TVESEAASYLDQISR	1669.8	2	3.6395	0.233
TVESITDIR	1034.1	2	3.4191	0.2794
TVESITDIRADIDKK	1704.9	2	3.1097	0.1307
TVESITDIRADIDKKYR	2024.3	3	3.3498	0.2952
TVESLEETLKK	1277.4	2	2.8807	0.2662
TVETRDGQVINETSQHHDDLE	2424.5	3	5.0933	0.3903
TVEVAEGEAVR	1160.3	2	4.2129	0.3825
TVEVAEGEAVRTPQSVTAK	1973.2	2	5.1057	0.4283
TVEVPFKGDVEHTIR	1727.9	2	3.7676	0.3198
TVEVPYKGDVENTILDILGGLR	2402.7	3	4.1194	0.3372
TVEYLHSQGVVHR	1525.7	2	3.4774	0.3702
TVFAEHISDECKR	1535.7	2	2.6023	0.2694
TVFDEAIR	951.1	2	2.4175	0.2042
TVFETLDIGWQLLR	1692.0	2	4.1769	0.2498
TVFFESLER	1128.3	2	2.801	0.2106
TVFGVEPDLTR	1234.4	2	2.9401	0.156
TVFGVEPDLTREGGSIPVTLTFQEATGK	2951.3	3	4.3894	0.2261
TVFQKENGTVTAANASTLNDGAAALVLMTADAAK	3366.7	3	6.4587	0.4594
TVFQKENGTVTAANASTLNDGAAALVLMTADAAKR	3522.9	3	6.7552	0.5266

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TVGEIKQFVSQLPHMQAAR	2141.5	3	3.5958	0.259
TVGFGTNNSEHITYLEHNPYEK	2551.7	3	4.5395	0.3471
TVGIADSNYNWFYGPESQLVFLDKFILK	3266.7	3	3.5759	0.1548
TVGIDDLTGEPLIQREDDKPETVIK	2783.1	3	4.1108	0.3085
TVGIDDLTGEPLIQREDDKPETVIKR	2939.3	3	4.7721	0.244
TVGLFLQGGKDWSPTLYIR	2152.5	3	5.1054	0.3784
TVGMLSNMIAFYDMAR	1821.2	2	4.3493	0.4465
TVGMVAGDEETYEVFADLFDPVIQER	2932.2	3	4.2306	0.3764
TVGQLYKEQLAK	1378.6	2	4.374	0.2445
TVGQLYKESLTK	1367.6	2	3.8873	0.3361
TVGVEPAADGKGVVVVIK	1739.0	2	4.8252	0.4474
TVGVEPAADGKGVVVVIKR	1895.2	2	2.655	0.1751
TVHTEWTQR	1158.2	2	2.8013	0.1113
TVHYLPILFIDQLSNR	1930.2	3	3.9346	0.1896
TVIAQHHVAPR	1229.4	2	2.473	0.2023
TVIDYNGER	1067.1	2	2.6942	0.243
TVIGDHGDELFSVFGAPFLK	2150.4	2	4.5421	0.4854
TVIGDHGDELFSVFGAPFLKEGASEEEIR	3151.4	3	5.2652	0.4028
TVIGDHGDELFSVFGAPFLKEGASEEEIRLSK	3479.8	3	6.0234	0.4538
TVIIEQSWGSPK	1345.5	2	4.3797	0.2686
TVIIHDRPDITHPR	1670.9	2	2.469	0.102
TVIKEGEEQLQTQHQK	1897.1	3	4.4862	0.2792
TVIKKDEQEHEFYK	1795.0	2	4.6353	0.4035
TVIPGMPTVIPPGLTR	1650.0	2	3.0183	0.2945
TVIQPGIYHPDIQLLHPINLEFLVNR	3041.5	3	3.9605	0.3085
TVITPDPNLSIDQVGVPR	1922.2	2	4.14	0.4014
TVIVHGFTLGEKGEK	1615.9	2	3.8751	0.3911
TVIVNMVDVAK	1189.5	2	2.6568	0.1176
TVKEEAEKPER	1316.4	2	3.5238	0.2211
TVKEEAEKPEREAK	1644.8	2	4.3848	0.2651
TVKENWKNLSDSEKELYIQHAK	2662.0	3	3.6349	0.1487
TVKEVLPALENNKEQIQK	2082.4	2	4.4547	0.34
TVKEVLPALENNKEQIQKIIETLTQQLQAK	3450.0	3	3.7096	0.2091
TVKHPTLLQDPDLR	1633.9	3	4.3593	0.3303
TVLCGTCGQPADKASASGSGAQVGGPISSGSSASSVTVTR	3641.0	3	6.712	0.504
TVLDPVTGDLSDTR	1489.6	2	3.8488	0.369

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TVLDQQQTPSR	1273.4	2	3.622	0.2641
TVLEHYALEDDPLAAFKQR	2217.5	3	3.3846	0.1734
TVLELMNPEAQLPQVYPFAADLYQK	2880.3	3	5.2632	0.3537
TVLELQYVLDKLGDDEVR	2106.4	2	4.103	0.3234
TVLELQYVLDKLGDDEVRTDLK	2563.9	3	4.1527	0.2797
TVLGQQILGQLDSSSLALPSEAK	2356.7	3	3.468	0.2482
TVLGTPEVLLGALPGAGGTQR	2008.3	3	4.3532	0.2918
TVLGTPEVLLGALPGAGGTQRLPK	2346.8	2	3.8634	0.1806
TVLIMELINNVAK	1458.8	2	5.2141	0.3651
TVLLSIQALLSAPNPDDPLANDVAEQWKTNEAQAIETAR	4205.6	3	4.8665	0.4126
TVLNSEVLEQR	1288.4	2	3.2614	0.219
TVLQIDDNVTSAVEGINR	1945.1	2	2.9398	0.3302
TVLQQVIEDGSKYGLK	1779.0	2	2.6275	0.2674
TVLQRPLSLIQGPPGTGK	1863.2	2	3.5355	0.2483
TVLRDNAIPTIFDLTSHLNNPHSR	2733.0	3	4.1059	0.2676
TVLSANADHMAQIEGLMDDVDFK	2521.8	2	5.4183	0.4302
TVLSANADHMAQIEGLMDDVDFKAK	2721.1	3	5.8786	0.3324
TVLSNVQEELDR	1403.5	2	3.2436	0.2538
TVLVIAHR	909.1	2	2.4715	0.1085
TVLVNADGEEVAMR	1504.7	2	4.0743	0.4602
TVLWNPEDLIPLPIPK	1846.2	2	2.8487	0.1907
TVMIPGPQLKPEEEYEEAQGEAQKPQLA	3112.5	3	4.158	0.2596
TVMPYISTTPAK	1309.6	2	3.0165	0.2831
TVMVQEGNVESAYR	1583.7	2	4.4489	0.3739
TVNVVQFEPSK	1248.4	2	3.3286	0.3035
TVNVVQFEPSKGAIGK	1674.9	2	3.6614	0.2191
TVPEELVKPEELSK	1598.8	2	3.2164	0.3615
TVPFCSTFAAFFTR	1595.8	2	3.198	0.3989
TVPKTVDNFVALATGEKGFGYK	2343.7	3	3.3532	0.2249
TVPLAGHVGFDSLPDQLVNK	2108.4	3	4.8798	0.4642
TVPNDATQTKENESKA	1733.8	2	2.8694	0.3919
TVPPAVTGITFLSGGQSEEEASINLNAINK	3059.4	3	5.2331	0.4187
TVQDALESLVAR	1302.5	2	3.6131	0.288
TVQDLTSVVQTLLQQMQDKFQTMSDQIIGR	3453.9	3	5.1399	0.4561
TVQGPPTSDDIFER	1562.7	2	3.5754	0.4863
TVQGSGHQEHINIHK	1685.8	2	3.9204	0.2803

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TVQHQDSQVNALEVTPDR	2038.2	2	3.3391	0.2975
TVQLTSSELESTLETLKAENQPIRDVLK	3144.5	3	3.5715	0.1141
TVQPVAMGPDGLPVDASSVSNNYIQTLGR	2988.3	3	5.0668	0.4295
TVQQHAGETDPVTTMR	1771.9	2	5.42	0.502
TVQQKLEQLNQYPDFNNYLIFVLTK	3058.5	3	5.197	0.1709
TVQSLEIDLDSMR	1507.7	2	4.631	0.4194
TVQSLEIDLDSMRNLK	1863.1	2	3.574	0.2394
TVQTAAANAASTAASSAAQNAFK	2153.3	3	4.3705	0.2936
TVQTAAANAASTAASSAAQNAFKGNQI	2565.7	3	4.4156	0.3289
TVQTDHNAVQR	1269.3	2	3.3963	0.3664
TVQYQNELHK	1260.4	2	2.8005	0.148
TVRDTLLALHQHGHSGPFESK	2331.6	3	3.8815	0.2922
TVSDGLHHPSQLHSK	1643.8	2	3.4279	0.3642
TVSDLIDQKVYELQASR	1966.2	3	5.7735	0.4946
TVSGVNGPLVILDHVK	1648.9	2	3.5559	0.3692
TVSGVNGPLVILDHVKFPR	2049.4	2	5.122	0.5302
TVSHEAEVHAESLQQKLESSQLQIAGLEHLR	3469.8	3	4.153	0.1222
TVSIEEFFGDLNNFR	1788.9	2	4.1409	0.3902
TVSKVDDFLANEAK	1537.7	2	4.0552	0.3004
TVSLGAGAKDELHIVEAEAMNYEGSPIK	2931.3	2	6.2083	0.4938
TVSLGAGAKDELHIVEAEAMNYEGSPIKVTLATLK	3658.2	3	8.5264	0.5877
TVSLLDENNVSSYLSK	1769.9	2	4.7742	0.3921
TVSLVHESFLDLSLPVLDDQSGKK	2629.0	3	4.7497	0.44
TVSNDSFFNFFAPPEVPESGDLDDDAEAILAADFEIGHFLR	4517.8	3	3.6658	0.3309
TVSPDRLELEAAQK	1557.7	2	3.4849	0.2667
TVSPDRLELEAAQKFLER	2103.4	3	4.5163	0.4088
TVSSHEVFLQR	1303.4	2	2.5953	0.2066
TVSTGTALSK	965.1	2	2.5846	0.1618
TVSTLHHVLQR	1291.5	2	3.4023	0.3979
TVTAMDVVYALK	1311.6	2	3.9985	0.4834
TVTAMDVVYALKR	1467.8	2	3.6997	0.4137
TVTEYKIDEDGKK	1526.7	2	4.0834	0.3313
TVTNAVVTVPAYFNDSQR	1983.2	2	5.2118	0.4427
TVTPALSSNVLPR	1355.6	2	3.6883	0.2101
TVTSATIVYHLAR	1432.6	2	2.8524	0.1383
TVVAGSSDAAQK	1134.2	2	2.7509	0.1872

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TVVDFETDVLFLVPTEIALAQHR	2615.0	3	4.6262	0.3249
TVVGQITVDMMYGGMR	1759.1	2	2.8055	0.3584
TVVNKDVFRDPALK	1602.9	2	3.8489	0.1848
TVVSGLVNHVPLEQMQNR	2022.3	2	4.4362	0.4341
TVVSGLVQFVPKEELQDR	2045.3	2	4.0014	0.3531
TVVTGIEMFHK	1262.5	2	3.4593	0.3296
TVWDWELMNDIKPIWQR	2231.6	2	2.7477	0.2027
TVWDWELMNDIKPIWQRPSK	2543.9	2	4.3751	0.3437
TVWDWELMNDIKPIWQRPSKEVEEDEYK	3566.0	3	4.6606	0.3376
TVWDWELMNDIKPIWQRPSKEVEEDEYKAFYK	4075.6	3	4.2812	0.1951
TVWLGHPEKR	1223.4	2	2.8906	0.1779
TVWSSGDDKEQLVK	1592.7	2	3.7569	0.294
TVYVGNLNSQTTTADQLLEFFK	2490.7	2	4.2386	0.4061
TWDHFWLNEGHTVYLER	2204.4	3	3.7425	0.2554
TWEQQQEVVSR	1390.5	2	3.9813	0.2324
TWGDLGAAAGGGTPSK	1446.5	2	2.5619	0.1899
TWIEGLTGLSIGPDFQK	1863.1	2	4.2724	0.3235
TWITNSPMADLFVVWAR	2008.3	2	3.5408	0.3618
TWNDPSVQQDIK	1431.5	2	4.0361	0.3159
TWNDPSVQQDIKFLPFK	2064.3	2	4.1495	0.3973
TWNDPSVQQDIKFLPFKVVEKK	2648.1	3	4.3561	0.3612
TWPDHGVPSDPGGVLDFLEEVHHK	2669.9	3	4.1341	0.2798
TWWNQFSVTALQLLQANR	2177.5	2	3.4419	0.2101
TWYAKLDEEAENLVATVVPTHLAAAVPEVAVYLK	3713.2	3	4.298	0.2473
TYADYESVNECMEGVCK	1942.1	2	3.5571	0.3562
TYAEPLTAAMVEFYTMSQER	2339.6	2	5.6476	0.5257
TYAYLFSHPSR	1342.5	2	3.3536	0.4426
TYDATTHFETTCDDIKNIYK	2380.6	3	4.7072	0.429
TYDATTHFETTCDDIKNIYKR	2536.8	3	4.6209	0.3778
TYDLPGNFLTQALTQR	1839.0	2	3.0802	0.1925
TYDLYITYDKYYQTPR	2104.3	3	3.6488	0.3822
TYDRDNSGMIDKNELK	1900.1	2	3.7881	0.2188
TYEDIDKR	1040.1	2	2.7302	0.2565
TYEDIKENLESR	1497.6	2	3.8621	0.3878
TYEEGLKHEANNPQLK	1872.0	2	4.6094	0.4573
TYEEGLKHEANNPQLKEGLQNMEAR	2901.2	3	5.8636	0.3898

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TYEQVLENLESK	1453.6	2	3.0022	0.246
TYEQVLENLESKR	1609.8	2	3.6431	0.3042
TYFPHFDLSHGSAQVK	1835.0	2	3.7886	0.504
TYGADLASVDFQHASEDAR	2054.1	2	5.4378	0.4904
TYGADLASVDFQHASEDARK	2182.3	2	5.4472	0.4965
TYGEIFEKFHPIR	1637.9	2	2.6431	0.2272
TYGEPESAGPSR	1251.3	2	3.3513	0.3052
TYGLPCHCPFKEGTYSLPK	2142.5	2	3.3606	0.2405
TYHALSNLPK	1144.3	2	2.8327	0.225
TYHSVGDSVLR	1234.3	2	2.6745	0.2269
TYIGEIFTQILVLPYVGK	2055.4	2	3.8838	0.2344
TYIPPKGETK	1134.3	2	2.553	0.182
TYIRQDNER	1195.3	2	2.6877	0.148
TYKYVNMQDPEMDMK	1894.2	2	4.8973	0.3745
TYLGDPIPYDPQITAEELAEK	2364.6	2	2.9108	0.2177
TYLHTYESEI	1256.3	2	2.9955	0.1235
TYLSEGPYYVKPVSTTAVEGAE	2362.6	2	4.51	0.3316
TYLVSGQPLEEIITYYPAMK	2317.7	2	5.0281	0.4366
TYNFLPEFLVSTQK	1687.9	2	4.3012	0.4146
TYNFLPEFLVSTQKTYGADLASVDFQHASEDAR	3723.0	3	4.9677	0.3678
TYNFLPEFLVSTQKTYGADLASVDFQHASEDARK	3851.2	3	3.7455	0.1238
TYNRVPLHKPTDWQK	1884.1	2	3.5216	0.266
TYPEWHVATEPVATWQNIQAAGTQK	2828.1	3	4.1909	0.3014
TYPKDPYQEEEWPQGFGQLTK	2542.7	3	3.3758	0.1309
TYQELLVNQNPIAQPLASR	2156.4	2	5.1074	0.4314
TYQFLQEYLDAIKK	1761.0	2	3.7478	0.3007
TYRPELIKDGK	1320.5	2	2.9694	0.1676
TYRPLNDVHIK	1356.6	3	4.0899	0.3626
TYRPLNDVHIKDITIHANPFAQ	2564.9	3	4.3361	0.3522
TYSAKLDNAR	1139.2	2	2.4453	0.2539
TYSEDNFEELQYFPNFYALLK	2632.9	3	5.2734	0.3312
TYSLGSALRPSTSR	1496.7	2	2.6326	0.384
TYSTSFTPMYHAVTK	1735.0	2	4.3826	0.5374
TYSVEYLPK	1100.2	2	2.5451	0.1927
TYSWDNAQVILVGNK	1708.9	2	3.9625	0.4024
TYSWDNAQVLLVGNK	1708.9	2	4.5098	0.3882

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
TYSYLNKLPVK	1326.6	2	3.1126	0.3378
TYSYLNKLPVKSEYPSIK	2131.5	3	4.3913	0.4631
TYSYLTPDLWK	1387.6	2	3.6773	0.3752
TYSYLTPDLWKETVFTK	2093.4	2	2.4298	0.1658
TYTAYVDLEKDFAAEVVHPGDLK	2582.8	3	4.6649	0.3977
TYTETVNHHYLLFQDTDLGSFHDLLR	3137.4	3	5.4785	0.3622
TYTIANQFPLNK	1410.6	2	4.0535	0.3287
TYTIANQFPLNKLTELLR	2136.5	3	3.5735	0.3651
TYTIRNEHVDYVDVGGAYVGPTQNR	2826.0	3	5.413	0.3992
TYTVNHETSHPPPSK	1695.8	2	2.8864	0.324
TYVGVVDGENELASPK	1678.8	2	4.2797	0.327
TYVTPPGTGFLPGDTAR	1750.9	2	3.7839	0.3633
TYWEDNKNSLISYLEQIHR	2410.6	3	5.6414	0.4853
TYYMSGGLQPVPIVFR	1829.2	2	4.3346	0.239
VAAALDDGSALGR	1216.3	2	3.7318	0.3529
VAAALDDGSALGRFER	1648.8	2	2.687	0.1776
VAAALPGMESTQDR	1446.6	2	3.2669	0.3663
VAAALTAMDKPLGR	1414.7	2	3.3814	0.3506
VAAENALSVAEEQIR	1600.8	2	4.0374	0.3538
VAAGLPPILVHTDAAQALGK	1943.3	2	3.5118	0.3845
VAAGLQIK	800.0	1	2.2286	0.1643
VAAGVLCELAQDKEAAEAIEAEGATAPLTELLHSR	3579.0	3	6.9206	0.5146
VAAHITGTR	926.1	2	2.683	0.3398
VAAIEALNDGELQK	1471.6	2	4.4704	0.1069
VAAIEALNDGELQKAIDLFTDAIK	2559.9	3	5.9854	0.1063
VAAIEALNDGELQKAIDLFTDAIKLNPR	3040.5	3	5.682	0.5298
VAAKLEVAPISDIIAIK	1752.1	2	3.6466	0.29
VAAKLEVAPISDIIAIKSPDTFVR	2555.0	3	6.3252	0.4991
VAALAEEKSR	1074.2	2	2.9667	0.2257
VAALFPALRPGGFQAHYR	1972.3	2	2.8485	0.1919
VAANAPK	670.8	1	1.7668	0.1859
VAANAVDPKNDSHVLIELHK	2171.4	3	4.302	0.337
VAAPDVVVPTLDTVR	1552.8	2	3.0866	0.2236
VAASIGNAQK	959.1	2	2.5244	0.1257
VAASNIVQMKDDHDK	1671.9	2	4.0605	0.4241
VAASVLNPYVK	1161.4	2	3.3666	0.2721

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VAATRQEIFQEQLAAVPEFR	2304.6	2	4.5318	0.4274
VAAYDKLEK	1037.2	2	2.7537	0.2345
VAAYDKLEKTK	1266.5	2	2.6602	0.1038
VACIGAWHPAR	1181.4	2	2.5871	0.1018
VADAATEVQHK	1169.3	2	3.083	0.3755
VADALTNAVAHVDDMPNALSALSDLHAHK	2998.3	3	6.7198	0.4984
VADALTNAVAHVDDMPNALSALSDLHAHKLR	3267.7	3	3.4218	0.3712
VADAMKQMQEK	1279.5	2	2.8436	0.2316
VADGLPLAASMQEDEQSGR	1975.1	2	3.4975	0.4129
VADGLPLAASMQEDEQSGRDLQQYQSQAK	3165.4	3	3.4277	0.3203
VADHSGQVK	941.0	2	2.6643	0.1747
VADHSGQVKTK	1170.3	2	2.5136	0.2057
VADIGLAAWGR	1129.3	2	3.6043	0.3609
VADILTQLLQTDDSAEFNLVNNALLSIFK	3207.6	2	3.8601	0.4247
VADILTQLLQTDDSAEFNLVNNALLSIFKMDAK	3653.2	3	4.7646	0.3684
VADISGDTQK	1034.1	2	3.1884	0.2765
VADISGDTQKAK	1233.4	2	3.541	0.1743
VADKIQLINNMLDKVNEMIIGGGMAFTFLK	3326.0	3	6.7813	0.4274
VADLSPIPVVLYSVPANTGLDLPVDAVVTLSQHPNIVGMK	4141.8	3	3.9336	0.2561
VADLTEQYNEQYGAVR	1857.0	2	5.497	0.396
VADPAYLPTQQDVLR	1686.9	2	4.2154	0.1833
VADPDHDHTGFLTEYVATR	2145.3	3	5.0389	0.5043
VADPTPFHIQAEVTMK	1785.1	2	4.3048	0.4354
VADQDGDSMATR	1266.3	2	3.0314	0.2687
VADQLRDQLEKGNLR	1756.0	2	3.5285	0.161
VADSSKGPDEAK	1204.3	2	3.3954	0.2433
VADSSKGPDEAKIK	1445.6	2	3.5219	0.1728
VADWTGATYQDKR	1511.6	2	3.6261	0.3709
VAEAEKQLGAAERDFIHTASISFLTPLR	3072.5	3	4.075	0.3743
VAEAHENIIHGSGATGK	1691.8	2	5.2553	0.516
VAEDEAEAAAAAK	1246.3	2	4.3647	0.4103
VAEEHAPSIVFIDEIDAIGTK	2255.5	3	4.7886	0.4872
VAEEHAPSIVFIDEIDAIGTKR	2411.7	3	5.4168	0.4626
VAEELALEQAKK	1329.5	2	3.3966	0.224
VAEELALEQAKKESEDQKR	2202.4	2	5.3477	0.4414
VAEELVAAAR	1029.2	2	3.3136	0.1941

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VAEGKQEEIQQK	1387.5	2	3.5814	0.1458
VAEIEHAEKEK	1283.4	2	3.3594	0.2511
VAEKEELEQGSRPAPTLEEEKIR	2639.9	3	4.808	0.2939
VAEKEGWPLDIR	1413.6	2	2.9066	0.1927
VAEKEPINK	1028.2	2	2.5815	0.1178
VAEKLDEIYVAGLVAHSDLDER	2443.7	3	6.3475	0.4995
VAEKLEALSVKEETKEDAEEK	2376.6	3	5.2554	0.3773
VAEKLEALSVKEETKEDAEEKQ	2504.7	3	4.9979	0.3774
VAELSSDDFHLDR	1504.6	2	3.0507	0.2083
VAELYSIHNSGDKSDIQDLLESVR	2689.9	3	4.3761	0.3588
VAENVADKNEEPSSNHIPHGK	2273.4	3	3.9385	0.209
VAEQAANDLR	1087.2	2	3.5291	0.2974
VAEQAANDLRAQVTELEDELTAAEDAK	2902.1	3	5.9685	0.417
VAEQAANDLRAQVTELEDELTAAEDAKLR	3171.4	3	5.8245	0.3544
VAEQTPLSALYLASLIK	1818.1	2	4.2071	0.4021
VAEQTPLTALYVANLIK	1845.2	2	5.0091	0.4142
VAEQVGIDRGDIPDLSQAPSSLLDALEQHLASLEGK	3774.1	3	6.6117	0.4097
VAEQVGIDRGDIPDLSQAPSSLLDALEQHLASLEGKK	3902.3	3	5.3173	0.333
VAEVEGEQVDNK	1317.4	2	4.2708	0.3281
VAEVEGEQVDNKAK	1516.6	2	4.3143	0.3092
VAEVLFDAADANAIEEVNLAYENVK	2709.0	3	4.3943	0.3408
VAEVLNDPENMEK	1488.6	2	3.0639	0.2422
VAFITGGGTGLGK	1178.4	2	3.8492	0.2767
VAFTGSTEVGK	1096.2	2	3.2499	0.1237
VAGALAEAGVGLEEIAK	1598.8	2	4.7346	0.4334
VAGALAEAGVGLEEIAKQVNVVTK	2367.7	3	4.034	0.346
VAGAQIQGAK	943.1	2	3.1478	0.1919
VAGDIESLLDR	1188.3	2	3.8861	0.3346
VAGGAAPSKPASAK	1212.4	2	2.798	0.2362
VAGGPQMIQLSLDGK	1514.8	2	3.57	0.2262
VAGHPLAQNER	1192.3	2	3.2542	0.3583
VAGHPNIVINNAAGNFISPTER	2292.5	2	6.5127	0.4305
VAGHSLGYGFVNYVTAK	1784.0	2	3.5215	0.3222
VAGIESHSELQISR	1526.7	2	3.9377	0.3968
VAGISLAYSSVQDVQK	1665.9	2	4.1571	0.4044
VAGMDVELTVEER	1448.6	2	3.669	0.3492

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VAGMLQSFQGK	1166.4	2	2.8063	0.3088
VAGNFHFAPGK	1145.3	2	2.6349	0.1735
VAGNPKPK	811.0	2	2.4597	0.1372
VAGQDGSVVQFK	1235.4	2	3.2715	0.2588
VAGSVTELIQAAEAMK	1618.9	2	4.9299	0.4626
VAGYAALLEQYQK	1454.7	2	4.2757	0.327
VAHAKEENLSMHQMLDQTLLELNNM	2911.3	3	3.3738	0.1224
VAHALAEGLGVIACIGEK	1752.1	2	6.0472	0.4866
VAHALAEGLGVIACIGEKLDER	2265.6	2	4.9548	0.5132
VAHALAEGLGVIACIGEKLDEREAGITEK	2994.4	3	3.8274	0.3316
VAHEPVAPPEDKESESEAK	2050.2	3	3.8887	0.3537
VAHEPVAPPEDKESESEAKVDGETASDSESR	3284.4	3	4.0956	0.3577
VAHFGYHWSLMER	1633.9	2	3.0633	0.4027
VAHHASENNR	1135.2	2	3.0717	0.247
VAHMEFCYQELCQLAAER	2142.5	2	3.6	0.2491
VAHMETSLGQAR	1300.5	2	2.7229	0.2213
VAHPIRPKPPSATSIPAILK	2094.5	2	3.1036	0.1275
VAHQLQALR	1036.2	2	2.9674	0.2376
VAHSDKPGSTSTASFR	1648.8	2	3.844	0.4026
VAHSFNCTPIEGMLSHQLK	2113.4	3	3.8383	0.3751
VAIAALEVLEEENLAENADKLGIILR	2808.2	3	4.7402	0.3099
VAIAALEVLEEENLAENADKLGIILRNELMK	3424.0	3	6.7076	0.4279
VAIAALEVLEEENLAENADKLGIILRNELMKLPSDVVTAVR	4462.2	3	5.1116	0.3958
VAIDNTNPDAASR	1344.4	2	3.7872	0.3999
VAIEHLDK	925.1	2	2.94	0.1829
VAIEHLDKISDSVLVDIKDTEPLIQTAK	3092.5	3	7.8223	0.5478
VAIHYINPPNPAKDNFTFK	2187.5	2	4.3891	0.3522
VAIIEELVVGYETSLK	1764.1	2	2.8743	0.2167
VAIIHQHLGR	1144.4	2	2.7835	0.2638
VAILVDDMADTCGTICHAADKLLSAGATK	2905.4	3	5.5189	0.3372
VAILVDDMADTCGTICHAADKLLSAGATR	2933.4	3	4.9117	0.4495
VAIVKPGVPMEIVLNK	1708.1	2	3.7756	0.3499
VAIVKPGVPMEIVLNKESR	2080.5	3	4.6888	0.3425
VAIYKLTGAVMHYGNMKFK	2172.6	2	3.3926	0.1112
VAKENNVDAVHPGYGFLSER	2203.4	3	4.1542	0.3187
VAKEVDPQGQR	1227.4	2	2.8682	0.1643

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VAKLDTSQWPLLLK	1612.9	2	3.4551	0.2658
VAKLIIQQCQQLHCLR	1895.3	2	2.9119	0.1016
VAKPVVEMDGDEMTR	1677.9	2	4.4357	0.4894
VAKQDAAMK	962.1	2	2.5672	0.1683
VAKVEPAVSSVVNSIQVLTSK	2156.5	2	3.2038	0.3557
VALDMTTLTIMR	1365.7	2	3.4689	0.3492
VALEIFQHSK	1172.4	2	2.4614	0.2637
VALENDDRSEEEKYTAVQR	2253.4	3	3.9081	0.1163
VALIGDAAHR	1023.2	2	2.4636	0.1533
VALIGSPVDLTYTYDHLGDSPK	2362.6	2	4.7677	0.4524
VALILQNVDLPN	1309.5	2	3.2978	0.1671
VALLLLDQGASPHAAAK	1676.0	2	3.0786	0.2204
VALLLLEKEVLDKNDMVELLGPRPFAEK	3181.8	3	6.5775	0.4742
VALLSGGGSGHEPAHAGFIGK	1963.2	2	5.3967	0.5149
VALNTLAR	858.0	2	2.6309	0.1077
VALNVSCANLLDKDIGSK	1861.2	2	4.3478	0.4485
VALQAEKLDHHPEWFNVYNK	2439.7	3	4.5415	0.4081
VALQFPDQLLGDAVAVAAR	1955.2	2	2.8927	0.1804
VALRGEDVPLTEQTVSQVLQSAK	2469.8	2	5.1497	0.4987
VALRGEDVPLTEQTVSQVLQSAKEQIK	2968.4	3	6.8474	0.4326
VALRNDSYTLHK	1417.6	3	3.9831	0.3369
VALSNMNVIDRKPYPDDENLVEVK	2760.1	3	5.6064	0.2933
VALSPAGVQNLVK	1296.5	2	2.9673	0.2245
VALTGLTVAEYFR	1440.7	2	4.9226	0.5025
VALTGLTVAEYFRDQEGQDVLLFIDNIFR	3344.8	3	6.2773	0.3839
VALVNDSLSDVTSTTSSR	1853.0	2	4.225	0.5434
VALVTFNSAAHNKPSLIR	1939.3	2	5.0377	0.4572
VALVTFNSAAHNKPSLIRDLLDTVLPHLYNETK	3692.2	3	3.9483	0.2111
VALVYGQMNEPPGAR	1602.8	2	5.3653	0.3575
VAMHILNNGR	1125.3	2	2.6561	0.299
VAMQDATAQMAMLQFISSGLSK	2329.7	3	6.3862	0.4942
VAMSHFEPNEYIHYDLLEK	2336.6	3	5.9168	0.4149
VANDNAPEHALRPGFLSTFALATDQGSK	2929.2	3	5.1529	0.3996
VANDNAPEHALRPGFLSTFALATDQGSKLGLSK	3427.8	3	4.0341	0.2322
VANEAEFILNR	1276.4	2	2.4372	0.1473
VANEAEFILSR	1249.4	2	3.0207	0.2108

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VANHMDGFQR	1175.3	2	3.0127	0.281
VANIIAEVAKNEFMR	1706.0	2	3.6675	0.2469
VANILHDDCAFLSAFGDVSKPER	2505.8	3	6.4396	0.5484
VANPKDIIHFFR	1457.7	3	3.9407	0.2089
VANPSGNLTETYVQDR	1764.9	2	5.0928	0.5318
VANREENEILPPDHLNGVKLEMDGHLNR	3211.6	3	3.3687	0.2485
VANVSLLALYK	1191.4	2	4.6668	0.3567
VAPAEPQEAPDSTAAGGSASK	1942.0	3	4.1847	0.4058
VAPAEPQEAPDSTAAGGSASKR	2098.2	2	4.2791	0.4192
VAPAPAVVK	852.1	1	2.6047	0.2536
VAPAPAVVKKQEAK	1436.7	2	2.8223	0.1919
VAPDEHPILLTEAPLNPKINR	2338.7	3	3.2469	0.1806
VAPEEHPTLLTEAPLNPK	1957.2	2	4.9461	0.3995
VAPEEHPVLLTEAPLNPK	1955.2	2	4.6567	0.3993
VAPEEHPVLLTEAPLNPKANR	2296.6	2	5.1964	0.5014
VAPEEHPVLLTEAPLNPKANREK	2553.9	2	5.0852	0.3994
VAPPGLTQIPQIQK	1490.8	2	2.7291	0.2605
VAPSAVLGPNVSIGK	1409.7	2	3.6213	0.4048
VAQEKDQLQEQLQALKESLKVTK	2656.0	3	6.1525	0.4529
VAQEQGGHPK	1051.1	2	2.9778	0.2387
VAQGVSGAVQDK	1159.3	2	3.6239	0.3153
VAQILKEPK	1026.3	2	3.1153	0.2087
VAQKELEEAVTSALQQETEKSK	2447.7	3	5.0594	0.4325
VAQLDQLLHYR	1356.6	2	3.534	0.3627
VAQLEQVYIR	1219.4	2	3.4304	0.2136
VAQPGPLEPEEPR	1419.6	2	2.9385	0.2137
VAQPTITDNKDGTVTVR	1816.0	2	4.0518	0.3957
VAQTEFDRQAEVTR	1650.8	2	3.1963	0.1395
VAQVAEITYGQK	1307.5	2	4.2892	0.3137
VARPPAAPELGALGSPDLSSLSLAVSR	2633.0	3	5.1847	0.2941
VASEAPLEHKPQVEASSPR	2033.2	2	4.3	0.4789
VASGPSPGEGISPQSAQAPQAPGDNHVVPVL	2965.2	3	4.963	0.2737
VASGPSPGEGISPQSAQAPQAPGDNHVVPVLR	3121.4	3	4.8578	0.4046
VASLEESEGNKQDLK	1647.8	2	4.2675	0.2973
VASLLEHHALQLCQQTGR	2005.3	3	3.6726	0.1836
VASPGSTIDTAPLSSVDSLINKFDSQLGGQAR	3233.5	3	3.9461	0.4277

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VASPSPSGSVLFTDEGVPK	1875.1	2	4.4021	0.3746
VASSPVMVSNPATR	1416.6	2	2.9123	0.2189
VASVLGTMEMGR	1251.5	2	3.6867	0.4391
VASVSQNAIVSAAGNIAR	1728.9	2	4.8235	0.4403
VASVYEAPGFFLDLEPIPGALDAVR	2648.0	3	4.4537	0.226
VATAQDDITGDGTTSNVLIIGELLK	2545.8	2	5.8808	0.454
VATAQDDITGDGTTSNVLIIGELLKQADLYISEGLHPR	4026.5	3	3.6479	0.2149
VATLNSEEESDPPTYKDAFPPLPEK	2776.0	3	4.1183	0.3552
VATPVDWKDGDSVMVLPTIPEEEAK	2728.1	3	4.6395	0.3237
VATPVDWKDGDSVMVLPTIPEEEAKK	2856.2	3	3.7204	0.1509
VATPVDWKDGDSVMVLPTIPEEEAKKLFPK	3341.9	3	5.4246	0.4058
VATQAVEDVLNIAKR	1627.9	2	3.6517	0.1162
VATWFNQPAR	1190.3	2	3.1256	0.1758
VAVAGCCHGELDKIYETLALAER	2462.8	3	5.0579	0.3701
VAVAIPNRPPDAVLTDTTSLNQAALYR	2868.2	3	5.4083	0.4476
VAVATPAK	756.9	1	2.1635	0.1616
VAVEAKNPADLPK	1352.6	2	3.2248	0.2141
VAVEEVDEEGK	1204.3	2	3.3151	0.3782
VAVEEVDEEGKFVR	1606.8	2	4.2397	0.4995
VAVEYLDPSPEVQK	1574.8	2	3.7913	0.3044
VAVFFSNTPTR	1239.4	2	2.8654	0.2572
VAVGAAAGGAGLR	1070.2	2	2.598	0.2494
VAVIQFSDDPKVEFLLNAHSSKDEVQNAVQR	3485.8	3	7.1308	0.4286
VAVLGASGGIGQPLSLLLK	1794.2	2	6.5468	0.4782
VAVLLLAGGQGTR	1255.5	2	2.5727	0.1426
VAVNDAHLLQYNHR	1650.8	2	4.4696	0.416
VAVNGVQLHYQQTGEGDHAVLLLPGMLGSGETDFGPQLK	4078.6	3	4.9333	0.305
VAVPLLSSGGQVAVLELR	1809.1	2	4.1887	0.3927
VAVPSTIHCDHLIEAQVGGEKDLR	2588.9	3	3.6724	0.3789
VAVPYSPAAGVDFELESFSER	2271.5	2	5.1218	0.505
VAVQAVQAMNR	1187.4	2	3.253	0.2184
VAVQGDVVR	943.1	2	2.5206	0.1771
VAVTEGCQPSR	1147.3	2	2.8718	0.3791
VAVVAGYGDVGK	1135.3	2	3.0975	0.1851
VAVVDYVEPSPQGTR	1617.8	2	4.5375	0.4608
VAVVGNVDAGK	1029.2	2	2.6697	0.1634

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VAVVNQIAR	970.2	2	2.559	0.1567
VAVVQYSDR	1037.2	2	2.6584	0.2802
VAVVQYSGTGQQRPER	1775.9	2	2.9793	0.1809
VAYFQSALDKLNEAIKLAK	2123.5	3	3.5538	0.3314
VAYLDPLELSEGK	1434.6	2	3.5545	0.3037
VAYVSFGPHAGK	1233.4	2	3.7197	0.424
VAYVSFGPHAGKLVAIVDVIDQNR	2569.9	3	5.1631	0.356
VCALLSCTSHKDYPFHEEF	2227.5	3	4.0244	0.2746
VCHAHPTLSEAFR	1468.7	2	2.8292	0.2121
VCLIGCGFSTGYGSAVK	1663.0	2	3.3212	0.1505
VCLIGCGFSTGYGSAVNVAK	1947.3	2	3.8762	0.2098
VDALEKSNTK	1105.2	2	3.0744	0.2976
VDALIDEIDFLR	1419.6	2	3.9776	0.1376
VDALLSAQPK	1042.2	2	2.4285	0.1236
VDALNDEINFLR	1419.6	2	4.2464	0.149
VDAQFGGIDQR	1206.3	2	3.5128	0.3679
VDATAETDLAK	1134.2	2	3.0959	0.3106
VDATAETDLAKR	1290.4	2	4.2518	0.4384
VDATAETDLAKRFDVSGYPTLK	2398.7	3	3.4904	0.1679
VDATEESDLAQQYGVR	1781.9	2	6.0767	0.4653
VDCDQHSDIAQR	1387.5	2	3.1284	0.1995
VDCTANTNTCNKYGVSGYPTLK	2350.6	3	3.7531	0.2913
VDDKVNFHFILFNNVDGHLYELDGR	2978.3	3	7.209	0.4435
VDDNEETIKK	1191.3	2	3.0045	0.1629
VDDVINVAGHR	1195.3	2	2.4968	0.1564
VDEFVTHNLSFDEINKAFELMHSGK	2909.2	3	4.4448	0.1543
VDELTTDLEILKAEIEEK	2089.3	2	3.366	0.3303
VDEREKQAALEEEQAR	1902.0	2	3.4561	0.1786
VDEVPDGAVKPPTNKLPIFFFGTHETAFLGPK	3471.0	3	3.8659	0.2101
VDFNVPMK	950.1	2	2.6698	0.2083
VDFNVPMKNNQITNNQR	2033.3	3	4.4492	0.391
VDFPQDQLTALTGR	1561.7	2	4.6475	0.4656
VDGETASDSESR	1253.2	2	3.1895	0.3633
VDGEYDLKVPR	1291.4	2	2.6399	0.1752
VDGHKDIQMPDGIR	1581.8	2	3.1557	0.3116
VDGLSDDHKIETQR	1613.7	2	3.0658	0.1616

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VDGNDVFAVYNATK	1513.6	2	4.4117	0.4588
VDHAGEYGANR	1189.2	2	2.8075	0.2969
VDHGAEIITQSPGR	1480.6	2	4.4777	0.4769
VDHQTGPIVWGEPGTNGQHAFYQLIHQGTK	3317.6	3	6.4819	0.5328
VDIDAPDVDVHGPDWHLK	2029.2	2	4.2996	0.4805
VDIDVPDVNIEGPDAK	1696.8	2	3.062	0.2206
VDIGDTIIYLVH	1358.6	2	2.8752	0.244
VDIIADAAYSIFQKPK	1780.1	2	3.389	0.303
VDISLENPGTSPALEAYSETAK	2293.5	2	3.4943	0.2347
VDIVAINDPFIDLNYMVYMFQYDSTHGK	3310.7	3	4.5345	0.1201
VDIVAINDPFIDLNYMVYMFQYDSTHGKFHGTVK	3980.5	3	3.9818	0.1893
VDKAAAAAAALQAK	1299.5	2	5.2151	0.3123
VDKGVVPLAGTDGETTTQGLDGLSER	2616.8	3	6.4346	0.2849
VDKGVVPLAGTNGETTTQGLDGLSER	2615.8	3	5.3894	0.5617
VDKLDASESLR	1233.4	2	2.8764	0.1819
VDKLYAGLKDLAEER	1720.9	2	3.4521	0.274
VDKSAADGPR	1016.1	2	2.8455	0.2046
VDLDTADFGYAVGEVEALVHEEAEVPTALEK	3318.6	3	4.8693	0.3114
VDLFYLHMPDHSTPVEETLR	2400.7	3	3.9267	0.1568
VDLGGFAGLFDLK	1352.6	2	4.6127	0.3852
VDLRNYLEGIYNVPVAAVR	2162.5	3	3.9963	0.3569
VDLVLEKEVAGLWIK	1713.1	2	2.7434	0.1424
VDLVLLGK	857.1	2	2.4918	0.1062
VDNDENEHQLSLR	1569.6	2	4.4418	0.3237
VDNEFDQR	1023.0	2	2.7536	0.319
VDNEILDYKDLAAIPK	1818.1	2	4.315	0.3659
VDNSSLTGESEPQTR	1620.7	2	4.3708	0.3869
VDNSSLTGESEPQTRSPDFTNENPLETR	3122.2	3	6.406	0.3885
VDQETLTEMVKPSIDYVR	2124.4	2	2.4228	0.1036
VDQGTLFELILAANYLDIK	2137.5	2	3.4682	0.3631
VDQIQEIVTGNPTVIK	1755.0	2	3.0439	0.2198
VDQSILTGESVSVIK	1575.8	2	3.5681	0.3438
VDSAATSGYEIGNPPDYR	1913.0	2	5.1117	0.4752
VDSFHESTEGK	1236.3	2	3.1635	0.3061
VDSFHESTEGKVGYELKDEIER	2568.7	3	4.8251	0.3472
VDSLLENLEKIEKEQSK	2003.2	3	4.2045	0.4177

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VDSTAKVAEIEHAEKEK	1885.1	3	3.4291	0.2942
VDTVNHLADELINSGHSDAATIAEWK	2808.0	3	4.5654	0.381
VDVEALENSAGATYIR	1708.9	2	4.2351	0.3732
VDVEFDYDGPLMK	1528.7	2	4.4009	0.4834
VDVEVPDVSLEGPEGK	1669.8	2	4.1798	0.354
VDVFNANSNLSSGPLPIFPLEQLVNKPVEELPEGVDPSR	4219.7	3	5.9111	0.44
VDVFREDLCTK	1325.5	2	2.7542	0.2689
VDVGKDQEFTVK	1365.5	2	3.8409	0.3384
VDVTEQPGLSGR	1258.4	2	4.1738	0.394
VDYKADEWLMK	1398.6	3	3.4066	0.1907
VDYLVTEEEINLTR	1694.9	2	3.2035	0.1333
VEAALDSR	860.9	2	2.437	0.1609
VEAIKEALMAHGLGNR	1710.0	3	4.4923	0.2891
VEAKPEVQSQPPR	1465.6	2	3.8151	0.3463
VEAQLQELQVK	1285.5	2	3.5841	0.1704
VEAQVYILSK	1150.3	2	2.6342	0.1866
VEDLAWHR	1026.1	2	2.6196	0.1892
VEDYEPYPDDGMGYGDYPK	2211.3	2	4.1429	0.3033
VEDYEPYPDDGMGYGDYPKLPDR	2692.9	3	3.3876	0.2042
VEEASPGRPSSVDTLLSPTALIDSILR	2825.2	3	3.5607	0.2228
VEEDDYPSEELLEDENAINAK	2423.5	2	3.0638	0.3285
VEEDVASDLVMKVDALLSAQPK	2358.7	3	4.1216	0.2391
VEEEAAQKNMALKK	1589.8	2	4.3	0.2518
VEEEEERNQILQNEK	1888.0	3	3.3885	0.1269
VEEEEERNQILQNEKK	2016.2	3	3.8363	0.1421
VEEEHTNAIGTLHGGLTATLVDNISTMALLCTER	3612.0	3	4.7176	0.2122
VEEEIQTLSQVLAAK	1658.9	2	3.9561	0.2286
VEEIAASK	846.9	1	2.5094	0.2386
VEEKEGIPPQQQR	1538.7	2	2.7516	0.1228
VEEQEPELTSTPNFVVEVIK	2288.5	2	5.04	0.3759
VEEQEPELTSTPNFVVEVIKNDDGKK	2946.2	3	4.2525	0.3074
VEEVGPYTYR	1213.3	2	2.4548	0.1434
VEFATLQEALAHALTEK	1872.1	2	3.9399	0.298
VEFATLQEALAHALTEKEGKDQELAK	2871.2	3	5.6743	0.3863
VEFEELCADLFER	1600.8	2	4.1788	0.4236
VEFLLNAHSSKDEVQNAVQR	2285.5	3	4.4498	0.3749

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VEFMDDTSR	1100.2	2	2.8566	0.2562
VEGDLKGPEVDIK	1399.6	2	2.9945	0.1537
VEGDLKGPEVDIKGPK	1681.9	2	3.531	0.2395
VEGFPTIYFAPSGDKK	1757.0	2	2.4853	0.2872
VEGFPTIYFAPSGDKKNPVKFEGGDRDLEHLSK	3680.1	3	4.0092	0.2725
VEGHVFPEFK	1189.3	2	2.6771	0.1634
VEGIVHPTTAEIDLKEDIGK	2165.4	2	5.0166	0.4881
VEGIVHPTTAEIDLKEDIGKALEK	2607.0	3	5.8349	0.4678
VEGQATDEKKEPK	1459.6	2	3.3096	0.1453
VEGTEPTTAFNLFVGNLNFNK	2313.6	2	5.0397	0.428
VEGTPSDPNPNDPR	1495.5	2	3.3146	0.1602
VEHAVAEGAK	1011.1	2	2.6572	0.1924
VEHNQVGEKTEER	1555.6	2	3.4779	0.3753
VEHSDLSFSK	1149.2	2	3.0774	0.3233
VEHTPDGVK	982.1	2	2.4248	0.1793
VEIAGPGFINVHLR	1522.8	2	2.9886	0.3187
VEIIANDQGNR	1229.3	2	3.8778	0.2388
VEIIANDQGNRITPSYVAFTPEGER	2778.0	3	4.3724	0.3428
VEIIANDQGNRITPSYVAFTPEGERLIGDAAK	3446.8	3	5.5347	0.4141
VEIKDVKLPVQLQR	1666.0	3	4.419	0.2763
VEILANDQGNR	1229.3	2	3.6605	0.2621
VEILANDQGNRTTPSYVAFTDTER	2698.9	3	5.1376	0.3873
VEITYTPSDGTQK	1439.5	2	3.2978	0.1678
VEKDGLILTSR	1231.4	2	3.5153	0.3347
VEKFDLVPVPTNLYGDFFTGDAYVILK	3062.5	3	4.4897	0.2901
VEKQVNDAVSK	1217.4	2	2.6364	0.1729
VEKVVVSNR	1030.2	2	2.6224	0.1231
VEKYTISQEAYDQRQDTVR	2330.5	3	3.3013	0.2633
VELEAKVDALNDEINFLR	2089.3	2	5.4548	0.3974
VELESRLEGLTDEINFLR	2134.4	2	2.4274	0.147
VELKGTVRPANDFNPDADAK	2158.4	3	4.3069	0.3606
VELLERELQELQDSLNAEREK	2542.8	3	5.0217	0.1932
VELNALMTDETISNVPILILGNK	2498.9	3	3.3709	0.1032
VELPGTAVPSVPEDAAPASR	1964.2	2	4.1111	0.4276
VELQELNDR	1116.2	2	2.708	0.1921
VELSDVQNPAISITENVLHFK	2354.6	3	3.2717	0.2515

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VELSEQQLQLWPSDVDKLSPTDNLPR	3009.3	3	4.3048	0.3229
VELSNGEKR	1032.1	2	2.6951	0.1144
VELVPPTPAEIPR	1418.7	2	3.1941	0.3193
VEMLDNLLDIEVAYSLLR	2107.5	2	4.3622	0.4646
VENMVDQLLR	1217.4	2	3.2767	0.2149
VENQENVSNLVIEDTELK	2074.2	2	5.5052	0.4732
VENQENVSNLVIEDTELKQVAYIYK	2940.3	3	3.4136	0.1585
VEPADASGTEKAFEPATGR	1934.1	2	4.5604	0.4435
VEPAVSSVVNSIQVLTSK	1858.1	3	4.9663	0.4704
VEPLRNELQKLEDDAKDNQQK	2511.7	3	4.5312	0.2169
VEPPLRSVLEQTK	1496.7	2	2.7531	0.1188
VEQATKPSFESGR	1436.6	2	3.9439	0.3576
VEQHVVDGK	1011.1	2	2.6611	0.2696
VEQHVVDGKER	1296.4	2	3.5592	0.4115
VEQIAAIAQELNELDYYDSPSVNAR	2810.0	3	6.1794	0.4478
VEQLGAEGNVEESQK	1617.7	2	5.0131	0.4117
VEQNAAPSHTK	1182.3	2	2.6858	0.2668
VEQVKFDATSMHVKPQVAAQQK	2470.8	3	5.6748	0.4055
VEQVLSLEPQHELK	1649.9	2	3.8577	0.2956
VERADGYEPPVQESV	1675.8	2	3.7358	0.3619
VESKINTDVQLDSQEKIGVK	2231.5	2	2.7808	0.1068
VESLSQVEVILQHSAADIAR	2166.4	3	3.3917	0.1944
VESVFETLVEDSAEEESTLTK	2343.5	2	5.5568	0.4248
VETDAAQAAVQSAFAVLLTQLIK	2388.7	3	3.8688	0.2764
VETGILKPGMVVTFAPVNVTTEVK	2531.0	3	3.6149	0.1381
VETGILRPGMVVTFAPVNITTEVK	2573.0	3	5.4224	0.4566
VETGVLKPGMVVTFAPVNVTTEVK	2517.0	2	5.5006	0.483
VETLRPHVVGSGGNDKEKEEFR	2484.7	3	5.5615	0.3809
VETPLEEAIKFLTPLK	1829.2	2	3.5051	0.205
VETSDEEIHDLHQR	1708.8	2	4.2441	0.3705
VEVDGSIMEGGGQILR	1660.9	2	3.61	0.2552
VEVERDNLAEDIMR	1689.9	3	4.1793	0.2948
VEVGKDQEFTVDTR	1623.7	2	3.8051	0.3766
VEVKEEKPSVSKEEKPSVSK	2244.5	3	4.6129	0.2525
VEVRPMMYVALTYDHR	1981.3	3	4.1727	0.1068
VEVTEFEDIK	1209.3	2	3.5206	0.3179

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VEYSEEELKTHISK	1692.8	2	4.3599	0.3585
VEYSEEELKTHISKGTLGK	2149.4	2	5.1149	0.4396
VFAARDDEAAAVALSSLIHALDDLDMVAIVR	3269.7	3	7.8124	0.5424
VFASLPQVER	1146.3	2	3.2669	0.2509
VFDAIMNFKKEETAK	1772.1	2	3.1854	0.2861
VFDEFKPLVEEPQNLIK	2046.4	3	5.5884	0.4432
VFDENKEDDLTELSHR	1948.0	3	3.2128	0.2956
VFDFTFSPEEMK	1477.7	2	3.6055	0.3751
VFDFTFSPEEMKQLNALNK	2259.6	3	4.1233	0.3316
VFDFTFSPEEMKQLNALNKNWR	2716.1	3	3.3618	0.2385
VFDGIPPPYDKK	1376.6	2	3.2628	0.2097
VFDHKQGTYGGYFR	1675.8	3	3.3212	0.1725
VFDKDGNGYISAAELR	1755.9	2	4.639	0.3056
VFDKEGNGTVMGAEIR	1723.9	2	4.5013	0.305
VFDKEGNGTVMGAELR	1723.9	2	4.6875	0.2958
VFDKLSPLHER	1341.5	2	3.2196	0.2266
VFDPQNDKPSK	1275.4	2	3.1185	0.1683
VFEEKTESEKYR	1545.7	2	3.7158	0.3542
VFEFGGPEVLK	1222.4	2	3.6502	0.2744
VFEGNRPTNSIVFTK	1709.9	2	3.5777	0.2162
VFEGPPKPEEPLKR	1623.9	2	4.0288	0.3089
VFEHDSVELNCK	1420.6	2	3.4533	0.2608
VFEHIGKK	958.1	2	2.6583	0.108
VFELMTSLHTK	1306.6	2	3.4001	0.2833
VFESIGKFGLALAVAGGVVNSALYNVDAGHR	3133.5	3	4.8232	0.3957
VFEVNASNLEK	1250.4	2	3.8903	0.2758
VFEVSLADLQNDEVAFR	1953.1	2	5.5909	0.4713
VFEVSLADLQNDEVAFRK	2081.3	2	3.8321	0.3613
VFGALKGAVDGGLSIPHSTK	1955.2	2	4.9582	0.3836
VFGAPNVVEDEIDQYLSK	2024.2	2	3.7072	0.3535
VFGEHKANDR	1173.3	2	2.7034	0.2213
VFGNEIKLEKPK	1402.7	2	3.2994	0.1223
VFHAGTQQQK	1144.3	2	2.468	0.1717
VFIGKDCIGGCSDLVSLQQSGELLTR	2740.2	3	4.0142	0.186
VFIGNLNTALVK	1289.5	2	2.882	0.2008
VFIGNLNTLVVK	1317.6	2	4.2389	0.3311

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VFIGNLNTLVVKK	1445.8	2	3.4932	0.2757
VFIPHGLIMDRTER	1685.0	2	2.7406	0.1247
VFITDDFHDMMPK	1596.9	2	4.4377	0.3082
VFKEENQKGDK	1322.4	2	2.4551	0.19
VFKEENQKGDKK	1450.6	2	3.4656	0.211
VFKQPSKPEIVSK	1487.8	2	3.4911	0.3142
VFKVYNEAGVTFT	1475.7	2	2.9754	0.2489
VFLAQK	705.9	1	2.0053	0.1231
VFLDPNILSDDGTVALR	1846.1	2	4.8856	0.3958
VFLENVIR	990.2	2	2.6709	0.133
VFLENVIRDAVTYTEHAK	2106.4	3	5.5172	0.4299
VFLENVIRDAVTYTEHAKR	2262.6	3	6.1704	0.4834
VFLLGEEVAQYDGAYK	1803.0	2	4.2941	0.1459
VFLQNLLSVSQAR	1475.7	2	3.7568	0.2929
VFLSLMETGWFDNLLLDIDKADAIVK	2968.5	3	3.9382	0.2345
VFNDMK	753.9	1	1.947	0.1134
VFNDMKVR	1009.2	2	2.5355	0.2272
VFNETPINPR	1187.3	2	2.5146	0.1431
VFNGSGKPIDRGPVVLAEDFLDIMGQPINPQCR	3585.1	3	4.5492	0.2836
VFNTTPDDLDLHVIYDVSHNIAK	2627.9	2	4.7616	0.4038
VFNVFCLYGNVEK	1532.8	2	4.7994	0.4002
VFNVTKENR	1107.2	2	2.4732	0.2116
VFNYNTLER	1156.3	2	2.8065	0.1866
VFPDKEVMLDAALALAAEISSK	2319.7	2	5.1628	0.4518
VFPDKEVMLDAALALAAEISSKSPVAVQSTK	3217.7	3	6.1421	0.4989
VFPGSTTEDYNLIVIER	1954.2	2	5.0521	0.409
VFQFLNAK	967.1	2	3.1493	0.2776
VFQSLPHENKPLTLSNYQTNK	2459.7	3	5.1349	0.3964
VFQSSANYAENFIQSIISTVEPAQR	2801.1	2	4.0992	0.3614
VFQTEAELQEVISDLQSK	2065.3	2	5.8656	0.363
VFQVEYAMK	1115.3	2	3.0588	0.209
VFSGLVSTGLK	1108.3	2	3.0937	0.3326
VFSGLVSTGLKVR	1363.6	2	3.532	0.2839
VFSNGADLSGVTEEAPLK	1835.0	2	5.6787	0.4094
VFSNGADLSGVTEEAPLKLSK	2163.4	2	5.2162	0.448
VFSVAITPDHLEPR	1581.8	2	3.4817	0.3942

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VFSVTHIK	931.1	2	2.6395	0.1284
VFTAITKHPDEK	1386.6	2	3.2296	0.205
VFTESEDRTASAEEIKAFEKELSHATIDSK	3370.6	3	5.0089	0.4077
VFTTQELVQAFTHAPATLEADR	2446.7	3	4.7981	0.4092
VFTTQELVQAFTHAPATLEADRGGK	2689.0	3	5.2475	0.4449
VFVDGHQLFDFYHR	1781.0	2	3.141	0.3478
VFVGGLSPDTSEEQIKEYFGAFGEIENIELPMDTK	3892.3	3	5.1918	0.3883
VFVHYTGWLLDGTK	1636.9	2	3.1555	0.4183
VFVQKEILDKFTEEVVK	2052.4	3	5.2419	0.3315
VFVQKEILDKFTEEVVKQTQR	2565.9	3	5.4605	0.3369
VFYELQHSDKPVGTK	1749.0	2	4.1999	0.3418
VFYSITGQGADTPPVGVFIIER	2367.7	2	3.9626	0.3287
VGAAEEELQK	1074.2	2	3.2061	0.1833
VGAAEEELQKSR	1317.4	2	3.2304	0.1909
VGAEDADGIDMAYR	1483.6	2	4.6872	0.3818
VGAENVAIVEPSER	1470.6	2	3.6371	0.3463
VGAGAPVYLAAVLEYLTAEILELAGNAARDNKK	3402.9	3	5.8328	0.4577
VGAGAPVYMAAVLEYLTAEILELAGNAAR	2935.4	3	6.2954	0.4813
VGAGAPVYMAAVLEYLTAEILELAGNAARDNK	3292.8	3	4.359	0.41
VGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	3420.9	3	5.2232	0.4864
VGAGSRPKPEAPMAK	1496.8	2	2.6664	0.1094
VGAHAGEYGAEALER	1530.6	2	3.9937	0.4497
VGAIPANALDDGQWSQGLISAAR	2311.5	3	5.1484	0.5825
VGATAAVYSAAILEYLTAEVLELAGNASK	2897.3	3	5.7438	0.1516
VGATAAVYSAAILEYLTAEVLELAGNASKDLK	3253.7	3	4.346	0.128
VGATAAVYSAAILKYLTAEVLELAGNASK	2896.3	3	5.2761	0.5274
VGATAAVYSAAILKYLTAEVLELAGNASKDLK	3252.7	3	3.9542	0.4598
VGAVDADKHHSLGGQYGVQGFPTIK	2582.9	3	6.7878	0.5193
VGDAIPAVEVFEGEPGNK	1829.0	2	4.5714	0.3266
VGDAIPAVEVFEGEPGNKVNLAELFK	2744.1	2	4.1705	0.4207
VGDKGTQLSGGQK	1275.4	2	2.4261	0.1067
VGDKIATR	860.0	2	2.973	0.1945
VGDKVLLPEYGGTK	1476.7	2	4.3277	0.3455
VGDKVLLPEYGGTKVVLDDKDYFLFR	2988.4	3	3.7045	0.2789
VGDPQELNGITR	1299.4	2	3.484	0.3918
VGDQILLAIKGQK	1383.7	2	3.3334	0.2439

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VGDSPIPGAGAYADDTAGAAAATGNGDILMR	2877.1	3	5.4952	0.3608
VGDSSGTAAAHK	1101.2	2	2.8687	0.2379
VGDSTPVSEKPVSAAVDANASESP	2315.4	2	4.5498	0.4148
VGDTLDLLIGEDKEAGTETVMR	2363.6	2	2.6012	0.1123
VGDTSLDPNDFDFTVTGR	1957.0	2	5.1946	0.4102
VGDVQGQESESQLPTK	1702.8	2	4.529	0.3683
VGDVYIPR	919.1	2	2.7217	0.2442
VGDYGSLSGR	1011.1	2	3.8662	0.3439
VGDYVYFENSSSNPYLIR	2124.3	2	5.0799	0.3963
VGDYVYFENSSSNPYLVR	2110.3	2	5.8062	0.4917
VGEAIETTQR	1104.2	2	3.0086	0.1291
VGEATETALTCLVEK	1564.8	2	2.5659	0.1978
VGEEDEEAAEAEAEAEEAER	2164.1	2	7.1824	0.5091
VGEEDEEAAEAEAEAEEAERAR	2391.4	2	4.6083	0.33
VGEFSGANK	909.0	2	2.4292	0.143
VGEFSGANKEK	1166.3	2	2.5468	0.1229
VGEFSGANKEKLEATINELV	2149.4	2	2.8051	0.1671
VGEIFSAAGAAFTK	1369.5	2	4.2765	0.4821
VGELKDDDFER	1323.4	2	2.5279	0.1508
VGELKDDDFERISELGAGNGGVVTK	2606.8	3	4.59	0.3328
VGELTNLTQIELR	1486.7	2	2.5328	0.1319
VGENADSQIK	1061.1	2	3.6043	0.2931
VGEPGQAGNPALVSAYGTGLEGGTTGIQSEFFINTTR	3699.0	3	5.3326	0.4198
VGEPKGYPPEDIFNLVGKK	2088.4	3	4.9824	0.2668
VGEPVALSEEERLK	1556.7	2	3.8839	0.3459
VGEPVALSEEERLKLAQQQAALLMQQEER	3295.7	3	6.8803	0.5525
VGEQAQVVIIDMNDPSNPIRRPISADSAIMNPASK	3736.2	3	4.8397	0.3341
VGERQPLLGPPESMREHVVAASK	2488.9	3	4.392	0.3932
VGESVFHTTR	1133.2	2	3.3692	0.393
VGETAPPNAYTVTDLVEYSIVIQQLSNGK	3108.4	3	4.4599	0.2559
VGETIIDLENR	1259.4	2	2.5683	0.2645
VGEVCHITCKPEYAYGSAGSPPK	2394.7	3	4.3651	0.3944
VGEVIVTK	845.0	2	2.5477	0.1999
VGEVIVTKDDAMLLK	1632.0	2	4.6734	0.467
VGEVIVTKDDAMLLKGKGDKAQIEKR	2843.3	3	5.6884	0.4553
VGEVTYVELFKDAEGK	1785.0	2	4.3259	0.4764

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VGEVTYVELLMDAEGK	1754.0	2	5.2002	0.472
VGEYSLYIGR	1157.3	2	3.4972	0.3019
VGFAEAAR	820.9	2	2.6237	0.242
VGFDKWPFMTTHTWGEDAR	2282.5	3	3.919	0.3039
VGFQYEGTYKWVNPHKL	2067.3	3	3.3932	0.3052
VGGAGNKIIQLIEGK	1497.8	2	4.1477	0.1691
VGGERFEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR	4438.9	3	3.874	0.3692
VGGHLRPGIVQSGGVVR	1689.0	3	3.7305	0.3075
VGGRLEDTKLIK	1329.6	3	3.3899	0.1593
VGGSGVNVNAK	1002.1	2	3.0283	0.2904
VGGSSVDLHR	1027.1	2	3.4715	0.3733
VGGTKPAGGDFGEVLNSAANASATTTEPLPEK	3088.3	3	4.8567	0.3817
VGGTKPAGGDFGEVLNSAANASATTTEPLPEKTQES	3533.8	3	5.838	0.4243
VGGTKPAGGDFGEVLNSAANASATTTEPLPEKTQESL	3646.9	3	7.0756	0.4802
VGGTSDVEVNEK	1234.3	2	3.9864	0.4039
VGGTSDVEVNEKK	1362.5	2	4.1299	0.2906
VGGTSDVEVNEKKDR	1633.7	2	4.2065	0.429
VGGTSDVEVNEKKDRVTDALNATR	2575.8	3	4.9567	0.3995
VGGVGPADTHEPLRPEAEPGELER	2513.7	3	3.3569	0.2654
VGGVQSLGGTGALR	1272.4	2	3.275	0.4027
VGGYILGEFGNLIAGDPR	1849.1	2	2.9615	0.2143
VGHSELVGEIIR	1309.5	2	3.4161	0.3869
VGHSELVGEIIRLEGDMATIQVYEETSGVSVGDPVLR	3957.4	3	4.8709	0.4399
VGHSIRHPDVEVDGFSELR	2150.3	2	4.361	0.4267
VGHSTAHDEIIPMSIR	1764.0	2	4.5548	0.4867
VGIADGHR	824.9	2	2.8707	0.1937
VGIGAFPTEQDNEIGELLQTR	2288.5	2	5.1697	0.3209
VGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDR	3635.2	3	4.0819	0.3242
VGIIAWHPTAR	1221.4	2	2.8632	0.2363
VGINYQPPTVVPGGDLAK	1826.1	2	4.6736	0.4686
VGIPKETPALTINR	1509.8	2	2.4951	0.2784
VGISPDKLR	985.2	2	3.1136	0.1764
VGIVAWHPTAR	1207.4	2	2.6357	0.1709
VGIVGNLASGK	1015.2	2	2.5495	0.1682
VGKETVQTTEDQILKR	1846.1	2	5.8866	0.4291
VGKGEPGAAPLSAPAFSLVFPFLK	2401.8	3	5.4606	0.4171

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VGKVEHGSVALPAIMR	1665.0	3	5.0193	0.4858
VGLADLHPDVFATAPR	1679.9	3	4.193	0.3381
VGLFHSDR	931.0	2	2.5854	0.2774
VGLGLGYLELPQINYK	1778.1	2	3.9898	0.3673
VGLKAPGIIPR	1121.4	2	3.1904	0.2463
VGLPLLSPEFLLTGVLK	1797.2	2	2.7284	0.1907
VGLQVVAVK	913.1	2	3.2169	0.2549
VGLQVVAVKAPGFGDNR	1728.0	3	4.2097	0.3153
VGLVASQKNDLDAVALMHPDGSAVVVVLNR	3089.6	3	5.4889	0.3306
VGLVQFSDTPVTEFSLNTYQTK	2475.7	3	4.661	0.4168
VGMEDMGHH	1013.1	2	2.444	0.1458
VGMQQMFALGER	1367.6	2	3.2667	0.2676
VGMRHYHLK	1141.4	2	2.4829	0.2015
VGNGFEEGTTQGPLINEK	1891.0	2	4.9349	0.3961
VGNGHSNEAALILHR	1588.8	3	3.7374	0.369
VGNHTAEGTGTNK	1286.3	2	3.6186	0.292
VGNHTAEGTGTNKK	1414.5	2	3.8195	0.3021
VGNIEIKDLMVGDEASELR	2089.4	2	4.3718	0.4299
VGNIIDTMITDAFLK	1651.9	2	4.9637	0.4293
VGNIIDTMITDAFLKADDYIEITGAGGKK	3071.5	3	4.4827	0.3466
VGNKYRLGR	1063.2	2	2.5709	0.1029
VGNLGLATSFFNEK	1497.7	2	4.4201	0.497
VGNLGLATSFFNER	1525.7	2	4.3119	0.4014
VGNLTVVGKEPESILQVLSQMEK	2499.9	2	4.4811	0.3914
VGNLTVVGKEPESILQVLSQMEKIVR	2868.4	3	3.518	0.2396
VGNMSESELGR	1179.3	2	3.0953	0.3693
VGNPWDPNVLYGPLHTK	1908.1	3	3.9832	0.3516
VGNQIFQSR	1049.2	2	3.0431	0.1515
VGNVEYFGLGNSPGFPLQYYPYYGK	2831.1	3	4.3532	0.2845
VGNVGQTNYAASK	1309.4	2	3.7652	0.4252
VGPDVVTDPAFLVTR	1586.8	2	2.6936	0.212
VGPVAATYPMLNK	1361.6	2	3.446	0.4052
VGPVSHHR	889.0	2	2.6121	0.2062
VGQADDSTKPTNK	1361.4	2	3.6693	0.2611
VGQASEIAR	931.0	2	2.44	0.2308
VGQAVDVVGQAGKPK	1453.7	2	5.0758	0.3716

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VGQDPVLR	884.0	2	2.6895	0.1224
VGQEIEVRPGIVSK	1511.7	2	3.6248	0.3404
VGQISFDLPR	1132.3	2	2.9174	0.3005
VGQLSEGAIAAIMQK	1516.8	2	4.9461	0.3682
VGQTAFDVADEDILGYLEELQK	2454.7	2	5.4799	0.4427
VGQTAFDVADEDILGYLEELQKKQNLLHSEKR	3689.1	3	3.7209	0.3253
VGQYVVDLTSFEQLALPVLR	2248.6	2	4.4487	0.4502
VGRPSNIGQAQPIIDQLAEEAR	2363.6	3	4.338	0.3475
VGSAADIPINISETDLSLLTATVVPPSGR	2895.3	2	4.6207	0.4463
VGSAKPGLQK	985.2	2	3.2322	0.1546
VGSEIER	789.9	1	1.8126	0.1009
VGSGDTNNFPYLEK	1541.6	2	4.7583	0.3765
VGSHEQPSGATLQR	1467.6	2	3.5376	0.1678
VGSHITGGDIYGIVSENSLIK	2160.4	2	6.2067	0.5506
VGSHITGGDIYGIVSENSLIKHK	2425.7	3	5.4699	0.4981
VGSHPEGGASWLSTAANFLSR	2145.3	2	5.0267	0.464
VGSLDNAHHVPGGGNVK	1658.8	2	3.8512	0.3821
VGSLDNAHHVPGGGNVKIDSQK	2230.4	2	4.2701	0.3002
VGSLDNVGHLPAGGAVK	1591.8	2	4.8224	0.4132
VGSLGLPAHPR	1104.3	2	3.2934	0.3323
VGSSGDIALHINPR	1436.6	2	3.8979	0.3929
VGSTENIKHQPGGGR	1537.7	2	4.1694	0.3986
VGSTKVPMTSGVK	1291.5	2	2.6374	0.2164
VGSTSENITQK	1164.2	2	3.1083	0.3115
VGTAQLALVAR	1099.3	2	3.1175	0.2594
VGTDKTGVKSEGST	1366.5	2	2.5081	0.1894
VGTEGLVDSFSQGLER	1694.8	2	2.5054	0.1032
VGTGEPCCDWVGDEGAGHFVK	2164.4	2	3.673	0.2156
VGTLVGEDKYGNKYYEDNKQFFGR	2829.1	3	3.9437	0.3278
VGVDGFGR	806.9	2	2.7283	0.3425
VGVDPLIIPTDYWK	1616.9	2	3.1513	0.1864
VGVEVPDVNIEGPEGK	1638.8	2	3.3613	0.2543
VGVGTSFGLPQTR	1319.5	2	2.9901	0.2485
VGVIGFPNVGK	1087.3	2	2.8481	0.1015
VGVKPVGSDPDFQPELSGAGSR	2200.4	2	5.2916	0.5008
VGVLAASMEAK	1076.3	2	3.156	0.3484

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VGVNGDHHGPGNQYLK	1692.8	2	2.5982	0.108
VGVNGFGR	805.9	2	2.4704	0.1078
VGVPTVDLDAQGR	1327.5	2	2.5734	0.3206
VGVSQQPEDSQQDLPGER	1970.0	2	5.275	0.3918
VGVVQFSNDVFPEFYLK	1989.3	2	5.9405	0.4912
VGWEQLLTTIAR	1387.6	2	4.4547	0.3563
VGWSVDFSRPQLGEDEFSYGFDGR	2751.9	3	3.3709	0.1376
VGYHLEDPLFHLESPR	1910.1	3	3.2098	0.1891
VHAASVNPIDVNMR	1523.7	2	3.5047	0.3691
VHACGVNPVETYIR	1558.8	2	3.2963	0.2337
VHAELADVLTEAVVDSILAIK	2207.6	2	7.7979	0.6307
VHAELADVLTEAVVDSILAIKK	2335.7	3	4.9322	0.4354
VHAEQVLNDKESHIK	1747.9	2	5.169	0.4918
VHAIQCDVRDPDMVQNTVSELIK	2612.0	3	4.1494	0.4371
VHATSTYR	935.0	1	2.1723	0.2249
VHAYIISYLKK	1335.6	3	3.2858	0.139
VHDSQKPQDQDKLSKEDVLSFIQMHR	3110.5	3	4.5353	0.3221
VHEELRNLGLYVK	1570.8	2	3.7953	0.3943
VHEKDNGDIK	1155.2	2	2.5204	0.214
VHELKEHNGQVTGIDWAPESNR	2517.7	3	5.2638	0.4457
VHELNEEIGK	1168.3	2	3.277	0.1594
VHELNEEIGKLLAK	1593.8	2	4.2925	0.4396
VHEMEKEHLNK	1394.6	2	3.6866	0.2336
VHEYNVLLETLSR	1573.8	2	4.721	0.4494
VHFEESSKLEDLLR	1702.9	3	3.9771	0.4405
VHFEESSKLEDLLRK	1831.1	2	2.9223	0.2319
VHFFTQDHKPSNPLEK	1925.1	2	2.9797	0.3469
VHFITDTLSKGETK	1576.8	2	3.7464	0.3894
VHFTAER	860.0	1	1.8185	0.1172
VHGIIKNGGVKPNIIPSYSELIYYFR	2979.5	3	3.4762	0.166
VHGLLK	666.8	1	1.696	0.1009
VHGPGIQSGTTNKPNK	1635.8	2	4.0657	0.4271
VHGPGIQSGTTNKPNKFTVETR	2369.6	2	5.523	0.4549
VHHEPQLSDK	1190.3	2	2.6188	0.2509
VHHEPQLSDKVHNDAQSFDYDHDAFLGAEEAK	3651.8	3	5.2396	0.3483
VHHPDYNNELTQFLPR	1981.2	3	3.599	0.3008

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VHIDIGADGR	1053.2	2	3.1467	0.2999
VHIEIGPDGR	1093.2	2	3.058	0.2354
VHIGQVIMSIR	1253.5	3	3.371	0.3094
VHKEDDGVPVICQVEHPAVTGNLQTQR	2971.3	3	5.5682	0.3943
VHKQELELLNNELLK	1821.1	2	4.1921	0.3324
VHLAEKGDGAELIWDKDDPSAMDFVTSAANLR	3473.8	3	6.15	0.4794
VHLASHAGELPFR	1434.6	2	3.3524	0.2721
VHLDIQVGEHANDYAEIAAK	2194.4	2	3.3167	0.3362
VHLDIQVGEHANDYAEIAAKDKLSELQLR	3277.6	3	3.9845	0.2907
VHLDIQVGEHANNYPEIAAK	2219.4	3	6.0092	0.4607
VHLDKAQQNNVEHK	1660.8	2	5.0567	0.3564
VHLDKAQQNNVEHKVETFSGVYK	2671.9	3	5.2291	0.4765
VHLDKAQQNNVEHKVETFSGVYKK	2800.1	3	5.5049	0.4864
VHLIGHSLGAHVAGEAGSK	1841.1	2	4.1111	0.3789
VHLMNPMVPGLTGSK	1581.9	2	3.6336	0.3259
VHLVGIDIFTGK	1299.5	3	4.2919	0.3604
VHLVGIDIFTGKK	1427.7	2	4.3005	0.3584
VHMFEAHSDYIR	1505.7	2	3.7088	0.4092
VHMTWVQPR	1154.4	2	2.6719	0.3471
VHNDAQSFDYDHDAFLGAEEAK	2480.5	3	4.4886	0.3131
VHNGMDDLILDGHNILDGLR	2218.5	3	4.2983	0.4377
VHPEIINENGNPSYK	1711.9	2	4.5331	0.3985
VHPVSTMIK	1012.3	1	2.2356	0.2554
VHQAAPLSDAPHDDAHGNFQYDHEAFLGR	3217.4	3	4.4109	0.3726
VHQILEGSNEVMR	1512.7	2	4.1759	0.3103
VHQLDVAIPLHLK	1483.8	2	2.4448	0.2088
VHQLETQNR	1125.2	2	2.9784	0.1236
VHQLYETIQR	1287.4	2	2.8137	0.2673
VHRDGPALSGPQSR	1477.6	2	3.0789	0.2769
VHSDEDNPER	1198.2	2	2.864	0.2965
VHSFPTLK	929.1	1	1.8559	0.197
VHSFTHEAPNQR	1423.5	2	3.5094	0.3942
VHSVAVIGAPFSQGQK	1625.9	2	4.7611	0.493
VHTECCHGDLLECADDRADLAK	2415.7	3	3.5081	0.2502
VHTGFDQHEQK	1326.4	2	2.7362	0.1677
VHTGFDQHEQKFTGLPR	1998.2	2	2.9256	0.3269

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VHTVEDYQAIVDAEWNILYDKLEK	2893.2	3	3.8497	0.1786
VHVGDEDFVHLR	1423.6	2	4.119	0.449
VHVIFNYK	1020.2	1	2.8224	0.191
VHVSEEGTEPEAMLQVLGPK	2151.4	2	3.7015	0.2314
VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK	3303.7	3	3.2974	0.1923
VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAKEDAANR	3960.3	3	6.1298	0.4626
VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAKEDAANRK	4088.5	3	5.8912	0.4908
VHVSGAR	725.8	1	1.6592	0.1164
VHVTQEDFEMAVAK	1604.8	2	2.9779	0.3403
VHVVDLKAESVAAPITVR	1905.2	3	3.5301	0.2719
VHYENNSPFLTITSMTR	2011.2	3	4.6701	0.3857
VHYETALAESEKK	1505.7	2	2.9739	0.275
VHYLEQQNKEIEAEIQALR	2312.6	3	4.9032	0.2402
VIAAEGEMNASR	1248.4	2	4.2837	0.4607
VIAATNRVDILDPALLR	1851.2	3	5.6807	0.3442
VIACDGGGGALGHPK	1352.5	2	2.9675	0.1773
VIADNVK	758.9	1	1.741	0.118
VIADNVKDWSK	1275.4	2	3.7273	0.3527
VIAEGDLGIVEK	1243.4	2	3.9414	0.373
VIAEKDKQIK	1172.4	2	2.6825	0.1768
VIAGFSLLNLLFK	1435.8	2	2.6444	0.1127
VIAHGKDHPTAATK	1446.6	2	4.1457	0.4212
VIAHPSFHNINFK	1524.8	2	2.9618	0.2967
VIAHSEYQK	1075.2	2	2.7982	0.2725
VIAHTQMR	956.1	2	2.5424	0.24
VIAINVDDPDAANYNDINDVK	2289.4	2	5.7084	0.4579
VIAINVDDPDAANYNDINDVKR	2445.6	2	5.291	0.4571
VIALGLPVPR	1035.3	2	2.7585	0.1423
VIATDINESKLQELEKYPGIQTR	2647.0	3	6.3076	0.4879
VIDDTNITR	1047.1	2	3.235	0.2883
VIDGLETLDELEKLPVNEK	2155.4	3	3.5312	0.2823
VIDLPGGGAAFVMEHLK	1755.1	2	3.239	0.2844
VIDPATATSVDLR	1358.5	3	3.2183	0.3106
VIDPATATSVDLRDIK	1714.9	2	3.5087	0.2956
VIDQEMQAIGGQK	1417.6	2	3.0189	0.1705
VIDRELYQQLQR	1561.8	2	4.4061	0.1364

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VIDVFAMPQSGTGVSVEAVDPVFQAK	2693.1	3	3.8096	0.2643
VIEASFPAGVDSSPR	1532.7	2	2.9471	0.2496
VIEDNEYTAR	1210.3	2	3.007	0.3375
VIEEQLEPAVEK	1384.6	2	2.85	0.1077
VIELVDKEDVHISTSQVAEIVATLEKEEK	3253.6	3	5.3955	0.4534
VIELVDKEDVHISTSQVAEIVATLEKEEKVEEKEK	3996.5	3	5.6797	0.5079
VIEPKDIHAK	1150.4	2	2.466	0.1182
VIEPLKDFHKDEVR	1726.0	3	3.8431	0.3336
VIEPQYFGLAYLFR	1717.0	2	3.1573	0.3897
VIESGPDQLNDNEYTK	1822.9	2	4.8901	0.4593
VIESTQDLGNDLAGVMALQR	2131.4	3	5.2597	0.3458
VIEVGNNDIDDVNIIVFR	2045.3	2	4.942	0.3925
VIFFLPWQK	1178.4	2	2.8278	0.2239
VIFGLFGK	881.1	2	2.6438	0.1138
VIFLEDDDVAAVVDGR	1733.9	2	4.6648	0.4516
VIFPAAEDKDQDLITIIGKEDAVR	2658.0	3	5.96	0.4135
VIFSGSLDFFSDSFFNSAVQK	2343.6	2	5.2934	0.4504
VIGANKNQEEEK	1359.5	2	3.2332	0.1015
VIGEDGQSVYK	1195.3	2	3.2011	0.3079
VIGEPTSLMDVFPTVVR	1861.2	2	4.2715	0.3483
VIGGDDLSTLTGK	1276.4	2	3.8743	0.4129
VIGGDDLSTLTGKNVLIVEDIIDTGKTMQTLLSLVR	3830.4	3	5.4109	0.3735
VIGIDHIK	895.1	2	2.9398	0.1498
VIGIDHIKELVDDSVNNVR	2136.4	3	4.5613	0.4064
VIGIDHIKELVDDSVNNVRKDDPTLLSSGR	3306.7	3	4.7117	0.3265
VIGLSSDLQQVGGASAR	1658.8	2	5.4345	0.4497
VIGMHYFSPVDK	1393.6	2	2.8595	0.3073
VIGMHYFSPVDKMQLLEIITTEK	2694.2	3	5.8803	0.3351
VIGNQSLVNELAFTAR	1733.0	3	4.9161	0.1095
VIGPFYEIVEDKK	1537.8	2	2.604	0.1171
VIGQDSSEIHFK	1360.5	2	2.8891	0.2865
VIGSGCNLDSAR	1192.3	2	2.8269	0.2564
VIGTLEEVHMPQNGINHPGITALAQAFAVNPLLR	3623.2	3	6.3422	0.4889
VIHDHFGIVEGLMTTVHAITATQK	2620.0	3	4.9773	0.3495
VIHDNFGIVEGLMTTVHAITATQK	2597.0	3	8.2468	0.5751
VIHDNFGIVEGLMTTVHAITATQKTVDGPSGK	3338.8	3	4.7555	0.4559

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VIHDNFGIVEGLMTTVHAITATQKTVDGPSGKLWR	3794.3	3	6.2975	0.5077
VIHGVINSFVHVEQYK	1870.1	2	4.046	0.4164
VIHLFDEKGNDLGNMHR	1996.2	3	3.4682	0.2829
VIHLSNLPHSGYSDSAVLK	2038.3	2	4.8975	0.3875
VIHLSNLPHSGYSDSAVLKLAEPYGK	2797.2	3	3.8695	0.2693
VIHSILNSPYAK	1342.6	2	3.3661	0.3105
VIHVVTSEMDNYEPGVYTEK	2311.6	2	6.1893	0.5547
VIIEKYYTR	1185.4	2	3.1349	0.1655
VIILGDSGVGK	1058.3	1	2.8942	0.3414
VIILGDSGVGKTSLMNQYVNK	2237.6	2	2.8158	0.1221
VIILTAAAQGIGQAAALAFAR	2027.4	3	4.7936	0.3747
VIISAPSADAPMFVMGVNHEK	2214.6	2	4.7213	0.4083
VIISAPSADAPMFVMGVNHEKYDNSLK	2935.4	2	4.1915	0.4977
VIISAPSADAPMFVMGVNHEKYDNSLKIISNASCTTNCLAPLAK	4637.4	3	4.0083	0.2998
VIIVVKDGPGFYTTR	1666.0	2	3.8417	0.2921
VIKDFMIQGGDFTR	1627.9	2	4.4808	0.4581
VIKDFMIQGGDFTRGDGTGGK	2200.5	2	4.9653	0.4392
VIKEYPGKEVK	1290.5	2	2.9087	0.1888
VILAEFDYKAEPLETFPFDQSK	2588.9	3	3.554	0.2276
VILAEFDYKAEPLETFPFDQSKER	2874.2	3	4.8442	0.3245
VILDLTPNYR	1204.4	2	3.113	0.2753
VILDLTPNYRGENSWFSTQVDTVATK	2956.3	3	6.2982	0.5009
VILDNEEQRELQKLEEGEVNVLDNLAAATDQLVQQR	4122.5	3	4.8198	0.3799
VILGNELPKFYDE	1537.7	2	3.1225	0.2973
VILGSEAAQQHPEEVR	1763.9	2	5.2671	0.4759
VILHLKEDQTEYLEER	2016.2	3	5.3424	0.4858
VILHLKEDQTEYLEERR	2172.4	3	4.4394	0.2657
VILHPTPNSPK	1203.4	2	2.5104	0.1585
VILPVSVDEYQVGQLYSVAEASK	2495.8	3	4.1579	0.3587
VILQDFTGVPAVVDFAAMR	2050.4	2	5.3642	0.5633
VILQDFTGVPAVVDFAAMRDAVK	2463.9	3	3.2623	0.1307
VIMVGSGGVGK	1004.2	2	2.5824	0.2314
VIMVTGDHPITAK	1382.7	2	3.8828	0.3896
VINAAHSFYNGTTTLPISDEDRTPR	2777.0	3	3.855	0.3483
VINAENAAHKSEK	1411.5	2	3.7025	0.3773
VINDKHDDVMAK	1385.6	2	3.8563	0.3509

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VINDPIHGHIELHPLLVR	2073.4	3	6.1018	0.465
VINEPTAAALAYGLDK	1646.9	2	5.0335	0.4676
VINEPTAAALAYGLDKSEDKVIAVYDLGGGTFDISILEIQK	4339.9	3	5.3778	0.437
VINQILTEMDGMSTK	1681.0	2	5.2361	0.4979
VINQILTEMDGMSTKK	1809.1	2	2.8747	0.2161
VINSVDIK	888.0	2	3.3301	0.2007
VINYEEFKK	1170.3	2	2.685	0.1846
VINYEEFKKALEELATKR	2182.5	3	3.307	0.2096
VIPEDGPAAQNPENVKR	1835.0	2	3.2475	0.4569
VIPELDGKLTGMAFR	1648.0	2	2.8911	0.2471
VIPELNGKLTGMAFR	1647.0	2	2.8876	0.4405
VIPSPFKHADIVTTTTHK	1993.3	2	3.1981	0.3659
VIPSQEHLNGPLPVPFTNGEIQKENSR	3002.3	3	3.9757	0.369
VIQALAMKGDVENIEVVQK	2085.5	3	4.7967	0.2224
VIQAQTAFSANPANPAILSEASAPIPHDGNLYPR	3532.9	3	5.6355	0.3729
VIQEGRGELPDFQDGTK	1890.0	2	4.0817	0.354
VIQEGRGELPDFQDGTKATFHYR	2665.9	3	4.3865	0.1724
VIQEIVDKSGVVR	1442.7	2	3.9375	0.281
VIQGDGVDINTLQEIVEGMK	2159.4	2	5.9555	0.5031
VIQGDGVDINTLQEIVEGMKQK	2415.7	2	4.1217	0.2952
VIQHNALEDR	1195.3	2	2.9349	0.303
VIQKVEAFEHR	1356.6	3	3.9	0.3334
VIQPHGGGSNPLEGTQHLQDVPYVMVR	2930.3	3	4.353	0.3198
VIQQLEGAFALVFK	1563.9	2	4.7916	0.3871
VIQQSLEQEEAEHKATK	1969.1	2	4.0271	0.2554
VIQTHPHANKLPLKDSFTYEDYR	2774.1	3	4.0514	0.3189
VIQVAAGSSNLKR	1343.6	2	3.7141	0.2006
VIQYFAIVAALGDGPGKK	1848.2	2	2.5107	0.1877
VIQYLAHVASSHK	1453.7	2	4.3791	0.4576
VIQYLAHVASSPK	1413.6	2	4.235	0.4382
VIQYLAYVASSHK	1479.7	2	4.4786	0.4905
VIRGWDEALLTMSKGEK	1934.2	3	3.8749	0.3569
VIRPLDQPSSFDATPYIK	2048.3	3	4.0298	0.3836
VISDGEQGGQQGHR	1468.5	2	3.3279	0.3527
VISELNGKNIEDVIAQGIGK	2098.4	2	5.5222	0.4383
VISGVLQLGNIVFK	1487.8	2	5.2343	0.4485

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VISGVLQLGNIVFKK	1616.0	2	3.9751	0.3534
VISHMLSSHGGEIFLHVLSSSR	2394.7	2	2.7509	0.2456
VISKHDLGHFMLR	1553.9	2	3.4084	0.3314
VISSIEQKTDTSDK	1551.7	2	4.3336	0.4171
VISSIEQKTDTSDKK	1679.9	2	3.7239	0.3463
VISSIEQKTER	1290.4	2	3.0523	0.314
VISSIEQKTERNEK	1661.8	2	4.0601	0.2315
VISSIEQKTSADGNEK	1706.8	2	4.7219	0.4165
VISTMSVGIDHLALDEIK	1942.3	2	3.594	0.3429
VISTMSVGIDHLALDEIKKR	2226.6	2	4.5019	0.4045
VISTTDAER	992.1	2	2.8494	0.1338
VISTTDAERQAVTPPGLQEAINDLVKK	2895.3	3	3.8493	0.2054
VITEEEKNFK	1237.4	2	3.4617	0.3211
VITEEEKNFKAFASLR	1883.1	2	5.0723	0.4926
VITEYLNAQESAK	1466.6	2	4.8907	0.3868
VITFHKKEPFELEAFYTNLHEVPYPDAR	3392.8	3	3.9475	0.1743
VITIMQNPR	1072.3	2	2.5596	0.1902
VITNQYNNPAGLYSSENISNFNNALESK	3103.3	3	5.7366	0.4997
VIVDFSSPNIAK	1290.5	2	3.893	0.2888
VIVQQPGER	1026.2	2	2.6525	0.2264
VIVVGNPANTNCLTASK	1702.0	2	3.9701	0.3512
VIVVWVGTNNHENTAEEVAGGIEAIVQLINTR	3447.8	3	4.1954	0.2112
VIYVLPMLTIKEDKGTGVVTSVPSDSPDDIAALR	3602.2	3	5.2895	0.3014
VKADQDSEAMKR	1378.5	2	3.7496	0.3628
VKADRDESSPYAAMLAAQDVAQR	2493.7	3	5.1383	0.3515
VKAEDTVTVENVLK	1545.8	2	3.9838	0.287
VKAEEDKIPLLVVGNK	1753.1	2	4.2311	0.456
VKAEEDKIPLLVVGNKSDLEER	2482.8	3	5.5231	0.448
VKAEGPGLSK	986.1	2	2.6366	0.1146
VKAEPAKIEAFR	1359.6	2	3.2814	0.3993
VKAEVQNLGGELVVSGVDSAMSLIQAAK	2815.2	3	3.6906	0.2717
VKAHGPGLEGGLVGKPAEFTIDTK	2422.8	3	4.0633	0.3216
VKALDEEVHK	1168.3	2	2.839	0.1397
VKALESALKEAK	1287.5	2	2.9572	0.2183
VKANSVKQEFEK	1407.6	2	3.393	0.3039
VKANSVKQEFEKQDELKR	2177.4	3	4.3008	0.3161

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VKAQTAPNKDVQR	1455.6	2	3.5814	0.3357
VKATAAPAGAPPQPQDLEFTKLPNGLVIASLENYSPVSR	4049.6	3	5.0449	0.3473
VKDALEFWLQAGVDGFQVR	2179.5	3	5.3284	0.446
VKDASPNQVAEK	1286.4	2	3.439	0.313
VKDAVQAVKR	1114.3	2	3.1596	0.2211
VKDDIESLHDK	1299.4	2	3.8287	0.2769
VKDDIESLHDKFK	1574.8	2	4.4871	0.3498
VKDDMTEVTGR	1251.4	2	3.0578	0.248
VKDEFSVDKEASAHISGDK	2063.2	2	4.4406	0.4199
VKDILQNVFKLEK	1574.9	2	3.4997	0.1097
VKDLESLFHR	1244.4	3	4.2587	0.3198
VKDLESLFHRSEVELAAALSDKR	2614.9	3	4.3963	0.3668
VKDLVLSVHNR	1280.5	2	2.6125	0.2048
VKDPNSGLPK	1055.2	2	2.5015	0.1002
VKDRDDFPVVLVGNK	1701.9	2	3.5144	0.1523
VKDSEDVPMVLVGNK	1630.9	2	3.138	0.3455
VKDTDDVPMILVGNK	1644.9	2	4.7205	0.3701
VKDTFNGNLPFLFK	1640.9	3	3.7763	0.3836
VKEALAGLLVTYPNSQEAENWKK	2589.9	3	3.961	0.1718
VKEDENVPFLLVGNK	1701.9	2	4.5788	0.3304
VKEDENVPFLLVGNKSDLEDKR	2545.8	3	4.4562	0.3008
VKEDKFENPDLFAK	1680.9	2	3.7017	0.3559
VKEDPDGEHAR	1253.3	2	3.3769	0.2388
VKEDPDGEHARR	1409.5	2	2.8951	0.195
VKEDSDEQIKQLEDALKDVQKR	2615.9	3	3.7477	0.2146
VKEEEAALAAK	1159.3	2	3.2792	0.2678
VKEEEIHSANK	1284.4	2	2.685	0.1444
VKEEEVHR	1026.1	2	2.6305	0.1486
VKEEIIEAFVQELR	1704.0	2	4.5825	0.4011
VKEESSSISSLKDEFTQR	2071.2	3	4.5002	0.4423
VKEFLHNQGK	1200.4	2	3.3133	0.2597
VKEGMNIVEAMER	1506.8	2	4.844	0.442
VKEHINSVSAMK	1343.6	2	2.9947	0.2619
VKEIGSTMSGR	1165.3	2	2.9214	0.228
VKEIVAQHTK	1153.4	2	2.8441	0.1801
VKEKEAELKEAEK	1531.7	2	4.3386	0.274

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VKEKEAELKEAEKELHEK	2168.4	3	3.9471	0.2328
VKELEDLEHLQLDFWR	2071.3	2	6.1265	0.5048
VKELEEELQHLK	1495.7	2	2.4588	0.1753
VKELEEQLENETLHKEIHNLK	2574.9	2	5.2865	0.3481
VKELGHSTQQFR	1430.6	2	3.1832	0.289
VKELLVDCYKPTEAFISGLLDK	2482.9	3	5.3255	0.4148
VKENFDKAR	1107.2	2	2.9157	0.1423
VKEPSVQEATSTSDILK	1833.0	2	2.4471	0.1001
VKEPSVQEATSTSDILKVPKPEPIPEPK	3045.5	3	3.7874	0.1389
VKEQLEAAKPEPVIEEVDLANLAPR	2760.1	3	5.3607	0.3496
VKESDKLVATSK	1305.5	2	3.6301	0.2662
VKETQEDKLEGGAAK	1603.8	2	3.7284	0.2621
VKETQEDKLEGGAAKR	1759.9	3	3.2783	0.1417
VKEVLPHVPLGVIQR	1685.1	3	3.3359	0.3421
VKEYQVETIVDTLCTNMLSDKEQLR	2957.4	3	4.634	0.4279
VKFIHDQTSPNPK	1511.7	2	4.3523	0.2969
VKGDVDVSLPK	1157.3	2	3.3129	0.222
VKGDVDVSVPK	1143.3	2	2.5191	0.1848
VKGDVDVTLPK	1171.4	2	2.5706	0.1899
VKGEEIYSMDEGIR	1626.8	2	2.7976	0.3117
VKGGGHVAQIYAIR	1469.7	2	4.2855	0.4691
VKGGNIDVHPSEK	1380.5	2	3.1661	0.212
VKGHFGPINSVAFHPDGK	1908.2	2	3.4873	0.3026
VKGLVLGPIHK	1161.5	2	2.9186	0.2886
VKGPVRMPTK	1113.4	2	2.4317	0.298
VKGTNIQENEYVK	1522.7	2	3.8348	0.391
VKHEVSGETVVFQGGALGK	1943.2	3	4.8694	0.3678
VKIGHYILGDTLGVGTFGK	1976.3	2	4.8286	0.4278
VKIHEATGMPAGK	1339.6	2	3.419	0.333
VKIHPNTVMVK	1266.6	2	2.7172	0.1738
VKIPEELKPWLVDDWDLITR	2466.9	3	3.7224	0.1989
VKIPEGTILTMDMLTVK	1890.3	3	5.4458	0.3696
VKISTEVGITNVDLSTVDKDQSIAPK	2759.1	3	6.0714	0.3824
VKKDDEEEDPLDQLISR	2030.2	2	4.7915	0.326
VKKEDEVQAIATLIEK	1815.1	2	4.1047	0.2724
VKKYEQGFITDPVVLSPK	2049.4	3	3.7906	0.1344

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4476.2	3	7.0789	0.4621
VKLAAVDATVNQVLASR	1756.0	2	5.9152	0.5202
VKLADIQIEQLNR	1540.8	3	4.1089	0.2204
VKLDDLLAYLPSDDSSLPKDVSPTQAK	2917.3	3	4.9212	0.3511
VKLDSPAGTALSPSGHTK	1767.0	2	3.923	0.2759
VKLEAEIATYR	1293.5	2	3.7534	0.2769
VKLEAEIATYRR	1449.7	2	2.4324	0.1651
VKLEEQLKETVEK	1573.8	2	4.7521	0.3109
VKLEGHELPADLPPHLVPPSKR	2430.8	3	3.8512	0.2934
VKLFTESTGVLALEDKELGR	2206.5	2	3.8879	0.3481
VKLGHTDILVGVK	1379.7	2	2.8122	0.2285
VKLPDGHELTFPNR	1623.8	2	3.1673	0.3406
VKLQEMEGTVK	1262.5	2	4.0366	0.1649
VKLTAELIEQAAQYTNAVR	2119.4	3	5.0472	0.4304
VKLTNAEGVEFK	1335.5	2	3.1404	0.3258
VKNELFKR	1034.2	2	2.4029	0.1779
VKNFGIWLR	1133.4	2	2.515	0.1564
VKNPEDLSAETMAK	1533.7	2	3.8792	0.2928
VKNQLKETTEAACR	1591.8	2	4.1813	0.2589
VKNSLLSLSDT	1177.3	2	2.5021	0.1827
VKNSQSFFSGLFGGSSK	1778.0	2	3.1623	0.2395
VKPAPDETSFSEALLK	1733.0	2	3.821	0.3342
VKPAPDETSFSEALLKR	1889.1	2	4.8818	0.469
VKPEEMMDERPK	1489.7	2	3.3109	0.1831
VKPFMTGAAEQIK	1420.7	2	2.9264	0.1963
VKPFVVRDAVVYPILVEFTR	2348.8	3	3.5163	0.1595
VKPLLQVSR	1040.3	2	2.4129	0.3303
VKPTLIAVRPPVPLPAPSHPASTNEPIVLED	3256.8	3	5.3554	0.4878
VKQDSESPK	1018.1	2	2.4335	0.117
VKQELLEEVKK	1343.6	2	4.0076	0.1741
VKQELLEEVKKELQK	1842.2	3	4.5912	0.2535
VKQLPLVKPYLR	1454.8	3	3.6063	0.2425
VKQQFMTTQDASK	1512.7	2	4.1445	0.3466
VKQQFMTTQDASKDGR	1841.0	2	4.655	0.4853
VKSPELQAEAK	1200.4	2	2.8385	0.187
VKSVLVDFLIGSGLK	1575.9	2	4.1555	0.4512

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VKTDDIAR	918.0	2	2.7583	0.1929
VKTDRPLPENPYHSR	1810.0	3	4.0799	0.3066
VKTEIEEELKSLDKEISEAFTSTGFDR	3103.4	3	5.0061	0.3375
VKTLAMDTILANAR	1517.8	2	4.011	0.317
VKTLTGKEIEIDIEPTDKVER	2414.7	3	6.0373	0.3046
VKTPSFGISAPQVSIPDVNVNLKGPK	2694.1	3	3.8829	0.3046
VKTSEDADELHK	1372.5	2	3.388	0.2688
VKTSEEQAEAK	1220.3	2	2.9735	0.1544
VKTSTVDLPIENQLLWQIDR	2369.7	3	3.7841	0.275
VKTSTVDLPIENQLLWQIDREMLNLYIENEGK	3804.3	3	6.6165	0.5145
VKTTGIVETHFTFK	1608.9	2	2.7425	0.1586
VKTYTDELTPIESAVSVFK	2128.4	2	5.4292	0.4653
VKVDESHK	942.1	2	2.8609	0.1412
VKVDNQHDFQDIASVVALTK	2228.5	3	4.737	0.4147
VKVDPSHDASK	1183.3	2	3.2079	0.3021
VKVDPSHDASKVKAEGPGLSK	2150.4	3	3.5166	0.2472
VKVEHVVSVLEK	1366.6	2	3.835	0.3599
VKVEPAVDTSR	1201.4	2	2.8523	0.2625
VKVEPSHDASK	1197.3	2	3.0837	0.2114
VKVFGPGVER	1088.3	2	3.0385	0.1661
VKVGKEDSSSAEFLEK	1753.9	2	4.9559	0.4427
VKVGKEDSSSTEFVEK	1769.9	2	4.5429	0.3285
VKVGVDGFGR	1034.2	2	3.1243	0.2865
VKVKDEPQR	1099.3	2	3.0439	0.1445
VKVLPTHDASK	1195.4	2	3.0648	0.2184
VKVNKDDIQK	1187.4	2	3.0121	0.1341
VKVSQAAADLLAYCEAHVR	2045.4	3	4.7283	0.3337
VKVSQAAADLLAYCEAHVREDPLIIPVPASENPFR	3821.4	3	3.233	0.1384
VKVWGNVGTVEWADPIEDPDPEVMAK	2883.2	3	5.0107	0.2091
VKVWGNVVTVEWADPVEEPDPEVMAK	2925.3	3	3.536	0.1375
VKWGDIEFPPPFGR	1645.9	2	3.1425	0.2924
VKYEETVFYGLQYILNK	2108.4	2	4.0054	0.3947
VKYETELAMR	1240.5	1	3.5366	0.2679
VLAALQERLDNVPHTPSSYIETLPK	2793.2	3	4.4985	0.4045
VLAAVYK	763.9	1	1.9562	0.1579
VLADPSDDTK	1061.1	2	2.9474	0.2731

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VLADPSDDTKGFFDPNTHENLTYLQLLER	3350.6	3	3.6778	0.1074
VLADPSDDTKGFFDPNTHENLTYR	2753.9	3	3.3301	0.2147
VLADTKELVSSK	1290.5	2	3.8757	0.432
VLAEKLAAIGEATR	1442.7	2	3.5472	0.3609
VLAFGAKPDSTLHTYFPSFLSR	2455.8	3	3.8012	0.258
VLAFTAVGDGPPSPTIQVK	1898.2	2	4.7931	0.3286
VLAGDKNFITAEELR	1676.9	2	4.6649	0.4779
VLAGDKNFITAEELRR	1833.1	2	2.9507	0.1189
VLAGETLSVNDPPDVLDR	1911.1	2	5.5446	0.4513
VLAGQTLDINMAGEPKPDRPK	2251.6	3	4.4746	0.3364
VLAHLAPLFDNPKLDKELR	2190.6	2	3.488	0.3519
VLAIAQNFV	975.2	2	2.431	0.1522
VLAKPQNTAEVQK	1426.6	2	3.9932	0.3518
VLALELFEQITK	1404.7	2	4.0629	0.4212
VLALGYKELGHLTHQQAR	2035.3	3	5.4364	0.4965
VLALPEPSPAAPTLRSELELTLGKLEQVR	3129.6	3	4.1429	0.4358
VLALSFDAPGR	1146.3	2	3.3334	0.3599
VLALSVETDYTFPLAEK	1897.2	2	5.7504	0.4952
VLALSVETDYTFPLAEKVK	2124.5	2	5.0345	0.4269
VLAMSGDPNYLHR	1473.7	2	4.0467	0.3028
VLANNSLSFEK	1222.4	2	3.5897	0.3001
VLANPGNSQVAR	1226.4	2	3.7889	0.3456
VLAPASTLQSSYQIPTENSMTAR	2466.8	3	4.964	0.3797
VLAQFGER	920.0	2	2.4958	0.1848
VLAQLLR	813.0	1	1.7335	0.1168
VLAQNSGFDLQETLVK	1763.0	3	4.248	0.3866
VLAQQGEYSEAIPILR	1788.0	2	4.1211	0.3656
VLASEKTSLSEK	1292.5	2	2.8438	0.2923
VLATAFDTTLGGR	1322.5	2	4.3067	0.4029
VLATQPGPGR	996.1	2	3.1766	0.1074
VLATVTKPVGGDK	1285.5	2	3.2129	0.3369
VLATVTKPVGGDKNGGTR	1771.0	2	4.005	0.421
VLAVNQENEHLMEDYEK	2062.2	2	5.4409	0.4085
VLAVNQENEHLMEDYEKLASDLLEWIR	3259.6	3	5.8061	0.4737
VLAVNQENEHLMEDYEKLASDLLEWIRR	3415.8	3	4.0497	0.282
VLAVNQENEQLMEDYEK	2053.2	2	5.3919	0.4055

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VLAVNQENEQLMEDYEKLASDLLEWIR	3250.6	3	5.0603	0.4184
VLAVNQENEQLMEDYEKLASDLLEWIRR	3406.8	3	3.3557	0.1567
VLAVTAIRENLISALEEAKK	2169.6	3	5.1486	0.3455
VLDAMLPYLINYYGNPHSR	2237.6	3	3.4294	0.3192
VLDASGHHETLIGEEQRPVFK	2363.6	3	3.2433	0.3139
VLDASWYSPGTR	1352.5	2	3.4353	0.3288
VLDAVRGSPAINVAVHVFR	2021.4	3	4.7311	0.3972
VLDDGELLVQQTK	1458.6	2	4.396	0.2026
VLDELTLAR	1030.2	2	3.8561	0.3336
VLDELTLARTDLEMQIEGLKEELAYLK	3135.6	3	6.1043	0.3812
VLDFEHFLPMLQTVAK	1889.3	3	5.0831	0.4274
VLDGLHNELQTIGFQIETIGK	2326.6	3	5.722	0.4002
VLDGLHNELQTIGFQIETIGKK	2454.8	3	6.1981	0.4324
VLDIIATINK	1100.3	2	3.4982	0.2486
VLDIIATINKGSIVWQEVFDDKAK	2704.1	3	5.4224	0.4547
VLDKLLLYLR	1246.6	2	3.538	0.2919
VLDLDLFR	991.2	2	3.2953	0.3128
VLDLDLFRVDKGGDPALIR	2113.4	3	3.7328	0.2691
VLDLGSPQLAMHSIR	1637.9	2	3.3052	0.3945
VLDLSGNALEALPPGQGLGPAEPPGLPQLQSLNLSGNR	3792.3	3	3.6214	0.3963
VLDNYLTSPLPEEVDETSAEDEGVSQR	2994.1	3	5.2261	0.5181
VLDNYLTSPLPEEVDETSAEDEGVSQRK	3122.3	3	3.9543	0.1624
VLDPFTIKPLDR	1414.7	1	2.6902	0.192
VLDPFTIKPLDRK	1542.8	2	2.5022	0.231
VLDQKEHR	1025.1	2	2.5961	0.1713
VLDQLSAGK	931.1	2	2.4629	0.1131
VLDQVETELQR	1330.5	2	2.7055	0.2645
VLDSGAPIKIPVGPETLGR	1920.2	2	5.1959	0.4285
VLDVNLMGTFNVIR	1591.9	2	4.8238	0.3153
VLDWGLQEQLWPHMEALRPR	2475.9	3	3.4652	0.349
VLEALELYNKLVNEAPVYSVYSK	2643.0	3	5.5978	0.3014
VLEDNSALDK	1104.2	2	2.5033	0.1611
VLEDRPLSDKGSGDSSQVTQVSPQR	2686.9	3	5.5176	0.4171
VLEDSDLK	919.0	1	2.54	0.1746
VLEDSDLKK	1047.2	2	2.9305	0.2008
VLEDSDLKKSDIDEIVLVGGSTR	2489.8	2	6.3937	0.3791

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VLEDSDLKKSDIDEIVLVGGSTRIPK	2828.2	3	5.2427	0.1894
VLEEANQAINPK	1326.5	2	3.1998	0.1686
VLEEEKEAINQETVQQR	2044.2	2	5.0348	0.3536
VLEEGSVEAR	1089.2	2	2.7616	0.2155
VLEFKAHEGEIEDLALGPDGKLVTVGR	2894.3	3	3.7543	0.2656
VLEGMEVVR	1032.2	2	3.6359	0.3622
VLEGMEVVRKVESTKTDSR	2164.5	3	3.5555	0.1483
VLEHQLLQTTK	1310.5	2	3.8786	0.3333
VLEKSPGK	858.0	2	2.5365	0.1733
VLELDNVKSEIIPMFSNLASDEQDSVR	3050.4	2	4.3348	0.3042
VLELDPALAPVVSR	1479.7	2	4.2996	0.4085
VLELEKTLEAER	1430.6	2	3.0178	0.2526
VLELIPQIANEQLTEELLIVNDNLNNVFLR	3479.0	3	3.9838	0.2646
VLELKEHKLDGK	1409.7	2	4.1714	0.2616
VLELNKKQESEDTAK	1732.9	2	4.2125	0.3344
VLELPYQGEELSMVILLPDDIEDESTGLKK	3375.8	3	3.995	0.2591
VLELPYQGEELSMVILLPDDIEDESTGLKKIEEQLTLEK	4460.1	3	4.3831	0.2925
VLELVSITANK	1187.4	2	3.7571	0.3049
VLENAEGAR	959.0	2	3.2159	0.2158
VLENLKNMIHETNEHTLPK	2261.6	3	4.5599	0.3013
VLEQDKAR	959.1	2	2.7086	0.1151
VLEQHKLTK	1096.3	2	2.9445	0.2269
VLEQLTGQTPVFSK	1547.8	2	4.4568	0.4249
VLEQLTGQTPVFSKAR	1775.0	2	4.1028	0.3195
VLESVVADLLNRFLGDYVENLNKSQLK	3078.5	3	4.7646	0.309
VLETAEDIQER	1303.4	2	4.2297	0.3461
VLETAEDIQERR	1459.6	2	3.0283	0.1013
VLETEAVDQPDVVQR	1698.9	2	4.5135	0.3538
VLETLQEKGER	1302.5	2	2.7153	0.1942
VLETPQEIHTVSSEAVSLLEEVITPR	2878.2	2	3.9445	0.4378
VLEVASGSGQHAAHFAR	1737.9	2	4.9538	0.4639
VLEVNPQNK	1041.2	2	2.4337	0.1354
VLEVYTTQPGVQFYTGNFLDGTLK	2692.0	3	3.6455	0.2644
VLEYLNQEK	1136.3	2	3.5636	0.2256
VLEYLNQEKAEK	1464.6	2	3.652	0.2884
VLEYLNQEKAEKGREHIA	2128.4	2	4.9592	0.393

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VLEYLTAEILELAGNAAR	1947.2	2	4.5451	0.2167
VLFASQEIPASPFR	1562.8	2	3.7366	0.4255
VLFDKVASQGEVVRK	1676.0	2	3.8724	0.3149
VLFPGNSTQYNILEGLEK	2023.3	2	4.4475	0.4197
VLFPGNSTQYNILEGLEKLK	2264.6	2	2.7136	0.3034
VLFPLGLGHAAEYVRPR	1896.2	2	3.0124	0.2912
VLFRPSDTANSSNQDALSSNTSLK	2553.7	3	5.7354	0.3403
VLFSSNGGVVK	1107.3	2	3.2804	0.2511
VLFVEKK	863.1	2	2.6007	0.1186
VLGAHILGPGAGEMVNEAALALEYGASCEDIAR	3299.7	3	3.9807	0.3247
VLGATLLPDLIQK	1381.7	2	3.9756	0.2924
VLGDVIEVHGK	1166.4	2	2.6588	0.3274
VLGDVIEVHGKHEERQDEHGFISR	2788.0	3	3.6572	0.2512
VLGEAMTGISQNAK	1419.6	2	4.6424	0.4824
VLGELWPLFGGR	1344.6	2	3.5461	0.1972
VLGESPVPHTVLNLKEPLYVGGAPDFSK	2965.4	3	6.0331	0.4282
VLGFSPVIIDR	1216.5	2	2.4305	0.1968
VLGHVNNILISAVLPTAFR	2035.4	2	4.0367	0.3554
VLGILAMIDEGETDWK	1791.1	2	5.4894	0.5057
VLGILAMIDEGETDWKVIAINVDDPDAANYNDINDVKR	4217.7	3	4.7656	0.3313
VLGKDHPDVAK	1179.4	2	3.5027	0.3534
VLGMDPLPSK	1057.3	2	2.7276	0.2593
VLGMDPLPSKMPK	1413.8	2	3.7103	0.322
VLGNPKSDEMNVK	1431.6	2	4.3911	0.4459
VLGQGEEWRGGDGINSIGGGQK	2215.4	3	4.2492	0.3315
VLGQPHHELDSK	1360.5	2	3.4936	0.1041
VLGSGAFGTVYK	1199.4	2	2.4754	0.1282
VLGSLEALEPVHYEEK	1814.0	2	2.8259	0.2198
VLGTAFDPFLGGK	1322.5	2	3.5503	0.3912
VLGTEAVQDPTKVEAHVR	1950.2	3	3.5281	0.3034
VLGTEDLYDYIDKYNIELDPR	2545.8	3	4.4442	0.2962
VLGVPIIVQASQAEK	1552.8	2	3.4755	0.3865
VLGYIQLGQK	1119.3	2	2.9345	0.1868
VLGYIQLGQKEGAK	1504.8	2	3.17	0.1346
VLHAEQEKAK	1153.3	2	2.9367	0.3057
VLHASLQSVLHKEESLGPK	2073.4	3	3.4728	0.4662

Peptide Sequence	Peptide mass (m/z)	Charge State	Xcorr	DelCn2
VLHDAQQQCR	1198.3	2	2.5166	0.3036
VLHDNFGIVKGLMTTVHAITATQK	2596.0	3	6.2562	0.5307
VLHFDQVTENTTEK	1661.8	2	2.9142	0.2358
VLHFPNPEDKKLEEIIHQITNVEALIAR	3268.8	3	3.3876	0.2744
VLHGEQYLELYKPLPR	1956.3	2	5.3227	0.476
VLHLLALRPYR	1351.7	2	2.6408	0.2526
VLHLQENNIQTISR	1665.9	2	3.4526	0.354
VLHMDRNPYYGGESASITPLEDLYK	2870.2	3	4.0157	0.1581
VLHMDRNPYYGGESASITPLEDLYKR	3026.4	3	8.5581	0.4775
VLHMDRNPYYGGESSSITPLEELYK	2900.2	3	5.9403	0.3903
VLHMDRNPYYGGESSSITPLEELYKR	3056.4	3	7.6783	0.4401
VLHMVGDKPVFSFQPR	1858.2	2	4.2448	0.3885
VLHNQLVLFHNAIAAYFAGNQK	2469.8	3	3.5764	0.2581
VLHPLEGAVVIIFKK	1664.1	3	3.5334	0.3084
VLHTALHSSSSYR	1458.6	2	3.2275	0.3256
VLHVSENPVPLTVR	1560.8	2	3.8202	0.4763
VLHYLAIQKPADLAR	1709.0	2	4.4346	0.3224
VLIAAHGNSLR	1151.3	2	3.4391	0.3752
VLIDWINDVLVGER	1641.9	2	2.5039	0.2028
VLIEGSINSVR	1187.4	2	3.2567	0.1835
VLIGALSPGLAADFLLK	1699.1	2	4.6411	0.3881
VLIGGDETPEGQR	1371.5	2	3.5707	0.3379
VLIPSYAAGSIIGK	1389.7	2	2.4752	0.1939
VLIQQHEDAK	1181.3	2	2.4838	0.1245
VLIQVGYEPLPPTIGR	1753.1	2	3.2523	0.2358
VLISFKANDIEK	1377.6	2	2.7074	0.1403
VLISTDVWAR	1160.3	2	3.3776	0.2062
VLITENDVKEGLQR	1614.8	2	4.0223	0.3325
VLITTDLLAR	1115.3	2	3.5274	0.3395
VLIVSEDPELPYMRPPLSK	2184.6	3	3.9982	0.3042
VLKAQAQSQK	1101.3	2	2.4927	0.1365
VLKDEIDVK	1059.2	2	2.5192	0.1561
VLKDQPPNSVEGLLNALR	1964.3	3	5.2148	0.4379
VLKDSLHEKFPDAGEDELLK	2284.6	3	4.7097	0.266
VLKEEGNELVK	1258.4	2	3.388	0.2175
VLKEEGNELVKK	1386.6	2	3.7055	0.1828

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VLKEFHQAGKPIGLCCIAPVLAAK	2508.1	3	5.3194	0.3049
VLKEVEAVIPDHCIFASNTSALPISEIAAVSK	3353.9	3	4.8998	0.4396
VLKEYKDVDKK	1365.6	2	3.4646	0.1932
VLKGDVEKLSK	1216.5	2	3.0912	0.1968
VLKKQDAFYKEQLAR	1838.1	2	4.7286	0.4243
VLKPNFAAAWEEVGDTFEKEETFALSSTK	3246.6	3	4.2824	0.3153
VLKQVHPDTGISSK	1509.7	2	4.7404	0.4542
VLLALFCHEPCRPLHQLATDSTFSLDQPGGTLDLTLIR	4193.8	3	4.494	0.2855
VLLATLSIPITPER	1523.8	2	2.5891	0.2736
VLLDDTQSEAAR	1318.4	2	3.4613	0.3198
VLLENQITHFR	1370.6	2	3.315	0.3153
VLLESEQFLTELTR	1678.9	2	5.5964	0.3877
VLLGETGKEK	1074.3	2	2.7151	0.1936
VLLGETGKEKLPR	1440.7	2	3.8291	0.2597
VLLGFSSDESDVEASPR	1808.9	2	3.1283	0.2746
VLLGGPGSFYWQGQLISDQVAEIVSK	2793.2	3	4.8744	0.2419
VLLGSVSGLAGGFVGTPADLVNVR	2299.7	2	5.4236	0.4895
VLLGVGDPK	898.1	2	2.7814	0.1883
VLLKEILEQGLFSK	1618.0	2	3.6139	0.3964
VLLKSDSPTGDVLLDETLKHIK	2422.8	3	4.4838	0.2661
VLLLSHLAR	1022.3	2	2.988	0.2544
VLLLSSPGLEELYR	1589.9	2	3.8922	0.3896
VLLLTGKPKPAGVLGAVNKPLSATGR	2559.1	3	5.2246	0.4626
VLLNDGGYYDPETGVFTAPLAGR	2426.7	2	3.0962	0.1033
VLLPEYGGTKVVLDDKDYFLFR	2589.0	3	3.4025	0.1971
VLLPEYGGTKVVLDDKDYFLFRDGDILGK	3287.7	3	3.7554	0.1811
VLLPVWEAEGLGLR	1552.8	2	3.584	0.479
VLLQGKGDSEHK	1311.5	2	2.9388	0.1242
VLLQGKGDSEHKR	1467.7	2	3.6738	0.427
VLLQSKDQITAGNAAR	1685.9	2	4.6533	0.3537
VLLSICSLLCDPNPDDPLVPEIAR	2594.0	2	3.8852	0.2911
VLLSLEHGLWAPNLHFHSPNPEIPALLDGR	3344.8	3	6.3938	0.3764
VLLTTQGVDMISK	1405.7	2	4.1993	0.3878
VLLVGLKGLGAEIAKNLILAGVK	2290.9	3	3.4026	0.165
VLLVLELQGLQK	1353.7	2	4.1172	0.3426
VLLVPGPEKEN	1195.4	2	2.7778	0.255

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VLMEKEFPGFLENQKDPLAVDK	2548.9	3	5.4113	0.4758
VLMEKEFPGFLENQKDPLAVDKIMK	2921.5	3	5.5874	0.2433
VLNDKFASFIDKVR	1652.9	2	2.5389	0.2507
VLNGNKVASEALAR	1442.6	2	2.9932	0.2805
VLNGPEGDGVPEAVVTLNNQIK	2264.5	2	4.9106	0.4777
VLNHFSIMQQR	1373.6	2	2.4091	0.2559
VLNLIQSWADAFR	1533.8	2	4.1343	0.4442
VLNNMEIGTSLFDEEGAK	1968.2	2	5.8759	0.384
VLNNMEIGTSLFDEEGAKIVK	2308.6	2	4.8906	0.4446
VLNNMEIGTSLFDEEGAKIVKDLMSK	2883.3	2	4.3807	0.346
VLNNMEIGTSLFDEEGAKIVKDLMSKAEK	3211.7	3	4.6727	0.2933
VLNQQLTNHIR	1336.5	2	3.2768	0.3482
VLNQQLTNHIRDTLPGLR	2089.4	3	3.2647	0.247
VLNSYWVGEDSTYK	1661.8	2	2.8785	0.275
VLNTEANVVR	1115.3	2	2.9523	0.2664
VLNYAPGPLDTDMQQLAR	2003.3	2	4.1214	0.3684
VLPAQATEYAFAFIQVPQDDDAR	2566.8	3	5.4165	0.3871
VLPAQATEYAFAFIQVPQDDDARTDAVDSVVR	3509.8	3	4.6871	0.484
VLPAVGISYVVYENMK	1783.1	2	3.7429	0.4333
VLPEFDTPGHTLSWGK	1785.0	2	4.1786	0.4602
VLPEFDTPGHTLSWGKGQK	2098.3	2	3.2647	0.1701
VLPGDYEILATHPTWALK	2025.3	2	3.2938	0.2136
VLPGVDALSNI	1098.3	2	3.3736	0.3947
VLPSDLDLLLHMNNAR	1822.1	2	4.0108	0.4581
VLPSITTEILK	1214.5	2	2.6584	0.3328
VLPSIVNEVLKSVVAK	1696.1	2	4.1593	0.391
VLPSIVNEVLKSVVAKFNASQLITQR	2855.4	3	5.0104	0.4439
VLPSQTPQPAHHTPDTR	1883.1	2	3.2756	0.2919
VLPTHDASK	968.1	1	2.0086	0.253
VLPTHDASKVK	1195.4	2	2.6375	0.2394
VLPTQPNPVDASR	1394.6	2	2.6949	0.2999
VLPTYDASKVTASGPGLSSYGVPASLPVDFAIDAR	3523.9	3	3.3864	0.1168
VLQALEGLK	971.2	1	3.2219	0.2201
VLQALGSEPIQYAVPVVK	1912.3	3	4.2842	0.3723
VLQAQGSSDPEEESVLYSNR	2209.3	2	5.0556	0.3859
VLQATVVAVGSGSK	1316.5	2	5.2932	0.5445

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VLQDMGLPTGAEGR	1444.6	2	4.2556	0.4365
VLQEGLLQLDSILSSLEPLHRPIESPGGSVLLR	3568.1	3	4.033	0.3015
VLQHAASNK	968.1	2	2.7448	0.2661
VLQHEKQVYDIAAK	1642.9	2	3.7929	0.3677
VLQHYQESDKGEELGPGNVQK	2356.5	2	6.7131	0.4746
VLQHYQESDKGEELGPGNVQKEVSSSFDHVIK	3585.9	3	5.1809	0.3872
VLQHYQESDKGEELGPGNVQKEVSSSFDHVIKETTR	4073.4	3	5.522	0.4459
VLQLINDNTATALSYGVFR	2096.4	2	6.3778	0.5336
VLQLSDTAIVPIGYHVPR	1979.3	2	4.4525	0.4638
VLQQFADNDVSR	1392.5	2	3.6593	0.3763
VLQQKLEAIEDDSVKETDSSSASAATPSK	3036.2	3	6.8737	0.4631
VLQQQGSQER	1173.3	2	3.1251	0.2594
VLQQVKAESEHK	1396.6	2	2.893	0.2554
VLQSALAAIR	1042.3	2	3.0939	0.2262
VLQSFTVDSSK	1211.3	2	3.6371	0.3905
VLQSFTVDSSKAGLAPLEVR	2118.4	2	5.2549	0.4253
VLQVSIGPGLPK	1208.5	2	3.4521	0.3216
VLQYHKPVQASYFETLR	2080.4	2	3.8875	0.3877
VLRDNIQGITKPAIR	1695.0	3	3.6337	0.1956
VLREQLQTEQDAPAATR	1927.1	3	4.4705	0.2627
VLRHEEFEEGCK	1476.6	2	3.2375	0.2576
VLRPPGGGSNFSLGFDEPTEQPVRK	2686.0	3	5.8015	0.2911
VLRPQVTAVAQQNQGEVPEPQDMK	2664.0	3	4.637	0.3623
VLSAPPHFHFGQTNR	1708.9	2	4.2298	0.4727
VLSEAAISASLEKFEIPVK	2032.4	3	3.5421	0.2889
VLSEDEEDVDFDIIHNANDTFTVK	2766.9	3	4.4219	0.3282
VLSGDLGQLPTGIR	1426.6	2	2.8408	0.255
VLSGDLGQLPTGIRDFVEHSAR	2368.6	3	3.4939	0.3718
VLSGQDTEDR	1120.2	2	2.4259	0.1488
VLSGTIHAGQPVK	1307.5	2	3.2731	0.4175
VLSHSSALTEHQK	1437.6	2	3.3292	0.3439
VLSIGDGIAR	1001.2	2	3.0765	0.2925
VLSIQSHVIR	1152.4	2	3.3234	0.3077
VLSKEFHLNESGDPSSK	1875.0	2	4.9559	0.3648
VLSLLSAPLGSGGFTLLHAAAAAGR	2351.7	2	3.7755	0.4909
VLSMAPGLTSVEIIPFR	1831.2	3	4.854	0.4949

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VLSNGVQFSR	1107.2	2	3.1338	0.3611
VLSQQAASVVKQEGGDNDLIER	2357.6	3	3.4203	0.2964
VLSRPNAQELPSMYQR	1890.2	2	4.6089	0.3784
VLSSHLMHSSLPGLTR	1736.0	2	3.3295	0.3579
VLSTDVDVILRK	1358.6	2	3.7156	0.2961
VLSTVHTHSSVK	1295.5	2	3.7641	0.4261
VLSVDESIIKPEQEFFTAPFEK	2554.9	3	3.2285	0.2036
VLSVPESTPFTAVLK	1588.9	2	2.6846	0.2957
VLTDAVDDITSIDDFLAVSENHILEDVNK	3202.5	3	3.6524	0.2022
VLTDSGSLDSTIPGIENTITVTTEQLTTASFPVGSKK	3810.2	3	3.5313	0.1229
VLTEDEMGHPEIGDAIAR	1954.2	2	4.8808	0.3717
VLTEIIASR	1002.2	2	3.0576	0.3462
VLTEIIASRTPEELR	1728.0	2	2.6642	0.1261
VLTELLEQER	1230.4	2	3.7582	0.1827
VLTFALSEEVRPQDTVSVIGGVAGGSK	2718.1	3	6.2103	0.4624
VLTFDLTKYPDANPNPNEQ	2177.4	2	4.3724	0.3528
VLTFYRKEPFTLEAYYSSPQDLPYPDPAIAQFSVQK	4211.7	3	4.2991	0.2155
VLTHFFEREPPAASWAVQPHYQLPTAFR	3297.7	3	5.407	0.2633
VLTIDPTEFK	1163.3	2	2.4908	0.2447
VLTILEQIPGMVVVADKTSELYQK	2676.2	3	3.9858	0.2829
VLTLSDDLER	1161.3	2	3.317	0.2143
VLTLSEDSPYETLHSFISNAVAPFFK	2914.3	3	5.2396	0.478
VLTLSERPLDFLDLERPPTTPQNEEIR	3180.6	3	4.2223	0.338
VLTPELYAELR	1304.5	2	2.622	0.15
VLTQPSQSAVR	1186.3	2	2.7368	0.1866
VLTVINQTQK	1144.3	2	3.0708	0.2025
VLTVINQTQKENIR	1656.9	2	4.32	0.3865
VLTVINQTQKENLR	1656.9	2	4.3065	0.4342
VLTVINQTQKENLRK	1785.1	2	4.4892	0.3259
VLVAQHDVYK	1172.4	2	3.2564	0.322
VLVAQHDVYKGLLPEELTPLILATQK	2890.4	3	5.8164	0.3973
VLVDGEEHVGFLK	1442.6	2	3.0277	0.3225
VLVDMDGVLADFEAGLLR	1934.2	2	6.0472	0.4706
VLVDQTTGLSR	1189.3	2	3.7923	0.4017
VLVDSSFGQPTTQGEAR	1792.9	2	5.4957	0.4902
VLVEPDAGAGVAVMK	1456.7	2	3.5377	0.3858

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VLVEQQQDR	1115.2	2	2.5702	0.2078
VLVFVMGK	893.2	2	3.0748	0.2666
VLVGGGTGFIGTALTQLLNAR	2059.4	2	5.7957	0.4593
VLVGKNFEDVAFDEKK	1839.1	3	4.5404	0.3417
VLVHPPQDGEDEPTLVQKEPVEAAPAAEPVPAST	3519.9	3	4.3707	0.2334
VLVNDAQKVTEGQQER	1815.0	2	4.9291	0.4418
VLVQNAAGSQEK	1244.4	2	3.4299	0.2441
VLVSLSAGGR	959.1	1	2.9676	0.2142
VLVSLSAGGRDEGNYLDDALVR	2320.5	3	5.7383	0.5446
VLVSLSAGGRDEGNYLDDALVRQDAQDLYEAGEK	3668.9	3	4.8989	0.4228
VLVSLSAGGRDEGNYLDDALVRQDAQDLYEAGEKK	3797.1	3	4.6008	0.3364
VLVTGATGLLGR	1157.4	2	4.2137	0.2437
VLVTGGAGYIGSHTVLELLEAGYLPVVIDNFHNAFR	3844.4	3	5.7165	0.4527
VLVVHDGFEGLAK	1384.6	2	3.4305	0.4087
VLWLADCDVSDSSCSSLAATLLANHSLR	2949.3	3	3.331	0.1011
VLWLDEIQQAVDEANVDEDR	2358.5	2	3.1993	0.301
VLYDFVMDDTISPYSR	1922.1	2	2.4732	0.1027
VLYFGDHLYSDLADLMLR	2142.5	2	3.1073	0.2944
VLYLGAASGTTVSHVSDIIGPDGLVYAVEFSHR	3432.8	3	4.2526	0.1971
VLYLGAASGTTVSHVSDIVGPDGLVYAVEFSHR	3418.8	3	5.9152	0.4009
VLYVQDSLEGEAR	1479.6	2	3.4289	0.2039
VMAGALEGDIFIGPK	1518.8	2	3.07	0.1039
VMAGALEGDLFIGPK	1518.8	2	4.3075	0.3193
VMALELGPHK	1095.3	2	2.7668	0.2583
VMALWHQLHVNTK	1577.9	2	3.5233	0.3493
VMATTGGMGMGPGGPGMITIPPSILNNPNIPNEIIHALQAGR	4197.9	3	5.2234	0.3678
VMAVDALASSHPLSTPASEINTPAQISELFDAISYSK	3863.3	3	6.7257	0.4569
VMDEVEKAR	1077.2	2	2.5675	0.2383
VMDKYTFELSR	1389.6	2	3.4284	0.2706
VMDMLHSMGPDTVVITSSDLPSPQGSNYLIVLGSQR	3847.4	3	5.0025	0.2885
VMDQHKLTR	1128.3	2	3.0616	0.3028
VMDRPGNYVEPTIVTGLGHDASIAHTETFAPILYVFK	4061.6	3	6.2296	0.4693
VMEGLDAFDDLMQHTHIQPWYLR	2817.2	3	5.3842	0.3678
VMEIVDADEKVR	1404.6	2	2.884	0.1247
VMEKETEK	994.1	2	2.6077	0.144
VMEKETEKR	1150.3	2	2.551	0.1814

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VMELESKLNEAKEEFTSGGPLGQK	2622.9	3	4.3928	0.272
VMENGLLFKELLQTPNFR	2150.5	2	2.5706	0.2585
VMFTEDLKLPASFDAR	1841.1	2	2.7488	0.122
VMGALNTVVENLHDPDKVSSVLALVGK	2807.3	3	4.6851	0.3503
VMGEVGK	719.9	1	1.9599	0.1761
VMGTFSTVTSTVK	1358.6	2	2.5646	0.1098
VMIPQDEYPEINFVGLLIGPR	2401.8	3	3.2899	0.1557
VMIYQDEVKLPAK	1534.8	2	3.7834	0.2072
VMKEFVGGNTPNVLTLVDNWYQVTQGIGR	3237.7	3	4.9911	0.4804
VMKGVDDLDFFIGDEAIEKPTYATK	2804.2	3	5.0796	0.4063
VMLGETNPADSKPGTIR	1787.0	2	5.2902	0.4062
VMLTTAGGTK	979.2	2	2.8553	0.3762
VMLVNSMNTVK	1236.5	2	2.6514	0.181
VMNILHR	883.1	2	2.5608	0.1521
VMNTGSQFVMEGVK	1527.8	2	4.3483	0.4474
VMPNAIVQSVGVSSGK	1573.8	2	3.8898	0.4172
VMPYVDILFGNETEAATFAR	2245.5	2	3.4054	0.2196
VMQEEIFGPILPIVPVK	1910.4	2	4.3743	0.4006
VMQEEIFGPILPIVPVKNVDEAINFINER	3325.9	3	3.9098	0.2007
VMQEQGTHPK	1155.3	2	3.2827	0.2973
VMQQQQQTTQQQLPQK	1943.2	2	4.5267	0.1869
VMQVLNADAIVVK	1400.7	2	3.8585	0.2188
VMQVVDEKLPGLLGNFPGPFEEEMK	2805.3	3	4.5956	0.2089
VMRVEYHFLSPYVSPK	1953.3	3	3.4295	0.159
VMSEFNNNFR	1258.4	2	2.6247	0.1788
VMSQEIQEQLHK	1470.7	2	4.0001	0.2808
VMSQEIQEQLHKQQEVIADK	2382.7	3	3.3138	0.1289
VMTDESGKSK	1082.2	2	2.5561	0.1076
VMTIAPGLFGTPLLTSLPEK	2086.5	2	4.2005	0.3825
VMVAEALDISRETYLAILMDR	2410.8	3	3.6035	0.3003
VMVDANEVPIQK	1343.6	2	3.8722	0.3494
VMVLDFVTPTPLGTR	1647.0	2	4.5742	0.4321
VMVQPINLIFR	1330.7	2	3.4152	0.2703
VMVTNVTSLLK	1205.5	2	3.5757	0.3074
VMYEKEAK	998.2	2	2.6537	0.1714
VNAGDQPGADLGPLITPQAK	1963.2	2	6.0812	0.5077

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VNAIEHVIIPR	1261.5	2	3.6239	0.3789
VNAVPRPIPEKK	1348.6	2	2.7028	0.2754
VNDFLAEIFKK	1324.5	2	2.9778	0.1094
VNDKNPHVALYALEVMESVVK	2356.7	3	4.0377	0.2977
VNDTIQIDLETGK	1446.6	2	2.9861	0.1119
VNDTIQIDLETGKITDFIK	2164.4	2	4.5487	0.3034
VNDVNEFAPVFVER	1635.8	2	3.0343	0.1055
VNEAREELMR	1247.4	2	2.6176	0.1964
VNESSHYDLAFTDVHFKPGQIR	2561.8	3	5.5586	0.3987
VNFAMNVGK	980.2	1	2.9255	0.3024
VNFDDYTVNLGGLKDHIK	2049.3	2	4.5619	0.3732
VNFEDDSRGK	1167.2	2	2.6471	0.1979
VNFHFILFNNVDGHLYELDGR	2520.8	3	3.2025	0.2189
VNFPENGFLSPDKLSLLEK	2148.4	2	4.1513	0.3355
VNFSPPGDTNSLFPGTWYLER	2398.6	2	2.5062	0.1996
VNFTVDQIR	1092.2	2	3.4717	0.3107
VNGDASPAAAESGAK	1345.4	2	3.9918	0.4449
VNGEDPYPHKFHVDISLTDFIQK	2701.0	3	3.4502	0.229
VNGRPLEMIEPR	1411.7	2	3.4049	0.2346
VNGVDDAANFR	1178.2	2	3.1998	0.3069
VNHFVPEAGSR	1213.3	2	3.2639	0.3053
VNHLYSDLSDALVIFQLYEK	2368.7	2	4.9267	0.3883
VNHPQVSALLGEEDEEALHYLTR	2621.8	3	5.2007	0.2702
VNHVEKPPKVESK	1491.7	2	3.024	0.2268
VNHVTLSQPK	1123.3	2	3.2955	0.3038
VNIAFNYDMPEDSDTYLHR	2301.5	2	5.4452	0.4565
VNIGQGSHPQK	1165.3	2	3.0337	0.327
VNIGQGSHPQKVKVFGPGVER	2234.5	3	4.8207	0.4312
VNIGSSFENRPMNVLK	1806.1	2	3.9756	0.1478
VNILFDFVK	1095.3	2	3.2009	0.1889
VNILFDFVKK	1223.5	2	2.9928	0.195
VNINAALVEDIINLEEVNEEMKSVIEALKDNFNK	3860.3	3	4.2707	0.2109
VNINGGAVSLGHPIGMSGAR	1908.2	2	4.8302	0.524
VNKEVER	874.0	2	2.4709	0.1548
VNKITITNDKGR	1359.6	2	2.7549	0.1581
VNKYGDTWDE	1227.3	2	3.1055	0.3621

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VNLAELFK	934.1	2	2.9304	0.249
VNLESPGPER	1098.2	2	2.8997	0.1864
VNLGVGAYR	949.1	2	2.485	0.159
VNLKYDSWHK	1290.5	2	2.7937	0.2892
VNLLSFTGSTQVGK	1451.6	2	4.5978	0.4021
VNLLYSR	865.0	1	1.7316	0.1553
VNLSAAQTLR	1073.2	2	3.2273	0.2897
VNMPPAVDPAEFFVLMER	2063.4	2	3.7638	0.4259
VNNASLIGLGYTQTLRPGVK	2102.4	3	3.256	0.1011
VNNRFELINIDDLEDDPVVNGER	2686.9	3	3.8882	0.135
VNNSSLIGLGYTQTLKPGIK	2104.4	3	5.2219	0.441
VNNSSLIGVGYTQTLRPGVK	2104.4	2	4.653	0.4192
VNNSTGTSEDPSLQR	1605.6	2	4.5254	0.374
VNNSTMLGASGDYADFQYLK	2195.4	2	5.4782	0.5307
VNPALAELNLR	1210.4	2	3.59	0.4223
VNPCIGGVILFHETLYQK	2032.4	2	4.9035	0.4192
VNPIQGLASK	1027.2	2	2.7306	0.2913
VNPSQTHNNLYAWGQETGAPILTDDVSLQVFMDHLKK	4169.6	3	6.5794	0.4641
VNPSQTHNNMYAWGQESGAPILTDDVSLQVFMDHLKK	4173.6	3	5.0277	0.3188
VNPTVFFDIAVDGEPLGR	1947.2	2	5.7117	0.5578
VNQIGSVTEAIQACK	1561.8	2	4.3497	0.5012
VNQIGSVTESIQACK	1577.8	2	4.4956	0.2127
VNQIGSVTESLQACK	1577.8	2	4.2353	0.326
VNQPASFAIR	1103.3	2	2.7344	0.2738
VNQQPNTSDKK	1259.4	2	2.5575	0.1309
VNQWTTNVVEQTLSQLTK	2090.3	2	5.123	0.4697
VNREIVSGMK	1133.3	2	2.7124	0.2072
VNSEQEHFLIVPFGLLYSEVTASSLVK	3008.4	3	3.6724	0.2876
VNSININQGSITFAGGPGRDGTIDFTPGSELLITK	3592.0	3	5.5762	0.4002
VNSKFDTIYQILLK	1683.0	2	4.5281	0.398
VNSKFDTIYQILLKK	1811.2	3	3.5522	0.2696
VNSQRPFNAEPPPELLTENYITPNPIFFTR	3503.9	3	5.3701	0.4134
VNSVSSGLAEEDLETLLQSR	2148.3	2	5.7291	0.4457
VNTFSALANIDLALEQGDALALFR	2563.9	3	4.271	0.324
VNTLIRPDGEK	1242.4	2	3.2689	0.2578
VNTLMHYNVR	1247.5	2	2.402	0.1159

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VNTSKGFLIDGYPR	1567.8	2	2.4688	0.2229
VNVDEVGGEALGR	1315.4	2	3.8411	0.3982
VNVDIINFGEEEVNTEK	1950.1	2	3.6685	0.2063
VNVDKVLER	1072.2	2	3.152	0.2247
VNVEAPDVNLEGLGGK	1611.8	2	4.3017	0.3385
VNVEHMTEK	1087.2	2	2.468	0.2727
VNVGAGSHPNK	1080.2	2	2.9396	0.3189
VNVGAGSHPNKVK	1307.5	2	3.6193	0.3789
VNVPGSQAQLK	1141.3	2	2.6075	0.2688
VNVPVIGGHAGK	1148.3	2	3.7287	0.3849
VNVTHKEEIILTPIEVAIEDMQK	2651.1	3	5.4343	0.4213
VNVTHKEEIILTPIEVAIEDMQKK	2779.2	3	3.39	0.2
VNVTVDYIRPASPATETVPAFSER	2620.9	3	5.395	0.469
VNVVAPGFVHTDMTK	1615.9	2	3.8252	0.3508
VNVYHHLVETLK	1452.7	2	3.4533	0.3839
VNYGAYINDFK	1304.4	2	3.8568	0.2765
VPADLGAEAGLQQLLGALR	1893.2	2	6.1694	0.5195
VPADLGAEAGLQQLLGALRELPRPK	2614.0	3	3.5057	0.2591
VPADTEVVCAPPTAYIDFAR	2136.4	3	4.7553	0.3432
VPAEGLEEVLTTPETVLTGHTEK	2451.7	3	4.2111	0.2908
VPAINVNDSVTK	1257.4	2	3.7464	0.3839
VPAQSESVR	973.1	2	2.5753	0.2097
VPASQPRPESKPESQIPPQRPQR	2610.9	3	4.1361	0.2382
VPDDIYKTHLENNR	1714.9	2	4.7448	0.45
VPDDIYKTHLENNRFGGSGSQVDSAR	2864.0	3	3.7158	0.2299
VPDKLLDSSTVTHLFK	1801.1	3	5.713	0.3465
VPDLKDLDPIGK	1310.5	2	3.7682	0.3886
VPDSTYEMIGGLDK	1525.7	2	3.4936	0.4086
VPEANSSWMDTVIR	1605.8	2	2.7757	0.1964
VPEARPNSMVVEHPEFLK	2080.4	3	4.344	0.3536
VPEEDLKR	986.1	2	2.4352	0.1114
VPEGLEDVSKYPDLIAELLR	2257.6	3	5.1929	0.3989
VPEGVAGAPNEAALLALMER	2009.3	2	5.6226	0.5449
VPENTMHAMQQK	1414.6	2	4.042	0.3634
VPERAPLPPPAPSQFQAR	1959.2	3	4.6445	0.4685
VPEVPTAPATDAAPK	1464.6	2	3.834	0.3258

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VPFDAATLHTSTAMAAQHGMDDDGTGQK	2875.1	3	5.8028	0.4688
VPFIHVGNQVVSELGPIVQFVK	2407.8	3	4.2764	0.2467
VPFLVAETPR	1129.3	2	3.0312	0.3151
VPFLVLECPNLK	1372.7	2	3.6295	0.2483
VPFPSIQAVK	1086.3	2	3.0512	0.2443
VPGNFHVSTHSATAQPQNPDMTHVIHK	2952.3	3	4.287	0.162
VPGPVQQALQSAEMSLDEIEQVILVGGATR	3137.6	3	3.7696	0.1698
VPGPVQQALQSAEMSLDEIEQVILVGGATRVPR	3490.0	3	5.2552	0.4521
VPHDPVALEEHFRDDDEGPVSNQGYMPYLNR	3598.9	3	4.484	0.3684
VPHNAAVQVYDYR	1532.7	2	3.5756	0.4758
VPHNAAVQVYDYREK	1790.0	2	2.8156	0.2691
VPHSLDLSSPNMANTVNAALKPLETLSR	2977.4	3	4.9452	0.5181
VPIDIDKTKVQNIHPVESAK	2232.6	3	5.6806	0.4794
VPINESFISMVIGR	1562.9	2	3.4983	0.4072
VPIPWVSGTSASTPVFGGILSLINEHR	2836.2	3	5.8357	0.5691
VPKKEESVKK	1172.4	2	2.8724	0.195
VPLALFALNR	1114.4	2	2.8867	0.3375
VPLKFPVQENASHLHGR	1930.2	2	4.2252	0.4292
VPLPSLSPTMQAGTIAR	1740.1	2	4.0634	0.4037
VPLQQNFQDNQFQGK	1791.9	2	4.638	0.4357
VPLVAEKPLKEPK	1448.8	2	3.3764	0.3409
VPPAINQFTQALDR	1570.8	2	3.321	0.4235
VPPVQVSPLIK	1177.5	2	3.3556	0.252
VPQAEGPPKR	1079.2	2	2.5895	0.3095
VPQIAFVITGGK	1230.5	2	2.7204	0.2404
VPQIEVETHK	1180.3	2	2.8075	0.2565
VPQVSTPTLVEVSR	1512.7	2	3.5301	0.4105
VPREQIVVDLSHPGVSEDDQVSR	2562.8	2	4.2754	0.3731
VPSENVLGEVGSGFK	1519.7	2	3.831	0.3622
VPSENVLGEVGSGFKVAMHILNNGR	2626.0	3	3.569	0.1086
VPSGFYVGSYVHGAMQSPSLHK	2349.7	3	3.6326	0.2848
VPSGGYSSINNVQDPQKPEPR	2270.4	3	3.219	0.2589
VPSHAVVAR	936.1	2	2.8757	0.2766
VPSLVGSFIR	1075.3	2	3.4657	0.2447
VPSLVGSFLR	1075.3	2	3.2723	0.1918
VPSPGYGSPAAGAASADTAAR	1875.0	2	3.5227	0.3401

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VPSTEAEALASSLMGLFEK	1981.3	2	4.8458	0.4353
VPSYQALLR	1047.2	2	2.7126	0.298
VPTADLEDVLPLAEDITNILSK	2367.7	2	5.5962	0.4274
VPTANVSVVDLTCR	1474.7	2	4.5475	0.4581
VPTANVSVVDLTCRLEKPAKYDDIK	2776.2	3	3.9819	0.3193
VPTANVSVVDLTCRLEKPAKYDDIKK	2904.4	3	5.534	0.3951
VPTTGIIEYPFDLENIIFR	2238.6	2	4.6818	0.3092
VPTTGIIEYPFDLQSVIFR	2196.5	2	4.265	0.3273
VPTVSRPYSFIEFDTFIQK	2275.6	3	4.1174	0.2549
VPVAVQGEDTVQSLTQGDGVAK	2199.4	3	4.2858	0.2338
VPVHDVTDASK	1168.3	2	3.5204	0.3114
VPVKDVVDPSK	1183.4	2	3.0429	0.1952
VPVPEDKYTAQVDAEEKEDVK	2390.6	3	4.9767	0.3462
VQAAEHTLR	1025.1	2	3.0778	0.2728
VQAAQSEAKVVSQYHELVVQAR	2441.7	3	3.8968	0.2825
VQAEREAAQSR	1245.3	2	2.5394	0.1246
VQAINVSSR	974.1	2	2.6124	0.1366
VQALTTDISLIFAALKDSK	2035.4	2	4.1753	0.452
VQAMQISSEKEEDDNEKR	2137.3	3	3.5921	0.3062
VQANLGAPDINIEGLDAK	1839.0	2	4.8658	0.3433
VQAQGHTLQVAGLR	1478.7	2	3.4994	0.4316
VQAQVIQETIVPKEPPPEFEFIADPPSISAFDLDVVK	4095.6	3	4.8236	0.4329
VQASLAANTFTITGHAETK	1961.2	2	5.2862	0.4748
VQASLSANTFAITGHAEAKPITEMLPGILSQLGADSLTSLR	4211.8	3	4.4581	0.2816
VQASLSANTFAITGHAEAKPITEMLPGILSQLGADSLTSLRK	4340.0	3	5.0252	0.3815
VQAVQPTLILQDGDVINLGDR	2265.6	3	5.6858	0.4618
VQAVVAVAR	913.1	2	3.1164	0.2274
VQCCLYFIAPSGHGLKPLDIEFMK	2711.3	3	3.6906	0.2733
VQDAVQQHQQK	1309.4	2	3.7404	0.2799
VQDDEVGDGTTSVTVLAAELLR	2289.5	2	6.0634	0.5004
VQDDVTKLDLR	1302.5	2	2.8664	0.1143
VQDHIQSR	983.1	2	2.5353	0.1423
VQEAVNYGLQVLDSAFEQLDIK	2480.8	3	5.1321	0.353
VQEEFDIDMDAPETER	1925.0	2	4.7098	0.4388
VQELETSLAELR	1388.5	2	3.006	0.1833
VQELQQQSAR	1187.3	2	3.288	0.1916

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VQENQMDKAR	1219.4	2	2.9819	0.1824
VQENSPGHR	1024.1	2	2.9334	0.2603
VQEQELKSEFEQNLSEK	2066.2	2	5.7467	0.4627
VQEQELKSEFEQNLSEKLSEQELQFR	3197.5	3	5.8924	0.4584
VQEQELKSEFEQNLSEKLSEQELQFRR	3353.6	3	4.9807	0.2529
VQEQELTR	1003.1	2	2.6824	0.1034
VQEQLHMAEK	1213.4	2	2.6305	0.1537
VQEQVHTLLSQDQAQAAR	2023.2	2	6.4578	0.5443
VQESADELQK	1147.2	2	3.3205	0.2044
VQESLKKQEGLLK	1500.8	2	4.632	0.2114
VQESTKGPDEAK	1289.4	2	4.2887	0.3248
VQESTKGPDEAKIK	1530.7	2	4.5932	0.3231
VQETGDIVISNAYVDLAPTSGTSAK	2537.8	3	4.6569	0.384
VQETGDIVISNAYVDLAPTSGTSAKTPSEGGK	3194.5	3	4.0504	0.2386
VQETGEIKEPLEISISQDVHDSK	2582.8	3	4.4703	0.1795
VQEVQVVGVKDDR	1471.6	2	3.8413	0.3919
VQGEAQKVER	1144.3	2	2.6879	0.1455
VQHVIHYQVPR	1376.6	2	3.406	0.2899
VQIAVANAQELLQR	1553.8	2	5.0256	0.3831
VQIEHISSLIK	1267.5	2	3.7495	0.3265
VQILKDYVR	1134.4	2	3.3281	0.2441
VQIYHNPTANSFR	1547.7	2	4.0796	0.3496
VQKEQADKLAR	1286.5	2	2.7531	0.2048
VQLDLAETDLSQGVAR	1715.9	2	5.5207	0.4444
VQLLQDLQDFFR	1522.7	2	4.3801	0.2527
VQLREQHLYYQDQLLPVSR	2386.7	3	5.2513	0.3739
VQLSGPQEAEKYVLHMIEDGEIFASINQK	3275.7	3	4.1264	0.3056
VQLSNDFDEYIMAIEQTIK	2258.5	2	4.6215	0.3408
VQLSNDFDEYIMAIEQTIKSGSDEVQVGQQR	3529.8	3	3.5586	0.1566
VQLVVGDGR	943.1	2	2.9906	0.191
VQNATLAVANITNADSATR	1931.1	2	5.7025	0.4951
VQNIHPVESAK	1222.4	2	3.6987	0.3681
VQNMALYADVGGK	1366.6	2	3.8432	0.3464
VQQAVWEHQR	1281.4	2	2.6399	0.1958
VQQELSRPGMLEMLLPGQPEAVAR	2651.1	3	4.5699	0.3114
VQQGERDFEQISK	1564.7	2	3.2582	0.1382

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VQQQEDEITVLK	1430.6	2	2.8197	0.1156
VQQQEDEITVLKAALADVLR	2240.5	3	3.3106	0.2091
VQQTVQDLFGR	1291.4	2	4.0284	0.3211
VQQVQPAMQAVIR	1468.8	2	4.4941	0.3577
VQRSEDTLKALEDFLASLR	2192.5	3	3.8607	0.3786
VQSATHFKK	1046.2	2	2.789	0.1225
VQSGNINAAK	1002.1	2	2.5328	0.108
VQSGSESVIQEYVDLR	1810.0	2	4.7331	0.3902
VQSHILHLEHDLVHVTR	2034.3	3	3.7984	0.4026
VQSINYNPFDQK	1453.6	2	2.5058	0.1768
VQSINYNPFDQKLYVYNDGYLLNYDLSVLQKPQ	3954.4	3	6.7462	0.5235
VQSLEGEKLSPK	1315.5	2	3.451	0.2606
VQSLQATFGTFESILR	1798.0	2	5.0197	0.5059
VQSSPNLLAAGR	1213.4	2	2.717	0.2098
VQSVEQIREVASGAAR	1700.9	2	3.2585	0.2027
VQTANEVKQAVEQQIQSHR	2194.4	3	3.6681	0.2011
VQTEKEEKEEAR	1476.6	2	3.5382	0.3278
VQTERPQPQTLQLDFLMK	2173.5	3	4.3121	0.3646
VQTLSNQPLLK	1241.5	2	3.1855	0.2003
VQTLSNQPLLKSPAPPLLHVAALGQK	2722.2	3	3.9723	0.2908
VQTRLEETQALLR	1557.8	2	3.712	0.2631
VQTTPPPAVQGQK	1351.5	2	2.6926	0.175
VQTVLGLVEPSKLGR	1596.9	2	3.6865	0.3581
VQVAEEGKR	1016.1	2	2.5035	0.1276
VQVAEHPR	936.1	2	2.6732	0.2409
VQVALEELQDLK	1385.6	2	4.4385	0.292
VQVALGNISSK	1116.3	2	2.5961	0.1885
VQVEYKGETK	1181.3	2	3.1334	0.2932
VQVLTAGSLMGLGDIISQQLVER	2428.8	3	4.4982	0.3454
VQVLTAGSLMGLGDIISQQLVERR	2585.0	3	3.6249	0.3096
VQVMVPEAETR	1259.5	2	2.9144	0.1506
VQVPNCDEIFYAGTGNLLLR	2223.5	3	3.6749	0.1143
VQVSYKGDTK	1125.3	2	2.6458	0.2572
VQVSYKGETK	1139.3	2	3.132	0.3582
VQYTLPDGSTLDVGPAR	1790.0	2	3.0173	0.1926
VRAGAVGAHLPASGLDIFGDLK	2165.5	2	2.985	0.2475

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VRAPMVNPTLGVHEADLLK	2061.4	3	5.1849	0.4005
VRDIAIATR	1015.2	2	2.9772	0.1148
VRDIEHLTSLDFFR	1749.0	2	3.5864	0.383
VRDIEHLTSLDFFRK	1877.1	3	3.9481	0.2872
VRDKLNNLVLFDK	1574.8	2	4.1058	0.3391
VRDKLNNLVLFDKATYDK	2153.5	3	5.0239	0.29
VRDLFALAR	1061.3	2	2.958	0.1814
VRDLQTQLEELQKK	1729.0	3	5.0724	0.2608
VRDQLGQELEELTASLFEEAHK	2543.8	3	5.658	0.3879
VRDVFEAK	964.1	2	2.6112	0.1169
VRDVLDFYNVPIQDR	1850.1	2	2.6646	0.17
VREAGQNVTFCCKASGTPMPKK	2353.8	2	2.4898	0.1253
VREEEIEVDSR	1361.4	2	3.1445	0.1963
VREEHQGENLDENLVPVAAAEGRPR	2787.0	3	3.8176	0.1837
VREELIDKKTESAVSQMQSVIELGR	2847.2	3	6.0604	0.5292
VREEVPLELVEAHVK	1748.0	3	5.0627	0.3144
VREEVPLELVEAHVKK	1876.2	3	4.654	0.2158
VREEYPDRIMNTFSVVPSPK	2365.7	2	3.8803	0.2065
VREFSITDLVPYSITLR	2010.3	2	3.8009	0.3208
VREFSITDVVPYPISLR	1992.3	2	5.4136	0.3986
VREFVGQLVAPLPLGTGALR	2094.5	2	3.4861	0.3573
VREHPLLGPYVEDLSK	1853.1	3	4.335	0.389
VREHSVLGPYVDGLSK	1757.0	2	4.1895	0.3821
VREIQEKLDAFIEALHQEK	2297.6	3	5.363	0.436
VREKLKISKINKGEK	1771.1	2	2.5344	0.1071
VRELELVYAR	1248.5	2	2.7035	0.1938
VRELFVQSEIFPLETPAFAIKEQGFR	3053.5	3	5.7262	0.484
VREMEEEAEKLKELQNEVEK	2461.7	3	5.544	0.237
VREQLEQELEELTASLFEEAHK	2629.9	3	3.7532	0.1013
VREVFGSGTACQVCPVHR	1946.2	2	3.2507	0.1937
VREWYGYHFPELVK	1824.1	2	3.1059	0.2075
VRFPSHFSSDLK	1420.6	2	2.8424	0.2611
VRFPSHFSSDLKDLLR	1918.2	3	4.7454	0.3153
VRGAVASVTFDDFHK	1649.8	2	3.4684	0.219
VRGAVASVTFDDFHKNSAR	2078.3	3	4.4714	0.2547
VRGEPLQVER	1183.3	2	2.8338	0.2533

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VRGPDAAPFLLGLLTNELPLPSPAAAGAPPAAR	3222.7	3	6.2436	0.4603
VRIDEYDYSKPIQGQQK	2068.3	2	4.6573	0.3628
VRIDQYQGADAVGLEEK	1892.1	3	4.681	0.32
VRIPAEVLILNSIVLPHK	2012.5	3	5.2109	0.3098
VRIPAEVLILNSIVLPHKELSR	2498.0	3	6.6473	0.3089
VRKDDLVLLKR	1355.7	2	2.9187	0.1391
VRKLELDILPLQEANAELSEK	2409.8	3	3.9879	0.1415
VRLAEAEETAR	1245.4	2	3.3605	0.2813
VRLLADPTGAFGKETDLLLDDSLVSIFGNR	3234.6	3	5.9652	0.5031
VRLLADPTGAFGKETDLLLDDSLVSIFGNRR	3390.8	3	3.4732	0.1008
VRLLSGDTYEAVVTAVDPVADIATLR	2746.1	3	3.8526	0.1417
VRNHYNEEMSNLR	1662.8	2	4.4152	0.2681
VRNNYDEEIISLK	1593.8	2	4.0101	0.211
VRPSEEMLELEKER	1746.0	3	3.7969	0.2108
VRPSSDLNNSTGQSPHHK	1962.1	3	4.1235	0.2724
VRQEESEQIK	1246.4	2	3.6902	0.1578
VRQEESEQIKTLNNK	1817.0	2	4.3737	0.2884
VRQEESEQIKTLNNKFASFIDKVR	2881.2	3	6.0696	0.2784
VRQLVEQVEQIQKEQNYQR	2416.7	3	4.437	0.1501
VRSLETENAGLR	1345.5	2	3.6974	0.3182
VRTDITYPAGFMDVISIDKTGENFR	2847.2	3	3.8539	0.2838
VRTELADK	932.1	2	2.548	0.1261
VRTELADKVTK	1260.5	3	4.104	0.2637
VRTELADKVTKLQVELDNVTGLLSQSDSK	3188.6	3	6.5858	0.6017
VRVDLPDKYPFK	1477.7	2	3.1592	0.1719
VRVEALQSGGGQER	1486.6	2	3.7088	0.311
VRVEGDNDKKNPR	1527.7	2	4.4239	0.3402
VRVELSNGEK	1131.3	2	3.2529	0.2163
VRVELSNGEKR	1287.5	3	3.4301	0.1065
VRVELSTGMPR	1245.5	2	2.8195	0.1722
VRVPTTGIIEYPFDLENIIFR	2493.9	2	5.5135	0.3334
VRVPTTGIIEYPFDLQSVIFR	2451.8	3	5.5492	0.3695
VRVSGQGLHEGHTFEPAEFIIDTR	2697.0	3	4.3881	0.2918
VRYSLDPENPTK	1419.6	2	3.6563	0.2745
VSADEDLKLSDLLK	1546.7	2	3.3095	0.2079
VSADNTVGR	919.0	2	2.774	0.1281

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VSAEKVNKTHSVNGITEEADPTIYSGK	2876.1	3	3.8515	0.2496
VSAFIDWIEETIASH	1718.9	2	4.3736	0.4171
VSAGEAVVNRVFDKLSPLHER	2324.6	3	5.5858	0.4332
VSAKNALESYAFNMK	1673.9	2	3.7056	0.3853
VSALDLAVLDQVEAR	1599.8	2	4.9107	0.4142
VSALGLSKDVYNSEYYHFR	2249.5	3	4.3191	0.3491
VSANKGEIGDATPFNDAVNVQK	2275.5	3	4.9878	0.3274
VSDATGQMNLTK	1265.4	2	3.9841	0.3608
VSDEAVKKDSELDKHLESR	2186.4	3	3.9101	0.3114
VSDIQELELDLIDKVEIDKTVLVTVR	2984.4	3	3.2865	0.1366
VSDIQWFR	1051.2	2	3.0729	0.1592
VSDKEKIDQLQEELLHTQLK	2395.7	3	5.2779	0.3249
VSDKVMIPQDEYPEINFVGLLIGPR	2831.3	3	4.6333	0.2884
VSDSISAQYPVVDHEFDAVVVGAGGAGLR	2917.2	3	4.5393	0.3427
VSDTVVEPYNATLSIHQLVENTDETYCIDNEALYDICFR	4495.9	3	4.5048	0.365
VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR	4481.9	3	5.8231	0.3843
VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFRTLK	4824.3	3	4.0251	0.2439
VSEADIQR	918.0	2	2.9203	0.1715
VSEADSSNADWVTK	1509.6	2	4.4222	0.338
VSEAIEKLVALLNTLDRWIDETPPVDQPSR	3406.8	3	3.7019	0.1368
VSEEAESQQQWDTSKGEQVSQNGLPAEQGSPR	3488.6	3	5.4274	0.342
VSEEIQKEIQDLEKTLDVFNIILAR	2945.4	3	6.1937	0.4475
VSEGGPAEIAGLQIGDK	1641.8	2	4.4637	0.4023
VSEGSPGMVSVGPLPK	1541.8	2	4.0961	0.4111
VSEKEKESIAR	1276.4	2	2.9121	0.2172
VSEKVSHVLAALQAGNR	1780.0	2	3.3812	0.2131
VSELFDKTR	1095.2	2	2.4996	0.1314
VSELHLEVK	1054.2	2	3.1212	0.2363
VSELKEELK	1075.2	2	3.4235	0.1694
VSELKEELKK	1203.4	2	2.8059	0.1748
VSEMQKLDAQVKELVLK	1959.3	3	4.3948	0.3086
VSENDFEDLLSNQGFSSR	2045.1	2	4.5631	0.4731
VSEQGLIEILK	1229.4	2	3.2676	0.1694
VSEQGLIEILKK	1357.6	2	3.4634	0.1761
VSEQVKNVK	1031.2	2	3.1928	0.138
VSEVKPSYR	1065.2	2	2.8725	0.1416

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VSEVKPTYR	1079.2	2	2.5165	0.1153
VSEYVPEIVNFVQK	1651.9	2	3.3483	0.2325
VSFELFADKVPK	1380.6	2	3.8612	0.3972
VSFELFADKVPKTAENFR	2099.4	2	4.953	0.4638
VSFQLQSR	965.1	2	2.5045	0.1786
VSFSYAGLSGDDPDLGPAHVVTVIAR	2644.9	3	4.2079	0.196
VSFTGSVPTGMK	1211.4	2	3.4939	0.3467
VSGAAPPRPGSSFAHFGFDEQLMHQIR	2941.3	3	6.0762	0.4047
VSGAQEMVSSAK	1194.3	2	3.2045	0.3545
VSGAQEMVSSAKDTVATQLSEAVDATR	2753.0	3	5.1906	0.2583
VSGELFAQAPVEQYPGIAVETVTDSSR	2852.1	3	3.6482	0.1209
VSGGLEVLAEK	1102.3	1	3.7189	0.2841
VSGGTPIKIEDPNQFVPLNTNPNEVLEKR	3207.6	3	4.7419	0.4138
VSGHVITDIVEGK	1354.5	2	2.9693	0.2525
VSGHVITDIVEGKK	1482.7	2	3.5906	0.4341
VSGLAGSIYR	1023.2	2	2.4553	0.1184
VSGQGLHEGHTFEPAEFIIDTR	2441.6	2	4.7987	0.4851
VSGSELVQK	947.1	2	3.1261	0.2117
VSGSELVQKFIGEGAR	1677.9	2	3.697	0.3774
VSGSFPEDSSKER	1425.5	2	3.1427	0.2824
VSGYLNLAADLAHNFTDGLAIGASFR	2695.0	3	4.5353	0.4606
VSHITFAHEVGHNFGSPHDSGTECTPGESK	3166.3	3	6.1304	0.4785
VSHKPSGLVMAR	1282.5	3	3.4693	0.2953
VSHLLGINVTDFTR	1572.8	2	4.7468	0.4548
VSHQAGDHWLIR	1419.6	2	3.394	0.3656
VSHQVAYGLHELLK	1594.8	2	3.6842	0.3068
VSHVLAALQAGNR	1336.5	2	4.3579	0.429
VSHVSTGGGASLELLEGK	1741.9	2	5.9911	0.555
VSHYIINSSGPRPPVPPSPAQPPPGVSPSR	3076.5	3	6.4112	0.4113
VSIHSLGHMTPVLSPQNLLSCDTHQQQGCR	3288.7	3	4.8548	0.2346
VSIKESSVAK	1048.2	2	2.4755	0.1751
VSILESLDKWER	1475.7	2	3.2969	0.3056
VSISEGDDKIEYR	1511.6	2	3.7223	0.4388
VSITEAMHR	1044.2	2	2.685	0.1072
VSKELVEKSEAVR	1474.7	2	2.8331	0.1981
VSKELVEKSEAVRQDEQQR	2259.5	3	3.6095	0.1562

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VSKELVEKSEAVRQDEQQRK	2387.6	3	3.327	0.1254
VSKNSETFPTILEEAKELVGR	2348.6	3	4.0499	0.2252
VSKPTLKEVVIVSATR	1728.1	3	4.8458	0.3084
VSKQEEASGGPTAPK	1486.6	2	3.6517	0.1987
VSKTGAEGAVLDEAKNINK	1945.2	3	4.271	0.3161
VSLANLKPNPGSK	1325.5	2	2.6072	0.1025
VSLAPQANLTELDIYSR	1891.1	2	3.7833	0.4056
VSLDPELEEALTSASDTELCDLAAILGMHNLITNTK	3830.3	3	4.0024	0.1858
VSLDVNHFAPDELTVK	1785.0	2	5.113	0.4582
VSLDVNHFAPDELTVKTK	2014.3	3	5.4663	0.4716
VSLEPHQGPGTPESK	1563.7	2	4.1148	0.2085
VSLERLDLDLTADSQPPVFK	2244.5	2	4.5744	0.4496
VSLFHTPHLR	1207.4	2	2.8159	0.2408
VSLFSHLPQYSR	1434.6	2	3.0594	0.3147
VSLLQGDLSEKEASLLDLKEHASSLASSGLK	3227.6	3	6.128	0.447
VSLRDSSLEADHVISAIPASVLSELLPAEAAPLAR	3600.1	3	6.2386	0.3877
VSMLAVEEYEEMQVNLELEKDLR	2769.1	3	3.395	0.1399
VSNEEVTEELLHVNDDLNNVFLR	2699.9	3	5.995	0.4538
VSNEEVTEELLHVNDDLNNVFLRYER	3148.4	3	4.1401	0.2912
VSNGAGTMSVSLVADENPFAQGALK	2464.7	2	6.2546	0.4558
VSNLEELPLNEYREYIK	2110.4	2	2.7232	0.1655
VSNLQYLHSYLTYIK	1843.1	2	4.4206	0.3839
VSNSGITRVEK	1190.3	2	3.1754	0.1576
VSNTLESR	906.0	2	2.9871	0.2148
VSNTLESRLDLIAQQMMPEVR	2431.8	2	4.0283	0.2492
VSNVDHNKR	1069.2	2	2.9046	0.251
VSPDMAIFITMNPGYAGR	1941.3	2	4.7263	0.3503
VSPESNEDISTTVVYR	1796.9	2	4.5338	0.5153
VSPETVDSVIMGNVLQSSSDAIYLAR	2753.1	3	5.3211	0.5304
VSPNELILGWYATGHDITEHSVLIHEYYSR	3501.8	3	5.069	0.4097
VSPSTSYTPSR	1182.3	2	2.7915	0.2335
VSPTGEKVTHTGQVYDDKDYR	2396.6	3	3.5769	0.2726
VSQAAADLLAYCEAHVREDPLIIPVPASENPFR	3594.1	3	5.8861	0.4992
VSQELKEPLHK	1308.5	2	2.4941	0.1345
VSQGKEPVHLLSLFK	1683.0	3	4.0875	0.3497
VSQGQLVVMQPEK	1443.7	2	4.053	0.2342

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VSQGQLVVMQPEKFQSK	1934.2	3	3.2982	0.165
VSQGSKDPAEGDGAQPEETPR	2156.2	2	6.2879	0.431
VSQGSKDPAEGDGAQPEETPRDGDKPEETQGK	3341.4	3	5.6086	0.3548
VSQGVEDGPDTK	1232.3	2	2.8044	0.3027
VSQGVEDGPDTKR	1388.5	2	2.9586	0.3202
VSQMAQYFEPLTLAAVGAASK	2183.5	2	5.6295	0.5415
VSQPIEGHAASFAQFK	1717.9	2	4.2543	0.4396
VSQQTEKTTTVK	1350.5	2	2.9369	0.2838
VSQSPSKDSEENPATEERPEK	2345.4	3	4.2347	0.2474
VSRDTLYEAVR	1309.5	2	3.0983	0.2416
VSRDTLYEAVREVLHGNQR	2243.5	3	3.5315	0.1264
VSREDFEWVYTDQPHADR	2251.4	3	3.7271	0.1895
VSRLEEELANLKDESKK	1989.2	2	2.8463	0.1703
VSRLETELDEEKNTVELLTDR	2490.7	3	5.3827	0.3485
VSSAEGAAKEEPK	1303.4	2	3.5403	0.302
VSSAEGAAKEEPKR	1459.6	2	3.3539	0.294
VSSAVKAELR	1060.2	2	3.2854	0.1716
VSSDEDLKLTELLR	1618.8	2	4.9563	0.3656
VSSDNVADLHEK	1314.4	2	2.7829	0.2407
VSSDNVADLHEKYSGSTP	1907.0	2	4.6552	0.4068
VSSDVIDQK	991.1	2	2.8127	0.1432
VSSDVIDQKVYEIQDIYENSWTK	2761.0	3	4.7854	0.3058
VSSFEEKMISDAIPELK	1924.2	3	4.5546	0.2983
VSSGVYEPVVIESH	1502.7	2	3.4096	0.3387
VSSGYVPPPVATPFSSK	1720.9	2	2.9272	0.1568
VSSHANAAQER	1170.2	2	3.3608	0.3611
VSSIDLEIDSLSSLLDDMTK	2182.4	2	2.62	0.3237
VSSPDYPER	1050.1	2	2.7077	0.2164
VSSQSFSEIER	1269.3	2	3.0846	0.1822
VSSSIQHPETPLHISGFHLPYKPKPPQETEK	3510.9	3	4.5645	0.2209
VSSTEGAAKEEPK	1333.4	2	3.103	0.1259
VSTEVDAR	876.9	1	2.1338	0.185
VSTHVIENIYLPAAQTMNSGTFNTTVDIK	3166.6	3	3.5756	0.2735
VSTISLPTAPPATGTK	1541.8	2	3.5873	0.3563
VSTLPAITLK	1043.3	1	1.6275	0.138
VSTLQDLLFHSDCVTLHCGLNEHNHHLINDFTVK	3902.4	3	4.8494	0.3191

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VSTTLNVAQAYYAR	1557.7	2	3.9605	0.4123
VSVADHSLHLSK	1293.5	2	3.8954	0.3917
VSVAHFGSR	960.1	2	2.8732	0.3552
VSVELTNSLFK	1237.4	2	3.1452	0.1312
VSVHVIEGDHR	1248.4	2	2.7351	0.2524
VSVLESMIDDLQWDIDKIR	2276.6	2	2.7626	0.1145
VSVPLIAQGNSYPSETTVK	1991.2	2	4.5179	0.4802
VSVSPVVHVR	1079.3	2	2.9849	0.3039
VSVVANTPSGPVEAFDFDEYQPEMLEK	3000.3	2	4.2672	0.4403
VSVVEPGNFIAATSLYSPESIQAIAK	2693.0	3	4.9654	0.3201
VSWQDLKDFMR	1425.6	2	2.5629	0.3139
VSYALLFGDYLPQNIQAAR	2140.4	2	4.6494	0.2247
VSYARPSSEVIKDANLYISGLPR	2536.9	3	4.8051	0.3832
VSYASLADVDKAVAAAK	1679.9	2	2.5912	0.188
VSYASLADVDKAVAAAKDAFENGEWGR	2842.1	3	4.5763	0.3506
VSYFPTVPGVYIVSTK	1758.1	2	3.7131	0.3371
VTADVINAAEKLQVVGR	1784.1	2	4.0244	0.3768
VTAEDKGTGNK	1120.2	2	3.4537	0.2525
VTAEDKGTGNKNK	1362.5	2	2.6058	0.1869
VTAEDKGTGNKNKITITNDQNR	2418.6	3	4.1636	0.244
VTAEVVLAHLGGGSTSR	1654.8	2	4.9694	0.5331
VTAIHIDPATHR	1331.5	2	3.3549	0.4
VTANNDKNR	1032.1	2	3.0054	0.2457
VTAPDVDLHLKAPK	1504.8	2	3.611	0.2914
VTAPQPAATNGDLASR	1569.7	2	3.5703	0.3865
VTAQGPGLEPSGNIANK	1653.8	2	4.6535	0.5019
VTASDPLDTLGSEGALSPGGVASLLR	2484.7	2	3.5518	0.2511
VTASDPLDTLGSEGALSPGGVASLLRLPR	2851.2	3	3.6104	0.2704
VTASGFPVILSAPWYLDLISYGQDWR	2956.3	3	4.8957	0.4571
VTASGFPVILSAPWYLDLISYGQDWRK	3084.5	3	3.8272	0.3019
VTASGPGLSSYGVPASLPVDFAIDAR	2548.8	2	5.5321	0.5143
VTDADAPNTPAWEAVYTILNDDGGQFVVTTNPVNNDGILK	4247.6	3	4.166	0.2761
VTDALNATR	961.1	2	3.7696	0.3306
VTDETSGCSLTCAQFHPDGLIFGTGTMDSQIK	3361.7	3	5.2463	0.4191
VTDFGDKVEDPTFLNQLQSGVNR	2580.8	3	5.5536	0.4212
VTDHLEALIDPFDLDVFTPHLNSNLHR	3130.5	3	6.948	0.4331

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VTDKLTPIHDR	1295.5	2	3.997	0.323
VTDPVGDIVSFMHSFEEK	2038.3	2	4.8872	0.5162
VTDPVGDIVSFMHSFEEKYGR	2414.7	3	3.6214	0.2488
VTDRNITLSLVANPSHLEAADPVVMGK	2849.3	3	5.639	0.4568
VTDTDFDGVEVR	1353.4	2	3.4763	0.2747
VTEDTSSVLR	1107.2	2	3.0061	0.1976
VTEEDFYKLVSEFTITK	2050.3	2	4.6943	0.4268
VTEEGTELSQR	1249.3	2	2.6974	0.1523
VTEFGGELHEDGGKLFCTSCNVVLNHVR	3062.4	3	5.3756	0.3033
VTEGLTDVILYHQPDDKKK	2200.5	2	3.8681	0.3374
VTEHGTPKPFR	1269.4	2	2.5183	0.3571
VTELALTASDR	1176.3	2	2.867	0.3344
VTELEQEKQVMQDELDRKEEQVLR	2974.3	3	4.6253	0.2893
VTENIPQIISFIEGIIAR	2014.4	3	3.7729	0.2704
VTEQLIEAINNGDFEAYTK	2156.3	2	4.5107	0.3837
VTETQKNER	1105.2	2	2.704	0.1626
VTFHNKGAYPLSIEPIGVR	2099.4	2	5.0679	0.4232
VTFSEDDEIINPEDVDPSVGR	2334.4	2	2.5948	0.1154
VTFVNFTVTR	1184.4	2	3.5426	0.3494
VTGADVPMPYAK	1249.5	2	3.785	0.2988
VTGDSQPKEQGQGDLK	1687.8	2	3.5085	0.1806
VTGEADVEFATHEDAVAAMAK	2163.4	3	3.6661	0.4242
VTGEADVEFATHEEAVAAMSK	2193.4	2	3.2493	0.1363
VTGEVLDILTR	1216.4	2	2.6857	0.2115
VTGEVLDILTRLPESVER	2027.3	3	4.6492	0.3082
VTGSLETKYR	1154.3	2	2.7887	0.3061
VTGTLETK	849.0	2	2.6512	0.1187
VTHALVNIR	1023.2	2	2.479	0.1516
VTHAVVTVPAYFNDAQR	1889.1	2	5.4264	0.417
VTHELQAMKDK	1300.5	2	3.3236	0.2238
VTHETSAHEGQTEAPSIDEK	2167.2	3	5.7103	0.564
VTHLFDVHSLEQQSEITPK	2209.4	3	5.1223	0.4178
VTHTGQVYDDKDYRR	1854.0	2	3.5989	0.2903
VTIAQGGVLPNIQAVLLPK	1932.3	3	5.9143	0.4303
VTIAQGYDALSSMANIAGYK	2074.3	2	5.3262	0.4839
VTIEYYSQLK	1244.4	2	3.2307	0.1538

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VTILGHVQR	1023.2	2	2.8919	0.1674
VTIMPKDIQLAR	1385.7	2	3.5955	0.2878
VTIPTDLIASSGDIIK	1643.9	2	3.2911	0.3316
VTKDGVTVAK	1018.2	2	3.5779	0.2766
VTKEQWDTIEELIR	1761.0	2	3.7928	0.2403
VTKEQWDTIEELIRK	1889.1	3	4.602	0.284
VTKLDRDPASGTALQEISFWLNLER	2861.2	3	5.655	0.3827
VTLAVSDLQK	1074.3	2	3.2434	0.2786
VTLDPVQLESSLLR	1570.8	2	2.6888	0.116
VTLDWAKPK	1058.3	2	2.6456	0.1801
VTLELGGK	817.0	1	1.9531	0.1424
VTLEYRPVIDK	1333.6	2	3.2461	0.1141
VTLLEGDHVR	1139.3	2	3.3705	0.2679
VTLLHHVLEEAEK	1518.7	2	3.6207	0.2207
VTLLHHVLEEAEKSHPDLLQLPR	2676.1	3	3.7188	0.3032
VTLLLFKDVK	1176.5	2	2.6017	0.1492
VTLSEGPHHVALFK	1535.8	2	3.9782	0.3513
VTLTLPVLNAAR	1268.5	2	3.0449	0.2951
VTLTSEEEAR	1135.2	2	3.4703	0.3453
VTLTSEEEARLK	1376.5	2	2.9849	0.1784
VTLTSEEEARLKK	1504.7	2	3.0554	0.1843
VTMDQLSTVHHEMGHIQYYLQYK	2823.2	3	3.5712	0.2031
VTMLFLGLHNVR	1400.7	2	3.1839	0.3698
VTMWVFEEDIGGK	1511.7	2	3.5024	0.2318
VTNDARENEMDENLEQVSGIIGNLR	2818.0	3	3.7507	0.2254
VTNGAFTGEISPGMIK	1622.9	2	5.1557	0.4159
VTNLHLMLQLVR	1437.8	2	4.0782	0.3597
VTNLSEDTR	1035.1	2	2.5874	0.1789
VTNSTELQHQLDKTK	1742.9	2	3.4557	0.3001
VTNVDEEKQR	1218.3	2	3.0756	0.1795
VTNVEWLLDALYGK	1621.9	2	2.5679	0.1556
VTPHGLEKVPGIFISR	1751.1	2	2.488	0.1058
VTPQSLFILFGVYGDVQR	2040.4	3	4.8978	0.4901
VTPTRTEIIILATR	1584.9	2	3.7278	0.2174
VTPVDYLLGVADLTGELMR	2063.4	2	5.2356	0.5253
VTQDELKEVFEDAAEIR	1993.2	3	5.014	0.4118

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VTQEEIKKEPEKPIDR	1940.2	3	4.3278	0.2886
VTQEEIKKEPEKPIDREK	2197.5	3	3.8651	0.2063
VTQLASYFEPLILAAVGVASK	2178.6	3	3.9406	0.3244
VTQLDLDGPKELSRR	1727.9	2	2.4972	0.1253
VTQLYMQLLHEIIR	1758.1	2	3.1757	0.2545
VTQSNFAVGYK	1214.4	2	2.7947	0.2199
VTQSNFAVGYKTDEFQLHTNVNDGTEFGGSIYQK	3797.1	3	5.3884	0.3372
VTQVDGHSSK	1058.1	2	3.1336	0.2736
VTQVDGNSPVR	1172.3	2	3.6858	0.2453
VTRVEFEELCADLFER	1957.2	3	4.2619	0.3401
VTSAHKGPDETLR	1411.5	2	3.5829	0.2971
VTSAHLFEVELQAAR	1671.9	2	2.7323	0.3136
VTSAVEALLSADSASR	1577.7	2	4.9084	0.4547
VTSEELHYFVQNHFTSAR	2166.3	2	5.2743	0.4625
VTSEGAGLQLQK	1231.4	2	4.0435	0.3455
VTSIADRLNVDFALIHKER	2198.5	3	3.3415	0.1745
VTSIQDWVQK	1204.4	2	3.4483	0.2748
VTSSEPPNPASSSK	1388.5	2	2.8891	0.1264
VTSVGNPTIKPHSVPSHTLPSHPVTPSSK	2990.4	3	4.9517	0.365
VTTAAAAAATSQDPEQHLTELREPAPGTNQR	3233.5	3	5.2314	0.355
VTTEIQLPSQSPVEEQSPASLSSLR	2684.9	3	4.3257	0.413
VTTEQYQKAAEEVEAK	1825.0	2	4.4277	0.4218
VTTHPLAK	867.0	1	2.0466	0.1006
VTTHPLAKDK	1110.3	2	2.7914	0.3572
VTTMDAELEFAIQPNTTGKQLFDQVVK	3025.4	3	3.513	0.2116
VTTQIDKEKK	1190.4	2	2.9385	0.1802
VTTVASHTSDSDVPSGVTEVVVK	2315.5	2	6.3538	0.5024
VTTVASHTSDSDVPSGVTEVVVKLFDSDPITVTVPVEVSR	4171.6	3	7.3899	0.5355
VTTVTEIGKDVIGLR	1601.9	2	3.4768	0.287
VTVAGGVHISGLHTESAPR	1889.1	3	3.8563	0.2774
VTVAGLAGKDPVQCSR	1601.9	2	4.5714	0.39
VTVIKAPHYPGIGPVDESGIPTAIR	2589.0	3	5.5395	0.5114
VTVKHLEEIVEK	1424.7	2	2.7879	0.284
VTVLFAGQHIAK	1284.5	2	4.1798	0.2292
VTVLFAGQHISK	1300.5	3	3.9383	0.3666
VTVLGHVQR	1009.2	2	2.8956	0.3283

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VTVLGVATAPQQVLSNGVPVSNFTYSPDTK	3091.5	3	3.5413	0.2221
VTVRFPPEASGYLHIGHAK	2080.4	3	4.6638	0.3562
VTVTEGGVKQEYR	1466.6	2	2.8432	0.2081
VTVVDVNESR	1118.2	2	3.6734	0.3131
VTYHPDGPEGQAYDVDFTPPFRR	2665.9	3	3.8448	0.2911
VTYKAPVPTGEVYFADSFDR	2263.5	2	4.9286	0.4386
VTYKAPVPTGEVYFADSFDRGTLSGWILSK	3306.7	3	3.9482	0.1462
VTYLVHNFEEGGGVAMGMYNQDK	2560.8	2	4.4865	0.4692
VTYPAK	678.8	1	1.9097	0.1049
VTYRPLDPDNYDKDLSFIK	2300.6	3	3.9658	0.2304
VTYTPMAPGSYLISIK	1742.1	2	2.6333	0.262
VTYYLDWIHHYVPK	1835.1	2	3.9075	0.3396
VVAEGFDSANGINISPDDKYIYVADILAHEIHVLEK	3957.4	3	5.7763	0.4281
VVAEKQEKR	1087.3	2	2.5981	0.1274
VVAEPVELAQEFR	1487.7	3	4.9854	0.4588
VVAGVANALAHKYH	1450.7	2	3.2738	0.3519
VVALDKNFHMK	1302.6	2	3.1004	0.1985
VVASGPGLEHGK	1151.3	2	3.4048	0.3486
VVATTQMQAADAR	1362.5	2	4.4664	0.4779
VVDAILGLAHHGNGQLR	1771.0	2	3.9576	0.3232
VVDALGNAIDGK	1172.3	2	4.2555	0.4207
VVDALGNAIDGKGPIGSK	1711.9	2	4.8533	0.5014
VVDFIDEGVNIGLEVK	1747.0	2	3.425	0.2557
VVDHYENPR	1129.2	2	3.2047	0.3563
VVDLLAPYAK	1089.3	2	3.1039	0.2795
VVDLLVIK	899.2	2	3.3896	0.2083
VVDLMAHMASK	1202.5	2	3.7633	0.406
VVDLMAHMASKE	1331.6	2	4.338	0.4263
VVDNPIYLSDMGAALTGAESHELQDVLEETNIPK	3671.0	3	5.349	0.4235
VVDNPIYLSDMGAALTGAESHELQDVLEETNIPKR	3827.2	3	4.4017	0.3231
VVDNPIYLSDMGAALTGAESHELQDVLEETNIPKRLYK	4231.7	3	4.7382	0.3614
VVDNTTAKEFADSLGIPFLETSAK	2554.8	2	5.5328	0.4802
VVDPFSKK	920.1	2	2.4795	0.1418
VVDPFSKKDWYDVKAPAMFNIR	2628.0	3	4.8748	0.311
VVDPIVSNFLQSFETAIEHNKEVEPLLGR	3282.7	3	3.5882	0.3645
VVDQQQVER	1101.2	2	2.4318	0.2655

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VVDRDSEEAEIIR	1531.7	2	3.2901	0.148
VVDSLYNK	938.1	2	3.0515	0.1479
VVDTTKESSR	1122.2	2	2.8828	0.2238
VVDVLDSIK	988.2	2	3.076	0.1451
VVDVLDSIKTK	1217.4	2	2.9433	0.3308
VVDYTTAKEFADSLGIPFLETSAK	2603.9	2	5.6548	0.4948
VVEIAPAAHLDPQLR	1629.9	2	4.166	0.3981
VVEKADSWVEKEEPAPSN	2015.2	2	4.0451	0.356
VVEKDNDVLLHWAPVEEAGDSTQILFSK	3141.5	3	4.6491	0.3362
VVEKEAETER	1190.3	2	3.0587	0.26
VVELLKDGSGR	1173.3	2	2.8387	0.2449
VVELPKTEEGLGFNIMGGKEQNSPIYISR	3207.6	3	4.7876	0.3963
VVESLDVGQDR	1217.3	2	3.8505	0.35
VVEVGSK	717.8	1	1.7225	0.1246
VVEVLAGHGHLYSR	1537.7	2	4.39	0.5041
VVFEQTK	851.0	2	2.7462	0.1595
VVFEQTKVIADNVKDWSK	2107.4	3	4.9007	0.4076
VVFGPELVSLGPEEQFTVLSLSAGRPK	2858.3	2	3.892	0.4048
VVFQEFR	925.1	2	2.4413	0.1555
VVFVFGPDKK	1136.4	2	2.4407	0.1135
VVGAMQLYSVDRK	1466.7	2	3.2989	0.3661
VVGAVGSDEKVAYLQK	1663.9	2	4.5831	0.2904
VVGAVIDQGLITR	1341.6	2	3.4977	0.235
VVGDVAYDEAKER	1451.6	2	3.4189	0.5014
VVGEHVEVHAR	1232.4	2	3.1209	0.229
VVGFHVLGPNAGEVTQGFAAALK	2283.6	2	5.2827	0.4846
VVGKEQGQNLAR	1299.5	2	3.4678	0.2229
VVGNPFDSKTEQGPQVDETQFK	2451.6	3	4.1672	0.1741
VVGPQQLHSETNER	1594.7	2	3.0199	0.3983
VVGRPQPQLQYVDALGYVSLFPLLLR	2943.5	3	3.6661	0.1811
VVGSEFVQKYLGEGPR	1766.0	2	3.6033	0.446
VVGSELIQKYLGDGPKLVR	2072.4	3	3.3275	0.3042
VVGVFTVPDKDGKADPLALAAEKDGTPVFKLPK	3425.0	3	4.3324	0.2031
VVGVKSEGEVAR	1230.4	2	3.1889	0.3437
VVGVLLGSWQK	1186.4	2	2.9083	0.2443
VVHASGDASYSAGDSGDAAAQPAFTGIK	2651.8	3	3.7603	0.2603

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VVHGEDAVPYSWPWQVSLQYEK	2618.9	3	3.7929	0.2266
VVHIMDFQR	1145.4	2	2.7556	0.3686
VVHLLNDQHLGVVTAATSLITTLAQK	2744.2	3	4.9327	0.4216
VVHLLNDQHLGVVTAATSLITTLAQKNPEEFK	3489.0	3	5.2657	0.478
VVHLSQEINHLQK	1545.8	3	3.8584	0.3401
VVHQDVAFTDPTLDSTEINVPQDILGIWVDPIDSTYQYIK	4548.0	3	3.4865	0.1581
VVHVNGYGK	973.1	1	2.423	0.2426
VVIGMDVAASEFFR	1541.8	2	3.465	0.4263
VVIHFTDGADGDLADLHR	1952.1	3	6.0721	0.408
VVIIGAGKPAAVVLQTK	1665.1	2	4.4313	0.4525
VVINVPIFKDKNTPSPFIETFTEDDEASR	3310.7	3	3.3917	0.2565
VVKEEEAIALAEK	1429.6	2	2.8993	0.1545
VVKELEDLQK	1201.4	2	3.4435	0.1181
VVKLENGEIETIAR	1571.8	2	4.0969	0.3794
VVKQASEGPLK	1156.4	1	3.2437	0.172
VVLAEVIQAFSAPENAVR	1914.2	2	4.2699	0.4936
VVLASASPR	900.1	2	2.9565	0.24
VVLAYEPVWAIGTGK	1603.9	3	4.9454	0.4859
VVLAYEPVWAIGTGKTATPQQAQEVHEK	3052.4	3	3.8131	0.3455
VVLAYEPVWAIGTGKTATPQQAQEVHEKLR	3321.8	3	4.9241	0.4298
VVLAYEPVWAIGTGKTATPQQDQEVHDK	3082.4	3	3.2828	0.1292
VVLDDKDYFLFR	1530.7	2	3.8549	0.4433
VVLDDKDYFLFRDGDILGK	2229.5	2	4.2411	0.2639
VVLDDKDYFLFRDGDILGKYVD	2606.9	3	4.1165	0.3914
VVLEAPDETTLKELAETLQQK	2356.7	3	3.236	0.1089
VVLEHEEVR	1110.2	2	2.4005	0.1848
VVLELKADVVPK	1310.6	2	3.7549	0.2153
VVLFEMEAR	1094.3	2	2.9768	0.2664
VVLHDGDPNEPVSDYINANIIMPEFETK	3158.5	3	4.8603	0.3455
VVLIGDSGVGK	1044.2	1	3.0292	0.1742
VVLIGDSGVGKSNLLSR	1715.0	2	4.3323	0.5217
VVLLEDLASQVGLR	1512.8	2	4.0764	0.3373
VVLPIEAPIR	1107.4	2	2.494	0.2302
VVLQQDPQQAR	1282.4	2	3.6245	0.2951
VVLRGVGGSQPPDIDKTELVEPTEYLVVHLK	3389.9	3	5.3274	0.4853
VVLSESVQVEKGDTEQEIQR	2274.5	3	5.3812	0.4242

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VVLSSQDKDK	1119.3	2	2.5618	0.204
VVLTAGPAQFGLDLSK	1616.9	2	2.9274	0.2526
VVLTQANK	873.0	1	1.7784	0.1338
VVLTQANKLGV	1142.4	2	3.4353	0.3344
VVLVLAGR	827.1	2	2.4666	0.141
VVLVNNILQNAQER	1610.8	2	4.5634	0.4353
VVLVTGAGAGLGR	1170.4	2	4.4113	0.4541
VVLWGSDYSKLQEVEVPEDFGPVR	2750.1	3	4.3742	0.2501
VVNEINIEDLCLTK	1603.9	2	2.7525	0.3311
VVNFIKGSSLNSR	1421.6	2	2.7597	0.1274
VVNGAAASQPPSKR	1382.6	2	3.1189	0.1092
VVNGPEILNK	1083.3	2	2.8014	0.1774
VVNISSMLGRMANPARSPYCITKFGVE	2942.5	3	5.0295	0.2462
VVNLHPLKK	1048.3	2	2.6085	0.3063
VVNPTQK	785.9	1	1.6759	0.1084
VVNVSSIMSVR	1191.4	2	4.5133	0.369
VVPENLGLQEGTHELCYNTACALIGQGQLNQAMK	3645.1	3	5.4845	0.4568
VVPLADIITPNQFEAELLSGR	2283.6	2	4.6334	0.4251
VVPLVQMGETDANVAK	1671.9	2	3.0123	0.3281
VVPSDLYPLVLGFLR	1689.0	3	3.9371	0.3932
VVPTEKGQLLAEQLGFDFFEASAK	2626.0	3	4.5365	0.3375
VVPTTDHIDTEKLK	1596.8	2	3.4302	0.3321
VVQGKEPAHLMSLFGGK	1799.1	2	4.5689	0.4318
VVQGKEPAHLMSLFGGKPMIIYK	2545.1	3	5.5631	0.4481
VVQHSNVVINLIGR	1548.8	2	3.7662	0.4354
VVQHSNVVINLIGRDWETK	2208.5	3	3.9378	0.3479
VVQLDVR	829.0	2	2.675	0.1373
VVQVSAGDSHTAALTDDGR	1900.0	2	4.1251	0.354
VVQVVKPHTPLIR	1486.8	2	3.4284	0.3414
VVRPDSELGERPPEDNQSFQYDHEAFLGK	3361.6	3	3.9763	0.3042
VVRPDSELGERPPEDNQSFQYDHEAFLGKEDSK	3821.0	3	3.6546	0.2685
VVRVPADLGAEAGLQQLLGALR	2247.6	2	5.103	0.4491
VVSAAVQAQHSATK	1397.6	2	3.841	0.3652
VVSEDFLQDVSASTK	1625.8	2	5.0808	0.4769
VVSETNDTK	993.1	1	3.2001	0.3361
VVSETNDTKVLRH	1498.7	2	4.0728	0.3326

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VVSKEESIVSSLR	1433.6	2	3.2756	0.3441
VVSPVLILDLISGDDDLEAQEDVTLEHLPESVLQDVIR	4186.7	3	5.0618	0.3899
VVSQYHELVVQAR	1528.7	2	4.3584	0.3459
VVSQYSSLLSPMSVNAVMK	2041.4	2	5.6517	0.4324
VVSSIEQK	890.0	1	2.2454	0.112
VVSSIEQKTEGAEK	1505.7	2	4.0452	0.3033
VVSSIEQKTEGAEKK	1633.8	2	4.4963	0.2208
VVSSSIVDKYIGESAR	1710.9	2	4.3193	0.501
VVSYRVPHNAAVQVYDYR	2137.4	3	4.4733	0.4381
VVTDTDETELAR	1349.4	2	3.8713	0.4514
VVTEKSPTDWALFTYEGNSNDIR	2643.8	3	5.1946	0.3814
VVTNYNSAHDQNSNLLIEYFR	2498.7	3	4.5674	0.4108
VVTTNYKPVANHQYNIEYER	2439.7	3	3.331	0.2255
VVTYGMANLLTGPK	1464.8	2	3.7028	0.4055
VVVAENFDEIVNNENK	1834.0	2	5.3201	0.4455
VVVDALSGLK	1001.2	2	3.8066	0.3127
VVVDALSGLKGDLAGR	1570.8	2	4.12	0.4649
VVVHKETEITPEDGED	1797.9	2	3.2	0.2945
VVVHKETELAEEGED	1684.8	2	4.571	0.4747
VVVHPLVLLSVVDHFNR	1944.3	3	5.1931	0.4809
VVVKAPDEETLIALLAHAK	2018.4	3	5.9129	0.2859
VVVLGLLPR	966.2	2	3.9111	0.2173
VVVQVLAEEPEAVLK	1623.9	2	4.0454	0.3942
VVVSHSTHR	1022.1	2	2.4304	0.1227
VVVTMEHSAK	1101.3	2	2.5351	0.1297
VVVTVEQTEEELER	1660.8	2	3.3456	0.1934
VVVVGDQSAGK	1059.2	2	3.0273	0.3086
VVVVGDQSAGKTSVLEMIAQAR	2259.6	3	5.2742	0.324
VVVVTGANTGIGKETAK	1644.9	2	4.2492	0.452
VVYENAYGQFIGPHR	1750.9	2	3.5382	0.1803
VVYGGGAAEISCALAVSQEADKCPTLEQYAMR	3332.8	3	3.8093	0.3232
VVYIFGPPVKEPPTDVTPTFLTTGVLSTLR	3246.8	3	6.0793	0.4267
VWAHYEEQPVEEVMPVLEEK	2442.7	3	4.2934	0.1859
VWAHYEEQPVEEVMPVLEEKER	2728.0	3	5.5841	0.3713
VWDAVSGDELMTLAHK	1773.0	2	5.4242	0.3542
VWDDGIIDPADTR	1473.6	2	4.2209	0.3472

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VWDLFPEADKVR	1475.7	2	2.9901	0.2745
VWGAPRNSDPALGLDDDPDAPAAQLAR	2790.0	3	4.3707	0.1587
VWGVPIPVFHHK	1416.7	2	2.8934	0.2189
VWITNGGLANIFTVFAK	1852.2	2	4.3716	0.1562
VWLDPNETNEIANANSR	1944.1	2	5.6643	0.5315
VWQVTIGTR	1060.2	2	3.1335	0.1755
VWSRNEDITEPQSILAAAEK	2258.5	2	5.4629	0.3642
VWSRNEDITEPQSILAAAEKAGMSAEQAQGLLEK	3673.1	3	6.0121	0.5018
VWYVSNIDGTHIAK	1603.8	2	4.0983	0.4326
VWYVSNIDGTHIAKTLAQLNPESSLFIIASK	3417.9	3	4.4998	0.2346
VYAALGNHDFHPK	1469.6	2	3.4706	0.3179
VYADGIFDLFHSGHAR	1806.0	2	4.2699	0.5068
VYAEADSQESADHLAHEVSLAVFQLAGGIGERPQPG	3751.0	3	4.8627	0.3785
VYAEADSQESADHLAHEVSLAVFQLAGGIGERPQPGF	3898.2	3	4.8715	0.4223
VYAEDPYKSFGLPSIGR	1900.1	2	2.939	0.3126
VYAILTHGIFSGPAISR	1803.1	2	4.6928	0.4566
VYALPEDLVEVKPK	1600.9	2	2.4724	0.1354
VYANGQHLFDFAHR	1675.8	2	4.5047	0.5668
VYAPASTLVDQPYANEGTVVVTER	2580.8	3	5.8429	0.5041
VYEFLDKLDVVR	1496.7	2	3.5169	0.3883
VYEGERPLTK	1192.3	2	2.9512	0.3323
VYEGERPLTKDNHLLGTFDLTGIPPAPR	3108.5	3	5.3035	0.4345
VYENVGLMQQQK	1437.6	2	4.1752	0.3176
VYEVATFYTMYNR	1657.9	2	3.7275	0.4903
VYFKDTHPK	1135.3	2	2.8658	0.2681
VYFQSPPGAAGEGPGGADDEGPVR	2331.4	3	4.2018	0.3593
VYGDIIHTPAKDR	1485.7	2	2.7712	0.1542
VYGSFLVNPESGYNVSLLYDLENLPASKDSIVHQAGMLKR	4427.0	3	3.7581	0.2178
VYIASSSGSTAIK	1284.4	2	4.2274	0.3804
VYIASSSGSTAIKK	1412.6	2	2.7847	0.2674
VYIGEEEKKIFLEK	1726.0	2	2.6929	0.2447
VYINLDKETK	1223.4	2	2.8575	0.1523
VYINYYDMNAANVGWNNSTFA	2428.6	2	4.4665	0.4654
VYISLLPLGDGLTLAFK	1821.2	2	2.869	0.2961
VYISSPHSSPAHNK	1524.7	2	3.1638	0.235
VYKEMYK	961.2	1	2.1237	0.1214

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
VYKEMYKTDLEKDIISDTSGDFR	2755.1	3	5.1099	0.431
VYKEMYKTDLEKDIISDTSGDFRK	2883.2	3	6.1864	0.4354
VYLLYRPGHYDILYK	1914.2	2	3.4418	0.1918
VYMGHGGKPWVSDFSHPHYLAGR	2599.9	3	5.0664	0.4495
VYNIEFNPPK	1221.4	2	3.0854	0.2303
VYNIEFNPPKTVGIDDLTGEPLIQR	2830.2	3	3.5339	0.234
VYNIEFNPPKTVGIDDLTGEPLIQREDDKPETVIKR	4141.6	3	3.9503	0.2981
VYNVTQHAVGIVVNK	1641.9	2	5.2534	0.3868
VYNVTQHAVGIVVNKQVK	1997.3	3	5.1431	0.4926
VYNYNHLMPTR	1408.6	2	3.8968	0.3404
VYNYVDWIKDTIAANS	1873.1	1	3.666	0.3659
VYNYVK	785.9	1	1.8639	0.102
VYQNHVQHLISEK	1595.8	2	4.2338	0.3114
VYQWDDPDPR	1291.4	2	3.2683	0.384
VYSEVHFTLAKPPSVVNR	2044.3	3	4.3877	0.3575
VYSLFLDESR	1229.4	2	3.1024	0.311
VYSPHVLNLTLIDLPGITK	2094.5	3	4.9795	0.3377
VYSRGDSEPLSEAAQAHTR	2075.2	3	4.6013	0.4211
VYSTSVTGSR	1057.1	2	3.1072	0.3491
VYTDVQQVASSLTHPR	1802.0	3	3.3294	0.2568
VYVAESLISSAGEGLFSK	1858.1	2	2.6416	0.2427
VYVGNLGNNGNK	1249.4	2	3.4865	0.267
VYVGNLGNNGNKTELER	1878.0	2	4.3821	0.3817
VYVGNLGTGAGK	1136.3	2	3.3107	0.3027
VYVGNLGTGAGKGELER	1720.9	2	4.1494	0.4293
VYVPALIFGQLLTSSNYDDDEKKVTGGR	3087.4	3	3.3699	0.1231
VYVPTGFSAFPFELLHTPEK	2280.6	2	4.3654	0.3389
VYVYLQHPAGIEPTPTLTLTGHDEFGR	3013.4	3	5.1555	0.3459
VYYFNHITNASQWER	1929.1	2	4.3496	0.4053
VYYTAGYNSPVK	1362.5	2	2.873	0.3215
VYYVDHVEKR	1308.5	2	3.2745	0.3333
WAAPVETLENIIATVDTR	2000.2	2	3.4702	0.3059
WAAVVVPSGEEQR	1428.6	2	3.792	0.2728
WAEGGGHSR	957.0	2	2.6441	0.2073
WAELLPLLQQCQVVR	1797.2	2	4.2952	0.2587
WAEYHADIYDK	1411.5	2	3.6962	0.3445

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
WAEYHADIYDKVSGDMQK	2157.3	3	4.9058	0.547
WAHLDIAGVMTNKDEVPYLR	2329.7	2	5.1958	0.4626
WAIAQLNYADMLK	1537.8	2	4.3487	0.2512
WAIAQLNYADMLKR	1694.0	3	3.706	0.2354
WALQAYQGQLLQEGATRLLR	2316.6	3	5.5758	0.1196
WALSQSNPSALR	1330.5	2	4.054	0.3468
WALSQSNPSALRETVVEVPQVTWEDIGGLEDVKR	3811.2	3	7.5224	0.5097
WARPPISMNFEVPFAPSGLK	2245.6	3	4.6431	0.3236
WATHGEPSPVNSHPQR	1800.9	2	5.3896	0.3758
WDAWNALGSLPK	1358.5	2	4.119	0.2555
WDDPYYDIAR	1314.4	2	2.9325	0.1749
WDKNSLTLEAVKR	1560.8	2	4.9386	0.3523
WDNNYGDGVSPMSWIGSVDILR	2482.7	2	4.5566	0.4875
WDPDKAGDKPHMQTYEVDLNK	2488.7	3	4.8782	0.3359
WDQSTFIGR	1110.2	2	2.7579	0.3205
WDQSTFLGR	1110.2	2	2.4726	0.2899
WDQTADQTPGATPK	1516.6	2	4.7683	0.4347
WDTGENPIYK	1223.3	2	2.615	0.2358
WDYEKNEWKK	1426.6	2	2.9943	0.2213
WDYPEGTPNGGSTTLPSAPPPASAGLK	2669.9	3	4.6201	0.2857
WEAAEGLLQEALDKDSGYPETLVNLIVLSQHLGKPPEVTNR	4533.1	3	5.1793	0.4524
WEFKHPQPFLR	1485.7	2	3.0709	0.3433
WENPLMGWASTADPLSNMVLTFSTK	2798.2	2	3.4886	0.3813
WEQGQADYMGADSFDNIKR	2232.4	2	4.7121	0.3685
WESERVLSFIPPDGNFRLISYRVSSQNLVAIPVYVK	4181.8	3	3.237	0.1309
WEVADLQPQLKIDK	1683.9	2	4.0333	0.3105
WFHPNITGVEAENLLLTR	2111.4	2	3.7839	0.3828
WFNGQPIHAELSPVTDFR	2115.3	2	3.4837	0.2273
WFQQKYDGIILPGK	1694.0	2	3.7274	0.361
WFVLKPNIISYYVSEDLKDK	2458.8	3	4.3611	0.3722
WFVLKPNIISYYVSEDLKDKK	2587.0	3	3.3911	0.2189
WGASTATTQK	1051.1	2	2.5528	0.2502
WGDAGAEYVVESTGVFTTMEK	2278.5	2	6.5843	0.4621
WGDEHIPGSPYR	1414.5	2	3.2355	0.134
WGDIEFPPPFGR	1418.6	2	2.8116	0.1115
WGDSVLLVDLTHEEMPQSIVEATSR	2814.1	3	3.6286	0.1061

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
WGFGLEELYGLALR	1624.9	2	2.8774	0.1775
WGFTKFNADEFEDMVAEK	2165.4	2	2.7412	0.1877
WGFTKFNADEFEDMVAEKR	2321.6	3	4.1156	0.245
WGLQDIDTIIDHASVGIMTLSPFDQMK	3033.5	3	3.6687	0.3451
WGPNHAADPIITR	1448.6	2	3.3328	0.2537
WGSQAFHNMR	1234.4	2	3.0211	0.1462
WGTDEAQFIYILGNR	1784.0	2	4.5503	0.3915
WGTDEEKFITIFGTR	1801.0	2	4.7074	0.4211
WGYSSTAITR	1142.2	2	2.7373	0.3007
WHELMLDKAPVLK	1580.9	2	4.2183	0.4428
WHFYDTVK	1096.2	2	2.4405	0.2398
WHLGVGPEGAFLPPHQGFHR	2240.5	2	5.2061	0.5232
WHNLPAHQGAVQDQPYQLPVEIDPLIASNTGMHR	3835.3	3	4.0675	0.2302
WHQTADFGYVPNPK	1660.8	2	4.2581	0.2889
WHWSSGSLVSYK	1437.6	3	4.3942	0.3652
WIAQDLSSLAGLLDQHGVR	2080.3	2	4.2771	0.3594
WIFKQDFSPEVLK	1637.9	2	3.4591	0.2411
WIGLDLSNGKPR	1356.6	2	2.9936	0.2753
WIHPASGR	924.0	1	1.7574	0.1682
WIKNTIAANS	1118.3	2	2.7986	0.1822
WISIMTER	1036.2	2	3.2021	0.1393
WITAKEDDLNSFNATDLKDLSSHQLNEFLAQTLQR	4064.4	3	7.5926	0.5535
WKAANDAGYFNDEMAPIEVK	2270.5	2	5.3769	0.3886
WKAGLYGLPR	1161.4	2	2.8557	0.2964
WKDEDISQK	1149.2	2	2.7087	0.1887
WKDSDEADLVLAK	1490.6	3	4.8389	0.3454
WKDTDEADLVLAK	1504.7	3	3.723	0.1526
WKEATIPGHLNSYTIK	1859.1	2	3.6481	0.293
WKELVDGAPLWLLK	1669.0	2	4.0458	0.1654
WKHPFFLDDR	1361.5	2	2.4049	0.1942
WKNFPSPVDAAFR	1535.7	2	2.7121	0.2361
WKPADLKEVTEEDLNNHFK	2314.5	2	3.6637	0.1826
WKPPMIDNPSYQGIWKPR	2214.6	2	3.1983	0.3708
WKRPTELLSNPQFIVDGATR	2329.6	3	6.1426	0.4192
WKYEKPDGSPVFIAFR	1941.2	2	4.5211	0.3411
WLAIDANAR	1030.2	2	2.9441	0.1628

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
WLAVDYENVRPDIVLLGK	2101.4	2	4.1122	0.3764
WLDLKDNPLDPVLAK	1738.0	3	4.3689	0.3055
WLDSDARNPPVVSK	1584.8	2	3.9587	0.3375
WLHNEDQMAVEK	1500.7	2	4.1932	0.4632
WLHNEDQMAVEKLSDGIR	2142.4	3	5.0703	0.3604
WLHSMTDDPPTTKPLTAR	2068.3	2	4.5703	0.2709
WLKDQELSPR	1272.4	2	2.6891	0.2087
WLKEDKLECSEELGDLVK	2135.4	2	5.858	0.4347
WLLAAAGVEFEEK	1463.7	2	4.6634	0.3447
WLLLTGISAQQNR	1500.7	2	4.3707	0.3572
WLPAGDALLQMITIHLPSPVTAQK	2602.1	2	4.5531	0.3889
WLPLEANPEVTNQFLK	1900.2	2	3.7886	0.3873
WLPVQESSTDDKKPGER	1973.1	2	3.9763	0.3122
WLQDLQEENESLKAHVQEVAQHNLK	2988.3	3	4.5197	0.217
WLSAAEEK	934.0	2	2.4529	0.1575
WLSAEIEDVKPAK	1486.7	2	3.7768	0.3562
WLVEPQIDDPNSNLEEAINEAEAITSVNSLGSK	3584.8	3	4.3033	0.3346
WLVIDPVPAAVPTQVAGPK	1959.3	2	3.9599	0.2415
WLVQVPR	898.1	2	2.5363	0.113
WLWEPTAPEKGKE	1571.8	2	2.9298	0.1923
WMEEQAQSLIDKTTAAFQQGK	2411.7	3	4.6086	0.2248
WMGPIPPAVNAR	1309.6	2	2.4153	0.1314
WNDGLDQYRLTPLELK	1962.2	2	3.834	0.2525
WNLDELPKFEK	1419.6	2	3.3652	0.1533
WNNTPMDEALHFGHHDVFK	2296.5	2	4.372	0.4736
WNTDNTLGTEISWENKLAEGLKLTLDTIFVPNTGKK	4049.5	3	4.2838	0.3185
WNTDNTLGTEITVEDQLAR	2177.3	2	5.18	0.3734
WNTDSVEEFLSEK	1584.7	2	3.0617	0.3899
WNTDSVEEFLSEKLERI	2096.3	2	2.5126	0.2783
WNTEDKVSHVSTGGGASLELLEGK	2515.7	3	5.9327	0.5236
WNTEDKVSHVSTGGGASLELLEGKVLPGVDALSNI	3595.0	3	3.7749	0.3389
WPDFNQEAYVGGTMVR	1871.1	2	2.7387	0.1225
WPDLHKNELK	1280.5	2	2.6698	0.1965
WPDLHSHHELK	1399.5	2	2.9155	0.1377
WPTETDVSSAK	1221.3	2	2.615	0.2829
WPTSGQLFLGHPK	1468.7	2	2.4281	0.1589

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
WQEVIPYTPAMQR	1619.9	2	2.6847	0.1424
WQFSMSAIKEEQELMEEINEDEPVKAK	3240.6	3	3.2741	0.1913
WQKEQESIIQQLQTSLHDR	2368.6	3	4.577	0.2586
WQQQGDLQDTK	1347.4	2	3.305	0.2861
WQQQGDLQDTKENR	1746.8	2	4.9073	0.4047
WQQQGDLQDTKENREEAR	2232.3	2	4.0365	0.198
WQSLKDLVK	1117.3	2	2.6082	0.1336
WQTLLSVDDLVEK	1546.7	2	4.2173	0.4049
WQTLLSVDDLVEKLVK	1887.2	2	3.92	0.322
WREEQMER	1164.3	2	2.5507	0.1108
WREEQMERLEALDANSR	2134.3	2	3.75	0.2291
WREHSAFQAPAVK	1527.7	3	4.1077	0.3048
WRPIASDEIVPGDIVSIGR	2081.4	3	3.3806	0.1127
WRYPSLSLHGIEGAFSGSGAK	2221.5	3	5.1257	0.4677
WSDQGPAQTSR	1233.3	2	3.286	0.343
WSGLLVTVGEVLEK	1530.8	2	4.4741	0.3628
WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK	3473.8	3	6.4738	0.5392
WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGKVLTPTQVK	4340.8	3	6.559	0.4749
WSKMDQLAK	1107.3	2	2.7566	0.2197
WSNAGELMELIR	1419.6	2	2.6025	0.1059
WSPIASTLPELVQR	1597.8	2	3.5072	0.2491
WSRPQAPITGYR	1432.6	2	2.7009	0.2831
WSTDDVQINDISLQDYIAVK	2324.5	2	5.6339	0.4822
WSTDDVQINDISLQDYIAVKEK	2581.8	3	4.897	0.3984
WSTLVEDYGMELR	1599.8	2	2.6144	0.1561
WTAISALEYGVPVTLIGEAVFAR	2464.8	2	4.474	0.4084
WTDENIDTVALK	1405.5	2	3.3728	0.2081
WTDENIDTVALKHFPNIDREK	2542.8	3	3.9927	0.299
WTEYGLTFTEK	1375.5	2	2.6458	0.2949
WTGMIIGPPR	1128.4	2	3.0758	0.3748
WTLLQEQK	1046.2	2	3.348	0.1517
WTPIIKDIMEDTIEDKLDTK	2405.7	2	3.5217	0.396
WTQLGAFYPFMR	1517.8	2	3.9929	0.3135
WTTAPKPTMADELYNQDYPIHSVEDR	3079.3	3	6.1534	0.4975
WTTAPKPTMADELYNQDYPIHSVEDRHK	3344.7	3	4.4423	0.2897
WTTEQQQR	1077.1	2	2.4604	0.1613

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
WTTSQLLQHPFVTVDSNKPIR	2468.8	3	3.6148	0.1252
WVAIQSVSAWPEK	1501.7	2	4.4401	0.3867
WVDINDKLK	1131.3	2	2.7347	0.1371
WVGADHADDIQYVFGKPFATPTGYRPQDR	3309.6	3	5.3659	0.4606
WVGGPEIELIAIATGGR	1740.0	2	4.5154	0.3912
WVPEITHHCPK	1347.6	2	2.4622	0.3246
WVPPLIGELYGLR	1513.8	3	4.2712	0.3389
WVTYFNKPDIDAWELR	2054.3	2	4.9632	0.4663
WVTYFNKPDIDAWELRK	2182.5	3	4.9005	0.4598
WVVIGDENYGEGSSR	1668.7	2	3.791	0.3982
WVVIGDENYGEGSSREHAALEPR	2572.7	3	3.9623	0.2815
WYDLMDNKDKGSS	1559.7	2	3.3181	0.23
WYFDVTEGK	1145.2	2	2.5542	0.1939
WYQMGAYQPFFR	1594.8	2	4.0238	0.3711
WYVNLHSLMDR	1434.6	2	2.8921	0.2773
WYVVGLAGNAILR	1432.7	2	4.1669	0.2429
WYVVQTNYDR	1344.5	2	2.98	0.1938
YAAELHLVHWNTK	1582.8	2	3.8334	0.3479
YAALLKDPTQALNEQGDSRNNSSVEDQK	3093.3	3	3.9231	0.1128
YAALSDQGLDIK	1294.4	2	2.5398	0.2529
YAALSVDGEDENEGEDYAE	2077.0	2	4.1192	0.4491
YAAVHVHTNAAR	1310.4	2	3.594	0.3588
YAAVTQFEATDAR	1443.5	2	3.1653	0.3175
YADALQEIIQER	1449.6	2	4.0956	0.2605
YADDTFTPAFVSTVGIDFK	2095.3	2	4.225	0.4498
YADEEIPR	993.1	2	2.7153	0.2386
YADEEIPRSPFK	1452.6	2	3.0058	0.1804
YADEMKEIQER	1412.6	2	3.6019	0.31
YADKLIAEGTVTLQEFEEEIAKYDR	2933.2	3	3.946	0.1942
YADLLLEKETLK	1436.7	2	4.2208	0.3276
YADLPGIAR	976.1	2	2.8393	0.3004
YADLSHNR	976.0	2	2.952	0.3444
YADLTEDQLPSCESLKDTIAR	2369.6	3	5.1585	0.3558
YAEAVTR	809.9	1	2.5205	0.1807
YAEDIFGELFTQANTFASR	2181.3	2	6.3027	0.4781
YAEERDRAEAEAR	1566.6	2	3.1928	0.1993

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YAEIVHLTLPDGTK	1557.8	2	3.9296	0.415
YAEIVHLTLPDGTKR	1714.0	3	4.733	0.3431
YAEKLIQEGK	1179.3	2	3.2094	0.2985
YAELLEEHRNSQK	1617.7	2	3.5653	0.2924
YAELLVSQGVVNQPEYEEEISKYDK	2932.2	3	4.2543	0.1964
YAETLFDILVAGGMLAPGGTLADDMMR	2830.3	2	3.0087	0.2132
YAFGQETNVPLNNFSADQVTR	2372.5	2	5.9046	0.4803
YAGEPVPFIEPPESFEFYAQQLRK	2844.2	3	4.0769	0.1991
YAGGTNDKGIGMGMTVPISFAVFPNEDGSLQKK	3431.9	3	3.7557	0.1868
YAGKDGYNYTLSK	1480.6	2	4.2337	0.3083
YAGPEDDAAITLAFSK	1669.8	2	3.8867	0.406
YAGSALQYEDVSTAVQNLQK	2186.4	2	5.7453	0.5229
YAHQSGFHVDR	1317.4	2	3.2337	0.3378
YAHVVLR	858.0	2	2.5376	0.1588
YAIAVNDLGTEYVHR	1721.9	2	3.9658	0.3518
YAICSALAASALPALVMSK	1881.3	2	3.0439	0.2275
YAIGSLNEGR	1080.2	2	2.8604	0.1937
YAKDALNLAQMQEQTLQLEQQSK	2680.0	3	4.5992	0.2756
YAKENPEKR	1135.3	2	2.794	0.1092
YALPLVGHR	1026.2	2	2.9249	0.2961
YALQMEQLNGILLHLESELAQTR	2672.1	2	6.7187	0.4861
YALQMEQLNGILLHLESELAQTRAEGQR	3213.6	3	4.6494	0.3257
YALSVGYR	929.1	2	2.8813	0.3201
YALTGDEVKK	1124.3	2	2.5716	0.2368
YALYDASFETK	1308.4	2	3.3147	0.3571
YALYDASFETKESR	1680.8	2	3.783	0.3259
YALYDATYETK	1338.4	2	4.4003	0.4134
YALYDATYETKESK	1682.8	2	3.945	0.3735
YANEVNSDAGAFKNSLKDLPDVQELITQVR	3336.7	3	5.3604	0.3826
YAPLHLVPLIER	1421.7	2	3.4783	0.3558
YAPSEAGLHEMDIR	1589.8	2	3.0716	0.3033
YAPSGFYIASGDVSGK	1619.8	2	5.1867	0.4854
YAPSGFYIASGDVSGKLR	1889.1	2	4.4439	0.4436
YAPTEAQLNAVDALIDSMSLAK	2322.6	2	6.211	0.5201
YAPTEVGLHEMHIK	1625.9	2	3.9957	0.4505
YASFQVENDQER	1486.5	2	3.7352	0.3351

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YASICQQNGIVPIVEPEILPDGDHDLKR	3121.5	3	6.8661	0.4616
YASNAVSEALIR	1294.4	2	4.2478	0.4066
YATALYSAASK	1146.3	2	3.5413	0.3853
YATALYSAASKQNKLEQVEKELLR	2755.1	3	4.0515	0.3664
YAVDDVQYVDEIASVLTSQKPSVLLTLR	3124.5	3	4.8374	0.3707
YAVLYQPLFDKR	1513.8	2	3.2186	0.3494
YAVTTGDHGIIR	1303.4	2	2.8929	0.1416
YDAFLASESLIK	1357.5	2	3.4001	0.2687
YDAVKEEK	982.1	2	2.6795	0.1822
YDDIEGANYFQQANELSK	2106.2	2	3.3683	0.135
YDDIKKVVK	1108.3	2	2.8829	0.2472
YDDLKKVVK	1108.3	2	2.6302	0.1882
YDDMAAAMK	1016.2	1	3.2539	0.3655
YDDMASAMK	1032.2	1	2.1535	0.358
YDDPEVQKDIK	1350.5	2	2.4079	0.142
YDDYSSSR	993.0	2	2.6564	0.2887
YDEIVKEVSAYIK	1557.8	2	3.2486	0.1618
YDEIVKEVSAYIKK	1685.9	3	4.2742	0.2601
YDEMVESMK	1132.3	2	3.2313	0.1804
YDEMVESMKK	1260.5	2	3.3758	0.3179
YDEYVNVKDFSDKINR	2006.2	3	3.8515	0.3953
YDGEDLAYTVK	1274.4	2	2.7173	0.3204
YDGIILPGK	976.2	2	3.1405	0.163
YDGKWEVEEMKESK	1758.9	3	4.2852	0.3097
YDGWFNNLR	1185.3	2	2.7827	0.3066
YDKSLHQAIEGDTSGDFLK	2125.3	3	3.8696	0.2664
YDLSGRPLNIKEDPDGENAR	2260.4	3	4.1719	0.353
YDNHVGTSK	1021.1	2	3.0078	0.194
YDNSLKIISNASCTTNCLAPLAK	2441.8	3	3.2892	0.1417
YDPSLKPLSVSYDQATSLR	2141.4	3	4.5175	0.4282
YDSPINSASHIPSSK	1603.7	2	3.4807	0.2891
YDVQHLQTALR	1344.5	2	3.0229	0.3028
YDYEEVEAEGANK	1517.5	2	4.7704	0.3787
YDYQRQPDSGISSIR	1785.9	2	3.4457	0.3238
YEAAGTLVTLSSAPTAIK	1794.0	2	3.2318	0.2991
YEAPQATDGLAGALDAR	1719.8	2	4.8849	0.438

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YEDFKEEGSENAVK	1645.7	2	4.074	0.3053
YEDFSNLGTTHLLR	1666.8	2	3.7161	0.397
YEDKDGKQPVGR	1392.5	2	3.7225	0.3706
YEEENFYLEPYLK	1737.9	2	4.2661	0.3539
YEEENFYLEPYLKEVIR	2235.5	3	3.6532	0.2254
YEEIDNAPEER	1365.4	2	3.2208	0.2932
YEEIVKEVSTYIK	1601.8	2	4.3697	0.3747
YEEIVKEVSTYIKK	1730.0	3	4.7709	0.4512
YEELQSLAGKHGDDLRR	1988.2	3	3.8172	0.359
YEEVSVSGFEEFHR	1715.8	2	2.7417	0.2521
YEGFFGLYR	1152.3	2	3.0511	0.3382
YEGGYPALTEVMNK	1572.8	2	4.0136	0.3305
YEHANDDKSSLK	1407.5	2	2.7874	0.2462
YEHLLQLLDLAQEK	1714.0	2	3.9685	0.2958
YEHLLQLLDLAQEKVDVANRLEK	2739.1	3	3.631	0.1479
YEIDLDTSDHAHLEHITR	2166.3	3	3.5739	0.373
YEIEETETVTK	1342.4	2	3.2122	0.2198
YEIKDIHVPPR	1367.6	3	3.4018	0.256
YEILTPNSIPK	1275.5	2	3.2395	0.2379
YEKDIAAYR	1129.2	2	3.196	0.2372
YEKEKFEEMIQQIK	1844.1	3	4.5899	0.3272
YEKPDGSPVFIAFR	1626.8	2	2.519	0.2528
YELGRPAANTK	1220.4	2	3.1901	0.3578
YEMFAQTLQQSR	1502.7	2	4.2737	0.3973
YEMLKEHER	1235.4	2	2.6532	0.1884
YENHSATAESSR	1352.3	2	2.7412	0.3073
YEQGFITDPVVLSPK	1693.9	2	2.5618	0.1238
YESGDHVAVYPANDSALVNQLGK	2448.6	3	4.9552	0.3517
YESLTDPSKLDSGK	1540.7	2	4.5396	0.3592
YESLTDPSKLDSGKELHINLIPNK	2713.0	3	4.7469	0.3702
YESLTDPSKLDSGKELHINLIPNKQDR	3112.4	3	5.8327	0.4116
YESLTDPSKLDSGKELK	1911.1	2	4.1252	0.4443
YESLTDPSKLDSGKELKIDIIPNPQER	3087.4	3	5.9953	0.4431
YESSALPSGQLTSLSEYASR	2147.3	2	6.2998	0.4819
YESSSYTDQFSR	1470.5	2	3.4138	0.3856
YESSTASALVA	1099.2	2	2.6332	0.2097

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YETELAMR	1013.2	2	2.7219	0.2714
YETTNKTYK	1148.2	2	2.7484	0.3061
YEVLKTENPGDASDLQGR	1993.1	2	5.5135	0.4996
YEVPLETPHVHSR	1564.7	2	3.6313	0.4409
YEVTSGGGGTSR	1171.2	2	2.6838	0.2819
YEWDVAEAR	1139.2	2	3.1718	0.3727
YEYVLHPR	1077.2	2	2.6932	0.2549
YFAGNLASGGAAGATSLCFVYPLDFAR	2741.1	2	5.0913	0.4942
YFAGTMAEETAPAVLER	1857.1	2	5.3023	0.4668
YFANKETDKQILQNR	1869.1	3	3.4793	0.2606
YFDENAAEDFEKHESVEYKPPKKPFVK	3273.6	3	5.157	0.3413
YFDGSGGNNHAVEHYR	1823.9	2	4.1545	0.4505
YFDGSGGNNHAVEHYRETGYPLAVK	2783.0	3	4.4381	0.4217
YFDKASYR	1050.1	2	2.6839	0.2274
YFDLGLPNRDQTDDQVTIDSALATQK	2926.1	3	6.1265	0.4385
YFDLGLPNRDQTDDQVTIDSALATQKYSVAVK	3573.9	3	5.4054	0.3511
YFDMWGGDVAPFIEFLK	2036.3	2	4.2327	0.2401
YFDPANGK	912.0	1	2.1752	0.2796
YFDRVDENNPEYLR	1830.9	2	2.7929	0.1205
YFDRVDENNPEYLRER	2116.2	2	3.0138	0.227
YFDSGDYNMAK	1311.4	2	3.2078	0.3717
YFEITDESPYVHYLNTFSSKEPQR	2952.2	3	4.079	0.3467
YFETSALKEEATK	1517.7	2	4.4327	0.432
YFGELLADLSR	1284.4	2	3.3401	0.3005
YFGELLADLSRK	1412.6	2	3.0577	0.2544
YFHTSVSRPGR	1307.4	2	2.4296	0.3134
YFHVVIAGPQDSPFEGGTFK	2197.4	2	4.7047	0.4183
YFILPDSLPLDTLLVDVEPK	2288.7	3	5.5301	0.5448
YFILPDSLPLDTLLVDVEPKVK	2516.0	2	3.4934	0.3574
YFKDHVEKDDIIK	1650.9	2	2.8267	0.2197
YFKLEPLQAYHR	1565.8	3	4.5927	0.3217
YFLAELLSEPNQTENDALEPEDLSQAAEQDE	3510.6	3	5.5876	0.5069
YFLAELLSEPNQTENDALEPEDLSQAAEQDEMR	3798.0	3	4.6221	0.4294
YFLAELLSEPNQTENDALEPEDLSQAAEQDEMRL	3911.2	3	5.3618	0.5287
YFLAELLSEPNQTENDALEPEDLSQAAEQDEMRLE	4040.3	3	5.1109	0.4765
YFLAELLSEPNQTENDALEPEDLSQAAEQDEMRLEL	4153.4	3	4.8776	0.4574

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YFLAELLSEPNQTENDALEPEDLSQAAEQDEMRLELQ	4281.6	3	6.0209	0.4781
YFLAELLSEPNQTENDALEPEDLSQAAEQDEMRLELQR	4437.8	3	5.0903	0.3672
YFLDNLDKLGEPDYIPSQQDILLAR	2938.3	3	4.7583	0.2737
YFLHQSHEER	1346.4	2	3.0307	0.3028
YFLHQSHEEREHAEK	1941.1	2	4.3136	0.4023
YFLHQSHEEREHAEKLMK	2313.6	3	4.0916	0.3343
YFLKPEVLQK	1265.5	2	2.9382	0.2837
YFNVHELEALLQEMSSK	2039.3	2	5.4142	0.4541
YFPAFEK	902.0	1	2.1477	0.2552
YFPGFDWFFLDPITSSGIK	2238.5	2	3.2515	0.3503
YFPTQALNFAFK	1447.7	2	3.9632	0.4214
YFPTQALNFAFKDK	1690.9	2	3.1507	0.2833
YFQFQEEGKEGENR	1761.8	2	4.7671	0.324
YFQHLLGK	1006.2	2	2.5427	0.1212
YFQNYSYGGVIQDDHIPFLR	2433.7	3	3.6773	0.2911
YFQNYSYGGVIQDDHIPFLRR	2589.8	3	4.1395	0.397
YFSEADKIK	1101.2	2	2.4476	0.1713
YFSERGDAVTK	1273.4	2	2.873	0.1357
YFSLKPEEKDEK	1513.7	2	3.4094	0.2781
YFTTTK	760.9	1	1.6726	0.1533
YFTWDPSRFPQPR	1697.9	2	2.7174	0.1143
YFVEAGAMAVR	1214.4	2	2.4473	0.1347
YFVQGMGYMPSASMTR	1827.1	2	5.0298	0.5455
YFYVSAEQVVQGMK	1649.9	2	3.4663	0.3438
YGAATANYMEVVSLLK	1731.0	2	4.505	0.4993
YGADVHTQSK	1106.2	2	3.0168	0.2643
YGAFGLPITVAHVDGQTHMLFGSDR	2691.0	3	4.2569	0.3761
YGAFVKPAVVTVGDFPEEDYGLDEI	2732.0	2	5.0558	0.406
YGAHNYHPLPVALER	1737.9	2	4.3123	0.4649
YGASLLHTYAGPSLLVLGPR	2086.4	2	3.5037	0.3696
YGASQVEDMGNIILAMISEPYNHR	2710.0	3	4.0362	0.2413
YGDFNKEVHK	1237.3	2	2.9663	0.2652
YGDGGSTFQSTTGHCVHMR	2042.2	3	3.5347	0.2294
YGDGIQLTR	1023.1	2	2.8415	0.2575
YGDLANWMIPGK	1365.6	2	3.2053	0.1575
YGDLLGHLK	1016.2	2	3.128	0.2195

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YGDLLPADGILIQGNDLKIDESSLTGESDHVKK	3542.9	3	5.0447	0.4241
YGDSGEQIAGFVK	1371.5	2	3.6412	0.389
YGDSGEQIAGFVKEFSHIAFLTIK	2659.0	3	3.4562	0.2537
YGDYNKEIHKPGYLANDR	2154.3	2	4.7742	0.4303
YGEAGEGPGWGGAHPR	1598.7	2	4.2483	0.4855
YGEDGLAGESVEFQNLATLKPSNK	2568.8	3	5.0646	0.4236
YGEDSEQFRDASK	1532.6	2	3.4536	0.361
YGEGDSLTLQQLK	1452.6	2	4.4022	0.4211
YGEIPAELR	1048.2	2	2.652	0.165
YGELISTPLVSKALSNRGQHSISYTLSR	3079.5	3	3.4998	0.2084
YGEPGEVFINK	1253.4	2	3.4488	0.3283
YGEPGEVFINKGK	1438.6	2	3.726	0.3358
YGFGEAGKPK	1054.2	2	2.4805	0.2774
YGFIEGHVVIPR	1387.6	2	4.1895	0.4007
YGFLWPGLNVPLMK	1636.0	2	3.565	0.2773
YGFNSHGLSVVEHR	1602.7	2	2.7548	0.223
YGFQEQLLYSVLEELVNSGR	2345.6	2	3.0162	0.2141
YGGDEIPFSPYR	1401.5	2	3.3443	0.177
YGGEEEDQPIYLAVK	1711.9	2	5.0179	0.4466
YGGEGAESMMGFFHELLK	2004.3	2	2.6845	0.1172
YGGELVPHFPAR	1343.5	2	3.37	0.3829
YGGETKVYVGNLGTGAGKGELER	2356.6	3	3.7544	0.2533
YGGGNYGPGGSGGSGGYGGR	1734.7	2	4.5452	0.4583
YGGHGYSHILTNVVPK	1743.0	2	4.0976	0.4157
YGGPNHIVGSPFK	1373.5	2	2.9718	0.2017
YGGPPPDSVYSGQQPSVGTEIFVGK	2567.8	3	3.7634	0.1847
YGGPPPDSVYSGQQPSVGTEIFVGKIPR	2934.3	3	4.5085	0.4041
YGGPPPDSVYSGVQPGIGTEVFVGK	2508.8	3	5.1611	0.3645
YGGPPPDSVYSGVQPGIGTEVFVGKIPR	2875.2	3	5.5804	0.34
YGGPYHIGGSPFK	1380.5	3	3.8843	0.3578
YGGQPLFSEKFPTLWSGAR	2142.4	3	4.7188	0.4661
YGGRDYSLDEFEANKILHQHLGAPEER	3146.4	3	5.8033	0.4414
YGGTFQNVSVQLPITLNK	1980.3	2	2.8186	0.1734
YGINTTDIFQTVDLWEGK	2101.3	2	6.1383	0.5662
YGISGELAMRPLASLSGGQK	2036.3	2	3.7008	0.3254
YGISNEKPEVK	1264.4	2	2.4817	0.1729

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YGISSMIQSQEKPDR	1739.9	2	4.0472	0.4493
YGIVDYMIEQSGPPSK	1785.0	2	2.5518	0.106
YGIVDYMIEQSGPPSKEILTLK	2482.9	3	4.5861	0.4247
YGIVLDAGSSR	1138.3	2	2.4612	0.1301
YGKDATNVGDEGGFAPNILENK	2310.5	3	6.1329	0.5601
YGKDATNVGDEGGFAPNILENKEGLELLK	3093.4	3	7.2242	0.3137
YGKDATNVGDEGGFAPNILENKEGLELLKTAIGK	3564.0	3	7.1124	0.5484
YGKDATNVGDEGGFAPNILENNEALELLK	3093.3	3	3.7278	0.2628
YGKDATNVGDEGGFAPNILENSEALELVK	3052.3	3	4.2835	0.2364
YGKDATNVGDEGGFAPNILENSEALELVKEAIDK	3608.9	3	3.3894	0.1786
YGKDATNVGDEGGFAPNILENSEALELVKEAIDKAGYTEK	4258.6	3	6.5354	0.4188
YGKIETIEVMEDR	1583.8	3	3.9605	0.3424
YGKLEVANLLLQK	1489.8	2	2.9712	0.1621
YGKSPYLYPLYGLGELPQGFAR	2490.8	3	5.8209	0.4707
YGLAAAVFTR	1069.2	2	3.5447	0.4029
YGLFKEENPYAR	1487.6	2	2.7596	0.233
YGLFPANYVELR	1442.6	2	2.7257	0.3218
YGLFPANYVELRQ	1570.8	2	3.8167	0.344
YGLIFHSTFIGR	1411.6	2	3.2361	0.2949
YGLIGLNGIGK	1105.3	2	2.7218	0.1096
YGLIPEEFFQFLYPK	1892.2	2	3.4175	0.3205
YGLIYHASLVGQTSPK	1735.0	2	3.5014	0.3738
YGLPDSLAILSEMGEVTDGMMDTK	2574.9	2	5.3398	0.5395
YGLVTYATYPK	1276.5	2	4.0026	0.3613
YGMNPHQTPAQLYTLQPK	2088.4	2	4.5417	0.2694
YGMWHFLLGDK	1367.6	2	2.4572	0.1939
YGNLGHVNIGAIQEPLAFILPK	2365.8	3	4.9148	0.2153
YGPIADVSIVYDQQSR	1812.0	2	5.0385	0.4555
YGPIVDVYVPLDFYTR	1918.2	2	4.2094	0.4905
YGPLLDLPELPFPELER	1999.3	2	4.0505	0.1963
YGPLSGVNVVYDQR	1567.7	2	4.1478	0.2544
YGPQYGHPPPPPPPPEYGPHADSPVLMVYGLDQSK	3787.2	3	6.1274	0.4806
YGPSLMPGGNK	1121.3	2	2.5562	0.2708
YGPSLMPGGNKEAWPHIK	1983.3	2	3.3146	0.3217
YGQFSGLNPGGRPITPPR	1915.1	3	3.6946	0.2159
YGQGAGEGSTR	1083.1	2	3.0857	0.334

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YGQGFYLISPSEFER	1794.0	2	3.8125	0.3221
YGQHPNIITLK	1284.5	2	2.4881	0.1644
YGQISEVVVVK	1221.4	2	3.5091	0.3739
YGQISEVVVVKDR	1492.7	3	3.936	0.3906
YGQNGDFTR	1058.1	2	3.2437	0.2908
YGQVTPLEIDILYQLADLYNASGR	2714.0	3	4.5851	0.3807
YGSALASAGDPGHPNHPLHASQNSAR	2613.7	3	3.926	0.3123
YGSDIVPFSK	1113.2	2	3.3521	0.3646
YGSDIVPFSKVDEEQMK	1973.2	2	5.4123	0.3821
YGSYNVFWTSNPGLPLLTEMVK	2517.9	3	4.3311	0.2342
YGVIILDEAHER	1415.6	2	2.6232	0.3451
YGVMDTTTAQGR	1300.4	2	4.1373	0.5153
YGVNPGPIVGTTR	1331.5	2	3.4366	0.3507
YGVQADRVDK	1151.3	2	2.9588	0.2186
YGVSGYPTLK	1085.2	1	3.3221	0.3888
YGYTHLSAGELLR	1480.6	3	4.6434	0.3777
YGYTHLSAGELLRDER	1881.0	2	4.0233	0.3842
YGYTHLSAGELLRDERKNPDSQYGELIEK	3383.7	3	4.6148	0.2846
YGYTHLSTGDLLR	1496.6	2	4.1472	0.4181
YGYTHLSTGDLLRSEVSSGSAR	2357.5	3	3.2648	0.1987
YHEEFEK	982.0	2	2.5167	0.1629
YHFNMGLLMGEAR	1539.8	2	2.6628	0.1854
YHFVPGTTAVLTQTVKPLTLELVEETVQAMEVE	3675.2	3	3.9071	0.27
YHGDSVASLGTQPDLGSALYQENYK	2714.9	3	6.5008	0.4157
YHGHSMSDPGVSYR	1593.7	3	3.3622	0.3231
YHGQLTK	847.0	1	2.3433	0.1746
YHIDLDPHFNDILGQHSR	2178.4	2	5.0046	0.3866
YHIEVNRVPAGNWVLIEGVDQPIVK	2847.3	3	3.5841	0.1079
YHLGAYTGDDVR	1367.4	2	3.5556	0.3387
YHNVGLSK	918.0	1	2.7127	0.2443
YHPDKNKEPGAEEK	1642.8	2	2.8084	0.2774
YHQIGSGK	890.0	1	2.5414	0.19
YHSDEYIK	1055.1	2	2.4945	0.1788
YHSLAPMYYR	1301.5	2	2.7723	0.1843
YHSYKDLSEFLR	1558.7	3	3.3956	0.3145
YHTEIVFAR	1136.3	2	2.4369	0.1646

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YHTINGHNAEVR	1411.5	2	3.8644	0.4283
YHTINGHNAEVRK	1539.7	2	3.3078	0.2878
YHTINGHNCEVK	1415.6	2	3.5546	0.2837
YHTSQSGDEMTSLSEYVSR	2178.3	2	5.7071	0.5217
YHTVKGHNCEVRK	1571.8	2	3.0356	0.2064
YHTVNGHNCEVR	1429.5	2	3.845	0.3803
YHVLVNLGK	1043.2	2	2.7689	0.1042
YHVLVNLGKK	1171.4	2	2.5339	0.193
YHVMANHNSLPILK	1637.9	2	2.9993	0.2086
YHVPVVVVPEGSASDTHEQAILR	2504.8	2	5.56	0.4833
YHYLGGR	866.0	1	2.2102	0.2903
YIAENGTDPINNQPLSEEQLIDIK	2716.0	3	5.1873	0.3665
YIAIASTTVETTDPEKEVEPALELLEPIDQK	3444.8	3	4.0252	0.2379
YIAIVSTTVETKEPEKEIRPALELLEPIEQK	3569.1	3	5.4423	0.4172
YIANLGHGLYPDMDPEHVGAFVDAVHK	2967.3	3	5.9786	0.4864
YIAPTVLTDVDPK	1432.6	2	3.241	0.2509
YICEKIMDINK	1370.7	2	2.7716	0.1037
YICENQDSISSK	1387.5	2	4.5958	0.4066
YIDENQDRYIK	1457.6	2	3.4723	0.2931
YIDENQDRYIKK	1585.7	2	3.341	0.2695
YIDITRPEEVKHQEQHHPELEDKDLDFK	3490.8	3	3.6835	0.2931
YIDLEPDTPLSPEELKEK	2117.3	3	3.3814	0.2233
YIDQEELNK	1152.2	2	3.6691	0.2083
YIDQEELNKTKPIWTR	2035.3	2	4.2289	0.4221
YIDQEELNKTKPIWTRNPDDITNEEYGEFYK	3851.1	3	5.3108	0.5218
YIDQEELNKTKPIWTRNPDDITQEEYGEFYK	3865.2	3	5.3768	0.4654
YIDTEHGGSQAR	1334.4	2	3.3218	0.3157
YIETDPANR	1079.1	2	2.7334	0.2535
YIEVFKSHR	1179.4	2	2.5102	0.2775
YIEVFKSSQEEVR	1614.8	2	4.5096	0.4139
YIGNMHGNEAVGR	1418.6	2	3.8209	0.415
YIGNMHGNEVVGR	1446.6	2	3.4037	0.3029
YIGTGHADTTK	1164.3	2	2.6857	0.2022
YIHLENLLAR	1242.5	2	2.8342	0.2609
YIIDKYGNHPAFYR	1758.0	2	3.2981	0.3526
YIIHKYPSLELER	1661.9	2	3.5555	0.3517

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YIITLHELLAHTPHEHVER	2309.6	3	3.399	0.2723
YIKDKYPNLQVIGGNVVTAAQAK	2491.9	3	4.519	0.3287
YILGNPLTPGVTQGPQIDKEQYDK	2676.0	2	4.3279	0.4828
YILGNPLTPGVTQGPQIDKEQYDKILDLIESGK	3645.1	3	4.609	0.2821
YILGNPLTPGVTQGPQIDKEQYDKILDLIESGKK	3773.3	3	5.0839	0.4498
YILGNPLTPGVTQGPQIDKEQYDKILDLIESGKKEGAK	4158.7	3	5.1666	0.3855
YINENLIVNTDELGR	1763.9	2	4.6255	0.3191
YINMLTR	911.1	2	2.5285	0.1416
YINMLTRPR	1164.4	1	1.9146	0.1263
YINTEHGGSQAR	1333.4	2	3.1807	0.1446
YIQHTYR	981.1	2	2.4041	0.2785
YIQPWESEFIDSQR	1798.9	3	3.5736	0.3369
YIQQTKPLTLER	1490.7	2	3.635	0.1315
YIRKPIDYTILDDIGHGVK	2217.6	3	3.4314	0.2545
YIRKPIDYTVLDDVGHGVK	2189.5	3	4.6373	0.3723
YISGSIHYSR	1183.3	2	2.6054	0.292
YISLIYTNYEAGKDDYVK	2156.4	2	5.2653	0.4634
YISPDQLADLYK	1426.6	2	4.0356	0.3756
YITGDQLGALYQDFVR	1860.1	2	5.4239	0.5297
YITGDQLGALYQDFVRDYPVVSIEDPFDQDDWAAWSK	4325.7	3	5.9262	0.4572
YITGTDILDMKLEDILESINSIK	2626.0	2	3.4326	0.2197
YITHESDDAR	1207.2	2	2.5399	0.2482
YITQNGDYQLR	1371.5	2	3.3957	0.3859
YIVLAKDFEK	1226.4	2	2.6231	0.2362
YIVPMLTVDGK	1236.5	2	3.1787	0.2879
YIYDSAFHPDTGEK	1643.7	2	4.3478	0.4626
YKAEDEK	882.9	1	2.5336	0.1339
YKAEDEKQR	1167.3	2	3.2287	0.2184
YKAEDEVQR	1138.2	2	3.3295	0.2245
YKAEDEVQRER	1423.5	2	2.5994	0.2483
YKAPFHQLR	1160.4	2	2.7232	0.1464
YKASITALEAK	1195.4	2	3.4018	0.3609
YKDAANLLNDALAIR	1661.9	2	3.853	0.3724
YKDAIHFYNK	1299.5	2	3.6592	0.3118
YKDDPVDLR	1121.2	2	2.803	0.2024
YKDDPVDLRLDIER	1747.9	2	2.8403	0.3673

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YKDEAQLYKEEHLR	1823.0	2	4.9886	0.455
YKDGTELELKENDIKPLTSFR	2497.8	3	5.438	0.3684
YKDILPFDHSR	1391.6	3	3.3314	0.1449
YKDINITKPASVFVQLR	1993.3	2	4.5257	0.318
YKDLDEDELLGNLSETELK	2225.4	3	4.4569	0.2422
YKDLDEDELLGNLSETELKQLETVLDDLDPENALLPAGFR	4533.9	3	4.6355	0.2967
YKDLVPDNSK	1179.3	2	3.1785	0.2449
YKDNPFSLGESFGSR	1704.8	2	2.637	0.2149
YKDSAQRDDMIFEDCGDVPSEPKER	2932.1	3	5.5999	0.4027
YKEAAHLLNDALAIR	1698.9	2	3.8538	0.3446
YKEALLGR	950.1	2	2.7299	0.2225
YKEATDLLHDALQIR	1787.0	2	2.6477	0.2723
YKEEFEKNK	1215.3	2	3.4469	0.2104
YKEETIEK	1040.1	2	2.4057	0.124
YKEEYAVLISEAQAIK	1856.1	2	4.5297	0.2231
YKEEYAVLISEAQAIKADLAAVEAK	2725.1	2	7.7791	0.5889
YKELGEKLSKDPNIVIAK	2046.4	2	5.9703	0.4011
YKETDLLILFK	1383.7	2	3.772	0.2426
YKETDLLILFKDDYFAK	2123.4	2	5.061	0.4854
YKEVAELTR	1109.3	2	2.8664	0.2377
YKGQHVPGSPFQFTVGPLGEGGAHK	2596.9	3	3.7797	0.3507
YKHFDWLYER	1457.6	2	2.4401	0.1574
YKHVEQNGEK	1232.3	2	2.5258	0.2231
YKLAVADAVIEK	1320.6	2	2.7618	0.231
YKLDKESYPVFYLFR	1969.3	2	5.3736	0.4776
YKLDKESYPVFYLFRDGDFENPVPYTGAVK	3560.0	3	4.5356	0.3212
YKLLGGLAVR	1090.3	2	2.6569	0.2347
YKNILPFDHSR	1390.6	2	3.3327	0.1038
YKNILPFDHTR	1404.6	2	3.7019	0.281
YKNREPLMPSPQFIK	1849.2	2	3.4397	0.3057
YKNWPESVYFFK	1608.8	2	2.6129	0.2098
YKPAVNQIECHPYLTQEK	2162.5	2	4.0812	0.3719
YKPESEELTAER	1452.5	2	3.4187	0.3422
YKPLDLRPKK	1258.5	2	2.7138	0.1615
YKPVCNQVECHPYFNQR	2126.4	2	4.2001	0.3022
YKPVCNQVECHPYFNR	1998.3	2	3.1819	0.2812

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YKPYEEALLQAEAPR	1779.0	2	3.9952	0.4004
YKQDVYLLPK	1267.5	2	2.9188	0.2264
YKQETEQLVSNLKEENTLLK	2408.7	3	4.2599	0.1906
YKQIFLGGVDKR	1424.7	2	3.5179	0.2955
YKQSLDDAAK	1139.2	2	2.8258	0.1586
YKRPGYGAYDAFK	1536.7	3	3.9245	0.3674
YKSVLAETEGILQK	1579.8	2	3.7985	0.2042
YKSYSPYDMLESIRK	1881.1	2	2.6549	0.2188
YKTPDFESTGLYSAMPR	1964.2	3	4.2464	0.4585
YKTQIDHYVGIAR	1564.8	2	4.1632	0.3986
YKVEGFPTIYFAPSGDK	1920.2	2	5.0245	0.4777
YKVEGFPTIYFAPSGDKK	2048.3	2	5.1197	0.4341
YKVEGFPTIYFAPSGDKKNPVK	2486.8	3	3.7624	0.2676
YKVEGFPTIYFAPSGDKKNPVKFEGGDR	3148.5	3	5.0432	0.4106
YKVEGFPTIYFAPSGDKKNPVKFEGGDRDLEHLSK	3971.4	3	5.3473	0.414
YKVEYPIMYSTDPENGHIFNCIQR	2919.3	3	3.9814	0.2383
YKVPDGKPENEFAFNAEFK	2231.4	2	4.1615	0.4014
YKVPDGKPENEFAFNAEFKDKDFAIDIIK	3390.8	3	5.7296	0.4544
YKYEDKDGK	1146.2	2	2.5502	0.162
YKYEDKDGKQPVGR	1683.8	2	4.8414	0.4182
YLAAGSSNAVK	1081.2	2	2.9864	0.1554
YLAEFATGNDR	1257.3	2	2.8833	0.2821
YLAEFATGNDRK	1385.5	2	3.2504	0.2664
YLAEFATGNDRKEAAENSLVAYK	2561.8	2	4.9438	0.316
YLAEKYEWDVAEAR	1743.9	2	5.0852	0.4379
YLAEVAAGDDKK	1280.4	2	3.7935	0.2713
YLAEVAAGDDKKGIVDQSQQAYQEAFEISK	3303.6	3	6.5788	0.3891
YLAEVAAGDDKKGIVDQSQQAYQEAFEISKK	3431.8	3	7.0678	0.4854
YLAEVACGDDRK	1340.5	2	3.2225	0.3524
YLAEVASGEK	1067.2	2	2.5783	0.1193
YLAEVASGEKK	1195.3	2	3.176	0.2651
YLAEVATGEKR	1237.4	2	3.1698	0.3081
YLAIHGMETLKGETK	1692.0	2	2.9142	0.1545
YLASGAIDGIINIFDIATGK	2053.3	2	5.3786	0.4952
YLDEDTIYHLQPSGR	1807.9	2	4.4481	0.402
YLDEIVKEVEAK	1436.6	2	2.6028	0.2762

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YLDFVFAVK	1102.3	2	2.8889	0.1873
YLDFVFAVKNENR	1615.8	2	2.5113	0.1216
YLDIPKMLDAEDIVGTARPDEK	2490.8	3	4.1818	0.2505
YLDIPKMLDAEDIVNTARPDEK	2547.9	3	4.2047	0.1753
YLDQMEDLYEDFHIVK	2059.3	2	4.9401	0.3935
YLDQMEDLYEDFHIVKLPLLPHEVR	3114.6	3	4.6931	0.3763
YLDSDTEKELQALYALQASIVKLDQPANLLR	3521.0	3	3.6926	0.1591
YLEANMTQSALPK	1466.7	2	3.3405	0.2168
YLECSALTQR	1184.3	2	2.6759	0.2795
YLEDKAQELAR	1336.5	2	2.4645	0.1747
YLEEERPFAIEQVTGMLLAK	2338.7	3	4.099	0.223
YLELLER	936.1	2	2.4435	0.1373
YLENGKDKLER	1365.5	2	3.1291	0.2218
YLENYDAIR	1157.3	2	3.0444	0.3488
YLESKEDVADALLQTDQSLSEKEK	2741.0	3	5.4185	0.3733
YLESLGEEQRK	1352.5	2	2.8271	0.1393
YLESLGEEQRKEAER	1838.0	2	2.6381	0.1022
YLEVQYKPQVHIQMTYPLQGLTR	2807.3	3	4.565	0.3876
YLFNQLFGEEDADQEVSPDRADPEAAWEPTEAEAR	3998.1	3	5.4693	0.3928
YLGDASVEPDPLQMPTFPPDYGFPER	2940.2	3	4.415	0.3042
YLGDASVEPDPLQMPTFPPDYGFPERK	3068.4	3	4.1384	0.2051
YLGFGTPSNLGK	1254.4	2	2.57	0.2518
YLGGTDDTVKKKDLFLDLIADVMFGVPSVIVAR	3598.2	3	5.2141	0.4901
YLGINSDGLVVGR	1363.5	2	3.265	0.3081
YLGLLENLR	1091.3	2	2.572	0.1497
YLGLLENVR	1077.3	2	3.0084	0.2432
YLGNTVDLSSFDFR	1634.8	2	3.426	0.1886
YLGQDYEQLR	1285.4	2	2.4518	0.1567
YLGQLHYLQSR	1378.6	2	2.7812	0.1593
YLHDESGLNRR	1360.5	2	2.5296	0.1938
YLHENLPIPQR	1380.6	2	2.9087	0.303
YLHLAREDTNNLFSVQFR	2224.5	3	4.3786	0.3871
YLHVGYIVPPAPEK	1583.9	2	3.8522	0.3439
YLHVRPQPLAGEDPPAYQAR	2279.5	3	4.3495	0.1953
YLIATSEQPIAALHR	1683.9	2	3.2969	0.3549
YLIATSEQPIAALHRDEWLRPEDLPIK	3176.6	3	4.4834	0.3763

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YLINLCGMDFPIK	1527.9	2	2.436	0.1221
YLIPNATQPESK	1361.5	2	3.2276	0.2216
YLKDLLGIQTTGPLELLQFDHGQSNPTYYIR	3596.0	3	4.2523	0.2537
YLKDVTLQK	1108.3	2	3.0183	0.221
YLKSEPIPESNDGPVK	1774.0	2	4.2664	0.3901
YLLDHFLSMGINK	1551.8	2	4.5367	0.4266
YLLETSGNLDGLEYK	1715.9	2	5.0455	0.5135
YLLETSGNLDGLEYKLHDFGYR	2604.9	3	3.7264	0.2755
YLLNLNLEPFSEK	1580.8	2	5.0833	0.2278
YLLQYQEPIPCEQLVTALCDIKQAYTQFGGK	3563.1	3	3.744	0.1911
YLLSQSSPAPLTAAEEELR	2076.3	2	5.4946	0.4511
YLLSQSSPAPLTAAEEELRQIK	2445.8	3	4.446	0.4104
YLMDEGAHLHIYDPK	1803.0	2	3.6016	0.1552
YLMEEDEDAYKK	1534.7	2	3.882	0.3663
YLMEEDEDAYKKQFSQYIK	2429.7	2	4.8508	0.4177
YLNEYGAPDAGGLEHVPLGWSYWYALEK	3200.5	3	3.9015	0.1154
YLNFFTK	933.1	2	2.4149	0.1616
YLNFVKGVVDSDDLPLNVSR	2251.5	3	6.1128	0.5521
YLNFVKGVVDSDDLPLNVSRETLQQHK	3116.5	3	3.9142	0.3041
YLNIFGESQPNPK	1507.7	2	2.7522	0.2589
YLNQDYEALRNECLEAGTLFQDPSFPAIPSALGFK	3920.4	3	5.3876	0.3551
YLNSGGFIGYAPYVNR	1792.0	2	4.2344	0.3664
YLNTNPVGGLLEYAR	1680.9	2	4.6102	0.4369
YLPDTLLLEECGLLR	1749.1	2	4.1189	0.4259
YLPELMAEKDSLDPSFTHAMQLLTAEIEK	3322.8	3	5.1497	0.492
YLPGHKLPPNVVAVPDVVQAAEDADILIFVVPHQFIGK	4108.8	3	4.0161	0.1545
YLPHSAGR	901.0	1	1.9023	0.1474
YLPRPANPDEIGNFIDENLK	2316.6	3	5.7257	0.367
YLQDLLAWVEENQHR	1915.1	2	3.8788	0.3608
YLQELDKDHAR	1388.5	2	2.627	0.2369
YLQEVIDVLETDGHFR	1935.1	2	4.2773	0.365
YLQEVIDVLETDGHFREK	2192.4	2	2.6821	0.1687
YLQLTQSELSSYHRK	1854.1	2	3.4023	0.1488
YLQQLAEKPLETR	1589.8	2	3.8024	0.1949
YLQTLTTIAAEK	1352.6	2	4.0066	0.3859
YLRAEPEDHYFLLTEPPLNTPENR	2916.2	3	4.6851	0.255

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YLREADFAR	1141.3	2	2.5184	0.2371
YLRIPDEIIDMVKEEVVAK	2261.7	3	5.9474	0.2622
YLRPPNTSLFVR	1463.7	3	3.6391	0.3057
YLSAQKPLLNDGQFR	1751.0	2	4.5288	0.4966
YLSEVASGDNK	1183.3	2	3.8113	0.3868
YLSEVASGDNKQTTVSNSQQAYQEAFEISK	3324.5	3	7.1778	0.4305
YLSEVASGDNKQTTVSNSQQAYQEAFEISKK	3452.7	3	5.5645	0.4689
YLSFHFK	942.1	2	2.5282	0.1462
YLSGIAHFLEK	1278.5	2	3.1448	0.2305
YLSHSEFKDLILPTIQK	2033.4	3	5.2596	0.298
YLSLEQKTEELEGQIK	1909.1	3	4.294	0.2326
YLSLEQKTEELEGQIKKLEADSLEVK	3022.4	3	3.3209	0.1457
YLSNAYAR	958.1	2	2.486	0.1483
YLSQLKDAHR	1231.4	2	3.2075	0.2047
YLSYTLNPDLIR	1468.7	2	3.7373	0.3777
YLTESYGTGQDIDDR	1733.8	2	4.0764	0.4379
YLTESYGTGQDIDDRIVEANPLLEAFGNAK	3301.6	3	6.0855	0.5053
YLTLDIFAGPPNYPFSDEY	2223.4	2	3.3692	0.3535
YLTVAAIFR	1054.3	2	3.3317	0.3282
YLTVAAVFR	1040.2	2	3.2819	0.333
YLTVATVFR	1070.3	2	2.7488	0.2926
YLTVQNTVR	1094.2	2	2.6066	0.2159
YLVAPDGKVVGAWDPTVSVEEVRPQITALVR	3366.9	3	3.4136	0.2127
YLVGACGRARGR	1279.5	2	2.4473	0.1066
YLVPDLVQEYIEKHNLYSSESEDRNAGVILAPLQR	4061.5	3	3.4014	0.2579
YLVVEPPEGDGALCLVCR	1934.3	2	2.5481	0.1518
YLYEIAR	928.1	2	3.1072	0.182
YLYPNIDKDHAFGK	1681.9	2	3.6757	0.4656
YLYRYPGGESYQDLVQR	2108.3	3	3.3313	0.1988
YLYTLVITDKEK	1486.7	2	3.7656	0.3718
YLYTLVITDKEKAEK	1815.1	2	5.1231	0.3148
YLYVDKNFINNPLAQADWAAK	2455.8	3	5.6061	0.446
YMAEALLLR	1080.3	2	3.2261	0.3185
YMAFAHDLMADAQR	1640.9	2	4.2206	0.5208
YMASGPVVAMVWQGLDVVR	2079.5	2	2.76	0.1951
YMDIEFDFKGDPLGGVISNYLLEK	2765.1	3	4.4639	0.2818

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YMDINFDFKGDPIGGHINNYLLEK	2815.2	3	5.2052	0.4141
YMDNDYAK	1020.1	2	2.7729	0.2674
YMEDYHQFHEDVKDAQELLR	2567.8	3	4.6562	0.3674
YMEENDQLKK	1298.4	2	3.2547	0.2675
YMIGVTYGGDDIPLSPYR	2018.3	2	5.9273	0.4603
YMMIVDPAISSSGPAGSYRPYDEGLRR	2990.4	3	3.3832	0.1744
YMNPAIVAPDAFDIIDLSAGGQLTTDQR	2994.3	2	3.8214	0.2833
YMNPAIVAPDAFDIIDLSAGGQLTTDQRR	3150.5	3	3.5029	0.2111
YMNSGPVVAMVWEGLNVVK	2094.5	2	5.5414	0.5219
YMSPMEAQEFGILDK	1760.0	2	3.2505	0.1625
YMSVNQAAQQLLEIVQNQR	2234.5	3	3.8937	0.2146
YMVADKFTELQK	1473.7	2	3.9599	0.4256
YMVSGTNVYGILR	1473.7	2	3.8197	0.3825
YNADEAR	838.8	1	1.8106	0.1395
YNALLAVQK	1020.2	2	2.8129	0.1743
YNAPTSHVTPSVK	1401.5	2	3.2047	0.2958
YNDKHIPGSPFTAK	1575.7	2	3.2689	0.3255
YNEDLELEDAIHTAILTLK	2202.4	2	6.1952	0.5261
YNEEERAQQEAEAAQR	1922.9	2	3.3895	0.2657
YNEETFGYEVPIKEEGDYVLVLK	2736.0	3	5.0842	0.4271
YNEQHVPGSPFTAR	1603.7	2	3.8175	0.3846
YNFPNPNPFVEDDMDKNEIASVAYR	2947.2	3	3.4843	0.3758
YNFPVEVEVPMER	1609.8	2	3.229	0.3799
YNHIDESEMK	1266.4	2	2.8023	0.119
YNHSHDQLVLTGSSDSR	1917.0	2	4.2946	0.3512
YNIEKDIAAHIK	1415.6	3	3.7485	0.2465
YNIEKDIAAHIKK	1543.8	2	3.8238	0.3257
YNIEKDIAAHLK	1415.6	2	4.2416	0.3112
YNIEKDIAAHLKK	1543.8	2	3.5613	0.2996
YNIEKDIAAYIK	1441.7	2	3.6825	0.3129
YNIEKDIAAYIKK	1569.8	3	4.4645	0.2947
YNILGTNAIMDK	1353.6	2	3.433	0.1594
YNILGTNTIMDK	1383.6	2	3.6951	0.2943
YNKWETIEAWTQQVATENPALISR	2850.1	3	4.4188	0.3905
YNLGLDLR	964.1	2	2.9386	0.1562
YNLHQIQGHSAPR	1521.7	3	3.3651	0.166

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YNLPESAPLIYNSFAQFLVK	2315.7	3	4.3708	0.3313
YNNQLATR	980.1	2	2.49	0.1297
YNPTWHCIVGR	1346.5	2	2.6878	0.3026
YNPVGASELRDLYLKTENYLGGEYFAR	3140.5	3	3.6389	0.2113
YNQLLRIEEELGSK	1692.9	2	4.1548	0.3525
YNQLLRIEEELGSKAK	1892.1	2	4.238	0.3392
YNQLMRIEEELGDEAR	1967.2	3	4.0635	0.2452
YNSDKSSTYVK	1292.4	2	3.4028	0.3772
YNVLGAETVLNQMR	1608.8	2	4.9826	0.4726
YNVPFLTFINKLDR	1741.0	2	3.3651	0.3413
YNYLKPR	954.1	2	2.5147	0.1022
YPALHKPENQDIDWGALEGETR	2540.7	3	4.2884	0.3161
YPASTVQILGAEK	1377.6	2	3.7648	0.3637
YPAVSAPK	833.0	1	1.6102	0.1256
YPDQWIVPGGGMEPEEEPGGAAVR	2542.8	2	3.4541	0.2105
YPEDKITPENLPQILLQLK	2253.6	2	2.8712	0.103
YPEEFALRDQEK	1525.6	2	3.6824	0.1526
YPGGESYQDLVQR	1512.6	2	3.1998	0.3012
YPGPQAEGDSEGLSQGLVDR	2076.2	2	5.5541	0.4918
YPGPQAEGDSEGLSQGLVDREK	2333.5	3	5.5422	0.4767
YPGSPGSYAAR	1126.2	2	2.4418	0.1645
YPHIKDGEDLKDHSTESK	2100.2	2	3.9447	0.3377
YPHLGQKPGGSDFLR	1672.9	2	3.2751	0.419
YPIEHGIITNWDDMEK	1962.2	2	4.6891	0.4006
YPIEHGIITNWDDMEKIWHHTFYNELR	3459.8	3	6.0395	0.3231
YPLFEGQETGKK	1397.6	2	3.0433	0.1843
YPMAVGLNK	993.2	2	2.4762	0.143
YPMEHGIITNWDDMEKIWHHTFYNELR	3477.9	3	4.38	0.2482
YPMEHGIVKDWNDMER	2021.3	2	4.3611	0.5231
YPMEHGVVR	1088.3	2	2.9994	0.2073
YPQLLPGIR	1057.3	2	2.7143	0.1843
YPSLSLHGIEGAFSGSGAK	1879.1	3	4.6297	0.3497
YPSPFFVFGEK	1318.5	2	2.4372	0.1616
YPYQSFQTPQHPSFLFQDKR	2515.8	2	4.4253	0.4184
YPYWPHQPIENL	1557.7	2	4.1272	0.2554
YQAAVSK	766.9	1	2.0272	0.1496

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YQASHPNLR	1086.2	2	2.5768	0.2801
YQAVTATLEEK	1253.4	2	3.5441	0.3042
YQDAETLYKEILTR	1743.9	2	3.8335	0.3849
YQDHEDIIIAELDATANELDAFAVHGFPTLK	3458.8	3	7.3586	0.5322
YQDIIHSIHLAR	1466.7	2	2.9372	0.342
YQDLGAYSSAR	1231.3	2	3.1237	0.3126
YQDTHPER	1046.1	2	2.7912	0.1427
YQDTPGVK	908.0	1	1.923	0.1275
YQDVDSETFISTR	1561.6	2	4.8027	0.4764
YQEALAKGDVTAQIALQPALK	2229.6	2	5.5929	0.5139
YQEALHLGSQLLR	1528.7	2	4.0975	0.4816
YQEEFEHFQQELDKK	1999.1	2	4.6566	0.3889
YQEEFEHFQQELDKKKEEFQK	2789.0	3	4.6275	0.3165
YQEIEEDRKKAELEGVAVTAPR	2532.8	3	5.7043	0.4617
YQEQGGEASPQR	1350.4	2	3.5056	0.3266
YQEQGGEASPQSR	1437.5	2	3.6018	0.3517
YQETFNVIER	1299.4	2	3.0406	0.376
YQEVTNNLEFAK	1456.6	2	3.7796	0.2816
YQFVREPEDEEEEEEEEEDEDEDLEELEVLER	4189.1	3	7.9385	0.5508
YQGVNLYVK	1084.2	2	2.6388	0.2197
YQILPLHSQIPR	1465.7	2	3.3	0.2901
YQILPLHSQIPREEQR	2008.3	2	3.6432	0.1644
YQKSTELLIR	1251.5	3	3.2722	0.247
YQLDKDGVVLFK	1425.7	2	4.0002	0.3585
YQLDKDGVVLFKK	1553.8	2	4.6863	0.4097
YQLDPTASISAK	1294.4	2	3.4386	0.2224
YQLEIKIPETYPFNPPK	2078.4	2	3.0345	0.1452
YQLEIKIPETYPFNPPKVR	2333.7	3	3.2321	0.3003
YQLLQLVEPFGVISNHLILNK	2439.9	2	5.4595	0.4053
YQLSIHKNPNTSEPQHLLVMK	2478.9	2	5.1286	0.3887
YQPFKPLSIGGIIILK	1788.2	2	3.1791	0.2296
YQPFKPLSIGGIIILKDTSEDIEELVEPVAAHGPK	3806.4	3	3.9245	0.2933
YQQAGLPLIVLAGK	1471.8	2	3.6956	0.3454
YQQEVDRIKEAVR	1634.8	2	2.9401	0.1954
YQRDYEEMASR	1448.5	2	2.7027	0.1029
YQRPEGL	863.0	2	2.4559	0.1302

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YQSGGGSVSENHMR	1509.6	2	4.0202	0.4457
YQVFFFGTHETAFLGPK	1990.2	2	4.0677	0.4215
YQVLLDGLVLQGLYQLLEPR	2331.7	3	4.0749	0.3371
YQVSWSLDHK	1263.4	2	3.0296	0.334
YQYGGLNSGRPVTPPR	1763.0	2	2.9146	0.2846
YRADTLGELDLER	1551.7	2	3.0857	0.2752
YRADTLGELDLERAPALGGSFAGLEPMGLLWALEPEKPLVR	4454.1	3	4.3617	0.4162
YRDHVTATQLIQK	1573.8	2	3.455	0.2698
YRDILKFPEELEHVESASK	2291.5	3	3.7445	0.1668
YRDLDEDEILGALTEEELR	2280.4	3	4.1588	0.3312
YRDLDEDEILGALTEEELRTLENELDELDPDNALLPAGLR	4570.9	3	4.3407	0.3372
YRDTVLLPQTSFPMK	1797.1	2	3.657	0.3395
YRDVSPFDHSR	1379.5	2	2.9889	0.1499
YREDLMAGIIIAGWDPQEGGQVYSVPMGGMMVR	3629.2	3	3.7844	0.233
YREWHHFLVVNMK	1760.1	3	3.3925	0.3279
YRGEYKDNALLAQLIQDK	2139.4	2	4.2901	0.3187
YRGEYKDNALLAQLIQDKLDAYK	2730.1	3	5.1556	0.3421
YRGFTIPEAFR	1357.5	2	2.8516	0.2787
YRGPGIFEDLQNYILEK	2056.3	3	4.7663	0.2484
YRGQHVTGSPFQFTVGPLGEGGAHK	2628.9	3	5.9208	0.4393
YRGSIHDFPGFDPNQDAEALYTAMK	2845.1	3	6.3946	0.5208
YRGVSFYEVPPHLFAVADTVYR	2587.9	3	4.165	0.3449
YRIPVPILPGLPMNNHGNYIVR	2535.0	3	5.845	0.3935
YRPDLIDMNTVAVQSNLANLEHAFYVAEK	3323.7	3	5.4944	0.3784
YRPEEVDIDAK	1335.4	2	2.4592	0.1653
YRPGTVALR	1033.2	2	2.4211	0.2261
YRPLFDYFLK	1362.6	2	2.6723	0.1132
YRQDDDQRSSHYDELLAAEAR	2539.6	3	4.4906	0.3958
YRQFPQLTR	1209.4	2	2.6567	0.1617
YRSDIHTEAVQAALAK	1774.0	2	4.0322	0.3401
YRVPDVLVADPPIAR	1682.0	3	3.7459	0.3055
YSALFLGVAYGATR	1489.7	2	4.2067	0.454
YSALHAKPNGLILQYGTAGFR	2278.6	3	4.5016	0.2912
YSAQTDITDDSLDR	1600.6	2	2.7615	0.1147
YSDFEWLKNELER	1729.9	2	3.265	0.1541
YSDFEWLKNELERDSK	2060.2	3	3.319	0.1738

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YSDFEWLR	1116.2	2	2.6418	0.2276
YSDFEWLRSELERESK	2075.2	3	3.442	0.1319
YSDFHDLHEK	1291.4	2	3.1503	0.3271
YSDIDIILLKGDVEEDETIPDSEQDIRPR	3375.6	3	4.4075	0.423
YSDIEPSTEGEVIFR	1742.9	2	4.3054	0.3347
YSDMIVAAIQAEK	1439.7	2	4.7585	0.406
YSDMIVAAIQAEKNR	1709.9	2	3.8776	0.4492
YSEKCHDFQCALLANLFASEGQPGK	2758.1	3	3.4517	0.1319
YSEKEDKYEEEIK	1690.8	2	4.443	0.3247
YSEKEDKYEEEIKLLSDK	2247.4	3	5.5842	0.3629
YSEKEDKYEEEIKLLSDKLK	2488.8	3	5.2204	0.3278
YSEKEDKYEEEIKLLSDKLKEAETR	3075.4	3	5.6312	0.3959
YSFHPVEDFPAPEEYKHFQR	2524.7	3	4.1648	0.3416
YSFKGPHLVQSDGTVPFWAHAGNAIPSSDQIR	3484.8	3	4.4497	0.4842
YSFLQFDPAPR	1341.5	2	3.1739	0.317
YSFTFELR	1063.2	2	2.7152	0.2485
YSGAYGASVSDEELK	1576.6	2	5.4153	0.471
YSGAYGASVSDEELKRR	1889.0	2	3.1236	0.1032
YSGKTEYQTTK	1306.4	2	2.7035	0.3405
YSGRPVNLMGTSL	1395.6	2	2.6957	0.2072
YSGTLNLDR	1039.1	2	2.6103	0.3002
YSGYFGGVTALSR	1378.5	2	3.9517	0.3158
YSHDFNFHINYGDLGFLGPEDLR	2727.9	3	5.9175	0.5159
YSHLQPGDHLTDITLK	1839.0	2	3.0593	0.1266
YSHNSLMVQAIK	1391.6	2	2.4539	0.1506
YSHVQEVQER	1275.4	2	2.9718	0.3022
YSHYNERDEIPHNDIALLK	2328.5	3	4.2458	0.2208
YSIAITWGGHHIPK	1580.8	2	3.1308	0.2781
YSIGEPTVPSTLAEEFTYNPFMR	2650.9	2	3.0634	0.3236
YSKEYGK	875.0	1	2.0538	0.1536
YSLDPENPTK	1164.2	2	2.8457	0.2337
YSLEPVAVELK	1248.5	2	2.8805	0.1183
YSLEQDIREKEEAIRQK	2136.4	3	3.358	0.1811
YSLKPNDQILAEDKHKELFDELVKK	3002.4	3	4.2519	0.2775
YSLSGGGTSSH	1053.1	2	2.6775	0.2851
YSLVEAKR	966.1	2	2.5389	0.1748

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YSNENLDLAR	1195.3	2	3.6575	0.3159
YSNFVSFPLYLNGR	1677.9	2	3.3044	0.1348
YSPEFKDPLIDKEYYR	2064.3	3	3.6458	0.2314
YSPTSPTYSPTSPVYTPTSPK	2259.5	2	5.1375	0.4375
YSQFINFPIYVWSSK	1880.1	2	5.4445	0.3825
YSQKEDKYEEEIKILTDK	2260.5	3	6.0212	0.3474
YSQKEDKYEEEIKILTDKLK	2501.8	3	5.5037	0.3277
YSQKEDKYEEEIKILTDKLKEAETR	3088.4	3	6.0357	0.4211
YSQKEDRYEEEIKVLSDKLKEAETR	3088.4	3	4.4354	0.2261
YSQLVVETIR	1208.4	2	3.4066	0.3297
YSQTGNYELAVALSR	1672.8	2	4.5228	0.4484
YSQVLANGLDNK	1322.4	2	4.2043	0.3451
YSQVLANGLDNKLREDLER	2234.5	3	3.8057	0.3062
YSQVLANGLDNKLREDLERLK	2475.8	3	3.3531	0.1383
YSSDVQEMILSSATADRIPIAVSGVR	2767.1	3	3.6109	0.269
YSTDVSVDEVK	1242.3	2	3.4436	0.407
YSTDVSVDEVKALASLMTYK	2221.5	2	5.3575	0.5825
YSVDIPLDK	1050.2	2	2.5305	0.2
YSVDIPLDKTVVNKDVFRDPALK	2634.0	2	3.7971	0.3815
YSVQLLTPANLLAK	1531.8	2	3.9571	0.313
YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHR	4102.6	3	4.3235	0.3049
YTAAVPYR	941.1	2	2.5487	0.2285
YTALDKWTNQLNSLNQAVVSK	2394.7	3	4.807	0.3954
YTCHVQHEGLPEPLTLR	1994.3	3	3.2634	0.1302
YTDATSKYESVMKTEPSIAEYTVR	2771.0	3	4.248	0.179
YTDDWFNSHGTR	1499.5	2	3.9382	0.4549
YTDQGGEEEEDYESEEQLQHR	2572.5	3	3.4881	0.3187
YTEFYHVPTHSDASK	1782.9	2	4.8692	0.503
YTEHKDIPLGIR	1442.6	2	2.9596	0.1293
YTELPYGREDVLK	1583.8	2	3.5179	0.2321
YTELPYGREDVLKEAVANKGPVSVGVDAR	3134.5	3	7.2714	0.5073
YTEQITNEK	1126.2	2	2.7959	0.1939
YTGSHKER	978.0	2	2.6151	0.2611
YTHAANTVVYSSNK	1555.7	2	3.4338	0.3241
YTHAANTVVYSSNKIDDTIR	2269.5	3	3.9983	0.3989
YTHFLTQHYDAKPQGR	1963.1	2	4.7574	0.35

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YTIAALLSPYSYSTTAVVTNPK	2361.7	2	5.4553	0.5318
YTIAALLSPYSYSTTAVVTNPKE	2490.8	2	5.9887	0.5367
YTIENPR	893.0	1	2.0191	0.1702
YTIHSQLEHLQSK	1584.8	2	4.0751	0.3148
YTIIIPENLKPQMK	1689.1	2	3.5504	0.3952
YTISQEAYDQRQDTVR	1974.1	2	3.32	0.1578
YTKEVYVPHPR	1389.6	2	3.6295	0.2704
YTKKVPQVSTPTLVEVSR	2033.4	3	4.1754	0.2018
YTLHYKTDAPLNIR	1705.9	3	3.6616	0.3054
YTLNVLEDLGDGQK	1565.7	2	3.461	0.344
YTLNVLEDLGDGQKANDDIIVNWVNR	2976.2	3	4.9501	0.3778
YTLPLYHAMMGGSEVAQTLAK	2282.7	3	4.1178	0.3085
YTLPPGVDPTQVSSSLSPEGTLTVEAPMPK	3100.5	3	6.4908	0.4969
YTPEQVAMATVTALHR	1789.0	2	4.3251	0.4632
YTPQSPTYTPSSPSYSPSSPSYSPTSPK	2980.1	3	4.8094	0.3234
YTPSGQAGAAASESLFVSNHA	2066.2	2	5.9424	0.5226
YTPSGQAGAAASESLFVSNHAY	2229.3	2	6.2398	0.5443
YTPSQQGVAFNSGAK	1555.7	2	3.9577	0.4205
YTPTQQGNMQVLVTYGGDPIPK	2408.7	2	5.1566	0.4118
YTPTSPSYSPSSPEYTPTSPK	2275.4	2	4.4545	0.4331
YTPVQQGPVGVNVTYGGDPIPK	2287.6	2	5.6191	0.5145
YTQVGPDHNR	1187.2	2	3.0889	0.2888
YTRPGLPTFSQEVLHK	1874.1	3	3.2046	0.1273
YTSIAEVQAQMEEEYLR	2061.3	2	2.7125	0.1906
YTSLMLR	884.1	1	2.0014	0.1592
YTTKHLNDETTSK	1538.6	2	3.8318	0.3003
YTTPEDATPEPGEDPR	1775.8	2	3.4563	0.3018
YTTPEDATPEPGEDPRVTR	2132.2	2	2.903	0.2157
YVAEIEKEKEENEK	1738.9	2	5.2256	0.3318
YVAEIEKEKEENEKKK	1995.2	2	4.3379	0.3277
YVALLKK	835.1	2	2.4826	0.1275
YVAQAHDKPR	1185.3	2	3.3057	0.3907
YVASYLLAALGGNSSPSAK	1870.1	2	5.9531	0.4734
YVASYLLAALGGNSSPSAKDIK	2226.5	2	4.6672	0.3912
YVASYVLEHLY	1357.5	2	3.6455	0.3913
YVATLGVEVHPLVFHTNR	2053.4	2	5.6273	0.5072

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YVAVMPPHIGDQPLTGAYTVTLDGR	2673.0	3	4.4629	0.2789
YVAVMPPHIGDQPLTGAYTVTLDGRGPSR	3070.5	3	3.9845	0.411
YVDEASKK	940.0	2	2.5233	0.2815
YVDEASKKEIKDILIQYDR	2327.6	3	5.8316	0.286
YVDFPITDVLQMMGR	1786.1	2	3.7034	0.3455
YVDLGGSYVGPTQNR	1626.8	2	4.5319	0.5246
YVDMSVK	842.0	1	1.9776	0.1584
YVDSEGHLYTVPIR	1649.8	2	3.691	0.3778
YVDSEGHLYTVPIREQGNIYKPNNK	2936.2	3	4.4397	0.3877
YVDTPFGKPSDALILGK	1822.1	2	4.0347	0.3489
YVDVLNPSGTQR	1349.5	2	2.8552	0.1169
YVDVPKPGMDVADAYVTFVR	2243.6	2	3.6508	0.3926
YVEAAWYPWWEQQGFFKPEYGRPNVSAANPR	3746.1	3	3.8676	0.2277
YVEPIEDVPCGNIVGLVGVDQFLVK	2704.1	3	4.529	0.2932
YVFDTHKR	1066.2	2	2.4116	0.1787
YVFLDPLAGAVTK	1394.6	2	3.5943	0.3184
YVFTDISYSIPHR	1598.8	2	2.9712	0.1775
YVGEKGIDIIIEMLANVNLSKDLSLLSHGGR	3356.9	3	6.4358	0.5163
YVGESEANIR	1138.2	2	3.1132	0.2732
YVGESEANIRK	1266.4	2	2.7463	0.2499
YVGETQPTGQIK	1321.5	2	3.4582	0.2977
YVGGQEHFAHLLILR	1754.0	2	4.1974	0.327
YVGSMVADVHR	1234.4	2	3.3875	0.4621
YVHDRFLVGPYQNTIGAAFVAK	2467.8	3	3.9753	0.1401
YVKELHLQENNIR	1656.9	2	4.0906	0.2466
YVLDDSDGLGREFDGIGAVSGGGATSR	2672.8	3	5.2762	0.3505
YVLEEAEQLEPR	1476.6	2	3.4653	0.2042
YVLENHPGTNSNYQMHLLK	2259.5	2	4.0103	0.3547
YVLENHPGTNSNYQMHLLKK	2387.7	2	4.9725	0.3865
YVLEPEISFTSDNSFAK	1948.1	2	4.9365	0.4207
YVLINWVGEDVPDAR	1746.9	2	4.5641	0.2901
YVNKEIQNAVNGVK	1576.8	3	4.9885	0.3799
YVNMQDPEMDMK	1501.7	2	3.5131	0.2304
YVPGSSGSSNTLPTADPFTGAGR	2240.4	2	4.1207	0.3981
YVPLDQEAYSR	1341.5	2	2.8629	0.3466
YVPVKGDHVIGIVTAK	1697.0	2	3.7356	0.2449

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YVQELPLEADGALR	1574.8	2	3.91	0.2595
YVQKGEYR	1043.2	2	2.5148	0.1681
YVQLPADEVDTQLLQDAAR	2146.3	3	4.9055	0.2518
YVQQVQVSCFNELEVCIHPDGVIPVLTFLR	3448.0	3	4.5155	0.1616
YVRPGGGFEPNFMLFEK	1989.3	2	3.5479	0.2202
YVRPGGGFVPNFQLFEK	1956.2	2	2.9566	0.2013
YVSHGATGK	920.0	1	2.654	0.3099
YVSSLTEEISK	1256.4	2	2.7779	0.1528
YVSSLTEEISKR	1412.6	2	3.3322	0.3607
YVVVTGITPTPLGEGK	1631.9	2	4.793	0.4129
YVWLVYEQDRPLK	1710.0	2	4.3714	0.4544
YVWLVYEQDRPLKCDEPILSNR	2738.1	3	4.3181	0.4004
YWGVASFLQK	1199.4	2	3.4436	0.2471
YWKEHHFEGIALVEK	1887.1	2	2.4814	0.1816
YWQQVIDMNDYQR	1759.9	2	4.4294	0.3327
YYAFPQMITPLVTKG	1730.1	2	3.5718	0.4451
YYALCGFGGVLSCGLTHTAVVPLDLVK	2798.3	3	4.6698	0.2645
YYASEIAGQTTSK	1419.5	2	4.5548	0.4948
YYDAKTEDKVR	1388.5	2	2.7906	0.2024
YYDDTYPSVKEQK	1636.7	2	3.9798	0.3261
YYDEIINALEEDPAAQKMQLAFR	2730.0	3	3.3605	0.1694
YYDSRPGGYGYGYGR	1731.8	2	2.8518	0.4367
YYGGAEVVDEIELLCQR	1958.2	2	4.7542	0.3837
YYGGGSEGGRAPK	1299.4	2	3.0407	0.2092
YYGLQILENVIK	1453.7	2	3.2882	0.2536
YYKNIGLGFK	1203.4	2	2.4092	0.1312
YYKNIGLGFKTPK	1529.8	3	4.03	0.3292
YYKVDENGKISR	1472.6	2	3.4302	0.3004
YYKVEPLDFGGTQK	1645.8	2	4.3476	0.2365
YYLAPKIEDEEGS	1514.6	2	3.034	0.3358
YYLDSLDRIGAADYQPTEQDILR	2716.9	3	6.2249	0.2214
YYLNDLDRVADPAYLPTQQDVLR	2740.0	3	5.351	0.2764
YYMDLKENQR	1360.5	2	2.4527	0.1785
YYPTEDVPR	1140.2	1	2.0427	0.2977
YYQTIGNHASYYK	1608.7	2	4.3391	0.3895
YYRESADPLGAWLQDAR	2012.2	3	4.2852	0.1733

Peptide Sequence	Peptide mass (*m/z*)	Charge State	Xcorr	DelCn2
YYTEFPTVLDITAEDPSK	2090.3	2	2.4658	0.1783
YYTVFDRDNNR	1463.5	2	2.4354	0.1013
YYTVFDRDNNRVGFAEAAR	2265.4	3	3.2337	0.1709
YYVTIIDAPGHR	1405.6	2	3.5667	0.1425
YYVTIIDAPGHRDFIK	1909.2	2	5.006	0.3987