

Mascot Search Results

Peptide View

MS/MS Fragmentation of **YSSMPDISGLSMSAR**

Found in **AT5G03280.1**, | Symbols: EIN2, PIR2, CKR1, ERA3, ORE3, ORE2 | EIN2 (ETHYLENE INSENSITIVE 2); transporter | chr5:788588-793065 FORWARD

Match to Query 9: 1680.695404 from(841.354978,2+)

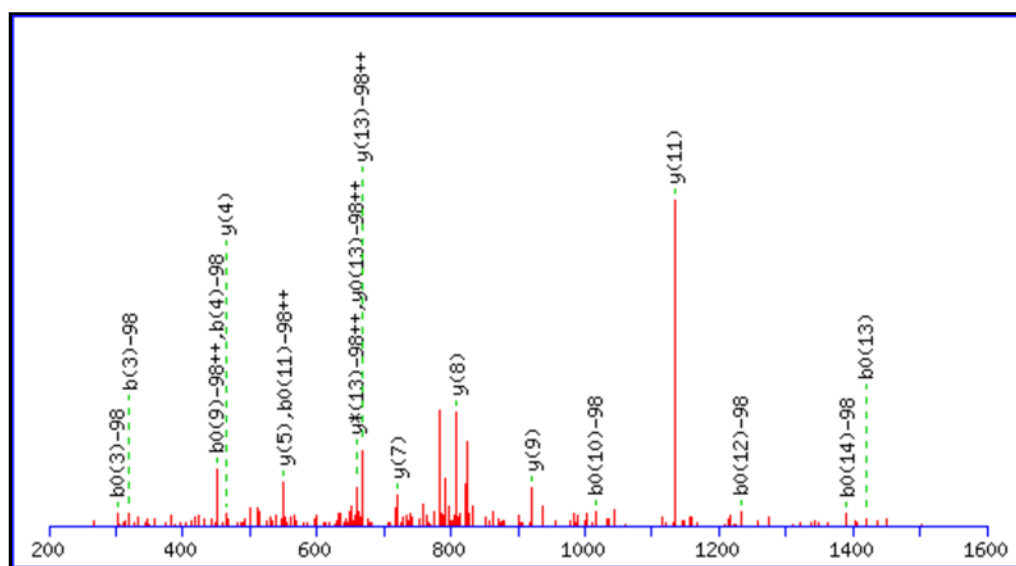
Title: PR4acn_grad.4816.4816.2.dta

Data file C:\Users\CooperB\Desktop\Ray\mgfs\MS2special.txt

Click mouse within plot area to zoom in by factor of two about that point

Or, 200 to 1600 Da

Label all possible matches ☐ Label matches used for scoring ☒



Monoisotopic mass of neutral peptide Mr(calc): 1680.6888

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

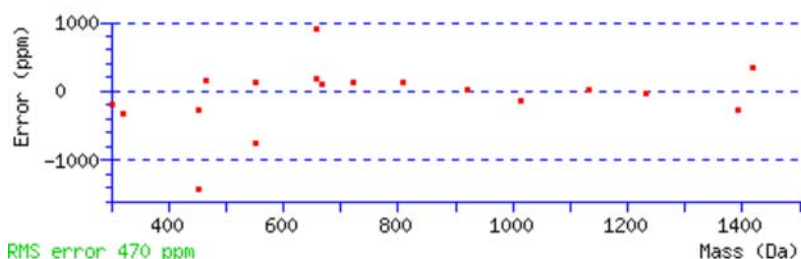
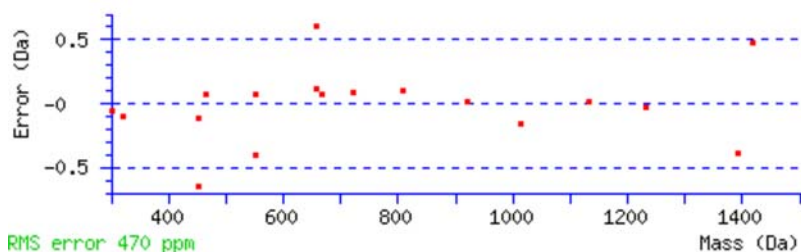
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 30 Expect: 0.026

Matches : 18/194 fragment ions using 25 most intense peaks ([help](#))

| # | b | b ⁺⁺ | b ⁰ | b ⁰⁺⁺ | Seq. | y | y ⁺⁺ | y* | y ^{*++} | y ⁰ | y ⁰⁺⁺ | # |
|----|-----------|-----------------|----------------|------------------|------|-----------|-----------------|-----------|------------------|----------------|------------------|----|
| 1 | 164.0706 | 82.5389 | | | Y | | | | | | | 15 |
| 2 | 251.1026 | 126.0550 | 233.0921 | 117.0497 | S | 1420.6559 | 710.8316 | 1403.6294 | 702.3183 | 1402.6453 | 701.8263 | 14 |
| 3 | 320.1241 | 160.5657 | 302.1135 | 151.5604 | S | 1333.6239 | 667.3156 | 1316.5973 | 658.8023 | 1315.6133 | 658.3103 | 13 |
| 4 | 451.1646 | 226.0859 | 433.1540 | 217.0806 | M | 1264.6024 | 632.8048 | 1247.5759 | 624.2916 | 1246.5919 | 623.7996 | 12 |
| 5 | 548.2173 | 274.6123 | 530.2068 | 265.6070 | P | 1133.5619 | 567.2846 | 1116.5354 | 558.7713 | 1115.5514 | 558.2793 | 11 |
| 6 | 663.2443 | 332.1258 | 645.2337 | 323.1205 | D | 1036.5092 | 518.7582 | 1019.4826 | 510.2449 | 1018.4986 | 509.7529 | 10 |
| 7 | 776.3284 | 388.6678 | 758.3178 | 379.6625 | I | 921.4822 | 461.2448 | 904.4557 | 452.7315 | 903.4717 | 452.2395 | 9 |
| 8 | 863.3604 | 432.1838 | 845.3498 | 423.1785 | S | 808.3982 | 404.7027 | 791.3716 | 396.1894 | 790.3876 | 395.6974 | 8 |
| 9 | 920.3818 | 460.6946 | 902.3713 | 451.6893 | G | 721.3661 | 361.1867 | 704.3396 | 352.6734 | 703.3556 | 352.1814 | 7 |
| 10 | 1033.4659 | 517.2366 | 1015.4553 | 508.2313 | L | 664.3447 | 332.6760 | 647.3181 | 324.1627 | 646.3341 | 323.6707 | 6 |

| | | | | | | | | | | | | |
|-----------|-----------|----------|------------------|-----------------|----------|-----------------|----------|----------|----------|----------|----------|----------|
| 11 | 1120.4979 | 560.7526 | 1102.4874 | 551.7473 | S | 551.2606 | 276.1339 | 534.2341 | 267.6207 | 533.2500 | 267.1287 | 5 |
| 12 | 1251.5384 | 626.2728 | 1233.5279 | 617.2676 | M | 464.2286 | 232.6179 | 447.2020 | 224.1047 | 446.2180 | 223.6126 | 4 |
| 13 | 1338.5704 | 669.7889 | 1320.5599 | 660.7836 | S | 333.1881 | 167.0977 | 316.1615 | 158.5844 | 315.1775 | 158.0924 | 3 |
| 14 | 1409.6076 | 705.3074 | 1391.5970 | 696.3021 | A | 246.1561 | 123.5817 | 229.1295 | 115.0684 | | | 2 |
| 15 | | | | | R | 175.1190 | 88.0631 | 158.0924 | 79.5498 | | | 1 |



NCBI **BLAST** search of [YSSMPDISGLSMSAR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

| Score | Mr(calc): | Delta | Sequence |
|-------|-----------|--------|---------------------------------|
| 29.9 | 1680.6888 | 0.0066 | YSSMPDISGLSMSAR |
| 29.7 | 1680.6888 | 0.0066 | YSSMPDISGLSMSAR |
| 5.6 | 1680.6888 | 0.0066 | YSSMPDISGLSMSAR |

neutral loss -98, S3 -18
neutral loss -98, S2 -18
neutral loss -98, S8 -18

MS2: High score 29.9, match probability 97%; +2 charge; b ion found for S3 [-18] but second rank position match is very close in score. Hedged to S3 but likely ambiguous because of close scores.

Mascot: <http://www.matrixscience.com/>