**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 135... | 1 | 33 | R.VNLVELGVYVS[+162.05282]DIR.A | S11(OGlycan / 162.0528) | Hex(1) | 959.8 | 694.7 | 2 | 869.4563 | 869.4671 | -12.36 | | 1737.9054 | 1737.9269 | Specific | 11 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 18.9753 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VNLVELGVYVS[+162]DIR.A z=2,scan#=sample=1 period=1 cycle=1205 experiment=9,scan time=18.9753

m/z errors, search tol=50.0 ppm

Sample S2 R.VNLVELGVYVS[+162.053]DIR.A

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 139... | 1 | 33 | R.VNLVELGVYVS[+162.05282]DIR.A | S11(OGlycan / 162.0528) | Hex(1) | 762.5 | 556.0 | 3 | 579.9755 | 579.9805 | -8.58 | | 1737.9120 | 1737.9269 | Specific | 11 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 19.3134 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VNLVELGVYVS[+162]DIR.A z=3,scan#=sample=1 period=1 cycle=1217 experiment=3,scan time=19.3134

m/z errors, search tol=50.0 ppm

Sample S2 R.VNLVELGVYVS[+162.053]DIR.A

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 135... | 1 | 33 | R.VNLVELGVYVS[+324.10565]DIR.A | S11(OGlycan / 324.1056) | Hex(2) | 1004.1 | 667.8 | 2 | 950.4798 | 950.4935 | -14.42 | | 1899.9523 | 1899.9797 | Specific | 11 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 18.8978 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VNLVELGVYVS[+324]DIR.A z=2,scan#=sample=1 period=1 cycle=1202 experiment=9,scan time=18.8978

m/z errors, search tol=50.0 ppm

Sample S1 R.VNLVELGVYVS[+324.106]DIR.A

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 135... | 1 | 33 | R.VNLVELGVYVS[+324.10565]DIR.A | S11(OGlycan / 324.1056) | Hex(2) | 864.6 | 617.5 | 3 | 633.9901 | 633.9981 | -12.57 | | 1899.9558 | 1899.9797 | Specific | 11 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 18.9186 | sample=1 perioc |

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

R.VNLVELGVYVS[+324]DIR.A z=3,scan#=sample=1 period=1 cycle=1203 experiment=4,scan time=18.9186

m/z errors, search tol=50.0 ppm

x:510.6436
y:0.004706

Sample S1 R.VNLVELGVYVS[+324.106]DIR.A

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 132... | 1 | 33 | R.VNLVELGVYYVS[+486.15847]DIR.A | S11(OGlycan / 486.1585) | Hex(3) | 946.0 | 617.4 | 2 | 1031.5021 | 1031.5199 | -17.28 | | 2061.9969 | 2062.0325 | Specific | 11 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 18.5571 | sample=1 perioc |

**Proteins**

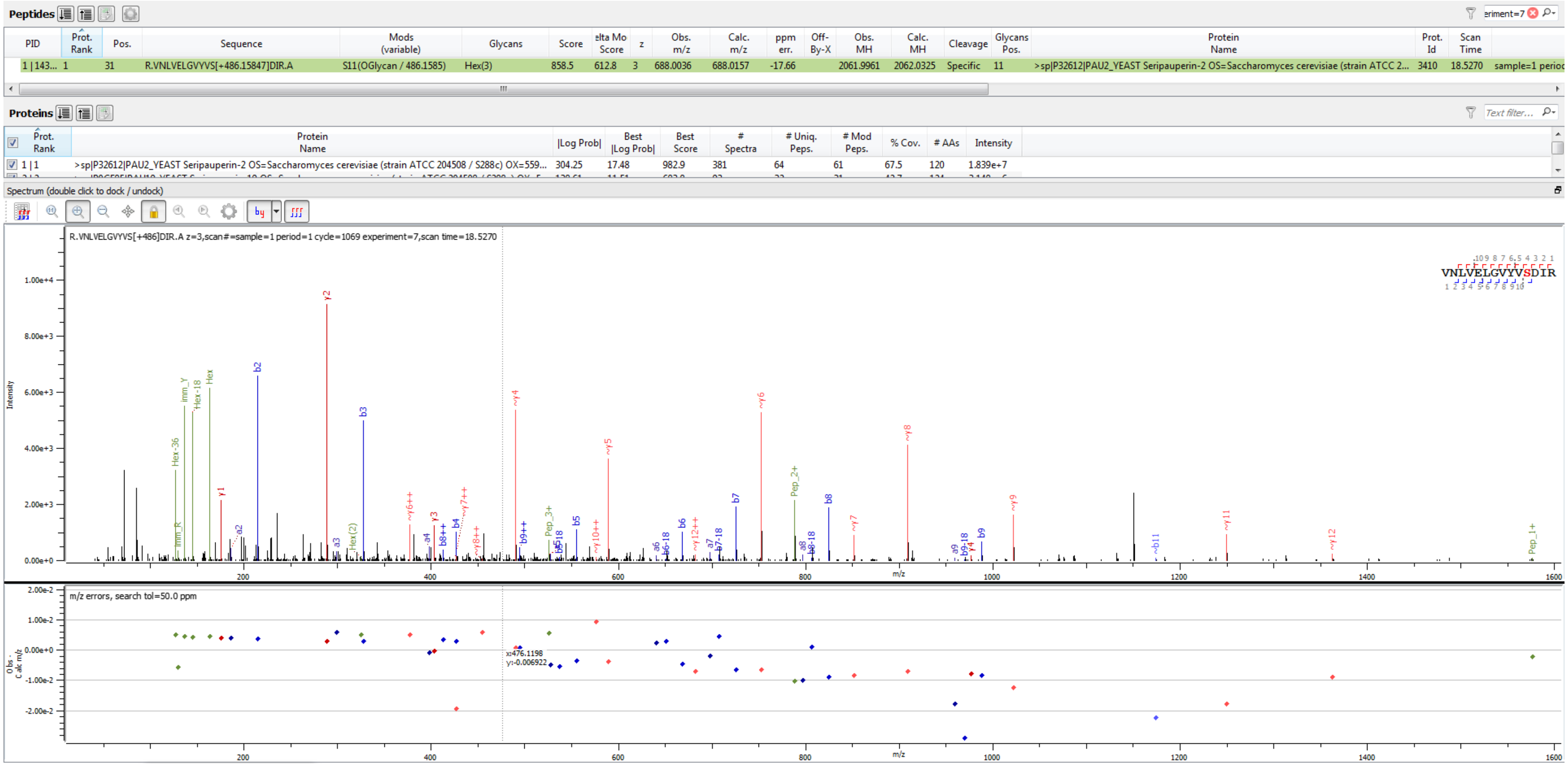
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VNLVELGVYYVS[+486]DIR.A z=2,scan#=sample=1 period=1 cycle=1190 experiment=17,scan time=18.5571

m/z errors, search tol=50.0 ppm

Sample S1 R.VNLVELGVYYVS[+486.158]DIR.A



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 143... | 1 | 31 | R.VNLVELGVYVS[+486.15847]DIR.A | S11(OGlycan / 486.1585) | Hex(3) | 858.5 | 612.8 | 3 | 688.0036 | 688.0157 | -17.66 | | 2061.9961 | 2062.0325 | Specific | 11 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 18.5270 | sample=1 perioc |

eriment=7

**Proteins**

Text filter...

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |

Spectrum (double click to dock / undock)

R.VNLVELGVYVS[+486]DIR.A z=3,scan#=sample=1 period=1 cycle=1069 experiment=7,scan time=18.5270

m/z errors, search tol=50.0 ppm

Sample S4 R.VNLVELGVYVS[+486.158]DIR.A

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 220... | 1 | 33 | R.VNLVELGVYVS[+648.21129]DIR.A | S11(OGlycan / 648.2113) | Hex(4) | 884.9 | 566.0 | 2 | 1112.5286 | 1112.5463 | -15.90 | | 2224.0500 | 2224.0853 | Specific | 11 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 18.5004 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VNLVELGVYVS[+648]DIR.A z=2,scan#=sample=1 period=1 cycle=1188 experiment=19,scan time=18.5004

m/z errors, search tol=50.0 ppm

Sample S1 R.VNLVELGVYVS[+648.211]DIR.A

**Peptides**

eriment=8

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 220... | 1 | 33 | R.VNLVELGVYVS[+648.21129]DIR.A | S11(OGlycan / 648.2113) | Hex(4) | 800.6 | 546.8 | 3 | 742.0241 | 742.0333 | -12.37 | | 2224.0578 | 2224.0853 | Specific | 11 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 18.5210 | sample=1 perioc |

**Proteins**

Text filter...

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VNLVELGVYVS[+648]DIR.A z=3,scan#=sample=1 period=1 cycle=1189 experiment=8,scan time=18.5210

m/z errors, search tol=50.0 ppm

Sample S1 R.VNLVELGVYVS[+648.211]DIR.A

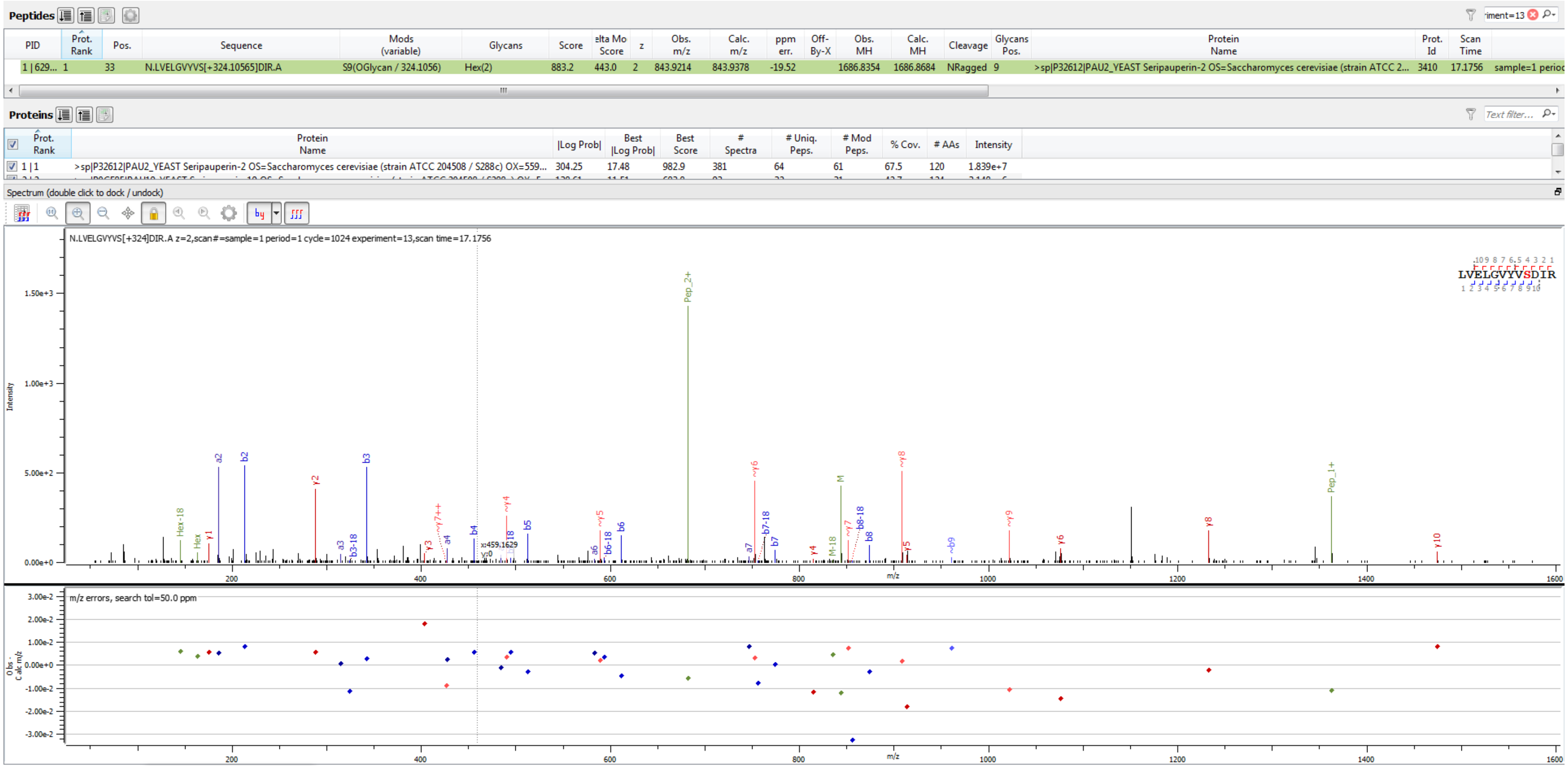
| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 210... | 1 | 29 | D.ERVNLVELGVYVS[+324.10565]DIR.A | S13(OGlycan / 324.1056) | Hex(2) | 902.7 | 670.1 | 3 | 729.0343 | 729.0460 | -16.03 | | 2185.0884 | 2185.1234 | NRagged | 13 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3461 | 17.8142 | sample=1 perioc |

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 248.32 | 15.68 | 955.8 | 342 | 58 | 55 | 67.5 | 120 | 1.797e+7 |

D.ERVNLVELGVYVS[+324]DIR.A z=3,scan#=sample=1 period=1 cycle=1061 experiment=10,scan time=17.8142

m/z errors, search tol=50.0 ppm

Sample S3 D.ERVNLVELGVYVS[+324.106]DIR.A



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 629... | 1 | 33 | N.LVELGVYVS[+324.10565]DIR.A | S9(OGlycan / 324.1056) | Hex(2) | 883.2 | 443.0 | 2 | 843.9214 | 843.9378 | -19.52 | | 1686.8354 | 1686.8684 | NRagged | 9 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 17.1756 | sample=1 perio |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |

N.LVELGVYVS[+324]DIR.A z=2,scan#=sample=1 period=1 cycle=1024 experiment=13,scan time=17.1756

m/z errors, search tol=50.0 ppm

Sample S4 N.LVELGVYVS[+324.106]DIR.A

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 132... | 1 | 33 | N.LVELGVYVS[+324.10565]DIR.A | S9(OGlycan / 324.1056) | Hex(2) | 617.3 | 348.6 | 3 | 562.9518 | 562.9610 | -16.28 | | 1686.8409 | 1686.8684 | NRagged | 9 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3461 | 17.2094 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 248.32 | 15.68 | 955.8 | 342 | 58 | 55 | 67.5 | 120 | 1.797e+7 |

Spectrum (double click to dock / undock)

N.LVELGVYVS[+324]DIR.A z=3,scan#=sample=1 period=1 cycle=1041 experiment=7,scan time=17.2094

m/z errors, search tol=50.0 ppm

Sample S3 N.LVELGVYVS[+324.106]DIR.A

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 113... | 1 | 93 | R.VITGVPWYSS[+324.10565]R.L | S10(OGlycan / 324.1056) | Hex(2) | 709.1 | 0.0 | 2 | 794.8781 | 794.8907 | -15.85 | | 1588.7489 | 1588.7741 | Specific | 10 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 15.1825 | sample=1 perioc |

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

R.VITGVPWYSS[+324]R.L z=2,scan#=sample=1 period=1 cycle=1074 experiment=10,scan time=15.1825

m/z errors, search tol=50.0 ppm

Sample S1 R.VITGVPWYS[+324.106]SR.L

Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 110... | 1 | 93 | R.VITGVPWYS[+324.10565]SR.L | S9(OGlycan / 324.1056) | Hex(2) | 614.4 | 0.0 | 3 | 530.2560 | 530.2629 | -13.04 | | 1588.7534 | 1588.7741 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.8885 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+324]SR.L z=3,scan#=sample=1 period=1 cycle=1064 experiment=4,scan time=14.8885

m/z errors, search tol=50.0 ppm

Sample S1 R.VITGVPWYS[+324.106]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 110... | 1 | 93 | R.VITGVPWYS[+486.15847]SR.L | S9(OGlycan / 486.1585) | Hex(3) | 747.1 | 11.2 | 2 | 875.9020 | 875.9171 | -17.27 | | 1750.7967 | 1750.8269 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.8687 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+486]SR.L z=2,scan#=sample=1 period=1 cycle=1063 experiment=15,scan time=14.8687

Sample S1 R.VITGVPWYS[+486.158]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 111... | 1 | 93 | R.VITGVPWYSS[+486.15847]R.L | S10(OGlycan / 486.1585) | Hex(3) | 686.5 | 0.0 | 3 | 584.2703 | 584.2805 | -17.50 | | 1750.7963 | 1750.8269 | Specific | 10 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 15.0018 | sample=1 perioc |

**Proteins**

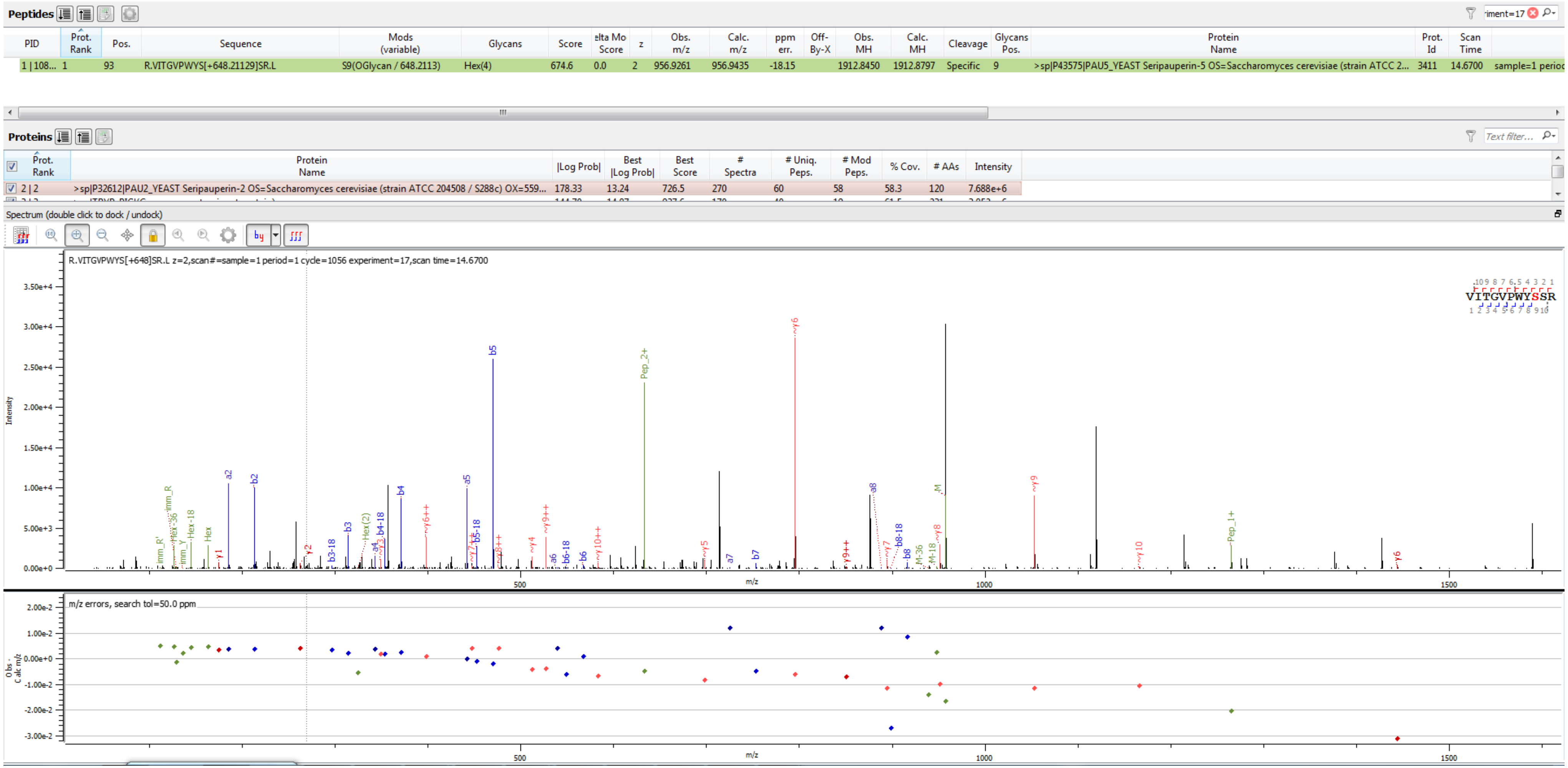
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYSS[+486]R.L z=3,scan#=sample=1 period=1 cycle=1068 experiment=2,scan time=15.0018

m/z errors, search tol=50.0 ppm

Sample S1 R.VITGVPWYS[+486.158]SR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 108... | 1 | 93 | R.VITGVPWYS[+648.21129]SR.L | S9(OGlycan / 648.2113) | Hex(4) | 674.6 | 0.0 | 2 | 956.9261 | 956.9435 | -18.15 | | 1912.8450 | 1912.8797 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.6700 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+648]SR.L z=2,scan#=sample=1 period=1 cycle=1056 experiment=17,scan time=14.6700

m/z errors, search tol=50.0 ppm

Sample S1 R.VITGVPWYS[+648.211]SR.L

**Peptides**

eriment=4

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 109... | 1 | 93 | R.VITGVPWYS[+648.21129]SR.L | S9(OGlycan / 648.2113) | Hex(4) | 683.1 | 0.0 | 3 | 638.2872 | 638.2981 | -17.16 | | 1912.8469 | 1912.8797 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.7448 | sample=1 perioc |

**Proteins**

Text filter...

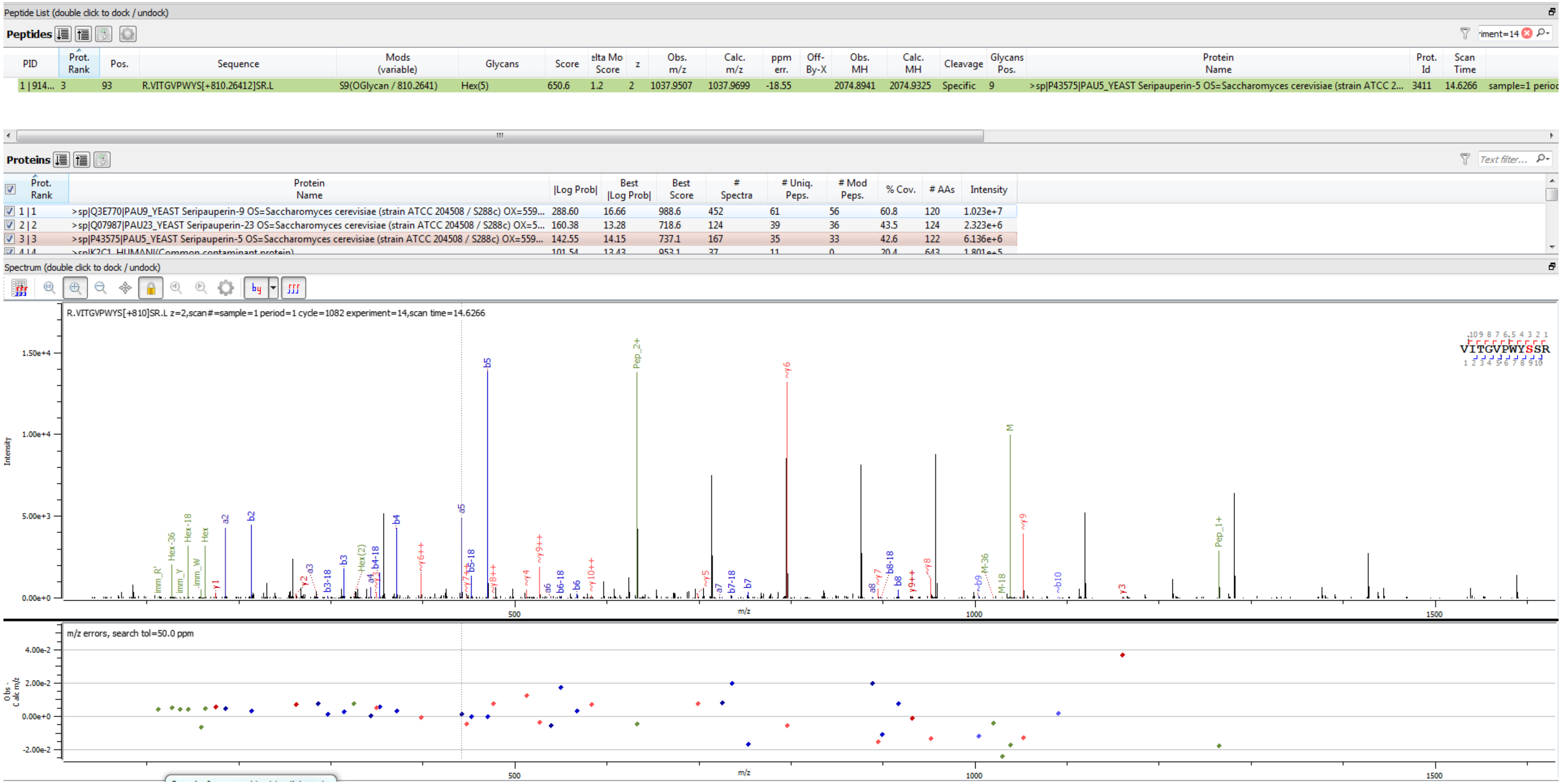
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+648]SR.L z=3,scan#=sample=1 period=1 cycle=1059 experiment=4,scan time=14.7448

m/z errors, search tol=50.0 ppm

Sample S1 R.VITGVPWYS[+648.211]SR.L



Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 914... | 3 | 93 | R.VITGVPWYS[+810.26412]SR.L | S9(OGlycan / 810.2641) | Hex(5) | 650.6 | 1.2 | 2 | 1037.9507 | 1037.9699 | -18.55 | | 2074.8941 | 2074.9325 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.6266 | sample=1 period |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ | 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |
| ☑ | 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 101.54 | 13.43 | 953.1 | 37 | 11 | 0 | 20.4 | 643 | 1.801e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+810]SR.L z=2,scan#=sample=1 period=1 cycle=1082 experiment=14,scan time=14.6266

Sample S6 R.VITGVPWYS[+810.264]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 107... | 1 | 93 | R.VITGVPWYS[+810.26412]SR.L | S9(OGlycan / 810.2641) | Hex(5) | 725.4 | 1.2 | 3 | 692.3033 | 692.3157 | -17.91 | | 2074.8954 | 2074.9325 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.5472 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+810]SR.L z=3,scan#=sample=1 period=1 cycle=1052 experiment=6,scan time=14.5472

m/z errors, search tol=50.0 ppm

Sample S1 R.VITGVPWYS[+810.264]SR.L

Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 130... | 3 | 93 | R.VITGVPWYS[+972.31694]SR.L | S9(OGlycan / 972.3169) | Hex(6) | 654.1 | 1.2 | 2 | 1118.9854 | 1118.9963 | -9.79 | | 2236.9635 | 2236.9854 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.3331 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|TRYP_PIG\|(Common contaminant protein) | 201.90 | 15.17 | 1032.1 | 433 | 52 | 23 | 59.3 | 231 | 4.729e+6 |
| ☑ | 2 \| 2 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 164.15 | 12.91 | 1037.3 | 98 | 28 | 4 | 35.8 | 643 | 4.850e+5 |
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |
| ☑ | 4 \| 4 | >sp\|K1C9_HUMAN\|(Common contaminant protein) | 66.04 | 18.99 | 1150.7 | 49 | 14 | 3 | 24.9 | 623 | 1.617e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+972]SR.L z=2,scan#=sample=1 period=1 cycle=1059 experiment=16,scan time=14.3331

m/z errors, search tol=50.0 ppm

Sample S2 R.VITGVPWYS[+972.317]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 180... | 1 | 93 | R.VITGVPWYS[+972.31694]SR.L | S9(OGlycan / 972.3169) | Hex(6) | 712.2 | 1.2 | 3 | 746.3205 | 746.3333 | -17.15 | | 2236.9470 | 2236.9854 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.2101 | sample=1 perioc |

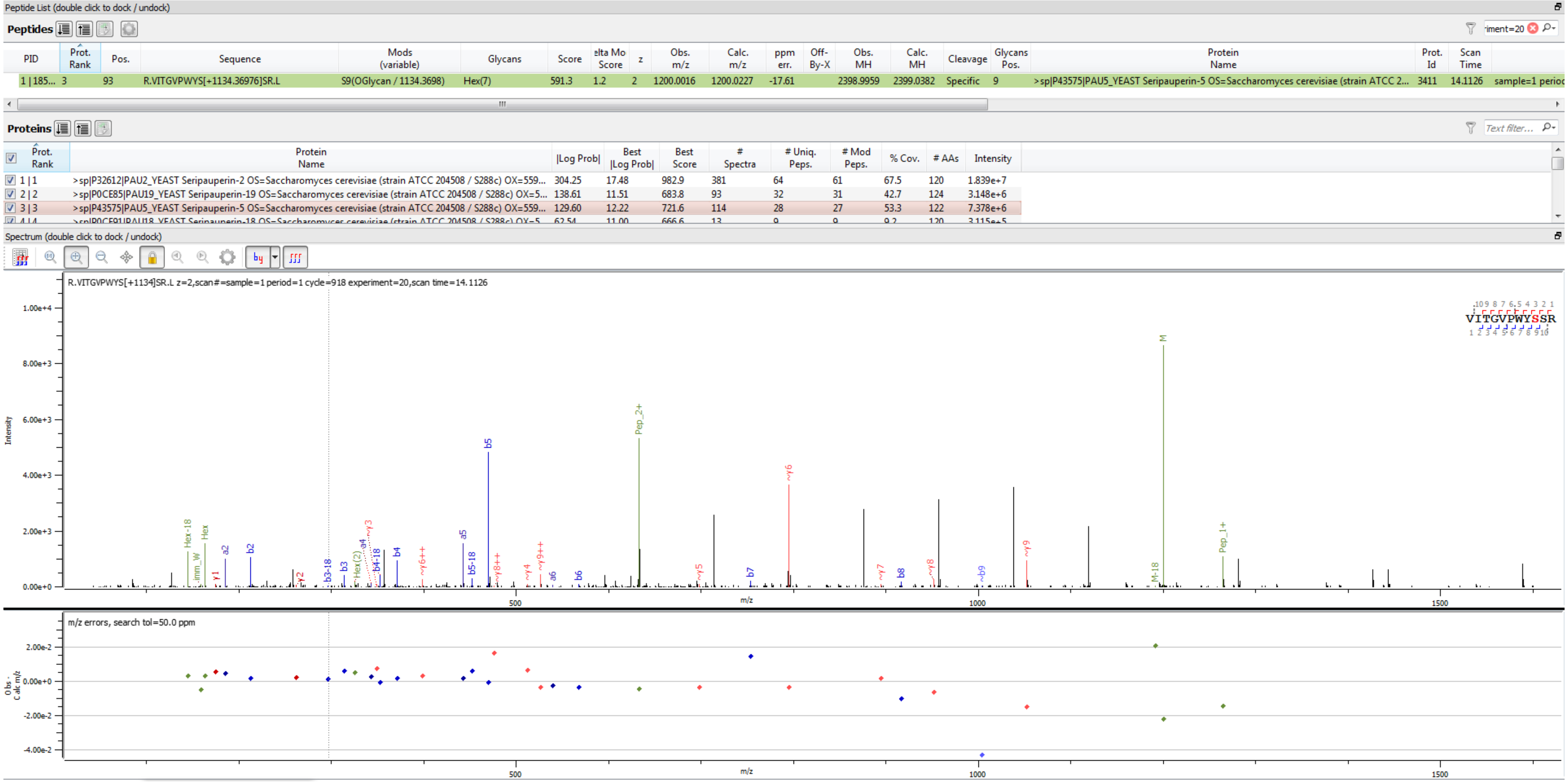
**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+972]SR.L z=3,scan#=sample=1 period=1 cycle=1040 experiment=11,scan time=14.2101

Sample S1 R.VITGVPWYS[+972.317]SR.L



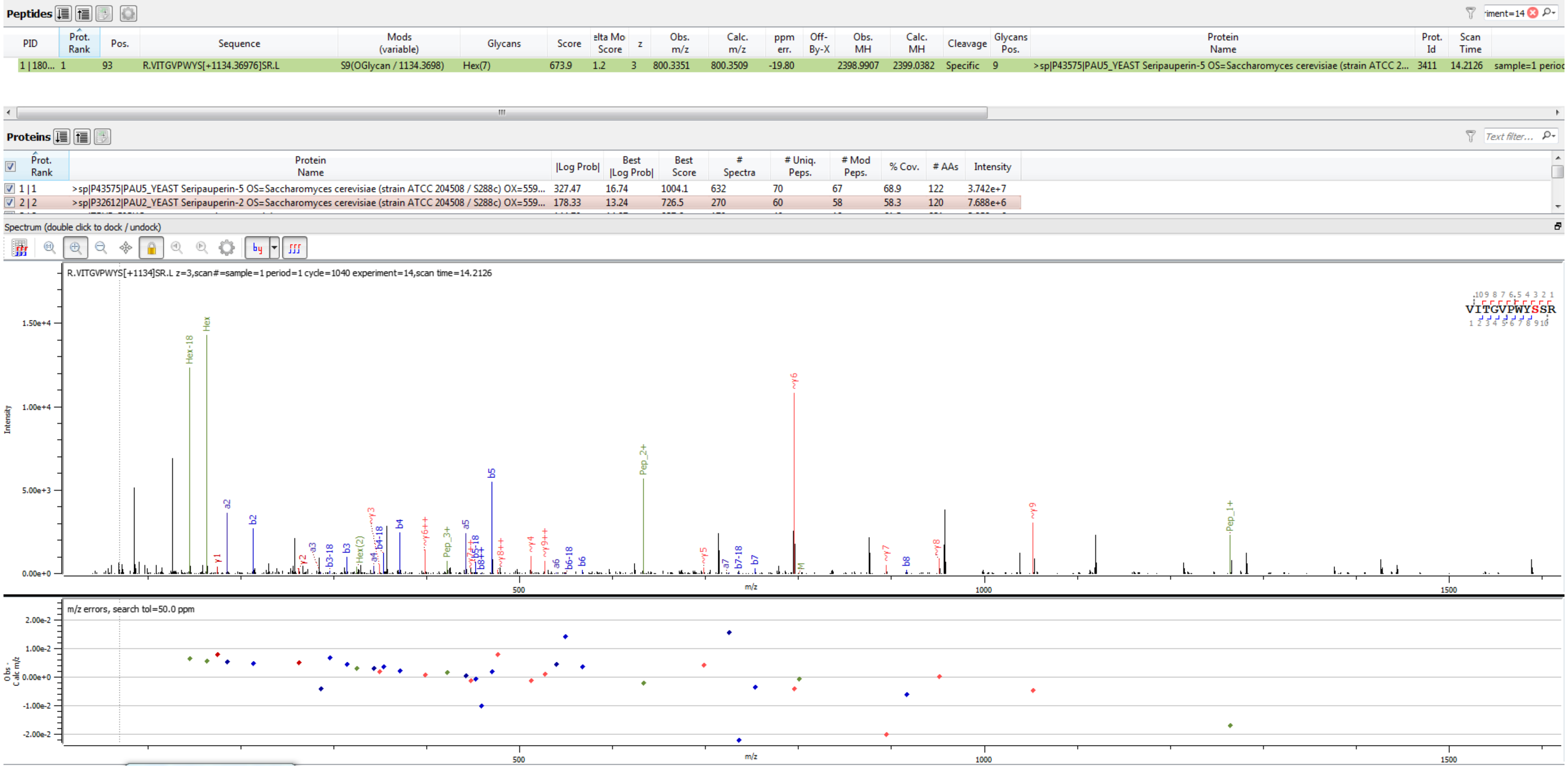
| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 185... | 3 | 93 | R.VITGVPWYS[+1134.36976]SR.L | S9(OGlycan / 1134.3698) | Hex(7) | 591.3 | 1.2 | 2 | 1200.0016 | 1200.0227 | -17.61 | | 2398.9959 | 2399.0382 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.1126 | sample=1 perioc |

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ | 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ | 4 \| 4 | >sp\|P0CF91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

R.VITGVPWYS[+1134]SR.L z=2,scan#=sample=1 period=1 cycle=918 experiment=20,scan time=14.1126

m/z errors, search tol=50.0 ppm

Sample S4 R.VITGVPWYS[+1134.370]SR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 180... | 1 | 93 | R.VITGVPWYS[+1134.36976]SR.L | S9(OGlycan / 1134.3698) | Hex(7) | 673.9 | 1.2 | 3 | 800.3351 | 800.3509 | -19.80 | | 2398.9907 | 2399.0382 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.2126 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+1134]SR.L z=3,scan#=sample=1 period=1 cycle=1040 experiment=14,scan time=14.2126

m/z errors, search tol=50.0 ppm

Sample S1 R.VITGVPWYS[+1134.370]SR.L

Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 179... | 1 | 93 | R.VITGVPWYS[+1296.42259]SR.L | S9(OGlycan / 1296.4226) | Hex(8) | 682.9 | 1.2 | 3 | 854.3515 | 854.3685 | -19.95 | | 2561.0399 | 2561.0910 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.0721 | sample=1 perio |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ | 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+1296]SR.L z=3,scan#=sample=1 period=1 cycle=1035 experiment=18,scan time=14.0721

m/z errors, search tol=50.0 ppm

Sample S1 R.VITGVPWYS[+1296.423]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 178... | 1 | 93 | R.VITGVPWYS[+1458.47541]SR.L | S9(OGlycan / 1458.4754) | Hex(9) | 613.5 | 1.2 | 3 | 908.3717 | 908.3861 | -15.89 | | 2723.1006 | 2723.1438 | Specific | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 13.9516 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ | 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+1458]SR.L z=3,scan#=sample=1 period=1 cycle=1031 experiment=12,scan time=13.9516

m/z errors, search tol=50.0 ppm

Sample S1 R.VITGVPWYS[+1458.475]SR.L

Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 157... | 3 | 93 | R.VITGVPWYSS[+972.31694]RL.K | S10(OGlycan / 972.3169) | Hex(6) | 413.9 | 1.7 | 2 | 1175.5192 | 1175.5384 | -16.33 | | 2350.0310 | 2350.0694 | CRagged | 10 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 15.6784 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |
| ☑ | 4 \| 4 | >sp\|K1C9_HUMAN\|(Common contaminant protein) | 66.04 | 18.99 | 1150.7 | 49 | 14 | 3 | 24.9 | 623 | 1.617e+5 |
| ☑ | 5 \| 5 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 44.94 | 6.66 | 595.2 | 47 | 17 | 17 | 9.7 | 124 | 3.884e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYSS[+972]RL.K z=2,scan#=sample=1 period=1 cycle=1104 experiment=15,scan time=15.6784

m/z errors, search tol=50.0 ppm

Sample S2 R.VITGVPWYSS[+972.317]RL.K

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 157... | 3 | 93 | R.VITGVPWYS[+972.31694]SRL.K | S9(OGlycan / 972.3169) | Hex(6) | 577.7 | 1.2 | 3 | 784.0136 | 784.0280 | -18.33 | | 2350.0264 | 2350.0694 | CRagged | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 15.6986 | sample=1 perioc |

eriment=8

**Proteins**

Text filter...

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |
| ☑ 4 \| 4 | >sp\|K1C9_HUMAN\|(Common contaminant protein) | 66.04 | 18.99 | 1150.7 | 49 | 14 | 3 | 24.9 | 623 | 1.617e+5 |
| ☑ 5 \| 5 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 44.94 | 6.66 | 595.2 | 47 | 17 | 17 | 9.7 | 124 | 3.884e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+972]SRL.K z=3,scan#=sample=1 period=1 cycle=1105 experiment=8,scan time=15.6986

m/z errors, search tol=50.0 ppm

Sample S2 R.VITGVPWYS[+972.317]SRL.K

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 169... | 3 | 93 | R.VITGVPWYS[+1134.36976]SRL.K | S9(OGlycan / 1134.3698) | Hex(7) | 582.9 | 1.2 | 3 | 838.0314 | 838.0456 | -17.01 | | 2512.0795 | 2512.1223 | CRagged | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 15.4899 | sample=1 perioc |

**Proteins**

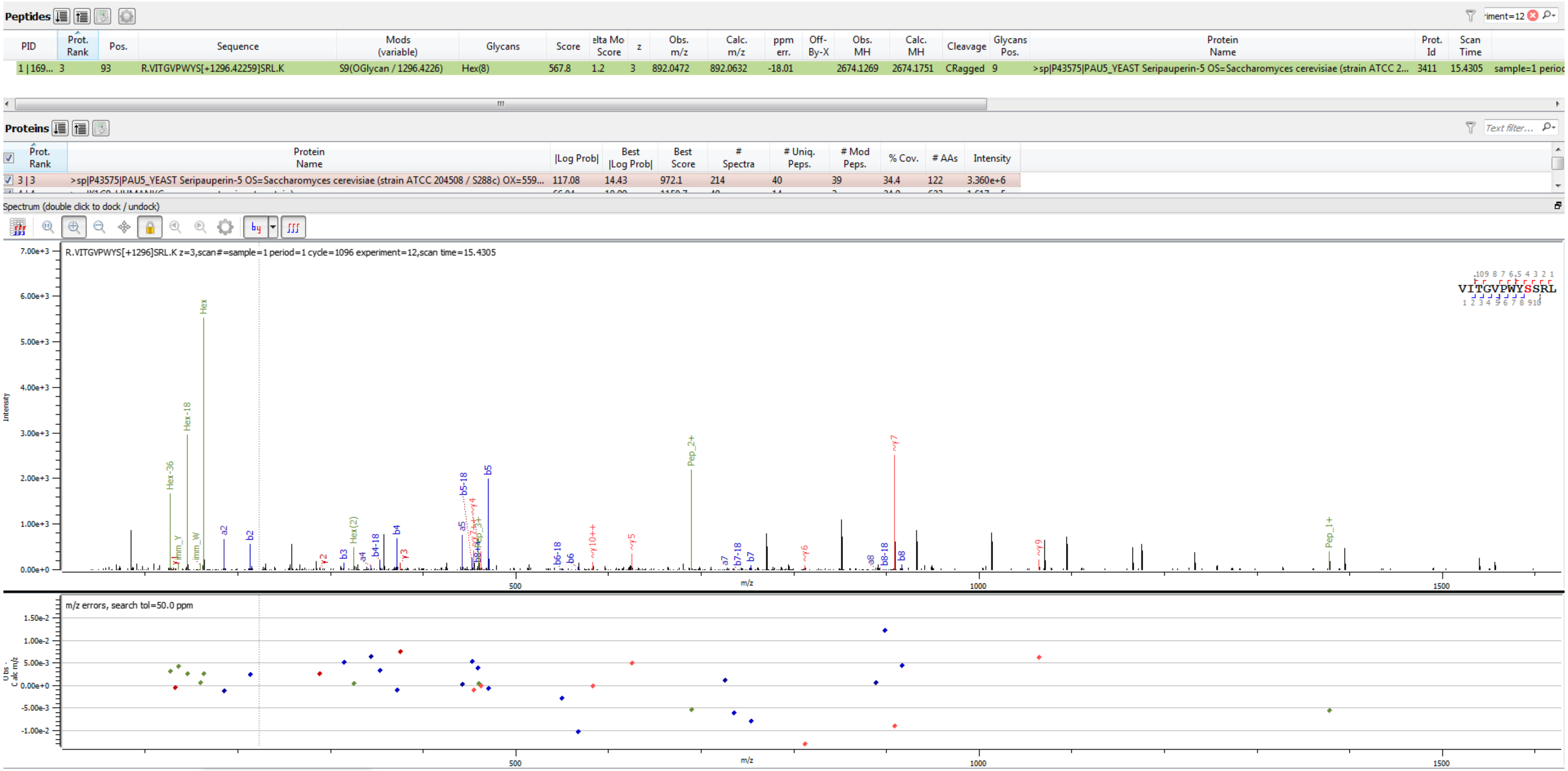
| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+1134]SRL.K z=3,scan#=sample=1 period=1 cycle=1098 experiment=12,scan time=15.4899

m/z errors, search tol=50.0 ppm

Sample S2 R.VITGVPWYS[+1134.370]SRL.K



| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 169... | 3 | 93 | R.VITGVPWYS[+1296.42259]SRL.K | S9(OGlycan / 1296.4226) | Hex(8) | 567.8 | 1.2 | 3 | 892.0472 | 892.0632 | -18.01 | | 2674.1269 | 2674.1751 | CRagged | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 15.4305 | sample=1 perioc |

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

R.VITGVPWYS[+1296]SRL.K z=3,scan#=sample=1 period=1 cycle=1096 experiment=12,scan time=15.4305

Sample S2 R.VITGVPWYS[+1296.423]SRL.K

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 121... | 1 | 91 | R.MITGVPWYSS[+486.15847]R.L | S10(OGlycan / 486.1585) | Hex(3) | 686.1 | 0.0 | 2 | 891.8856 | 891.9031 | -19.62 | | 1782.7640 | 1782.7990 | Specific | 10 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3461 | 15.1760 | sample=1 perioc |

**Proteins**

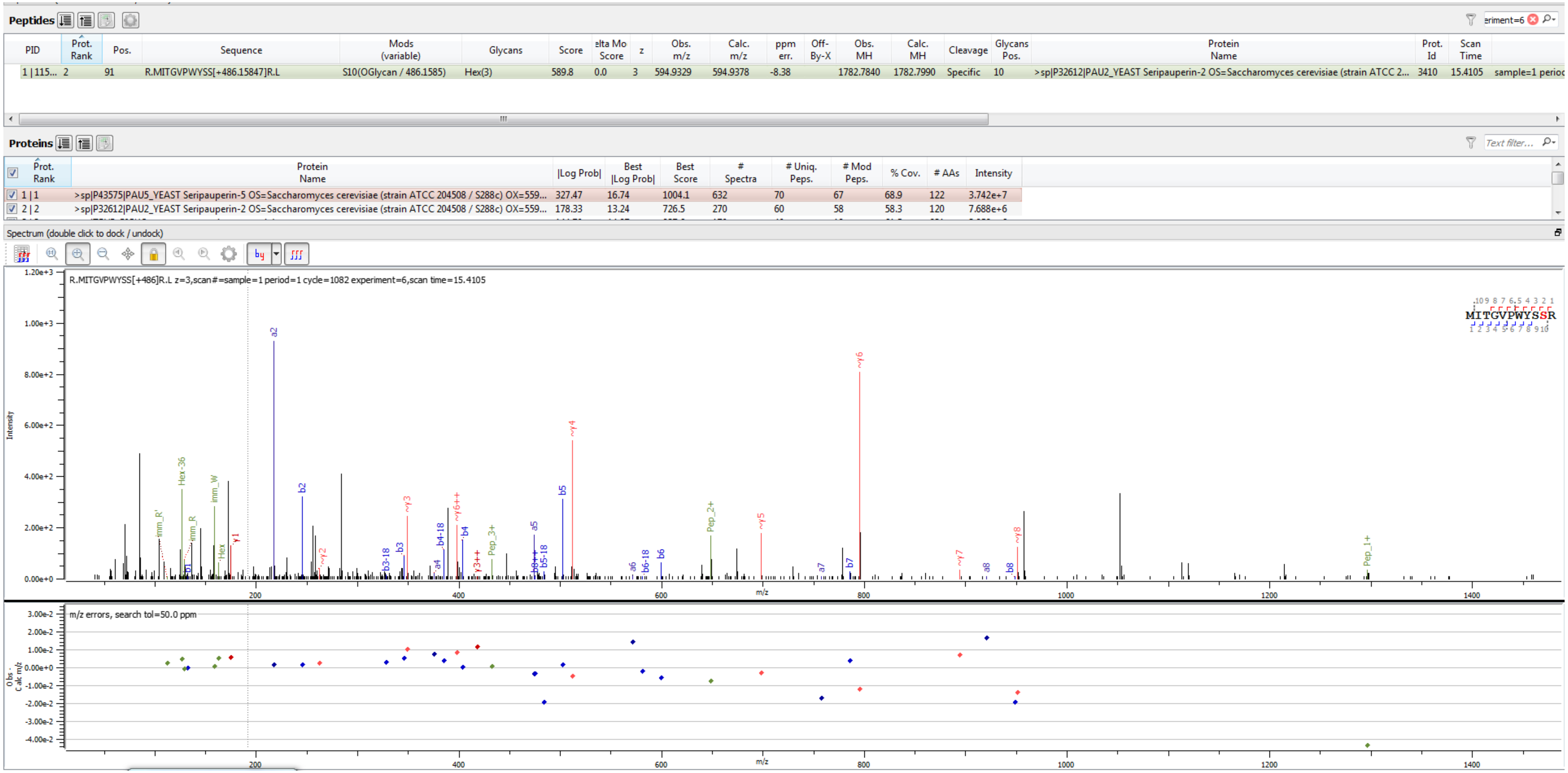
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 248.32 | 15.68 | 955.8 | 342 | 58 | 55 | 67.5 | 120 | 1.797e+7 |

Spectrum (double click to dock / undock)

R.MITGVPWYSS[+486]R.L z=2,scan#=sample=1 period=1 cycle=971 experiment=12,scan time=15.1760

m/z errors, search tol=50.0 ppm

Sample S3 R.MITGVPWYSS[+486.158]R.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 115... | 2 | 91 | R.MITGVPWYSS[+486.15847]R.L | S10(OGlycan / 486.1585) | Hex(3) | 589.8 | 0.0 | 3 | 594.9329 | 594.9378 | -8.38 | | 1782.7840 | 1782.7990 | Specific | 10 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 15.4105 | sample=1 perio |

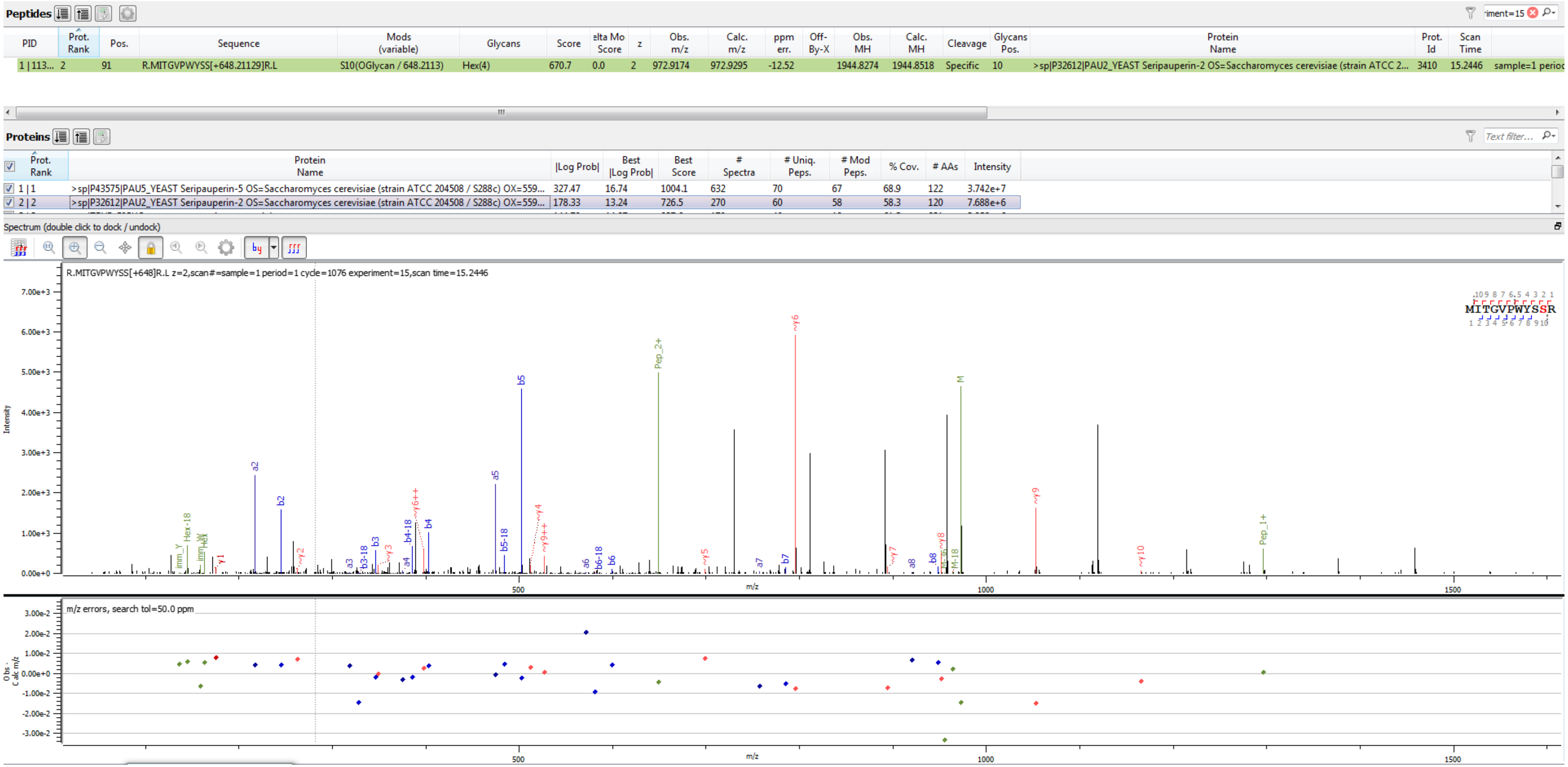
**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.MITGVPWYSS[+486]R.L z=3,scan#=sample=1 period=1 cycle=1082 experiment=6,scan time=15.4105

Sample S1 R.MITGVPWYSS[+486.158]R.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 113... | 2 | 91 | R.MITGVPWYSS[+648.21129]R.L | S10(OGlycan / 648.2113) | Hex(4) | 670.7 | 0.0 | 2 | 972.9174 | 972.9295 | -12.52 | | 1944.8274 | 1944.8518 | Specific | 10 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 15.2446 | sample=1 perio |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.MITGVPWYSS[+648]R.L z=2,scan#=sample=1 period=1 cycle=1076 experiment=15,scan time=15.2446

m/z errors, search tol=50.0 ppm

Sample S1 R.MITGVPWYSS[+648.211]R.L

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 120... | 1 | 91 | R.MITGVPWYSS[+648.21129]R.L | S10(OGlycan / 648.2113) | Hex(4) | 647.1 | 0.0 | 3 | 648.9425 | 648.9554 | -19.95 | | 1944.8130 | 1944.8518 | Specific | 10 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3461 | 15.0832 | sample=1 perioc |

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 248.32 | 15.68 | 955.8 | 342 | 58 | 55 | 67.5 | 120 | 1.797e+7 |

R.MITGVPWYSS[+648]R.L z=3,scan#=sample=1 period=1 cycle=968 experiment=5,scan time=15.0832

Sample S3 R.MITGVPWYSS[+648.211]R.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 187... | 2 | 91 | R.MITGVPWYS[+810.26412]SR.L | S9(OGlycan / 810.2641) | Hex(5) | 658.5 | 1.2 | 2 | 1053.9396 | 1053.9559 | -15.52 | | 2106.8719 | 2106.9046 | Specific | 9 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 15.0441 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ | 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+810]SR.L z=2,scan#=sample=1 period=1 cycle=1069 experiment=18,scan time=15.0441

m/z errors, search tol=50.0 ppm

Sample S1 R.MITGVPWYS[+810.264]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 187... | 2 | 91 | R.MITGVPWYS[+810.26412]SR.L | S9(OGlycan / 810.2641) | Hex(5) | 726.5 | 1.2 | 3 | 702.9597 | 702.9731 | -19.03 | | 2106.8645 | 2106.9046 | Specific | 9 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 15.0671 | sample=1 perioc |

**Proteins**

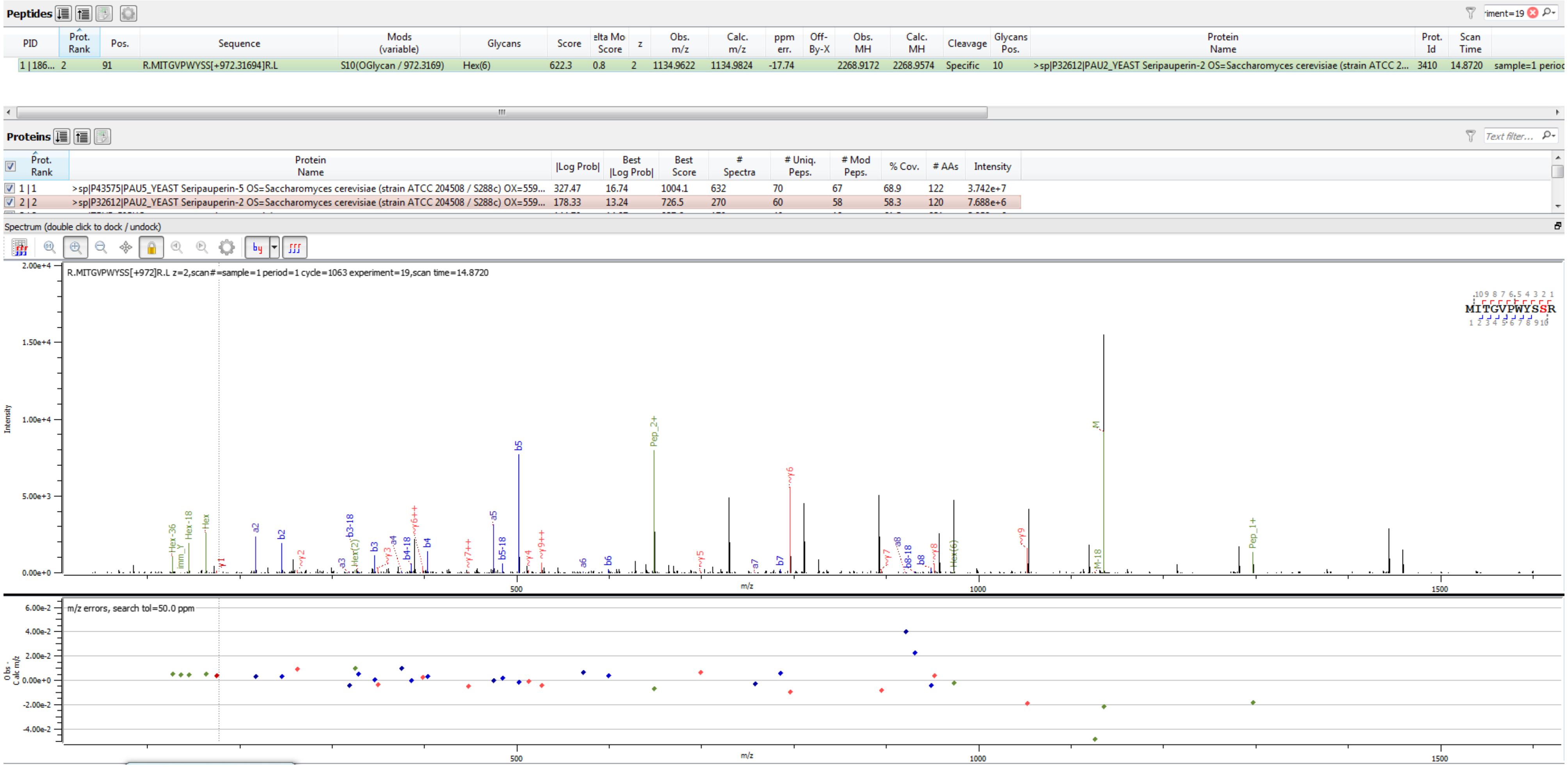
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+810]SR.L z=3,scan#=sample=1 period=1 cycle=1070 experiment=11,scan time=15.0671

m/z errors, search tol=50.0 ppm

Sample S1    R.MITGVPWYS[+810.264]SR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 186... | 2 | 91 | R.MITGVPWYSS[+972.31694]R.L | S10(OGlycan / 972.3169) | Hex(6) | 622.3 | 0.8 | 2 | 1134.9622 | 1134.9824 | -17.74 | | 2268.9172 | 2268.9574 | Specific | 10 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 14.8720 | sample=1 perioc |

**Proteins**

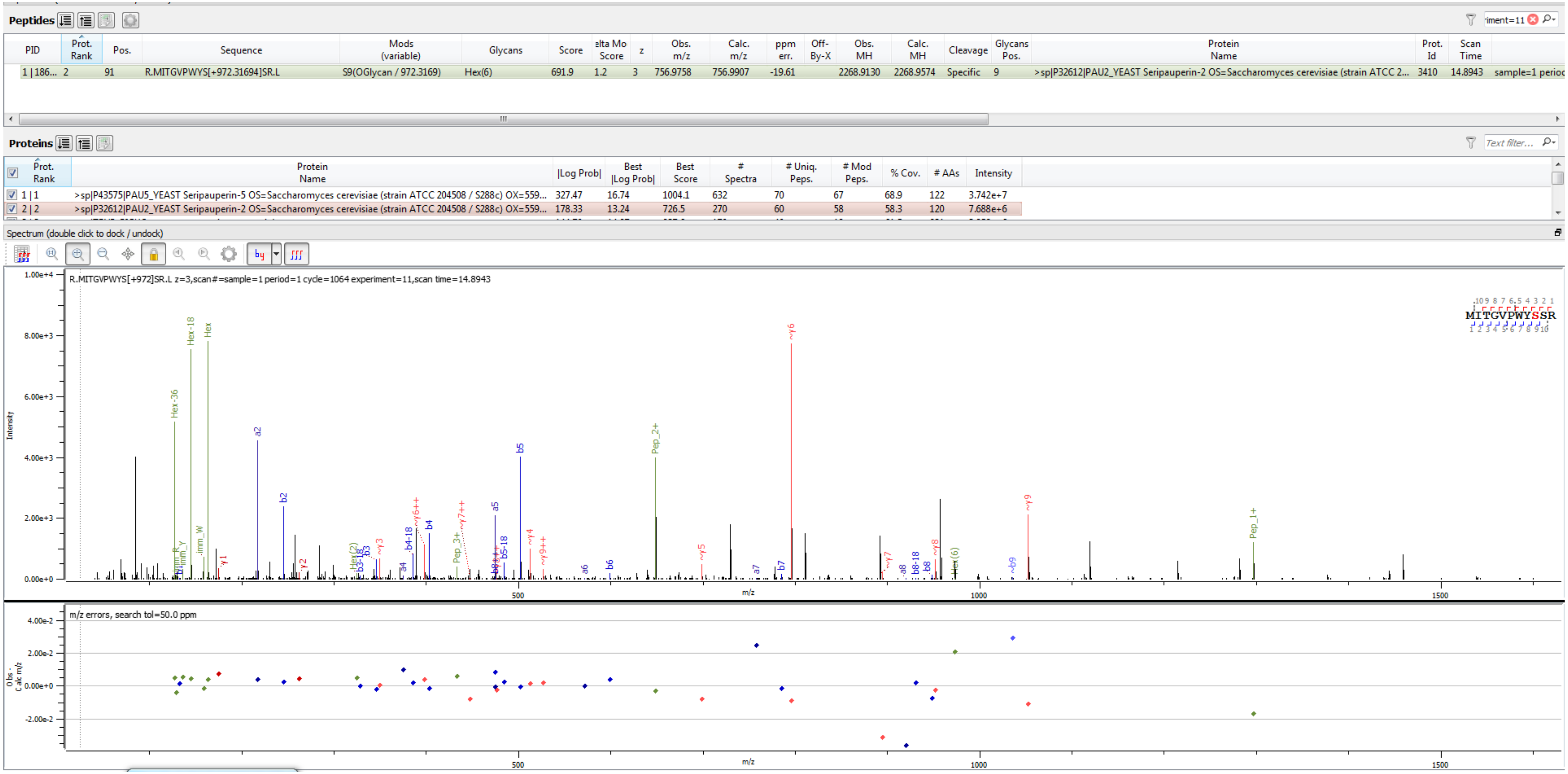
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.MITGVPWYSS[+972]R.L z=2,scan#=sample=1 period=1 cycle=1063 experiment=19,scan time=14.8720

m/z errors, search tol=50.0 ppm

Sample S1 R.MITGVPWYS[+972.317]SR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 186... | 2 | 91 | R.MITGVPWYS[+972.31694]SR.L | S9(OGlycan / 972.3169) | Hex(6) | 691.9 | 1.2 | 3 | 756.9758 | 756.9907 | -19.61 | | 2268.9130 | 2268.9574 | Specific | 9 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 14.8943 | sample=1 perioc |

**Proteins**

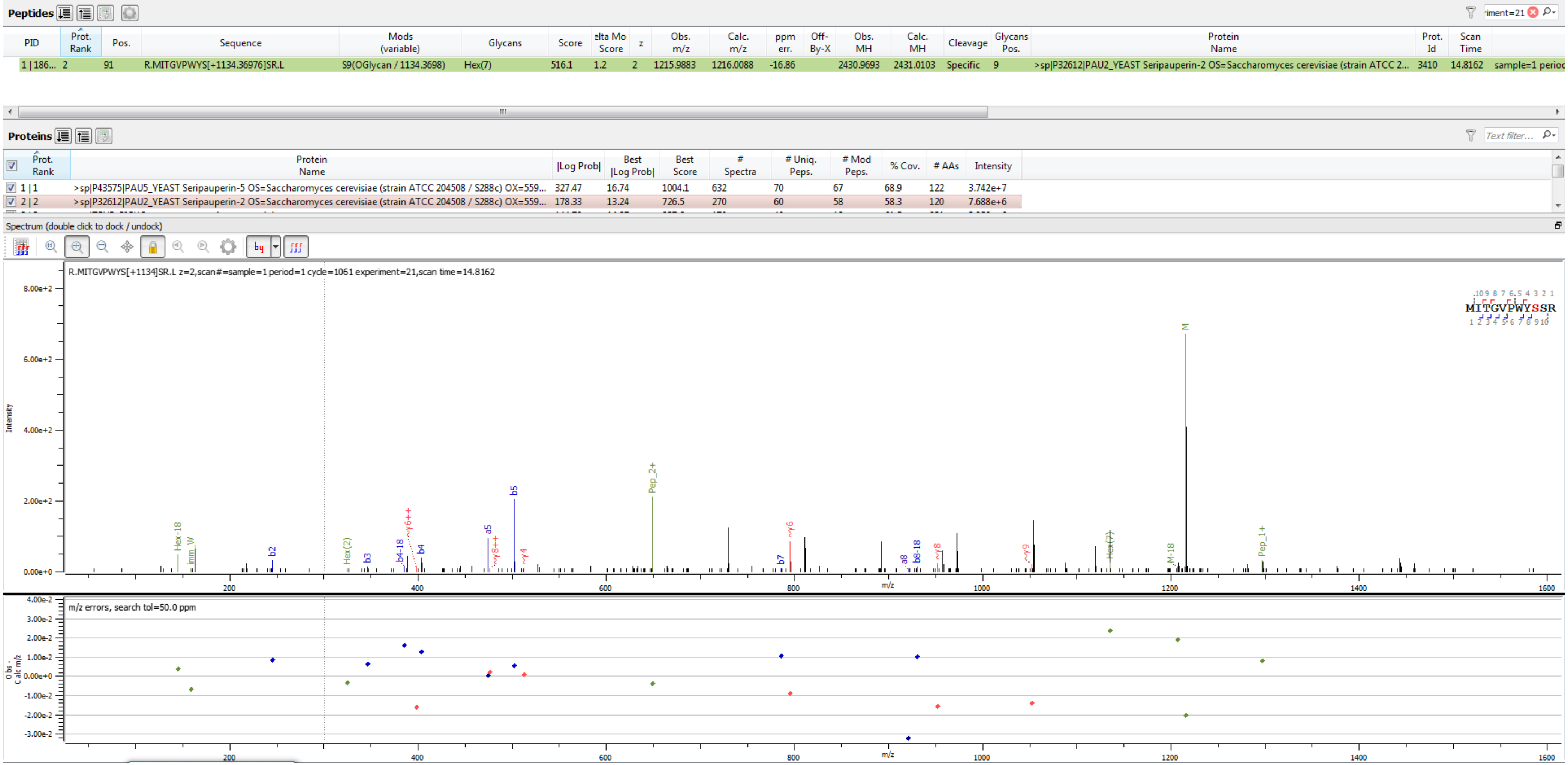
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+972]SR.L z=3,scan#=sample=1 period=1 cycle=1064 experiment=11,scan time=14.8943

m/z errors, search tol=50.0 ppm

Sample S1 R.MITGVPWYS[+972.317]SR.L



| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 186... | 2 | 91 | R.MITGVPWYS[+1134.36976]SR.L | S9(OGlycan / 1134.3698) | Hex(7) | 516.1 | 1.2 | 2 | 1215.9883 | 1216.0088 | -16.86 | | 2430.9693 | 2431.0103 | Specific | 9 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 14.8162 | sample=1 perioc |

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

R.MITGVPWYS[+1134]SR.L z=2,scan#=sample=1 period=1 cycle=1061 experiment=21,scan time=14.8162

Sample S1 R.MITGVPWYS[+1134.370]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 132... | 1 | 91 | R.MITGVPWYS[+1134.36976]SR.L | S9(OGlycan / 1134.3698) | Hex(7) | 636.2 | 1.2 | 3 | 810.9955 | 811.0083 | -15.75 | | 2430.9720 | 2431.0103 | Specific | 9 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3461 | 14.7986 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 101.54 | 13.43 | 953.1 | 37 | 11 | 0 | 20.4 | 643 | 1.801e+5 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+1134]SR.L z=3,scan#=sample=1 period=1 cycle=1088 experiment=14,scan time=14.7986

m/z errors, search tol=50.0 ppm

Sample S6 R.MITGVPWYS[+1134.370]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 814... | 3 | 21 | A.APATT[+648.21129]TLSPSDER.V | T5(OGlycan / 648.2113) | Hex(4) | 389.1 | 11.4 | 3 | 665.2840 | 665.2951 | -16.65 | | 1993.8375 | 1993.8707 | NRagged | 5 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 8.4575 | sample=1 perioc |

**Proteins**

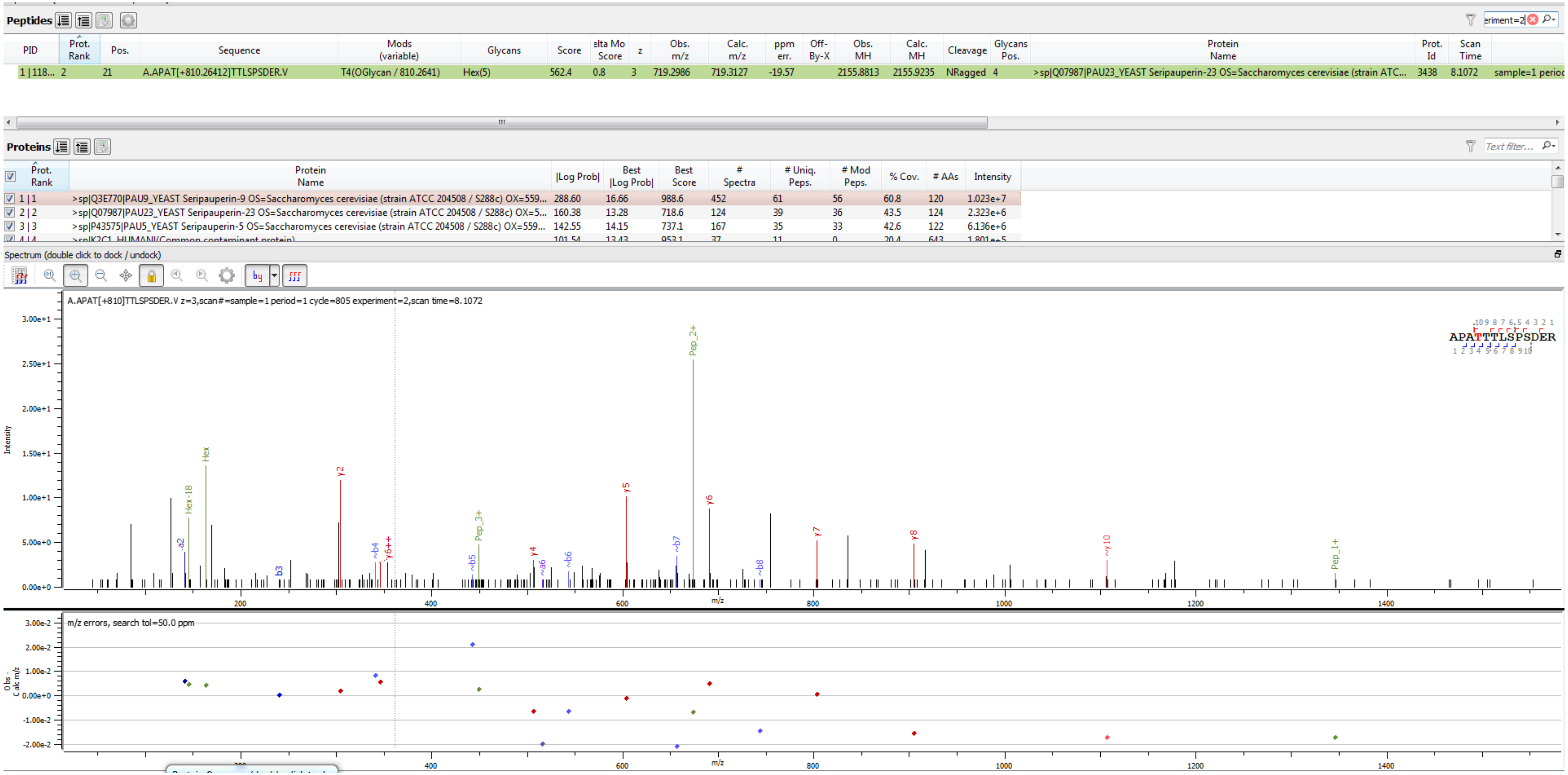
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 248.32 | 15.68 | 955.8 | 342 | 58 | 55 | 67.5 | 120 | 1.797e+7 |

Spectrum (double click to dock / undock)

A.APATT[+648]TLSPSDER.V z=3,scan#=sample=1 period=1 cycle=745 experiment=5,scan time=8.4575

m/z errors, search tol=50.0 ppm

Sample S3 A.APATT[+648.211]TLSPSDER.V



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 118... | 2 | 21 | A.APAT[+810.26412]TTLSPSDER.V | T4(OGlycan / 810.2641) | Hex(5) | 562.4 | 0.8 | 3 | 719.2986 | 719.3127 | -19.57 | | 2155.8813 | 2155.9235 | NRagged | 4 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 8.1072 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 101.54 | 13.43 | 953.1 | 37 | 11 | 0 | 20.4 | 643 | 1.801e+5 |

Spectrum (double click to dock / undock)

A.APAT[+810]TTLSPSDER.V z=3,scan#=sample=1 period=1 cycle=805 experiment=2,scan time=8.1072

m/z errors, search tol=50.0 ppm

Sample S6 A.APAT[+810.264]TTLSPSDER.V

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 118... | 2 | 21 | A.APATTT[+972.31694]LSPSDER.V | T6(OGlycan / 972.3169) | Hex(6) | 702.4 | 0.0 | 3 | 773.3154 | 773.3303 | -19.32 | | 2317.9315 | 2317.9763 | NRagged | 6 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 8.1732 | sample=1 perioc |

**Proteins**

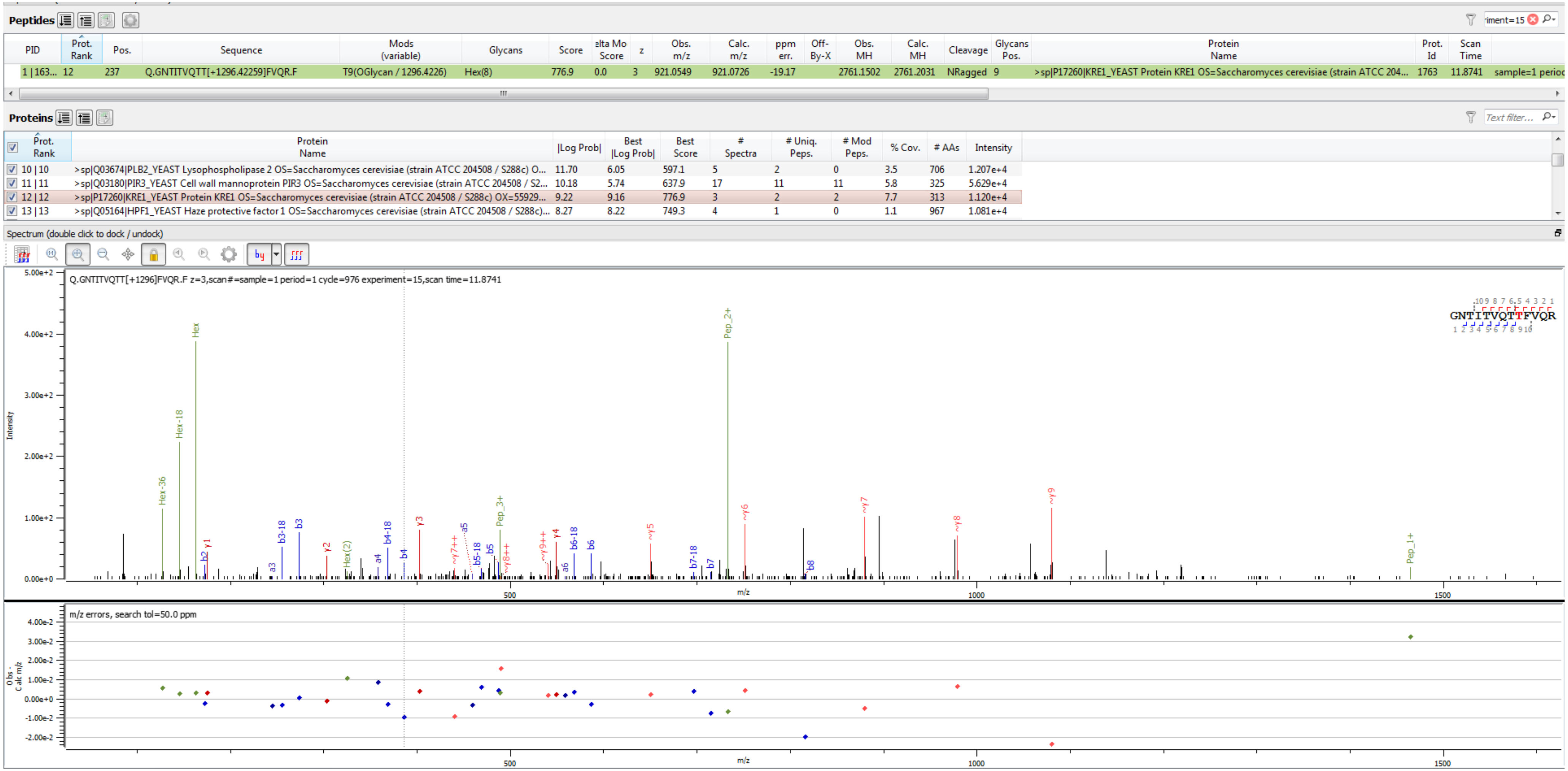
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 101.54 | 13.43 | 953.1 | 37 | 11 | 0 | 20.4 | 643 | 1.801e+5 |

Spectrum (double click to dock / undock)

A.APATTT[+972]LSPSDER.V z=3,scan#=sample=1 period=1 cycle=807 experiment=2,scan time=8.1732

m/z errors, search tol=50.0 ppm

Sample S6 A.APATTT[+972.317]LSPSDER.V



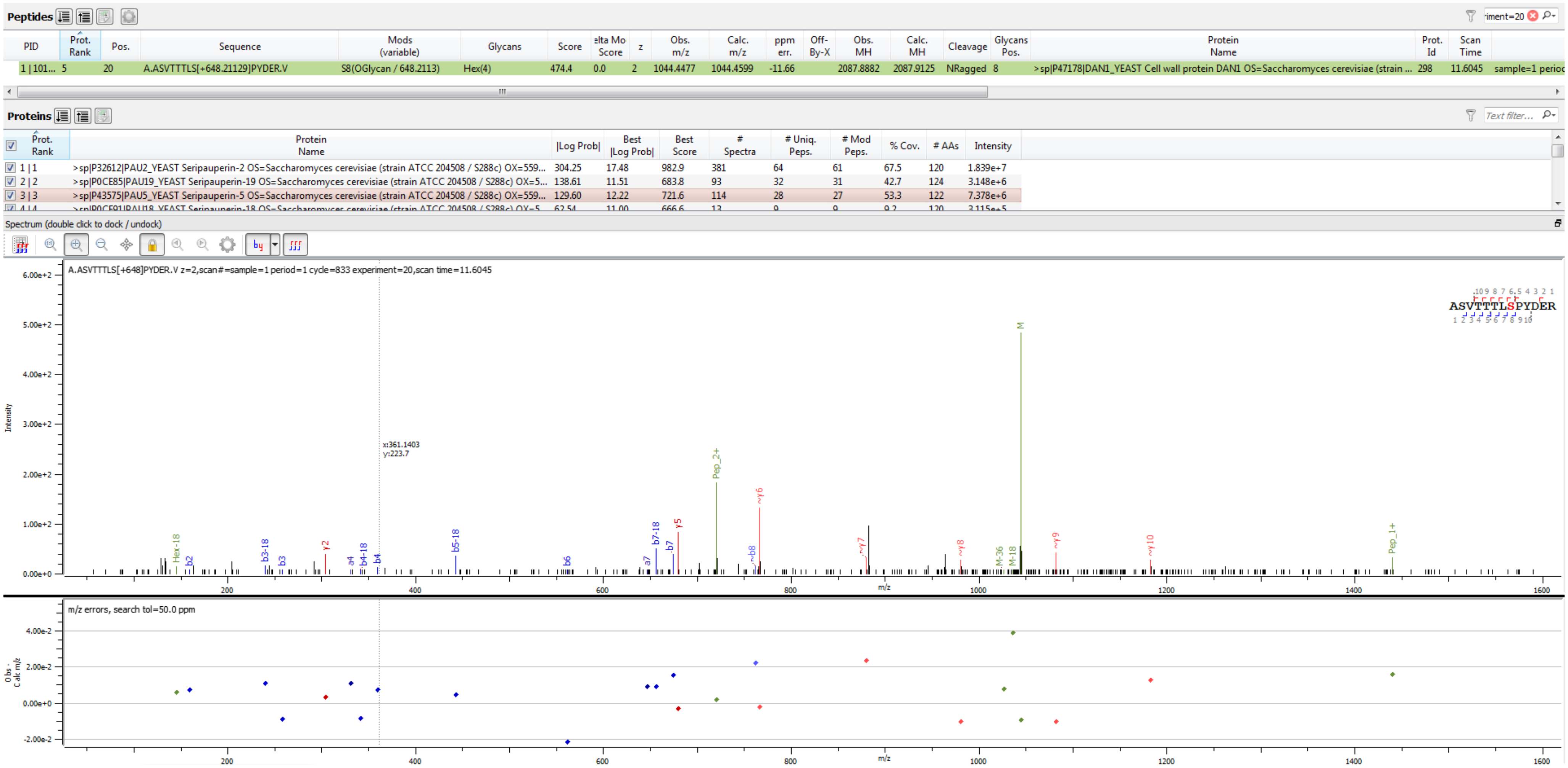
| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 163… | 12 | 237 | Q.GNTITVQTT[+1296.42259]FVQR.F | T9(OGlycan / 1296.4226) | Hex(8) | 776.9 | 0.0 | 3 | 921.0549 | 921.0726 | -19.17 | | 2761.1502 | 2761.2031 | NRagged | 9 | >sp\|P17260\|KRE1_YEAST Protein KRE1 OS=Saccharomyces cerevisiae (strain ATCC 204… | 1763 | 11.8741 | sample=1 perioc |

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 10 \| 10 | >sp\|Q03674\|PLB2_YEAST Lysophospholipase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) O… | 11.70 | 6.05 | 597.1 | 5 | 2 | 0 | 3.5 | 706 | 1.207e+4 |
| ☑ | 11 \| 11 | >sp\|Q03180\|PIR3_YEAST Cell wall mannoprotein PIR3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S2… | 10.18 | 5.74 | 637.9 | 17 | 11 | 11 | 5.8 | 325 | 5.629e+4 |
| ☑ | 12 \| 12 | >sp\|P17260\|KRE1_YEAST Protein KRE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=55929… | 9.22 | 9.16 | 776.9 | 3 | 2 | 2 | 7.7 | 313 | 1.120e+4 |
| ☑ | 13 \| 13 | >sp\|Q05164\|HPF1_YEAST Haze protective factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c)… | 8.27 | 8.22 | 749.3 | 4 | 1 | 0 | 1.1 | 967 | 1.081e+4 |

Q.GNTITVQTT[+1296]FVQR.F z=3,scan#=sample=1 period=1 cycle=976 experiment=15,scan time=11.8741

m/z errors, search tol=50.0 ppm

Sample S2 Q.GNTITVQTT[+1296.423]FVQR.F



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 101... | 5 | 20 | A.ASVTTTLS[+648.21129]PYDER.V | S8(OGlycan / 648.2113) | Hex(4) | 474.4 | 0.0 | 2 | 1044.4477 | 1044.4599 | -11.66 | | 2087.8882 | 2087.9125 | NRagged | 8 | >sp\|P47178\|DAN1_YEAST Cell wall protein DAN1 OS=Saccharomyces cerevisiae (strain ... | 298 | 11.6045 | sample=1 perioc |

**Proteins**

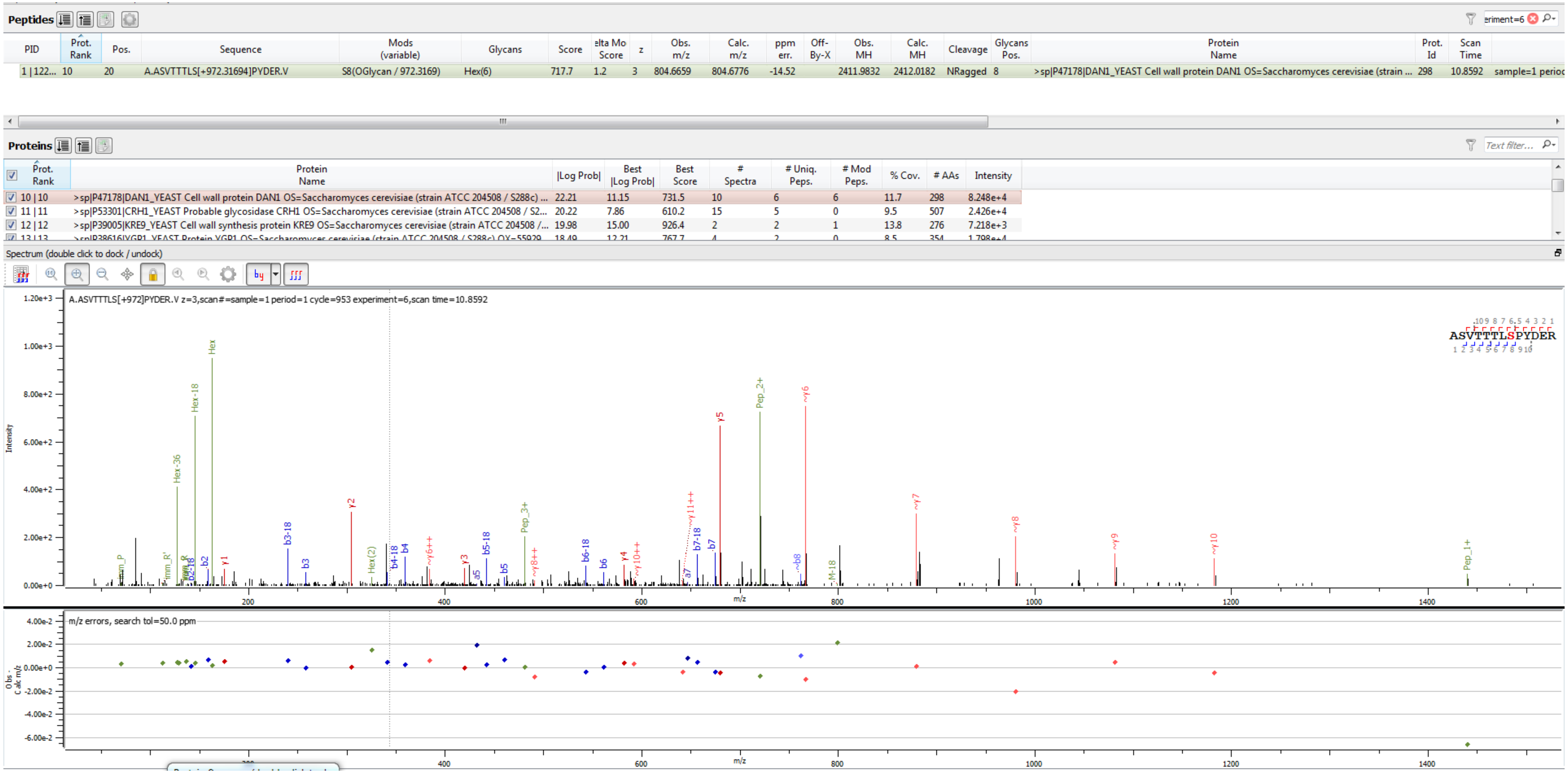
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CF91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

A.ASVTTTLS[+648]PYDER.V z=2,scan#=sample=1 period=1 cycle=833 experiment=20,scan time=11.6045

m/z errors, search tol=50.0 ppm

Sample S4 A.ASVTTTLS[+648.211]PYDER.V



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 122... | 10 | 20 | A.ASVTTTLS[+972.31694]PYDER.V | S8(OGlycan / 972.3169) | Hex(6) | 717.7 | 1.2 | 3 | 804.6659 | 804.6776 | -14.52 | | 2411.9832 | 2412.0182 | NRagged | 8 | >sp\|P47178\|DAN1_YEAST Cell wall protein DAN1 OS=Saccharomyces cerevisiae (strain ... | 298 | 10.8592 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 10 \| 10 | >sp\|P47178\|DAN1_YEAST Cell wall protein DAN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) ... | 22.21 | 11.15 | 731.5 | 10 | 6 | 6 | 11.7 | 298 | 8.248e+4 |
| ☑ 11 \| 11 | >sp\|P53301\|CRH1_YEAST Probable glycosidase CRH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S2... | 20.22 | 7.86 | 610.2 | 15 | 5 | 0 | 9.5 | 507 | 2.426e+4 |
| ☑ 12 \| 12 | >sp\|P39005\|KRE9_YEAST Cell wall synthesis protein KRE9 OS=Saccharomyces cerevisiae (strain ATCC 204508 /... | 19.98 | 15.00 | 926.4 | 2 | 2 | 1 | 13.8 | 276 | 7.218e+3 |
| ☑ 13 \| 13 | >sp\|P38616\|YGP1_YEAST Protein YGP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=55929 | 18.49 | 12.21 | 767.7 | 4 | 2 | 0 | 8.5 | 354 | 1.798e+4 |

Spectrum (double click to dock / undock)

A.ASVTTTLS[+972]PYDER.V z=3,scan#=sample=1 period=1 cycle=953 experiment=6,scan time=10.8592

m/z errors, search tol=50.0 ppm

Sample S6 A.ASVTTTLS[+972.317]PYDER.V

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 356... | 2 | 116 | K.DGIYT[+324.10565]AIPK.- | T5(OGlycan / 324.1056) | Hex(2) | 683.8 | 321.7 | 2 | 651.3173 | 651.3216 | -6.59 | | 1301.6273 | 1301.6358 | Specific | 5 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 13.3804 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |

Spectrum (double click to dock / undock)

K.DGIYT[+324]AIPK.- z=2,scan#=sample=1 period=1 cycle=894 experiment=9,scan time=13.3804

m/z errors, search tol=50.0 ppm

Sample S4 K.DGIYT[+324.106]AIPK.-

**Peptides**

eriment=2

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 117... | 3 | 21 | A.AATTTLSQS[+972.31694]DER.V | S9(OGlycan / 972.3169) | Hex(6) | 733.4 | 0.0 | 3 | 751.3006 | 751.3146 | -18.70 | | 2251.8873 | 2251.9294 | NRagged | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 7.1528 | sample=1 perioc |

**Proteins**

Text filter...

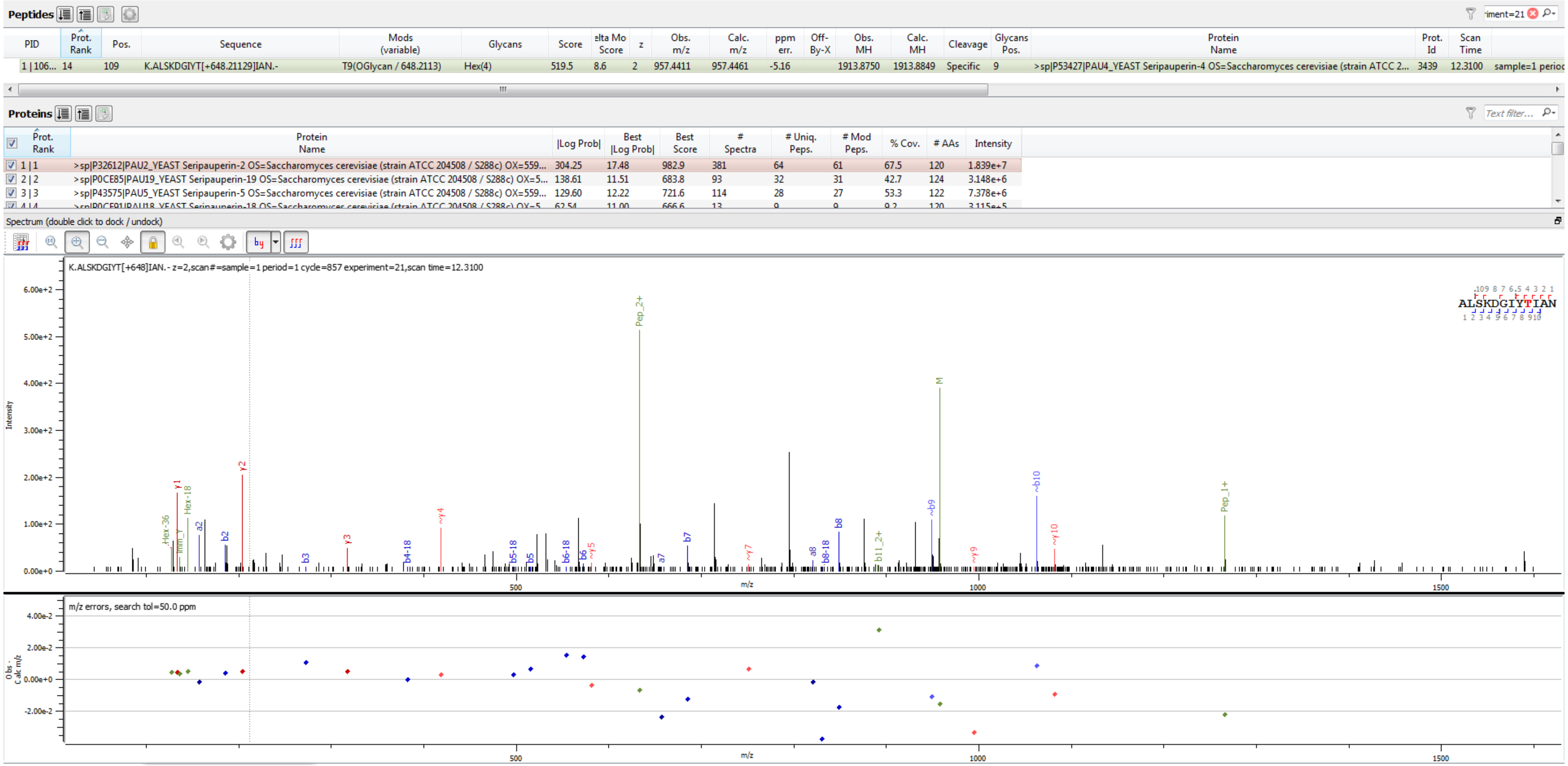
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 10 \| 10 | >sp\|P47178\|DAN1_YEAST Cell wall protein DAN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) ... | 22.21 | 11.15 | 731.5 | 10 | 6 | 6 | 11.7 | 298 | 8.248e+4 |
| ☑ 11 \| 11 | >sp\|P53301\|CRH1_YEAST Probable glycosidase CRH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S2... | 20.22 | 7.86 | 610.2 | 15 | 5 | 0 | 9.5 | 507 | 2.426e+4 |
| ☑ 12 \| 12 | >sp\|P39005\|KRE9_YEAST Cell wall synthesis protein KRE9 OS=Saccharomyces cerevisiae (strain ATCC 204508 /... | 19.98 | 15.00 | 926.4 | 2 | 2 | 1 | 13.8 | 276 | 7.218e+3 |
| ☑ 13 \| 13 | >sp\|P38616\|YGP1_YEAST Protein YGP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=55929 | 18.49 | 12.21 | 767.7 | 4 | 2 | 0 | 8.5 | 354 | 1.798e+4 |

Spectrum (double click to dock / undock)

A.AATTTLSQS[+972]DER.V z=3,scan#=sample=1 period=1 cycle=732 experiment=2,scan time=7.1528

m/z errors, search tol=50.0 ppm

Sample S6 A.AATTTLSQS[+972.317]DER.V



| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 106... | 14 | 109 | K.ALSKDGIYT[+648.21129]IAN.- | T9(OGlycan / 648.2113) | Hex(4) | 519.5 | 8.6 | 2 | 957.4411 | 957.4461 | -5.16 | | 1913.8750 | 1913.8849 | Specific | 9 | >sp\|P53427\|PAU4_YEAST Seripauperin-4 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3439 | 12.3100 | sample=1 perioc |

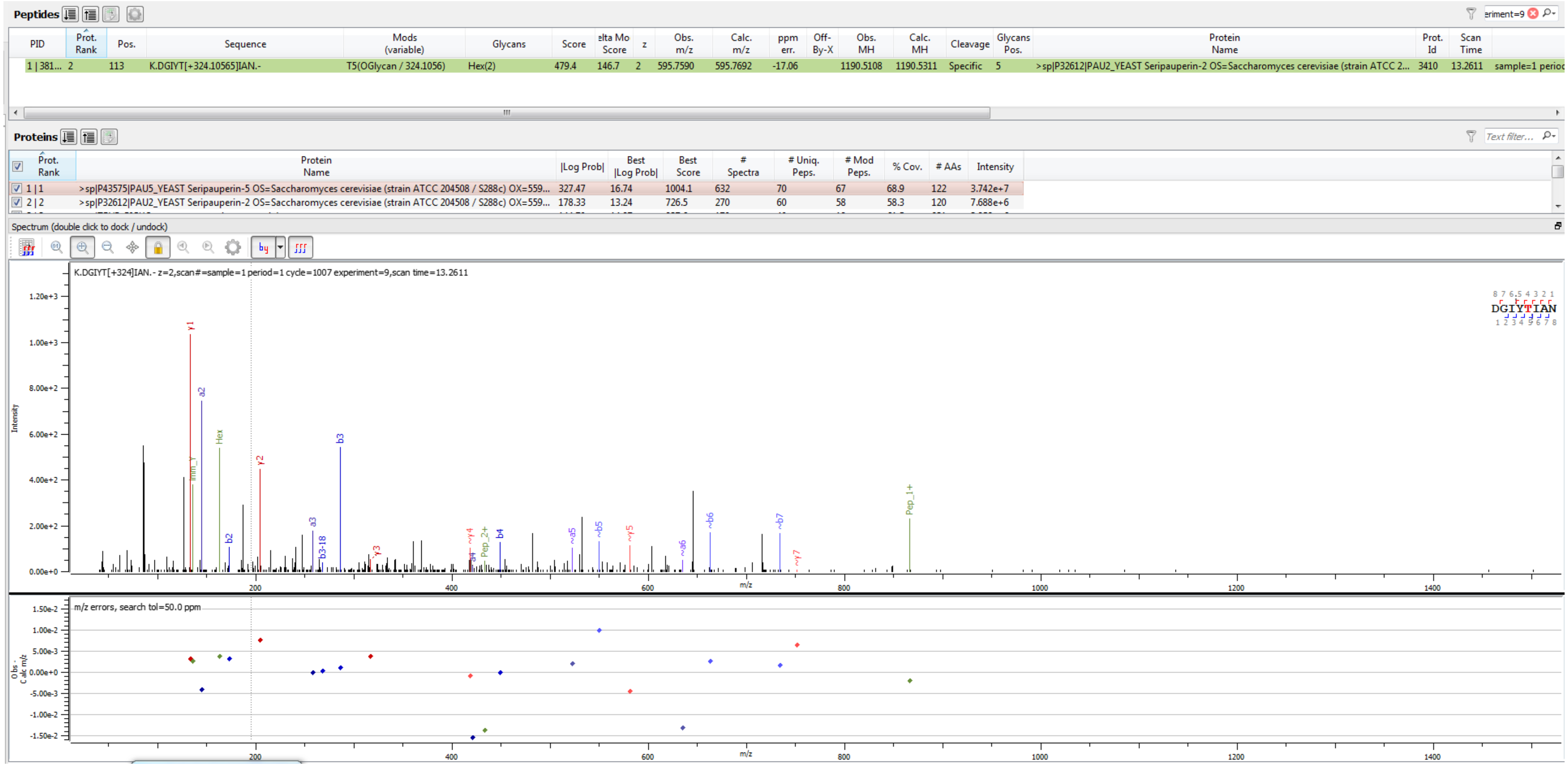
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CF91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

K.ALSKDGIYT[+648]IAN.- z=2,scan#=sample=1 period=1 cycle=857 experiment=21,scan time=12.3100

m/z errors, search tol=50.0 ppm

Sample S4 K.ALSKDGIYT[+648.211]IAN.-



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 381... | 2 | 113 | K.DGIYT[+324.10565]IAN.- | T5(OGlycan / 324.1056) | Hex(2) | 479.4 | 146.7 | 2 | 595.7590 | 595.7692 | -17.06 | | 1190.5108 | 1190.5311 | Specific | 5 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 13.2611 | sample=1 perioc |

**Proteins**

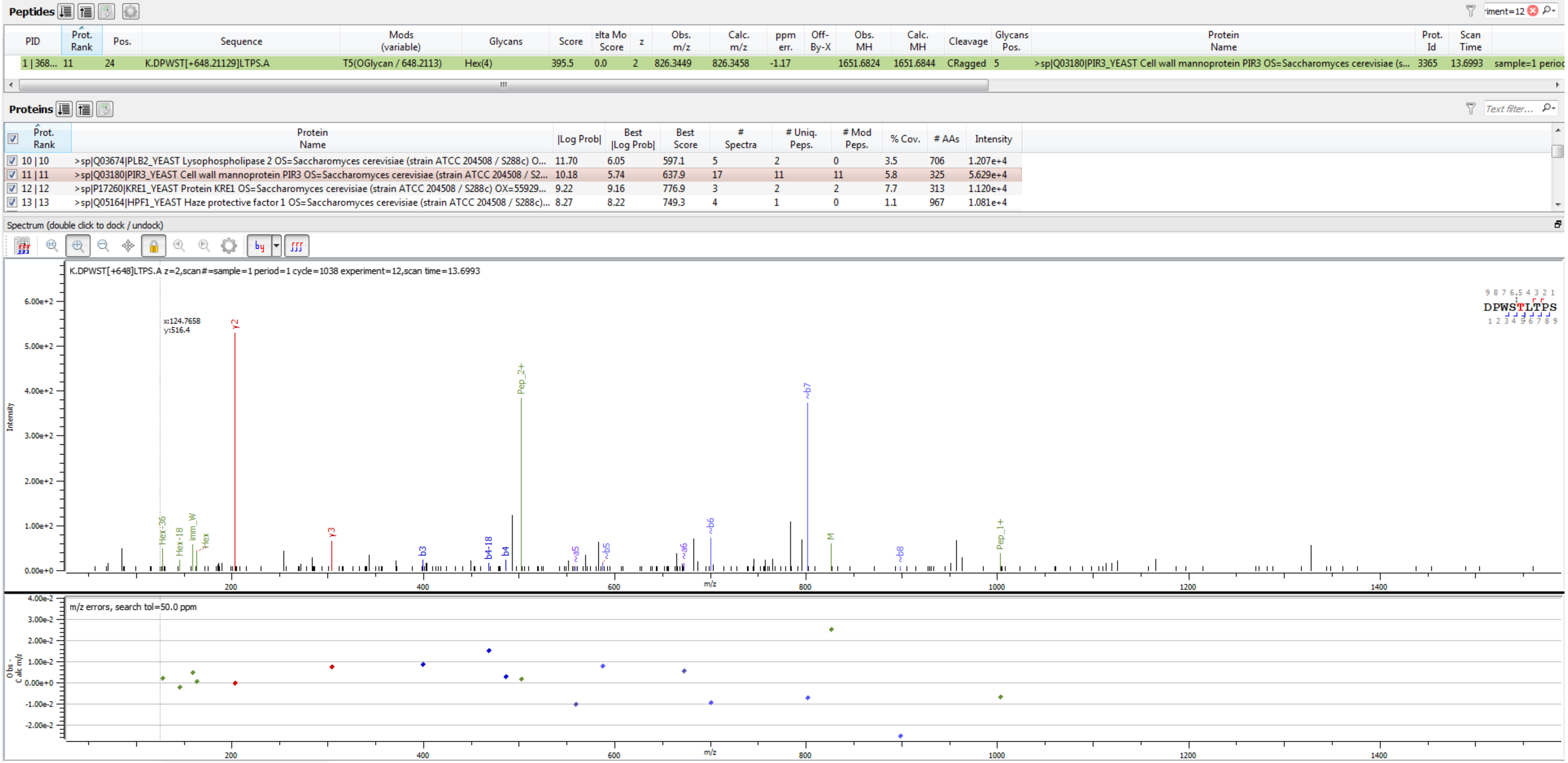
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

K.DGIYT[+324]IAN.- z=2,scan#=sample=1 period=1 cycle=1007 experiment=9,scan time=13.2611

m/z errors, search tol=50.0 ppm

Sample S1 K.DGIYT[+324.106]IAN.-



**Peptides**

iment=12

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 368... | 11 | 24 | K.DPWST[+648.21129]LTPS.A | T5(OGlycan / 648.2113) | Hex(4) | 395.5 | 0.0 | 2 | 826.3449 | 826.3458 | -1.17 | | 1651.6824 | 1651.6844 | CRagged | 5 | >sp\|Q03180\|PIR3_YEAST Cell wall mannoprotein PIR3 OS=Saccharomyces cerevisiae (s... | 3365 | 13.6993 | sample=1 perioc |

**Proteins**

Text filter...

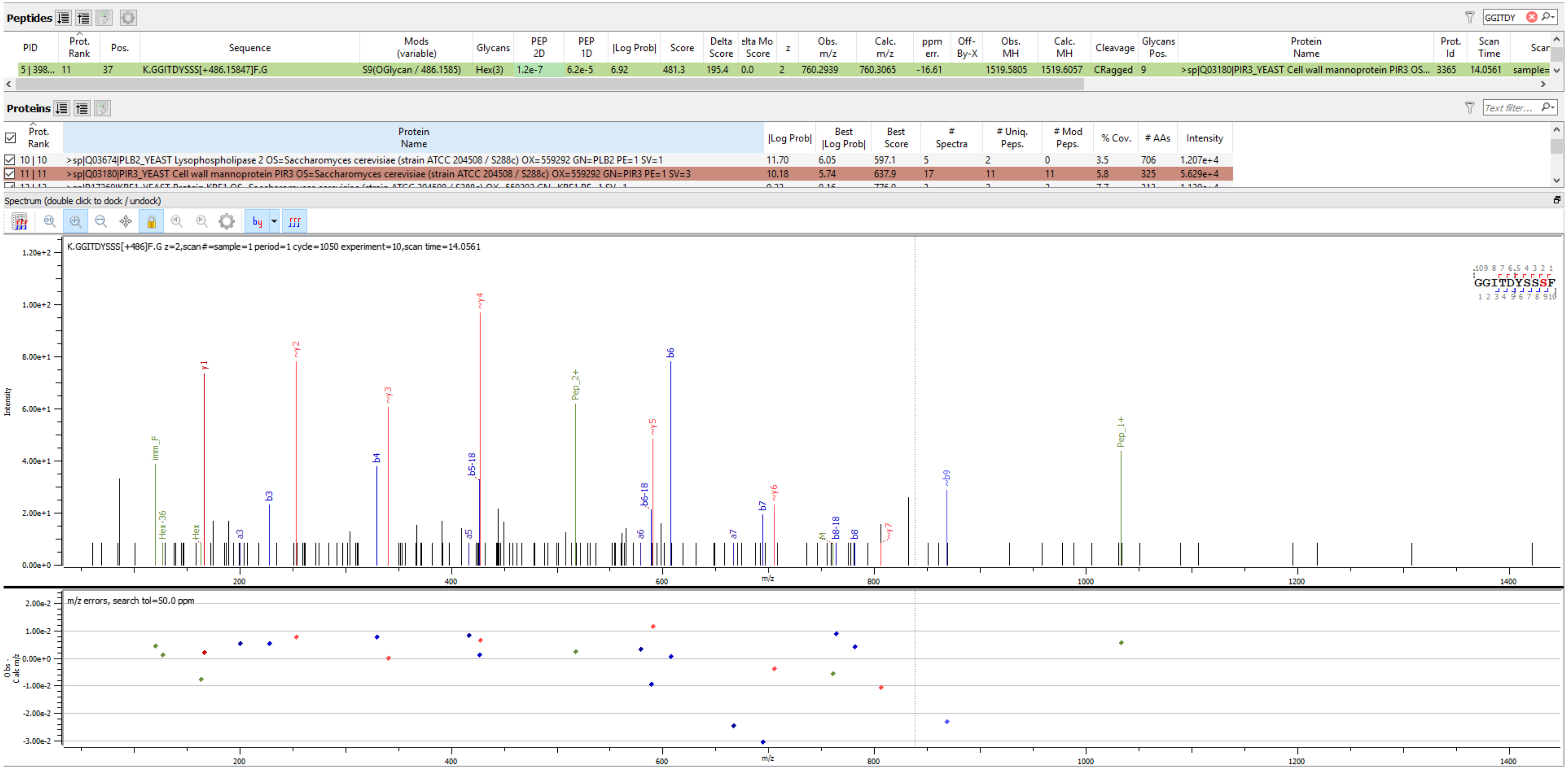
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 10 \| 10 | >sp\|Q03674\|PLB2_YEAST Lysophospholipase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) O... | 11.70 | 6.05 | 597.1 | 5 | 2 | 0 | 3.5 | 706 | 1.207e+4 |
| ☑ 11 \| 11 | >sp\|Q03180\|PIR3_YEAST Cell wall mannoprotein PIR3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S2... | 10.18 | 5.74 | 637.9 | 17 | 11 | 11 | 5.8 | 325 | 5.629e+4 |
| ☑ 12 \| 12 | >sp\|P17260\|KRE1_YEAST Protein KRE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=55929... | 9.22 | 9.16 | 776.9 | 3 | 2 | 2 | 7.7 | 313 | 1.120e+4 |
| ☑ 13 \| 13 | >sp\|Q05164\|HPF1_YEAST Haze protective factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c)... | 8.27 | 8.22 | 749.3 | 4 | 1 | 0 | 1.1 | 967 | 1.081e+4 |

Spectrum (double click to dock / undock)

K.DPWST[+648]LTPS.A z=2,scan#=sample=1 period=1 cycle=1038 experiment=12,scan time=13.6993

m/z errors, search tol=50.0 ppm

Sample S2 K.DPWST[+648.211]LTPS.A



**Peptides**

GGITDY

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | Scar |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 5 \| 398... | 11 | 37 | K.GGITDYSSS[+486.15847]F.G | S9(OGlycan / 486.1585) | Hex(3) | 1.2e-7 | 6.2e-5 | 6.92 | 481.3 | 195.4 | 0.0 | 2 | 760.2939 | 760.3065 | -16.61 |  | 1519.5805 | 1519.6057 | CRagged | 9 | >sp\|Q03180\|PIR3_YEAST Cell wall mannoprotein PIR3 OS... | 3365 | 14.0561 | sample= |

**Proteins**

Text filter...

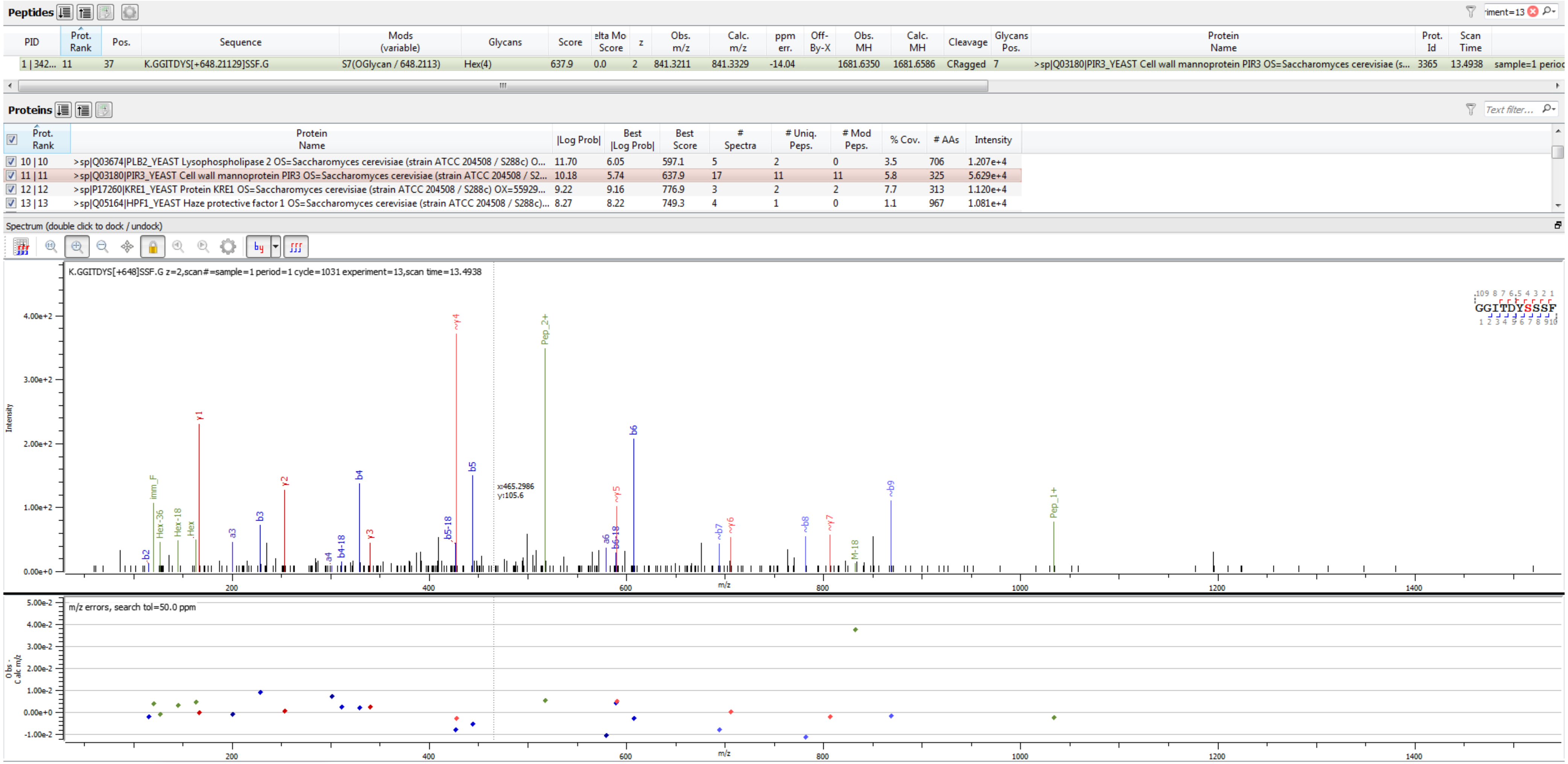
| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 10 \| 10 | >sp\|Q03674\|PLB2_YEAST Lysophospholipase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PLB2 PE=1 SV=1 | 11.70 | 6.05 | 597.1 | 5 | 2 | 0 | 3.5 | 706 | 1.207e+4 |
| ☑ | 11 \| 11 | >sp\|Q03180\|PIR3_YEAST Cell wall mannoprotein PIR3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559292 GN=PIR3 PE=1 SV=3 | 10.18 | 5.74 | 637.9 | 17 | 11 | 11 | 5.8 | 325 | 5.629e+4 |

Spectrum (double click to dock / undock)

K.GGITDYSSS[+486]F.G z=2,scan#=sample=1 period=1 cycle=1050 experiment=10,scan time=14.0561

m/z errors, search tol=50.0 ppm

Sample S2    K.GGITDYSSS[+486.158]F.G



**Peptides**

iment=13

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 342... | 11 | 37 | K.GGITDYS[+648.21129]SSF.G | S7(OGlycan / 648.2113) | Hex(4) | 637.9 | 0.0 | 2 | 841.3211 | 841.3329 | -14.04 | | 1681.6350 | 1681.6586 | CRagged | 7 | >sp\|Q03180\|PIR3_YEAST Cell wall mannoprotein PIR3 OS=Saccharomyces cerevisiae (s... | 3365 | 13.4938 | sample=1 perioc |

**Proteins**

Text filter...

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 10 \| 10 | >sp\|Q03674\|PLB2_YEAST Lysophospholipase 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) O... | 11.70 | 6.05 | 597.1 | 5 | 2 | 0 | 3.5 | 706 | 1.207e+4 |
| ☑ 11 \| 11 | >sp\|Q03180\|PIR3_YEAST Cell wall mannoprotein PIR3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S2... | 10.18 | 5.74 | 637.9 | 17 | 11 | 11 | 5.8 | 325 | 5.629e+4 |
| ☑ 12 \| 12 | >sp\|P17260\|KRE1_YEAST Protein KRE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=55929... | 9.22 | 9.16 | 776.9 | 3 | 2 | 2 | 7.7 | 313 | 1.120e+4 |
| ☑ 13 \| 13 | >sp\|Q05164\|HPF1_YEAST Haze protective factor 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c)... | 8.27 | 8.22 | 749.3 | 4 | 1 | 0 | 1.1 | 967 | 1.081e+4 |

Spectrum (double click to dock / undock)

K.GGITDYS[+648]SSF.G z=2,scan#=sample=1 period=1 cycle=1031 experiment=13,scan time=13.4938

m/z errors, search tol=50.0 ppm

Sample S2     K.GGITDYS[+648.211]SSF.G

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 464... | 2 | 94 | R.VITGVPWYST[+324.10565]R.L | T10(OGlycan / 324.1056) | Hex(2) | 567.4 | 0.0 | 2 | 801.8850 | 801.8985 | -16.88 | | 1602.7627 | 1602.7897 | Specific | 10 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 14.5391 | sample=1 perioc |

**Proteins**

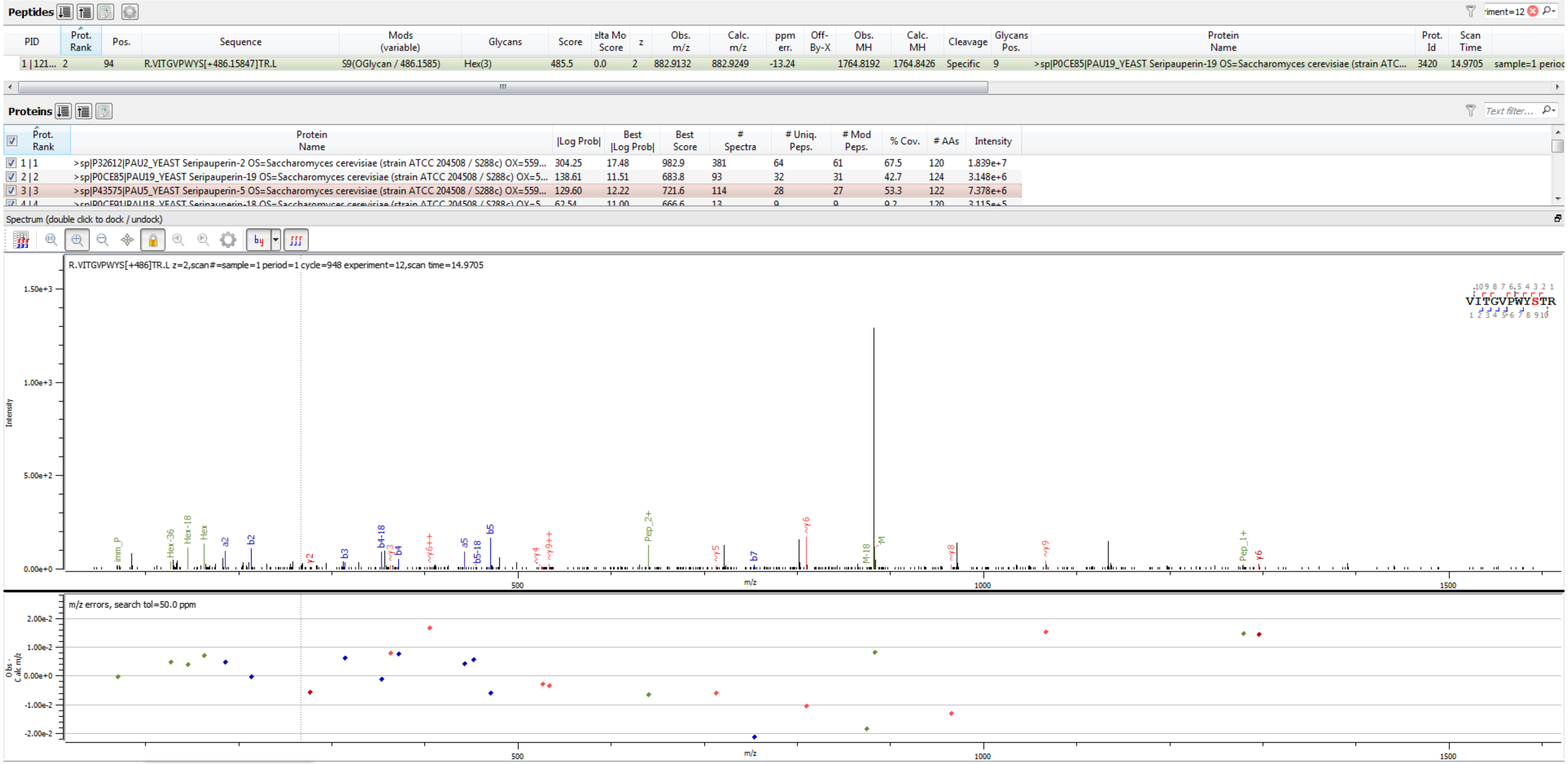
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 101.54 | 13.43 | 953.1 | 37 | 11 | 0 | 20.4 | 643 | 1.801e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYST[+324]R.L z=2,scan#=sample=1 period=1 cycle=1079 experiment=12,scan time=14.5391

m/z errors, search tol=50.0 ppm

Sample S6 R.VITGVPWYST[+324.106]R.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 121... | 2 | 94 | R.VITGVPWYS[+486.15847]TR.L | S9(OGlycan / 486.1585) | Hex(3) | 485.5 | 0.0 | 2 | 882.9132 | 882.9249 | -13.24 | | 1764.8192 | 1764.8426 | Specific | 9 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 14.9705 | sample=1 perioc |

**Proteins**

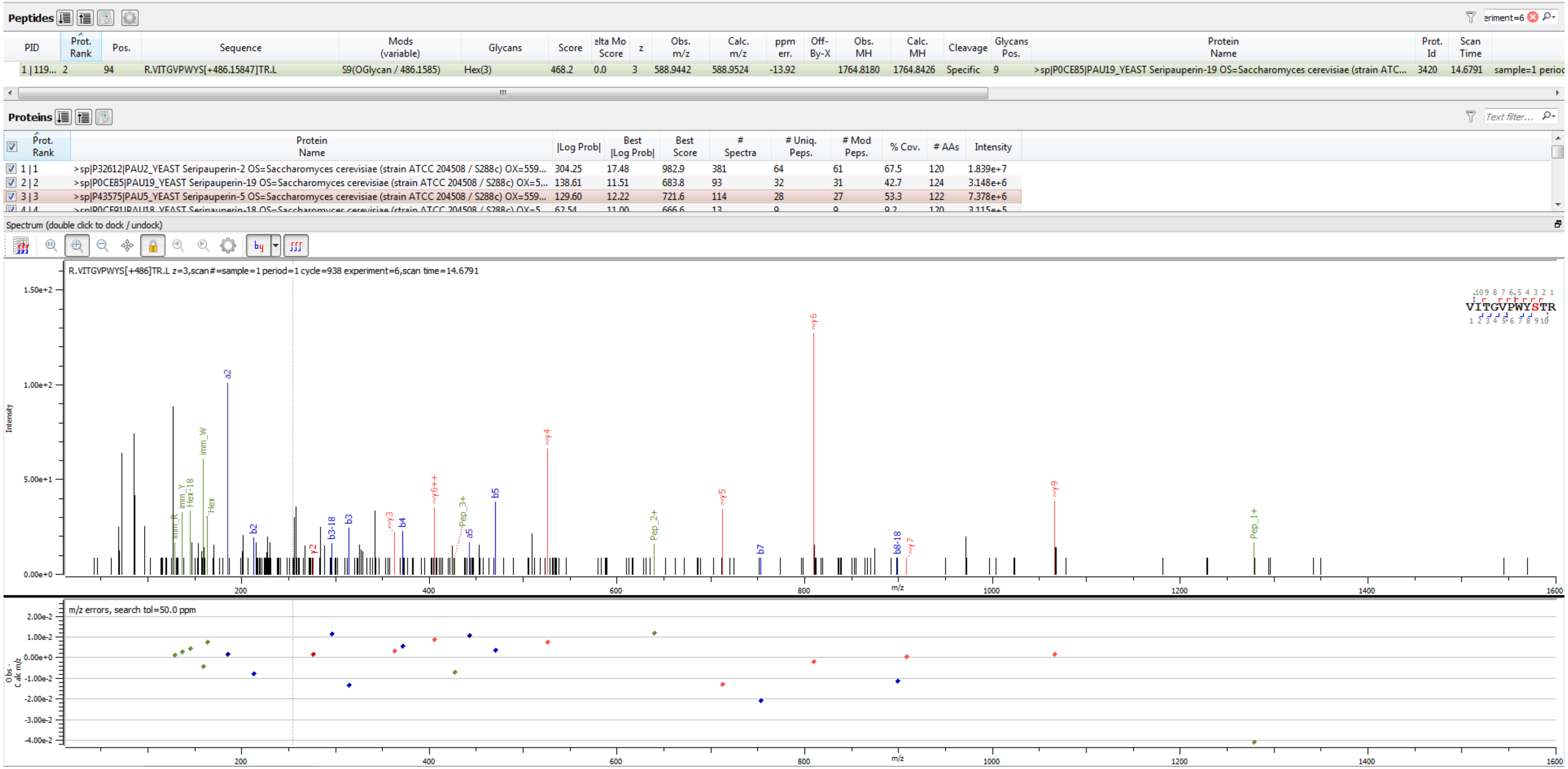
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CF91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+486]TR.L z=2,scan#=sample=1 period=1 cycle=948 experiment=12,scan time=14.9705

m/z errors, search tol=50.0 ppm

Sample S4 R.VITGVPWYS[+486.158]TR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 119... | 2 | 94 | R.VITGVPWYS[+486.15847]TR.L | S9(OGlycan / 486.1585) | Hex(3) | 468.2 | 0.0 | 3 | 588.9442 | 588.9524 | -13.92 | | 1764.8180 | 1764.8426 | Specific | 9 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 14.6791 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CF91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

R.VITGVPWYS[+486]TR.L z=3,scan#=sample=1 period=1 cycle=938 experiment=6,scan time=14.6791

m/z errors, search tol=50.0 ppm

Sample S4 R.VITGVPWYS[+486.158]TR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 936... | 2 | 94 | R.VITGVPWYST[+648.21129]R.L | T10(OGlycan / 648.2113) | Hex(4) | 659.4 | 0.0 | 2 | 963.9353 | 963.9513 | -16.62 | | 1926.8633 | 1926.8954 | Specific | 10 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 14.9432 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 101.54 | 13.43 | 953.1 | 37 | 11 | 0 | 20.4 | 643 | 1.801e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYST[+648]R.L z=2,scan#=sample=1 period=1 cycle=1093 experiment=13,scan time=14.9432

m/z errors, search tol=50.0 ppm

Sample S6 R.VITGVPWYST[+648.211]R.L

**Peptides**

eriment=5

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 115... | 3 | 94 | R.VITGVPWYST[+648.21129]R.L | T10(OGlycan / 648.2113) | Hex(4) | 594.7 | 0.0 | 3 | 642.9572 | 642.9700 | -19.83 | | 1926.8572 | 1926.8954 | Specific | 10 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 14.4496 | sample=1 perio |

**Proteins**

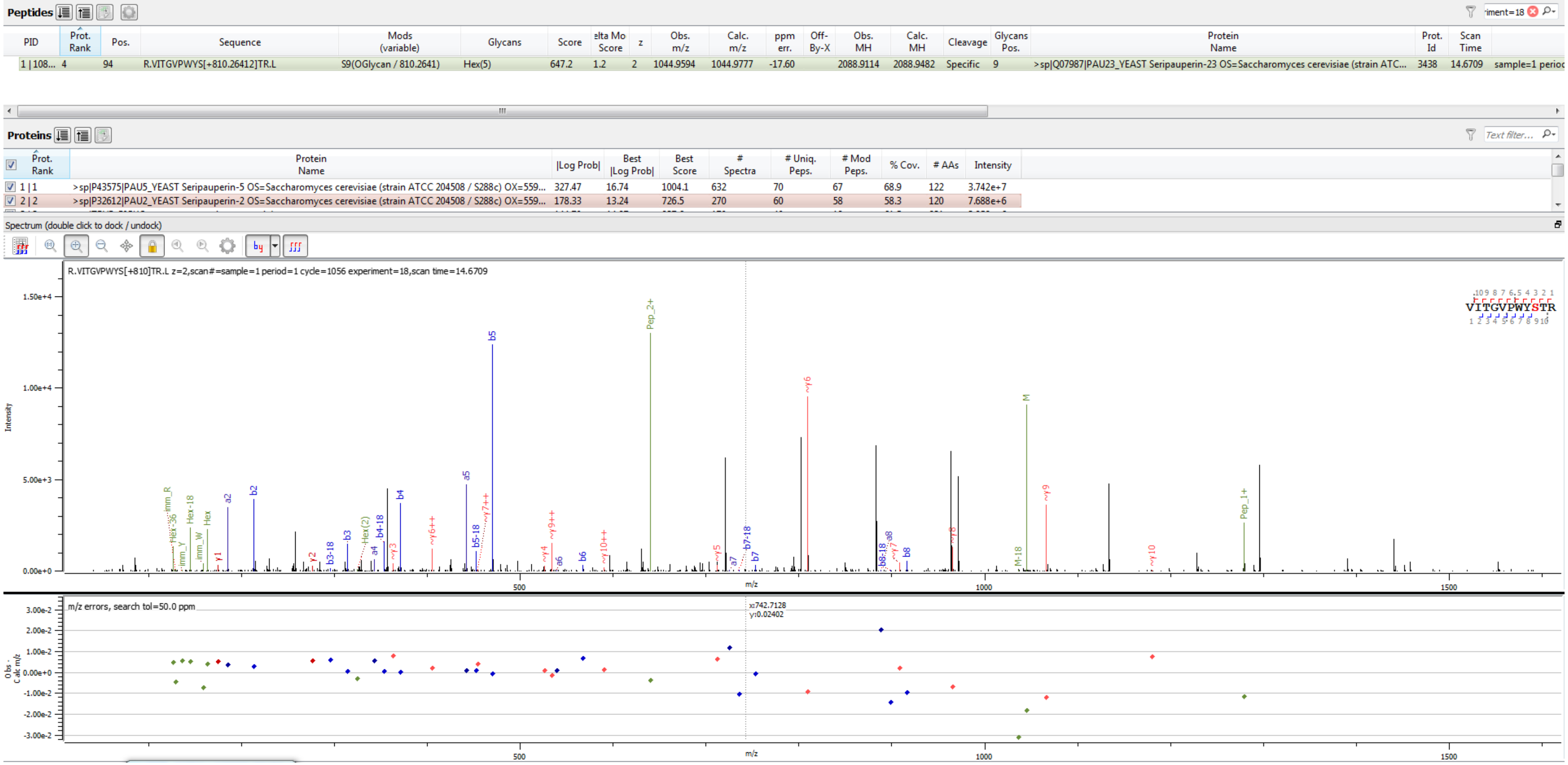
Text filter...

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 248.32 | 15.68 | 955.8 | 342 | 58 | 55 | 67.5 | 120 | 1.797e+7 |

Spectrum (double click to dock / undock)

R.VITGVPWYST[+648]R.L z=3,scan#=sample=1 period=1 cycle=946 experiment=5,scan time=14.4496

Sample S3 R.VITGVPWYST[+648.211]R.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 108... | 4 | 94 | R.VITGVPWYS[+810.26412]TR.L | S9(OGlycan / 810.2641) | Hex(5) | 647.2 | 1.2 | 2 | 1044.9594 | 1044.9777 | -17.60 | | 2088.9114 | 2088.9482 | Specific | 9 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 14.6709 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+810]TR.L z=2,scan#=sample=1 period=1 cycle=1056 experiment=18,scan time=14.6709

m/z errors, search tol=50.0 ppm

x:742.7128
y:0.02402

Sample S1 R.VITGVPWYS[+810.264]TR.L

**Peptides**

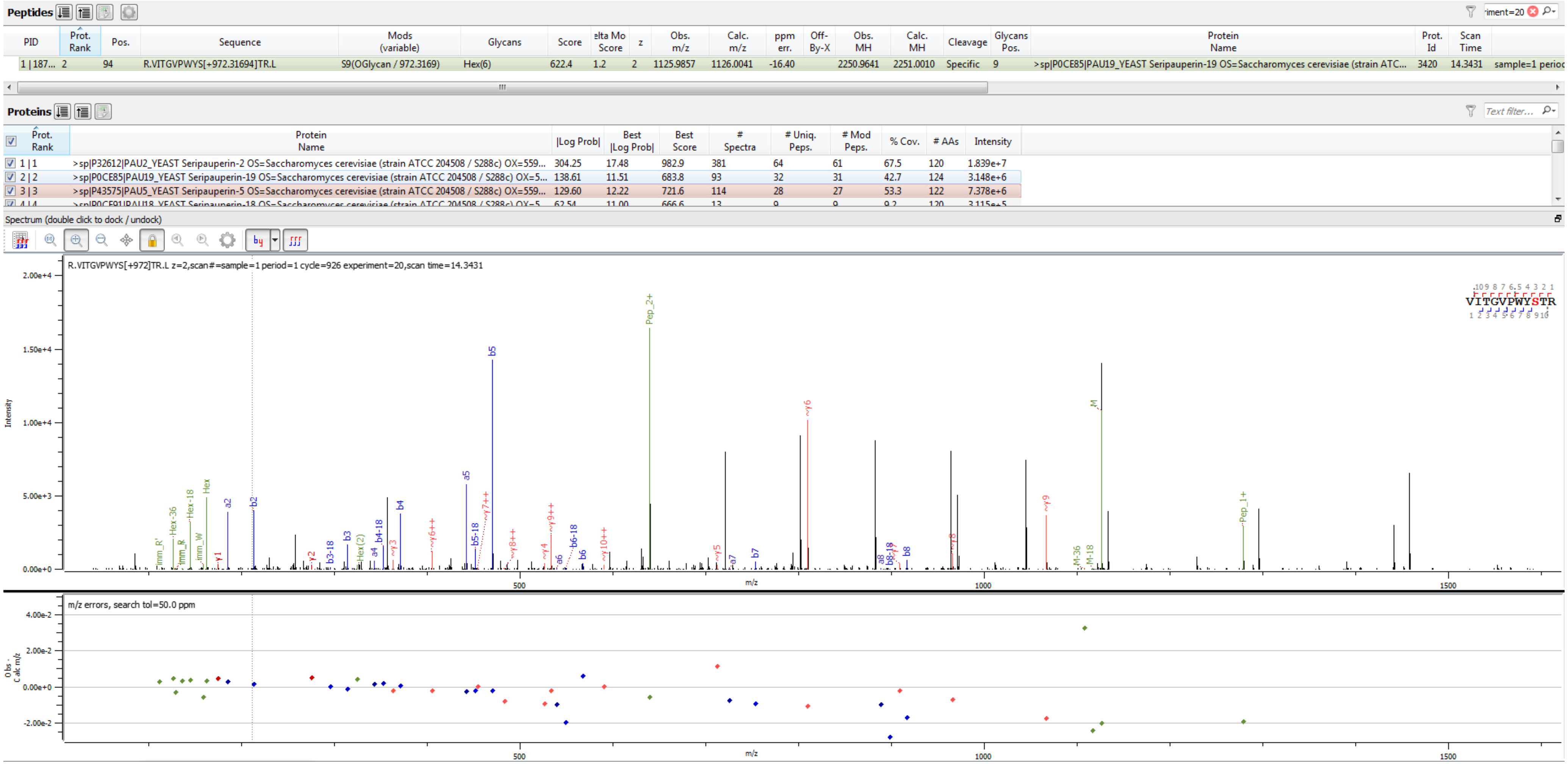
| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 927... | 2 | 94 | R.VITGVPWYS[+810.26412]TR.L | S9(OGlycan / 810.2641) | Hex(5) | 711.5 | 1.2 | 3 | 696.9746 | 696.9876 | -18.69 | | 2088.9092 | 2088.9482 | Specific | 9 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 14.8259 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 101.54 | 13.43 | 953.1 | 37 | 11 | 0 | 20.4 | 643 | 1.801e+5 |

R.VITGVPWYS[+810]TR.L z=3,scan#=sample=1 period=1 cycle=1089 experiment=12,scan time=14.8259

Sample S6 R.VITGVPWYS[+810.264]TR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 187... | 2 | 94 | R.VITGVPWYS[+972.31694]TR.L | S9(OGlycan / 972.3169) | Hex(6) | 622.4 | 1.2 | 2 | 1125.9857 | 1126.0041 | -16.40 | | 2250.9641 | 2251.0010 | Specific | 9 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 14.3431 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ | 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ | 4 \| 4 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+972]TR.L z=2,scan#=sample=1 period=1 cycle=926 experiment=20,scan time=14.3431

m/z errors, search tol=50.0 ppm

Sample S4 R.VITGVPWYS[+972.317]TR.L

**Peptides**

eriment=7

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 131... | 2 | 94 | R.VITGVPWYS[+972.31694]TR.L | S9(OGlycan / 972.3169) | Hex(6) | 699.7 | 1.2 | 3 | 750.9908 | 751.0052 | -19.20 | | 2250.9578 | 2251.0010 | Specific | 9 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 14.6208 | sample=1 perioc |

**Proteins**

Text filter...

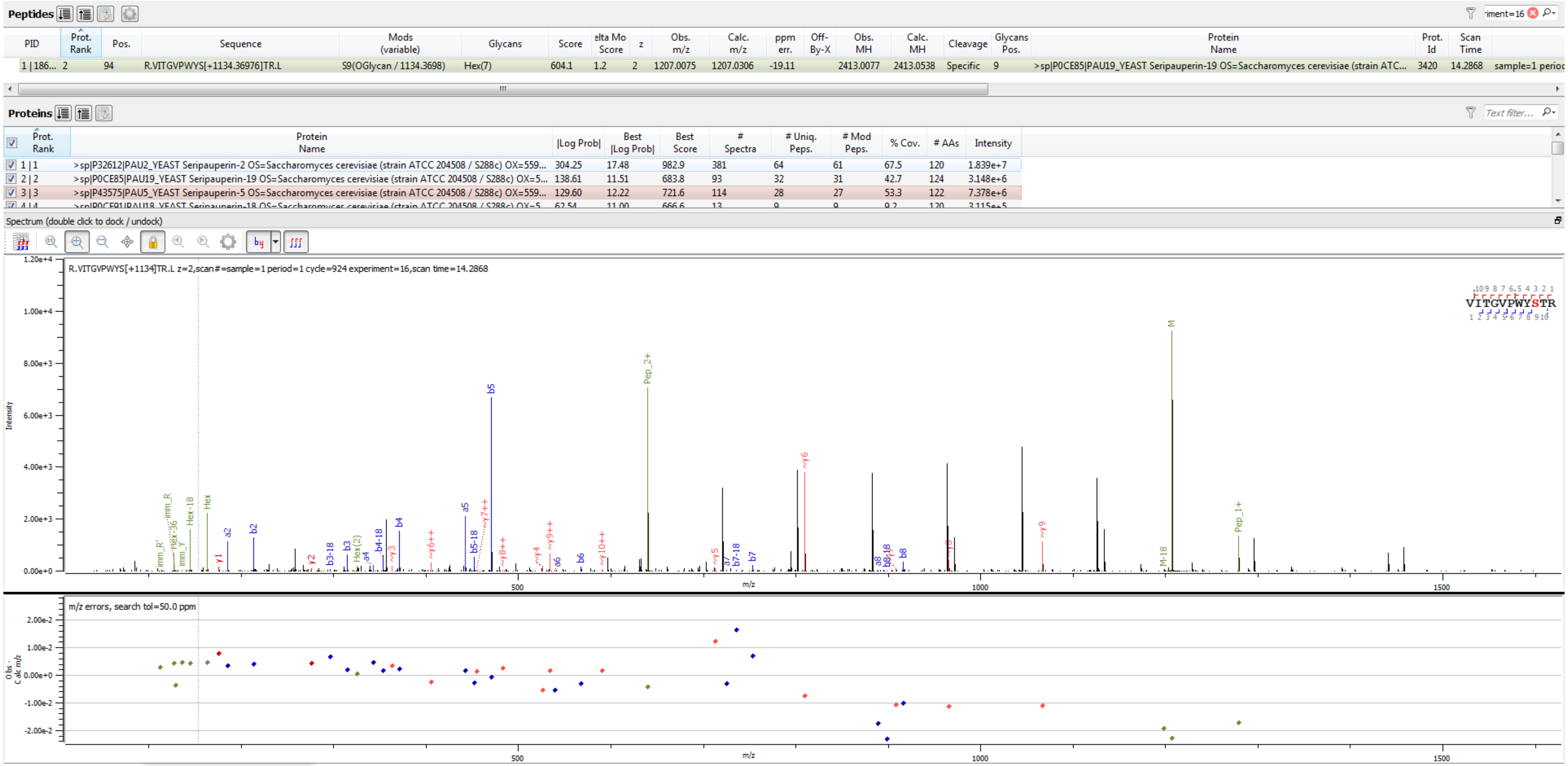
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 101.54 | 13.43 | 953.1 | 37 | 11 | 0 | 20.4 | 643 | 1.801e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+972]TR.L z=3,scan#=sample=1 period=1 cycle=1082 experiment=7,scan time=14.6208

m/z errors, search tol=50.0 ppm

Sample S6 R.VITGVPWYS[+972.317]TR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 186... | 2 | 94 | R.VITGVPWYS[+1134.36976]TR.L | S9(OGlycan / 1134.3698) | Hex(7) | 604.1 | 1.2 | 2 | 1207.0075 | 1207.0306 | -19.11 | | 2413.0077 | 2413.0538 | Specific | 9 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 14.2868 | sample=1 perio |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ | 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ | 4 \| 4 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+1134]TR.L z=2,scan#=sample=1 period=1 cycle=924 experiment=16,scan time=14.2868

m/z errors, search tol=50.0 ppm

Sample S4 R.VITGVPWYS[+1134.370]TR.L

**Peptides**

iment=11

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 129... | 2 | 94 | R.VITGVPWYS[+1134.36976]TR.L | S9(OGlycan / 1134.3698) | Hex(7) | 659.5 | 1.2 | 3 | 805.0098 | 805.0228 | -16.14 | | 2413.0149 | 2413.0538 | Specific | 9 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 14.3391 | sample=1 perioc |

**Proteins**

Text filter...

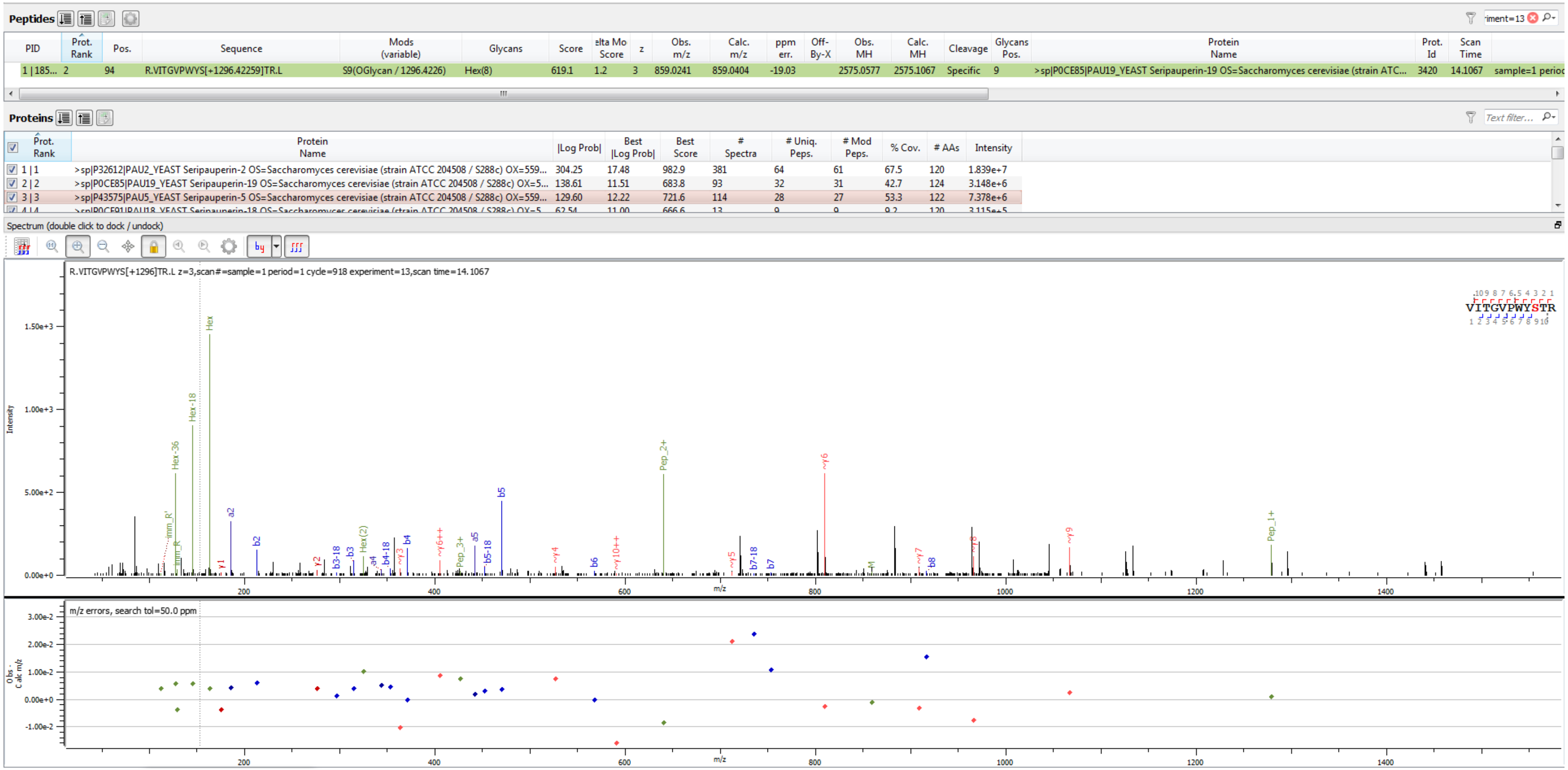
| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ | 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |
| ☑ | 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 101.54 | 13.43 | 953.1 | 37 | 11 | 0 | 20.4 | 643 | 1.801e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+1134]TR.L z=3,scan#=sample=1 period=1 cycle=1072 experiment=11,scan time=14.3391

m/z errors, search tol=50.0 ppm

Sample S6 R.VITGVPWYS[+1134.370]TR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 185... | 2 | 94 | R.VITGVPWYS[+1296.42259]TR.L | S9(OGlycan / 1296.4226) | Hex(8) | 619.1 | 1.2 | 3 | 859.0241 | 859.0404 | -19.03 | | 2575.0577 | 2575.1067 | Specific | 9 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 14.1067 | sample=1 perio |

**Proteins**

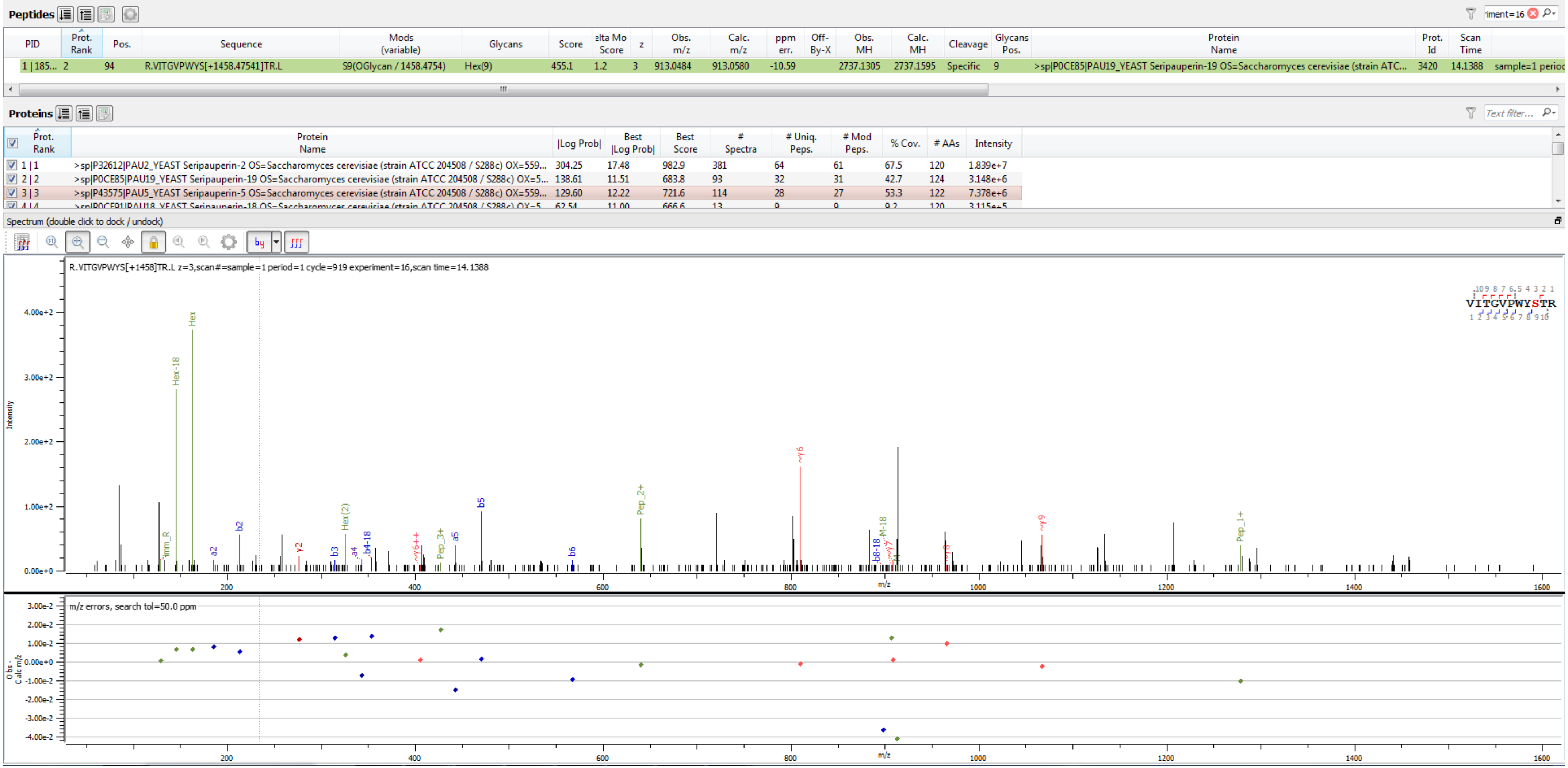
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CF91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+1296]TR.L z=3,scan#=sample=1 period=1 cycle=918 experiment=13,scan time=14.1067

m/z errors, search tol=50.0 ppm

Sample S4 R.VITGVPWYS[+1296.423]TR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 185... | 2 | 94 | R.VITGVPWYS[+1458.47541]TR.L | S9(OGlycan / 1458.4754) | Hex(9) | 455.1 | 1.2 | 3 | 913.0484 | 913.0580 | -10.59 | | 2737.1305 | 2737.1595 | Specific | 9 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 14.1388 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CF91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

R.VITGVPWYS[+1458]TR.L z=3,scan#=sample=1 period=1 cycle=919 experiment=16,scan time=14.1388

m/z errors, search tol=50.0 ppm

Sample S4 R.VITGVPWYS[+1458.475]TR.L

**Peptides**

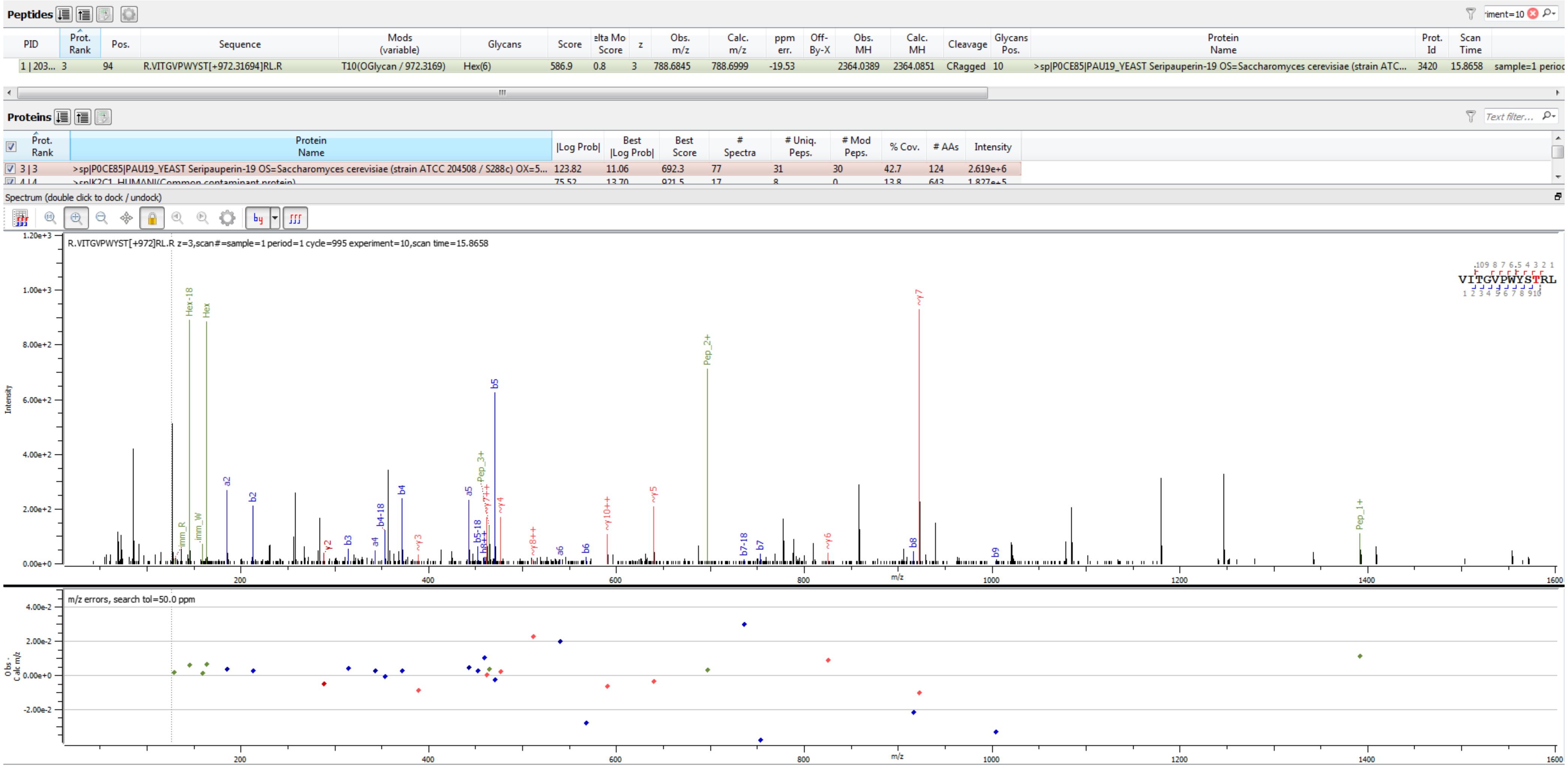
| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 193... | 2 | 94 | R.VITGVPWYS[+972.31694]TRL.R | S9(OGlycan / 972.3169) | Hex(6) | 465.5 | 1.2 | 2 | 1182.5227 | 1182.5462 | -19.84 | | 2364.0382 | 2364.0851 | CRagged | 9 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 15.8694 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |

R.VITGVPWYS[+972]TRL.R z=2,scan#=sample=1 period=1 cycle=979 experiment=13,scan time=15.8694

Sample S R.VITGVPWYS[+972.317]TRL.R



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 203... | 3 | 94 | R.VITGVPWYST[+972.31694]RL.R | T10(OGlycan / 972.3169) | Hex(6) | 586.9 | 0.8 | 3 | 788.6845 | 788.6999 | -19.53 | | 2364.0389 | 2364.0851 | CRagged | 10 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 15.8658 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 123.82 | 11.06 | 692.3 | 77 | 31 | 30 | 42.7 | 124 | 2.619e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 75.52 | 13.70 | 921.5 | 17 | 8 | 0 | 13.8 | 643 | 1.827e+5 |

Spectrum (double click to dock / undock)

R.VITGVPWYST[+972]RL.R z=3,scan#=sample=1 period=1 cycle=995 experiment=10,scan time=15.8658

m/z errors, search tol=50.0 ppm

Sample S3 R.VITGVPWYST[+972.317]RL.R

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | ɘlta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 170... | 5 | 94 | R.VITGVPWYS[+1296.42259]TRL.R | S9(OGlycan / 1296.4226) | Hex(8) | 536.3 | 1.2 | 3 | 896.7207 | 896.7351 | -16.04 | | 2688.1476 | 2688.1907 | CRagged | 9 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 15.7642 | sample=1 perioc |

**Proteins**

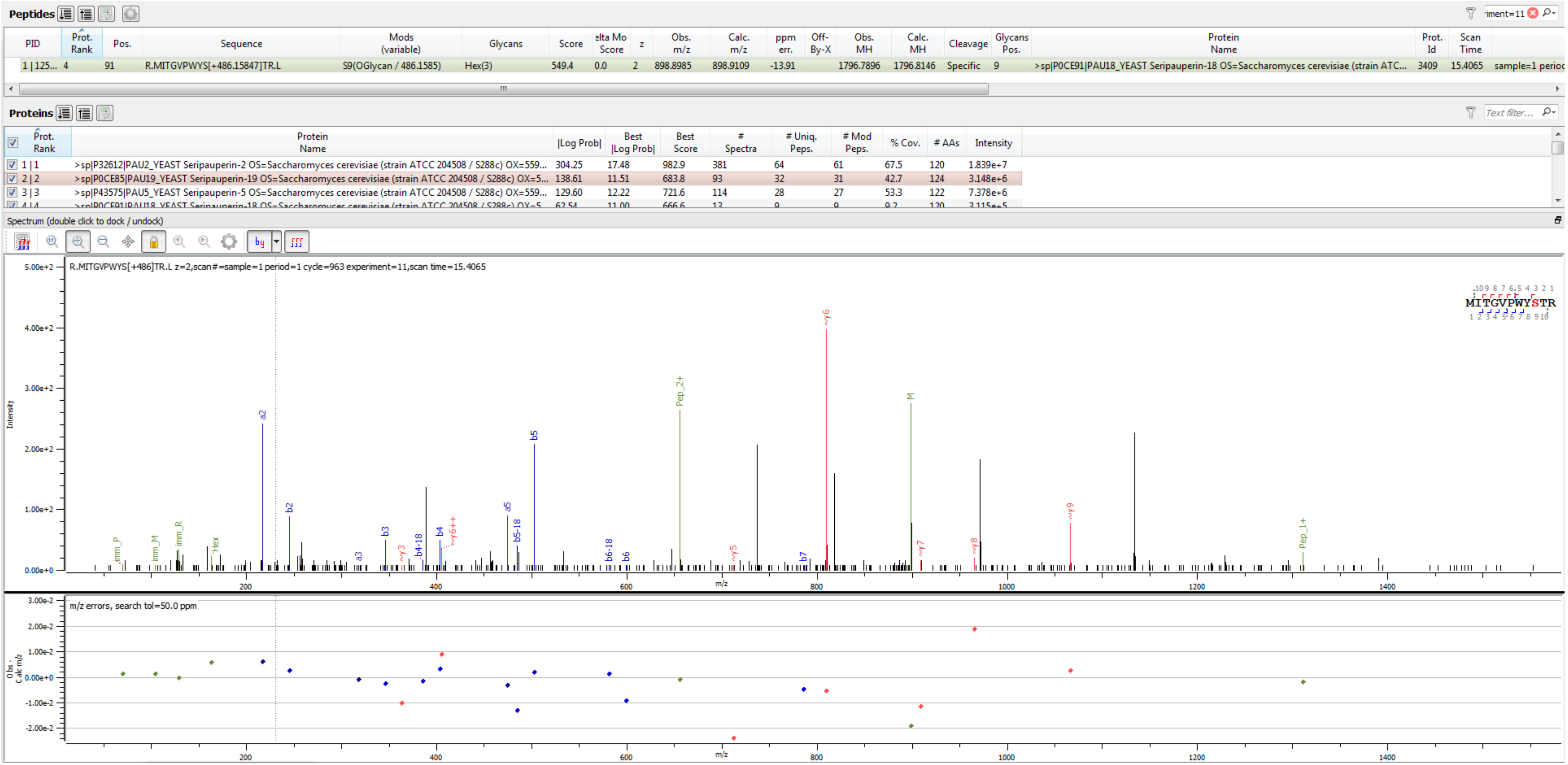
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

Spectrum (double click to dock / undock)

R.VITGVPWYS[+1296]TRL.R z=3,scan#=sample=1 period=1 cycle=1107 experiment=12,scan time=15.7642

m/z errors, search tol=50.0 ppm

Sample S2 R.VITGVPWYS[+1296.423]TRL.R



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 125... | 4 | 91 | R.MITGVPWYS[+486.15847]TR.L | S9(OGlycan / 486.1585) | Hex(3) | 549.4 | 0.0 | 2 | 898.8985 | 898.9109 | -13.91 | | 1796.7896 | 1796.8146 | Specific | 9 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATC... | 3409 | 15.4065 | sample=1 perioc |

iment=11

**Proteins**

Text filter...

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+486]TR.L z=2,scan#=sample=1 period=1 cycle=963 experiment=11,scan time=15.4065

m/z errors, search tol=50.0 ppm

Sample S4 R.MITGVPWYS[+486.158]TR.L

Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 115... | 5 | 91 | R.MITGVPWYS[+648.21129]TR.L | S9(OGlycan / 648.2113) | Hex(4) | 603.0 | 0.0 | 2 | 979.9187 | 979.9374 | -19.04 | | 1958.8301 | 1958.8674 | Specific | 9 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATC... | 3409 | 15.3883 | sample=1 perioc |

**Proteins**

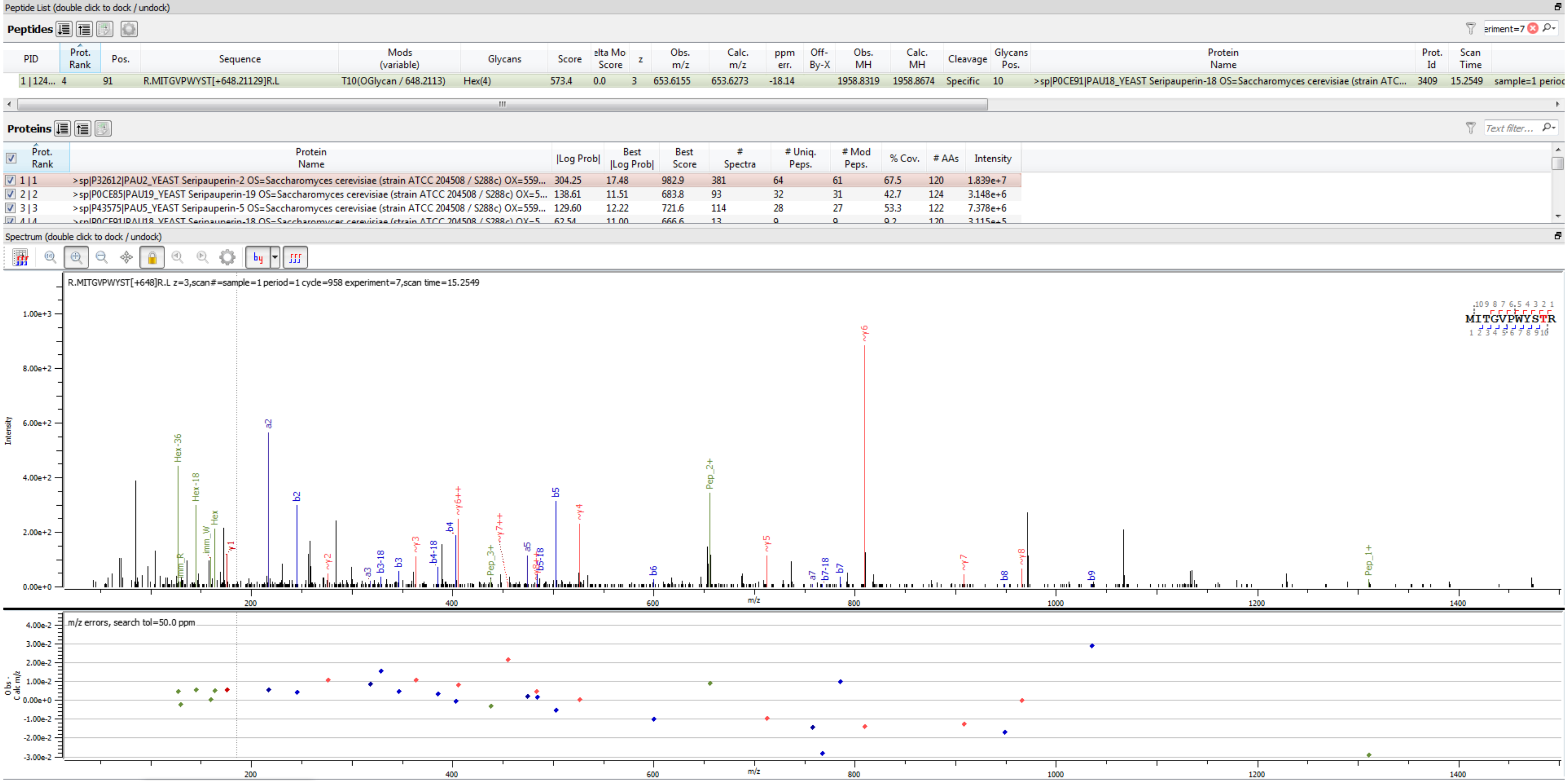
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+648]TR.L z=2,scan#=sample=1 period=1 cycle=1081 experiment=14,scan time=15.3883

m/z errors, search tol=50.0 ppm

Sample S1 R.MITGVPWYS[+648.211]TR.L



Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 124... | 4 | 91 | R.MITGVPWYST[+648.21129]R.L | T10(OGlycan / 648.2113) | Hex(4) | 573.4 | 0.0 | 3 | 653.6155 | 653.6273 | -18.14 | | 1958.8319 | 1958.8674 | Specific | 10 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATC... | 3409 | 15.2549 | sample=1 perioc |

**Proteins**

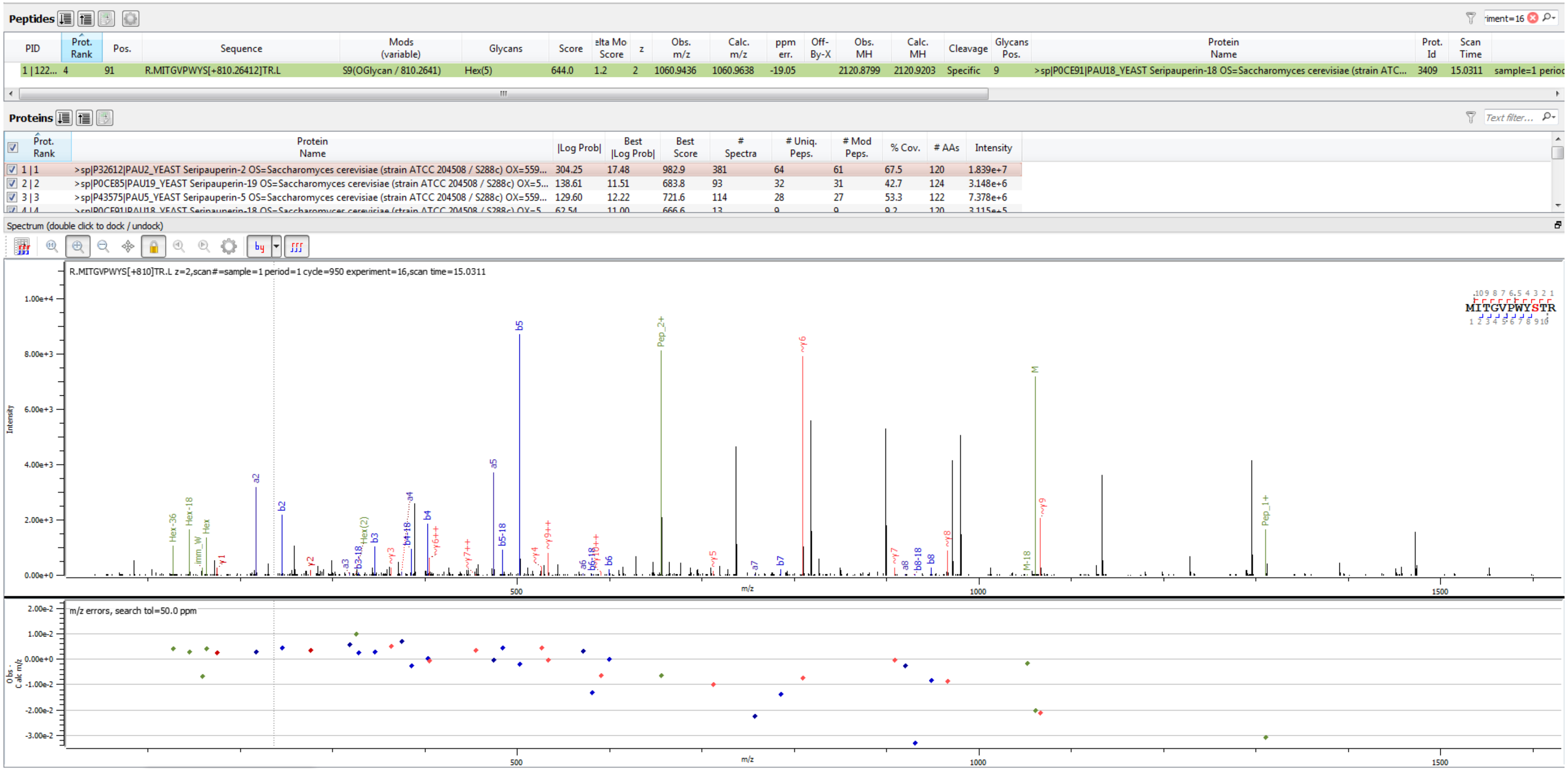
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

R.MITGVPWYST[+648]R.L z=3,scan#=sample=1 period=1 cycle=958 experiment=7,scan time=15.2549

m/z errors, search tol=50.0 ppm

Sample S4 R.MITGVPWYS[+648.211]TR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 122... | 4 | 91 | R.MITGVPWYS[+810.26412]TR.L | S9(OGlycan / 810.2641) | Hex(5) | 644.0 | 1.2 | 2 | 1060.9436 | 1060.9638 | -19.05 | | 2120.8799 | 2120.9203 | Specific | 9 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATC... | 3409 | 15.0311 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+810]TR.L z=2,scan#=sample=1 period=1 cycle=950 experiment=16,scan time=15.0311

m/z errors, search tol=50.0 ppm

Sample S4 R.MITGVPWYS[+810.264]TR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 957... | 6 | 91 | R.MITGVPWYS[+810.26412]TR.L | S9(OGlycan / 810.2641) | Hex(5) | 684.2 | 1.2 | 3 | 707.6310 | 707.6449 | -19.79 | | 2120.8783 | 2120.9203 | Specific | 9 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATC... | 3409 | 15.2348 | sample=1 perio |

**Proteins**

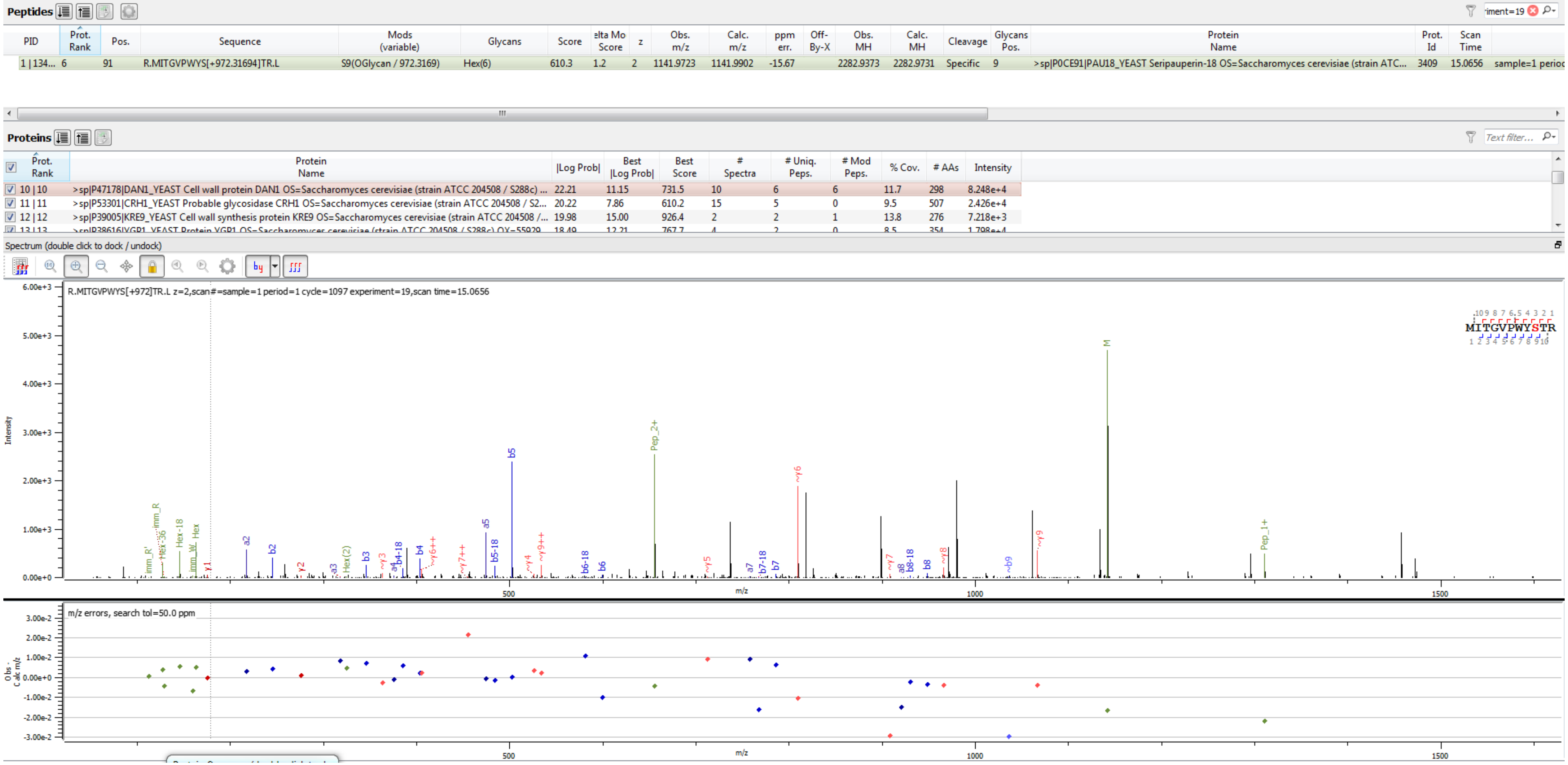
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 10 \| 10 | >sp\|P47178\|DAN1_YEAST Cell wall protein DAN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) ... | 22.21 | 11.15 | 731.5 | 10 | 6 | 6 | 11.7 | 298 | 8.248e+4 |
| ☑ 11 \| 11 | >sp\|P53301\|CRH1_YEAST Probable glycosidase CRH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S2... | 20.22 | 7.86 | 610.2 | 15 | 5 | 0 | 9.5 | 507 | 2.426e+4 |
| ☑ 12 \| 12 | >sp\|P39005\|KRE9_YEAST Cell wall synthesis protein KRE9 OS=Saccharomyces cerevisiae (strain ATCC 204508 /... | 19.98 | 15.00 | 926.4 | 2 | 2 | 1 | 13.8 | 276 | 7.218e+3 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+810]TR.L z=3,scan#=sample=1 period=1 cycle=1103 experiment=10,scan time=15.2348

m/z errors, search tol=50.0 ppm

Sample S6 R.MITGVPWYS[+810.264]TR.L



**Peptides**

iment=19

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 134... | 6 | 91 | R.MITGVPWYS[+972.31694]TR.L | S9(OGlycan / 972.3169) | Hex(6) | 610.3 | 1.2 | 2 | 1141.9723 | 1141.9902 | -15.67 | | 2282.9373 | 2282.9731 | Specific | 9 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATC... | 3409 | 15.0656 | sample=1 perioc |

**Proteins**

Text filter...

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 10 \| 10 | >sp\|P47178\|DAN1_YEAST Cell wall protein DAN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) ... | 22.21 | 11.15 | 731.5 | 10 | 6 | 6 | 11.7 | 298 | 8.248e+4 |
| ☑ 11 \| 11 | >sp\|P53301\|CRH1_YEAST Probable glycosidase CRH1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S2... | 20.22 | 7.86 | 610.2 | 15 | 5 | 0 | 9.5 | 507 | 2.426e+4 |
| ☑ 12 \| 12 | >sp\|P39005\|KRE9_YEAST Cell wall synthesis protein KRE9 OS=Saccharomyces cerevisiae (strain ATCC 204508 /... | 19.98 | 15.00 | 926.4 | 2 | 2 | 1 | 13.8 | 276 | 7.218e+3 |
| ☑ 13 \| 13 | >sp\|P38616\|YGP1_YEAST Protein YGP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=55929 | 18.49 | 12.21 | 767.7 | 4 | 2 | 0 | 8.5 | 354 | 1.798e+4 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+972]TR.L z=2,scan#=sample=1 period=1 cycle=1097 experiment=19,scan time=15.0656

m/z errors, search tol=50.0 ppm

Sample S6 R.MITGVPWYS[+972.317]TR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 191... | 4 | 91 | R.MITGVPWYS[+972.31694]TR.L | S9(OGlycan / 972.3169) | Hex(6) | 636.6 | 1.2 | 3 | 761.6496 | 761.6625 | -16.96 | | 2282.9344 | 2282.9731 | Specific | 9 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATC... | 3409 | 14.9982 | sample=1 perioc |

**Proteins**

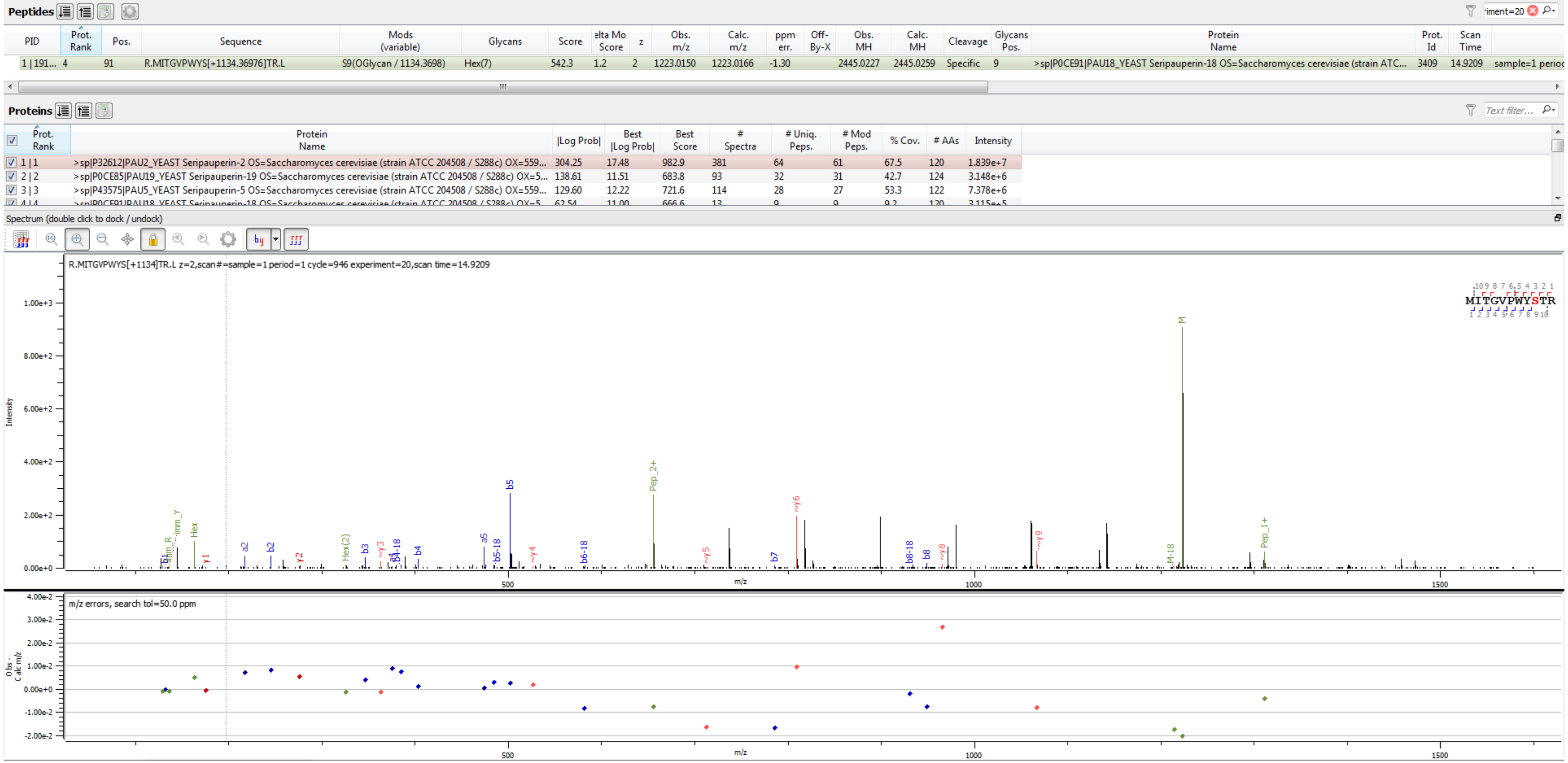
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+972]TR.L z=3,scan#=sample=1 period=1 cycle=949 experiment=11,scan time=14.9982

m/z errors, search tol=50.0 ppm

Sample S4 R.MITGVPWYS[+972.317]TR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 191... | 4 | 91 | R.MITGVPWYS[+1134.36976]TR.L | S9(OGlycan / 1134.3698) | Hex(7) | 542.3 | 1.2 | 2 | 1223.0150 | 1223.0166 | -1.30 | | 2445.0227 | 2445.0259 | Specific | 9 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATC... | 3409 | 14.9209 | sample=1 perioc |

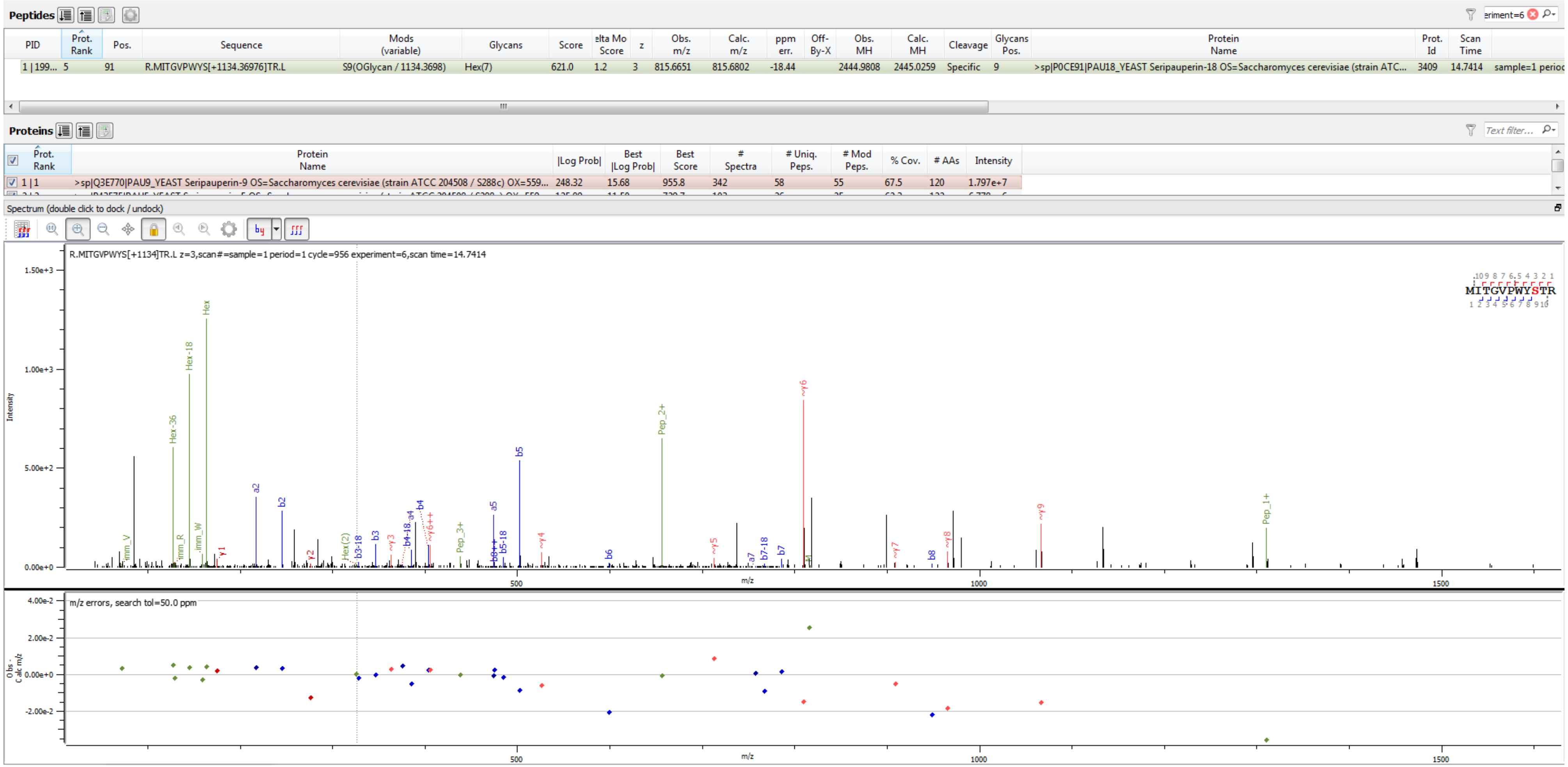
**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

R.MITGVPWYS[+1134]TR.L z=2,scan#=sample=1 period=1 cycle=946 experiment=20,scan time=14.9209

Sample S4

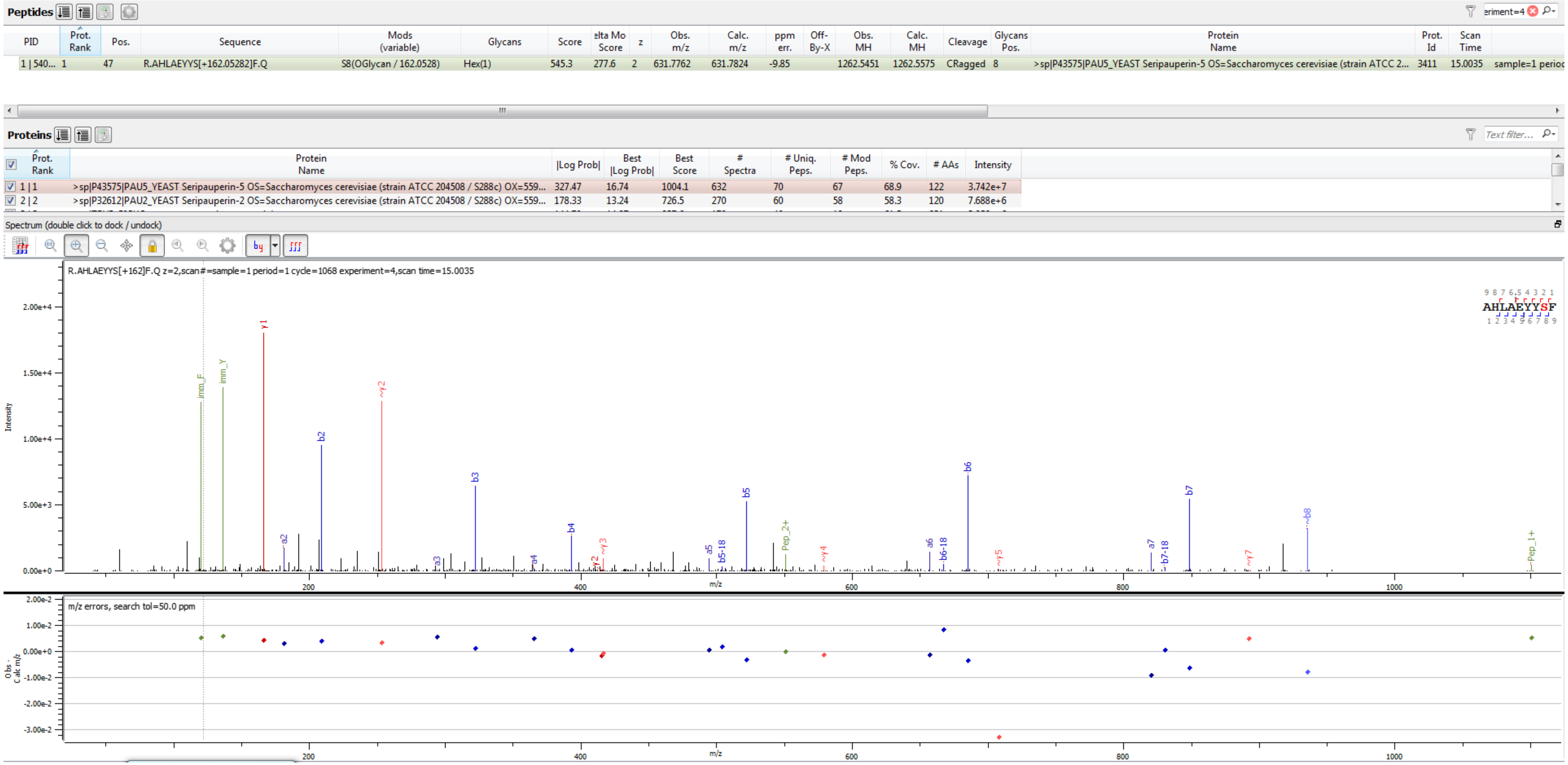


| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 199... | 5 | 91 | R.MITGVPWYS[+1134.36976]TR.L | S9(OGlycan / 1134.3698) | Hex(7) | 621.0 | 1.2 | 3 | 815.6651 | 815.6802 | -18.44 | | 2444.9808 | 2445.0259 | Specific | 9 | >sp\|P0CE91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATC... | 3409 | 14.7414 | sample=1 perioc |

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 248.32 | 15.68 | 955.8 | 342 | 58 | 55 | 67.5 | 120 | 1.797e+7 |

R.MITGVPWYS[+1134]TR.L z=3,scan#=sample=1 period=1 cycle=956 experiment=6,scan time=14.7414

Sample S3 R.MITGVPWYS[+1134.370]TR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 540... | 1 | 47 | R.AHLAEYYS[+162.05282]F.Q | S8(OGlycan / 162.0528) | Hex(1) | 545.3 | 277.6 | 2 | 631.7762 | 631.7824 | -9.85 | | 1262.5451 | 1262.5575 | CRagged | 8 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 15.0035 | sample=1 perioc |

**Proteins**

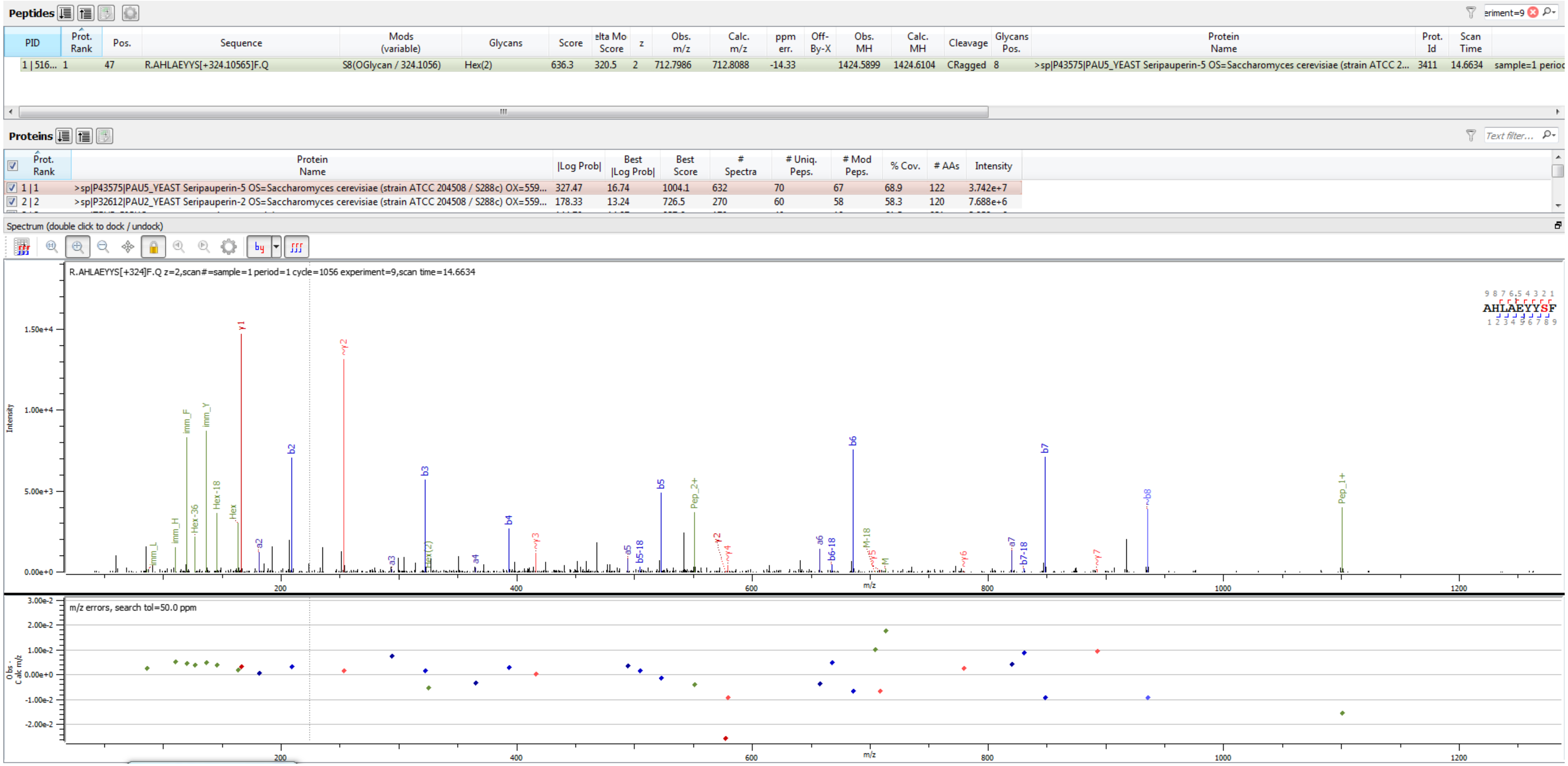
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.AHLAEYYS[+162]F.Q z=2,scan#=sample=1 period=1 cycle=1068 experiment=4,scan time=15.0035

m/z errors, search tol=50.0 ppm

Sample S1 R.AHLAEYYS[+162.053]F.Q



**Peptides**

eriment=9

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 516... | 1 | 47 | R.AHLAEYYS[+324.10565]F.Q | S8(OGlycan / 324.1056) | Hex(2) | 636.3 | 320.5 | 2 | 712.7986 | 712.8088 | -14.33 | | 1424.5899 | 1424.6104 | CRagged | 8 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.6634 | sample=1 perioc |

**Proteins**

Text filter...

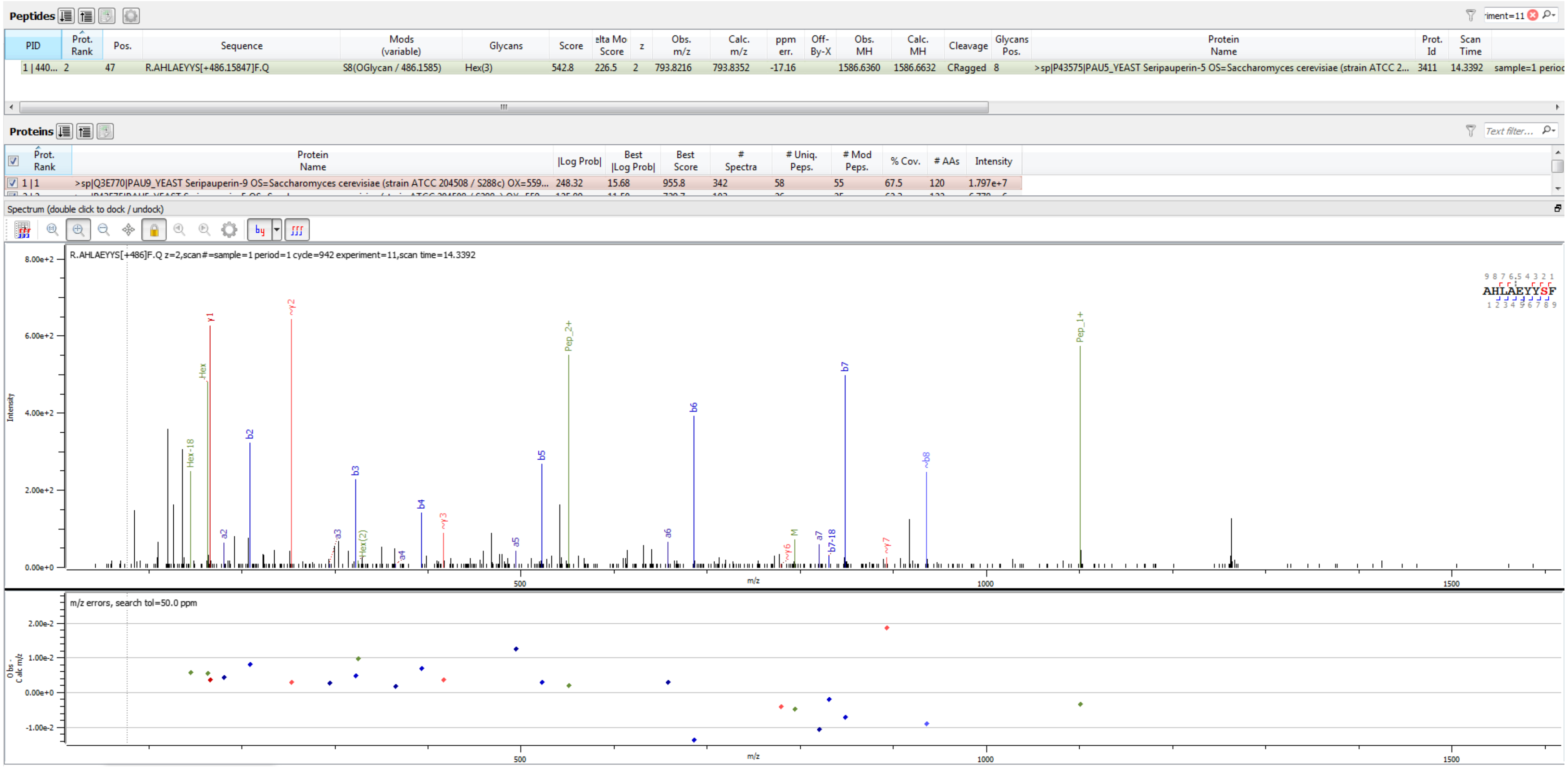
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.AHLAEYYS[+324]F.Q z=2,scan#=sample=1 period=1 cycle=1056 experiment=9,scan time=14.6634

m/z errors, search tol=50.0 ppm

Sample S1 R.AHLAEYYS[+324.106]F.Q



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 440... | 2 | 47 | R.AHLAEYYS[+486.15847]F.Q | S8(OGlycan / 486.1585) | Hex(3) | 542.8 | 226.5 | 2 | 793.8216 | 793.8352 | -17.16 | | 1586.6360 | 1586.6632 | CRagged | 8 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.3392 | sample=1 perioc |

**Proteins**

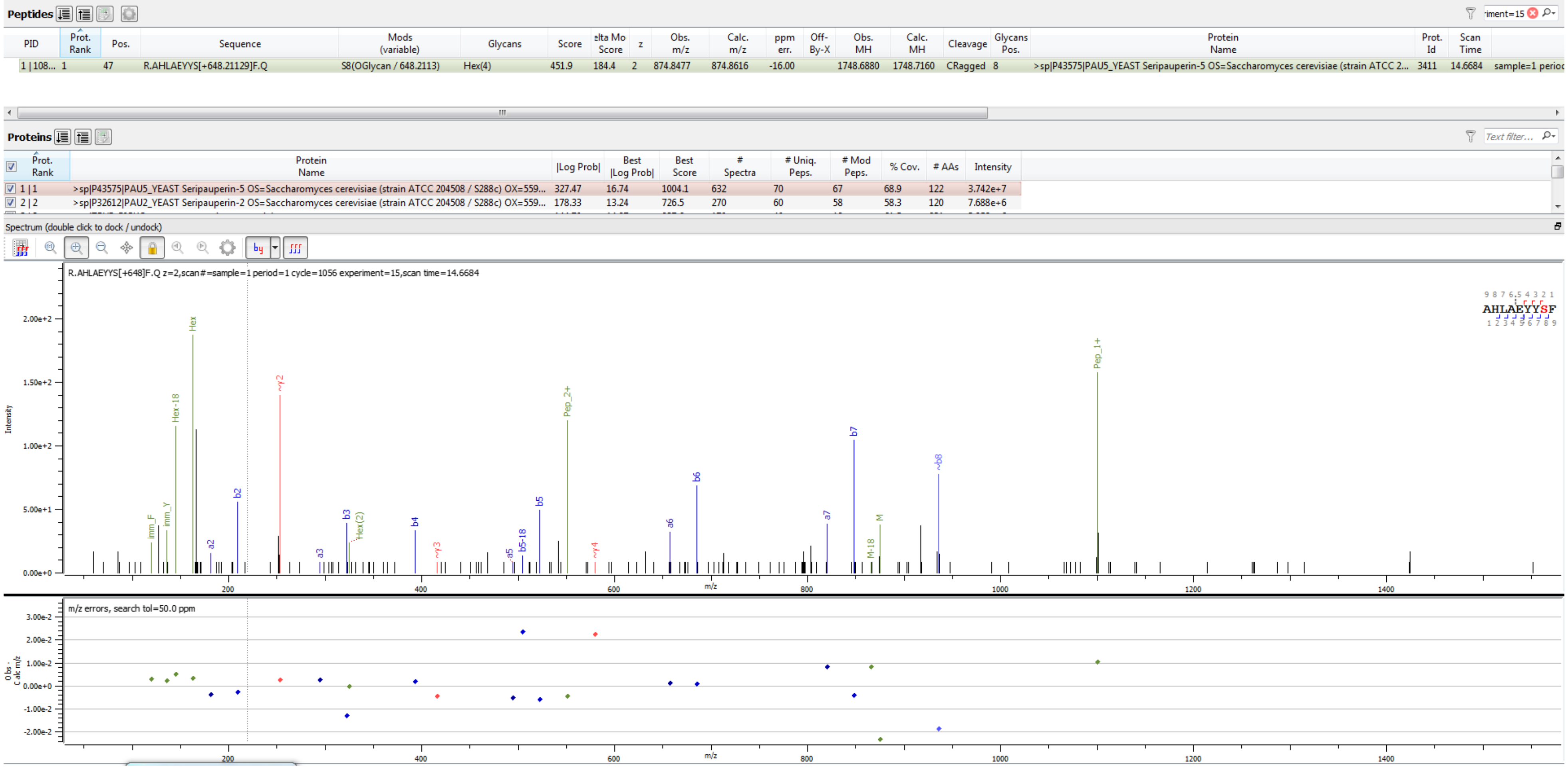
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 248.32 | 15.68 | 955.8 | 342 | 58 | 55 | 67.5 | 120 | 1.797e+7 |

Spectrum (double click to dock / undock)

R.AHLAEYYS[+486]F.Q z=2,scan#=sample=1 period=1 cycle=942 experiment=11,scan time=14.3392

m/z errors, search tol=50.0 ppm

Sample S3 R.AHLAEYYS[+486.158]F.Q



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 108... | 1 | 47 | R.AHLAEYYS[+648.21129]F.Q | S8(OGlycan / 648.2113) | Hex(4) | 451.9 | 184.4 | 2 | 874.8477 | 874.8616 | -16.00 | | 1748.6880 | 1748.7160 | CRagged | 8 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.6684 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ | 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Sample S1 R.AHLAEYYS[+648.211]F.Q

Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 511... | 2 | 45 | R.AHLAQYYS[+162.05282]F.Q | S8(OGlycan / 162.0528) | Hex(1) | 529.6 | 336.8 | 2 | 631.2811 | 631.2904 | -14.69 | | 1261.5550 | 1261.5735 | CRagged | 8 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 14.6023 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.AHLAQYYS[+162]F.Q z=2,scan#=sample=1 period=1 cycle=1054 experiment=4,scan time=14.6023

m/z errors, search tol=50.0 ppm

Sample S1 R.AHLAQYYS[+162.053]F.Q

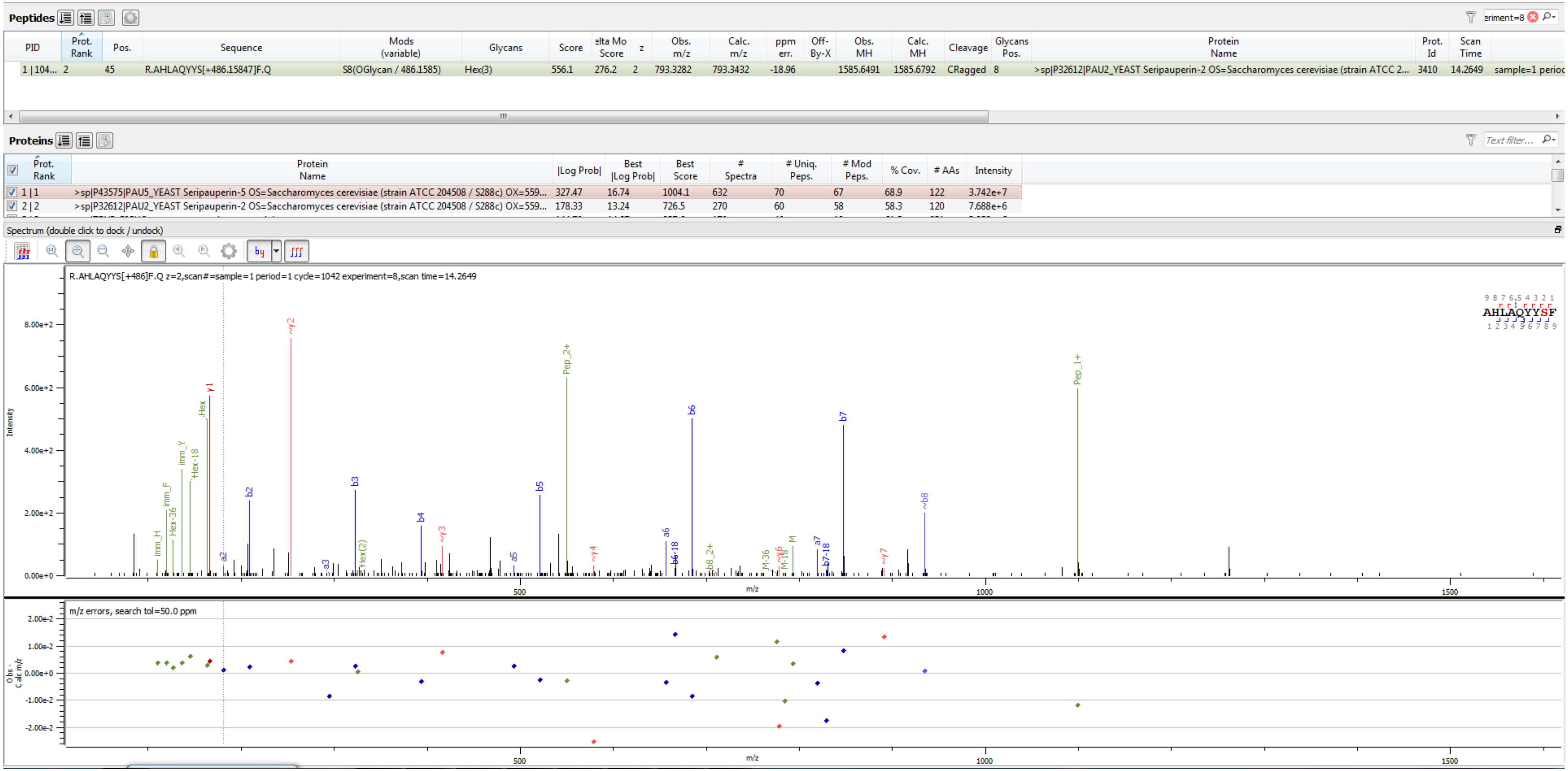
| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 506... | 2 | 45 | R.AHLAQYYS[+324.10565]F.Q | S8(OGlycan / 324.1056) | Hex(2) | 619.5 | 349.5 | 2 | 712.3077 | 712.3168 | -12.84 | | 1423.6081 | 1423.6264 | CRagged | 8 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 14.4929 | sample=1 perioc |

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ | 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

R.AHLAQYYS[+324]F.Q z=2,scan#=sample=1 period=1 cycle=1050 experiment=9,scan time=14.4929

m/z errors, search tol=50.0 ppm

Sample S1 R.AHLAQYYS[+324.106]F.Q



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 104... | 2 | 45 | R.AHLAQYYS[+486.15847]F.Q | S8(OGlycan / 486.1585) | Hex(3) | 556.1 | 276.2 | 2 | 793.3282 | 793.3432 | -18.96 | | 1585.6491 | 1585.6792 | CRagged | 8 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 14.2649 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ | 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.AHLAQYYS[+486]F.Q z=2,scan#=sample=1 period=1 cycle=1042 experiment=8,scan time=14.2649

m/z errors, search tol=50.0 ppm

Sample S1 R.AHLAQYYS[+486.158]F.Q

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 114... | 1 | 45 | R.AHLAQYYS[+648.21129]F.Q | S8(OGlycan / 648.2113) | Hex(4) | 429.1 | 198.2 | 2 | 874.3673 | 874.3696 | -2.68 | | 1747.7273 | 1747.7320 | CRagged | 8 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 14.1683 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |

Spectrum (double click to dock / undock)

R.AHLAQYYS[+648]F.Q z=2,scan#=sample=1 period=1 cycle=920 experiment=16,scan time=14.1683

m/z errors, search tol=50.0 ppm

Sample S4 R.AHLAQYYS[+648.211]F.Q

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off- By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 6483 | 1 | 102 | R.LKPAISSALS[+486.15847]K.D | S10(OGlycan / 486.1585) | Hex(3) | 468.1 | 0.0 | 2 | 800.9109 | 800.9244 | -16.89 | | 1600.8144 | 1600.8415 | Specific | 10 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3461 | 10.6253 | sample=1 perioc |

**Proteins**

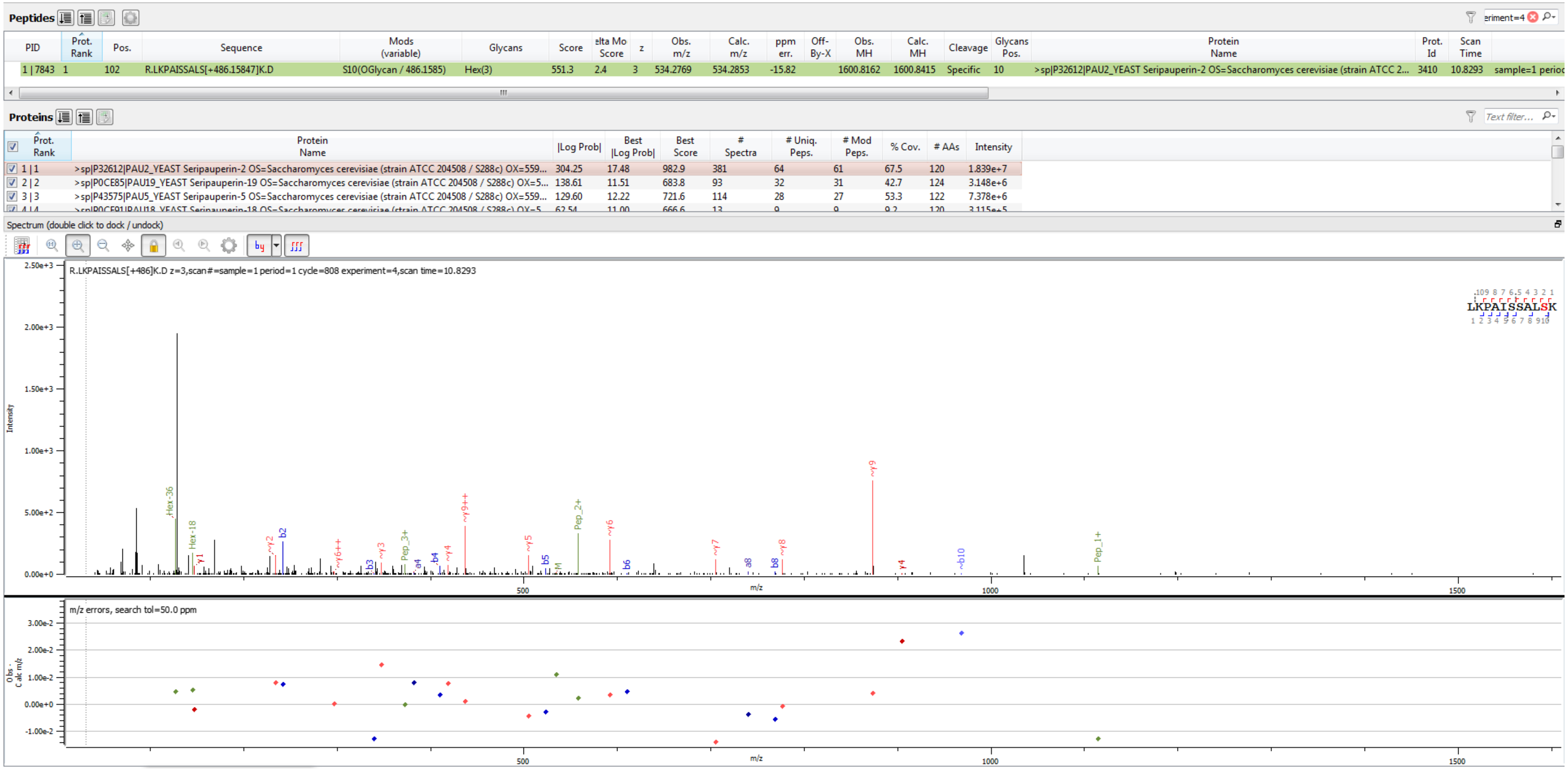
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 248.32 | 15.68 | 955.8 | 342 | 58 | 55 | 67.5 | 120 | 1.797e+7 |

Spectrum (double click to dock / undock)

R.LKPAISSALS[+486]K.D z=2,scan#=sample=1 period=1 cycle=817 experiment=14,scan time=10.6253

m/z errors, search tol=50.0 ppm

Sample S3    R.LKPAISSALS[+486.158]K.D



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 7843 | 1 | 102 | R.LKPAISSALS[+486.15847]K.D | S10(OGlycan / 486.1585) | Hex(3) | 551.3 | 2.4 | 3 | 534.2769 | 534.2853 | -15.82 | | 1600.8162 | 1600.8415 | Specific | 10 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 10.8293 | sample=1 perio |

**Proteins**

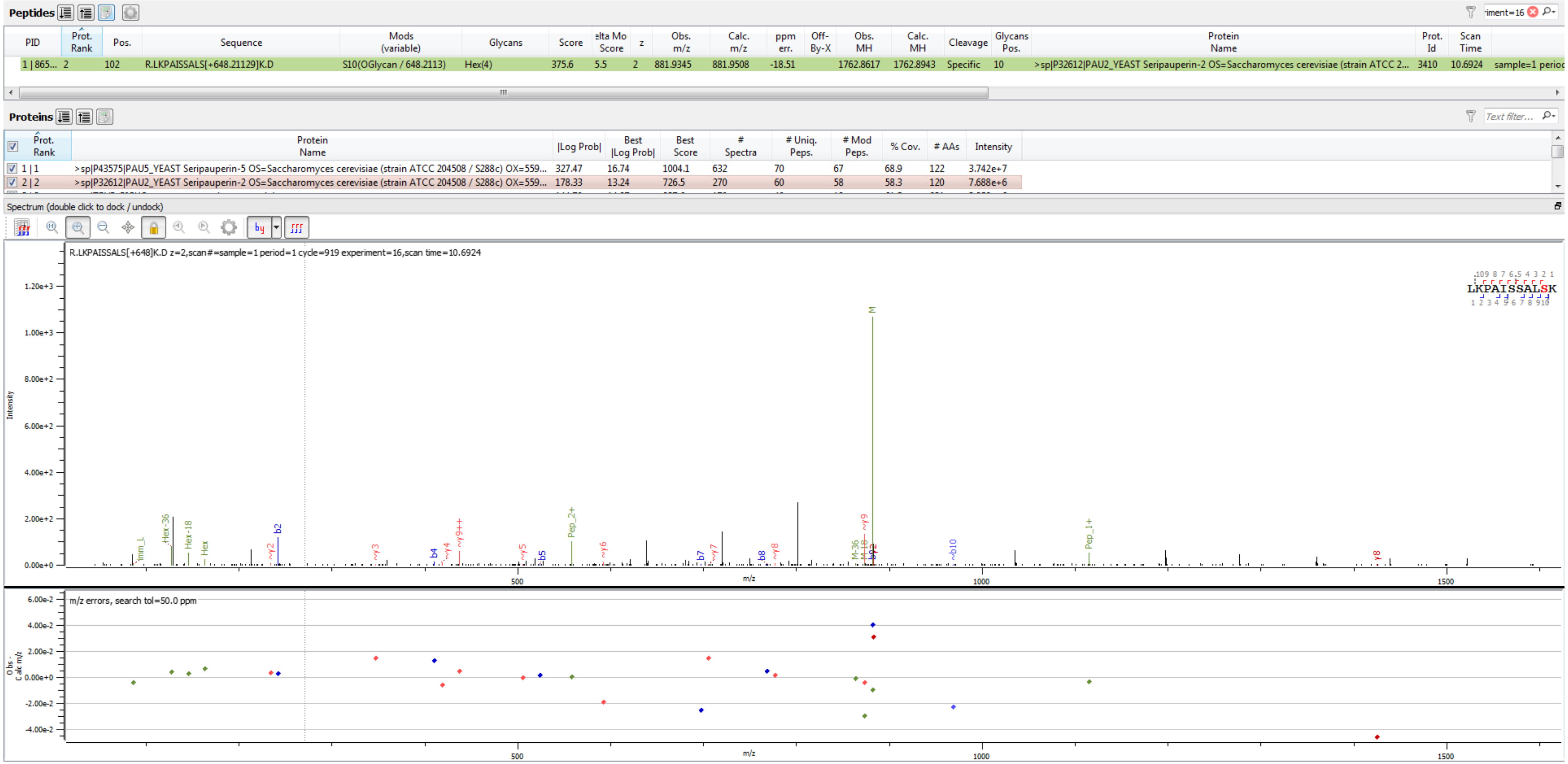
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |
| ☑ 4 \| 4 | >sp\|P0CF91\|PAU18_YEAST Seripauperin-18 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 62.54 | 11.00 | 666.6 | 13 | 9 | 9 | 9.2 | 120 | 3.115e+5 |

Spectrum (double click to dock / undock)

R.LKPAISSALS[+486]K.D z=3,scan#=sample=1 period=1 cycle=808 experiment=4,scan time=10.8293

m/z errors, search tol=50.0 ppm

Sample S4 R.LKPAISSALS[+486.158]K.D



**Peptides**

iment=16

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 865... | 2 | 102 | R.LKPAISSALS[+648.21129]K.D | S10(OGlycan / 648.2113) | Hex(4) | 375.6 | 5.5 | 2 | 881.9345 | 881.9508 | -18.51 | | 1762.8617 | 1762.8943 | Specific | 10 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 10.6924 | sample=1 perioc |

**Proteins**

Text filter...

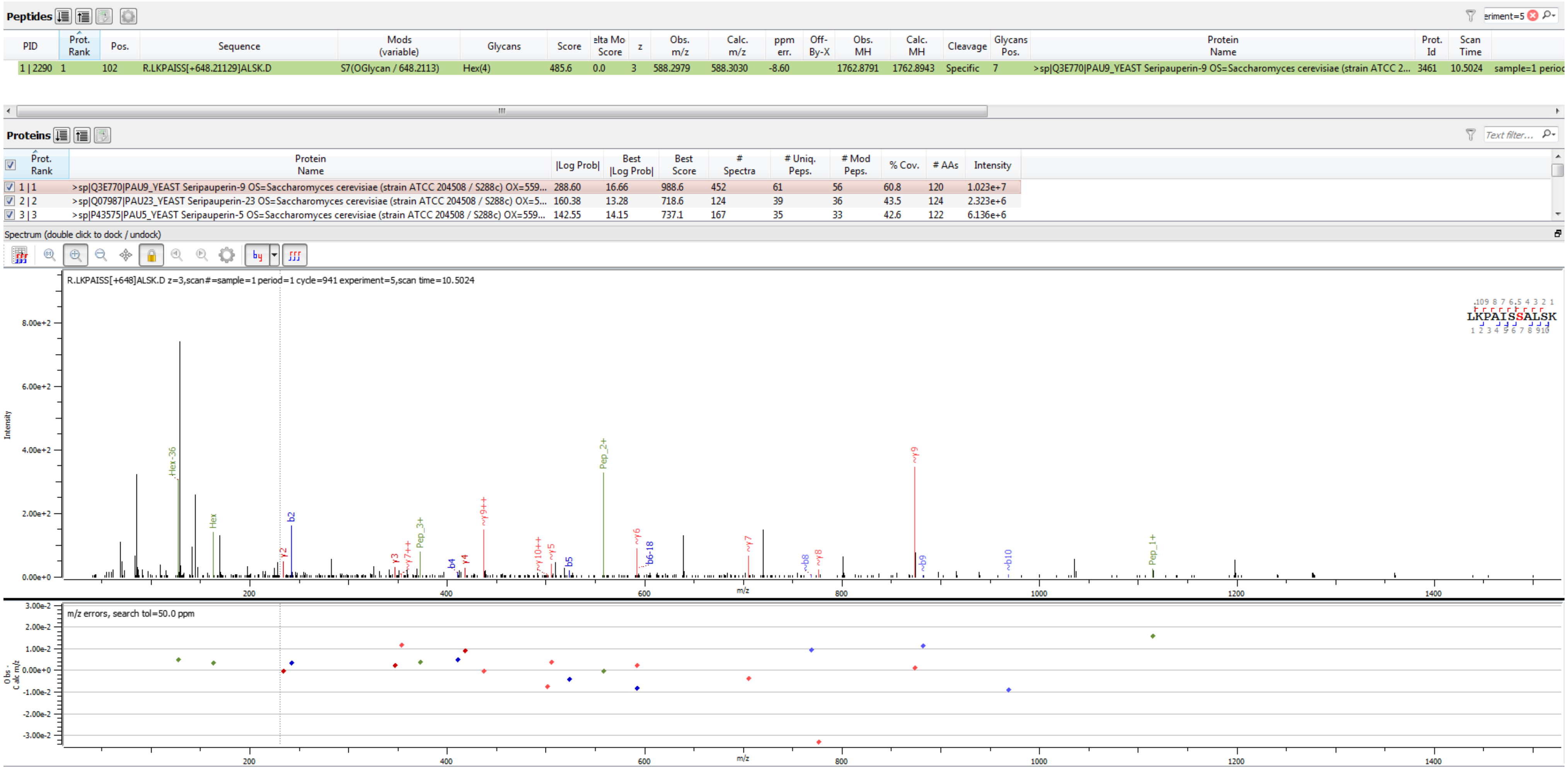
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.LKPAISSALS[+648]K.D z=2,scan#=sample=1 period=1 cycle=919 experiment=16,scan time=10.6924

m/z errors, search tol=50.0 ppm

Sample S1 R.LKPAISSALS[+648.211]K.D



**Peptides**

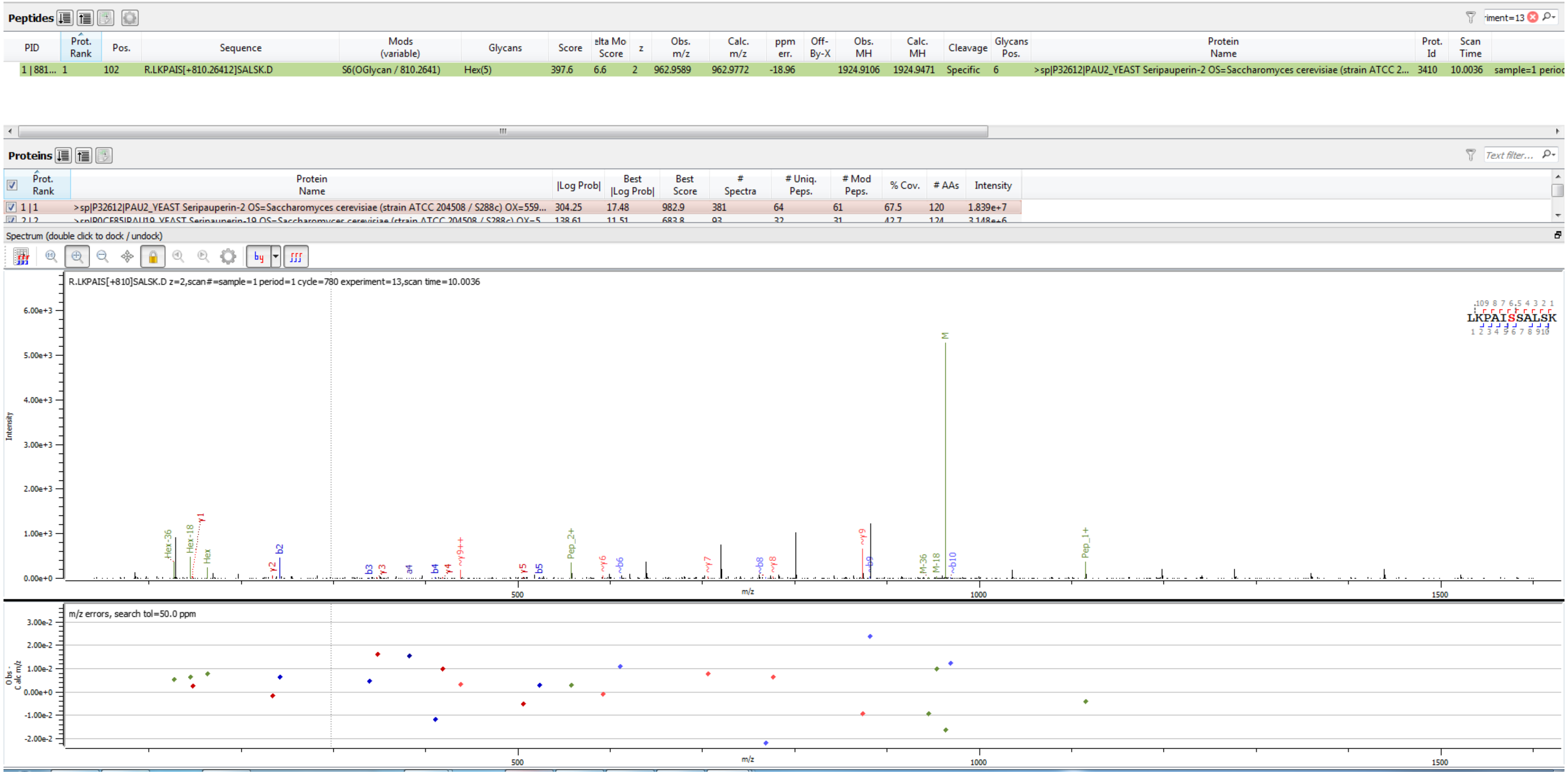
| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 2290 | 1 | 102 | R.LKPAISS[+648.21129]ALSK.D | S7(OGlycan / 648.2113) | Hex(4) | 485.6 | 0.0 | 3 | 588.2979 | 588.3030 | -8.60 | | 1762.8791 | 1762.8943 | Specific | 7 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3461 | 10.5024 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ | 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |

Spectrum (double click to dock / undock)

Sample S6 R.LKPAISS[+648.211]ALSK.D



| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 881... | 1 | 102 | R.LKPAIS[+810.26412]SALSK.D | S6(OGlycan / 810.2641) | Hex(5) | 397.6 | 6.6 | 2 | 962.9589 | 962.9772 | -18.96 | | 1924.9106 | 1924.9471 | Specific | 6 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 10.0036 | sample=1 perioc |

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |

R.LKPAIS[+810]SALSK.D z=2,scan#=sample=1 period=1 cycle=780 experiment=13,scan time=10.0036

m/z errors, search tol=50.0 ppm

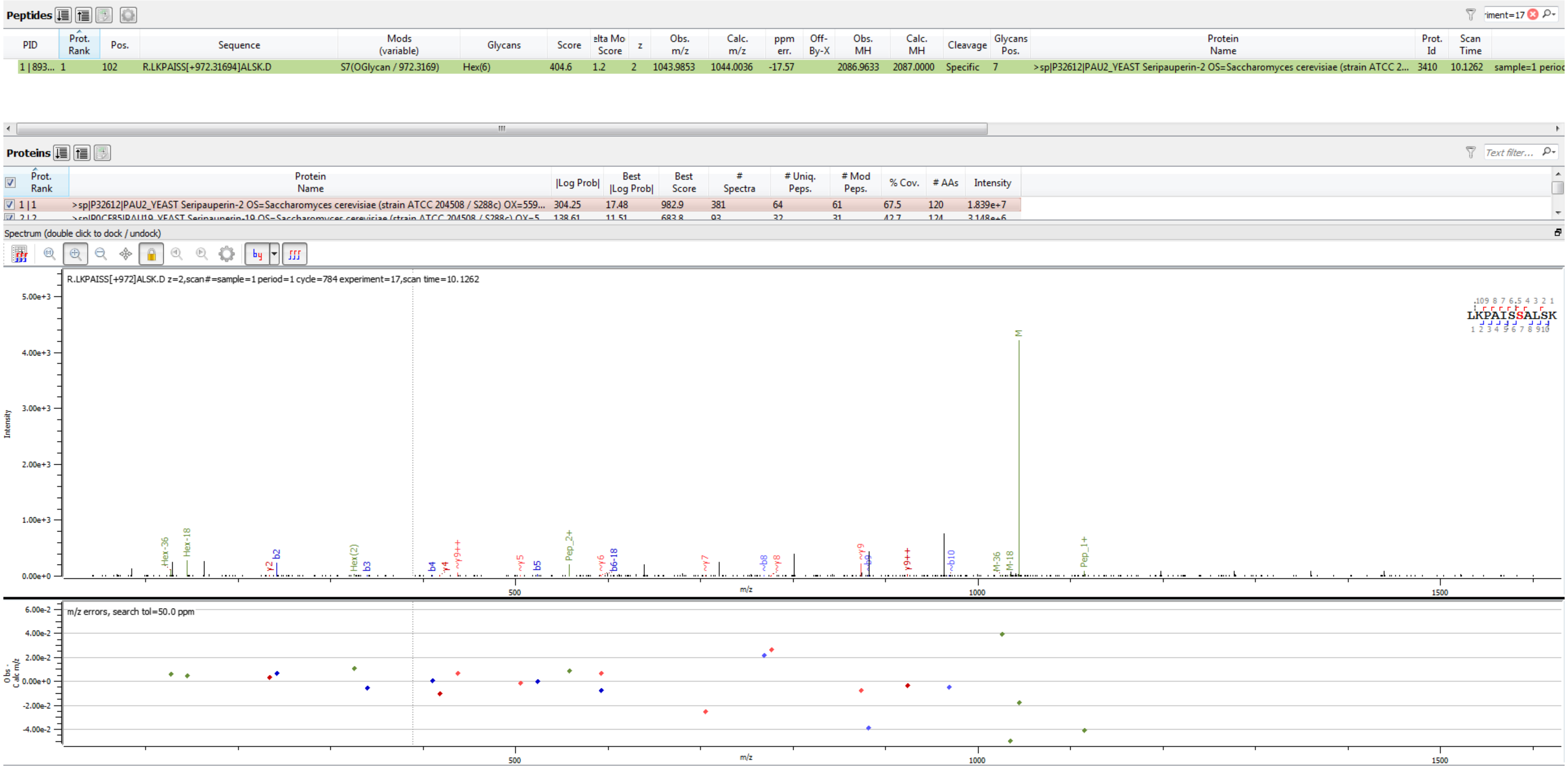
Sample S1 R.LKPAIS[+810.264]SALSK.D

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 830... | 2 | 102 | R.LKPAISS[+810.26412]ALSK.D | S7(OGlycan / 810.2641) | Hex(5) | 516.9 | 0.0 | 3 | 642.3138 | 642.3206 | -10.57 | | 1924.9268 | 1924.9471 | Specific | 7 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 10.3352 | sample=1 perioc |

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

R.LKPAISS[+810]ALSK.D z=3,scan#=sample=1 period=1 cycle=907 experiment=5,scan time=10.3352

Sample S1 R.LKPAISS[+810.264]ALSK.D



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 893... | 1 | 102 | R.LKPAISS[+972.31694]ALSK.D | S7(OGlycan / 972.3169) | Hex(6) | 404.6 | 1.2 | 2 | 1043.9853 | 1044.0036 | -17.57 | | 2086.9633 | 2087.0000 | Specific | 7 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 10.1262 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CF85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5 | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |

Spectrum (double click to dock / undock)

Sample S4 R.LKPAISS[+972.317]ALSK.D

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 875... | 1 | 102 | R.LKPAISS[+972.31694]ALSK.D | S7(OGlycan / 972.3169) | Hex(6) | 524.9 | 1.2 | 3 | 696.3297 | 696.3382 | -12.13 | | 2086.9746 | 2087.0000 | Specific | 7 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 9.9411 | sample=1 perioc |

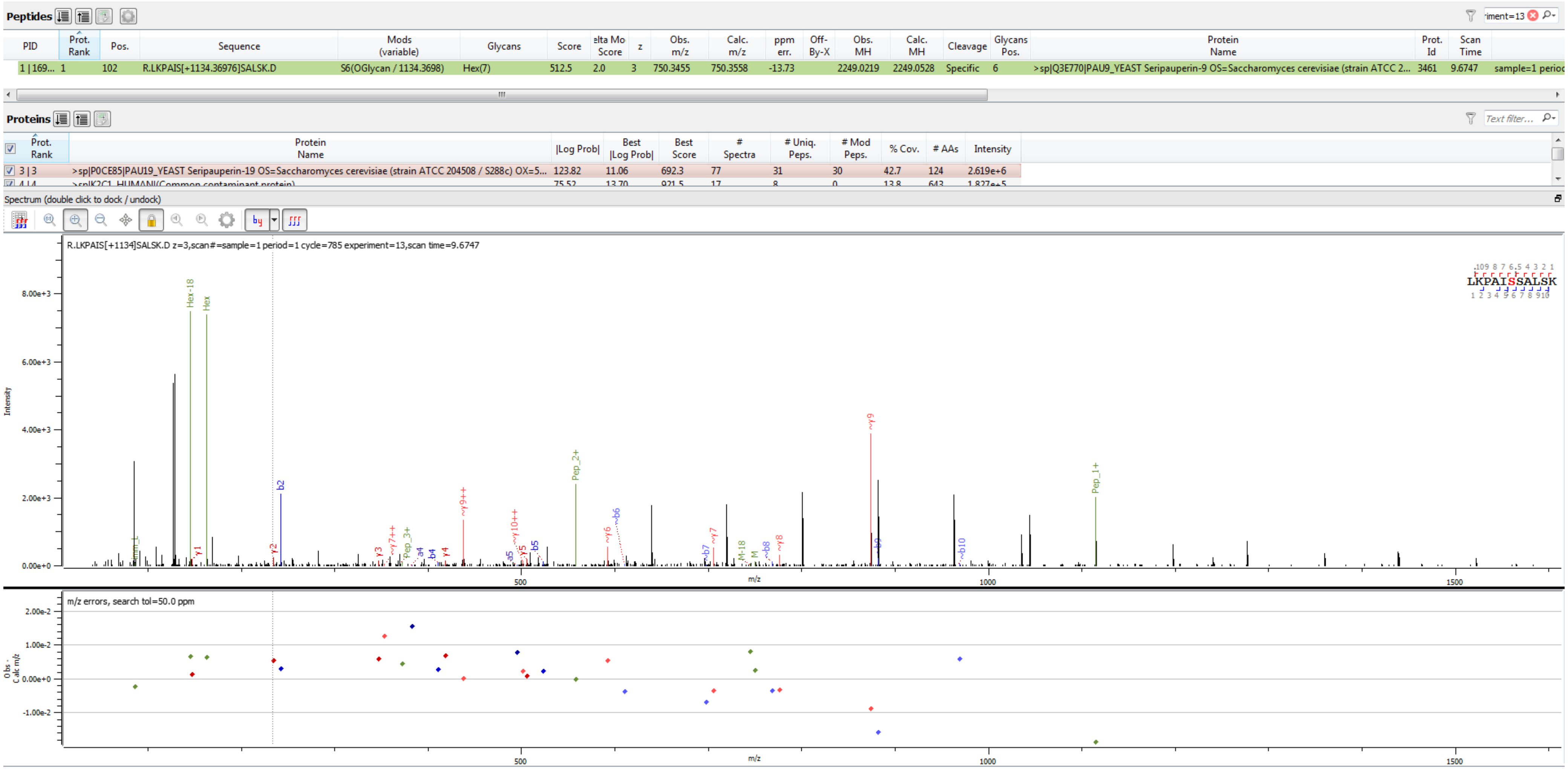
**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |

Spectrum (double click to dock / undock)

R.LKPAISS[+972]ALSK.D z=3,scan#=sample=1 period=1 cycle=778 experiment=10,scan time=9.9411

Sample S4 R.LKPAISS[+972.317]ALSK.D



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 169... | 1 | 102 | R.LKPAIS[+1134.36976]SALSK.D | S6(OGlycan / 1134.3698) | Hex(7) | 512.5 | 2.0 | 3 | 750.3455 | 750.3558 | -13.73 | | 2249.0219 | 2249.0528 | Specific | 6 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3461 | 9.6747 | sample=1 perioc |

iment=13

**Proteins**

Text filter...

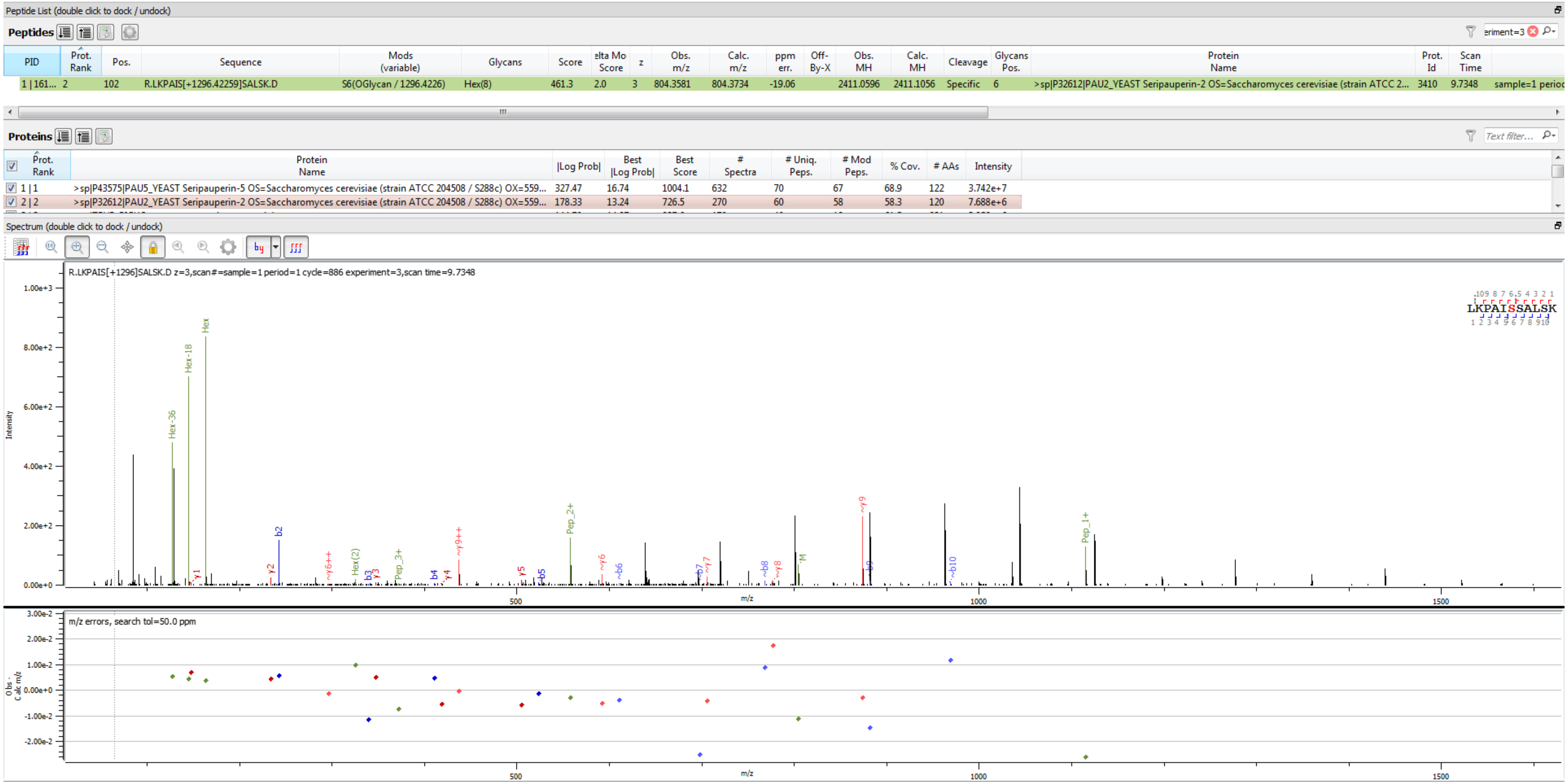
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 123.82 | 11.06 | 692.3 | 77 | 31 | 30 | 42.7 | 124 | 2.619e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 75.52 | 13.70 | 921.5 | 17 | 8 | 0 | 13.8 | 643 | 1.827e+5 |

Spectrum (double click to dock / undock)

R.LKPAIS[+1134]SALSK.D z=3,scan#=sample=1 period=1 cycle=785 experiment=13,scan time=9.6747

m/z errors, search tol=50.0 ppm

Sample S3 R.LKPAIS[+1134.370]SALSK.D


Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 161... | 2 | 102 | R.LKPAIS[+1296.42259]SALSK.D | S6(OGlycan / 1296.4226) | Hex(8) | 461.3 | 2.0 | 3 | 804.3581 | 804.3734 | -19.06 | | 2411.0596 | 2411.1056 | Specific | 6 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 9.7348 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |
| ☑ 2 \| 2 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 178.33 | 13.24 | 726.5 | 270 | 60 | 58 | 58.3 | 120 | 7.688e+6 |

Spectrum (double click to dock / undock)

R.LKPAIS[+1296]SALSK.D z=3,scan#=sample=1 period=1 cycle=886 experiment=3,scan time=9.7348

Sample S1 R.LKPAIS[+1296.423]SALSK.D

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 111... | 3 | 95 | V.ITGVPWYS[+648.21129]TR.L | S8(OGlycan / 648.2113) | Hex(4) | 482.1 | 0.0 | 2 | 914.4069 | 914.4171 | -11.17 | | 1827.8066 | 1827.8270 | NRagged | 8 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 13.9354 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 123.82 | 11.06 | 692.3 | 77 | 31 | 30 | 42.7 | 124 | 2.619e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 75.52 | 13.70 | 921.5 | 17 | 8 | 0 | 13.8 | 643 | 1.827e+5 |

Spectrum (double click to dock / undock)

V.ITGVPWYS[+648]TR.L z=2,scan#=sample=1 period=1 cycle=928 experiment=16,scan time=13.9354

m/z errors, search tol=50.0 ppm

Sample S3 V.ITGVPWYS[+648.211]TR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 100... | 5 | 95 | V.ITGVPWYST[+810.26412]R.L | T9(OGlycan / 810.2641) | Hex(5) | 468.8 | 0.0 | 2 | 995.4310 | 995.4435 | -12.56 | | 1989.8548 | 1989.8798 | NRagged | 9 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 13.9113 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

Spectrum (double click to dock / undock)

V.ITGVPWYST[+810]R.L z=2,scan#=sample=1 period=1 cycle=1045 experiment=17,scan time=13.9113

m/z errors, search tol=50.0 ppm

Sample S2 V.ITGVPWYST[+810.264]R.L

Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 101... | 5 | 95 | V.ITGVPWYS[+810.26412]TR.L | S8(OGlycan / 810.2641) | Hex(5) | 448.0 | 0.0 | 3 | 663.9558 | 663.9648 | -13.58 | | 1989.8528 | 1989.8798 | NRagged | 8 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 14.0252 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

Spectrum (double click to dock / undock)

V.ITGVPWYS[+810]TR.L z=3,scan#=sample=1 period=1 cycle=1049 experiment=9,scan time=14.0252

m/z errors, search tol=50.0 ppm

Sample S2 V.ITGVPWYS[+810.264]TR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 126... | 5 | 95 | V.ITGVPWYS[+972.31694]TR.L | S8(OGlycan / 972.3169) | Hex(6) | 445.2 | 1.2 | 2 | 1076.4524 | 1076.4699 | -16.26 | | 2151.8976 | 2151.9326 | NRagged | 8 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 13.7051 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

Spectrum (double click to dock / undock)

V.ITGVPWYS[+972]TR.L z=2,scan#=sample=1 period=1 cycle=1038 experiment=19,scan time=13.7051

m/z errors, search tol=50.0 ppm

Sample S2 V.ITGVPWYS[+972.317]TR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 126... | 5 | 95 | V.ITGVPWYS[+972.31694]TR.L | S8(OGlycan / 972.3169) | Hex(6) | 538.7 | 1.2 | 3 | 717.9694 | 717.9824 | -18.08 | | 2151.8937 | 2151.9326 | NRagged | 8 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 13.7270 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

V.ITGVPWYS[+972]TR.L z=3,scan#=sample=1 period=1 cycle=1039 experiment=10,scan time=13.7270

m/z errors, search tol=50.0 ppm

Sample S2 V.ITGVPWYS[+972.317]TR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 190... | 3 | 95 | V.ITGVPWYS[+1134.36976]TR.L | S8(OGlycan / 1134.3698) | Hex(7) | 466.6 | 1.2 | 2 | 1157.4751 | 1157.4964 | -18.41 | | 2313.9428 | 2313.9854 | NRagged | 8 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 13.4854 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 123.82 | 11.06 | 692.3 | 77 | 31 | 30 | 42.7 | 124 | 2.619e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 75.52 | 13.70 | 921.5 | 17 | 8 | 0 | 13.8 | 643 | 1.827e+5 |

Spectrum (double click to dock / undock)

V.ITGVPWYS[+1134]TR.L z=2,scan#=sample=1 period=1 cycle=913 experiment=19,scan time=13.4854

m/z errors, search tol=50.0 ppm

Sample S3 V.ITGVPWYS[+1134.370]TR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 150... | 5 | 95 | V.ITGVPWYS[+1134.36976]TR.L | S8(OGlycan / 1134.3698) | Hex(7) | 492.5 | 1.2 | 3 | 771.9868 | 772.0000 | -17.08 | | 2313.9459 | 2313.9854 | NRagged | 8 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 13.5215 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

Spectrum (double click to dock / undock)

V.ITGVPWYS[+1134]TR.L z=3,scan#=sample=1 period=1 cycle=1032 experiment=11,scan time=13.5215

m/z errors, search tol=50.0 ppm

Sample S2 V.ITGVPWYS[+1134.370]TR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 100... | 3 | 94 | V.ITGVPWYS[+810.26412]SR.L | S8(OGlycan / 810.2641) | Hex(5) | 545.2 | 0.0 | 2 | 988.4244 | 988.4357 | -11.45 | | 1975.8415 | 1975.8641 | NRagged | 8 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 13.8496 | sample=1 perio |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

Spectrum (double click to dock / undock)

V.ITGVPWYS[+810]SR.L z=2,scan#=sample=1 period=1 cycle=1043 experiment=15,scan time=13.8496

m/z errors, search tol=50.0 ppm

Sample S2 V.ITGVPWYS[+810.264]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 834... | 1 | 94 | V.ITGVPWYSS[+810.26412]R.L | S9(OGlycan / 810.2641) | Hex(5) | 580.7 | 0.0 | 3 | 659.2827 | 659.2929 | -15.52 | | 1975.8335 | 1975.8641 | NRagged | 9 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 13.8578 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 136.57 | 14.25 | 968.4 | 163 | 30 | 27 | 28.7 | 122 | 1.440e+6 |

Spectrum (double click to dock / undock)

V.ITGVPWYSS[+810]R.L z=3,scan#=sample=1 period=1 cycle=1053 experiment=7,scan time=13.8578

Sample S5 V.ITGVPWYSS[+810.264]R.L

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 126... | 3 | 94 | V.ITGVPWYS[+972.31694]SR.L | S8(OGlycan / 972.3169) | Hex(6) | 481.7 | 1.2 | 2 | 1069.4505 | 1069.4621 | -10.91 | | 2137.8936 | 2137.9170 | NRagged | 8 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 13.5588 | sample=1 perioc |

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

V.ITGVPWYS[+972]SR.L z=2,scan#=sample=1 period=1 cycle=1033 experiment=20,scan time=13.5588

m/z errors, search tol=50.0 ppm

Sample S2 V.ITGVPWYS[+972.317]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 125... | 3 | 94 | V.ITGVPWYS[+972.31694]SR.L | S8(OGlycan / 972.3169) | Hex(6) | 532.3 | 1.2 | 3 | 713.3003 | 713.3105 | -14.33 | | 2137.8863 | 2137.9170 | NRagged | 8 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 13.5199 | sample=1 perioc |

**Proteins**

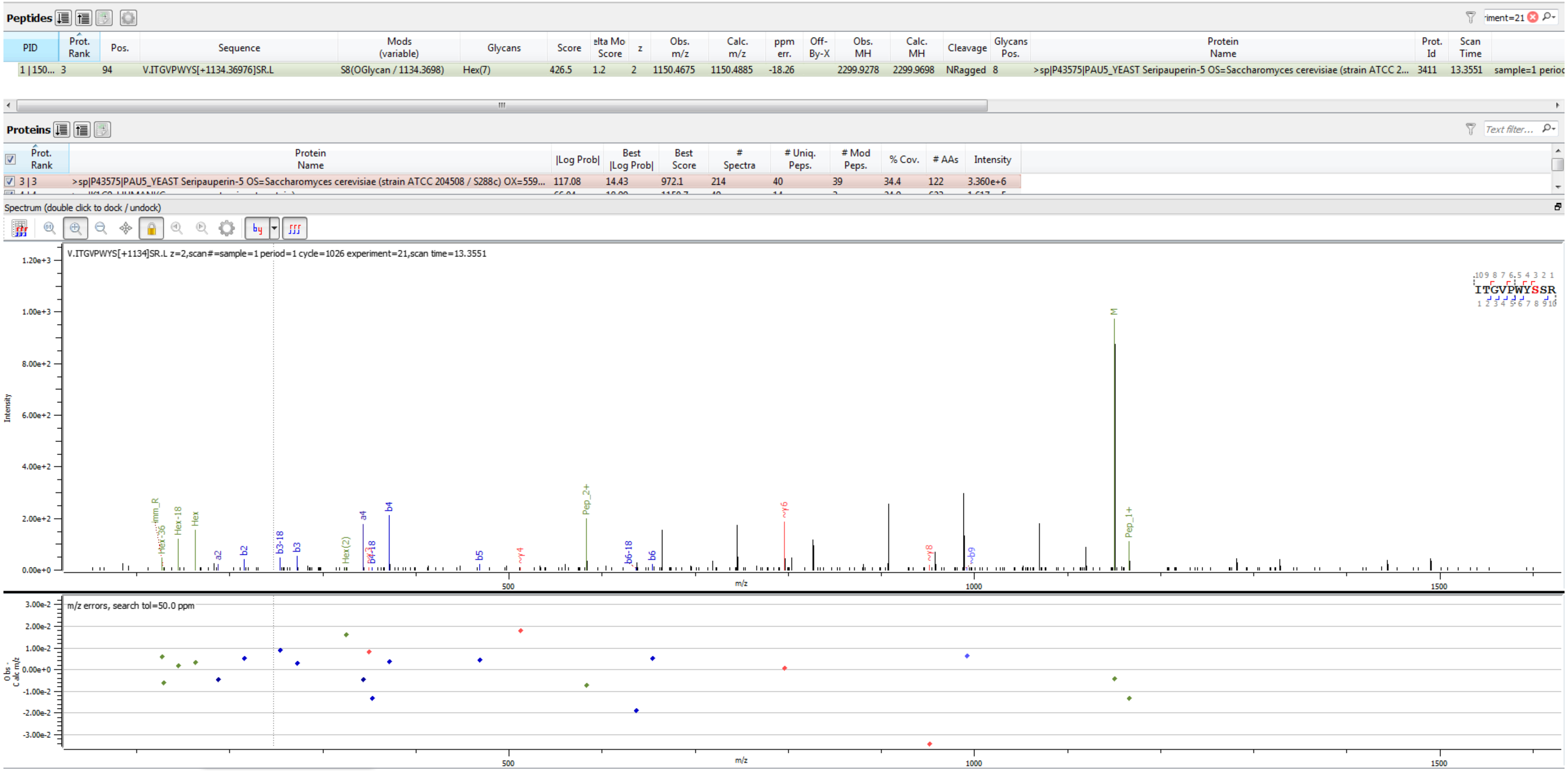
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

Spectrum (double click to dock / undock)

V.ITGVPWYS[+972]SR.L z=3,scan#=sample=1 period=1 cycle=1032 experiment=9,scan time=13.5199

m/z errors, search tol=50.0 ppm

Sample S2 V.ITGVPWYS[+972.317]SR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 150… | 3 | 94 | V.ITGVPWYS[+1134.36976]SR.L | S8(OGlycan / 1134.3698) | Hex(7) | 426.5 | 1.2 | 2 | 1150.4675 | 1150.4885 | -18.26 | | 2299.9278 | 2299.9698 | NRagged | 8 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2… | 3411 | 13.3551 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559… | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

V.ITGVPWYS[+1134]SR.L z=2,scan#=sample=1 period=1 cycle=1026 experiment=21,scan time=13.3551

Sample S2 V.ITGVPWYS[+1134.370]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 473... | 1 | 47 | R.AHLAEYYS[+324.10565]FQ.A | S8(OGlycan / 324.1056) | Hex(2) | 573.4 | 326.7 | 2 | 776.8299 | 776.8381 | -10.56 | | 1552.6526 | 1552.6689 | CRagged | 8 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 14.0075 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |

Spectrum (double click to dock / undock)

R.AHLAEYYS[+324]FQ.A z=2,scan#=sample=1 period=1 cycle=1033 experiment=10,scan time=14.0075

m/z errors, search tol=50.0 ppm

Sample S1 R.AHLAEYYS[+324.106]FQ.A

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 953... | 2 | 105 | R.LRPAISSALS[+648.21129]K.D | S10(OGlycan / 648.2113) | Hex(4) | 559.8 | 0.0 | 3 | 597.6273 | 597.6383 | -18.53 | | 1790.8673 | 1790.9005 | Specific | 10 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 10.5948 | sample=1 perioc |

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559 | 129.60 | 12.22 | 721.6 | 114 | 28 | 27 | 53.3 | 122 | 7.378e+6 |

R.LRPAISSALS[+648]K.D z=3,scan#=sample=1 period=1 cycle=800 experiment=12,scan time=10.5948

Sample S4 R.LRPAISSALS[+648.211]K.D

**Peptides**

eriment=3

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 805... | 2 | 105 | R.LRPAISSALS[+810.26412]K.D | S10(OGlycan / 810.2641) | Hex(5) | 554.9 | 0.0 | 3 | 651.6456 | 651.6559 | -15.94 | | 1952.9222 | 1952.9533 | Specific | 10 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 10.3538 | sample=1 perio |

**Proteins**

Text filter...

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |

Spectrum (double click to dock / undock)

R.LRPAISSALS[+810]K.D z=3,scan#=sample=1 period=1 cycle=936 experiment=3,scan time=10.3538

m/z errors, search tol=50.0 ppm

Sample S6 R.LRPAISSALS[+810.264]K.D

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 172... | 3 | 105 | R.LRPAIS[+972.31694]SALSK.D | S6(OGlycan / 972.3169) | Hex(6) | 501.0 | 2.0 | 3 | 705.6641 | 705.6736 | -13.42 | | 2114.9777 | 2115.0061 | Specific | 6 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 9.9368 | sample=1 perioc |

**Proteins**

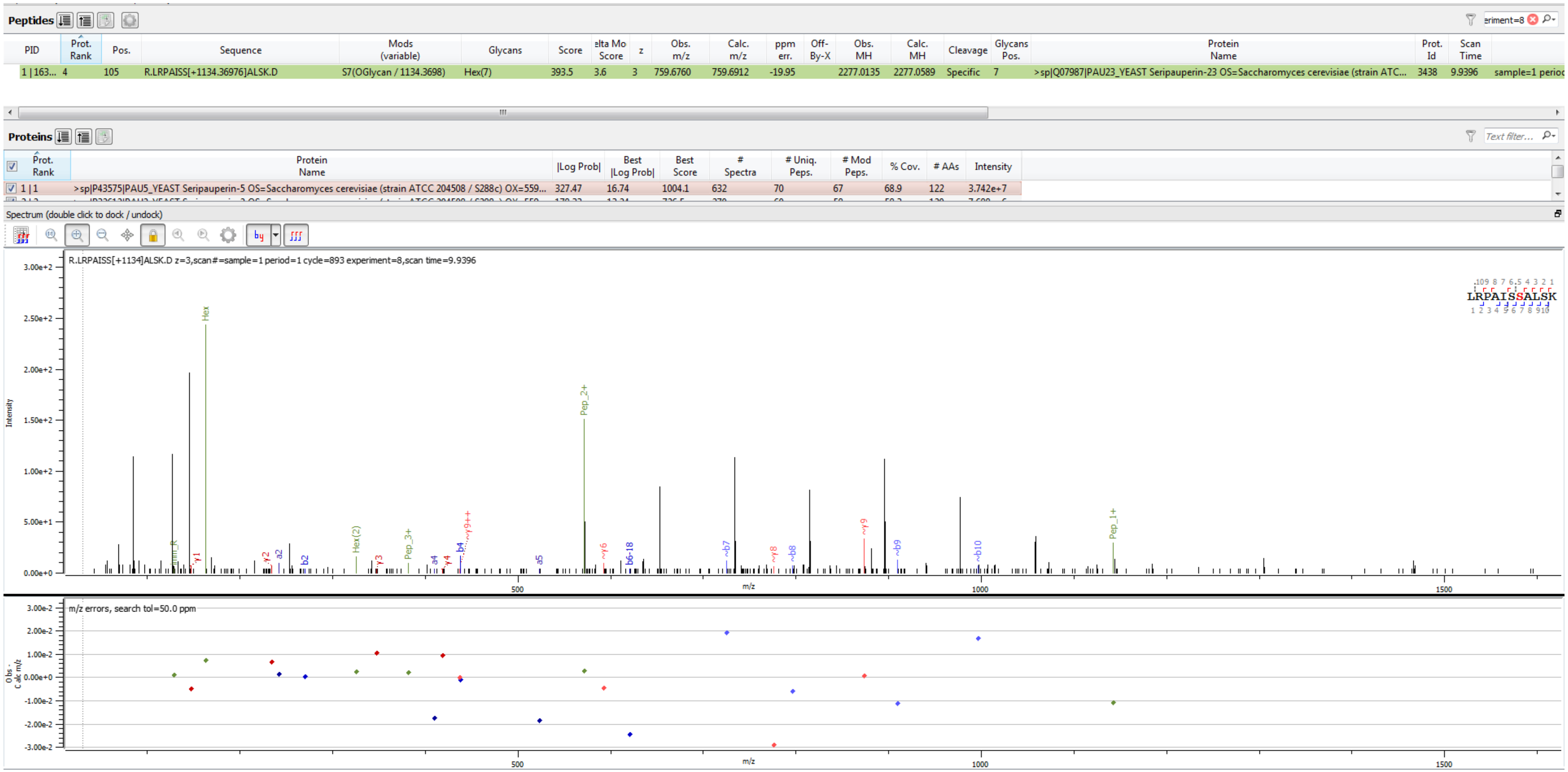
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 123.82 | 11.06 | 692.3 | 77 | 31 | 30 | 42.7 | 124 | 2.619e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 75.52 | 13.70 | 921.5 | 17 | 8 | 0 | 13.8 | 643 | 1.827e+5 |

Spectrum (double click to dock / undock)

R.LRPAIS[+972]SALSK.D z=3,scan#=sample=1 period=1 cycle=794 experiment=5,scan time=9.9368

m/z errors, search tol=50.0 ppm

Sample S3 R.LRPAIS[+972.317]SALSK.D



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 163... | 4 | 105 | R.LRPAISS[+1134.36976]ALSK.D | S7(OGlycan / 1134.3698) | Hex(7) | 393.5 | 3.6 | 3 | 759.6760 | 759.6912 | -19.95 | | 2277.0135 | 2277.0589 | Specific | 7 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 9.9396 | sample=1 perio |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |

Spectrum (double click to dock / undock)

R.LRPAISS[+1134]ALSK.D z=3,scan#=sample=1 period=1 cycle=893 experiment=8,scan time=9.9396

m/z errors, search tol=50.0 ppm

Sample S1 R.LRPAISS[+1134.370]ALSK.D

**Peptides**

iment=15

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 165... | 2 | 105 | R.LRPAIS[+1296.42259]SALSK.D | S6(OGlycan / 1296.4226) | Hex(8) | 230.7 | 2.0 | 3 | 813.6931 | 813.7088 | -19.29 | | 2439.0647 | 2439.1117 | Specific | 6 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 9.7650 | sample=1 perioc |

**Proteins**

Text filter...

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5 | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |

Spectrum (double click to dock / undock)

R.LRPAIS[+1296]SALSK.D z=3,scan#=sample=1 period=1 cycle=772 experiment=15,scan time=9.7650

m/z errors, search tol=50.0 ppm

Sample S4 R.LRPAIS[+1296.423]SALSK.D

**Peptides**

iment=13

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 112... | 1 | 92 | M.ITGVPWYSS[+648.21129]R.L | S9(OGlycan / 648.2113) | Hex(4) | 551.3 | 0.0 | 2 | 907.3915 | 907.4093 | -19.65 | | 1813.7757 | 1813.8113 | NRagged | 9 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 13.8662 | sample=1 perioc |

**Proteins**

Text filter...

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |

Spectrum (double click to dock / undock)

M.ITGVPWYSS[+648]R.L z=2,scan#=sample=1 period=1 cycle=910 experiment=13,scan time=13.8662

m/z errors, search tol=50.0 ppm

Sample S4 M.ITGVPWYSS[+648.211]R.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 190... | 1 | 92 | M.ITGVPWYS[+1134.36976]SR.L | S8(OGlycan / 1134.3698) | Hex(7) | 463.1 | 1.2 | 3 | 767.3167 | 767.3281 | -14.82 | | 2299.9357 | 2299.9698 | NRagged | 8 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3461 | 13.3300 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 123.82 | 11.06 | 692.3 | 77 | 31 | 30 | 42.7 | 124 | 2.619e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 75.52 | 13.70 | 921.5 | 17 | 8 | 0 | 13.8 | 643 | 1.827e+5 |

M.ITGVPWYS[+1134]SR.L z=3,scan#=sample=1 period=1 cycle=908 experiment=15,scan time=13.3300

m/z errors, search tol=50.0 ppm

x:305.5880
y:0.03569

Sample S3 M.ITGVPWYS[+1134.370]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 180... | 1 | 92 | M.ITGVPWYS[+1296.42259]SR.L | S8(OGlycan / 1296.4226) | Hex(8) | 474.5 | 1.2 | 3 | 821.3375 | 821.3457 | -10.00 | | 2461.9980 | 2462.0226 | NRagged | 8 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3410 | 13.1470 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ | 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5 | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |

Spectrum (double click to dock / undock)

M.ITGVPWYS[+1296]SR.L z=3,scan#=sample=1 period=1 cycle=886 experiment=17,scan time=13.1470

m/z errors, search tol=50.0 ppm

Sample S4 M.ITGVPWYS[+1296.423]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 358... | 1 | 104 | R.LKPAISS[+324.10565]AL.S | S7(OGlycan / 324.1056) | Hex(2) | 496.0 | 8.1 | 2 | 612.3255 | 612.3345 | -14.67 | | 1223.6437 | 1223.6617 | CRagged | 7 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 13.0583 | sample=1 perio |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |

Spectrum (double click to dock / undock)

R.LKPAISS[+324]AL.S z=2,scan#=sample=1 period=1 cycle=1000 experiment=2,scan time=13.0583

m/z errors, search tol=50.0 ppm

Sample S1 R.LKPAISS[+324.106]AL.S

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 315... | 1 | 104 | R.LKPAIS[+486.15847]SAL.S | S6(OGlycan / 486.1585) | Hex(3) | 481.0 | 2.0 | 2 | 693.3480 | 693.3609 | -18.64 | | 1385.6887 | 1385.7145 | CRagged | 6 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 12.7191 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |

Spectrum (double click to dock / undock)

R.LKPAIS[+486]SAL.S z=2,scan#=sample=1 period=1 cycle=988 experiment=14,scan time=12.7191

m/z errors, search tol=50.0 ppm

Sample S1 R.LKPAIS[+486.158]SAL.S

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 255... | 1 | 104 | R.LKPAISS[+648.21129]AL.S | S7(OGlycan / 648.2113) | Hex(4) | 403.4 | 11.2 | 2 | 774.3733 | 774.3873 | -18.09 | | 1547.7393 | 1547.7673 | CRagged | 7 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 2... | 3411 | 12.4284 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |

R.LKPAISS[+648]AL.S z=2,scan#=sample=1 period=1 cycle=978 experiment=16,scan time=12.4284

m/z errors, search tol=50.0 ppm

Sample S1 R.LKPAISS[+648.211]AL.S

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 189... | 17 | 93 | M.LTMVPWYS[+972.31694]SR.L | S8(OGlycan / 972.3169) | Hex(6) | 444.4 | 1.2 | 2 | 1106.4530 | 1106.4716 | -16.89 | | 2211.8986 | 2211.9360 | NRagged | 8 | >sp\|Q12218\|TIR4_YEAST Cell wall protein TIR4 OS=Saccharomyces cerevisiae (strain A... | 4963 | 14.7199 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|P32612\|PAU2_YEAST Seripauperin-2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 304.25 | 17.48 | 982.9 | 381 | 64 | 61 | 67.5 | 120 | 1.839e+7 |
| ☑ | 2 \| 2 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5 | 138.61 | 11.51 | 683.8 | 93 | 32 | 31 | 42.7 | 124 | 3.148e+6 |

Spectrum (double click to dock / undock)

M.LTMVPWYS[+972]SR.L z=2,scan#=sample=1 period=1 cycle=939 experiment=20,scan time=14.7199

m/z errors, search tol=50.0 ppm

Sample S4 M.LTMVPWYS[+972.317]SR.L

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 897... | 10 | 92 | M.LTMVPWYS[+1134.36976]SR.L | S8(OGlycan / 1134.3698) | Hex(7) | 384.4 | 1.2 | 3 | 791.9855 | 792.0011 | -19.74 | | 2373.9419 | 2373.9888 | NRagged | 8 | >sp\|P10863\|TIR1_YEAST Cold shock-induced protein TIR1 OS=Saccharomyces cerevisi... | 4256 | 14.9474 | sample=1 perioc |

**Proteins**

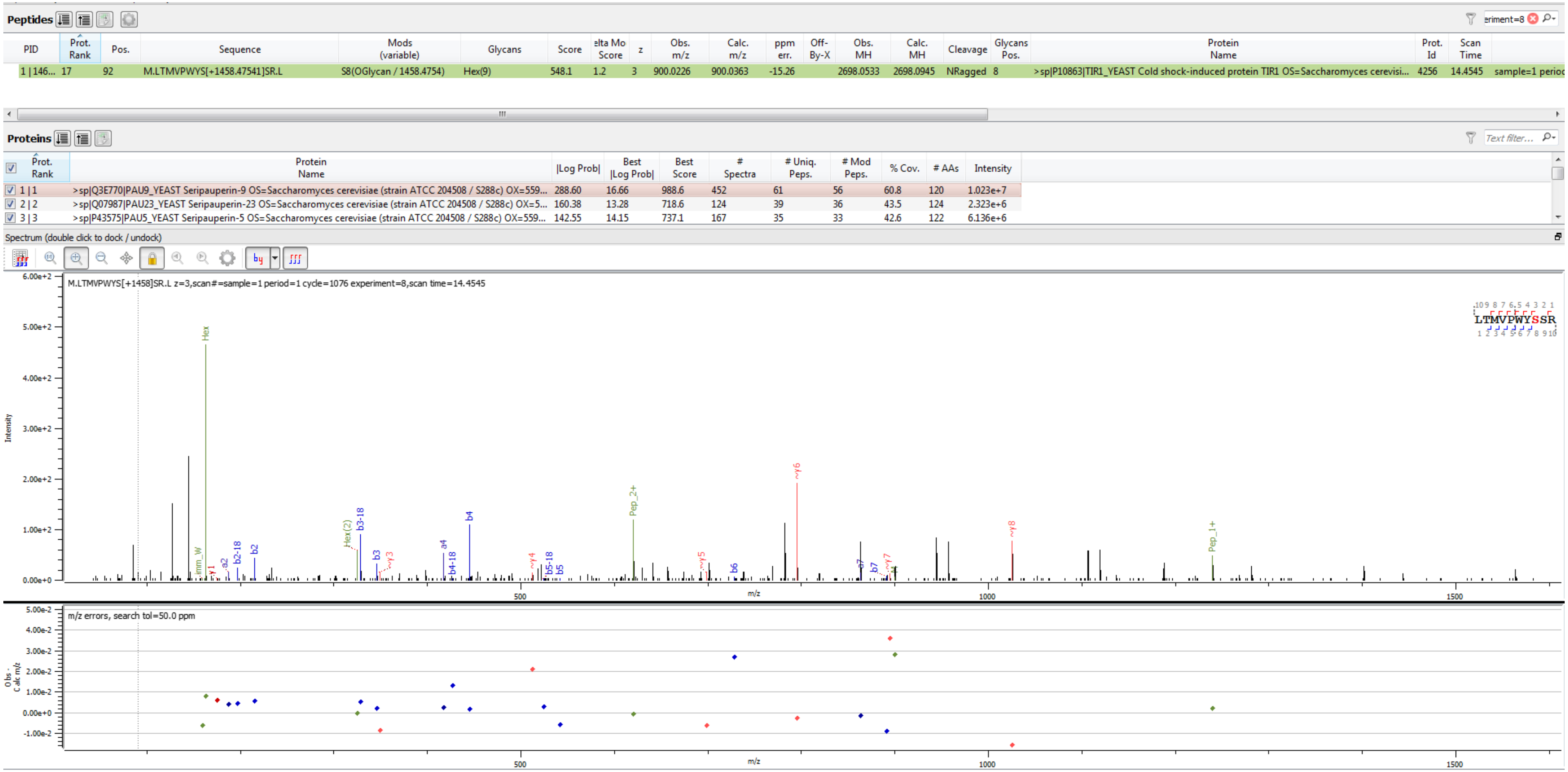
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 136.57 | 14.25 | 968.4 | 163 | 30 | 27 | 28.7 | 122 | 1.440e+6 |

Spectrum (double click to dock / undock)

M.LTMVPWYS[+1134]SR.L z=3,scan#=sample=1 period=1 cycle=1089 experiment=10,scan time=14.9474

m/z errors, search tol=50.0 ppm

Sample S4 M.LTMVPWYS[+1134.370]SR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 146... | 17 | 92 | M.LTMVPWYS[+1458.47541]SR.L | S8(OGlycan / 1458.4754) | Hex(9) | 548.1 | 1.2 | 3 | 900.0226 | 900.0363 | -15.26 | | 2698.0533 | 2698.0945 | NRagged | 8 | >sp\|P10863\|TIR1_YEAST Cold shock-induced protein TIR1 OS=Saccharomyces cerevisi... | 4256 | 14.4545 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |

Spectrum (double click to dock / undock)

M.LTMVPWYS[+1458]SR.L z=3,scan#=sample=1 period=1 cycle=1076 experiment=8,scan time=14.4545

m/z errors, search tol=50.0 ppm

Sample S6 M.LTMVPWYS[+1458.475]SR.L

**Peptides**

iment=13

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 262... | 3 | 105 | R.LRPAISS[+486.15847]AL.S | S7(OGlycan / 486.1585) | Hex(3) | 481.0 | 17.7 | 2 | 707.3562 | 707.3640 | -10.92 | | 1413.7052 | 1413.7206 | CRagged | 7 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATC... | 3420 | 12.7089 | sample=1 peri |

**Proteins**

Text filter...

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P0CE85\|PAU19_YEAST Seripauperin-19 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 123.82 | 11.06 | 692.3 | 77 | 31 | 30 | 42.7 | 124 | 2.619e+6 |
| ☑ 4 \| 4 | >sp\|K2C1_HUMAN\|(Common contaminant protein) | 75.52 | 13.70 | 921.5 | 17 | 8 | 0 | 13.8 | 643 | 1.827e+5 |

Spectrum (double click to dock / undock)

R.LRPAISS[+486]AL.S z=2,scan#=sample=1 period=1 cycle=887 experiment=13,scan time=12.7089

m/z errors, search tol=50.0 ppm

Sample S3 R.LRPAISS[+486.158]AL.S

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 218... | 2 | 105 | R.LRPAIS[+648.21129]SAL.S | S6(OGlycan / 648.2113) | Hex(4) | 412.1 | 1.4 | 2 | 788.3810 | 788.3904 | -11.86 | | 1575.7548 | 1575.7735 | CRagged | 6 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATC... | 3438 | 12.6460 | sample=1 perioc |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |

Spectrum (double click to dock / undock)

R.LRPAIS[+648]SAL.S z=2,scan#=sample=1 period=1 cycle=1014 experiment=8,scan time=12.6460

m/z errors, search tol=50.0 ppm

Sample S6 R.LRPAIS[+648.211]SAL.S

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 266... | 15 | 34 | R.AVVTVT[+648.21129]QY.V | T6(OGlycan / 648.2113) | Hex(4) | 467.7 | 56.6 | 2 | 764.8377 | 764.8480 | -13.47 | | 1528.6682 | 1528.6887 | CRagged | 6 | >sp\|P36135\|UTH1_YEAST Probable secreted beta-glucosidase UTH1 OS=Saccharomyc... | 4486 | 12.6868 | sample=1 perioc |

**Proteins**

| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

Spectrum (double click to dock / undock)

R.AVVTVT[+648]QY.V z=2,scan#=sample=1 period=1 cycle=1003 experiment=10,scan time=12.6868

m/z errors, search tol=50.0 ppm

Sample S2 R.AVVTVT[+648.211]QY.V

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 244... | 15 | 34 | R.AVVTVT[+810.26412]QY.V | T6(OGlycan / 810.2641) | Hex(5) | 293.0 | 27.4 | 2 | 845.8661 | 845.8744 | -9.79 | | 1690.7250 | 1690.7416 | CRagged | 6 | >sp\|P36135\|UTH1_YEAST Probable secreted beta-glucosidase UTH1 OS=Saccharomyc... | 4486 | 12.5372 | sample=1 perio |

**Proteins**

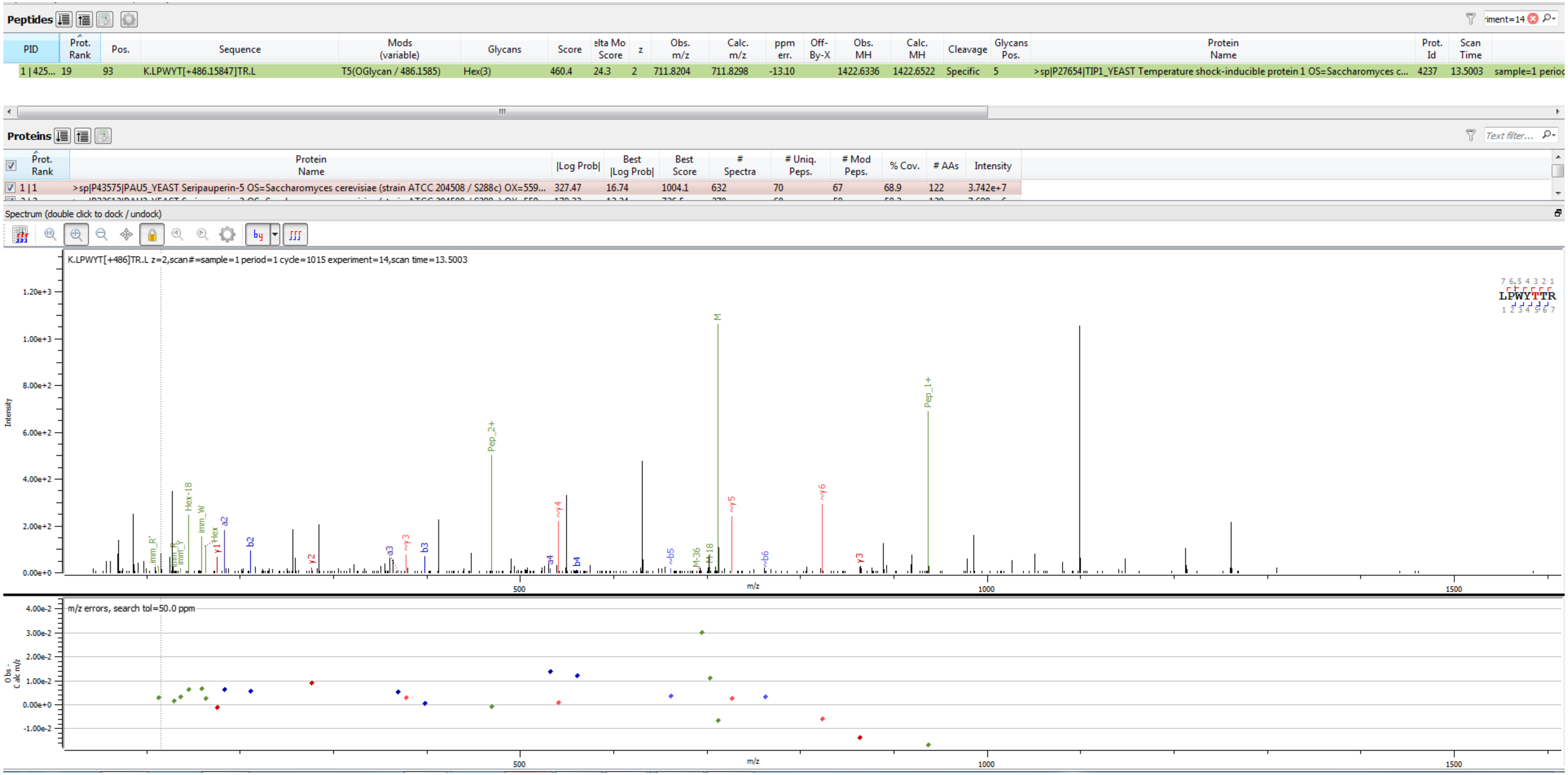
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 117.08 | 14.43 | 972.1 | 214 | 40 | 39 | 34.4 | 122 | 3.360e+6 |

Spectrum (double click to dock / undock)

R.AVVTVT[+810]QY.V z=2,scan#=sample=1 period=1 cycle=998 experiment=11,scan time=12.5372

m/z errors, search tol=50.0 ppm

Sample S2 R.AVVTVT[+810.264]QY.V



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 425... | 19 | 93 | K.LPWYT[+486.15847]TR.L | T5(OGlycan / 486.1585) | Hex(3) | 460.4 | 24.3 | 2 | 711.8204 | 711.8298 | -13.10 | | 1422.6336 | 1422.6522 | Specific | 5 | >sp\|P27654\|TIP1_YEAST Temperature shock-inducible protein 1 OS=Saccharomyces c... | 4237 | 13.5003 | sample=1 perioc |

**Proteins**

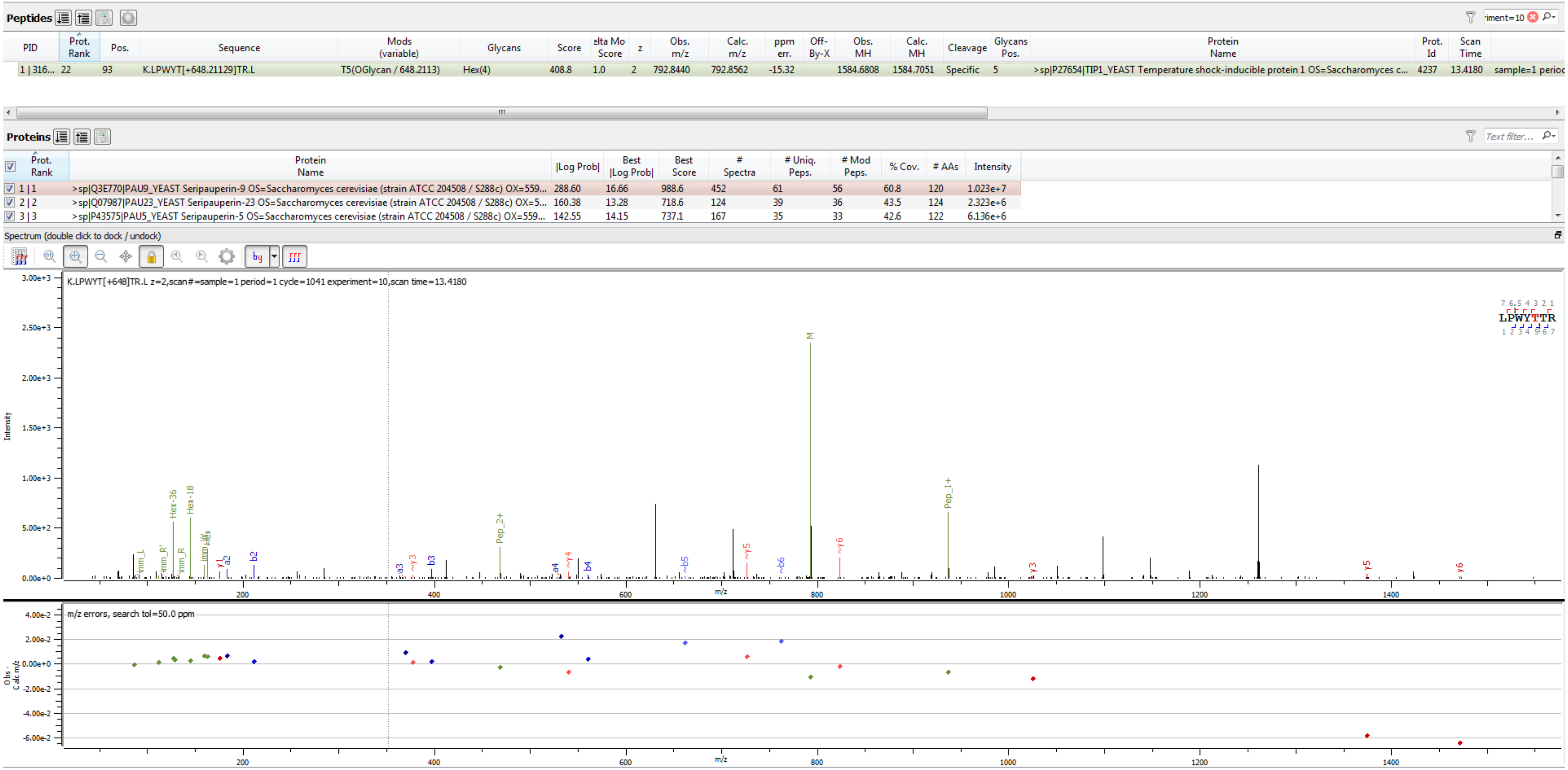
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 327.47 | 16.74 | 1004.1 | 632 | 70 | 67 | 68.9 | 122 | 3.742e+7 |

Spectrum (double click to dock / undock)

K.LPWYT[+486]TR.L z=2,scan#=sample=1 period=1 cycle=1015 experiment=14,scan time=13.5003

m/z errors, search tol=50.0 ppm

Sample S1 K.LPWYT[+486.158]TR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 316... | 22 | 93 | K.LPWYT[+648.21129]TR.L | T5(OGlycan / 648.2113) | Hex(4) | 408.8 | 1.0 | 2 | 792.8440 | 792.8562 | -15.32 | | 1584.6808 | 1584.7051 | Specific | 5 | >sp\|P27654\|TIP1_YEAST Temperature shock-inducible protein 1 OS=Saccharomyces c... | 4237 | 13.4180 | sample=1 perioc |

**Proteins**

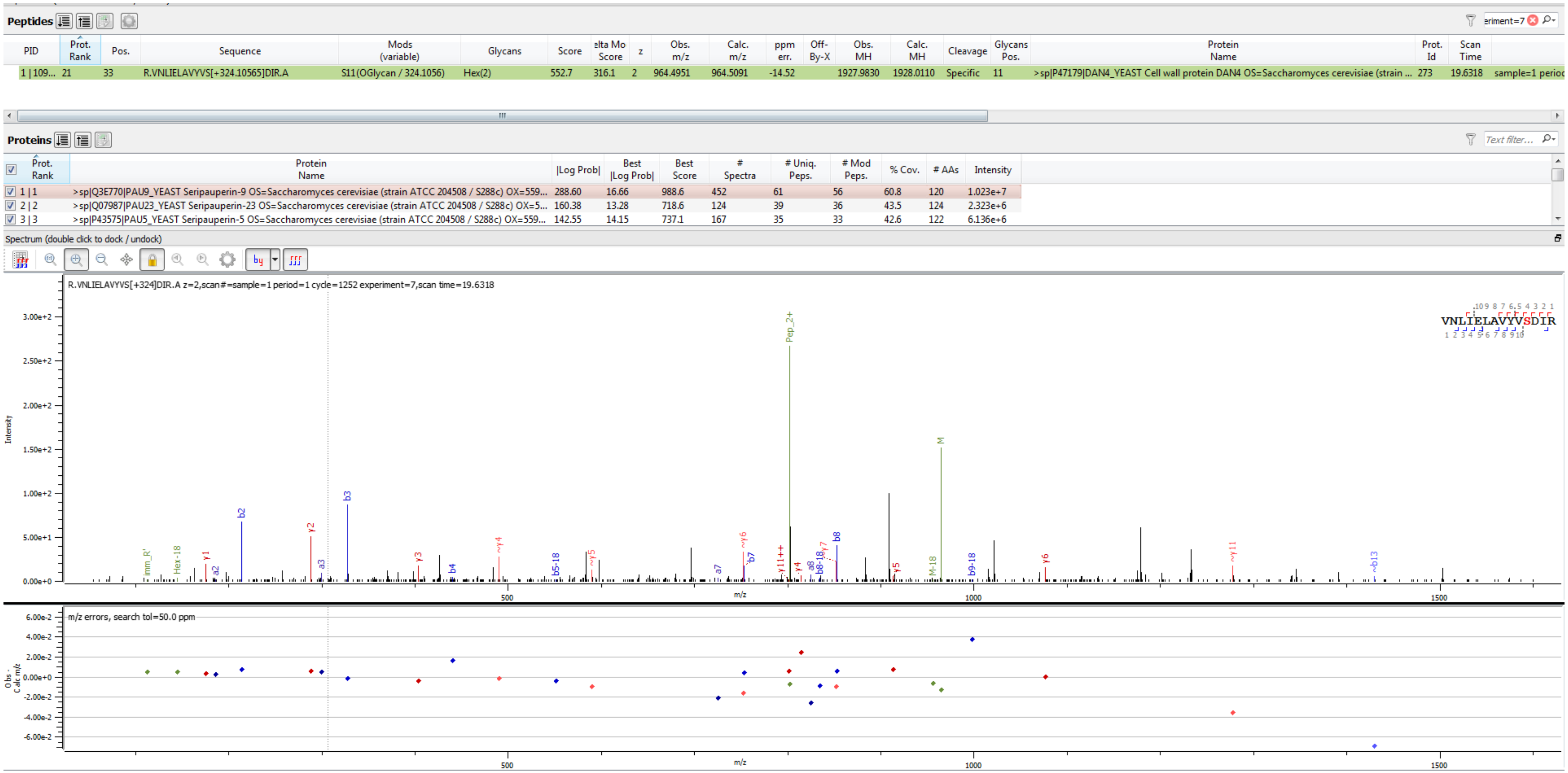
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |

Spectrum (double click to dock / undock)

K.LPWYT[+648]TR.L z=2,scan#=sample=1 period=1 cycle=1041 experiment=10,scan time=13.4180

m/z errors, search tol=50.0 ppm

Sample S6 K.LPWYT[+648.211]TR.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 109... | 21 | 33 | R.VNLIELAVYVS[+324.10565]DIR.A | S11(OGlycan / 324.1056) | Hex(2) | 552.7 | 316.1 | 2 | 964.4951 | 964.5091 | -14.52 | | 1927.9830 | 1928.0110 | Specific | 11 | >sp\|P47179\|DAN4_YEAST Cell wall protein DAN4 OS=Saccharomyces cerevisiae (strain ... | 273 | 19.6318 | sample=1 perioc |

**Proteins**

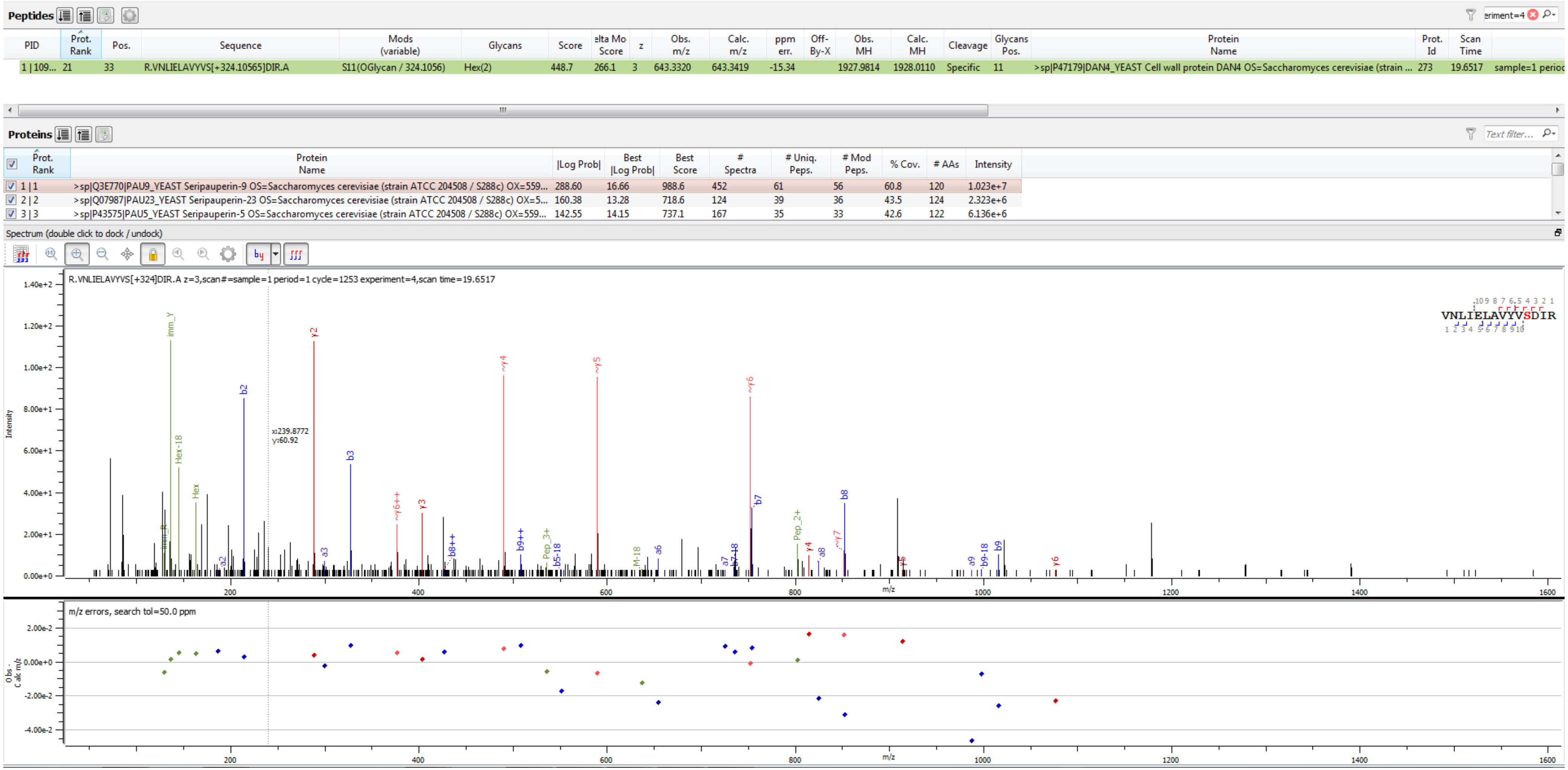
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |

Spectrum (double click to dock / undock)

R.VNLIELAVYVS[+324]DIR.A z=2,scan#=sample=1 period=1 cycle=1252 experiment=7,scan time=19.6318

m/z errors, search tol=50.0 ppm

Sample S6 R.VNLIELAVYVS[+324.106]DIR.A



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Scan Time | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 109... | 21 | 33 | R.VNLIELAVYVS[+324.10565]DIR.A | S11(OGlycan / 324.1056) | Hex(2) | 448.7 | 266.1 | 3 | 643.3320 | 643.3419 | -15.34 | | 1927.9814 | 1928.0110 | Specific | 11 | >sp\|P47179\|DAN4_YEAST Cell wall protein DAN4 OS=Saccharomyces cerevisiae (strain ... | 273 | 19.6517 | sample=1 perio |

**Proteins**

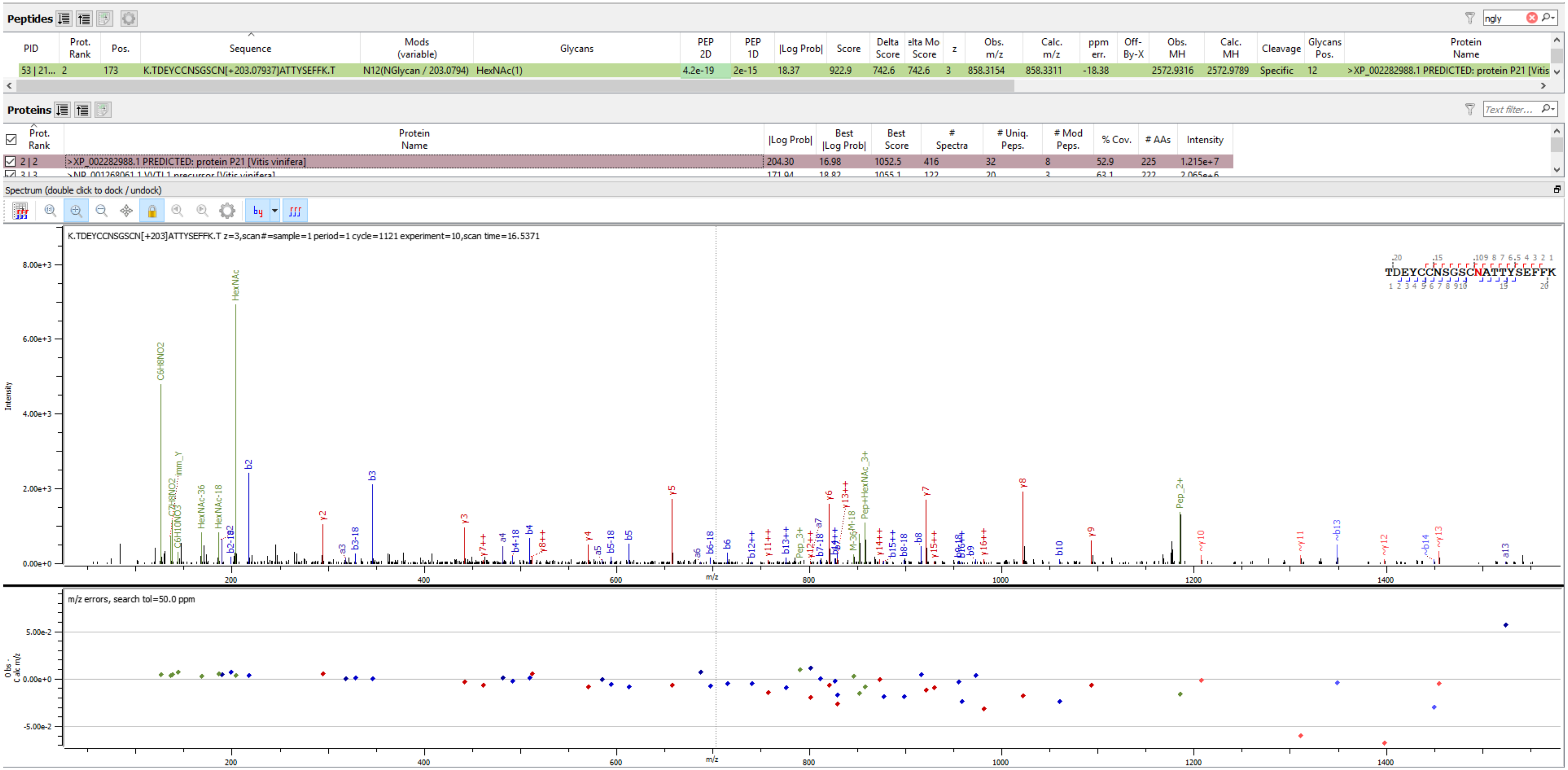
| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >sp\|Q3E770\|PAU9_YEAST Seripauperin-9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 288.60 | 16.66 | 988.6 | 452 | 61 | 56 | 60.8 | 120 | 1.023e+7 |
| ☑ | 2 \| 2 | >sp\|Q07987\|PAU23_YEAST Seripauperin-23 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=5... | 160.38 | 13.28 | 718.6 | 124 | 39 | 36 | 43.5 | 124 | 2.323e+6 |
| ☑ | 3 \| 3 | >sp\|P43575\|PAU5_YEAST Seripauperin-5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) OX=559... | 142.55 | 14.15 | 737.1 | 167 | 35 | 33 | 42.6 | 122 | 6.136e+6 |

Spectrum (double click to dock / undock)

R.VNLIELAVYVS[+324]DIR.A z=3,scan#=sample=1 period=1 cycle=1253 experiment=4,scan time=19.6517

m/z errors, search tol=50.0 ppm

Sample S6 R.VNLIELAVYVS[+324.106]DIR.A



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 53 \| 21... | 2 | 173 | K.TDEYCCNSGSCN[+203.07937]ATTYSEFFK.T | N12(NGlycan / 203.0794) | HexNAc(1) | 4.2e-19 | 2e-15 | 18.37 | 922.9 | 742.6 | 742.6 | 3 | 858.3154 | 858.3311 | -18.38 |  | 2572.9316 | 2572.9789 | Specific | 12 | >XP_002282988.1 PREDICTED: protein P21 [Vitis |

**Proteins**

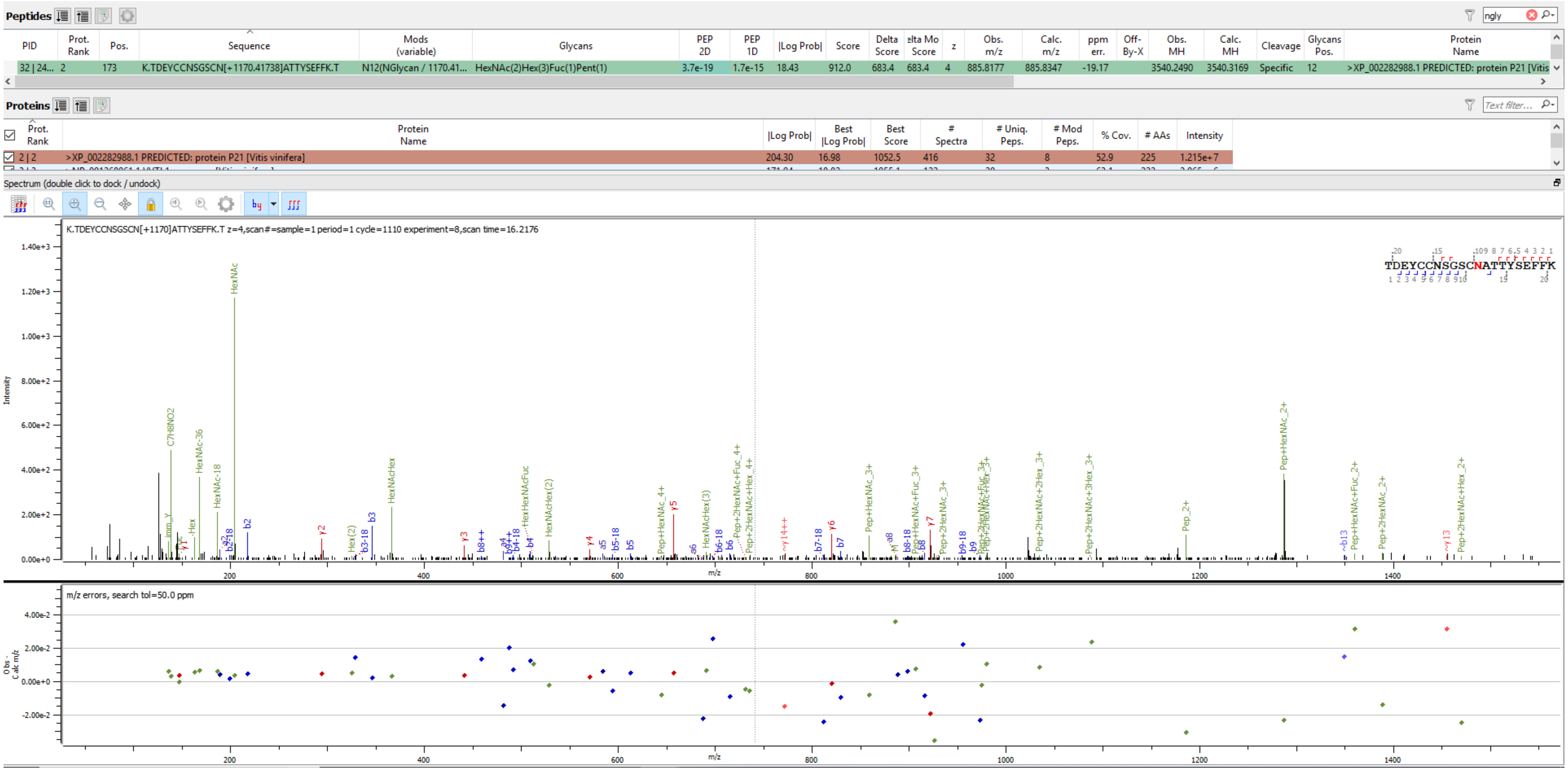
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >XP_002282988.1 PREDICTED: protein P21 [Vitis vinifera] | 204.30 | 16.98 | 1052.5 | 416 | 32 | 8 | 52.9 | 225 | 1.215e+7 |
| ☑ 3 \| 3 | >NP_001268061.1 VVTL1 precursor [Vitis vinifera] | 171.94 | 18.82 | 1055.1 | 122 | 20 | 3 | 63.1 | 222 | 2.065e+6 |

Spectrum (double click to dock / undock)

K.TDEYCCNSGSCN[+203]ATTYSEFFK.T z=3,scan#=sample=1 period=1 cycle=1121 experiment=10,scan time=16.5371

m/z errors, search tol=50.0 ppm

Sample S1 K.TDEYCCNSGSCN[+203.079]ATTYSEFFK.T



**Peptides**

ngly

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 32 \| 24... | 2 | 173 | K.TDEYCCNSGSCN[+1170.41738]ATTYSEFFK.T | N12(NGlycan / 1170.41... | HexNAc(2)Hex(3)Fuc(1)Pent(1) | 3.7e-19 | 1.7e-15 | 18.43 | 912.0 | 683.4 | 683.4 | 4 | 885.8177 | 885.8347 | -19.17 |  | 3540.2490 | 3540.3169 | Specific | 12 | >XP_002282988.1 PREDICTED: protein P21 [Vitis |

**Proteins**

Text filter...

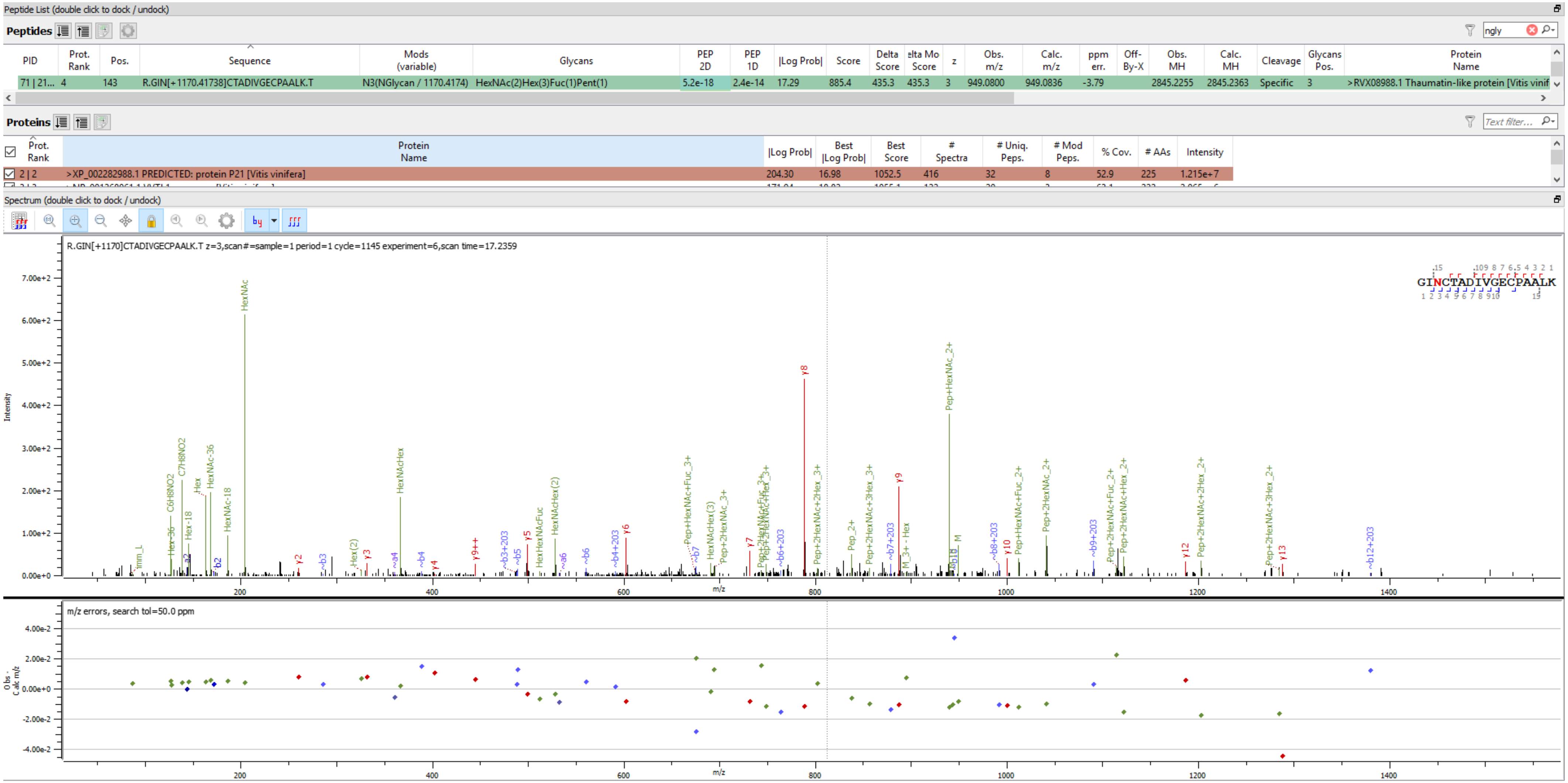
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >XP_002282988.1 PREDICTED: protein P21 [Vitis vinifera] | 204.30 | 16.98 | 1052.5 | 416 | 32 | 8 | 52.9 | 225 | 1.215e+7 |

Spectrum (double click to dock / undock)

K.TDEYCCNSGSCN[+1170]ATTYSEFFK.T z=4,scan#=sample=1 period=1 cycle=1110 experiment=8,scan time=16.2176

m/z errors, search tol=50.0 ppm

Sample S1 K.TDEYCCNSGSCN[+1170.417]ATTYSEFFK.T



Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 71 \| 21... | 4 | 143 | R.GIN[+1170.41738]CTADIVGECPAALK.T | N3(NGlycan / 1170.4174) | HexNAc(2)Hex(3)Fuc(1)Pent(1) | 5.2e-18 | 2.4e-14 | 17.29 | 885.4 | 435.3 | 435.3 | 3 | 949.0800 | 949.0836 | -3.79 |  | 2845.2255 | 2845.2363 | Specific | 3 | >RVX08988.1 Thaumatin-like protein [Vitis vinif |

**Proteins**

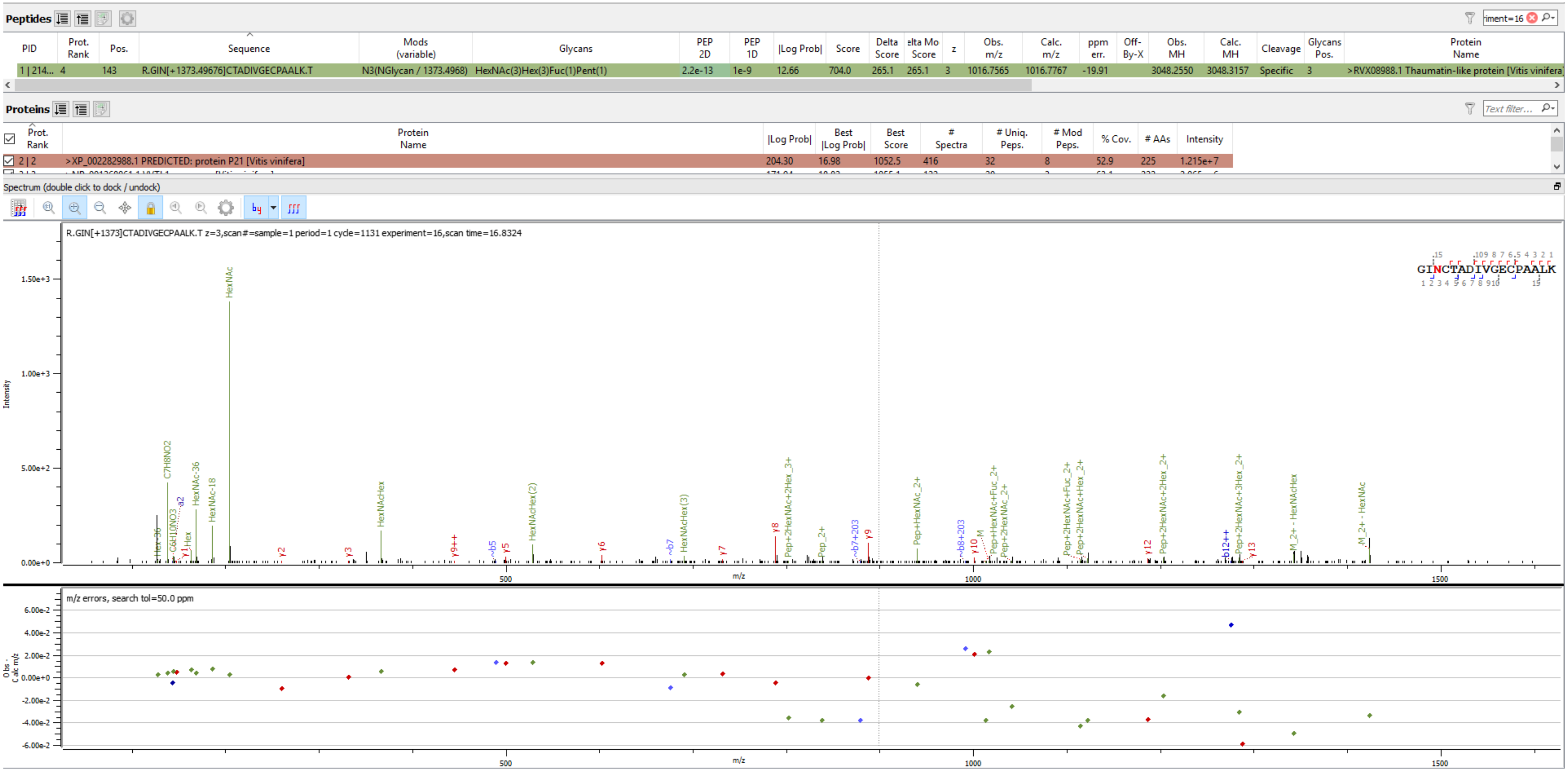
| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 2 \| 2 | >XP_002282988.1 PREDICTED: protein P21 [Vitis vinifera] | 204.30 | 16.98 | 1052.5 | 416 | 32 | 8 | 52.9 | 225 | 1.215e+7 |

Spectrum (double click to dock / undock)

R.GIN[+1170]CTADIVGECPAALK.T z=3,scan#=sample=1 period=1 cycle=1145 experiment=6,scan time=17.2359

m/z errors, search tol=50.0 ppm

Sample S1 R.GIN[+1170.417]CTADIVGECPAALK.T



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 \| 214... | 4 | 143 | R.GIN[+1373.49676]CTADIVGECPAALK.T | N3(NGlycan / 1373.4968) | HexNAc(3)Hex(3)Fuc(1)Pent(1) | 2.2e-13 | 1e-9 | 12.66 | 704.0 | 265.1 | 265.1 | 3 | 1016.7565 | 1016.7767 | -19.91 | | 3048.2550 | 3048.3157 | Specific | 3 | >RVX08988.1 Thaumatin-like protein [Vitis vinifera] |

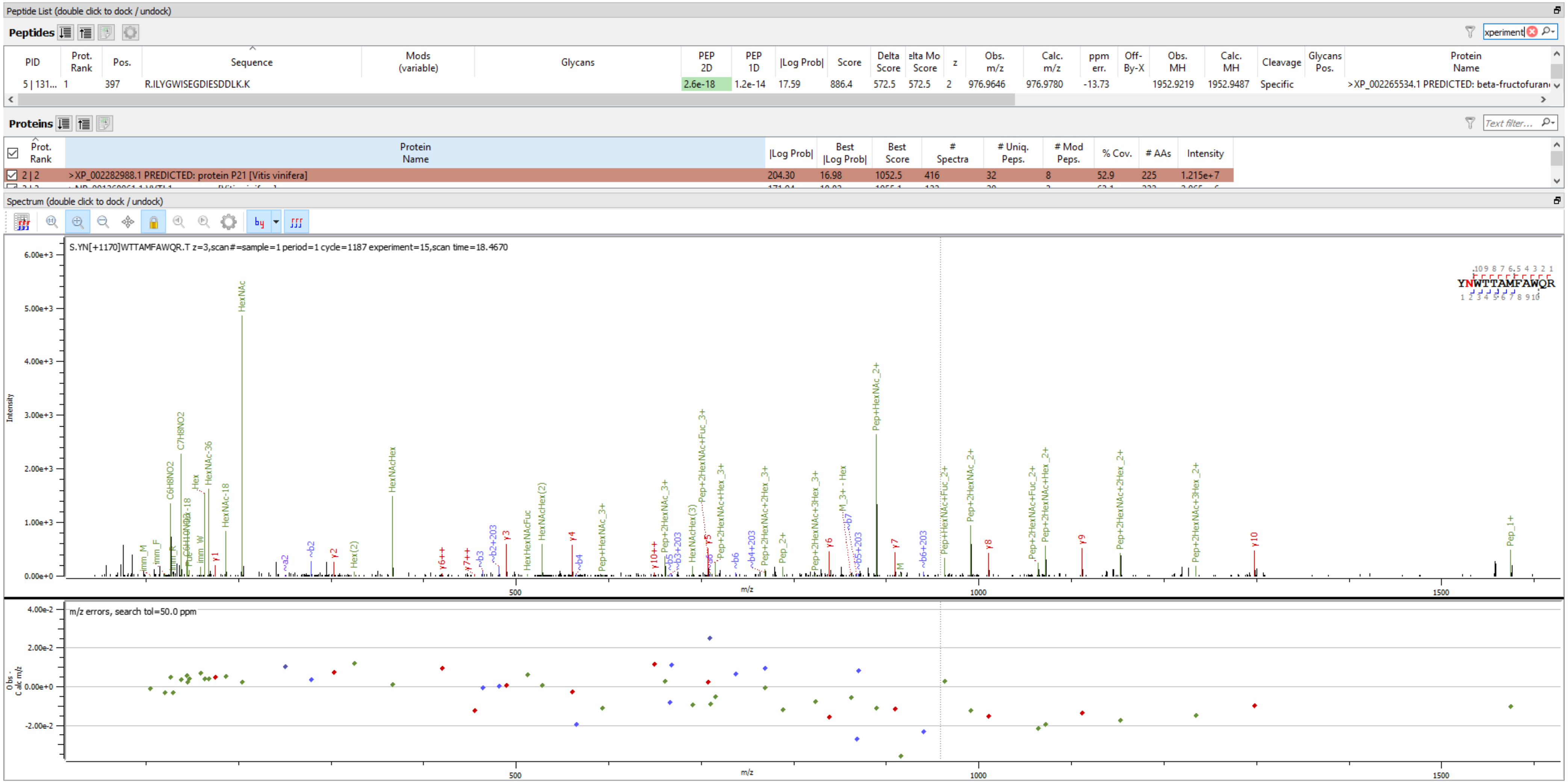
**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >XP_002282988.1 PREDICTED: protein P21 [Vitis vinifera] | 204.30 | 16.98 | 1052.5 | 416 | 32 | 8 | 52.9 | 225 | 1.215e+7 |

Spectrum (double click to dock / undock)

R.GIN[+1373]CTADIVGECPAALK.T z=3,scan#=sample=1 period=1 cycle=1131 experiment=16,scan time=16.8324

Sample S1 R.GIN[+1373.497]CTADIVGECPAALK.T



Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 5 \| 131... | 1 | 397 | R.ILYGWISEGDIESDDLK.K |  |  | 2.6e-18 | 1.2e-14 | 17.59 | 886.4 | 572.5 | 572.5 | 2 | 976.9646 | 976.9780 | -13.73 |  | 1952.9219 | 1952.9487 | Specific |  | >XP_002265534.1 PREDICTED: beta-fructofuran |

**Proteins**

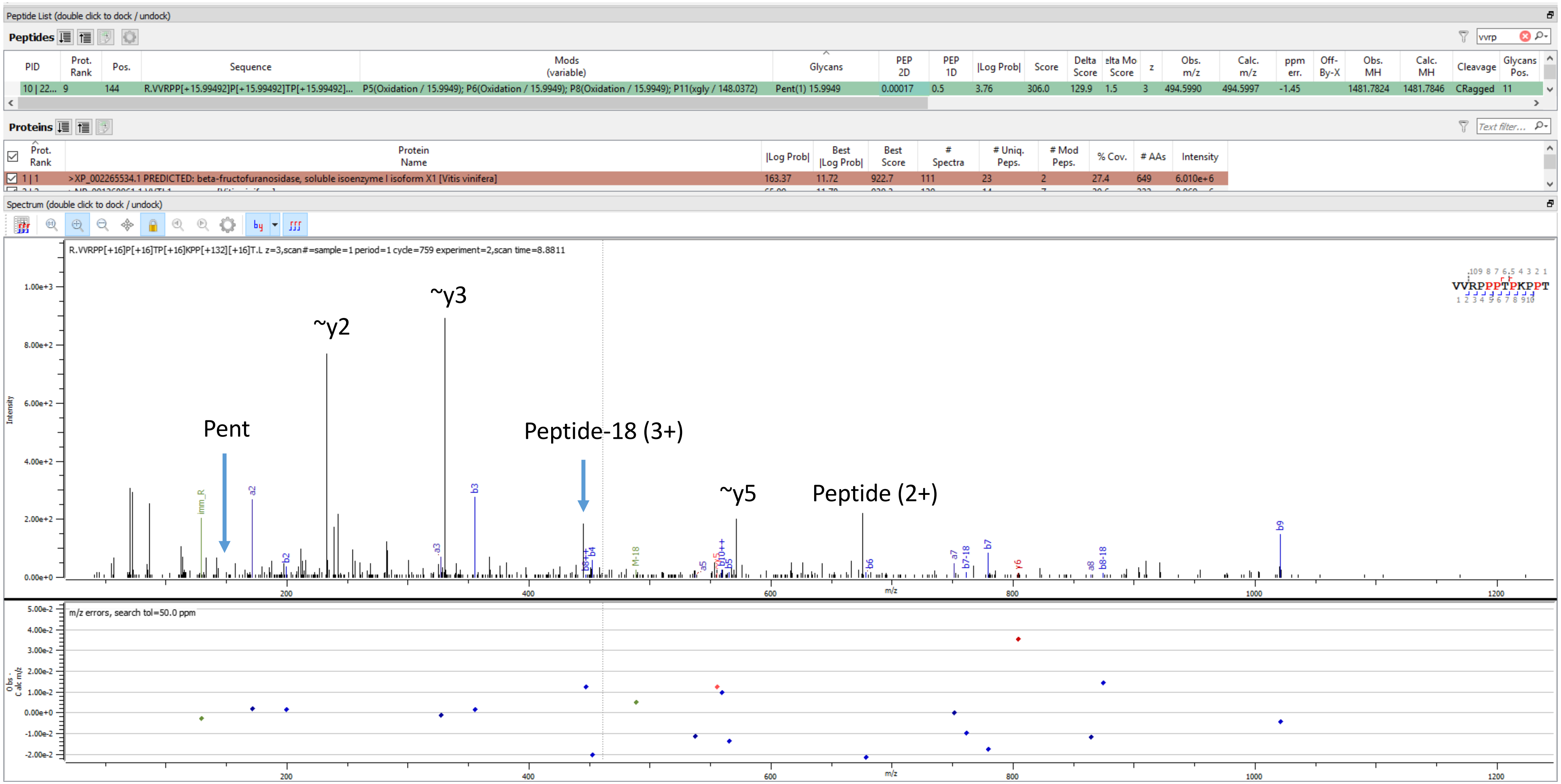
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 2 \| 2 | >XP_002282988.1 PREDICTED: protein P21 [Vitis vinifera] | 204.30 | 16.98 | 1052.5 | 416 | 32 | 8 | 52.9 | 225 | 1.215e+7 |

Spectrum (double click to dock / undock)

S.YN[+1170]WTTAMFAWQR.T z=3,scan#=sample=1 period=1 cycle=1187 experiment=15,scan time=18.4670

m/z errors, search tol=50.0 ppm

Sample S1 S.YN[+1170.417]WTTAMFAWQR.T



Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 10 \| 22... | 9 | 144 | R.VVRPP[+15.99492]P[+15.99492]TP[+15.99492]... | P5(Oxidation / 15.9949); P6(Oxidation / 15.9949); P8(Oxidation / 15.9949); P11(xgly / 148.0372) | Pent(1) 15.9949 | 0.00017 | 0.5 | 3.76 | 306.0 | 129.9 | 1.5 | 3 | 494.5990 | 494.5997 | -1.45 |  | 1481.7824 | 1481.7846 | CRagged | 11 |

**Proteins**

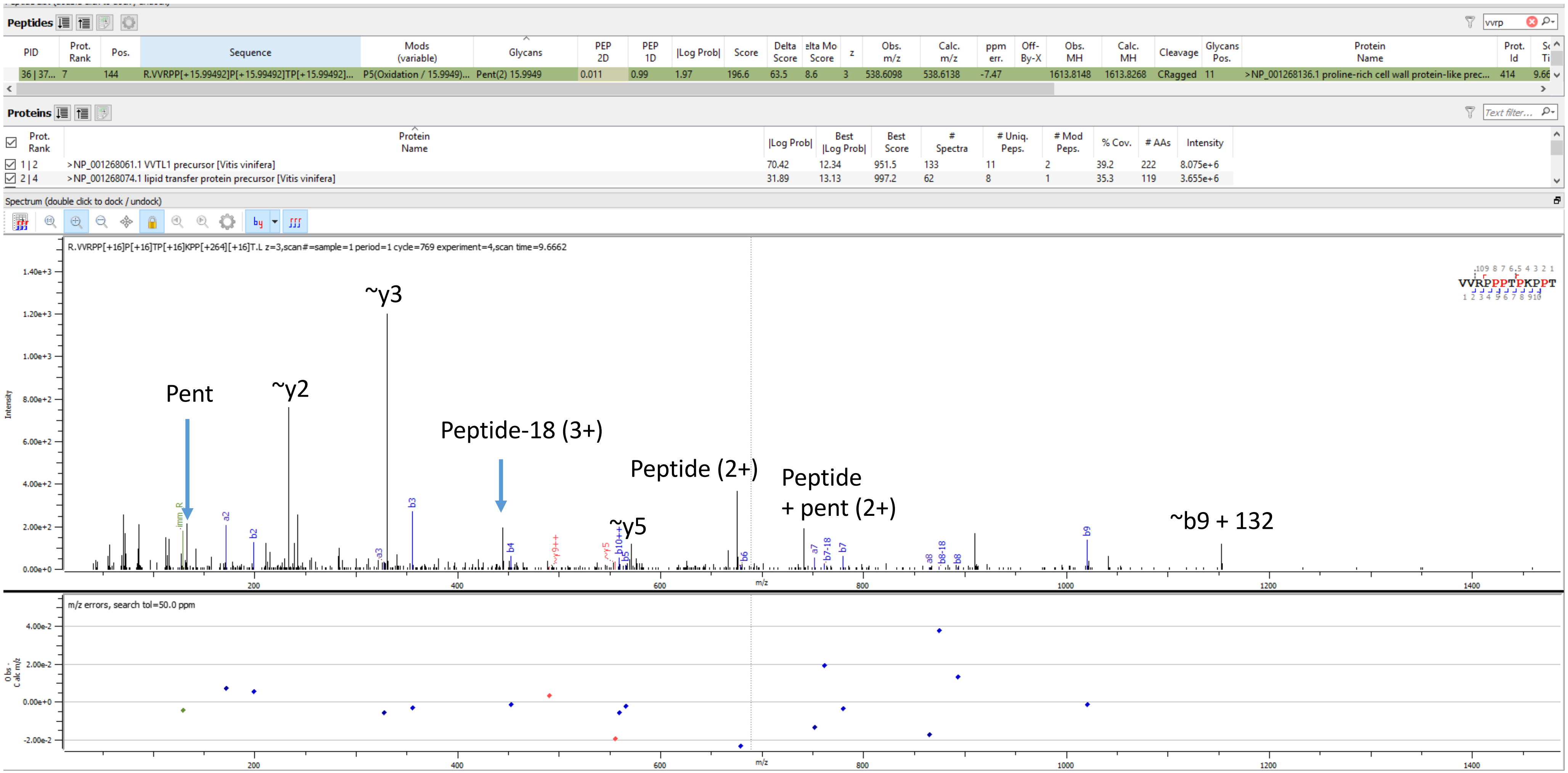
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 1 \| 1 | >XP_002265534.1 PREDICTED: beta-fructofuranosidase, soluble isoenzyme I isoform X1 [Vitis vinifera] | 163.37 | 11.72 | 922.7 | 111 | 23 | 2 | 27.4 | 649 | 6.010e+6 |

Spectrum (double click to dock / undock)

R.VVRPP[+16]P[+16]TP[+16]KPP[+132][+16]T.L z=3,scan#=sample=1 period=1 cycle=759 experiment=2,scan time=8.8811

m/z errors, search tol=50.0 ppm

Sample S3 R.VVRPP[+15.995]P[+15.995]TP[+15.995]KPP[+132.042][+15.995]T.L



**Peptides**

vvrp

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name | Prot. Id | Sc Ti |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 36 \| 37... | 7 | 144 | R.VVRPP[+15.99492]P[+15.99492]TP[+15.99492]... | P5(Oxidation / 15.9949)... | Pent(2) 15.9949 | 0.011 | 0.99 | 1.97 | 196.6 | 63.5 | 8.6 | 3 | 538.6098 | 538.6138 | -7.47 |  | 1613.8148 | 1613.8268 | CRagged | 11 | >NP_001268136.1 proline-rich cell wall protein-like prec... | 414 | 9.66 |

**Proteins**

Text filter...

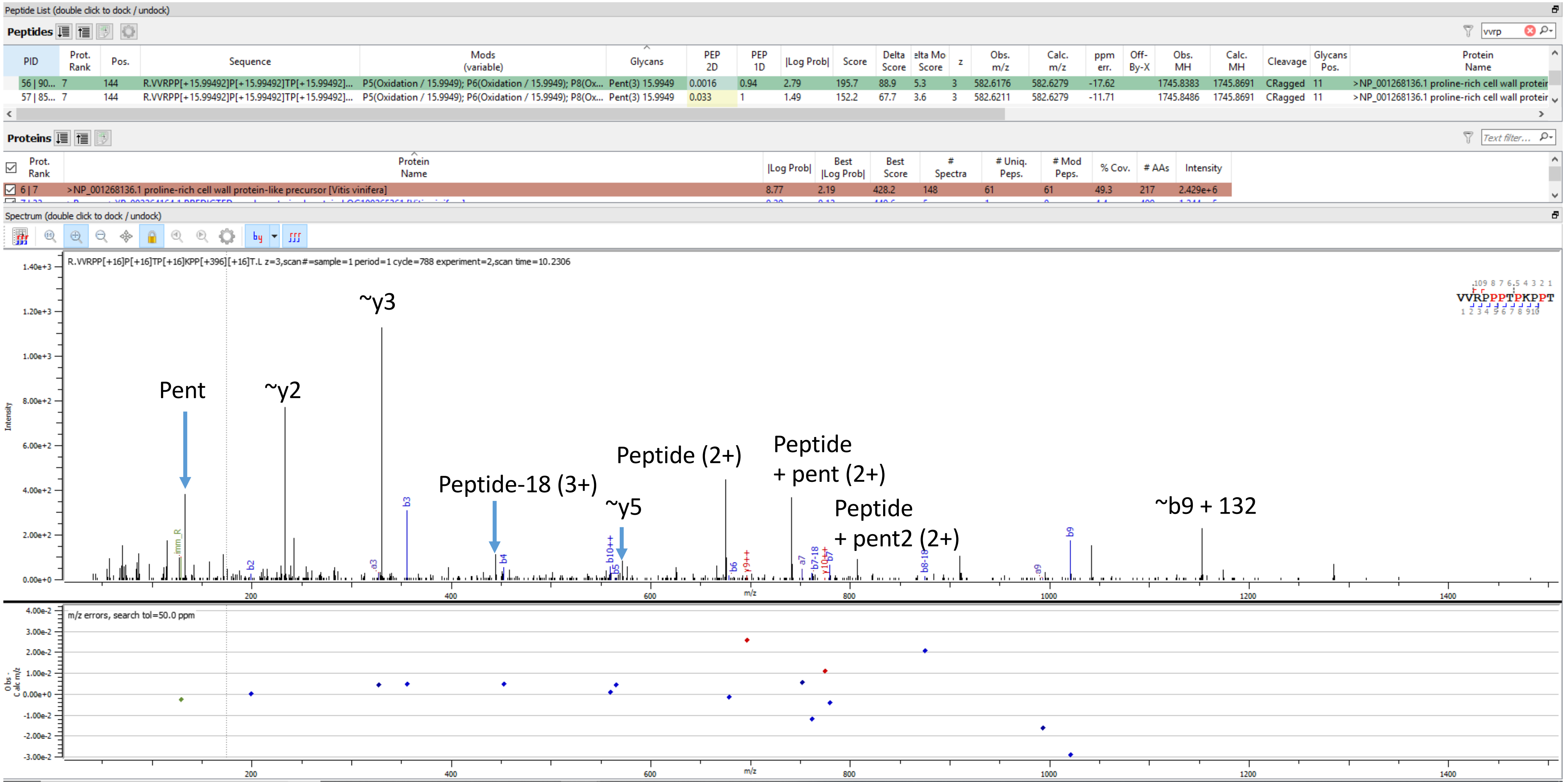
| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 2 | >NP_001268061.1 VVTL1 precursor [Vitis vinifera] | 70.42 | 12.34 | 951.5 | 133 | 11 | 2 | 39.2 | 222 | 8.075e+6 |
| ☑ | 2 \| 4 | >NP_001268074.1 lipid transfer protein precursor [Vitis vinifera] | 31.89 | 13.13 | 997.2 | 62 | 8 | 1 | 35.3 | 119 | 3.655e+6 |

Spectrum (double click to dock / undock)

R.VVRPP[+16]P[+16]TP[+16]KPP[+264][+16]T.L z=3,scan#=sample=1 period=1 cycle=769 experiment=4,scan time=9.6662

m/z errors, search tol=50.0 ppm

Sample S4 R.VVRPP[+15.995]P[+15.995]TP[+15.995]KPP[+264.085][+15.995]T.L



Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 56 \| 90... | 7 | 144 | R.VVRPP[+15.99492]P[+15.99492]TP[+15.99492]... | P5(Oxidation / 15.9949); P6(Oxidation / 15.9949); P8(Ox... | Pent(3) 15.9949 | 0.0016 | 0.94 | 2.79 | 195.7 | 88.9 | 5.3 | 3 | 582.6176 | 582.6279 | -17.62 |  | 1745.8383 | 1745.8691 | CRagged | 11 | >NP_001268136.1 proline-rich cell wall protei |
| 57 \| 85... | 7 | 144 | R.VVRPP[+15.99492]P[+15.99492]TP[+15.99492]... | P5(Oxidation / 15.9949); P6(Oxidation / 15.9949); P8(Ox... | Pent(3) 15.9949 | 0.033 | 1 | 1.49 | 152.2 | 67.7 | 3.6 | 3 | 582.6211 | 582.6279 | -11.71 |  | 1745.8486 | 1745.8691 | CRagged | 11 | >NP_001268136.1 proline-rich cell wall protei |

**Proteins**

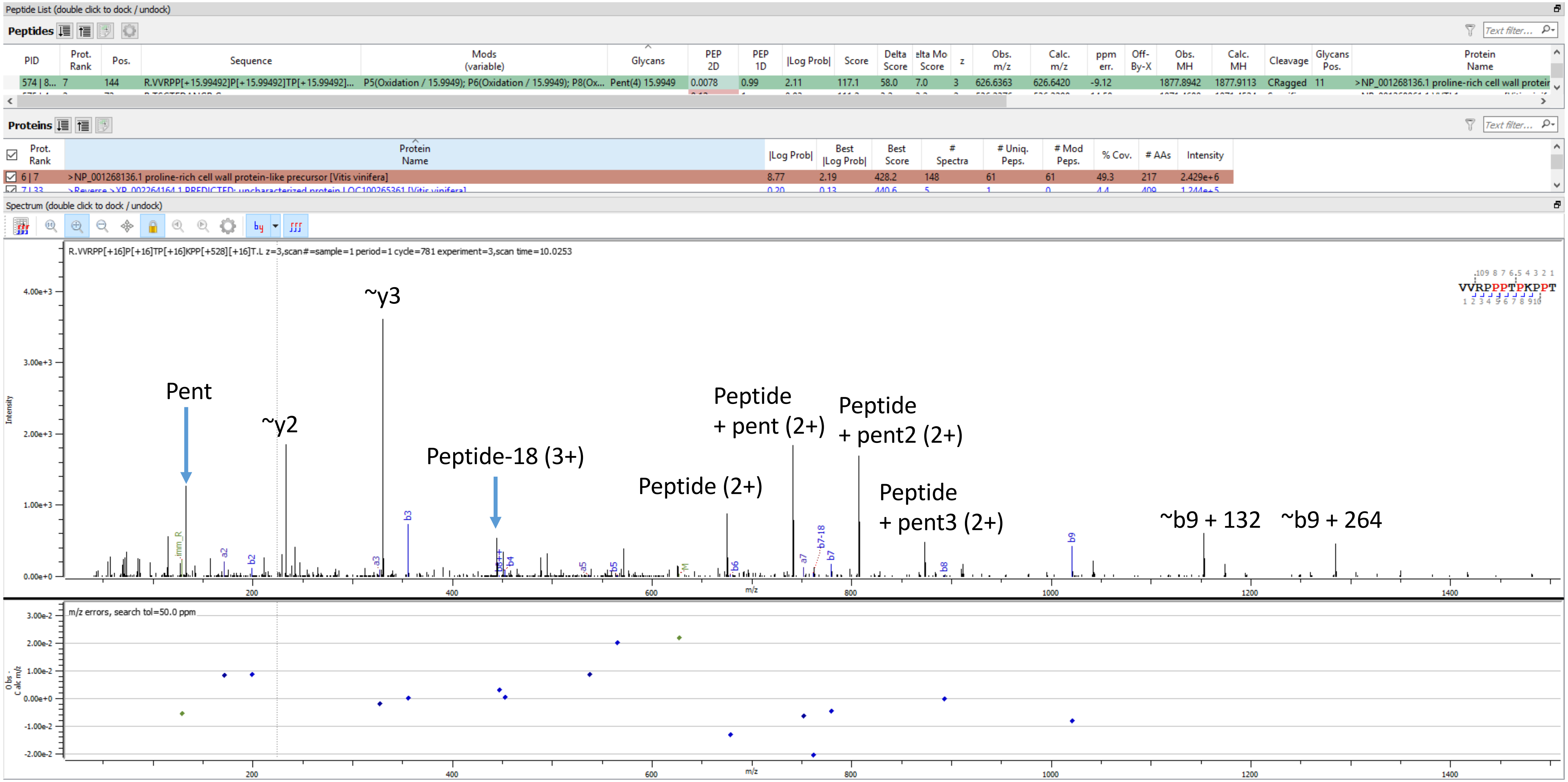
| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 6 \| 7 | >NP_001268136.1 proline-rich cell wall protein-like precursor [Vitis vinifera] | 8.77 | 2.19 | 428.2 | 148 | 61 | 61 | 49.3 | 217 | 2.429e+6 |

Spectrum (double click to dock / undock)

R.VVRPP[+16]P[+16]TP[+16]KPP[+396][+16]T.L z=3,scan#=sample=1 period=1 cycle=788 experiment=2,scan time=10.2306

m/z errors, search tol=50.0 ppm

Sample S4 R.VVRPP[+15.995]P[+15.995]TP[+15.995]KPP[+396.127][+15.995]T.L



Peptide List (double click to dock / undock)

**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 574 \| 8... | 7 | 144 | R.VVRPP[+15.99492]P[+15.99492]TP[+15.99492]... | P5(Oxidation / 15.9949); P6(Oxidation / 15.9949); P8(Ox... | Pent(4) 15.9949 | 0.0078 | 0.99 | 2.11 | 117.1 | 58.0 | 7.0 | 3 | 626.6363 | 626.6420 | -9.12 |  | 1877.8942 | 1877.9113 | CRagged | 11 | >NP_001268136.1 proline-rich cell wall protein |

**Proteins**

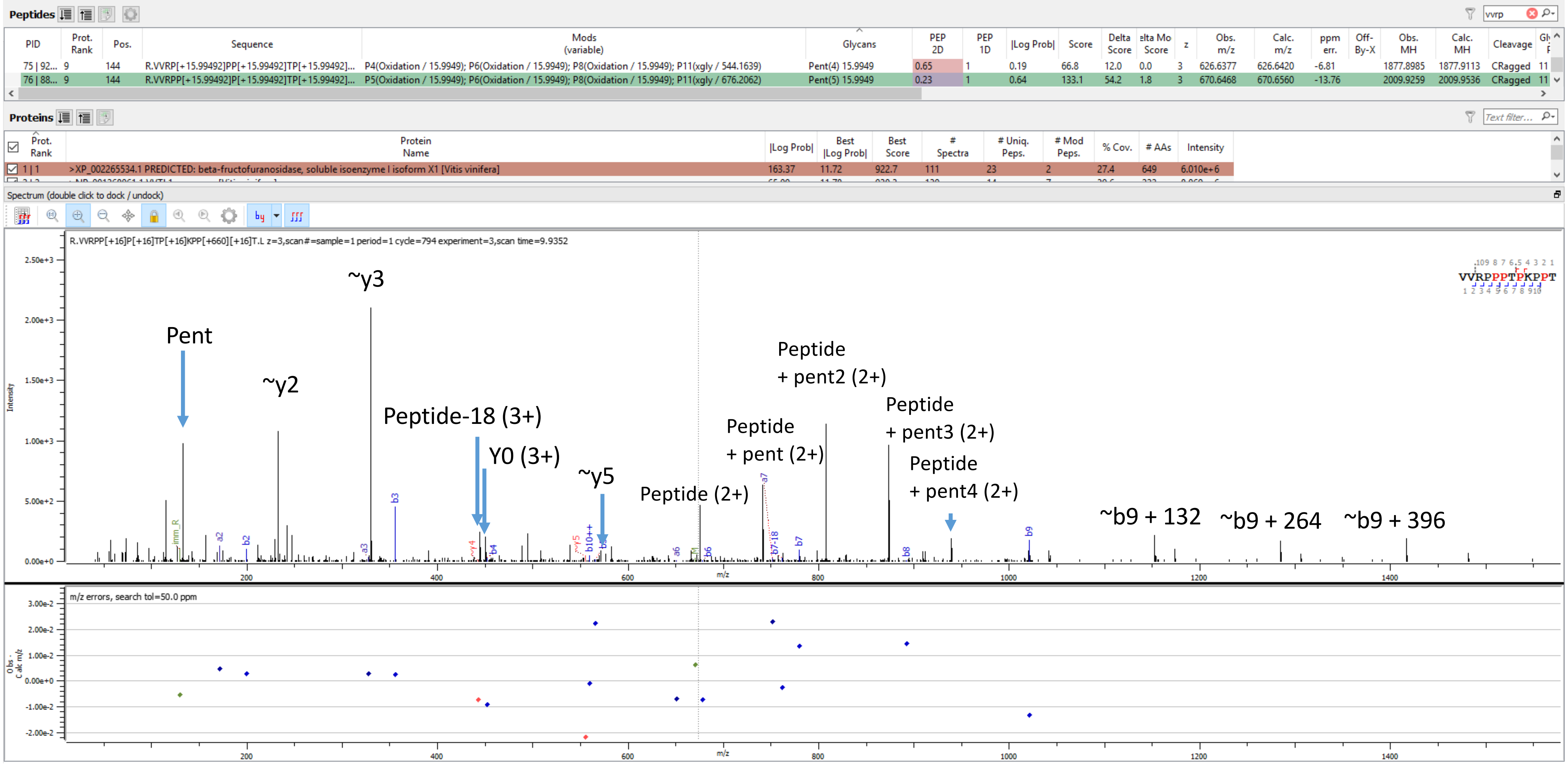
| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 6 \| 7 | >NP_001268136.1 proline-rich cell wall protein-like precursor [Vitis vinifera] | 8.77 | 2.19 | 428.2 | 148 | 61 | 61 | 49.3 | 217 | 2.429e+6 |

Spectrum (double click to dock / undock)

R.VVRPP[+16]P[+16]TP[+16]KPP[+528][+16]T.L z=3,scan#=sample=1 period=1 cycle=781 experiment=3,scan time=10.0253

m/z errors, search tol=50.0 ppm

Sample S4 R.VVRPP[+15.995]P[+15.995]TP[+15.995]KPP[+528.169][+15.995]T.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Gl F |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 75 \| 92... | 9 | 144 | R.VVRP[+15.99492]PP[+15.99492]TP[+15.99492]... | P4(Oxidation / 15.9949); P6(Oxidation / 15.9949); P8(Oxidation / 15.9949); P11(xgly / 544.1639) | Pent(4) 15.9949 | 0.65 | 1 | 0.19 | 66.8 | 12.0 | 0.0 | 3 | 626.6377 | 626.6420 | -6.81 | | 1877.8985 | 1877.9113 | CRagged | 11 |
| 76 \| 88... | 9 | 144 | R.VVRPP[+15.99492]P[+15.99492]TP[+15.99492]... | P5(Oxidation / 15.9949); P6(Oxidation / 15.9949); P8(Oxidation / 15.9949); P11(xgly / 676.2062) | Pent(5) 15.9949 | 0.23 | 1 | 0.64 | 133.1 | 54.2 | 1.8 | 3 | 670.6468 | 670.6560 | -13.76 | | 2009.9259 | 2009.9536 | CRagged | 11 |

**Proteins**

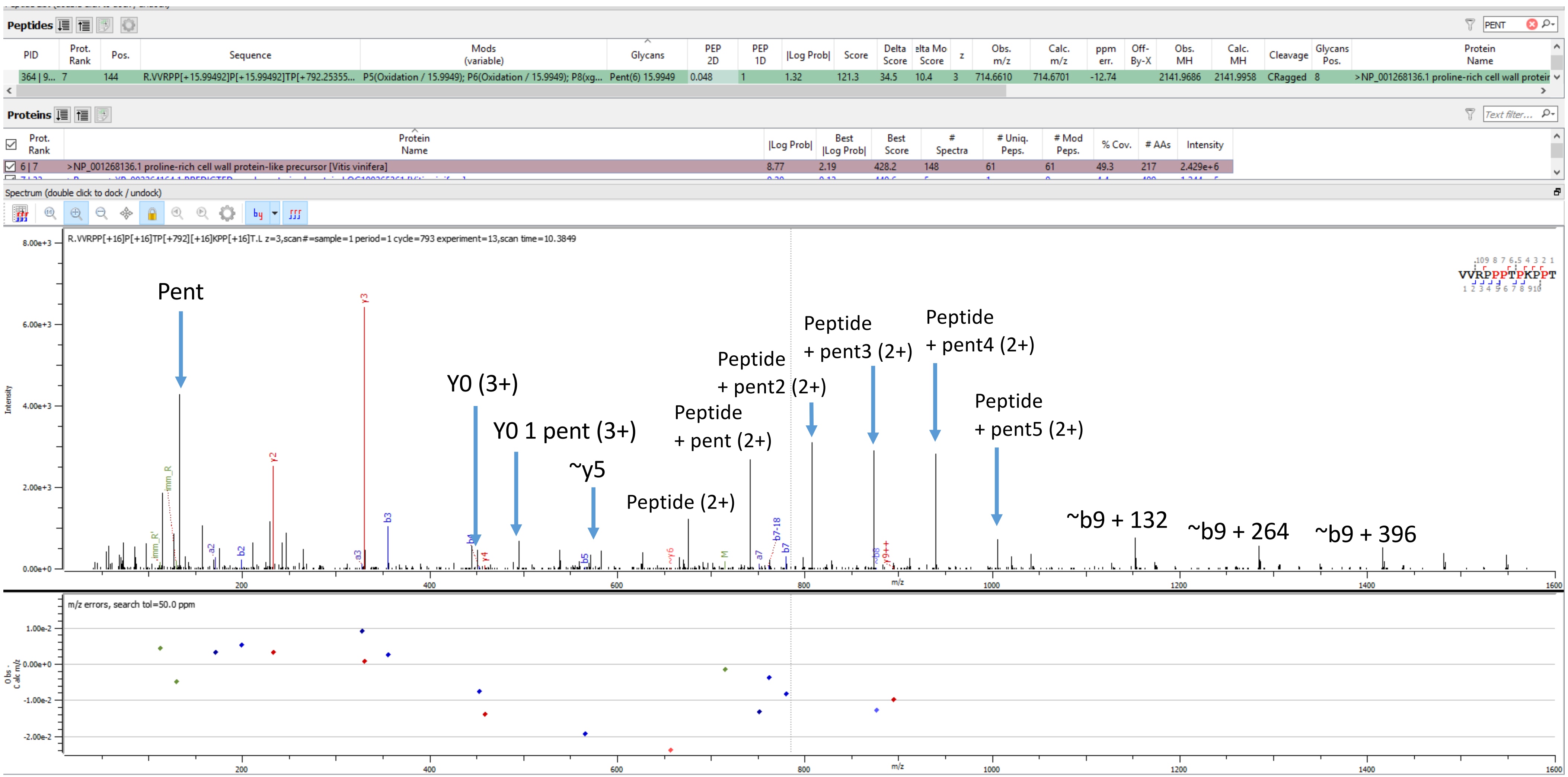
| ☑ | Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ☑ | 1 \| 1 | >XP_002265534.1 PREDICTED: beta-fructofuranosidase, soluble isoenzyme I isoform X1 [Vitis vinifera] | 163.37 | 11.72 | 922.7 | 111 | 23 | 2 | 27.4 | 649 | 6.010e+6 |

Spectrum (double click to dock / undock)

R.VVRPP[+16]P[+16]TP[+16]KPP[+660][+16]T.L z=3,scan#=sample=1 period=1 cycle=794 experiment=3,scan time=9.9352

m/z errors, search tol=50.0 ppm

Sample S3 R.VVRPP[+15.995]P[+15.995]TP[+15.995]KPP[+660.211][+15.995]T.L



**Peptides**

| PID | Prot. Rank | Pos. | Sequence | Mods (variable) | Glycans | PEP 2D | PEP 1D | \|Log Prob\| | Score | Delta Score | elta Mo Score | z | Obs. m/z | Calc. m/z | ppm err. | Off-By-X | Obs. MH | Calc. MH | Cleavage | Glycans Pos. | Protein Name |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 364 \| 9... | 7 | 144 | R.VVRPP[+15.99492]P[+15.99492]TP[+792.25355... | P5(Oxidation / 15.9949); P6(Oxidation / 15.9949); P8(xg... | Pent(6) 15.9949 | 0.048 | 1 | 1.32 | 121.3 | 34.5 | 10.4 | 3 | 714.6610 | 714.6701 | -12.74 |  | 2141.9686 | 2141.9958 | CRagged | 8 | >NP_001268136.1 proline-rich cell wall protei |

**Proteins**

| ☑ Prot. Rank | Protein Name | \|Log Prob\| | Best \|Log Prob\| | Best Score | # Spectra | # Uniq. Peps. | # Mod Peps. | % Cov. | # AAs | Intensity |
|---|---|---|---|---|---|---|---|---|---|---|
| ☑ 6 \| 7 | >NP_001268136.1 proline-rich cell wall protein-like precursor [Vitis vinifera] | 8.77 | 2.19 | 428.2 | 148 | 61 | 61 | 49.3 | 217 | 2.429e+6 |

Spectrum (double click to dock / undock)

R.VVRPP[+16]P[+16]TP[+792][+16]KPP[+16]T.L z=3,scan#=sample=1 period=1 cycle=793 experiment=13,scan time=10.3849

m/z errors, search tol=50.0 ppm

Sample S4 R.VVRPP[+15.995]P[+15.995]TP[+792.254][+15.995]KPP[+15.995]T.L