## Interpretation of MS<sup>3</sup> and MS<sup>4</sup> spectra acquired during top down analysis of CLR chains.

The nomenclature for fragment ions defined by Macek et al in [Mol Cell Proteomics. 5(5):949-958] was adopted.

We thus marked as  $\hat{y}$ , the fragment ions containing the C-terminal residue of the btype fragment selected for MS<sup>3</sup> or MS<sup>4</sup>.

We marked as  $\hat{b}$ , the fragment ions containing the N-terminal residue of the y-type fragment selected for MS<sup>3</sup> or MS<sup>4</sup>.

We chose to label as 'y' the fragments whose mass matched the theoretical m/z of y-type fragment ions, even though they came from MS<sup>3</sup> or MS<sup>4</sup> fragmentation of b ions.







ITMS<sup>3</sup> of the b<sub>13</sub><sup>+</sup> ion at m/z 1250.6014 (1+), produced by FTMS<sup>2</sup> analysis of m/z 1102.41 (10+) or 1104.02 (10+) (CLR-B) Q(pyro)LSCTGP\*PAIP\*GI





ITMS<sup>3</sup> of the y<sub>9</sub><sup>2+</sup> ion at m/z 535.3027 (2+), produced by FTMS<sup>2</sup> analysis of m/z 1102.41 (10+) or 1104.02 (10+) (CLR-B, 1-97) YKATQKIAF



ITMS<sup>3</sup> of the  $y_{20}^{2+}$  ion at m/z 1103.5312 (2+), produced by FTMS<sup>2</sup> analysis of m/z 1256.71 (8+) (CLR-C, 1-90) (PGP)\*MGIP\*GEPGEEGRYKQKF

## FKQKYRGEE G - P - EGP\* -GP **FKQKYR GEEGP** -EGP\*IGMPGP\* **RYKQKF** P\*GE P\*GP G PGEE G **Y**14<sup>2+</sup> 819.33 100 90 80 70 Relative Abundance 07 09 09 **Y**16<sup>2+</sup> 904.33 30 681.25 18 669.91 **%**6 869.33 **b**9 868.17 20 569.17 2+ **Y**<sub>17</sub><sup>2+</sup> ĥ b' 1018.92 b 541.17 10 456.25 337.66 970.02 621.33 398.92 1216.25 1338.67 268.17 1280.50 1533.25 1640.83 0 200 400 600 800 1000 1200 1400 1600 1800 m/z

ITMS<sup>3</sup> of the y<sub>20</sub><sup>3+</sup> ion at m/z 736.0229 (3+), produced by FTMS<sup>2</sup> analysis of m/z 1256.71 (8+) (CLR-C, 1-90)

## P\*GPMGIP\*GEPGEEGRYKQKF



ITMS<sup>3</sup> of the  $y_{14}^{2+}$  ion at m/z 819.3975 (2+), produced by FTMS<sup>2</sup> analysis of m/z 1256.71 (8+) (CLR-C, 1-90) P\*GEPGEEGRYKQKF



P\*GPMGIP\*GEP\*GEEGRYKQKF





P\*GPMGIP\*GEPGEEGRYKQKFQSVF



ITMS<sup>4</sup> of the fragment at m/z 399.17 (1+), produced by ITMS<sup>3</sup> analysis of m/z 889.7638 (3+) (CLR-C, 1-94)

This ion corresponds to fragment  $b_4$  produced from sequence P\*GPMGIP\*GEP\*GEEGRYKQKFQSVF. P\*GPM



ITMS<sup>3</sup> of the y<sub>14</sub><sup>2+</sup> ion at m/z 827.3938 (2+), produced by FTMS<sup>2</sup> analysis of m/z 1258.71 (8+) (CLR-C, 1-90)

P\*GEP\*GEEGRYKQK



ITMS<sup>3</sup> of the y<sub>18</sub><sup>2+</sup> ion at m/z 1050.0091 (2+), produced by FTMS<sup>2</sup> analysis of m/z 1314.36 (8+) (CLR-C, 1-94)

P\*GEPGEEGRYKQKFQSVF



ITMS<sup>3</sup> of the y<sub>18</sub><sup>2+</sup> ion at m/z 1058.0063 (2+), produced by FTMS<sup>2</sup> analysis of m/z 1316.38 (8+) (CLR-C, 1-94) P\*GEP\*GEEGRYKQKFQSVF



P\*GPMGIP\*GEP\*GEEGRYKQKFQSVF



ITMS<sup>4</sup> of m/z 569.33 (1+), produced by ITMS<sup>3</sup> analysis of m/z 895.0957 (3+) (CLR-C, 1-94) This ion corresponds to fragment  $\hat{b}_6$  produced from sequence P\*GPMGIP\*GEP\*GEEGRYKQKFQSVF

## P\*GPMGI