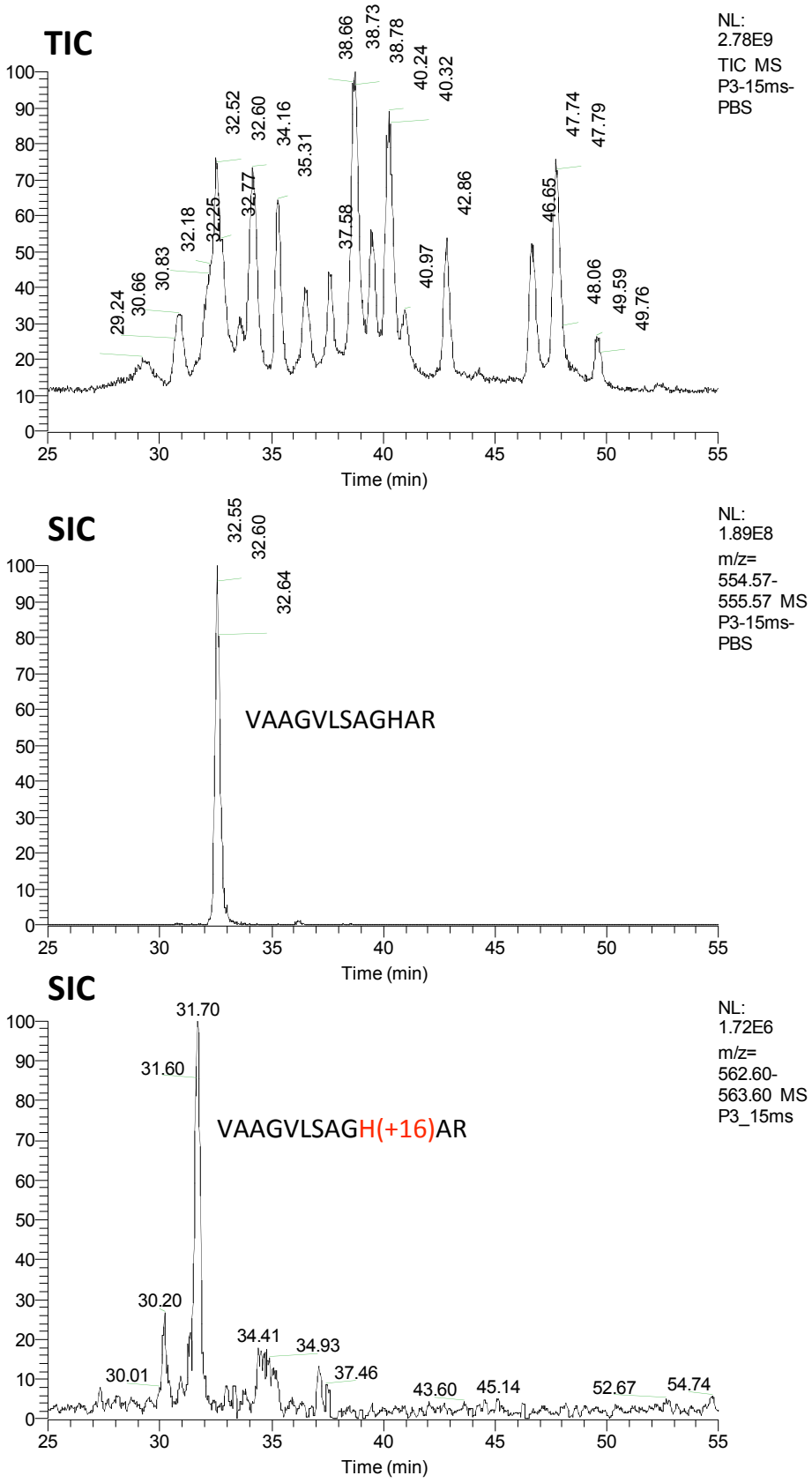
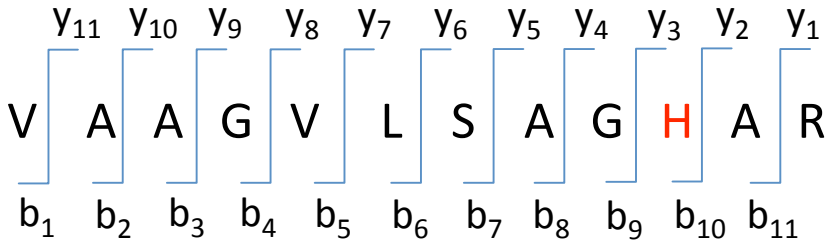
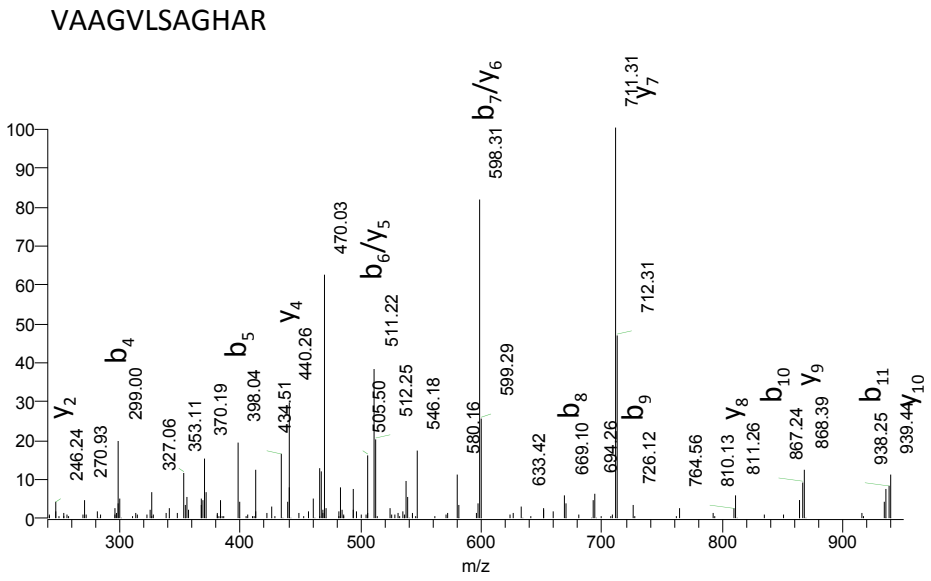

TIC
NL:
2.78E9
TIC MS
P3-15ms-
PBS
29.24
30.66
30.83
32.18
32.25
32.52
32.60
32.77
34.16
35.31
37.58
38.66
38.73
38.78
40.24
40.32
40.97
42.86
46.65
47.74
47.79
48.06
49.59
49.76
Time (min)
SIC
NL:
1.89E8
m/z=
554.57-
555.57 MS
P3-15ms-
PBS
32.55
32.60
32.64
VAAGVLSAGHAR
Time (min)
SIC
NL:
1.72E6
m/z=
562.60-
563.60 MS
P3_15ms
31.70
31.60
VAAGVLSAGH(+16)AR
30.20
30.01
34.41
34.93
37.46
43.60
45.14
52.67
54.74
Time (min)

Figure S2.


y11 y10 y9 y8 y7 y6 y5 y4 y3 y2 y1
V A A G V L S A G H A R
b1 b2 b3 b4 b5 b6 b7 b8 b9 b10 b11


VAAGVLSAGHAR
m/z

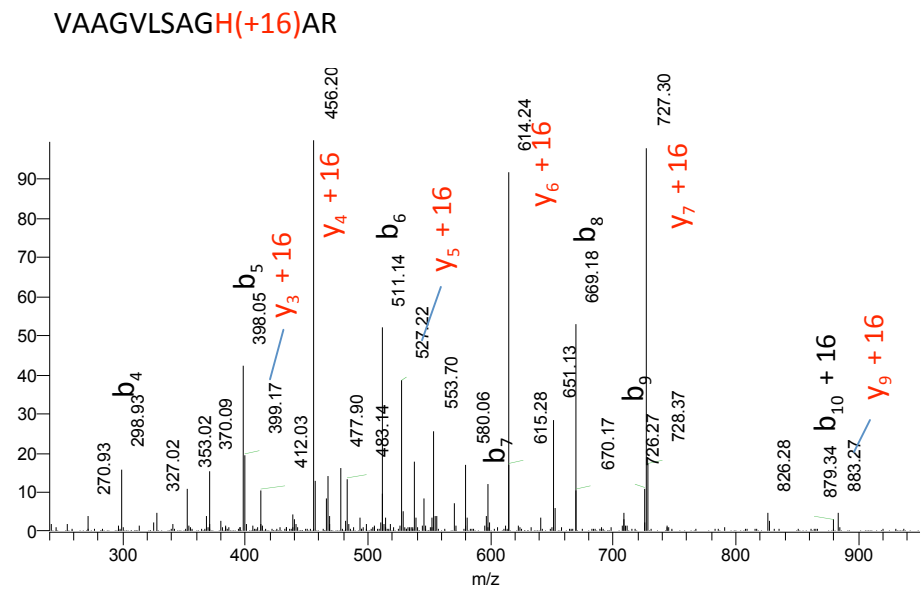

VAAGVLSAGH(+16)AR
m/z

Figure S3.

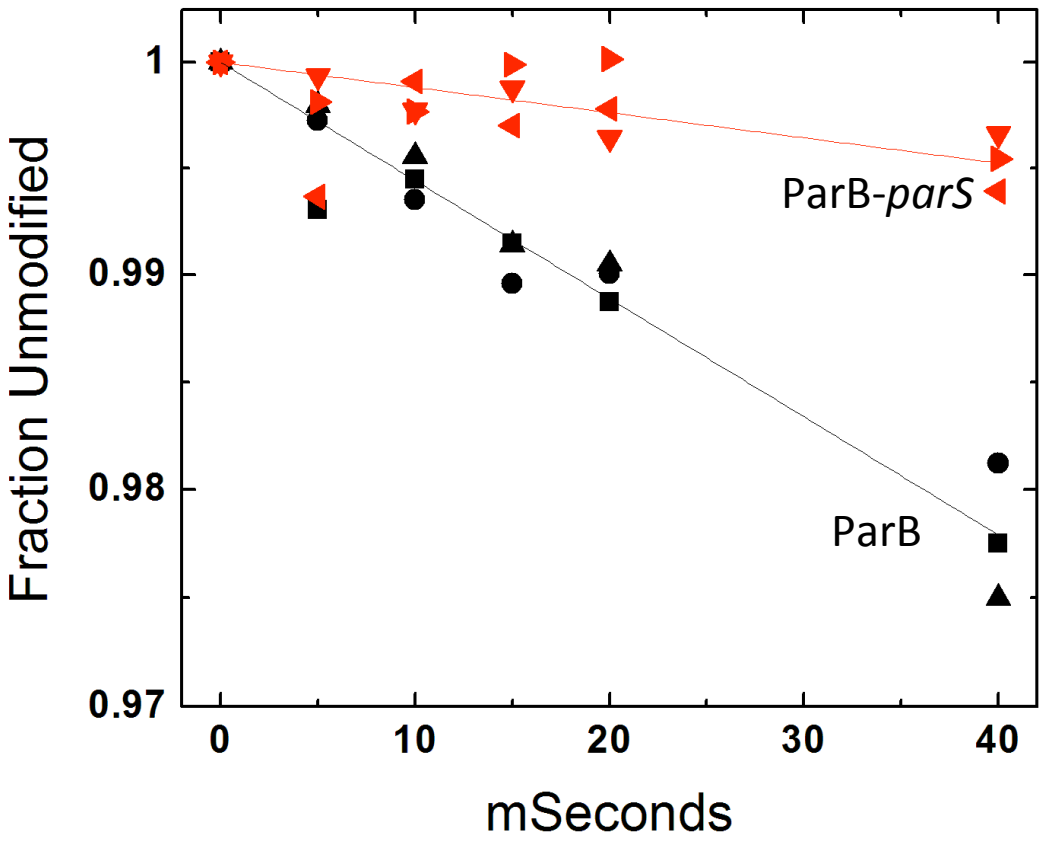

Fraction Unmodified
1
0.99
0.98
0.97
0
10
20
30
40
mSeconds
ParB-parS
ParB

Figure S4.

Figure S2. The top panel shows a typical total ion current chromatogram (TIC) of a peptic digest of X-ray irradiated (15ms) ParB, represented by software XCalibur 2.01 (Thermo Electron). The middle panel shows the selected ion chromatogram (SIC) for the native (unmodified) and modified (+16 m/z shift, single peak) peptide 211-222 and their relative abundance after 15ms of X-ray irradiation.

Figure S3. MS/MS fragmentation of native and modified peptide 211-222, which shows +16 modification at H220.

Figure S4. A representative dose response plot for peptide, 211-222 VAAGVLSAGH(+16)AR. The fraction of unmodified peptide at any exposure is calculated by the following equation:

$$Fraction\ Unmodified = \frac{Unmodified\ peak\ area}{(Unmodified\ peak\ area + Modified\ peak\ area)}$$

The peak areas are calculated from the selected ion chromatogram. A time evolution of SICs are used to calculated fraction unmodified vs. exposure time. Hydroxyl radical modification rate constants are determined from the single exponential curve fitting as described in Experimental Methods.