

Supplementary information

Profiling patterns of glutathione reductase inhibition by the natural product illudin S and its acylfulvene analogues

Xiaodan Liu and Shana J. Sturla*

Department of Medicinal Chemistry, College of Pharmacy, University of Minnesota, Minneapolis, Minnesota 55455

Figure S1. Inhibition of GR by carmustine.

Figure S2. Effect of GSSG and NADPH on the GR inhibition by carmustine.

Figure S3. Effects on the GR Fluorescence Spectrum by carmustine under Different Conditions.

Figure S4. LC/MS spectrum derived from GR-carmustine adduct.

Table S1. Mass of *y* and *b* ions from the IAA- and HMAF- modified GR active site sequence by trypsin digestion.

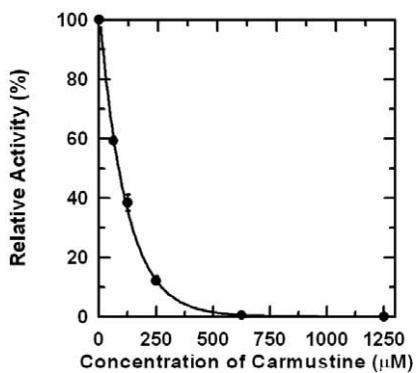


Figure S1. Inhibition of GR by carmustine. GR (5 nM) was incubated with carmustine in the presence of NADPH (150 μ M) for 30 min at 25 °C, carmustine, 62.5, 125, 250, 625, 1250 μ M.

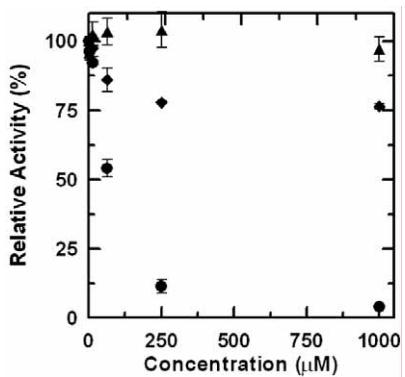


Figure S2. Effect of NADPH and GSSG on the GR Inhibition by carmustine. GR (5 nM) was incubated with carmustine (2.5, 12.5, 62.5, 250, 1000 μ M) in the presence (●) and absence (◆) of NADPH (150 μ M), or in the presence (▲) of GSSG (0.25 mM) for 30 min at 25 °C, and then the activity was measured.

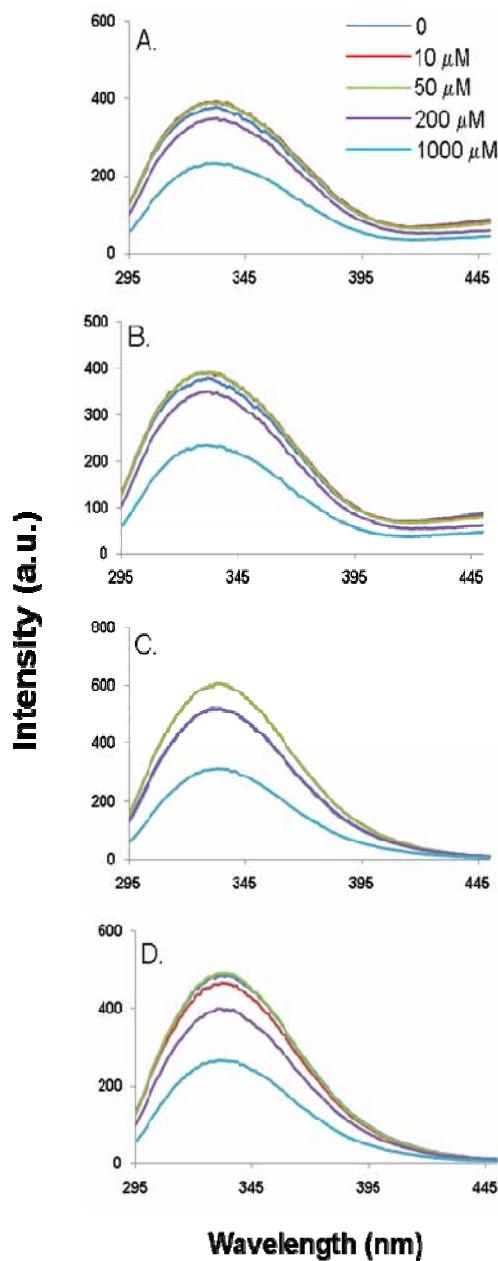


Figure S3. GR fluorescence spectrum changes in the presence of varying concentration of carmustine. Carmustine (0.01, 0.05, 0.20, 1.00 mM) was allowed to react with GR (2 μ M) in a total volume of 500 μ L TE buffer for 30 min at 25 °C under different conditions: a. the absence of NADPH; b. in the presence of NADPH (100 μ M); c. in the absence of NADPH and in the presence of GSSG (400 μ M); d. in the presence of NADPH (100 μ M) and GSSG (400 μ M).

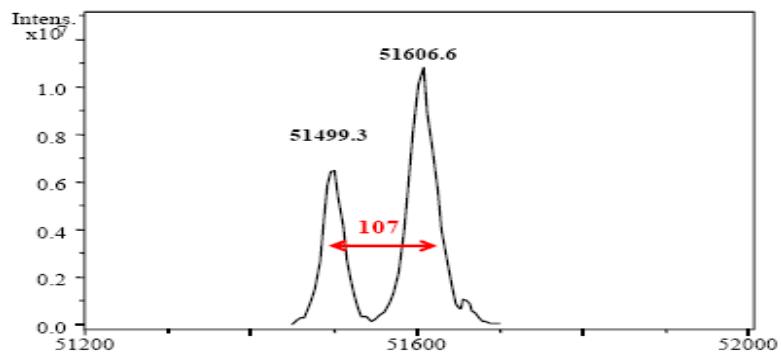


Figure S4. LC/MS spectra derived from GR-carmustine adduct. GR (5 nmol) was allowed to react with carmustine (0.25 mM) in 1 mL TE buffer containing NADPH (1 mM) for 3 h at 25 °C. Unbound compound was removed before LC/MS analysis.

Table 1. Mass of *y* and *b* ions from the IAA- and HMAF- modified GR active site sequence by trypsin digestion.

HMAF	IAA	b		Active site sequence		y	IAA	HMAF
			1	A	14			
185.1	185.1	185.1	2	L	13	1246.6	1360.7	1738.6
242.1	242.1	242.1	3	G	12	1133.5	1247.6	1625.5
299.2	299.2	299.2	4	G	11	1076.5	1190.6	1568.5
400.2	400.2	400.2	5	T	10	1019.5	1133.5	1511.5
749.2	560.2	503.2	6	C	9	918.5	1032.5	1410.5
848.3	659.3	602.3	7	V	8	815.4	872.5	1061.4
962.3	773.4	716.3	8	N	7	716.4	773.4	962.4
1061.4	872.4	815.4	9	V	6	602.3	659.4	848.3
1118.4	929.5	872.4	10	G	5	503.3	560.3	749.3
1467.4	1089.5	975.4	11	C	4	446.2	503.3	692.2
1566.5	1188.6	1074.5	12	V	3	343.2	343.2	
1663.6	1285.6	1171.6	13	P	2	244.2	244.2	
			14	K	1	147.1	147.1	

*Numbers in red represent corresponding *y* or *b* ion mass plus one molecular mass of IAA or HMAF.

*Number in blue represent corresponding *y* or *b* ion mass plus two molecular masses of IAA or HMAF.