

Table S1. Quantitative Real Time PCR (qRT-PCR) primers used for quantifying glucosinolate biosynthetic and hydrolysis-related gene transcript abundance in *Raphanus sativus*.

Gene target	RadishBase ID ^a	GeneBank ID	Description	Pathway	Primer(5'-3')
<i>CYP79B1</i>	UN28455	XM_018591728.1	Cytochrome P450 Tryptophan N-monooxygenase	Indolic (synthesis)	F AAGCAGCTAAACACCGAGATAG R GTCATAGGTCTTGAGGCGAATAG
<i>CYP83B1</i>	UN51198	XM_018603411.1	cytochrome P450	Indolic (synthesis)	F GACATCCCAAATCTCCCTTATCT R GCGTCTGCTATGGTTTCTCTAT
<i>CYP79F1</i>	UN19600	XM_018584676.1	cytochrome P450 dihomomethionine-N-hydroxylase	Aliphatic (synthesis)	F TACATTACCACCCTCTCCTCTT R GAGTTTCTCTCCGGCTGATTAC
<i>CYP83A1</i>	UN22968	XM_018629165.1	cytochrome P450	Aliphatic (synthesis)	F GGAAACCAAACCAAAGAGCATAG R CGGAGAAAGTGAGCAAGTGATA
<i>MYROSINASE4</i>	UN18772	XM_018634237.1	myrosinase	hydrolysis	F CCTTTGGATGCGAGAGAGTAAG R GGCTTCTTAAGCCCACGTATAG
<i>NITRILE-SPECIFIER</i>	UN26475	XM_018584970.1	nitrile specifier	hydrolysis	F CCAGCCCTTTCTTACCATCAA R GAAGTGGGAGAGGTTGGATAAG
APS kinase	UN65099	XM_018630545.1	5'-adenylylsulfate kinase	synthesis	F TCGGAAACTCGACGAACATAAA R ACTAAGACCAGTGACCCAAATC
<i>MYB28</i>	UN76555	XM_018596832.1	Transcription factor Myb-related protein 28	Aliphatic (synthesis)	F TCGGTCATAGCGAGACATTTAC R TTGTGAGTCACGGGATCAATAC
<i>ACTIN7</i>	UN84481	XM_018620829.1	Actin2/7	reference	F CCTGGATAGCAACATACAT R GCATCACACTTTCTACAAC

^a <http://bioinfo.bti.cornell.edu/cgi-bin/radish/EST/>

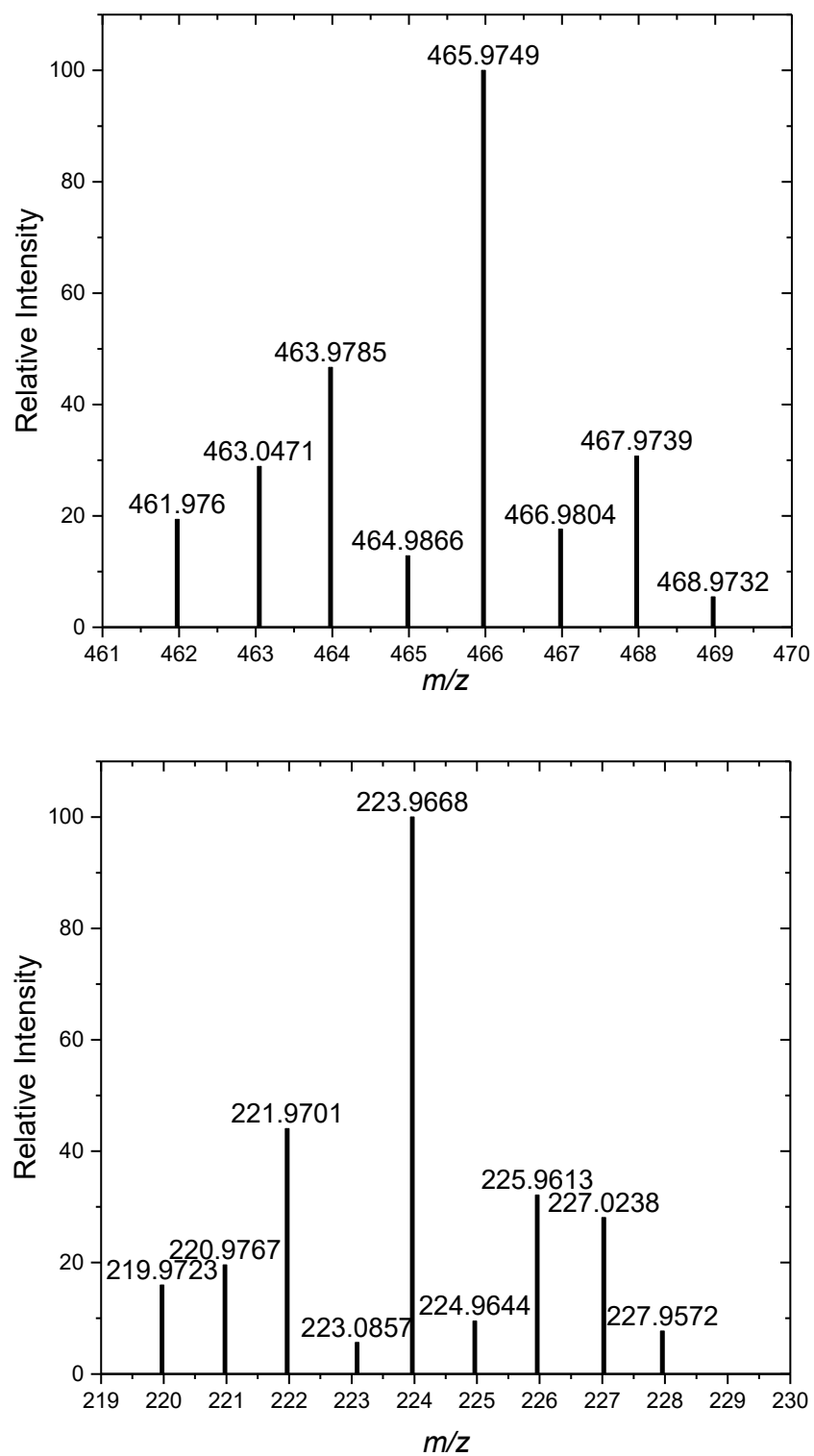


Figure 1. Selenium isotope clusters for the tentatively identified 4MSeB3 pseudomolecular ion and its major selenium-containing daughter ion.

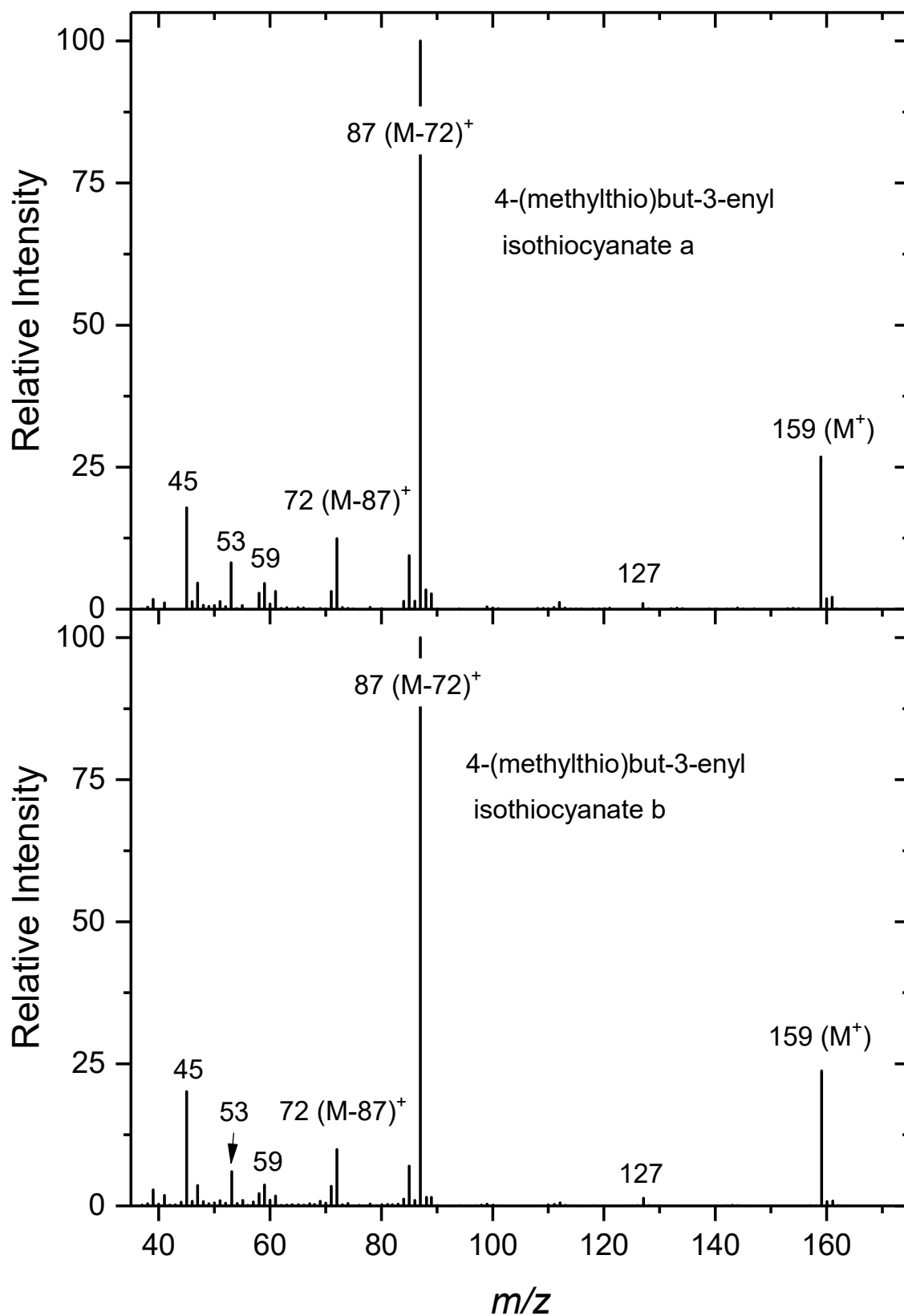


Figure 2. EI-MS fragmentation patterns of the two isomers of 4MTB3-ITC.

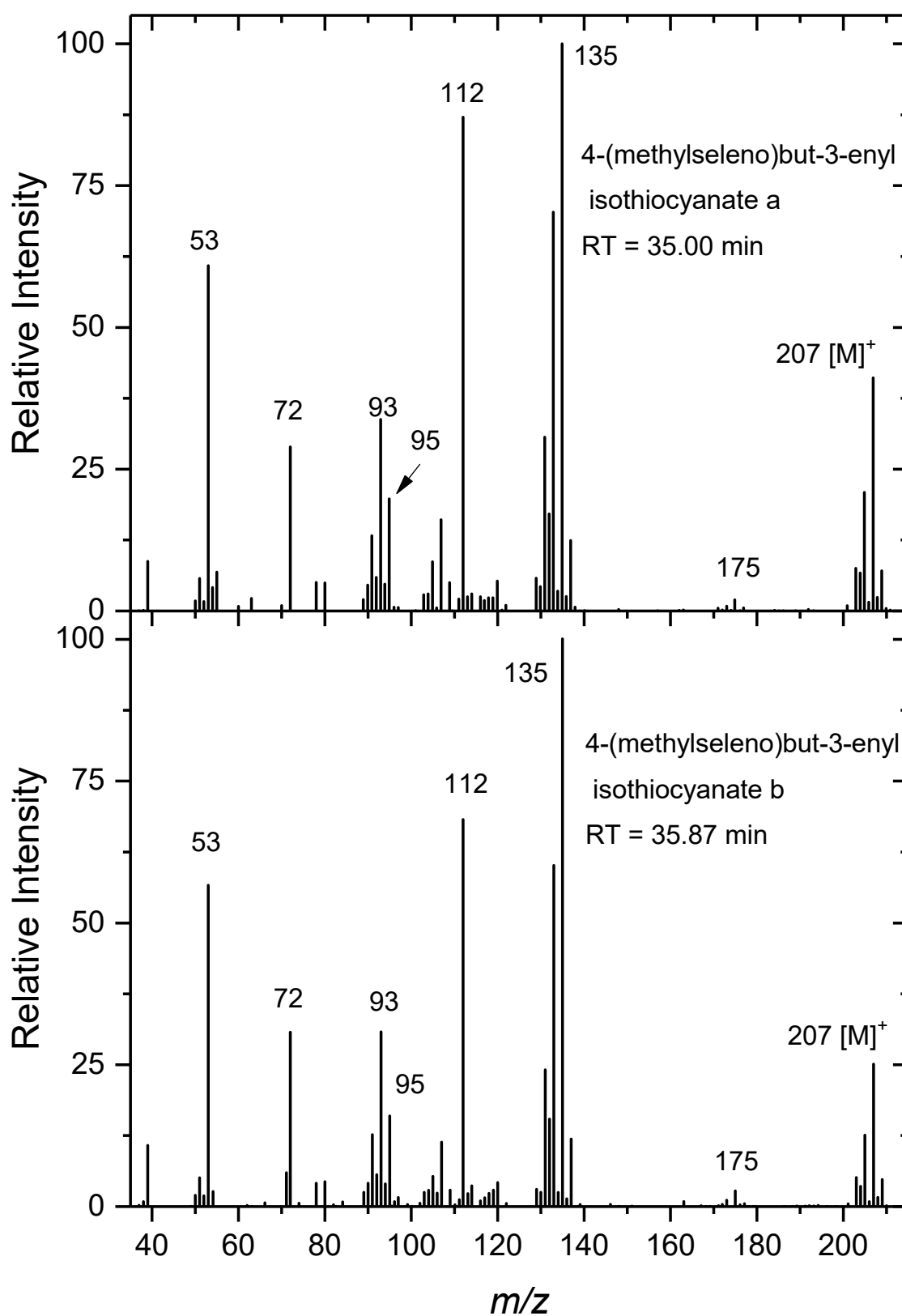


Figure 3. EI-MS fragmentation patterns of the two isomers of the proposed compound 4MSeB3-ITC.