**Supplemental materials**

**MATERIALS AND EXPERIMENTAL METHODS**

***HPLC analysis of extracellular and intracellular ITCs and the metabolites.*** An aliquot of the TCA supernatant (300 μL) or the culture medium (400 μL directly from culture plates) was analyzed by HPLC with a UV detector SPD-10A (Shimadzu, Columbia, MD) and a β-RAM detector (Inus System, Tampa, FL) on a Phenomenex C18 HPLC column (5μm, 4.6 × 250 mm) eluted at 1 mL/min with a gradient mobile phase consisting of 25 mM sodium phosphate (pH 5.4; mobile phase A) and 100% methanol (mobile phase B). The linear gradient for PEITC metabolites was: 0% B for the first 5 min, increased to 100% B from 5 to 55 min, then kept at 100% B from 55 to 65 min. The linear gradient for SFN metabolites was: 0% B for the first 5 min, increased to 50% B from 5 to 55 min, then increased to 100% B from 55 to 65 min, then kept at 100% B from 65 to 75 min. The scintillation cocktail flow rate was set at 3 mL/min.

***Determination of protein carbonyls by ELISA.*** After ITC treatment, cell pellet ($4x10^6$ cells) was lysed in 200 μl buffer (50 mM phosphate, 0.1% Triton X-100, pH 7.4) on ice for 30 min. The cell lysate at 10 μg/mL in PBS buffer was incubated in a NUNC Maxisorp plate in tetra-plicate (200 μl) overnight at 4°C. DNPH solution (0.1 mM) was allowed to react for 45 min at room temperature before washing with PBS/Ethanol (1:1, v/v). Nonspecific binding sites were blocked at room temperature with 5% milk (Bio-Rad) in PBS for 2 h. After washing, rabbit anti-DNPH primary antibody (Sigma-Aldrich; 1:4000) was applied and incubated for 1 h at 37 °C. Following washing with PBST (0.1% Tween 20), anti-rabbit IgG conjugated to peroxidase (GE Healthcare; 1:5000) was also incubated at 37 °C for 1 h. The reaction was visualized by treatment with 200 μL 0.6 mg/mL *o*-phenylenediamine in substrate buffer (50 mM phosphate, 25 mM acetic acid, 1.3 mM $H_2O_2$, pH 5.0) and stopped by the addition of 100 μL sulfuric acid (2 N) after 15 min.

Absorbance at 490 nm was measured. Seven carbonyl standards (0–6 nmol protein carbonyl/mg protein) were generated from a combination of sodium borohydride reduction or iron-catalysed oxidation of bovine serum albumin and calibrated as previously described (30) to construct a standard curve, from which the carbonyl content of the protein samples was calculated.

***Identification of ITC binding sites by mass spectrometry.*** BSA (1mg/mL) was mixed with 2 mM DTT and the mixture was incubated at 37 ºC for 30 min, before it was purified by a two-in-series Sephadex G25 desalting column. The reduced BSA was incubated in the presence or absence of 1 mM either PEITC or SFN at 37 ºC for 2 h. ITC-treated and native BSA were digested with modified trypsin (Promega, Madison, WI) and analyzed by matrix-asssisted laser desorption/ionization time-of-flight/time-of-flight mass spectrometer (MALDI-TOF/TOF) (4700 Proteomics Analyzer, Applied Biosystems, Foster City, CA) to obtain accurate masses of the peptides. The BSA peptide digests were spotted onto a 192 well stainless steel MALDI target plate after mixing 0.5 µl of peptides with 0.5 µl of pre-solubilized α-cyano-4-hydroxycinnamic acid matrix (Agilent Technologies, Paolo Alto, CA), and air-dried at room temperature. The instrument was operated in reflector mode, and the MS data were acquired from *m/z* range 600-4000 with external calibration. Each MS spectrum represents 1000 laser acquisitions averaged from 20 sub-spectra each consisting of 50 laser shots on the sample.