

Covalent Small Molecule Inhibitors of Ca^{2+} -Bound S100B

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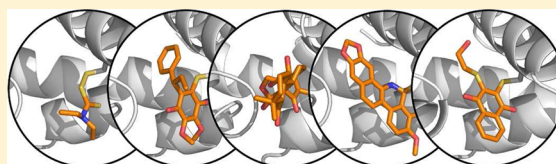
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S Supporting Information

ABSTRACT: Elevated levels of the tumor marker S100B are observed in malignant melanoma, and this EF-hand-containing protein was shown to directly bind wild-type (wt) p53 in a Ca^{2+} -dependent manner, dissociate the p53 tetramer, and inhibit its tumor suppression functions. Likewise, inhibiting S100B with small interfering RNA (siRNA^{S100B}) is sufficient to restore wild-type p53 levels and its downstream gene products and induce the arrest of cell growth and UV-dependent apoptosis in malignant melanoma. Therefore, it is a goal to develop S100B inhibitors (SbIXs) that inhibit the S100B–p53 complex and restore active p53 in this deadly cancer. Using a structure–activity relationship by nuclear magnetic resonance approach (SAR by NMR), three persistent binding pockets are found on S100B, termed sites 1–3. While inhibitors that simultaneously bind sites 2 and 3 are in place, no molecules that simultaneously bind all three persistent sites are available. For this purpose, Cys84 was used in this study as a potential means to bridge sites 1 and 2 because it is located in a small crevice between these two deeper pockets on the protein. Using a fluorescence polarization competition assay, several Cys84-modified S100B complexes were identified and examined further. For five such SbIX–S100B complexes, crystallographic structures confirmed their covalent binding to Cys84 near site 2 and thus present straightforward chemical biology strategies for bridging sites 1 and 3. Importantly, one such compound, SC1982, showed an S100B-dependent death response in assays with WM115 malignant melanoma cells, so it will be particularly useful for the design of SbIX molecules with improved affinity and specificity.



Covalent small molecule inhibitors of Ca^{2+} -bound S100B

Despite improvements in chemotherapy, BRAF/MEK inhibitors, cytokine treatments, immunotherapies, vaccines, and combinatorial approaches for treating malignant melanoma (MM),^{1–5} long-term survival (>3 years) remains very poor for a majority of patients (>70%), and side effects from these treatments are sometimes quite severe.^{2,6,7} These issues are even more problematic after the onset of metastasis and/or when drug-resistant mechanisms arise.^{5,8} As with many cancers, survival from MM is most promising when it is detected early, so the development of useful biomarkers for detection and more recently for personalized medicine approaches is ongoing.^{9,10} One such marker, S100B, is especially important to monitor because its level is elevated in >90% of MM patients and its protein level correlates directly with poor survival (<1 year) and relapse, and it is especially predictive when used in combination with other diagnostic indicators.^{11–13} On the other hand, for the few MM patients (5–10%) who have low levels of S100B, the MM vaccine is most effective at providing longer survival times.^{14,15}

The S100B protein is a marker for melanoma, and when its level is elevated, it contributes to disease progression.^{16,17} While

the mechanism of elevated S100B levels toward MM progression is not fully understood, it contributes to lowering protein levels of the tumor suppressor p53 in a Ca^{2+} -dependent manner.^{18,19} Specifically, p53 is sequestered by Ca^{2+} -bound S100B (Ca^{S100B}), its phosphorylation in the C-terminal negative regulator domain blocked,^{20–23} its oligomerization disrupted,¹⁹ and its degradation promoted.^{18,19,24,25} Because p53 is typically wild-type in MM,^{26,27} efforts are underway to specifically inhibit formation of the Ca^{S100B} –p53 complex^{16,28,29} and restore p53 levels, particularly in cases in which the cancer is resistant to kinase inhibitors or other therapeutic options.³⁰ As a proof of principle, blocking the Ca^{S100B} -dependent effect on p53 via RNA interference or by small molecule inhibitors (also known as SbIXs) restores p53 protein levels and its tumor suppression activities, including UV-activated apoptosis.^{17,18,31} One such inhibitor, pentamidine

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(also termed SBI1), entered stage II clinical trials for the treatment of relapsed or refractory malignant melanoma in patients with wild-type p53 and detectable S100B (www.clinicaltrials.gov, identifier NCT00729807). However, despite this promising line of inquiry, efficacy, specificity, and toxicity issues need to be improved significantly for SBIx lead molecules and warrant further investigation using drug design approaches.

In previous structure–function studies of S100B,^{32–35} three persistent binding sites were identified in ^{Ca}S100B–target and ^{Ca}S100B–SBIx complexes (Figure 1). Site 1 interactions were

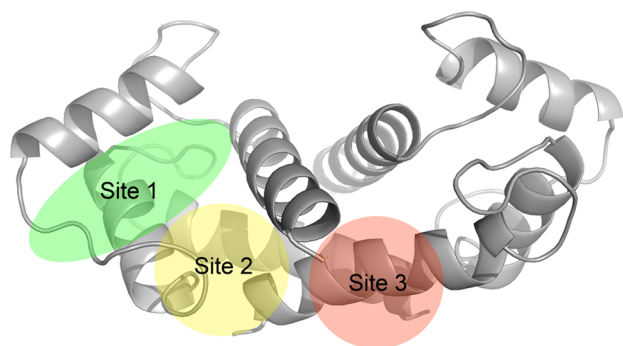


Figure 1. Binding sites 1–3. Shown is a ribbon diagram of the S100B dimer with the three persistent binding sites shaded. The sites were identified in ^{Ca}S100B–target and ^{Ca}S100B–SBIx complexes. Site 1 interactions were first highlighted via the structure of ^{Ca}S100B bound to the C-terminal regulatory domain of p53,²⁰ while sites 2 and 3 were elucidated in the detailed characterization of the ^{Ca}S100B–SBI1 complex.³⁶

first highlighted via the structure of ^{Ca}S100B bound to the C-terminal regulatory domain of p53,²⁰ while sites 2 and 3 were elucidated in the detailed characterization of the ^{Ca}S100B–SBI1 complex.³⁶ Here we describe a series of inhibitors, which occupy only the central binding site on ^{Ca}S100B (site 2) through a covalent attachment to Cys84. To fully characterize this binding site, a series of “site 2” ^{Ca}S100B–SBIx complexes were subjected to crystallization trials. Five new ^{Ca}S100B–SBIx complexes were identified (i.e., for ^{Ca}S100B–SC124, ^{Ca}S100B–SBI4172, ^{Ca}S100B–SC1982, and ^{Ca}S100B–SC1475). As a group, these “site 2” inhibitors display a meaningful effect in cellular assays on their own, but as discussed here, they also provide promise for defining how to link SBIx molecules bound in sites 1 and 3, as part of a new chemical scaffold, which can occupy all three persistent binding pockets within ^{Ca}S100B, simultaneously. These data also identify a common conformational change that occurs as a result of “site 2” occupation, which is necessary to consider in future therapeutic design efforts.

EXPERIMENTAL PROCEDURES

Purification. ¹⁵N-labeled S100B (rat and bovine) was expressed and purified (>99%) with methods similar to those described previously.^{37,38} The concentrations of S100B stock solutions were determined using the Bio-Rad Protein Assay (Bio-Rad Inc., Hercules, CA). The S100B was stored at a concentration of ~10 mM in 0.25 mM Tris (pH 7.2) and 0.25 mM DTT at –20 °C until use.

Fluorescence Polarization Competition Assay (FPCA). The LOPAC1280 (Sigma-Aldrich) compound library was screened using an adaptation of a previously reported

fluorescence polarization competition assay.³⁵ Briefly, the compounds were screened for binding to ^{Ca}2+-loaded S100B by measuring changes in fluorescence polarization upon competition with the TAMRA-labeled version of peptide TRTK12, which is derived from CapZ protein residues 265–276 (TRTKIDWNKILS). The FPCA was performed in 0.2 μ M S100B (rat), 25 nM TAMRA-TRTK12, 50 mM HEPES (pH 7.2), 100 mM KCl, 15 mM NaCl, 10 mM CaCl₂, 0.01% Triton X-100, and 0.3% DMSO in 1536-well plates with 8 μ L per well.

NMR Spectroscopy. Purified ¹⁵N-labeled S100B (rat) protein was dialyzed against 0.25 mM Tris (pH 7.5) and 0.25 mM DTT and concentrated to 10–15 mM using Amicon Ultra centrifugal filter units with a 10 kDa molecular weight cutoff; the concentration was determined using Bradford reagent (Bio-Rad), and protein was then aliquoted and stored at –20 °C. The ^{Ca}2+-loaded S100B–SBIx heteronuclear single-quantum coherence (HSQC) samples contained 0.5 mM S100B subunit, 0.625 mM SBIx, 0.34 mM NaN₃, 15 mM NaCl, 5% DMSO-*d*₆, 10 mM CaCl₂, 10% D₂O, 0.2% TPEN, and 10 mM Hepes, adjusted to pH 7.2 with HCl. HSQC NMR data were collected at 37 °C with a Bruker Avance 800 US2 (800.27 MHz for protons) instrument equipped with pulsed-field gradients, four frequency channels, and triple-resonance, z-axis gradient cryogenic probes. Data were processed with NMRPipe, and proton chemical shifts were reported with respect to the H₂O or HDO signal taken as 4.608 ppm relative to external TSP (0.0 ppm). The ¹⁵N chemical shifts were indirectly referenced as previously described using the following ratio of the zero-point frequency: 0.10132905 for ¹⁵N to ¹H. A series of three-dimensional HNCA, HNCOCa, ¹⁵N-edited NOESY-HSQC, and ¹⁵N-edited HMQC-NOESY-HSQC NMR experiments were conducted, and the data were sufficient to unambiguously assign all the observable backbone ¹H, ¹⁵N, and ¹³C chemical shift values of S100B in the compound-bound state (Figures S1–S5 of the Supporting Information).

Crystallographic Studies. Crystallization. All crystallization experiments were conducted using vapor diffusion methods and performed as follows using purified ¹⁵N-labeled S100B (bovine) protein. ^{Ca}S100B–SBI4172 crystals were grown in sitting drops consisting of a 0.75:0.75 μ L protein solution [20 mg/mL S100B, 10 mM cacodylate (pH 7.2), 7.5 mM CaCl₂, and 2 mM SBI4172 prepared in DMSO-*d*₆] and mother liquor [20% 2-methyl-2,4-pentanediol, 0.1 M Hepes (pH 7.0), and 7.5 mM CaCl₂]. ^{Ca}S100B–SBI4434 crystals were grown in sitting drops consisting of a 0.75:0.75 μ L protein solution [40 mg/mL S100B, 10 mM cacodylate (pH 7.2), 7.5 mM CaCl₂, and 4 mM SBI4434 prepared in DMSO-*d*₆] and mother liquor [40% 2-methyl-2,4-pentanediol, 0.1 M cacodylate (pH 6.0), and 7.5 mM CaCl₂]. ^{Ca}S100B–SC1982 crystals were grown in sitting drops consisting of a 0.75:0.75 μ L protein solution [40 mg/mL S100B, 10 mM cacodylate (pH 7.2), 7.5 mM CaCl₂, and 4 mM SC1982 prepared in DMSO-*d*₆] and mother liquor [40% 2-methyl-2,4-pentanediol, 0.1 M Tris (pH 8.0), and 7.5 mM CaCl₂]. ^{Ca}S100B–SC1475 crystals were grown in sitting drops consisting of a 0.75:0.75 μ L protein solution [40 mg/mL S100B, 10 mM cacodylate (pH 7.2), 7.5 mM CaCl₂, and 4 mM SC1475 prepared in DMSO-*d*₆] and mother liquor [40% 2-methyl-2,4-pentanediol, 0.1 M Bis-Tris (pH 6.0), and 7.5 mM CaCl₂]. ^{Ca}S100B–SC124 crystals were grown in sitting drops consisting of a 0.75:0.75 μ L protein solution [40 mg/mL S100B, 10 mM cacodylate (pH 7.2), 7.5 mM CaCl₂, and 4 mM SC124 prepared in DMSO-*d*₆] and mother liquor [40% 2-methyl-2,4-pentanediol, 0.1 M Hepes

Table 1. Statistics of Reflection Data and Structure Refinements^a

	SC124	SC1475	SC1982	SBi4172	SBi4434
space group	P21	P21	C2221	P21	P21
unit cell dimensions (Å)	34.7, 56.5, 48.3	35.0, 58.1, 47.9	34.6, 90.0, 60.8	35.0, 57.1, 48.0	35.2, 56.3, 48.1
unit cell angles (deg)	90.0, 110.1, 90.0	90.0, 111.2, 90.0	90.0, 90.0, 90.0	90.0, 111.0, 90.0	90.0, 108.8, 90.0
resolution range (Å)	35.35–1.58	35.40–2.18	36.17–1.65	44.82–1.73	21.69–1.08
no. of reflections observed	83472 (9120)	30768 (4167)	55035 (7875)	55396 (8136)	244228 (12126)
no. of unique reflections	23617 (3115)	9152 (1259)	11752 (1673)	17118 (2517)	70592 (3504)
no. of reflections in the R_{free} set	1201	935	1173	869	2006
completeness (%)	97.8 (89.1)	96.7 (91.7)	99.9 (99.8)	92.6 (94.2)	92.2 (93.0)
redundancy	3.5 (2.9)	3.4 (3.3)	4.7 (4.7)	3.2 (3.2)	3.5 (3.5)
$\langle I/\sigma \rangle$	22.6 (3.5)	11.6 (2.3)	22.7 (2.6)	13.8 (2.4)	9.0 (3.0)
R_{sym}^b	0.029 (0.325)	0.051 (0.461)	0.045 (0.613)	0.038 (0.452)	0.068 (0.351)
R_{cryst}^c	0.215	0.213	0.177	0.230	0.192
R_{free}^d	0.253	0.251	0.214	0.268	0.211
no. of amino acids	179	180	90	179	181
no. of protein atoms	1445	1454	751	1446	1464
no. of hetero atoms	20	46	29	30	36
no. of waters	173	19	137	76	321
rmsd ^e for bond lengths (Å)	0.020	0.013	0.012	0.024	0.015
rmsd ^e for bond angles (deg)	1.056	1.304	1.231	1.372	1.133
mean B factor (Å ²)	28.92	48.73	20.67	39.00	14.91
protein atoms (Å ²)	27.69	48.00	18.61	38.74	13.62
hetero atoms (Å ²)	44.54	71.95	28.82	38.00	22.01
water atoms (Å ²)	37.36	48.65	30.21	44.32	25.09
Ramachandran outliers (%)	0.0	0.0	0.0	0.0	0.0
Ramachandran favored (%)	100.0	98.9	100.0	98.9	99.4

^aThe numbers in parentheses represent values from the highest-resolution shell (1.66–1.58 Å for SC124, 2.3–2.18 Å for SC1475, 1.74–1.65 Å for SC1982, 1.82–1.73 Å for SBi4172, and 1.10–1.08 Å for SBi4434). Atom counts do not include H. ^b $R_{\text{sym}} = \sum_h (\sum_j |I_{hj}| - \langle I_h \rangle) / \sum_j |I_{hj}|$, where h is the set of Miller indices, j is the set of observations of reflection h , and $\langle I_h \rangle$ is the mean intensity. ^c $R_{\text{cryst}} = \sum_h ||F_{o,h}| - |F_{c,h}|| / \sum_h |F_{o,h}|$. ^d R_{free} was calculated using a percentage of the complete data set excluded from refinement. ^eDeviations from ideal values.

(pH 7.0), and 7.5 mM CaCl₂]. The crystals were grown over a period of 1–14 days at 295 K. Crystals were flash-cooled directly from the crystallization drop.

Data Collection and Processing. Diffraction data for ^{Ca}S100B–SBi4172 crystals were collected at the Northeastern Collaborative Access Team (NE-CAT) 24ID-C beamline at the Advanced Photon Source (Argonne National Laboratory, Argonne, IL). Data were recorded at 100 K on a PILATUS detector and processed by NE-CAT's RAPD automated processing (<https://rapd.nec.aps.anl.gov/rapd>), which uses XDS³⁹ for integration and scaling. A 1.73 Å data set was collected at a wavelength of 0.97920 Å while the crystal was being oscillated by 1.0° each frame. The space group was determined to be P21.

Diffraction data for ^{Ca}S100B–SC124, ^{Ca}S100B–SBi4434, and ^{Ca}S100B–SC1982 crystals were collected remotely^{40,41} at Stanford Synchrotron Radiation Lightsource (SSRL) beamline 7-1. Data were recorded at 100 K on an ADSC Q315 (315 mm × 315 mm) detector with collection strategies generated by BLU-ICE.⁴² ^{Ca}S100B–SC124 and ^{Ca}S100B–SC1982 data sets were processed and integrated by AUTODS,⁴³ while S100B–SBi4434 data sets were processed and integrated by MOSFLM⁴⁴ within the CCP4 program suite.⁴⁵ A 1.58 Å ^{Ca}S100B–SC124 data set was collected at a wavelength of 1.1271 Å while the crystal was being oscillated by 0.6° each frame. The space group was determined to be P21. A 1.08 Å ^{Ca}S100B–SBi4434 data set was collected at a wavelength of 1.00 Å while the crystal was being oscillated by 0.35° each frame. The space group was determined to be P21. A 1.65 Å ^{Ca}S100B–SC1982 data set was collected at a wavelength of

1.1271 Å while the crystal was being oscillated 0.45° each frame. The space group was determined to be C2221.

Diffraction data for ^{Ca}S100B–SC1475 crystals were collected remotely^{40,41} at Stanford Synchrotron Radiation Lightsource (SSRL) beamline 12-2. Data were recorded at 100 K on a PILATUS detector with collection strategies generated by BLU-ICE,⁴² and processing and integration were performed by AUTODS.⁴³ A 2.18 Å data set was collected at a wavelength of 0.97950 Å while the crystal was being oscillated by 0.15° each frame. The space group was determined to be P21. Diffraction data statistics are summarized in Table 1.

Structure Determination and Refinement. To determine the structure of ^{Ca}S100B in complex with SBiXs, we performed molecular replacement (MR). A search model from a previous S100B structure [Protein Data Bank (PDB) entry 1MHO^{46,47}] was generated by removing coordinates for ligands and water. Molecular replacement was conducted within the AUTOMR⁴⁸ function of the PHENIX⁴⁹ software suite. The models were finished by manual building within COOT.⁵⁰ The models were refined by the PHENIX.REFINE⁵¹ function of the PHENIX⁴⁹ software suite. Ligands and waters were incorporated into the models by visual inspection of the $|F_o| - |F_c|$ omit maps. The structure refinement statistics are summarized in Table 1.

Cell-Based Assay with WM115 Malignant Melanoma Cells. The malignant melanoma cell line, WM115, was obtained from American Type Tissue Collection (ATCC) and cultured in minimum essential medium (Invitrogen) supplemented with 10% heat-inactivated fetal bovine serum (FBS) and 100 units/mL penicillin-streptomycin (PS). The cells were infected with SMARTvector 2.0 lentiviral particles

containing either nontargeting scrambled or anti-S100B shRNA according to manufacturer's recommendations (Thermo Scientific-Dharmacon). The following day, the medium containing lentivirus was removed, the cells were washed twice with PBS and trypsinized, and each well was expanded into a 24-well plate containing growth medium supplemented with puromycin (0.5 $\mu\text{g/mL}$). Upon confluence, the wells were trypsinized and single-cell diluted into 96-well plates. Positive clones with a reduction in the level of S100B protein expression were maintained in puromycin-containing medium.⁵²

A cellular screen was then developed with these WM115 cell lines, and further test compounds were shown to bind S100B *in vitro*. In this cellular assay, the ability of SBiX molecules to inhibit the growth of WM115 melanoma cells infected with shRNA lentivirus (Dharmacon) targeting S100B (shRNA^{S100B}, i.e., low S100B) or a scrambled control (shRNA^{scrambled}, i.e., high S100B) was examined quantitatively. The methods used were similar to those used previously and included the use of a Biomek FX Laboratory Automation Workstation (Beckman-Coulter) equipped with a 96-channel pipetting head.⁵³ Specifically, 20 μL of MEM (Corning) supplemented with 10% fetal bovine serum, 0.5 $\mu\text{g/mL}$ puromycin, and 1% Pen/Strep was added to each well of a 384-well, clear bottom, tissue culture plate (Corning) containing 600 cells per well such that growing uninhibited they reach 80% confluence in 5 days. After the cells had grown for 24 h at 37 °C in a 5% CO₂ humidity-controlled incubator, 20 μL of the compound was added directly to the cell culture medium, while control cultures received an equivalent amount of DMSO. After being incubated for an additional 4 days, the cells were lysed by transferring 20 μL of lysis buffer consisting of 1.8% Igepal with a 1:10000 dilution of SYBR Green I (10000 \times , Invitrogen) to each well. The plates were then returned to the incubator for 24 h. The fluorescence intensity was then read through the bottom of the plate using a PolarStar fluorescent plate reader (BMG) using 485 nm excitation and 520 nm emission filters. The SYBR Green fluorescence is used to measure total DNA that in turn correlates with the cell number as previously described.⁵⁴ The EC₅₀ of each compound was determined using serial dilutions and performed in a minimum of three replicates. Hill curves of each replicate were generated using Origin Data Analysis Software.

To analyze changes in total p53 protein levels upon treatment with SC1982, WM115 cells were seeded in triplicate at a density of 70 \times 10⁵ cells in 60 mm dishes in 1 \times MEM (Cellgro) supplemented with 10% FBS, 100 units/mL PS, and 0.5 $\mu\text{g/mL}$ puromycin and allowed to adhere overnight. The following day, the old medium was removed and new medium containing 5 μM SC1982 or DMSO was added. The cells were harvested 4 h post-treatment using cold 1 \times RIPA lysis buffer [0.5 M Tris-HCl (pH 7.4), 1.5 M NaCl, 2.5% deoxycholic acid, 10% Igepal, and 10 mM EDTA] and subjected to Western blotting.

Western blotting was performed using 30 μg of cell lysates loaded on a 12% sodium dodecyl sulfate–polyacrylamide gel electrophoresis gel (NuPage), which was subsequently transferred to PVDF membranes (Millipore) and reacted with p53 mouse monoclonal antibody (DO-1, Santa Cruz), mouse anti-S100B antibody (BD Biosciences), and mouse anti-GAPDH antibody at dilutions recommended by the manufacturers. The blots were then reacted with goat anti-mouse secondary antibodies (Kirkegaard & Perry Laboratories) and treated

with Immobilon Western Chemiluminescent HRP Substrate (Millipore) at dilutions recommended by the manufacturer.

RESULTS

The binding of ^{Ca}S100B to p53 downregulates tumor suppressor activity in cancer cells such as malignant melanoma,^{18,24} so a search for small molecule inhibitors that bind ^{Ca}S100B and prevent formation of the ^{Ca}S100B–p53 complex was undertaken. A fluorescence polarization competition assay (FPCA) was performed against the 1280-compound Library of Pharmacologically Active Compounds (LOPAC1280). Because of the location of Cys84 within the ^{Ca}S100B binding pocket (i.e., between sites 1 and 3), the focus of this investigation was a series of covalent complexes from this that were predicted to covalently bind at Cys84 of ^{Ca}S100B. SBi4172 is a structural analogue of the covalent modifier SC0844³⁵ and was thought to bind similarly. SC124, or disulfiram, is a known covalent modifier.⁵⁵ The chemical nature of SBi4434 suggests the possibility of adduct formation and is confirmed here. To gain additional opportunities for characterization of covalent adducts, compounds were also taken from a previously reported screen versus the 2000-compound Spectrum Collection.³⁵ The compounds characterized in this study include SC1982 and SC1475, which were reported in the previous study as being dependent on Cys84 for binding, but the formed covalent adducts were not investigated.³⁵ Cellular and biophysical characterization of these covalently bound inhibitors was explored, including their three-dimensional structures when bound to ^{Ca}S100B (Tables 1–4).

Table 2. Cellular Assays^a

compound	high S100B EC ₅₀ (μM)		low S100B EC ₅₀ (μM)		T-test	ratio (\mp)	n
	mean	SD	mean	SD			
SC124	0.06	0.06	0.23	0.38	0.321	3.57	6
SC1475	13.87	1.70	13.81	5.00	0.980	1.00	6
SC1982	5.05	1.13	8.95	2.68	0.001	1.77	8
SBi4172	2.07	1.29	3.11	1.43	0.127	1.50	9
SBi4434	FI		FI				

^aAssays used WM115 melanoma cells transfected with shRNA^{scrambled} (i.e., high S100B) or shRNA^{S100B} (i.e., low S100B).

Table 3. Calculated rmsd's (angstroms) of Models from C^α Atoms of 1MHO^a

^{Ca} S100B–SC124	0.382 (0.381)	0.435 (0.328)
^{Ca} S100B–SC1475	0.329 (0.258)	0.325(0.256)
^{Ca} S100B–SC1982	0.391 (0.279)	
^{Ca} S100B–SBi4172	0.518 (0.378)	0.546 (0.382)
^{Ca} S100B–SBi4434	0.310 (0.279)	0.319 (0.252)

^aOne or both modeled protein chains (when applicable) are compared to the single-protein chain within 1MHO. Numbers in parentheses are the calculated rmsd's of only globally conserved residues 1–84.

NMR Studies. Backbone resonance assignments were completed for each SBiX–S100B complex using standard multidimensional heteronuclear NMR data, and the chemical shift perturbations in ^{Ca}S100B (with or without the compound) were evaluated as described for other S100B inhibitors.^{31,33–36} In general, the SBiX complexes studied here showed the largest perturbations within a well-defined binding pocket of ^{Ca}S100B comprising helices 3 and 4 and loop 2 (termed the “hinge”

Table 4. Measured Distortions of the Zinc Binding Site^a

	His15	His25	His85	Glu89
SC1982	95.5°	19.1°	0.7 Å	1.9 Å
SBi4172	76.9°		1.4 Å	2.5 Å
SBi4434		28.1°	67.9°	1.5 Å
SC1475	68.2°		0.8 Å	1.3 Å
SC124	82.9°		1.0 Å	1.6 Å
SC0844 ³⁵	38.3°	2.8 Å	157.7°	5.0 Å
SC0322 ³⁵	31.2°	31.7°	49.1°	not applicable

^aShown are averaged movements of side chains in angstroms (directional movement of C^γ) or degrees (swing of C^β–C^γ). As Glu89 was not modeled in 1MHO, directional measurements are from the carbonyl carbon atom of Phe88.

region). These observations are consistent with the FPCA, which identified SBiXs that compete with TRTK12 peptide binding.

Chemical Shift Assignments. Titrations of compound into ^{Ca}S100B were monitored using ¹H–¹⁵N HSQC NMR experiments, as previously described.^{32–34} Because perturbations were not always easily tracked during the titration, a series of HNCA, HNCOC, ¹⁵N-edited NOESY-HSQC, and ¹⁵N-HNH (HMQC-NOESY-HSQC) NMR experiments were collected at the end of each titration to unambiguously assign all the chemical shift values in the compound-bound state. The reaction products for five small molecules (SC124, SC1475, SC1982, SBi4172, and SBi4434) bound to ^{Ca}S100B were assessed by monitoring perturbations of backbone ¹H–¹⁵N HSQC correlations after the compounds were added and fully reacted (Figure 2 and Figures S1–S5 of the Supporting Information).

In the presence of SC124, many of the ¹H–¹⁵N HSQC correlations of ^{Ca}S100B were perturbed, with the most significant perturbations (≥mean ± SD) occurring for residues in loop 2 (His42) and helix 4 (Ser78, Thr81, Thr82, Ala83, Glu86, Phe87, and His90). Likewise, several other residues in

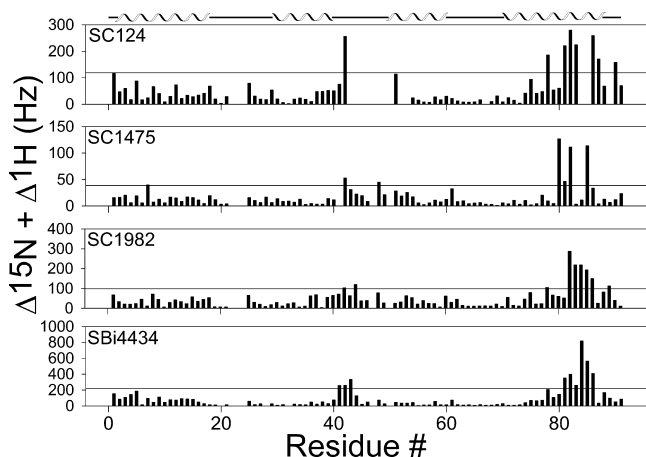


Figure 2. Assigned two-dimensional ¹H–¹⁵N HSQC NMR spectra. The binding of five small molecules (SC124, SC1475, SC1982, SBi4172, and SBi4434) to ^{Ca}S100B was assessed by monitoring perturbations of backbone ¹H–¹⁵N HSQC NMR experiments. Chemical shift perturbations in NMR spectra for ^{Ca}S100B in the presence of SBi4172 could not be measured as the compound caused ^{Ca}S100B to form soluble aggregates. The solid horizontal line is plotted at the mean perturbation (in hertz) plus one standard deviation for each data set.

loop 2 (Phe43, Leu44, Glu45, and Glu46) and helix 4 (Cys84, His85, and Glu89) either broadened and/or disappeared upon addition of SC124.

Similarly, residues in loop 2 and helix 4 were perturbed for modifications via SC1982 (loop 2, His42 and Leu44; helix 4, Ser78, Thr82, Ala83, Cys84, His85, Glu86, and Glu89) and SBi4434 (loop 2, Ser41, His42, and Phe43; helix 4, Thr81, Thr82, Ala83, Cys84, His85, and Glu86). For SC1475, changes in loop 2 (His42 and Lys48), helix 4 (Val80, Thr81, Thr82, and His85), and helix 1 (Met7) were found in solution. These data are all consistent with the notion that SC124, SC1475, and SC1982 all react with Cys84 because loop 2 and helix 4 are in the proximity of each other in the crystallographic structures of ^{Ca}S100B and have been previously described to facilitate the binding of small molecules. For SBi4172, the chemical shift perturbations during the reaction could not be measured because the compound induced aggregation of ^{Ca}S100B (Figure S4 of the Supporting Information). To further characterize the structural impact of covalent modifications at Cys84 on ^{Ca}S100B, we next determined the structures of the S100B complexes with each compound by X-ray crystallography.

Crystallographic Studies. Covalent Modifications at Cys84 Affect Target Binding of ^{Ca}S100B. The structures of ^{Ca}S100B–inhibitor complexes (SC124, SC1475, SC1982, SBi4172, and SBi4434) are compared, each of which was confirmed to have the SBiX molecule covalently bound to Cys84 of ^{Ca}S100B (Figure 3). In all five of these structural models, each ^{Ca}S100B subunit consists of four helices (helix 1, E2–G19; helix 2, K28–L40; helix 3, E49–D61; helix 4, D69–F88), two small antiparallel β-strands, and a Ca²⁺ ion bound to both the typical and noncanonical EF-hand calcium binding domains. Likewise, the typical EF-hand is in the “open” Ca²⁺-bound conformation, as is generally found in ^{Ca}S100B structures,²⁵ and the dimer interface is aligned as a symmetric X-type four-helix bundle comprising helices 1, 1', 4, and 4'.^{32,34–36,47} Comparison of these five structures to that of ^{Ca}S100B (PDB entry 1MHO⁴⁷) with no drug target reveals a strong conservation of the global fold (Table 3); however, deviations in the positions of several side chains in the target binding site of ^{Ca}S100B were observed, as necessary, to accommodate the binding of various SBiX molecules. These include residues in helix 4 and/or loop 4 and in helix 1 (i.e., His15) in some cases, as described below (i.e., for the ^{Ca}S100B–SC124 complex). The specifics of each structure also provide details of potential synthetic strategies for engineering a single molecule that occupies all three persistent “pockets” within the S100B target binding site, so the individual structures and specific structural changes will be discussed in some detail.

^{Ca}S100B–SC124. The X-ray structure of a product resulting from mixing SC124 (disulfiram) with Ca²⁺-bound S100B (^{Ca}S100B–SC124) was determined at 1.58 Å resolution (Figure 4). The asymmetric unit included two ^{Ca}S100B subunits (chains A and B) forming the biologically active form of dimeric ^{Ca}S100B. Residues Met0–Phe88 and Met0–Glu89 were modeled in chains A and B, respectively. In the final refined model (*R*_{crys} and *R*_{free} values of 0.215 and 0.253, respectively), all residues were in the favored (100%) regions of the Ramachandran plot with no outliers (Table 1). Each subunit of ^{Ca}S100B–SC124 was found to coordinate two calcium ions as is typical of S100 proteins,³⁸ and electron density was also clearly observed in the target binding sites for

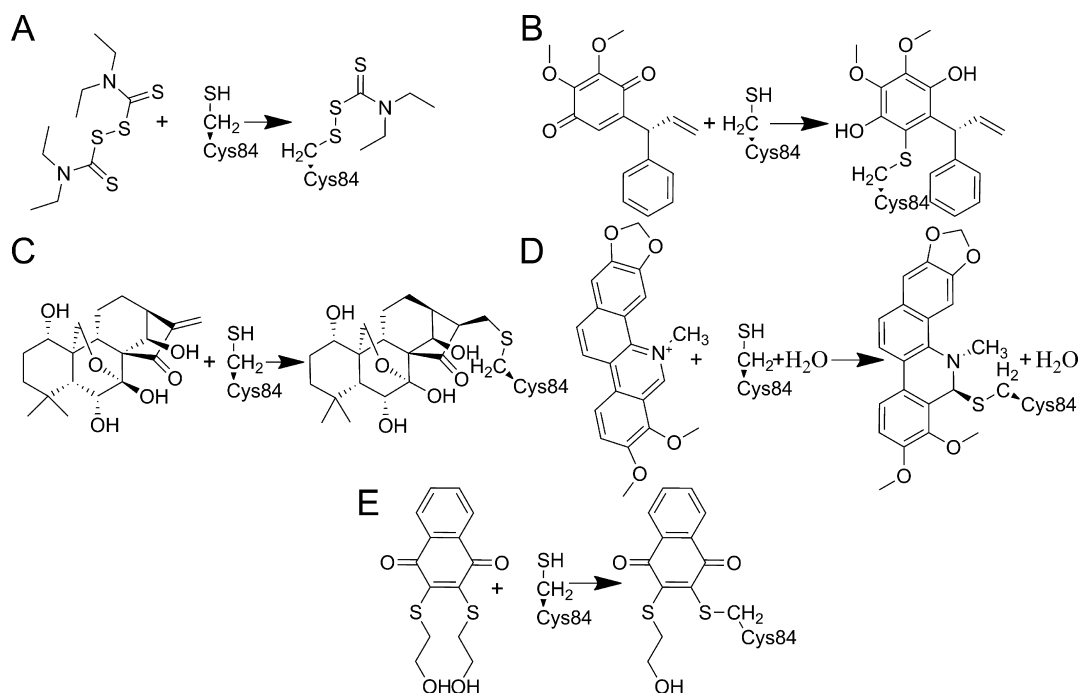


Figure 3. Chemical modification of Cys84 of CaS100B . Shown are schematics that provide an overview of the chemical modification of Cys84 by compounds (A) SC124, (B) SC1475, (C) SC1982, (D) SBI4172, and (E) SBI4434.

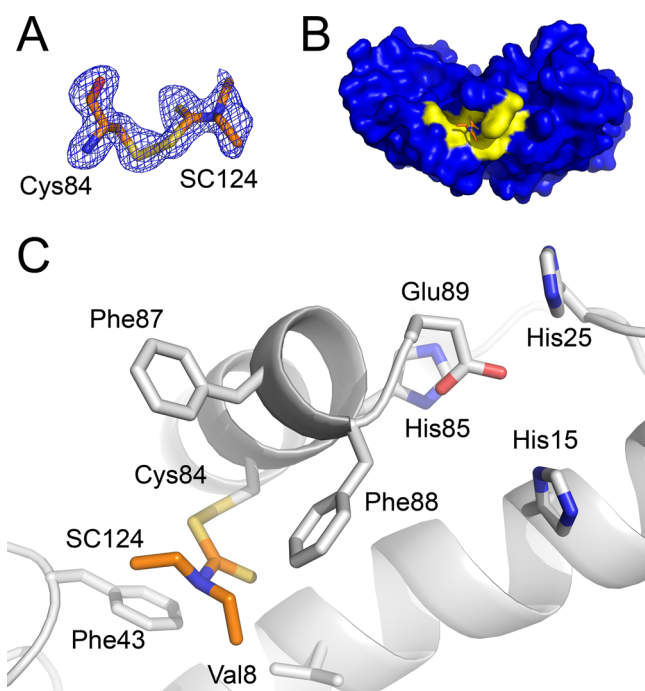


Figure 4. Crystallographic structure of the CaS100B-SC124 complex. (A) Shown is an $|F_o| - |F_c|$ electron density omit map of SC124 covalently bound to Cys84 of CaS100B with the map contoured at the 2.5σ level. (B) Dimeric CaS100B is rendered in a surface diagram with residues within 4 Å of the SC124 colored yellow. SC124 is found within persistent binding site 2. (C) SC124 is situated within the hydrophobic pocket formed by Val8, Phe43, Phe87, and Phe88. SC124 makes no hydrogen bonds. The neighboring Zn^{2+} binding site composed of Glu89, His15, His25, and His85 is also rendered.

each subunit of CaS100B as a result of nucleophilic attack of Cys84 by SC124 (Figures 3 and 4). The structure of the bound product was also consistent with what has been found

previously with other protein adducts involving SC124⁵⁵ (Figure 3). Interestingly, though, the Cys84-bound SC124 adduct has somewhat different positions in each subunit of CaS100B , and this was the first indication that this region, termed site 2, of CaS100B can accommodate various orientations for small inhibitors. Curiously, the binding of SC124 causes the side chain of Glu89 in one subunit to occupy a pocket that can tightly coordinate a Zn^{2+} ion,^{36,56,57} and as a result, His15 is reoriented. Note, in Zn^{2+} -bound structures of CaS100B described elsewhere,^{36,56,57} Zn^{2+} is coordinated by residues His15, His25, His85, and Glu89.

S100B-SC1475. The X-ray structure of a product resulting from mixing SC1475 (3,4-dimethoxydalbergione) with Ca^{2+} -bound S100B (CaS100B-SC1475) was determined at 2.18 Å resolution (Figure 5). The asymmetric unit included two CaS100B subunits (chains X and A) of CaS100B , and in both chains, residues Met0–Glu89 were modeled into the electron density. In the final refined structure (R_{crys} and R_{free} values of 0.213 and 0.251, respectively), all residues were in the most favored (98.9%) or allowed (1.1%) regions of the Ramachandran plot with no outliers (see Table 1). In each subunit, two Ca^{2+} ions, one SC1475 molecule, and 19 waters were resolved from the calculated electron density of the CaS100B-SC1475 structure. It was also clear that SC1475 covalently modified CaS100B via nucleophilic substitution of Cys84 into the benzoquinone moiety of the drug. Such a reaction is not uncommon, has been observed in toxic metabolites of acetaminophen, and results in the tautomerization of the moiety (Figure 3), as previously found.⁵⁸ Upon inspection, no hydrogen bonds were observed from residues of CaS100B to SC1475, but the small molecule was situated in a hydrophobic pocket defined by residues in loop 2, termed the “hinge region” of S100B (Phe43) and helix 4 (Ile80, Ala83, Phe87, and Phe88). Specifically, the hydroquinone moiety of SC1475 stacks with Phe43, and the alkene moiety aligns favorably with the aromatic ring of Phe87. His15 is observed to swing outward

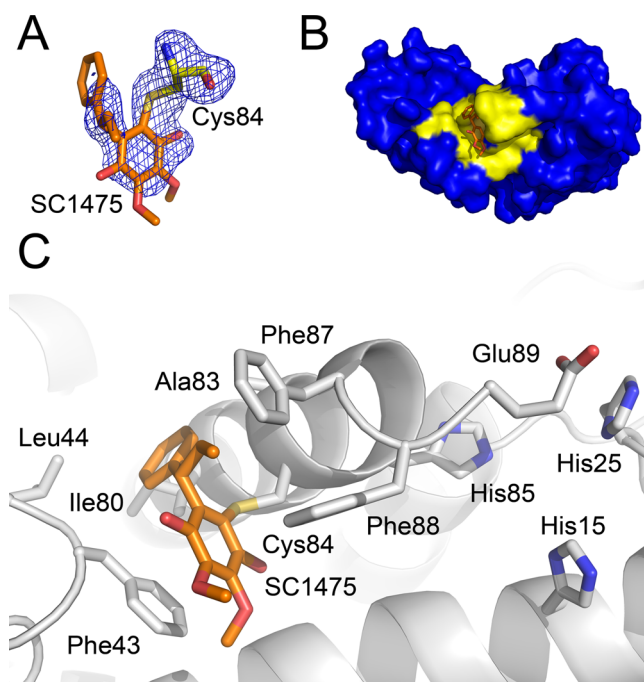


Figure 5. Crystallographic structure of the CaS100B –SC1475 complex. (A) Shown is an $|F_o| - |F_c|$ electron density omit map of SC1475 covalently bound to Cys84 of CaS100B with the map contoured at the 2.5σ level. (B) Dimeric CaS100B is rendered in a surface diagram with residues within 4 Å of the SC1475 colored yellow. SC1475 is found within persistent binding site 2. (C) SC1475 is situated within the hydrophobic pocket formed by Phe43, Leu44, Ile80, Ala83, Phe87, and Phe88. SC1475 makes no hydrogen bonds. The neighboring Zn^{2+} binding site composed of Glu89, His15, His25, and His85 is also rendered.

from the Zn^{2+} binding site as observed in other CaS100B –SBIx structures, and unlike CaS100B complexes of SBI4172, SC124, and SC1982, Glu89 does not invade the Zn^{2+} binding site (*vide infra*).

CaS100B –SC1982. The X-ray structure of CaS100B bound to SC1982 (Rubescensin A; CaS100B –SC1982) was determined at 1.65 Å resolution (Figure 6). The asymmetric unit contained one CaS100B subunit, and density for Met0–Glu91 could be readily modeled with the second subunit mapped on the basis of its location within the crystal symmetry. In the final refined model (R_{cryst} and R_{free} values of 0.177 and 0.214, respectively), all residues were in the highly favored (100%) region of the Ramachandran plot with no outliers (Table 1). Each subunit of CaS100B –SC1982 was found to coordinate two Ca^{2+} ions (one in each EF-hand), and one SC1982 molecule occupied each of the target protein binding sites via covalent modification (in the region termed site 2). Specifically, the alkene of SC1982 is reduced via Michael addition from the thiol of Cys84 from CaS100B ⁵⁹ (Figure 3). After covalent attachment, SC1982 makes two hydrogen bonds to the backbone carbonyls of loop 2 (His42 and Phe43) and forms several hydrophobic interactions with residues in the target binding pocket of CaS100B , including those in loop 2 (Phe43) and helix 4 (Ile80, Phe87, and Phe88). His15 is once again observed to move outward from the Zn^{2+} binding site, and like the structures of CaS100B –SC124 and CaS100B –SBI4172, the covalent binding of SC1982 causes the side chain of Glu89 to intrude into a region of the protein, which can bind Zn^{2+} , and causes the side chain of His15 to rotate away fairly drastically.

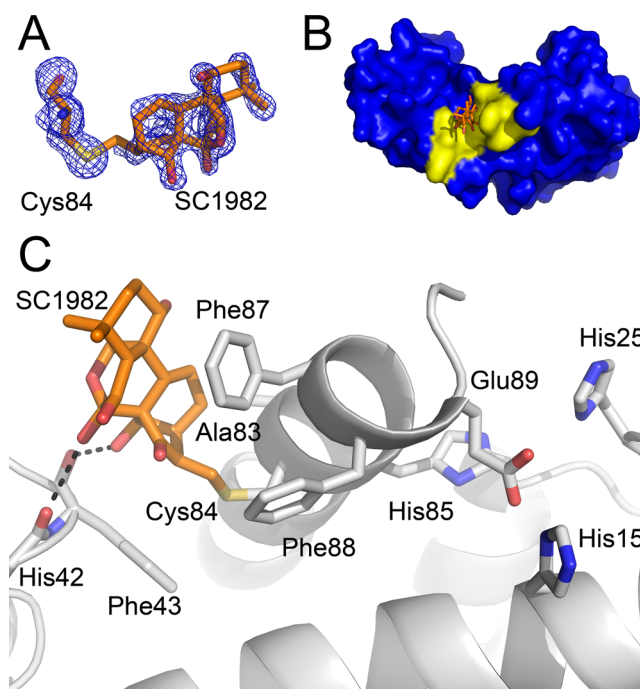


Figure 6. Crystallographic structure of the CaS100B –SC1982 complex. (A) Shown is an $|F_o| - |F_c|$ electron density omit map of SC1982 covalently bound to Cys84 of CaS100B with the map contoured at the 2.5σ level. (B) Dimeric CaS100B is rendered in a surface diagram with residues within 4 Å of the SC1982 colored yellow. SC1982 is found within persistent binding site 2. (C) SC1982 is situated within the hydrophobic pocket formed by Phe43, Ala83, Phe87, and Phe88. SC1982 makes hydrogen bonds to the backbone carbonyls of His42 and Phe43. The neighboring Zn^{2+} binding site composed of Glu89, His15, His25, and His85 is also rendered.

Electron density for a highly coordinated atom that is too dense to be water was identified. As calcium is prevalent in the system and because of the identity of the contributors in the coordination (Asp63, Asp69, and six water molecules), a third calcium ion was modeled into this density (confirmed by anomalous difference maps).

CaS100B –SBI4172. The X-ray structure of chelerythrine-bound CaS100B , CaS100B –SBI4172, was determined at 1.73 Å resolution (Figure 7). The asymmetric unit in the drug complex included two S100B subunits (chains A and B) forming the biologically active dimeric form of CaS100B . In chain A, residues Met0–Glu89 were modeled into the electron density, and in chain B, only Ser1–Glu89 could be resolved. Each subunit of the CaS100B –SBI4172 complex coordinated two Ca^{2+} ions; however, only one molecule of SBI4172 could be observed and was located in the model for chain B. Sparse density was observed in the analogous binding pocket of chain A, but it was not sufficiently well defined for accurate modeling of the SBI4172 inhibitor. A more detailed analysis of chain A showed that a lack of density in the second subunit likely occurred as a result of spatial restraints imposed by the crystal packing. In the final refined model (R_{cryst} and R_{free} values of 0.230 and 0.268, respectively), all residues in both subunits were in the favored (98.9%) or allowed regions (1.1%) of the Ramachandran plot with no outliers (Table 1). As clearly defined by the calculated electron density maps, SBI4172 was found to react with Cys84 via hydration of a double bond of SBI4172⁶⁰ (Figure 3). Once SBI4172 was covalently bound, a dioxole oxygen atom of SBI4172 was found to make water-bridged interactions with the

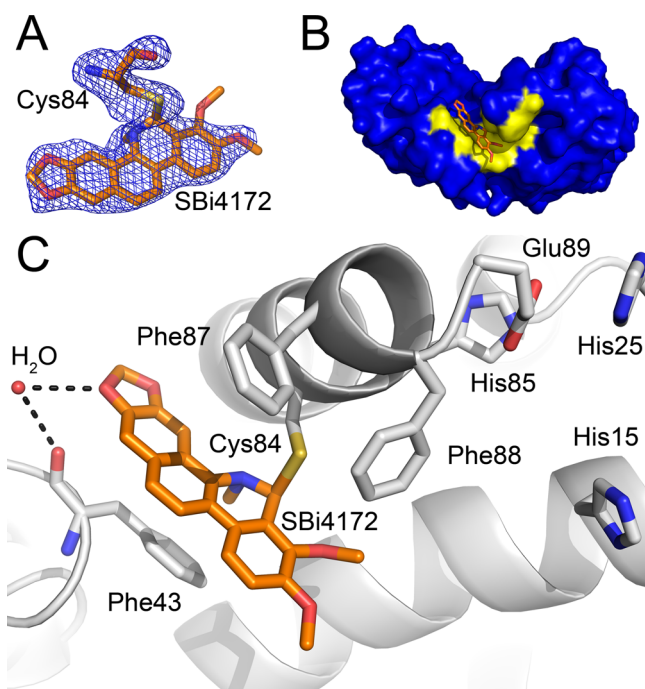


Figure 7. Crystallographic structure of the CaS100B-SBi4172 complex. (A) Shown is an $|F_o| - |F_c|$ electron density omit map of SBI4172 covalently bound to Cys84 of CaS100B with the map contoured at the 2.5σ level. (B) Dimeric CaS100B is rendered in a surface diagram with residues within 4 Å of the SBI4172 colored yellow. SBI4172 is found within persistent binding site 2. (C) SBI4172 is situated within the hydrophobic pocket formed by Phe43, Phe87, and Phe88. SBI4172 makes a water-bridged interaction with the backbone carbonyl of Phe43. The neighboring Zn^{2+} binding site composed of Glu89, His15, His25, and His85 is also rendered.

backbone carbonyl of Phe43. Otherwise, SBI4172 was situated in a hydrophobic pocket composed of side chains within loop 2 (Phe43), helix 4 (Ile80, Ala83, Phe87, and Phe88), and helix 1' (Val7, Val8, and Ile11). Like the earlier inhibitor-bound CaS100B complexes, the side chain moiety of His15 was found to move out of the established Zn^{2+} binding site of CaS100B .

CaS100B-SBi4434 . The X-ray structure of SBI4434 {2,3-bis[(2-hydroxyethyl)thio]-1,4-naphthoquinone} bound to CaS100B (CaS100B-SBi4434) was determined at 1.08 Å resolution (Figure 8). The asymmetric unit included two S100B subunits (chains A and X) forming the biologically active dimeric form of S100B. In chain A, residues Met0–Glu91 were modeled while only residues Met0–Phe88 of chain X could be resolved. Each subunit in the CaS100B-SBi4434 structure bound two calcium ions and a SBI4434 molecule. In the final refined model (R_{cryst} and R_{free} values of 0.192 and 0.211, respectively), all residues were in the favored (99.4%) or allowed regions (0.6%) of the Ramachandran plot with no outliers (Table 1). Sole among the structures described here, the high resolution of the diffraction data produced by the CaS100B-SBi4434 crystal allowed for the inclusion of riding hydrogen atoms in this particular model. As clearly defined by the calculated electron density maps, SBI4434 covalently modifies CaS100B at Cys84. As seen, the thiol of Cys84 substitutes for one of the thioglycol moieties of SBI4434 (Figure 3). The second thioglycol moiety is allowed much conformational flexibility as evidenced by the sparse electron

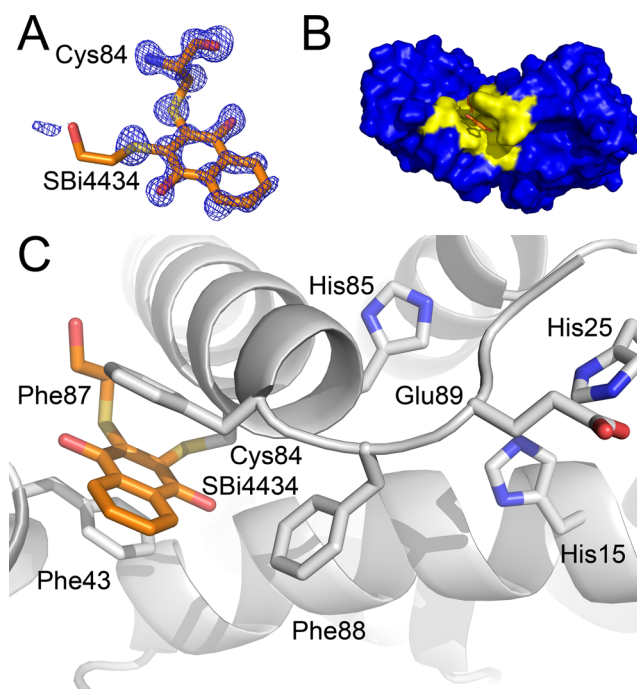


Figure 8. Crystallographic structure of the CaS100B-SBi4434 complex. (A) Shown is an $|F_o| - |F_c|$ electron density omit map of SBI4434 covalently bound to Cys84 of CaS100B with the map contoured at the 2.5σ level. (B) Dimeric CaS100B is rendered in a surface diagram with residues within 4 Å of the SBI4434 colored yellow. SBI4434 is found within persistent binding site 2. (C) SBI4434 is situated within the hydrophobic pocket formed by Phe43, Phe87, and Phe88. SBI4434 makes no hydrogen bonds. The neighboring Zn^{2+} binding site composed of Glu89, His15, His25, and His85 is also rendered.

density for these atoms as well as the alternative conformations of the moiety modeled in the two inhibitor molecules. The compound does not make any hydrogen bonds with the protein but is nestled in a hydrophobic pocket formed by loop 2 and helix 4 with the aromatic rings of SBI4434 stacked between the side chains of Phe43 and Phe87. In this model, His85 swings out of the Zn^{2+} binding site.

Coordinates and structure factors have been deposited in the Protein Data Bank as entries 4PE1 for CaS100B-SC124 , 4PE4 for CaS100B-SC1475 , 4PE7 for CaS100B-SC1982 , 4PDZ for CaS100B-SBi4172 , and 4PE0 for CaS100B-SBi4434 .

Cell-Based Assay. To determine whether covalent modification of Cys84 affects cell proliferation in malignant melanoma, its effect on the growth of WM115 malignant melanoma cells, which express elevated levels of the S100B protein, was measured as described previously.⁵³ Briefly, proliferation of WM115 cells stably transfected with either shRNA^{scrambled} (i.e., high S100B) or shRNA^{S100B} (i.e., low S100B) was evaluated in triplicate following a 4 day incubation in the absence or presence of each compound at varying concentrations (Table 2). For each titration, knockdown of the S100B protein was confirmed by Western blot analysis (3-fold decrease; $n = 4$) (Figure 9), and EC_{50} values were determined using the average of three or more titrations. With SC1475 as an exception (ratio of 1.00), it was found that lower concentrations of SC124, SC1982, and SBI4172 were needed to inhibit cell growth with the shRNA^{scrambled} versus the shRNA^{S100B} knockdown WM115 cells ($1.50 < \text{ratio} < 3.57$). This is consistent with the compounds having specificity

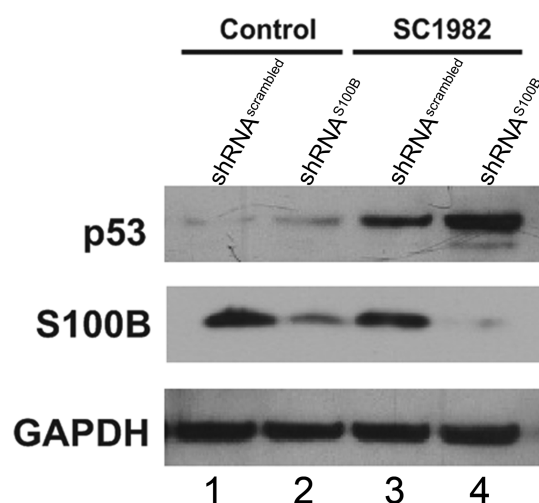


Figure 9. Western blot analysis. The control without drug was treated with the same DMSO concentration (0.01%). The addition of SC1982 did not affect the protein levels of S100B in the shRNA^{scrambled} or shRNA^{S100B} cell lines. However, both shRNA^{scrambled} and shRNA^{S100B} cell lines had a measurable gain in total p53 protein levels in the presence of SC1982. This result along with an observation of S100B expression-dependent growth inhibition suggests that SC1982 displays an on-target effect of S100B inhibition with subsequent p53 restoration.

toward S100B-containing cells; however, only titrations with SC1982 were shown to be S100B-selective (1.77-fold) with a statistically significant *t*-test ($p = 0.001$; $n = 8$). Consistent with this result, p53 levels were 2-fold higher ($n = 4$) in the presence than in the absence of SC1982 (in Figure 9, compare lanes 1 and 3 and lanes 2 and 4, respectively). This result along with an observation of S100B expression-dependent growth inhibition suggests that SC1982 displays an on-target effect of S100B inhibition with subsequent p53 restoration. The last compound, SBi4434, showed fluorescence interference with the SYBR Green dye, so it was excluded from further evaluation.

DISCUSSION

Malignant melanoma is the fifth and seventh most common cancer among men and women,⁶¹ respectively, so the discovery of novel therapeutics for its treatment remains a high priority. Elevated S100B is a prognostic indicator for assessing disease progression, disease recurrence, and metastatic potential in patients with MM.^{62–68} It is also established that S100B not only is a clinical marker but also binds to and negatively regulates p53 at the protein level.^{18,19} While the p53 tumor suppressor protein is mutated in many human cancers,⁶⁹ it is typically wild-type (wt, >90%) in MM,^{26,27} so restoring p53 protein by inhibiting S100B represents a novel therapeutic strategy for treating MM. While low-molecular weight compounds that block the p53 binding site on S100B and inhibit formation of the S100B–p53 complex exist, improving their affinity, efficacy, and specificity remains a priority. Thus, S100B represents a new cancer target, and improved SBiXs should provide novel therapeutic(s) for treating MM by restoring active p53 protein.²⁷

Structure–function characterizations of five novel inhibitors of the ^{Ca}S100B–p53 interaction are presented here. Of the five compounds, SC1982 has the most significant hydrogen bonding network within the ^{Ca}S100B binding pocket, and interestingly, it demonstrated the highest level of target specific

activity in the WM115 cellular assay. Note that despite the relatively low EC₅₀ of SC124, expectations should be tempered when considering this compound. SC124 is small with a scaffold lacking complexity. It forms no hydrogen bonds with the target protein and lacks even a consistent binding pose within the two monomers of S100B. These details leave little potential for SC124 as a therapeutic that would not be sequestered elsewhere within the cell, and unsurprisingly, it lacks statistically significant S100B expression-dependent growth inhibition.

Such target specific effects are important when considering the relationship between off-target effects and toxicity. This is particularly important when considering the therapeutic application of covalent modifiers because their off-target effects are not uncommon and are often severe. One successful example of a drug linked to the protein via Michael addition is Afatinib, which is used in the treatment of metastatic non-small cell lung carcinoma (NSCLC).^{70,71} The target specific effect of SC1982 (Figure 9 and Table 2) is reassuring and warrants further investigation as a chemical scaffold for engineering novel SBiX molecules. In fact, SC1982 and each compound presented here offer a new chemical scaffold for continued SAR studies for improving affinity and specificity.

These structures can be used for guiding the design of new inhibitors using multiple approaches. The most straightforward of these is via “tethering” new functional moieties onto the existing covalently bound compound(s) and keeping the covalent bond in place.⁷² A second strategy is to develop quickly reversible covalent modifications, as described previously,⁷³ for the inclusion of an α -cyanoacrylamide functionality. This modification increases the intrinsic reactivity of an olefin and eliminates the formation of irreversible adducts. Such an approach could enhance the bioavailability and selectivity of the inhibitory compound. For Cys84 of ^{Ca}S100B, such a cyanoacrylamide (or cyanoacrylate) would react with cysteine thiols under physiological conditions in an energetically favorable manner and become rapidly reversible, including having off rates on the subsecond to second time scales.⁷¹ In this situation, the level of off-site targeting is significantly reduced, and the covalent nature of the adduct for the target of interest is long-lived, as needed for therapeutic efficacy.

A third approach to obtaining high-affinity, high-specificity S100B inhibitors with these data is to engineer compounds that make use of all three persistent pockets in the p53 binding site. In this regard, the inhibitors presented here are particularly important because they are located within the persistent binding pocket termed “site 2”. Therefore, regardless of whether these inhibitors are covalently bound, they provide exquisite detail for how to connect chemical moieties in sites 1 and 3. Therefore, the inhibitors presented here can be considered in combination with chemical functionalities described in previous structural studies of other SBiXs^{33–36} to produce a ligand capable of binding all three persistent binding sites simultaneously. The simultaneous occupation of sites 1 and 2 will be of interest first because “site 3” binders within ^{Ca}S100B have been thoroughly described elsewhere.

Although the mechanisms involved in adduct formation may differ between compounds, SC124, SC1475, SC1982, SBi4172, and SBi4434 (as well as for SC0844 and SC322³⁵ studied previously), together these compounds comprise a subset of S100B inhibitors that impact the conformational state of ^{Ca}S100B in a similar manner. In particular, an adduct added to

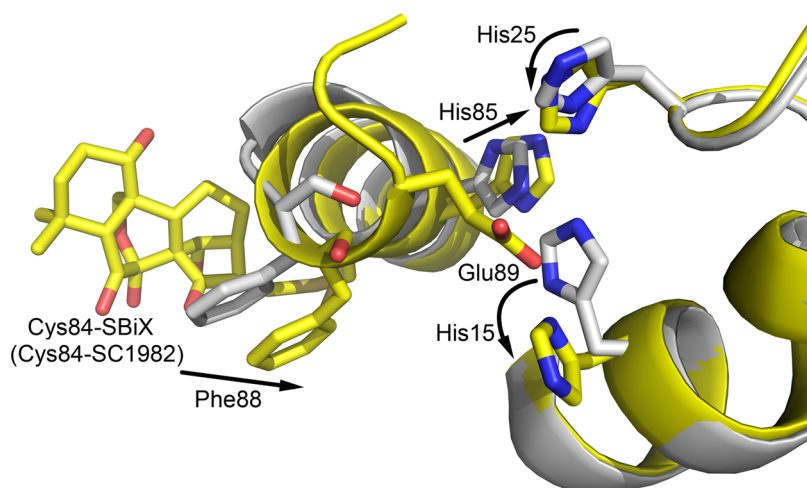


Figure 10. Distortion of the zinc binding site is a hallmark of the S100B covalent inhibitor family. Shown are ribbon diagrams of $C^{a}S100B$ in the presence (yellow) and absence (gray) of a covalent modifier (SC1982) with residues and ligands of interest shown as sticks. The covalent modifier family of SBiXs is hallmarked by perturbation in the conformational state of the residues forming the Zn^{2+} binding site (His15, His25, His85, and Glu89). Commonly, Glu89 is seen intruding on the Zn^{2+} with a subsequent displacement of a histidine side chain.

Cys84 clashes with side chains on helix 4 and thereby rotates a Zn^{2+} binding residue, Glu89, into a new location. As a result, residues comprising the Zn^{2+} binding site (His15, His25, His85, and Glu89) are subsequently reordered. Although the particulars of this effect on the Zn^{2+} binding site may be unique to an individual compound and may or may not have an effect on S100B activities, the covalent modifier family of SBiXs described here is “hallmarked” by this common structural perturbation (Figure 10). Table 4 lists the effect through measurements of directional movements of atoms and torsions of residue side chains. The most disruptive feature of this conformational change is an intrusion of Glu89 into the Zn^{2+} site with a subsequent exit of one of the localized histidine side chains. Further investigation may prove this to be a meaningful observation because the oxidation of Cys84 has functional implications with regard to the regulation of S100B by redox.⁷⁴ The inhibitory properties of these compounds may in part be attributed to the manipulation of this natural regulatory Zn^{2+} binding feature of S100B and are very likely functionally important.

Although we have demonstrated a restoration in p53 levels alongside the inhibition of S100B, it must be noted that within WM115 malignant melanoma cells, S100B has been associated with factors other than p53. For instance, S100B was found to enhance cell viability and modulate MAPK signaling by binding directly to the p90 ribosomal S6 kinase (RSK). The formation of this complex blocks ERK-dependent phosphorylation of RSK and sequesters RSK into the cytosol, preventing it from acting on nuclear targets. Thus, S100B has been shown to increase the level of cell survival in malignant melanoma by contributing to abnormal ERK/RSK signaling.⁵² Also, a target of S100B is the receptor for advanced glycation end products (RAGE). RAGE is upregulated in late metastatic stages of samples from melanoma patients. The overexpression of RAGE is associated with mesenchymal-like morphologies in WM115 cells and results in greater migration abilities and reduced proliferation properties. This supports a role of RAGE in the metastatic switch of melanoma cells. Interestingly, overexpression of RAGE results in the increased level of expression of S100B and lower levels of p53, ERK1/2, cyclin E, and NF- κ B.⁷⁵

■ ASSOCIATED CONTENT

■ Supporting Information

Figures S1–S5 show overlaid two-dimensional 1H – ^{15}N HSQC spectra of $C^{a}S100B$ and $C^{a}S100B$ –SBiX complexes. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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Notes

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ABBREVIATIONS

MM, malignant melanoma; SBI_X, S100B inhibitor where *X* is a number; CaS100B, calcium-bound S100B; NMR, nuclear magnetic resonance; HSQC, heteronuclear single-quantum coherence; rmsd, root-mean-square deviation; SD, standard deviation.

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