

High-Throughput Screening for Human Lysosomal β -N-Acetyl Hexosaminidase Inhibitors Acting as Pharmacological Chaperones

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SUMMARY

The adult forms of Tay-Sachs and Sandhoff diseases result when the activity of β -hexosaminidase A (Hex) falls below $\sim 10\%$ of normal due to decreased transport of the destabilized mutant enzyme to the lysosome. Carbohydrate-based competitive inhibitors of Hex act as pharmacological chaperones (PC) in patient cells, facilitating exit of the enzyme from the endoplasmic reticulum, thereby increasing the mutant Hex protein and activity levels in the lysosome 3- to 6-fold. To identify drug-like PC candidates, we developed a fluorescence-based real-time enzyme assay and screened the Maybridge library of 50,000 compounds for inhibitors of purified Hex. Three structurally distinct micromolar competitive inhibitors, a bisnaphthalimide, nitro-indan-1-one, and pyrrolo[3,4-d]pyridazin-1-one were identified that specifically increased lysosomal Hex protein and activity levels in patient fibroblasts. These results validate screening for inhibitory compounds as an approach to identifying PCs.

INTRODUCTION

Pharmacological chaperones (PC), as small molecule therapeutics, represent a novel paradigm for the treatment of disorders arising from mutations that destabilize and thus reduce protein levels [1–3]. In these cases, the mutation affects the equilibrium between the folded and unfolded states of the protein, shifting it away from the functional (folded) conformation. Improperly folded mutant (or wild-type) proteins are then cleared by the “protein quality control systems” (QC) associated with the synthetic machinery in the cytosol and endoplasmic reticulum (ER) [4]. By preferentially binding to the native-like structure of the mutant protein, PCs, typically compounds acting as antagonists/inhibitors, shift the equilibrium back

toward the functional conformation, which is deemed “competent for release” by the protein cells’ QC [5]. Depending on the target protein, this treatment has been shown to result in increased levels of the functional mutant protein in the cytosol [6], specific organelles (e.g., the lysosome) [2], or the cell surface [7].

The PC approach has been shown to successfully enhance the enzyme levels of five different mutant lysosomal enzymes that lead to the chronic form of the lysosomal storage disorders, GM2 gangliosidosis [8], Fabry [9], Gaucher [10], and Morquio B diseases [11]. GM2 gangliosidosis, arising from the neuronal storage of GM2 ganglioside (GM2), occurs in three variants: Tay-Sachs disease (TSD), Sandhoff disease (SD), and the AB variant. The former two result from mutations in the evolutionarily related *hexa* or *hexb* genes, encoding the α or β subunits, respectively, of heterodimeric β -N-acetyl-hexosaminidase A (Hex A, $\alpha\beta$) [12]. Two other homodimeric Hex isozymes exist (i.e., Hex B [$\beta\beta$] and Hex S [$\alpha\alpha$]), but cannot utilize GM2 ganglioside as a substrate.

Whereas both the α and/or β active sites of dimeric Hex can hydrolyze neutral synthetic N-acetyl hexosamine-terminal substrates, only the α site of Hex A and Hex S can efficiently utilize negatively charged substrates (e.g., 6-sulphated GlcNAc [13, 14]). Therefore, total Hex activity can be measured with 4-methylumbelliferyl β -N-acetylglucosaminide (MUG), whereas 4-methylumbelliferyl β -N-acetylglucosamine-6-sulfate (MUGS) is used to measure Hex A and Hex S activity [14]. Substrates based on 4-methylumbelliferone (MU) are available and used to diagnose enzyme deficiencies in the other lysosomal storage disorders (LSD).

The more common infantile TSD (ITSD) variant of GM2 gangliosidosis results from absent α subunits and elevated amounts of Hex B, such that levels of total Hex activity (MUG) are near normal. Less common is infantile SD (ISD), resulting from an absence of β subunits and very low levels of Hex activity associated with the unstable Hex S isozyme. In contrast to the infantile forms, adult TSD (ATSD) and adult SD (ASD) are chronic, slowly progressive, neurodegenerative diseases that vary in age onset. In many cases, they are associated with missense

mutations, usually producing thermolabile Hex A with residual activity (MUGS) and protein levels that are <10%, but >2% of normal. The correlation between clinical phenotypes and residual activity indicates that there is a surprisingly low critical threshold level of Hex A activity (i.e., the level of Hex A needed to prevent GM2 ganglioside storage) of ~10% of normal [15].

The majority of patients with ATSD possess a missense mutation in exon 7 of the α subunit gene (i.e., α G269S [12]). This and similar point mutations do not directly affect the α -active site of Hex A or the interface between its α and β subunits [13, 16], but are believed to result in increased amounts of misfolded α -protein in the ER, which are in turn retained by its QC and degraded [17]. Since only a small proportion of the newly synthesized mutant α -precursor can adopt the proper conformation necessary to form heterodimers and become transport competent, there are reduced levels of both Hex A activity and protein in the lysosome.

Previously, we used conventional carbohydrate-based Hex inhibitors (e.g., N-acetyl glucosamine thiazoline [NGT]) to enhance the stability, protein levels, and enzyme activity of mutant Hex A in ATSD fibroblasts, and Hex S levels in ISD patient fibroblasts [8]. NGT is a stable thiazoline derivative of the oxazoline reaction intermediate formed by lysosomal Hex and other members of glycoside hydrolase family GH20 [18, 19]. The 3D structures of GH20 family members, human Hex (hHex) B [13, 20], hHex A [16], *Streptomyces plicatus* Hex [21], and *Serratia marcescens* chitobiase [22], have been determined, the former three in complex with NGT. Although these enzymes have an overall identity of less than 25%, their active site residues share greater than 95% identity, and are superimposable to less than 1.5 Å rmsd [13, 21].

In all examples to date, compounds acting as PCs in cells have also been competitive inhibitors of the target enzyme [2], their effectiveness often varying with the nature of the mutation [23], but generally correlating with their bioavailability and K_i [24]. Potential PCs have been identified for only a minority of the 40 known gene products that, when mutated, can result in an LSD. High-throughput screening (HTS) of small molecule libraries has been used to identify specific drug-like inhibitory compounds for proteins with [25] or without [26, 27] known structures or mechanisms of action. It is proposed that HTS of a library of compounds for inhibitors of the target enzyme would also result in the identification of candidate PCs, which could then be evaluated by a secondary live cell-based assay. Thus, we developed a real-time MU-based enzyme assay and coupled it with HTS, utilizing purified human placental Hex as a target to identify several drug-like inhibitors. Subsequently, lysates from patient cells grown in the presence of these compounds were demonstrated to have enhanced levels of Hex A (ATSD) or Hex S (ISD) activity and protein. This approach represents a facile and efficient strategy for identification of candidate PCs in small molecule libraries for any lysosomal enzyme with an available MU-based substrate by first screening for inhibitory compounds.

RESULTS AND DISCUSSION

Development of an Assay to Continuously Monitor Hex Activity

Conventional MU-based substrate assays for the known lysosomal glycosidases are end-point assays, which are less convenient for HTS because they are more prone to false-positives (quenchers) or false-negatives (fluorescent compounds) [28]. Consequently, we developed a real-time MU-based enzyme assay and coupled it with HTS of the 50,000 small-molecule compound Maybridge library to identify drug-like inhibitory compounds against highly purified placental human lysosomal Hex.

As the MU fluorophore, released by Hex and other lysosomal enzymes, has a pKa of 7.8 that is higher than the acidic pH optimums of these enzymes, an endpoint assay was used. Recently, it has been shown that the released MU fluorophore can be continuously and efficiently monitored at an acidic pH by decreasing the excitation wavelength from 365 nm to 330 nm [29], but with no change in emission optimum (450 nm). With this assay, the rate of MU hydrolysis was linear over 25 min, with an apparent K_m of 0.35 mM at room temperature. For the HTS, a lower concentration of substrate was chosen (60 μ M) to diminish the quenching effects of the substrate [30].

Since all of the test compounds were dissolved in DMSO, we checked for effects of DMSO on Hex A activity. DMSO inhibited Hex A activity by more than 50% at the concentrations at which the library compounds were screened (compounds tested at 20 μ M gave the equivalent of 0.26 M DMSO in the assays) (Figure 1A). Furthermore, since V_{max} remained constant, whereas K_m increased with increasing DMSO concentrations, DMSO was found to be a competitive inhibitor of Hex (Figure 1A), with a K_i of 0.17 ± 0.02 M.

Primary Biochemical Screen: Identification of Candidate Hex Inhibitors

To identify inhibitors, the activity of purified hHex A was evaluated in the presence of each of 50,000 compounds from the Maybridge small-molecule library. Inhibitory compounds in the library were expected to reduce the residual activity of Hex A relative to the residual activity of the enzyme treated with DMSO (high controls). Despite the fact that DMSO was a weak competitive inhibitor of Hex A, the HTS was successful in identifying Hex inhibitory compounds.

Replicate assays for each compound were plotted as a single (x, y) coordinate (Figure 1B). The majority (>75%) of these values differed by less than 1.4-fold, and fell near the $x = y$ diagonal (i.e., the replicates were generally reproducible). The average Z' statistic [31] of 0.67 for the two replicates was well within the acceptable range for a robust and interpretable screen [32]. The statistical cut-off for the "hit" threshold, based on the standard deviations of the high (DMSO only) and low (NGT and DMSO) control values, was determined to be 69%. Since this resulted in >600 hits, the hit threshold was empirically set to 50%

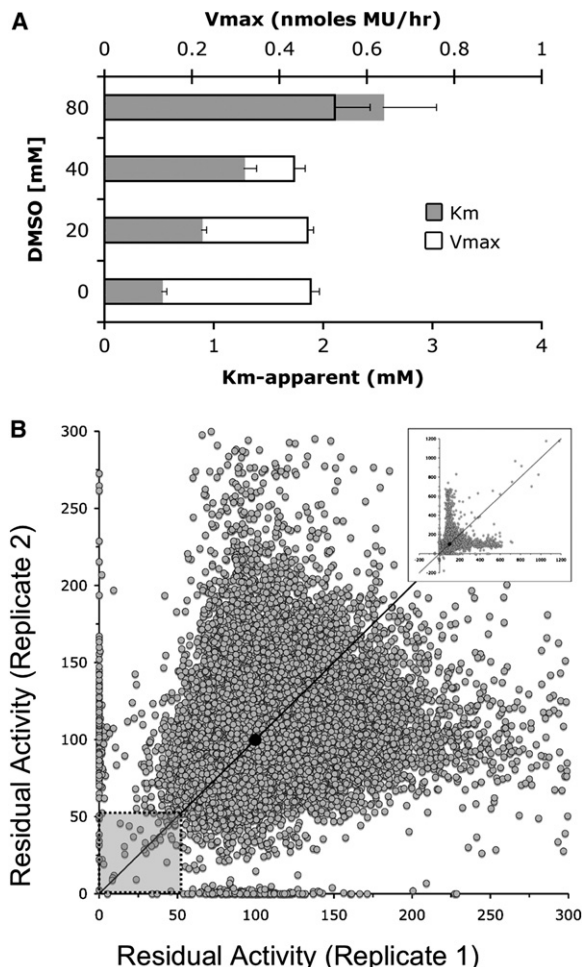


Figure 1. Primary Screen of a 50,000 Compound Maybridge Library for Hex A Inhibitors in the Presence of DMSO, a Competitive Inhibitor of Hex A

(A) The change in K_m (gray bars) and V_{max} (bars outlined in black) versus increasing concentrations of DMSO ($n = 3$). Error bars refer to standard deviation.

(B) A portion of the replicate plot of residual Hex A activity (0%–300%) in the presence of individual compounds from the Maybridge library (inset: entire replicate plot [0%–1200%] for all compounds). Diagonal line denotes compounds with identical activities in both replicates. The hit zone containing candidate inhibitory compounds and average residual activity is denoted by the shaded box and filled circle, respectively. Residual activity values for each compound are provided in the Supplemental Data.

residual activity, which lowered the number of compounds to be evaluated to a more manageable 64 (0.13% hit rate).

Secondary Screen: Validation of Candidate Inhibitors from Primary Screen

By virtue of their semilogarithmic sigmoidal dose-response curve, which is typical of an inhibitor, only 24 of the 64 hits were confirmed as bona fide inhibitors (Table 1). Interestingly, the 24 confirmed hits were also compounds that replicated best in the primary screen. The in-

hibitory activities of these compounds (Table 1) span three orders of magnitude (i.e., one compound had an IC_{50} of 0.2 μ M, two were $>6 \mu$ M, 16 ranged from 12 to 79 μ M, and six ranged from 105 to 385 μ M). These results confirm the utility of coupling the real-time enzyme assay based on 4-MU substrates with HTS to identify inhibitory compounds for Hex and other lysosomal enzymes from a library of small-molecule compounds.

Singleton compounds, which had an $IC_{50} > 100 \mu$ M, or had reactive groups (e.g., compound M-49773, which bore a reactive thiol group [known to inactivate Hex]), were not examined further. Similarly, cyclic thiol compounds, represented by M-27352 and M-26024, were eliminated from the study, as they have been found to be promiscuous inhibitors, identified in other HTS using different enzymes. Compounds such as M-28324 and M-00659, which were difficult to dissolve and/or precipitated readily in aqueous solutions above 10 μ M, also were not examined further.

The majority of compounds identified by HTS that inhibited Hex were substituted bicyclic and tricyclic nitrogen-containing heterocycles. The structures of these compounds differ greatly from known azasugar-based Hex inhibitors, and represent novel scaffolds that could be further optimized for use as specific Hex inhibitors.

Three of the 24 compounds, M-22971, M-31850, and M-45373, were chosen to be evaluated in greater detail. M-31850 had the lowest IC_{50} identified (200 nM), and three additional, structurally related compounds (M-13862, M-31867, and M-31860; i.e., bearing the 1,8 naphthalimide moiety compounds) were also identified with IC_{50} s $> 10 \mu$ M. The other two compounds, M-22971, an indan-1-one, and M-45373, bearing a pyrrolo[3,4-d]pyridazin-1-one moiety, were found to have IC_{50} s $< 10 \mu$ M (1.8 and 5.8 μ M IC_{50} , respectively). Furthermore, compounds M-31850 and M-22971 contained scaffolds found in the drugs, Alrestatin [33] and Indacrinone [34], that have been approved for use in humans. Although compound M-22971 has a structure common to bidentate ligands (i.e., one capable of binding a metal ion), Hex does not require a metal ion for activity.

Inhibitory Activities of the HTS Inhibitors of Hex toward Other Members of Glycosidase Family GH20 and Human O-GlcNAcase

In order to determine the selectivity of the HTS inhibitors, their activities were evaluated against hHex A and hHex B, Jack Bean Hex (JBHex), the plant ortholog of lysosomal hHex, bacterial Hex from *Streptomyces plicatus* (SpHex), and chitobiase B from *Serratia marcescens* (SmCHB); all are members of the GH20 glycosidase family. Human O-GlcNAcase (hOGN), a member of the GH84 family of glucosaminidases that has a reaction mechanism similar to Hex [35], was also tested with the HTS inhibitors (Table 2). Glycosidases in both of these families use substrate assisted catalysis and are all inhibited by NGT to different degrees [19, 21, 35].

Although all of the HTS inhibitors show activity toward both Hex A and B isozymes, there was a 2-fold difference

Table 1. List of Inhibitory Compounds Verified in a Secondary Screen Showing Corresponding Structure, Identification Number and IC₅₀ (μM) Values

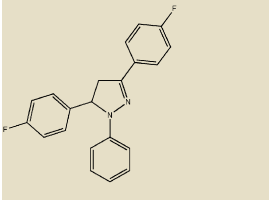
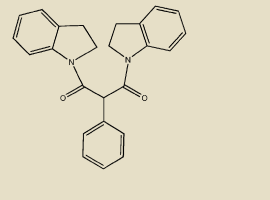
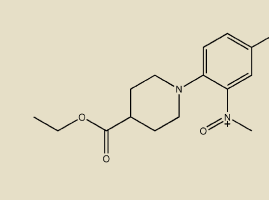
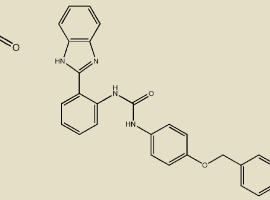
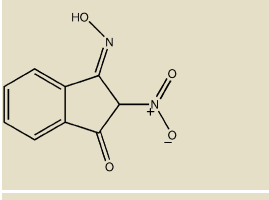
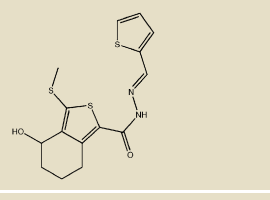
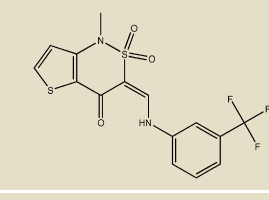
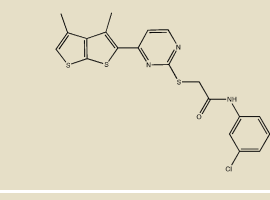
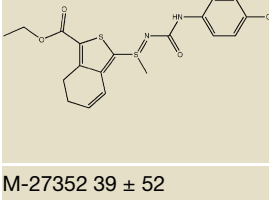
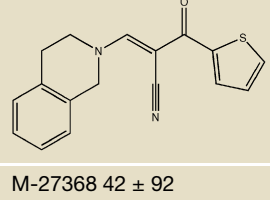
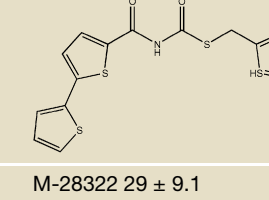
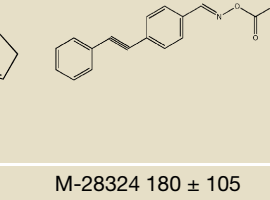
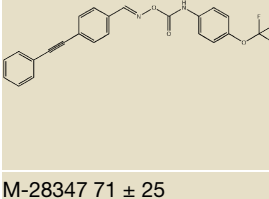
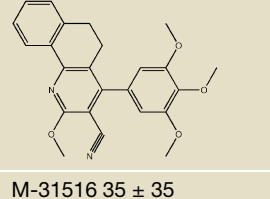
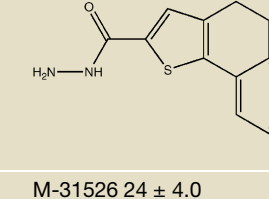
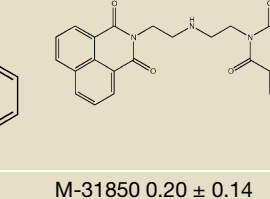
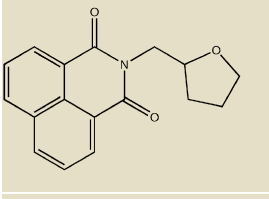
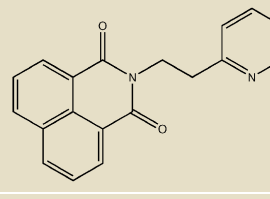
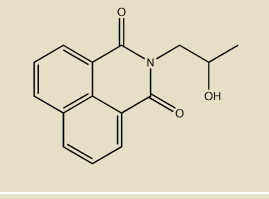
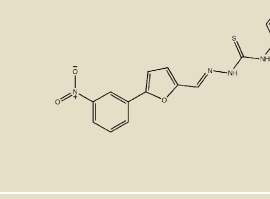
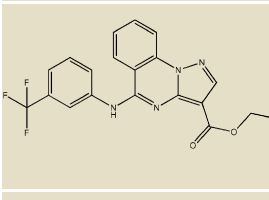
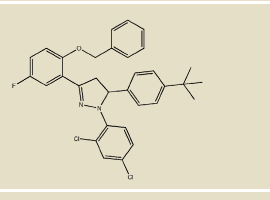
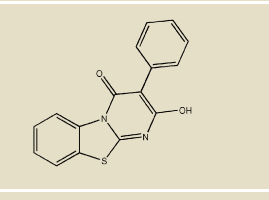
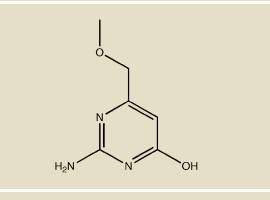
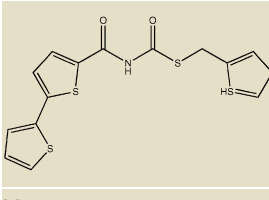
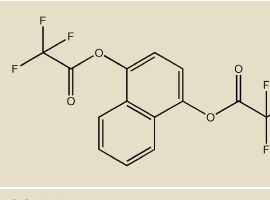
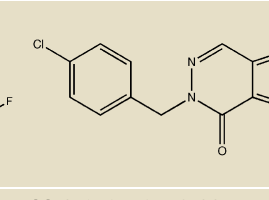
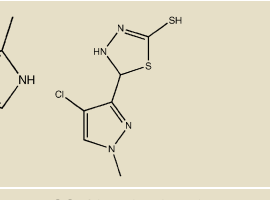
			
M-00573 6.5 ± 4.3	M-00659 34 ± 21	M-02984 65 ± 99	M-19672 12 ± 14
			
M-22971 1.8 ± 2.6	M-26024 30 ± 6.7	M-26463 270 ± 256	M-26553 20 ± 7.2
			
M-27352 39 ± 52	M-27368 42 ± 92	M-28322 29 ± 9.1	M-28324 180 ± 105
			
M-28347 71 ± 25	M-31516 35 ± 35	M-31526 24 ± 4.0	M-31850 0.20 ± 0.14
			
M-31860 138 ± 111	M-31862 108 ± 53	M-31867 31 ± 15	M-32527 42 ± 69
			
M-34700 45 ± 12	M-35014 162 ± 94	M-37955 72 ± 32	M-38728 44 ± 62
			
M-42881 77 ± 54	M-44054 93 ± 82	M-45373 5.8 ± 0.44	M-49773 79 ± 35

Table 2. Summary of IC₅₀ Values for the Confirmed Inhibitory Compounds against Human Hex Isozymes, a Panel of Family-20 Glucosaminidases, and O-GlcNAcase

Inhibitor ^a	hHexA	hHexB	JBHex	SpHex	SmHex	hOGN
DMSO	350 ± 31	98 ± 20	300 ± 13	NI (380)	NI (380)	NA
NGT	0.00027 ^b	0.00019 ^b	0.00028 ^c	>0.020 ^d	>3.0 ^d	0.00007 ^e
M-22971 ^f	0.027 ± 0.006	0.071 ± 0.01	0.23 ± 0.07	>1.0	NI (1.0)	NI (2.0)
M-31850	0.0060 ± 0.0018	0.0031 ± 0.0015	0.28 ± 0.04 ^g	>0.5	NI (0.3)	NI (1.0)
M-45373	0.020 ± 0.008	0.040 ± 0.05	NI (0.6)	NI (0.6)	NI (0.6)	NI (2.0)

hOGN, human O-GlcNAcase; NA, not applicable; NI, noninhibitor. IC₅₀ Values are presented (mM).

^aBased on endpoint assay (1.6 mM MUG).

^bK_i (mM) was determined with MUG substrate.

^cK_i was determined with pNP-GlcNAc substrate [19].

^dHighest concentration (mM) at which compound was evaluated.

^eK_i (mM) as shown in Macauley et al. [35], Table 2.

^fBased on 1.5 mM pNP-GlcNAc substrate.

^gIncomplete dose-response curve; estimated IC₅₀ (mM).

in the IC₅₀ values for the two isozymes. Thus, DMSO and M-31850 have lower IC₅₀ values for Hex B as compared with Hex A, while the reverse is true for both M-22971 and M-45373. M-45373 did not display any inhibitory activity toward JBHex, even at concentrations approaching 1 mM. Although the two HTS inhibitors, M-22971 and M-31850, showed some activity toward SpHex, their IC₅₀ values decreased more than 30- and 100-fold, respectively, relative to hHex. Most significantly, none of the HTS compounds M-22971, M-31850, or M-45373 showed any inhibitory activity toward hOGN, even though this enzyme readily hydrolyzes MUG (K_m = 0.43 mM) and NGT functions as an effective competitive inhibitor (K_i = 70 nM) [35]. None of the three HTS inhibitors, even at concentrations approaching 1 mM, showed any inhibitory activity toward an unrelated lysosomal glycosidase, glucocerebrosidase (Cerezyme).

NGT, the compound mimicking the reaction intermediate common to all members of family 20 and 84 glycosidases, showed the broadest range of inhibitory activity against the enzymes listed in Table 2. This is not surprising, as NGT interacts only with the conserved residues that directly participate in substrate binding and catalysis. The specificity shown for the hHex isozymes by the compounds identified through HTS suggests that they likely interact with only a few of the same conserved active-site residues, requiring interactions with other peripheral, non-conserved residues at or near the active site of hHex A/B for high affinity binding.

Evaluation of Chaperoning Potential of HTS Hex Inhibitors in ISD Patient Fibroblasts

The ability of the HTS inhibitors to act as PCs was evaluated using a cell line from a patient with ISD (i.e., only expresses Hex S). This isozyme is intrinsically unstable and was shown previously to be very responsive to the chaperoning effects of NGT [8] (e.g., similar treatment of ISD or ATSD with NGT resulted in a 6-fold increase in Hex S activity, but only a 3-fold increase in Hex A activity

[8]). All three compounds, M-31850, M-22971, and M-45373, produced a dose-dependent increase in MUG hydrolysis (Hex S levels) in lysates from treated ISD cells (Figure 2A). The increase was specific to Hex, as a similar increase was not observed in hydrolysis of MUGal by lysosomal enzyme β-galactosidase (Figure 2B). Clearly, the three inhibitory compounds function as specific PCs for Hex.

Compared to NGT, which is most effective in enhancing enzyme activities at 1 mM [8], both M-31850 and M-45373 were maximally effective as PCs at 100- and 10-fold lower concentrations, respectively. In contrast, M-22971 produced a maximal response near 1 mM. Although effective as PCs, the parallel decrease in relative activity of both MUG and MUGal seen at concentrations above 1 mM are indicative of the cellular toxicity of M-31850 and M-22971 at elevated levels. Bisnaphthalimide compounds are toxic to cells in the nanomolar to micromolar range, depending on the number of amines and length of alkylamine linker [36].

Treatment of ATSD Fibroblasts with HTS Compounds Results in Increased Levels of Mature/Proteolytically Processed α Subunit in Lysosomes

To demonstrate that the compounds identified by HTS can enhance the functional levels of the G269S mutant α subunit, ATSD patient fibroblasts were grown in the presence of M-22971, M-31850, and M-45373 at concentrations shown to be optimal in ISD cells. Western blotting with an anti-Hex A antibody showed that treatment of ATSD fibroblasts with the HTS compounds resulted in increased levels of α subunit (Figure 3A). In comparison to untreated cells (media only), the DMSO- and HTS inhibitor-treated cells showed increased levels of a 56 kDa band, corresponding to the processed, mature α subunit (α_m) found in wild-type fibroblasts. Densitometric quantitation of the α_m band demonstrated a clear increase in levels of α subunit protein that closely paralleled the increase in specific MUGS activity found in the lysates of

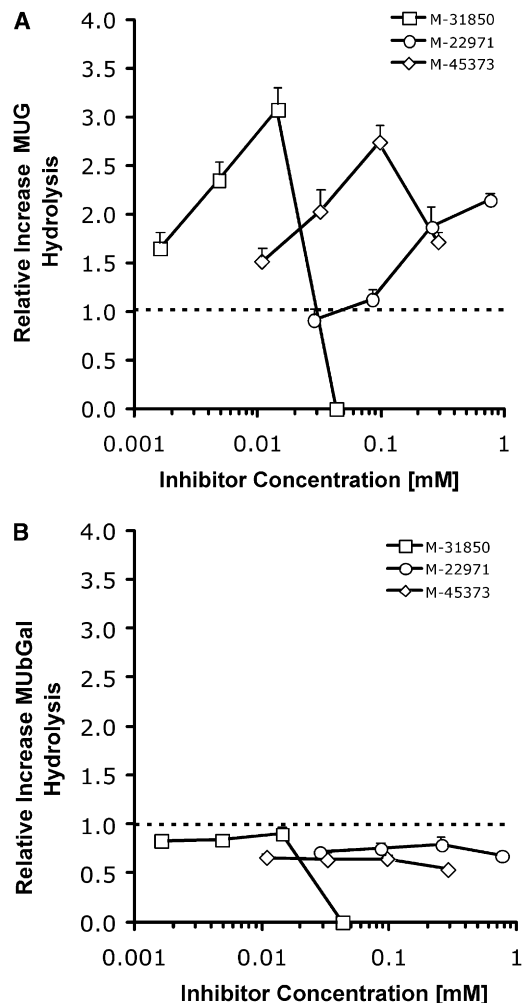


Figure 2. Dose-Dependent Increase in MUG Activity Following Growth of ISD Fibroblasts in Media Containing HTS-Derived Inhibitory Compounds

ISD fibroblasts were grown in media containing different concentrations of M-22971, M-31850, M-45373, or DMSO for 5 days, lysed, and MUGS or MUBGal activity determined ($n = 4$). The relative increases in MUG (A) or MUBGal (B) hydrolysis were determined as: (MU fluorescence of the inhibitor-treated cells)/(MU fluorescence of mock [DMSO]-treated cells). Dashed line denotes no change in activity. Error bars refer to standard deviation.

inhibitor-treated cells (Figure 3B). Not surprisingly, since DMSO is a weak competitive inhibitor of Hex, it also acted as a weak PC, increasing the amount of α_m approximately 1.5-fold relative to untreated cells. However, one cannot exclude the possibility that DMSO may enhance Hex activity by other mechanisms, as it has been reported to enhance protein levels by acting as a nonspecific chemical chaperone [37] and was found to increase mRNA levels of IL-1 β by augmenting promoter activity [38].

The proteolytic processing of lysosomal enzymes occurs post-ER (i.e., in lysosomes or late endosomes [39, 40]). D'azzo et al. [41] previously demonstrated that the α G269S Hex A is retained in the ER, resulting in barely de-

tectable levels of α_m . Thus, the increased levels of α_m in the presence of the HTS inhibitors suggests that the compounds function as PCs, increasing the levels of α subunit that can be transported from the ER to the lysosome.

To conclusively demonstrate that the inhibitor-treated cells have increased levels of Hex A in the lysosomes, a lysosome-enriched fraction was prepared from DMSO and M-31850-treated fibroblasts (Figure 3C). This method has been previously used to isolate an ER-depleted lysosomal fraction by magnetic chromatography following labeling of fibroblasts by iron-dextran colloid [8, 42]. There was an approximately 10-fold increase in Hex (MUGS)- and acid phosphatase (MUP)-specific activity in the lysosomal fraction. More importantly, MUGS activity was increased 3-fold both in the postnuclear supernatant and lysosome-enriched fractions, consistent with the hypothesis that increased levels of Hex A in treated cells are found in the lysosome. The activity of lysosomal acid phosphatase was not significantly affected in either fraction from M-31850-treated cells. Fibroblasts do not synthesize significant levels of the higher gangliosides (e.g., GM1 ganglioside [43]). Thus, the ATSD and ASD cells used in this study do not store appreciable amounts of GM2 ganglioside. However, our data strongly imply that patient cells that do synthesize higher gangliosides (i.e., neurons) would benefit from M-31850 treatment.

These results validate the approach for identifying novel PC by first performing an HTS for Hex-inhibitory compounds. The strongest inhibitors identified, M-22971, M-31850, and M-45373, are structurally distinct from the known hHex inhibitors, the majority of which are azasugars [19, 44] and iminocyclitol derivatives [45]. These HTS-derived inhibitors can serve as new, more drug-like frameworks that can be further optimized by high-throughput combinatorial chemistry [45]. This approach could be applied to the naphthalimide derivatives, as they can be readily synthesized via a straightforward, single-step scheme [46].

Examination of the Mechanism by Which Compound M-31850 Acts as a PC for Hex A

Bisnaphthalimide compound, M-31850, was examined in greater detail in terms of its mechanism of binding, because (1) it was active in cells at the lowest concentration of the HTS compounds examined, (2) several naphthalimide derivatives, Elinafide (LU79533), and Alrestatin had been evaluated or approved for use in humans, and (3) other naphthalimide congeners can be easily synthesized. To confirm that M-31850 functions as a PC in a manner similar to NGT (i.e., it binds at [or near] the active site and is capable of increasing the stability of the enzyme [8]), the effects of the compound on enzyme kinetics and thermal denaturation were analyzed. M-31850 increased the half-life of the mutant Hex A from ATSD cells more than 2-fold at 44°C relative to the enzyme heated in the presence of DMSO (Figure 4A). It acts as a classic competitive inhibitor of Hex (K_m increases and V_{max} is unaffected by increasing amounts of M-31850), with a K_i of $0.8 \pm 0.1 \mu\text{M}$ (Figure 4B).

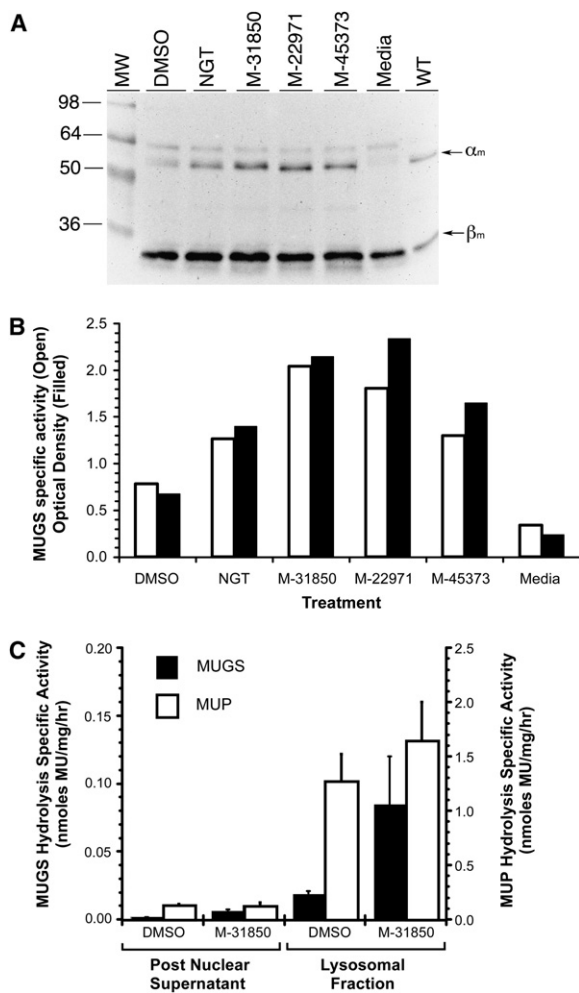


Figure 3. Increased MUGS Activity in Treated ATSD Fibroblasts Is Associated with an Increase in the Mature α Subunit Protein and Levels of the Active Hex A Isozyme

(A) ATSD cells were treated for 5 days with DMSO (1%), NGT (1 mM), M-31850 (0.002 mM), M-22971 (1 mM), or M-45373 (0.1 mM). Following resolution of the α and β subunits by SDS-PAGE and subsequent transfer to nitrocellulose, the blot was probed with rabbit polyclonal anti-hHex A antibody. Positions of the lysosomally processed, mature α subunits (α_m) and β subunits (β_m) in mock (media) or inhibitor-treated fibroblasts are denoted by arrows to the left of the blot. Position of Mr markers are shown to the left of the blot.

(B) The increase in MUGS activity parallels the increase in amount of mature α subunit from lysates of treated ATSD fibroblasts. The specific MUGS activity (nanomoles MU released/mg total cell protein/hr) of lysates used to produce the western blot in (A) is shown plotted (open bars) adjacent to the optical density of the α_m band (filled bars) from the western blot in (A).

(C) Increased MUGS (Hex A) activity is found in the lysosomal fraction of M-31850-treated ATSD cells. Comparison of MUGS activity (nanomoles/mg of total cell protein/hr) in the postnuclear supernatant (PNS) and lysosome (lyso)-enriched fractions from M-31850 (0.002 mM)-treated (filled bar) ATSD fibroblasts. Error bars refer to standard deviation.

All of the mononaphthalimide derivatives, M-31860, M-31862, and M-31867 (Tables 1 and 3) from the secondary screen had IC_{50} values that were at least 100-fold higher than the bisnaphthalimide, M-31850 (Table 3). All

of these derivatives contained a small hydrophobic group N-linked to the underlying naphthalimide by a short alkyl chain that lacked a secondary amine. Similarly, the decreased inhibitory activity of the mononaphthalimides, BTB12933 and 5141402, further underline the importance of the second naphthalimide moiety.

The critical role of the secondary amine group in the linker bridging the two naphthalimide moieties was underscored by the loss of all inhibitory activity when it was replaced by an ether linkage in the analogous position in compound 7916963. The behavior of this compound suggests that the secondary amine in M-31850 may be involved in the formation of a hydrogen bond with an unidentified residue in Hex A. Although reduced more than 10-fold, the inhibitory activity of compound 5141402 suggests that an analogously positioned hydroxyl group could provide the necessary hydrogen atom. The importance of the N-alkylamine linker for inhibitory activity of both the mono- and bisnaphthalimide derivatives, compound 5141402 and M-31850, is reminiscent of recently described iminocyclitol-based Hex inhibitors bearing an N-alkylamine moiety [47].

The attenuated inhibitory activity of compound 5141402, lacking the second naphthalimide, suggests that it may provide additional hydrophobic contacts important for high-affinity binding. It is surprising that there is an ~ 8 -fold decrease in the inhibitory activity of LU79553, as it bears two naphthalimide groups and the position of the amine in the linker relative to the naphthalimide group is identical to that in M-31850. This suggests that the two naphthalimide groups must be spaced appropriately in order to effectively bind Hex A. The second active site in Hex A is not a candidate for the site that binds the second naphthalimide group in M-31850, as the measured distance between the two active sites is more than 2.5 times the size of the alkylamine linker in M-31850. However, the proposed hydrophobic aglycon pockets just outside either active site of Hex A [20, 47] remain possible candidates.

On the basis of the inhibitory activity of the naphthalimide derivatives in Table 2, and the fact that M-31850 is a competitive inhibitor, the following binding model is proposed. One of the naphthalimide groups binds directly in the substrate binding pocket of Hex A, while the second naphthalimide moiety binds to a secondary hydrophobic patch (e.g., an aglycon binding site). An appropriately sized linker between the two naphthalimide groups is needed to span the two sites, and must also be able to form a stabilizing hydrogen bond with an acidic acceptor residue on the surface of Hex A.

Compound M-31850 was evaluated in greater detail in part due to its close similarity to LU79553 (Elinafide), which previously had been evaluated in phase-I clinical trials as a solid tumor chemotherapeutic due to its DNA intercalating ability and inhibitory activity against topoisomerase I [46]. Although Elinafide did not proceed further in clinical trials [48, 49] due to its toxicity at therapeutic doses, these results demonstrate the utility of using the inhibitory compounds as seeds to identify in-trial or FDA-approved drugs. Since the goal of the HTS screen was

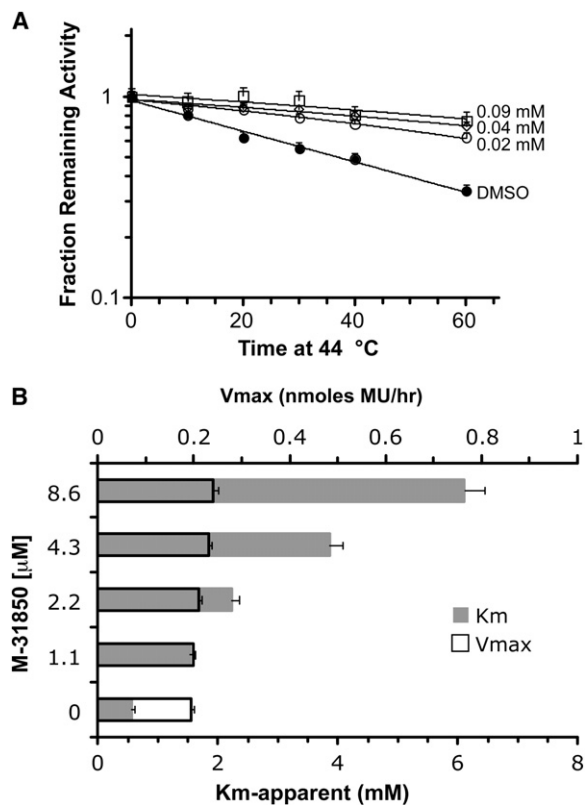


Figure 4. M-31850 Attenuates Thermal Denaturation of Hex A, α Gly269Ser Mutant at 44°C and It is a Competitive Inhibitor

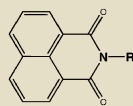
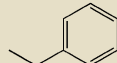
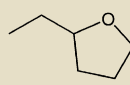
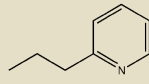
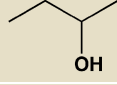

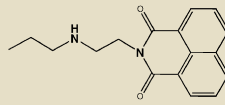
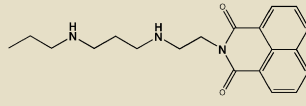
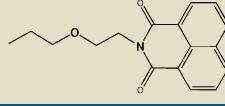
(A) Partially purified mutant Hex A from ATSD fibroblasts was heated at 44°C in the presence of DMSO (mock-treated; filled symbols) or different concentrations of M-31850 (open symbols) for 10, 20, 30, 40, or 60 min. "Fraction remaining MUGS activity," (y axis) was calculated using the formula: (MU fluorescence of inhibitor-treated sample heated for a given time)/(MU fluorescence of inhibitor-treated sample left at 4°C [time = 0 min]) (n = 3) (i.e., 1 = no change). Error bars refer to standard deviation.

(B) The change in K_m (gray bars) and V_{max} (bars outlined in black) versus inhibitor concentration is shown for M-31850 (n = 3) with MUG substrate. Michaelis-Menten plots were used to determine K_m and V_{max} in the absence and presence of increasing concentrations of M-31850 (dissolved in water). Error bars refer to standard deviation.

to identify more drug-like PCs, compounds such as Elinafide would be expected to expedite the development of therapeutics for the treatment of ATSD [50].

SIGNIFICANCE

In Tay-Sachs disease (TSD) and Sandhoff disease (SD), inadequate levels of Hex A ($\alpha\beta$ -dimer) in the lysosome result in the intralysosomal accumulation of GM2 ganglioside in neuronal cells. Although the more common infantile forms have no residual enzyme activity, the late-onset, adult, and juvenile forms have 2%–8% of normal activity. To date, carbohydrate-based inhibitors of Hex (e.g., NGT) act as pharmacological chaperones (PCs), enhancing lysosomal

Table 3. Inhibitory Activity of Naphthalimide Derivatives against Purified Human HexA		
ID	Substituent (-R)	IC ₅₀ (μ M)
Parent ^a		
PHG 00876		NI (200) ^{c,d}
M-31860		138 \pm 111 ^e
M-31862		108 \pm 53 ^e
M-31867		31 \pm 15 ^e
BTB12933	-H	18 \pm 1.5
5141402		16 \pm 1.5
M-31850		0.6 \pm 0.3
LU79953		4.6 \pm 1.9
7916963		NI (200)

NI, noninhibitor.

^a General structure naphthalimide derivatives evaluated.

^b N-linked R groups from naphthalimide derivatives.

^c Highest concentration at which compound was evaluated.

^d IC₅₀ values based on 0.06 mM MUG (continuous).

^e IC₅₀ values based on 0.06 mM MUG (endpoint).

Hex enzyme levels in cells of late-onset patients above the ~10% critical threshold.

We have developed a high-throughput screening (HTS) method to identify novel drug-like inhibitors of Hex utilizing a fluorescence-based real-time enzyme assay. The simplicity and efficiency of this strategy to identify inhibitors utilizing existing methylumbelliferone-based substrates can be exploited to quickly identify candidate drug-like PC for other lysosomal storage disorders where there is a nonexistent or limited panel of inhibitory compounds available for the deficient enzyme.

Three structurally distinct single-digit micromolar Hex inhibitors were identified that did not inhibit other lysosomal enzymes or neutral, cytosolic O-GlcNAcase.

Unlike the majority of Hex inhibitors that are azasugar derivatives, these compounds consist of novel frameworks found in FDA-approved drugs, such as Alrestatin and Indacrinone. All of the HTS-derived inhibitors were shown to function as PCs, since they enhanced the levels and activity of Hex S and mutant Hex A in infantile SD and adult TSD (ATSD) patient fibroblasts, respectively. Importantly, the approximately 3-fold increase in protein and enzyme activity levels in the lysosomes from M-32850-treated ATSD cells would be expected to raise Hex A levels above the critical 10% threshold. These results validate the approach of using HTS for inhibitory compounds to identify candidate drug-like PCs.

EXPERIMENTAL PROCEDURES

Chemicals and Reagents

A total of 50,000 drug-like compounds from the Maybridge collection (Maybridge PLC, UK) were used in the initial screen. Compounds evaluated in the secondary screen and their derivatives were reordered from Maybridge PLC (UK) or Chembridge (USA) and solubilized using DMSO or water. Fluorogenic substrates purchased from Sigma (USA) included 4-methylumbelliferyl β -D-glucopyranoside (MUGlc), 4-methylumbelliferyl β -D-galactosaminide (MUGal), 4-methylumbelliferyl phosphate (MUP), MUG, and MUGS. The colorimetric substrate p-nitrophenol β -D-N-acetyl glucosaminide (Sigma) was also used to monitor Hex A activity. Placental hHex A was prepared as previously described [51], and NGT was synthesized and purified as previously described [52, 19].

Cell Lines

The following cell lines were used: 1766 (ATSD) was from an ~40-yr-old female patient diagnosed with the chronic (adult) form of TSD (kindly provided by Dr. J.R. Donat, University of Saskatchewan, Kinsmen Children's Centre, Saskatoon, Saskatchewan, Canada) homozygous for the α G269S mutation (Molecular Diagnostics Laboratory, SickKids, Toronto, ON, Canada); 294 (ISD) was from an ISD patient, homozygous for the 16 kb *hexb* deletion mutation [53, 54]. All cell lines were grown in α -minimal essential media (α -MEM; Invitrogen, USA) supplemented with 10% fetal calf serum (FCS; Sigma), and antibiotics Penicillin/Streptomycin (Invitrogen, USA) at 37°C in a humidified CO₂ incubator.

Primary Screening

The statistical test resulting in the Z' factor [31] measured the variability of the rate values for Hex in the presence (low control) and absence (high control) of the Hex inhibitor, NGT. To control for plate-to-plate variability, enzyme activity was expressed according to the equation:

$$RA = \left(\frac{r - \mu_L}{\mu_H - \mu_L} \right) \cdot 100$$

where RA is residual activity, r is rate in the presence of the library compound, μ_L is mean low control rate (i.e., activity in the presence of NGT and DMSO), and μ_H is mean high control rate (i.e., activity in the presence of DMSO only). Reactions were set up in black-walled 384-well plates with the SAGIAN Core System (Beckman Coulter, Inc. Fullerton, CA, USA) equipped with an ORCA arm for labware transportation, a Biomek FX with a 96 channel head for liquid handling, and an Analyst HT (Molecular Devices Corp., Sunnyvale, CA, USA) for fluorescence detection. All reactions were performed in duplicate (separate plates). High controls (32 wells) consisted of Hex A (100 ng/ml) in citrate phosphate (CP) buffer containing 0.0025% human serum albumin (HSA) and 2% DMSO. Low controls (32 wells) additionally contained NGT at 360 μ M. Test wells contained 20 μ M of each library compound. To

take into account the effects of DMSO on enzyme activity, the expressed residual activity for the two replicates in Figure 1B was normalized to 100% ($100 \times [\text{raw activity}/\text{mean activity}]$).

Secondary Screening

The dose-response curves of the 64 hits from the primary screen were determined by the continuous MUG Hex assay in the presence of seven concentrations (0.1–100 μ M) of the putative inhibitor diluted in DMSO. Data were fit to the equation:

$$v = \frac{a}{1 + \left(\frac{[I]}{IC_{50}} \right)^s}$$

where v = background corrected reaction rate, a = the rate in the absence of the inhibitor, [I] = the concentration of the inhibitor, and s = the slope factor, with either Grafit (v.4.0.010; Erithacus Software, Surrey, UK) or Kaleidagraph (Synergy Software, PA, USA), to calculate IC₅₀ values. Compounds exhibiting sigmoidal dose-response curves were selected as bona fide inhibitors.

Hex Activity Assays

Hex A/B/S activity was measured by release of 4-methylumbelliferyl fluorophore from MUG. Total assay volume was 50 μ l, and contained 10 mM citrate-phosphate buffer, pH 4.3, 0.025% HSA. For enzyme activity monitored continuously, reactions were initiated with 75 μ M MUG at room temperature and monitored for 7 min with 330 nm and 450 nm excitation and emission filters, respectively. For the endpoint assay, the reaction at 37°C was terminated by raising the pH to 10.5, above the pKa of 4-MU, with 0.1 M 2-amino 2-methyl 1-propanol. The increase in fluorescence was measured using a Spectramax Gemini EM MAX (Molecular Devices Corp, Sunnyvale, CA) fluorometer, and detected at excitation and emission wavelengths set to 365 nm and 450 nm, respectively.

Activity of JBHex (Vector Labs, USA) and SpHex (New England Biolabs, USA) in the presence of DMSO, NGT, and the HTS compounds were evaluated identically to procedures used for hHex. In the case of *Serratia marcescens* chitinase (glucosaminidase) (kindly provided by C. Vorgias [22, 55]), activity was monitored at pH 7.5 under otherwise identical conditions. The activity of hOGN was performed with 0.5 mM, 4-nitrophenyl N-acetyl β -D-glucosaminide substrate and reaction conditions as described by Macauley et al. [35].

For primary and secondary screening of the compounds, enzyme activity was monitored continuously on the Analyst HT (Molecular Devices Corp) fluorometer, as describe above. Steady-state kinetic parameters were established with a range of MUG substrate (1.6–0.003 mM) and enzyme concentrations (1–0.01 mg/ml). The inhibitory activity of compounds that were fluorescent (M-31850 and derivatives) or quenched (M-22971) near the emission maxima of MU were also confirmed with the colorimetric substrate pNP-GlcNAc and conditions described for the MUG endpoint assay, except that absorbance was measured at 405 nm.

Kinetic parameters (K_m , V_{max} , and K_i) were determined by fitting the nonlinear least square data to the Michaelis-Menten equation with Kaleidagraph (Synergy Software) according to Kakkar et al. [56].

Heat Inactivation Assay

Heat inactivation experiments were performed with Hex A from ATSD fibroblasts treated with NGT (1 mM) for 5 days, as previously described [8], with Hex B removed by ion exchange chromatography. For heat inactivation experiments, equal amounts of total protein (0.1–0.5 μ g) from enriched mutant Hex A fractions were diluted in CP buffer (pH 4.2), containing 0.5% HSA. Diluted samples of the enzyme containing Hex inhibitors or DMSO were split into two aliquots; one was left on ice, and the other heat-treated at 44°C. The heat-treated enzyme was cooled on ice until completion of the time series. For assaying enzyme activity, samples were pre-equilibrated to 37°C for 10 min, followed by addition of MUGS substrate, and incubated at 37°C for a further 30 min.

Evaluating Chaperoning Activity of Compounds in Cell Culture

ISD fibroblasts were seeded onto 96 well tissue culture plates (Costar) at 10,000–50,000 cells per plate (~50% confluence). The following day, the medium was replaced with fresh α -MEM-FCS with or without a test compound to be evaluated (1:100 dilution). Test compounds were either dissolved in water (NGT) or DMSO. Mock- or compound-treated cells were evaluated in triplicate and grown for 5 days at 37°C in a humidified CO₂ incubator.

To measure Hex S activity in treated ISD fibroblasts, media was removed, cells were washed twice with PBS, and subsequently lysed by the addition of 10 mM citrate-phosphate buffer (pH 4.8), containing 0.1% HSA and 0.1% Triton X-100. One aliquot (25 μ l) of the lysate was mixed with an equal volume of MUG and assayed for total Hex activity. To control for variability in cell numbers between replicate wells, the remaining aliquot of the lysate was used to assay for lysosomal β -galactosidase, with the substrate MUGal [8] by the endpoint assay described above.

Western Blotting

Lysates prepared from ATSD cells were subjected to SDS-PAGE on a 10% bis-acrylamide gel, and the separated proteins were transferred to nitrocellulose. A rabbit polyclonal antibody against hHex A was used as previously described [57]. Blots were developed with chemiluminescent substrate according to the manufacturer's protocol (Amersham, Biosciences, UK). Bands were visualized and optical density quantitated using a high sensitivity gel documentation system (Fluorchem 8000) consisting of a cooled CCD camera coupled with Alpha Innotech software (Alpha Innotech Corp., USA).

Purification of Iron-Dextran-Labeled Lysosomes

Lysosomal fractions were prepared from ATSD fibroblasts treated with DMSO or M-31850 (1 mM) for 5 days, followed by labeling with iron-dextran colloid and subsequent purification by magnetic chromatography, as previously described [8]. Lysosomal, acid phosphatase, and Hex A were monitored fluorometrically with the substrates MUP and MUGS, respectively, as previously described [8].

Mass Spectrometry

The mass of selected secondary hits was confirmed by the Advanced Proteomic Centre at Sickkids (Toronto, ON, Canada) with a QToF mass spectrometer (Waters/Micromass, Manchester, UK).

Supplemental Data

Supplemental Data are available online at <http://www.chembiol.com/cgi/content/full/14/2/153/DC1/>.

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