



# Identification of aryl sulfonamides as novel and potent inhibitors of Nav1.5

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## ABSTRACT

We describe the synthesis and biological evaluation of a series of novel aryl sulfonamides that exhibit potent inhibition of Nav1.5. Unlike local anesthetics that are currently used for treatment of Long QT Syndrome 3 (LQT-3), the most potent compound (-)-6 in this series shows high selectivity over hERG and other cardiac ion channels and has a low brain to plasma ratio to minimize CNS side effects. Compound (-)-6 is also effective in shortening prolonged action potential durations (APDs) in a pharmacological model of LQT-3 syndrome in pluripotent stem cell-derived cardiomyocytes (iPSC-CMs). Unlike most aryl sulfonamide Nav inhibitors that bind to the channel voltage sensors, these Nav1.5 inhibitors bind to the local anesthetic binding site in the central pore of the channel.

The cardiac voltage-gated sodium channel Nav1.5 (*SCN5A* gene) is expressed mainly in the cell membrane of cardiomyocytes, including the sarcolemma of atrial and ventricular myocytes, Purkinje fibers, sinoatrial, and atrio-ventricular nodes.<sup>1</sup> The rapid upstroke of the cardiac action potential and the rapid impulse conduction through cardiac tissue is due to sodium influx via Nav1.5 channels. Mutations in the *SCN5A* gene result in the genesis of a variety of cardiac arrhythmias. Hundreds of unique *SCN5A* mutations have been identified in patients, with the vast majority being in two primary inherited cardiomyopathies, either long QT syndrome type 3 (LQT-3, gain-of-function)<sup>2–5</sup> or Brugada syndrome (BrS, loss-of-function).<sup>6</sup> In addition, *SCN5A* mutations have also been reported in association with other cardiac disorders, including sick sinus syndrome,<sup>7</sup> atrial standstill,<sup>8</sup> cardiac conduction defect (CCD),<sup>9</sup> atrial fibrillation (AF),<sup>10,11</sup> and dilated cardiomyopathy (DCM).<sup>12</sup>

Sodium channel blocker therapy has been extensively used in treating cardiac arrhythmias, with many therapeutically useful antiarrhythmic agents targeting Nav1.5 (e.g. local anesthetics such as mexiletine 1).<sup>13</sup> Although these drugs are widely used, they suffer from dose-limiting adverse effects, especially nausea and dizziness.<sup>14</sup> Ranolazine (2), structurally similar to other class I antiarrhythmic agents, is currently marketed for the treatment of chronic angina. Although the mechanism of its antianginal effects is not known, 2 does inhibit Nav1.5, and has significant antiarrhythmic effects in both ventricles and atria.

Unfortunately, 2 blocks  $\beta$ -adrenergic receptors, and inhibits a number of cardiac ion currents (e.g., human ether-à-go-go-related gene, hERG).<sup>15,16</sup> A more potent compound, GS-967 (3), was found to have high brain penetration and high activity on brain sodium channel isoforms (e.g., Nav1.1, Nav1.2, & Nav1.6).<sup>17</sup> Eleclazine (4), purportedly selective over brain sodium channel isoforms, was discontinued from clinical development.<sup>18</sup>

In an effort to identify structurally distinct Nav1.5 inhibitors with high selectivity over hERG and limited brain exposure, the corporate compound repository was surveyed. Aryl sulfonamide *rac*-5 was found to be a modest Nav1.5 inhibitor. We were intrigued by its structural feature because aryl sulfonamide is a well-known structure for subtype selective inhibitors of Nav1.7 and, in general, displays low hERG activity and low central nervous system (CNS) penetration. Herein, we describe our efforts in the optimization of *rac*-5 that led to the identification of a series of novel Nav1.5 inhibitors including (-)-6, a potent Nav1.5 inhibitor with high selectivity over hERG and other cardiac ion channels and low brain penetration.

The synthesis of these aryl sulfonamides is exemplified by *rac*-6 as illustrated in Scheme 1, in general, via a S<sub>N</sub>Ar reaction joining a 3-substituted piperidin-4-ol left-hand fragment (LHF) with a suitably protected heteroaryl sulfonamide right-hand fragment (RHF) through an oxygen linkage. Construction of the LHF (*rac*-11) was commenced by

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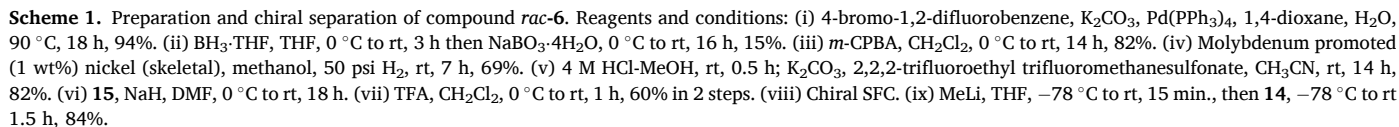
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Taking *rac-5* as a starting point, our initial structure–activity relationship (SAR) studies focused on replacing the 1,2,4-thiadiazole moiety in *rac-5* to improve hNav1.5 potency, and investigating different five- and six-membered nitrogen-containing heterocycles. This effort provided us several compounds with improved hNav1.5 activity relative to *rac-5*: the 4-thiazole *rac-17* (IC<sub>50</sub> = 1.18 μM) and 6-fluoropyridine *rac-23* (IC<sub>50</sub> = 0.70 μM) were revealed to be the two most potent hNav1.5 inhibitors. A

Compound *rac*-**33** showed an attractive profile due to good hN<sub>A</sub>V1.5 potency and *in vitro* microsomal stability. Therefore, we decided to study this compound further. The optically pure enantiomers were obtained by chiral separation and evaluated individually; however, the absolute stereochemistry could not be determined readily, and instead the first eluting enantiomer from the chiral column was assigned as (-)-**33** ( $[\alpha]_D^{21} = -18.90$ , *c* 2.1, DMF) and the second eluting enantiomer was assigned as (+)-**33** ( $[\alpha]_D^{21} = +18.74$ , *c* 2.1, DMF). (-)-**33** was slightly more potent with an IC<sub>50</sub> value of 0.24 μM on hN<sub>A</sub>V1.5.



**Table 1**Nav1.5 activity of compounds *rac*-5, and *rac*-16 – *rac*-

Compd <sup>a</sup>	Het	hNav1.5 IC <sub>50</sub> (μM) <sup>b</sup>	Compd <sup>a</sup>	Het	hNav1.5 IC <sub>50</sub> (μM) <sup>b</sup>
<i>rac</i> -5		7.83	<i>rac</i> -16		25.05
<i>rac</i> -17		1.18	<i>rac</i> -18		4.65
<i>rac</i> -19		7.14	<i>rac</i> -20		>30
<i>rac</i> -21		25.49	<i>rac</i> -22		4.32
<i>rac</i> -23		0.70	<i>rac</i> -24		5.04
<i>rac</i> -25		1.29	<i>rac</i> -26		13.21
<i>rac</i> -27		1.10	<i>rac</i> -28		6.33

<sup>a</sup> All compounds exhibited spectral data consistent with their proposed structures and had analytical purities >94% as determined by HPLC.

<sup>b</sup> IC<sub>50</sub>s were an average of at least two independent determinations using automated voltage clamp electrophysiology.

We subsequently discovered analog *rac*-6, which was about 4-fold more potent than *rac*-33. However, this improvement came at the cost of lower microsomal stability. We postulated that the increased metabolic clearance of *rac*-6 might be due to the absence of the 2-fluoro substituent of the central phenyl ring; disappointingly, addition of a 2-fluorine in *rac*-36 did not lead to improvement in metabolic stability. Furthermore, replacement of the central phenyl ring with a pyridyl ring, compound *rac*-37, displayed similar metabolic stability as *rac*-33, but with erosion of hNav1.5 activity. For comparison, the 4-thiazole analog *rac*-38 was also prepared and found to be not as efficient as its 6-fluoropyridine counterpart *rac*-33 in Nav1.5 inhibition and metabolic stability, consistent with the earlier SAR.

Chiral separation of *rac*-6 provided two optically pure enantiomers (-)-6 ([α]<sub>D</sub><sup>21</sup> = -7.95, c 2.1, DMF) and (+)-6 ([α]<sub>D</sub><sup>21</sup> = +7.52, c 2.1, DMF). (-)-6 was about 4-fold more potent than (+)-6 with an IC<sub>50</sub> value of 0.039 μM on hNav1.5. Further evaluation of (-)-6 suggested that (-)-6 had 16-, 7-, and 6-fold selectivity over CNS sodium channel isoforms hNav1.1, 1.2, and 1.6 (IC<sub>50</sub>s of 0.62, 0.27, and 0.23 μM, respectively), when measured by whole cell voltage clamp (EP). The EP protocol used to optimize potency on Nav1.5 was designed to maximize interaction with the high affinity state of the channel and best approximate the K<sub>d</sub> for binding to Nav1.5, especially for potent compounds that have slow kinetics of binding equilibration. We have found that using this protocol for selectivity assessments can overestimate the true selectivity of compounds that have differentiated rates of equilibrium with distinct channel isoforms. For this reason, we also measured compound isoform selectivity with a different (V<sub>1/2</sub>) protocol that we believe better assesses the physiologically relevant selectivity. In this selectivity protocol, potency (IC<sub>50</sub>) on hNav1.5, 1.1, 1.2, 1.6 changed to 0.11, 0.09, 0.012, and 0.11 μM, respectively, suggesting that the apparent selectivity seen in the SAR protocol is not likely to translate to an *in vivo* setting.

Compound (-)-6 was also evaluated in a sodium influx assay<sup>21</sup> for its inhibitory activities on hNav1.5, 1.1, 1.2, 1.6 and 1.7, and exhibited IC<sub>50</sub> values of 0.044, 0.56, 0.27, 0.11, and 0.22 μM, respectively.

**Table 2**Nav1.5 activity and metabolic stability of compounds *rac*-23, and *rac*-29 – *rac*-

Compound <sup>a</sup>	Ar	X	Y	HET	hNav <sub>1.5</sub> IC <sub>50</sub> (μM) <sup>b</sup>	HLM, MLM CL <sub>hep</sub> (mL/min/ kg)
<b>38.</b>						
<i>rac</i> -23		C (F)	C (H)		0.70	16, 70
<i>rac</i> -29		C (F)	C (H)		0.68	17, 71
<i>rac</i> -30		C (F)	C (H)		0.46	13, 53
<i>rac</i> -31		C (F)	C (H)		0.61	11, 62
<i>rac</i> -32		C (F)	C (H)		0.47	13, 49
<i>rac</i> -33		C (F)	C (H)		0.26	7.5, 49
(-)-33	enantiomer 1				0.24	9.0, 50
(+)-33	enantiomer 2				0.43	7.0, 45
<i>rac</i> -34		C (F)	C (H)		4.58	nd <sup>c</sup>
<i>rac</i> -35		C (F)	C (H)		>30	nd <sup>c</sup>
<i>rac</i> -6		C (H)	C (F)		0.065	15, 65
(-)-6	enantiomer 1				0.039	13, 63
(+)-6	enantiomer 2				0.17	14, 74
<i>rac</i> -36		C (F)	C (F)		0.031	14, 65
<i>rac</i> -37		C (H)	N		1.55	8.4, 63
<i>rac</i> -38		C (F)	C (H)		0.75	14, 70

<sup>a</sup> All compounds exhibited spectral data consistent with their proposed structures and had analytical purities >94% as determined by HPLC.

<sup>b</sup> IC<sub>50</sub>s were an average of at least two independent determinations using automated voltage clamp electrophysiology.

<sup>c</sup> nd: not determined.

Compounds (-)-33 and (-)-6 were found to have negligible inhibition on CYPs 1A2, 3A4, 2C19, 2D6, and moderate inhibition on CYP2C9 (IC<sub>50</sub>s of 6.9, and 2.2 μM for (-)-33 and (-)-6, respectively). Importantly, (-)-6 was highly selective, when tested by voltage clamp against a panel of heterologously expressed cardiac ion channels including hERG, Kv2.1, Kv1.5, Kv3.2, HCN2, HCN4, Kv4.2KChIP2.2, Kv4.3KChIP2.2,

K<sub>v</sub>LQT1/mink, Ca<sub>v</sub>1.2, Ca<sub>v</sub>2.2, Ca<sub>v</sub>3.1, Ca<sub>v</sub>3.3, GABA, TRPV1, and 5-HT3A. For example, (-)-6 showed 5% inhibition on hERG at 10  $\mu$ M concentration.

The pharmacokinetic (PK) properties of (-)-33 and (-)-6 were determined in mouse (Table 3). Consistent with the predicted CL<sub>hep</sub> and high plasma protein binding (99.8% bound), both compounds exhibited low plasma clearance (CL), moderate terminal half-lives ( $t_{1/2}$ ) and low volume of distribution ( $V_{ss}$ ). The oral bioavailability of (-)-33 and (-)-6 were 45%, and 39%, respectively. In addition, both (-)-33 and (-)-6 exhibited low brain levels, suggesting that the activity on CNS sodium channel isoforms was not a concern.

Next, we evaluated the activity of (-)-6 in shortening prolonged action potential durations (APDs) like those often observed in long QT syndrome-3 (LQT-3) patients carrying gain-of-function *SCN5A* mutations. The *Anemonia sulcata* toxin II (ATX-II) is known to slow the inactivation of Na<sub>v</sub>1.5<sup>22</sup>, thereby increasing total sodium flux and simulating a gain-of-function *SCN5A* mutation that causes a persistent sodium current, which would lead to a prolongation of the APD. In this study we used an ATX-II-induced model of prolonged APD in human induced pluripotent stem cell cardiomyocytes (iPSC-CMs) utilizing current clamp to record the APD of spontaneously beating iPSC-CMs. Only cells with maximum diastolic potentials < -75 mV and ventricular-like AP morphology (upstroke velocity > 70 V/s) were used. With the addition of 15–30 nM ATX-II, prolongation of the APD was observed in the iPSC-CMs with a 25–100% increase in APD<sub>90</sub>, depending on the sensitivity of the cell (Fig. 2). Addition of 100 nM (-)-6 (2.5  $\times$  Na<sub>v</sub>1.5 IC<sub>50</sub>) concurrently with ATX-II shortened the ATX-II-induced prolongation by 84%, returning it close to vehicle. Compound (-)-6 showed no effect on AP amplitude or maximum diastolic membrane potential (Fig. S2A in supplementary data), however, it did cause a small reduction in upstroke velocity dV/dt(V<sub>max</sub>) of 23% (Fig. S2B in supplementary data).

It has been reported that mexiletine (1), ranolazine (2), GS-967 (3) and eleclazine (4) inhibit the Na<sub>v</sub>1.5 late (persistent) current ( $I_{Na}$ ) (Fig. 1), which is enhanced in LQT3 patients and other cardiac pathological conditions, such as ischemic heart disease.<sup>13,17,18</sup> By blocking the late sodium current during ischemia, these drugs inhibit the subsequent sodium-calcium overload within the myocyte that is normally a hallmark of an ischemic cell.<sup>23</sup> We therefore determined the selectivity of (-)-6 for inhibiting the Na<sub>v</sub>1.5 late  $I_{Na}$  over the Na<sub>v</sub>1.5 peak  $I_{Na}$ . Analogous to the iPSC experiment, ATX-II was used to generate Na<sub>v</sub>1.5 late  $I_{Na}$  in HEK cells stably expressing hNa<sub>v</sub>1.5 and both peak and late Na<sub>v</sub>1.5 currents were measured at a holding potential of -95 mV, similar to the resting membrane potential of the iPSC cardiomyocytes. Unfortunately, the ratio of IC<sub>50</sub> values for inhibition of peak and late  $I_{Na}$  by (-)-6 was only 1.1-fold (peak/late IC<sub>50</sub> 17.7/15.8 nM). This suggests that in the ATX-II-induced iPSC model at least, it appears that the efficacy is mainly driven by total Na<sub>v</sub>1.5 inhibition at the resting membrane

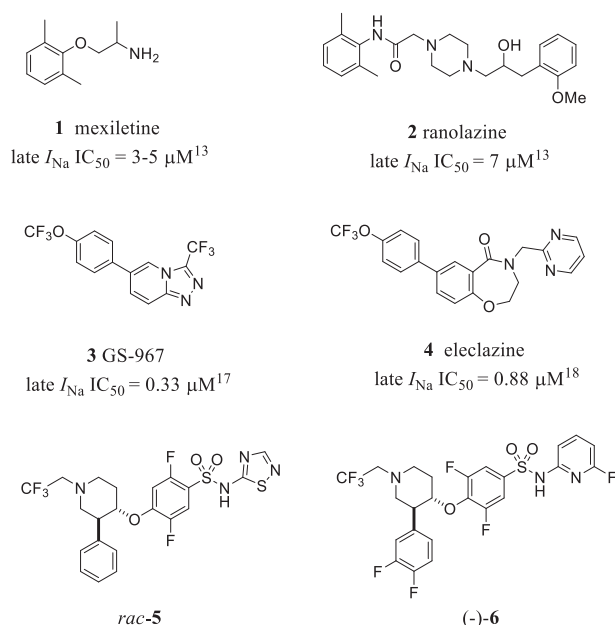


Fig. 1. Selected Na<sub>v</sub>1.5 inhibitors and compounds *rac*-5 and (-)-6.

potential of a cardiomyocyte, rather than selective block of late  $I_{Na}$  as (-)-6 had a reduction in prolonged APD yet no peak/late selectivity.

To investigate the binding mode of Na<sub>v</sub>1.5 inhibition, we performed mutagenesis studies using compounds *rac*-17 and *rac*-23 (Table 4). Recently, subtype-selective aryl sulfonamide Na<sub>v</sub> inhibitors with an anionic warhead have been shown to bind to a positively charged gating residue, the fourth Arg in segment S4 (R4) in the Na<sub>v</sub>1.7 voltage sensor of domain IV (VSD4).<sup>24,25</sup> Therefore, we evaluated the binding of compounds *rac*-17 and *rac*-23 on the equivalent VSD4 R1631A (R4A) mutation in Na<sub>v</sub>1.5 using the VSD4 blocker GX-4195<sup>25</sup> as a control. This mutant led to more than 18-fold decrease in Na<sub>v</sub>1.5 potency for GX-4195, however, no clear potency drop was observed for *rac*-17 or *rac*-23, suggesting that *rac*-17 and *rac*-23 do not have interactions with the positively charged gating residue (R4) in VSD4. Furthermore, *rac*-23 was also evaluated on VSD4 R1622A (R1A), R1625A (R2A), R1628A (R3A) and R1634A (R5A) mutants to determine if it engaged any of the other highly conserved arginines in VSD4. Again, no clear potency change was observed (IC<sub>50</sub>s of 1.29, 0.81, 0.82 and 1.21  $\mu$ M, respectively). We next hypothesized that this class of compounds might be binding to a corresponding conserved arginine in VSD2 instead of R4 in VSD4, thereby imparting its inhibitory activity through VSD2, similar to the peptide toxin ProTx-II.<sup>26</sup> We evaluated *rac*-23 on a VSD2 R814A (R3A) mutant, which corresponds to R4 in VSD4, but saw no clear impact of the mutation (IC<sub>50</sub> of 0.41  $\mu$ M).

We continued to investigate the binding site for this class of compounds by site directed mutagenesis of phenylalanine 1759 to alanine (F1759A) in the pore domain of the Na<sub>v</sub>1.5 channel followed by functional analysis. This residue, found in VSD4-S6, is known to be essential for binding of some antiarrhythmic agents, such as ranolazine,<sup>27</sup> in addition to the local anesthetics (e.g., lidocaine).<sup>28</sup> The potency of (-)-33 for the mutated channel was reduced by >40-fold (IC<sub>50</sub> > 10  $\mu$ M), suggesting that these aryl sulfonamide Na<sub>v</sub>1.5 inhibitors bind to the local anesthetic binding site in the pore domain.

We further tested the ability of compounds (-)-33 and (-)-6 to displace the [<sup>3</sup>H]BNZA ligand. This ligand has been shown to bind to the pore of Na<sub>v</sub>1.5 and most clinical local anesthetics inhibit binding of [<sup>3</sup>H]BNZA.<sup>29</sup> This was also the case for (-)-33 and (-)-6 with  $K_i$  values of 2.02 and 0.37  $\mu$ M, respectively. Furthermore, in voltage clamp studies of Na<sub>v</sub>1.5 expressed heterologously in HEK cells, the state-dependence of block for (-)-6, was only 24-fold when comparing the shift in IC<sub>50</sub> at

Table 3

PK profiles of compounds (-)-33 and (-)-6<sup>a</sup>.

Compound	(-)-33	(-)-6
iv		
CL (mL/min/kg)	1.8	3.8
$t_{1/2}$ (h)	4.3	2.6
$V_{ss}$ (L/Kg)	0.6	0.8
AUC ( $\mu$ M.h)	16	7.6
po		
$C_{max}$ ( $\mu$ M)	5.2	3.6
$t_{1/2}$ (h)	4.1	2.7
AUC ( $\mu$ M.h)	72	30
F (%)	45	39
$C_b/C_p$ @ 2 h ( $\mu$ M) (ratio)	2.62/9.37 (0.28)	2.03/6.44 (0.32)

<sup>a</sup> Average of 3 male FVB mice. Intravenous dosed with 1 mg/kg of compound (-)-33 or (-)-6 in PEG400 and 50% 2-Hydroxypropyl- $\beta$ -cyclodextrin in saline (40:60). Orally dosed with 10 mg/kg of compound (-)-33 or (-)-6 as a suspension in 0.5% w/w methyl cellulose and 0.2% v/v tween 80 in water.



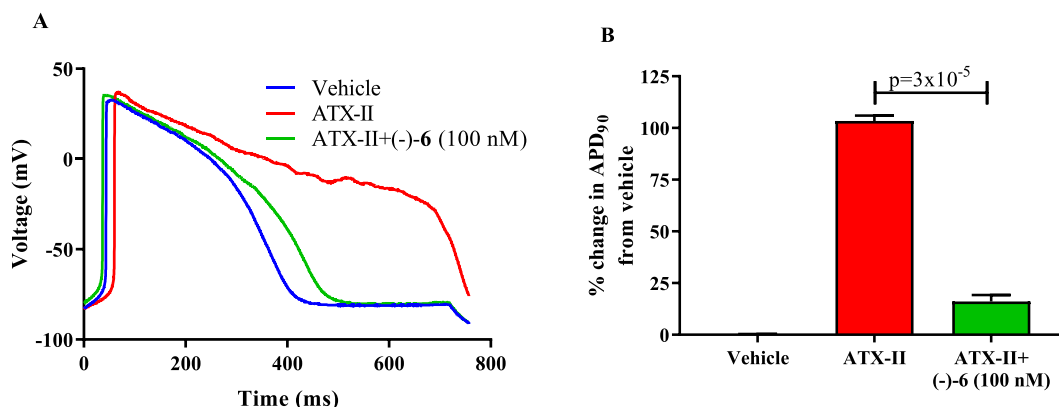


Fig. 2. Reversal of ATX-II-induced APD<sub>90</sub> by 100 nM (-)-6 in human iPSC-CM. Statistical significance of results were analyzed by T-test using Prism version 7 (GraphPad Software).

Table 4

Mutagenesis studies of *rac*-17, *rac*-23 and GX-4195.

Compound	hNav1.5 IC <sub>50</sub> (μM)	hNav1.5 VSD4 R4A IC <sub>50</sub> (μM)
<i>rac</i> -17	1.18	1.17
<i>rac</i> -23	0.70	0.57
GX-4195	0.55	> 10

rested state (-120 mV) to a partially inactivated state (-95 mV) (Fig. S1 in supplementary data). This fold change is similar to lidocaine (35-fold), a pore-binding local anesthetic, but much smaller than a VSD4 binding sodium channel inhibitor such as GX-674 (2400-fold),<sup>25</sup> further supporting our conclusion that these aryl sulfonamides bind to the pore domain.

In summary, we have described the discovery of a series of novel aryl sulfonamide Nav1.5 inhibitors. Mutagenesis studies suggest that these potent Nav1.5 inhibitors bind to the local anesthetic binding site in the pore domain. The tool compound (-)-6 is a potent Nav1.5 inhibitor with significant advantages over currently available class I antiarrhythmic agents including its high selectivity over hERG and other cardiac ion channels, as well as its low brain penetration. Nonetheless, (-)-6 is effective in shortening prolonged APDs induced by ATX-II in human iPSC-CMs. (-)-6 represents a new probe in the research of the pharmacological functions on Nav1.5.

The molybdenum-promoted (1 wt%) nickel (skeletal) catalyzed reduction of epoxides method provides a valuable synthetic entry to *trans* cyclic alcohols. Although the mechanism of the *trans* stereochemistry from this reduction is not known, this catalyst appears to be essential for this transformation. Potentially, enantioselective epoxidation of olefin **8** could be realized using Jacobsen's salen-type catalyst,<sup>30</sup> leading to the asymmetric synthesis of enantiomer (-)-6 or (+)-6 that could be assigned according to its optical rotation or its biological activities, thereby the absolute stereochemistry of (-)-6 could be determined.

#### Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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#### Appendix A. Supplementary data

Preparation and chiral separation of compound *rac*-6; <sup>1</sup>H NMR spectra of *rac*-10 and its *cis*-isomer; protocols for Nav1.5 *in vitro* profiling and efficacy assessment protocol in human iPSC-CMs. Supplementary data to this article can be found online at <https://doi.org/10.1016/j.bmcl.2021.128133>.

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