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# Small molecule McI-1 inhibitors for the treatment of cancer

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# Abstract

The Bcl-2 family of proteins serves as primary regulators of apoptosis. Myeloid cell leukemia 1 (Mcl-1), a pro-survival member of the Bcl-2 family of proteins, is overexpressed and the Mcl-1 gene is amplified in many tumor types. Moreover, the overexpression of Mcl-1 is the cause of resistance to several chemotherapeutic agents. Thus, Mcl-1 is a promising cancer target. This review highlights the current progress on the discovery of small molecule Mcl-1 inhibitors.

#### Keywords

Mcl-1; myeloid cell leukemia-1; inhibitors; small molecule; BH3-mimetic

# 1. Introduction

Apoptosis is a natural process for eliminating unwanted or damaged cells that represent a threat to the health of an organism. This process is highly regulated, and the B-cell lymphoma-2 (Bcl-2) family of proteins serve as the main regulators. Indeed, dysregulation and evasion of apoptosis is one of the hallmarks of cancer.(Hanahan & Weinberg, 2000, 2011)

Members of the Bcl-2 family proteins share conserved sequences in regions known as Bcl-2 homology (BH) domains (BH1–BH4).(Korsmeyer, 1999; Pang, et al., 2012) Members within the same family can have opposite effects. The anti-apoptotic or pro-survival proteins, including Bcl-2, Bcl-X<sub>L</sub>, Bcl-w, Bfl-1/A1 and Mcl-1,(Adams & Cory, 2007) keep cells alive; whereas, the pro-apoptotic proteins (e.g., Bim, tBid, Bad, Puma, Noxa, Bak, and Bax)(Youle & Strasser, 2008) promote cell death. The relative levels of the anti- and pro-apoptotic proteins govern whether a cell will live or die. Recently, much has been learned about how the Bcl-2 proteins regulate apoptosis.(Burlacu, 2003; M. F. van Delft & Huang,

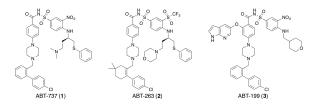
#### **Conflict of Interest Statement**

The authors declare that there are no conflicts of interest.

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2006; Volkmann, et al., 2014) Upon triggering a death signal, a subset of the pro-apoptotic proteins with homology only in the BH3 region cause Bak and Bax to homo-oligomerize and form pores in the mitochondrial membrane leading to cytochrome c release into the cytosol. This activates the caspase cascade and causes cell death. The anti-apoptotic proteins block cell death by binding and sequestering, with varying specificity the BH3-only proteins.(L. Chen, et al., 2005) The binding specificity and affinity exhibited by the antiapoptotic proteins for the pro-apoptotic proteins is defined by hydrophobic and electrostatic interactions between the BH3 region of the pro-apoptotic proteins and the binding groove formed by the BH1, BH2 and BH3 regions of the anti-apoptotic proteins. (Dutta, et al., 2010; Moldoveanu, et al., 2014; Sattler, et al., 1997) Of the BH3-only proteins, Bim and Puma are the least selective, binding to all five anti-apoptotic proteins. Bad binds strongly to Bcl-2, Bcl-X<sub>L</sub> and Bcl-w; whereas, Noxa binds exclusively to Mcl-1 and Bfl-1/A1. These observations suggest that apoptosis is regulated by the interactions between particular subsets of these proteins and that apoptosis can be initiated by the inhibition of the prosurvival members of the Bcl-2 family proteins. Indeed, this has been demonstrated by the BH3-mimetics ABT-737 (1)(Oltersdorf, et al., 2005) and its orally available derivative ABT-263 (2; navtioclax)(Tse, et al., 2008) which bind to Bcl-2, Bcl-X<sub>L</sub> and Bcl-w. As expected, ABT-737 and ABT-263 induce apoptosis in tumor cells that are dependent on Bcl-2 and Bcl-X<sub>L</sub>. More recently, a selective Bcl-2 inhibitor was discovered (ABT-199) that also demonstrates the utility of inhibitors of the Bcl-2 family.(Souers, et al., 2013) Indeed, Navitoclax and ABT-199 have shown efficacy in several clinical trials in patients with lymphoid malignancies that are believed to be Bcl-2 dependent. (Choo, et al., 2014; Roberts, et al., 2012; Tse, et al., 2008) However, there are some cancers that cannot be treated by these compounds alone. Several studies have shown that upregulation of Mcl-1 is a key factor in the development of resistance to ABT-737 and ABT-263 resistance in several tumor types.(Konopleva, et al., 2006; Tahir, et al., 2007; Mark F van Delft, et al., 2006)

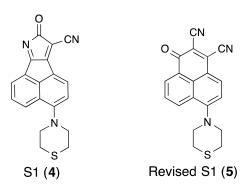


Mcl-1 has a number of functions and features that make it unique among the anti-apoptotic Bcl-2 family members. Mcl-1 is essential for early embryogenesis(Rinkenberger, et al., 2000) as well as the development and maintenance of lymphocytes(Dzhagalov, et al., 2008; Opferman, et al., 2003), neurons(Arbour, et al., 2008), synovial fibroblasts(Liu, et al., 2005) and hematopoietic stem cells(Opferman, et al., 2005). Mcl-1 is also unique in that it has a very short half-life of <1–4 h, depending on cellular conditions(Yang-Yen, 2006), and multiple pathways tightly regulate Mcl-1 transcription, translation, and degradation. (Thomas, et al., 2010) Structurally, Mcl-1's N-terminus also differs from that of the other anti-apoptotic Bcl-2 proteins in that it contains two PEST (proline/glutamic acid/serine/ threonine–containing) regions.(Germain & Duronio, 2007) Indeed, the N-terminal region may serve as a regulatory domain for Mcl-1's rate of turnover, localization, and

phosphorylation, and may thus provide a mechanism to rapidly fine-tune the expression of Mcl-1 in response to environmental and cellular input.(Thomas, et al., 2010)

There is a lot of evidence to suggest that Mcl-1 is an important cancer target. For example, Mcl-1 overexpression is one of the most common genetic aberrations observed in human cancer, (Beroukhim, et al., 2010; G. Wei, et al., 2012) including lung(L. X. Song, et al., 2005), breast(Ding, et al., 2007), prostate(Krajewska, et al., 1996), pancreatic(Miyamoto, et al., 1999), ovarian and cervical cancers(Brotin, et al., 2010), as well as melanoma(Boisvert-Adamo, et al., 2009) and leukemia(Andersen, et al., 2005; Derenne, et al., 2002; Kang, et al., 2008). Furthermore, Mcl-1 overexpression induces resistance against the aforementioned Bcl-2-inhibitors, as well as a number of widely used anticancer therapies including paclitaxel, (Wertz, et al., 2011) vincristine (Wertz, et al., 2011) and gemcitabine (S.-H. Wei, et al., 2008). Moreover, RNA-mediated knockdown of Mcl-1 has shown tumor growth inhibition and cell death in Mcl-1 overexpressing lung, colon, ovarian and lymphoma cells. (Akgul, 2008; Boisvert-Adamo, et al., 2009; W. Chen, et al., 2010; Chetoui, et al., 2008; Hauck, et al., 2009; Keuling, et al., 2009; Konopleva, et al., 2006; Lucas, et al., 2012; Moulding, et al., 2000; Qin, et al., 2006; Thallinger, et al., 2003) Silencing of Mcl-1 also restores sensitivity in chemoresistant cells.(Lin, et al., 2007; Meng, et al., 2007; Taniai, et al., 2004) Given these data, Mcl-1 represents a very promising cancer target. An Mcl-1 inhibitor would be expected to be useful as a single agent against cancers that depend on Mcl-1 for survival and in combination with other drugs where Mcl-1 overexpression is the major resistance factor.

This Review focuses on the current state of Mcl-1 inhibitors. Although peptide-based inhibitors have been described, including stapled alpha-helix of Bcl-2 domains (SAHB) (Muppidi, et al., 2012; Stewart, et al., 2010), alpha-/beta-peptide foldamers(Smith, et al., 2013) and reverse BH3 (rBH3) peptides(Placzek, et al., 2011), we focus this review on small molecule inhibitors that have been reported to function as BH3-mimetics. As proposed by Lessene and coworkers true BH3-mimetics should exhibit Bak/Bax-dependant biological activity and high-affinity binding to at least one Bcl-2 family pro-survival protein, specifically Mcl-1 in the case of this review.(Lessene, et al., 2008) Therefore, Obatoclax (GX15-070)(Nguyen, et al., 2007), a putative pan-inhibitor that binds to all Bcl-2 family pro-survival proteins with low affinity(Nguyen, et al., 2007; Tse, et al., 2008) and kills wild-type and Bak/Bax-deficient cells with equal potency(Vogler, et al., 2009), as well as other chemical entities that exert their biological activities through possible off-target or unknown mechanisms of action are not included in this review.(Billard, 2013) In addition, this review does not cover molecular entities disclosed exclusively within patents. This information has been reviewed in detail elsewhere(Bajwa, et al., 2012).



Efforts aimed at designing novel DNA intercalating agents led to the discovery of S1 (4), a rigid, planar chromophore, which exhibited anti-tumor activity yet surprisingly lacked the ability to intercalate into DNA.(Zhang, et al., 2007) The structure of S1 was originally reported as possessing an 8-oxo-8*H*-acenaphtho[1,2-*b*]pyrrole-9-carbonitrile (4) backbone. However, the structure was later revised by Song et al. to a 1-oxo-1H-phenalene-2,3dicarbonitrile (5).(T. Song, Chen, et al., 2013) S1 has been touted as a pan-Bcl-2 family inhibitor as it has been reported to bind to Mcl-1 ( $K_d = 58$  nM, Bid-BH3, FPA) and Bcl-2  $(K_d = 310 \text{ nM}, \text{Bid-BH3}, \text{FPA})$ , disrupt Bax/Bcl-2 and Bak/Mcl-1 complexes in a dose- and time-dependent manner, and induce Bax/Bak-dependent apoptosis.(Zhang, et al., 2010) However, Eastman and co-workers suggest that S1 does not function as a pan-Bcl-2 inhibitor in cells but rather it upregulates the BH3-only protein Noxa, which inhibits Mcl-1 and leads to its degradation and an increase in cellular sensitivity to apoptosis.(Albershardt, et al.) Furthermore, S1 has been shown to rapidly increase reactive oxygen species (ROS) which leads to the induction of endoplasmic reticulum (ER)-mediated stress.(Soderquist, et al., 2013) Finally, Zhong et al. have reported that S1-mediated cell death may be in part due to the induction of autophagy through (ER) stress and disruption of the interaction of Beclin 1 with Bcl-2.(Zhong, et al., 2012) Thus, S1-mediated cell death could be caused by several different mechanisms.

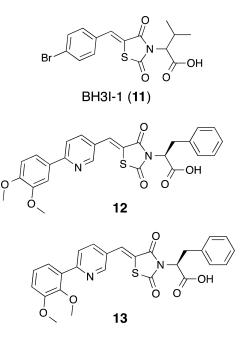
#### 3. S1 Derivatives

Zhang and co-workers have disclosed a number of S1 derivatives using scaffold hopping approaches. Based on their NMR-derived model for the binding of S1 to Mcl-1, Song et al. selected the C3 and C6 positions of S1 (**5**, Fig. 1) for synthetic elaboration in order to extend further along the hydrophobic BH3-binding groove.(T. Song, Li, et al., 2013; T. Song, et al., 2014) Structure–activity studies at the C3 and C6 positions led to the identification of **6**, which binds Mcl-1 (IC<sub>50</sub> = 10 nM, Bim-BH3, ELISA) and Bcl-2 (IC<sub>50</sub> = 20 nM, Bim-BH3, ELISA) with increased affinity relative to S1 (Mcl-1, IC<sub>50</sub> = 95 nM; Bcl-2, IC<sub>50</sub> = 715 nM, Bim-BH3, ELISA). Preliminary cell studies indicate that compound **6** exhibits increased apoptotic activity compared to S1.

Additionally, Zhang and co-workers employed a fragment-based strategy to identify two novel Mcl-1 inhibitors. As shown in Figure 2, screening of several fragments derived from the dissection of the unrevised S1 structure using a fluorescence polarization assay led to the

identification of two novel hits: a 2-cyanoacetamide (7)(Zhang, Song, et al., 2013), and a 2-hydroxynicotinonitrile (9)(Zhang, Liu, et al., 2013). Synthetic elaboration of these molecules yielded compounds **8**, which is 6-fold more potent than S1, and **10**, which is equipotent to S1.

#### 4. A\*STAR Compounds



By synthesizing and screening a small, focused library of pyridine-based rhodanine derivatives of BH3I-1 (11)(Lugovskoy, et al., 2002), that binds to Bcl-2 at the BH3 site, Bernardo et al. identified two constitutional isomers, structurally-differentiated by the relative position of two methoxy groups. Compound 12 binds exclusively to Mcl-1 ( $K_d = 10 \mu$ M, ITC), and compound 13 binds Mcl-1 ( $K_d = 0.25 \mu$ M, ITC) with greater affinity and also binds to Bcl-X<sub>L</sub> ( $K_d = 3.4 \mu$ M, ITC). (Bernardo, et al., 2010) While NMR-guided docking studies suggest that compounds 12 and 13 bind to the BH3-binding groove, the interaction(s) responsible for the difference in selectivity observed as a result of such a subtle structural change have not yet been identified. Although Bernardo and coworkers did not provide data validating the biological activity of the these compounds, compounds 12 and 13 were evaluated alongside other putative Mcl-1-inhibitors by Varadarjan et al. (Varadarajan, et al., 2013) This follow-up study determined that neither compound killed cells, even at high concentrations (<30 nM), as a single agent or in combination with ABT-737.

#### 5. Compounds from Takeda Pharmaceutical Company

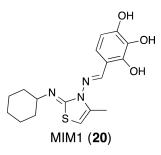
The desire to overcome Mcl-1 over-expression in cancer cells treated with Bcl-2 family inhibitors has prompted interest in the discovery of dual inhibitors, such as an Mcl-1/Bcl-X<sub>L</sub> dual inhibitor. To this end, Tanaka et al. analyzed known inhibitors of Mcl-1 such as compound **14**(Elmore, et al., 2008) (Fig. 3) and the reported Bcl-X<sub>L</sub> inhibitor, ABT-737, for two complimentary binding motifs. Merging of the two scaffold fragments, **15** and the

arylsulfonamide portion of ABT-737, resulted in compound **17**, which binds to both Mcl-1 ( $IC_{50} = 88$  nM, Bid-BH3, TR-FRET) and Bcl-  $X_L$  ( $IC_{50} = 3.7$  nM, Bid-BH3, TR-FRET). (Tanaka, et al., 2013) Compound **16**, the des-methyl analog of **17**, was cocrystallized with Mcl-1 (PDB ID 3WIY) and Bcl-  $X_L$  (PDB ID 3WIZ) and, for the most part, confirmed the contribution of each half of the molecule for binding to the respective anti-apoptotic proteins (Fig. 4). The portion of the molecule derived from ABT-737 does not appear to contribute much towards the binding of Mcl-1.

#### 6. University of Michigan Compounds

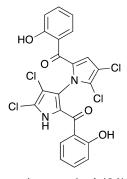
Abulwerdi et al. identified *N*-(4-hydroxynaphthalen-1-yl)arylsulfonamide **18** (Fig.5) as part of a high-throughput screen (HTS) of 53,000 synthetic small molecules using a fluorescence polarization assay.(Abulwerdi, et al., 2014) Aided by NMR-based docking models and SAR studies, elaboration of the initial hit led to compound **19**, which exhibits selective affinity for Mcl-1 ( $K_d = 180$  nM, Bid-BH3, FPA) over other pro-survival Bcl-2 family members (9- to 59-fold). Experiments in leukemia cell lines show that compound **19** inhibited cell growth and activated caspase-3 in a dose-dependent manner. Further, compound **19** shows moderate cytotoxicity against Bak/Bax-deficient cells, suggesting that apoptosis is Bak/Bax-dependent.

#### 7. MIM1



Cohen and coworkers screened a library of over 70,000 small molecules in a highthroughput competition fluorescence polarization-based assay for their ability to displace a fluorescently labeled Mcl-1 SAHBA(Stewart, et al., 2010) from Mcl-1.(Cohen, et al., 2012) In addition, the library was counter-screened for activity against Bcl- X<sub>L</sub>, and the resulting hits were excluded from the hit pool to select compounds that selectively bind to Mcl-1. Following a series of increasingly stringent confirmatory assays, 28 compounds were progressed into liposome- and cell-based assays. Mcl-1 Inhibitor Molecule 1 (**20**; MIM1) was ultimately selected based on a combination of biological and physicochemical properties. MIM1 was shown to bind selectively to Mcl-1 with modest affinity (IC<sub>50</sub> = 4.78  $\mu$ M, Bid-BH3, FPA), trigger Bax/Bak-dependent apoptosis in leukemia cells, and to act in concert with ABT-737 by down-regulation of Mcl-1. However, a recent evaluation of putative Mcl-1 inhibitors disclosed that MIM1 induced Bak-dependent apoptosis only at high concentrations (>10  $\mu$ M) and that it failed to induce apoptosis in Mcl-1-, Bcl-2- and Bcl-X<sub>L</sub>-dependent cell lines.(Varadarajan, et al., 2013) Taken together, these data suggest that MIM1's inhibitory effects may be cell-line dependent.

#### 8. Marinopyrrole A (Maritoclax)



marinopyrrole A(21)

Marinopyrrole A (**21**), a natural product isolated from an obligate marine *Streptomyces*, has received considerable attention due to its promising antibiotic activity against methicillin-resistant *Staphylococcus aureus* (MRSA).(Haste, et al., 2011; Hughes, et al., 2009; Nicolaou, et al., 2011) Marinopyrrole A, which was named Maritoclax, was found to also selectively bind to Mcl-1 (IC<sub>50</sub> = 10.1  $\mu$ M, Bim-BH3, ELISA), decrease Mcl-1 protein levels via proteasomal degradation and induce apoptosis in Mcl-1-dependent, but not Bcl-2- and Bcl-X<sub>L</sub>-dependent, leukemia(Doi, et al., 2012) and melanoma cells(Pandey, et al., 2013). However, Eichhorn and coworkers disclosed that marinopyrrole A was equally effective against Bcl-2-dependent leukemia cells compared to Mcl-1-dependent cells, and that treatment with marinopyrrole A had no effect upon Mcl-1 expression levels.(Eichhorn, et al., 2013) Furthermore, the follow-up report indicates that marinopyrrole A does not lead to the degradation of Mcl-1 as no affect on Mcl-1 expression levels was observed upon treatment with this compound.

#### 9. Compounds from Eutropics Pharmaceuticals

Richard et al. screened a library of 315,000 compounds in a high-throughput fluorescence polarization-based assay for the ability of compounds to inhibit Mcl-1.(Richard, et al., 2013) A subsequent FP assay was used as a counter-screen to the primary assay to identify compounds that displayed selectivity for Mcl-1 over Bcl-X<sub>L</sub>. Evaluation of the hits identified in the HTS campaign for their synthetic tractability and quality gave the team their lead compound, the 7-hydroxyquinoline **22** (Fig. 6). Analysis of compound **22** identified a number of perceived liabilities, namely, the carboxylic acid and the 4-chloro groups, which were subsequently modified or eliminated. Synthetic modification and further SAR studies resulted in compound **23**, which yielded IC<sub>50</sub>s of 310 nM for Mcl-1 and 40  $\mu$ M for Bcl-X<sub>L</sub> (Bim-BH3, FPA). Compound **23** was found to induce dose-dependent cytochrome c release and antiproliferative activity against several Mcl-1 dependent cell lines. Furthermore, the authors demonstrate that the cellular activity and selectivity of cell lines correlates with the degree of mitochondrial priming as determined by BH3 profiling(Certo, et al., 2006).

#### 10. AbbVie Compounds

An NMR-based fragment screen against Mcl-1 of a 17,000 fragment library conducted by a team at AbbVie revealed a number of hits. Two of these hits were selected for additional studies based on the criteria of binding efficiency and synthetic tractability: (1) aryl sulfonamide 24 and (2) salicylic acid 26 (Fig. 7). (Petros, et al., 2014) In the absence of high resolution crystal structures, the binding modes for the respective fragments were determined by alternate means. The binding mode for the aryl sulfonamide fragment 24 was determined with the aid of nuclear Overhauser effect (NOE) restraint-driven docking and, in the case of the salicylic acid fragment **26**, the binding mode was elucidated by simply docking the fragment into the BH3-binding groove guided by a single electrostatic-contact restraint. The aryl sulfonamide fragment was elaborated into compound 25, which exhibited an IC<sub>50</sub> of 30 nM (Noxa-BH3, FPA) against Mcl-1, and the salicylic acid fragment was elaborated into compound 27, which yielded an IC<sub>50</sub> of 570 nM (Noxa-BH3, FPA). Cocrystal structures of aryl sulfonamide 28 (PDB ID 40Q5) and salicylate 29 (PDB ID 40Q6) were subsequently obtained (Fig. 8). Notably, the acid moieties of both 28 and 29 are fixed in the same region, and the hydrophobic naphthyl moiety of the more potent aryl sulfonamide 28 is located deep within the hydrophobic pocket of Mcl-1.

# 11. Vanderbilt University Compounds

An NMR-based screen of a large fragment library (>13,800 compounds) by Friberg and coworkers led to the identification of several chemically distinct classes of fragment hits. Two of these hits, 5,6-ring-fused heterocyclic carboxylic acids, and a group of hydrophobic aromatics linked to a polar headpiece. (Friberg, et al., 2013) NMR-guided docking of the fragments revealed that the fragments bound in a mutually exclusive fashion in two closely situated binding sites within a large hydrophobic pocket. Based on this structural information, two fragments were merged together to produce compounds with markedly improved binding affinities (e.g., **30** and **31**, Fig. 9). Further analoging led to the discovery of the indole-2-carboxylic acid 33, which was a potent inhibitor of Mcl-1 ( $K_d = 55$  nM, Bak-BH3, FPA) that displayed a 16-fold selectivity over Bcl-2 and 270-fold over Bcl-X<sub>I</sub> (870 nM and  $>15 \mu$ M, respectively, Bak-BH3, FPA). Cocrystal structures of compounds 32 (PDB ID 4HW3) and 33 (PDB ID 4HW2) bound to Mcl-1 confirmed that the merged compounds occupy both pockets identified by the initial fragments and that the carboxylic acid moiety interacts with R263 (Fig. 10). Further analysis of the X-ray structure aided in rationalizing the SAR observed in the merged series and illuminated opportunities to improve the potency by accessing additional binding sites.

# 12. Conclusion

Significant effort has been directed towards the discovery of Bcl-2 and Bcl- $X_L$  inhibitors which has culminated in a number of very potent Bcl-2 family inhibitors such as ABT-737(Oltersdorf, et al., 2005), navitoclax (ABT-263)(Tse, et al., 2008), and ABT-199(Souers, et al., 2013). The remarkable in vitro and in vivo biological activities observed preclinically and in the clinic clearly demonstrates the feasibility of targeting the Bcl-2 family proteins with small molecule inhibitors. In contrast to the advances made in

drugging Bcl-2 and Bcl- $X_L$ , the discovery of Mcl-1 inhibitors has lagged behind. This is unfortunate, since Mcl-1 appears to also be a promising cancer target. Encouragingly, the last half-decade has witnessed a rapid surge of interest towards the discovery of Mcl-1 inhibitors. This has resulted in a significant number of small molecule BH3-mimetics comprising a range of structurally diverse chemotypes. There remain, however, questions regarding the chemical liabilities, i.e., the inclusion of possible "bad actors" (Baell, 2010), and the non-drug-like physicochemical properties of some of the reported inhibitors. Also, the lack of in vivo data for the majority of proposed Mcl-1 inhibitors is striking.

The moderate potency of Mcl-1 inhibitors reported to date (Table 1) is likely responsible for the lack of convincing in vivo activity. It is tempting to speculate that the experiences observed in the discovery of Bcl-2 and Bcl- $X_L$  inhibitors(Oltersdorf, et al., 2005; Souers, et al., 2013; Tse, et al., 2008) will be reflected in the Mcl-1 inhibitors. By comparison, a clinically useful Mcl-1 inhibitor may need to exhibit in vitro affinities approaching the low picomolar range. At present, there are no reported Mcl-1 inhibitors, peptide or small molecule-based, exhibiting this level of affinity for Mcl-1.

The discovery of potent Mcl-1 inhibitors is a unique challenge due to key structural differences between the BH3-binding grooves of Mcl-1 and Bcl-2 proteins. Unlike Bcl-2, the P2 pocket of Mcl-1 (Fig. 11), as confirmed by cocrystal structures of small molecule inhibitors bound to Mcl-1(Friberg, et al., 2013; Petros, et al., 2014; Tanaka, et al., 2013), has a high degree of plasticity. Indeed, the P2 pocket of Mcl-1 expands to form a large, hydrophobic cavity in the presence of ligands. The P4 pocket of Mcl-1, however, is less well defined and more solvent exposed.(Czabotar, et al., 2007) As such, this pocket is shallower and less hydrophobic than that found in Bcl-X<sub>L</sub>. The importance of the P2 pocket in Mcl-1 has been confirmed experimentally by the results of two NMR-based fragment screening campaigns against Mcl-1 conducted by Friberg et al. and Petros et al. (Friberg, et al., 2013; Petros, et al., 2014). These two studies disclosed that fragments, bind exclusively in P2. In contrast, the NMR-based screen leading up to the discovery of ABT-737 resulted in the discovery of two fragments bound to two distinct areas of Bcl-XL, P2 and P4.(Oltersdorf, et al., 2005) Future efforts to develop potent and specific ligands for Mcl-1 will need to fully exploit the binding opportunities available within the proximity of the P2 pocket as opportunities to gain significant contributions towards affinity from interactions outside of this region appear, at present, to be limited.

Significant advancements have been made over the past few years towards the discovery of Mcl-1 inhibitors. However, the Mcl-1 inhibitors described to date are still at a very early stage. Given the concerns described above, significant challenges still remain. With the recent increase in interest it is likely that these challenges will be overcome, and these efforts will lead to novel Mcl-1 inhibitors for the treatment of cancer.

#### Abbreviations

Bad	Bcl-2-associated death promoter
Bak	Bcl-2 homologous antagonist/killer

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Bax	Bcl-2 associated X
Bcl-2	B-cell lymphoma-2
BH	Bcl-2 homology
BH3	Bcl-2 homology domain 3
Bcl-XL	B-cell lymphoma-extra large
Bim	Bcl-2 interacting mediator
Bfl-1/A1	Bcl-2-related protein A1
Mcl-1	myeloid cell leukemia-1
Noxa	phorbol-12-myristate-13-acetate-induced protein 1
Puma	p53 upregulated modulator of apoptosis
SAHB	stapled alpha-helix of Bcl-2 domains
SAR	structure activity relationships
SPR	surface plasmon resonance
tBid	truncated BH3-interacting domain death agonist

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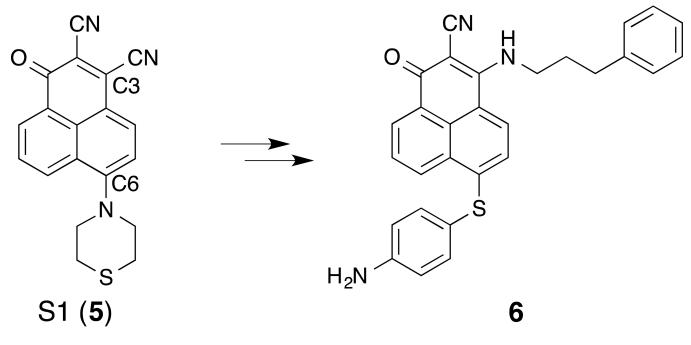
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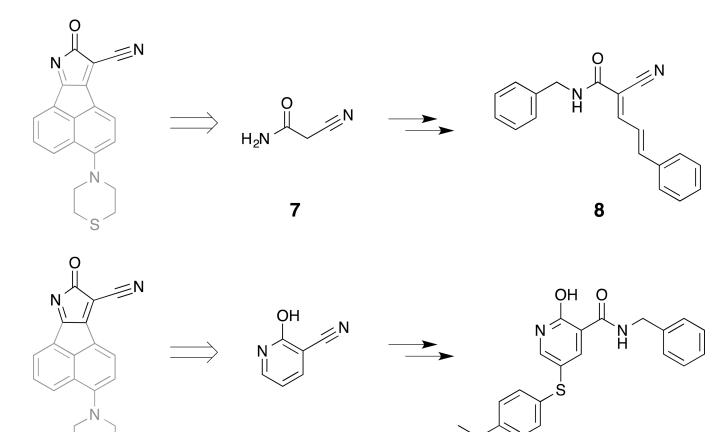
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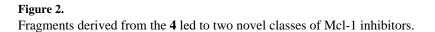




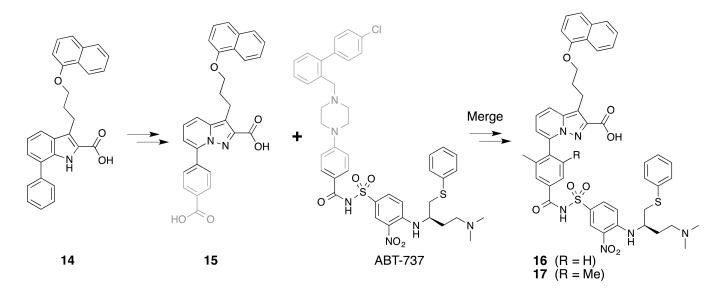
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#### Figure 3.

Merging of fragments derived from two known inhibitors of Mcl-1 and Bcl- $X_L$  resulted in novel dual-inhibitors.

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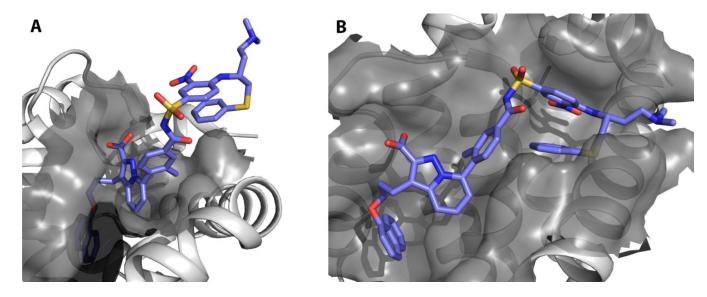
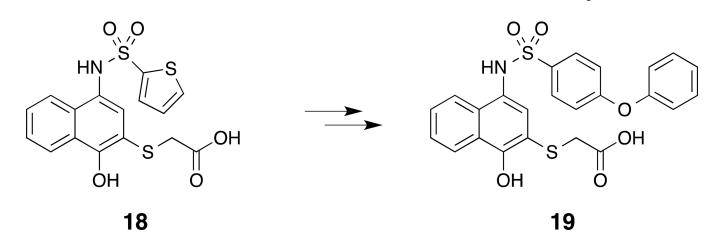
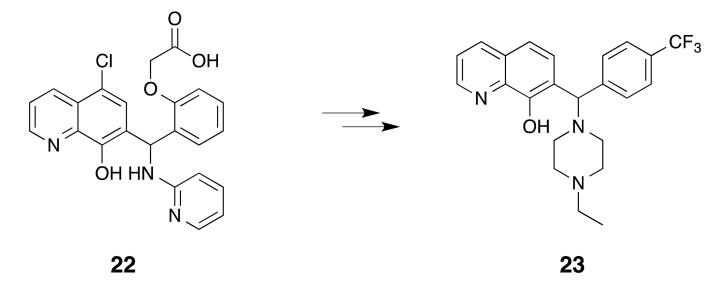


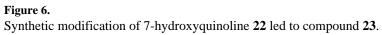
Figure 4. Crystal structures of 15 bound to Mcl-1 (A) and to Bcl- $X_L$  (B).



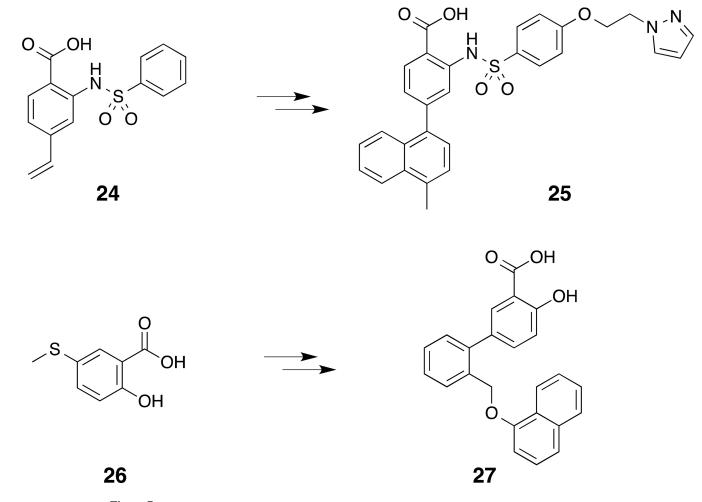


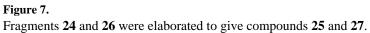
Discovery of an *N*-(4-hydroxynaphthalen-1-yl)sulfonamide Mcl-1 inhibitor.





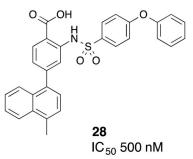
Belmar and Fesik



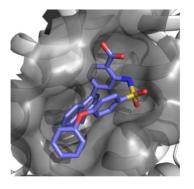


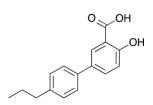
Belmar and Fesik

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**29** ΙC<sub>50</sub> 3.3 μΜ

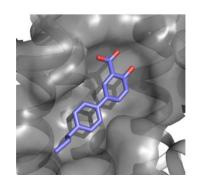
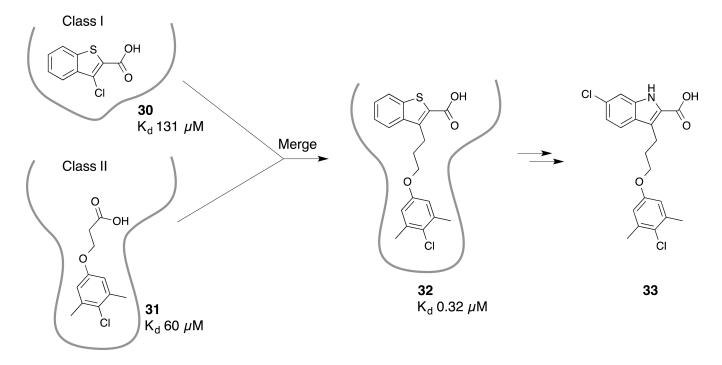
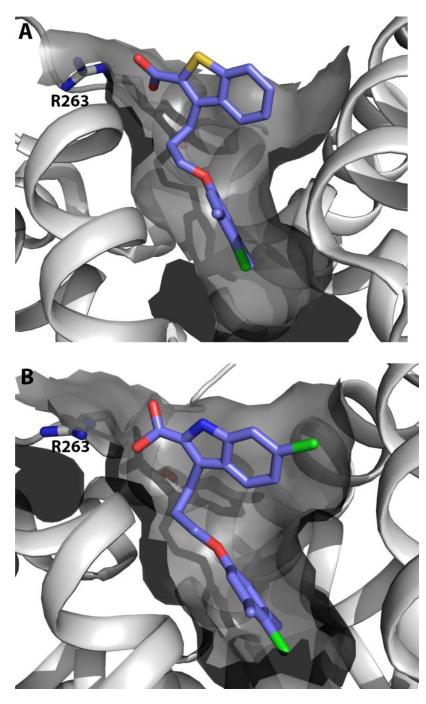


Figure 8. Cocrystal structures of aryl sulfonamide 28 and salicylate 29 with Mcl-1.



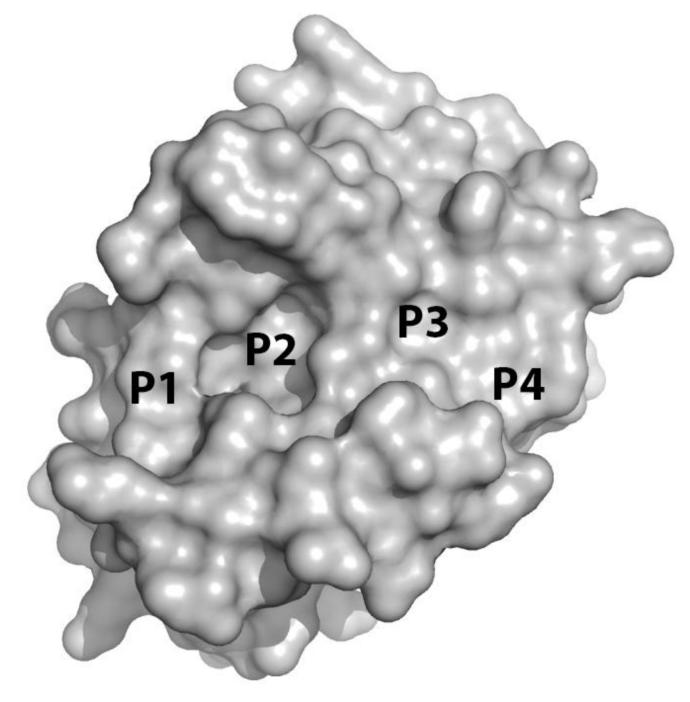
#### Figure 9.

Merging fragments from two distinct classes produced a compound with significantly improved binding affinity.



#### Figure 10.

Cocrystal structures of benzothiophene-2-carboxylic acid **32** (A) and indole-2-carboxylic acid **33** (B).



**Figure 11.** X-ray structure of Mcl-1 (PDB ID 3MK8).

#### Table 1

#### Small molecule Mcl-1 inhibitors.

	Inhibi	tion/Selectivity		
Compound	Mcl-1	Bcl-2	Bcl-X <sub>L</sub>	Reference
S1 (5)	K <sub>d</sub> 58 nM	K <sub>d</sub> 310 nM	NA	T. Song, Chen, et al. (2013)
6	IC <sub>50</sub> 10 nM	IC <sub>50</sub> 20 nM	NA	T. Song, et al. (2014)
8	K <sub>d</sub> 160 nM	NA	NA	Zhang, Song, et al. (2013)
10	IC <sub>50</sub> 54 nM	NA	NA	Zhang, Liu, et al. (2013)
12	$K_d \ 10 \ \mu M$	NA	$K_d\!>\!\!750~\mu M$	Bernardo, et al. (2010)
13	K <sub>d</sub> 250 nM	NA	$K_d 3.4 \ \mu M$	Bernardo, et al. (2010)
16	IC <sub>50</sub> 610 nM	NA	IC <sub>50</sub> 4.4 nM	Tanaka, et al. (2013)
17	IC <sub>50</sub> 88 nM	NA	IC <sub>50</sub> 3.7 nM	Tanaka, et al. (2013)
19	K <sub>d</sub> 180 nM	$K_d$ 7.6 $\mu M$	K <sub>d</sub> 10.6 μM	Abulwerdi, et al. (2014)
MIM1 (20)	$IC_{50}4.8\mu M$	NA	$IC_{50}\!>\!\!50\mu M$	Cohen, et al. (2012)
marinopyrrole A (21)	$IC_{50}10\mu M$	NA	$IC_{50} > 80 \ \mu M$	Doi, et al. (2012)
23	IC <sub>50</sub> 310 nM	NA	$IC_{50}40\mu M$	Richard, et al. (2013)
25	IC <sub>50</sub> 30 nM	NA	NA	Petros, et al. (2014)
27	IC <sub>50</sub> 570 nM	NA	NA	Petros, et al. (2014)
33	K <sub>d</sub> 55 nM	K <sub>d</sub> 870 nM	$K_d\!>\!\!15~\mu M$	Friberg, et al. (2013)

Abbreviations: NA, not available at time of writing.

\*Determined using varying competitive binding assays and ITC.