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Development of Small Molecule Non-peptide Formyl Peptide Receptor (FPR) Ligands and Molecular Modeling of Their Recognition

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Abstract: Formyl peptide receptors (FPRs) are G protein-coupled receptors (GPCRs) expressed on a variety of cell types. These receptors play an important role in the regulation of inflammatory reactions and sensing cellular damage. They have also been implicated in the pathogenesis of various diseases, including neurodegenerative diseases, cataract formation, and atherogenesis. Thus, FPR ligands, both agonists and antagonists, may represent novel therapeutics for modulating host defense and innate immunity. A variety of molecules have been identified as receptor subtype-selective and mixed FPR agonists with potential therapeutic value during last decade. This review describes our efforts along with recent advances in the identification, optimization, biological evaluation, and structure–activity relationship (SAR) analysis of small molecule non-peptide FPR agonists and antagonists, including chiral molecules. Questions regarding the interaction at the molecular level of benzimidazoles, pyrazolones, pyridazin-3(2*H*)-ones, N-phenylureas and other derivatives with FPR1 and FPR2 are discussed. Application of computational models for virtual screening and design of FPR ligands is also considered.

1. INTRODUCTION

Formyl peptide receptors (FPRs) are G protein-coupled receptors (GPCR) that play an important role in leukocyte activation and chemotaxis [1]. These receptors were originally identified for their ability to bind and be stimulated by *N*-formyl peptides, which are produced by bacteria but can also be released from damaged mitochondria during tissue injury [2-4]. Phylogenetic analysis has revealed that FPRs belong to a family of chemosensory GPCR [5], and structurally related members of these receptors expressed in the vomeronasal organs of mammals appear to have an olfactory function associated with the identification of pathogenic states [6, 7]. It has been proposed that FPRs act as sensors of pathogen-derived products that recruit leukocytes to sites of infection, where these cells exert antibacterial effector functions and clear cell debris [8, 9]. Indeed, targeted disruption of the fpr1 gene coding for the mouse counterpart of human FPR1 renders mice more susceptible to bacterial infection without other significant phenotypic alterations [10], supporting the role of FPRs in innate host defense based on recognition of bacterial-derived agonists. However, the expression pattern of FPRs in nonphagocytic cells suggests that these receptors also participate in functions other than innate immunity and may represent unique targets for therapeutic

drug design [9, 11-13]. For example, it was recently found that aging Fpr1 knockout mice develop spontaneous lens degeneration, suggesting FPR agonists may be useful in drug therapy for cataracts [14].

In humans, there are three FPR isoforms: FPR1 and FPR2 exhibiting 69% amino acid homology to each other, and FPR3 with 56% amino acid sequence identity to FPR1 and 83% to FPR2 [1]. These receptors are expressed on a variety of cell types, including neutrophils, macrophages, T lymphocytes, immature dendritic cells, epithelial cells, hepatocytes, fibroblasts, astrocytes, microvascular endothelial cells, and platelets [1, 15-17]. In mice, the FPR family consists of eight genes, including genes for mFpr1, mFpr2, and mFpr-rs1, which are expressed in leukocytes. Recently, mFpr1/mFpr2 was found to be expressed in dendritic and glial cells [8, 18-20]. Five distinct Fprs, including mFpr-rs1, mFpr-rs3, mFpr-rs4, mFpr-rs6, and mFpr-rs7, are expressed in mouse vomeronasal sensory neurons [5]. Mouse Fpr1 has a 76% sequence identity to human FPR1; however, its putative ligand-binding domains resemble those of human FPR2 rather than FPR1 [8, 21].

Being expressed in the majority of white blood cells, FPRs play an important role in the regulation of inflammatory reactions and cellular dysfunction [15, 22]. A variety of endogenous and pathogen-associated molecules can bind FPR1 and FPR2 with high affinity. Several studies have described intestinal proinflammatory properties for *N*-formyl peptides (e.g., *f*MLF), such as in colonic

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inflammation *in vivo* [23-25], suggesting a possible role in the etiology of inflammatory bowel disease in humans when bacterial chemotactic peptides breach mucosal defenses. Furthermore, involvement of ƒMLF in the pathogenesis of pouchitis, ulcerative colitis, and Crohn's disease is also suggested [26-28]. Fehr *et al.* [29] reported that ƒMLF could substitute for the place of the second endotoxin injection in provoking the generalized Shwartzman reaction in rabbits. When injected into rabbits, ƒMLF causes dose-dependent transient hypotension, as well as neutropenia, thrombocytopenia, and a decrease in systemic vascular resistance [30, 31]. Moreover, ƒMLF causes a variable degree of bronchoconstriction after inhalation of this peptide by rabbits [32]. Similarly, leucopenia occurs rapidly after inhalation of ƒMLF by humans and could contribute to bronchial inflammation during bacterial infection [33].

FPR2 behaves as a "pattern recognition" receptor that can be activated by a wide variety of unrelated ligands. These include acute-phase serum amyloid A (SAA), annexin 1, urokinase plasminogen activator receptor (uPAR), the V3 region of HIV-1 envelope glycoprotein gp120, a 42-amino-acid form of β-amyloid, human prion peptide, cathelicidin LL-37, and other molecules (reviewed in [1, 11, 34, 35]). Some of these endogenous FPR2 agonists may play pathophysiological roles. For example, binding of SAA to FPR2 contributed to the destruction of bone and cartilage via the promotion of synoviocyte hyperplasia and angiogenesis in rheumatoid arthritis [36]. Recently, it was proposed that FPR2 could be involved in pathogenic mechanisms of atherogenesis via FPR2-dependent SAA-stimulated foam cell formation [37, 38]. Other examples of FPR involvement in multiple diseases have been recently reviewed [39]. These authors concluded that FPRs form a very attractive family of pharmacological targets and suggested that "the studies of specific agonists and antagonists for FPRs will be of great significance for better understanding of the roles of these receptors in physiology and pathophysiology [39]."

2. THERAPEUTIC EFFICACY OF FPR LIGANDS

Various approaches to activate or inhibit FPR-dependent pathways have been considered for therapeutic development. For example, antagonists that inhibit binding of FPR agonists decrease leukocyte chemotaxis and can potentially diminish release of pro-inflammatory molecules. In addition, some of therapeutic effects of FPR agonists may be related to homo- and/or cross-desensitization mechanisms. Finally, an integral role of FPR agonists in promoting the resolution of inflammatory reactions has been demonstrated [40, 41].

There is evidence that bioactive ligands acting as FPR agonists or antagonists might serve as useful therapeutics in host defense and as immunomodulatory activators to enhance selective innate immune responses in order to reduce detrimental effects associated with inflammation, infectious diseases, and cancer [42-45]. Various endogenous and synthetic peptide FPR agonists have been used to study the potential therapeutic efficacy in models of pathological processes. For example, FPR2 agonist, annexin 1 fragment 2-26 (Anxa1$_{2-26}$), reduced the lipopolysaccharide (LPS)-induced cerebrovascular inflammatory response in a murine model [46], significantly enhanced gastric ulcer healing [47], and

prevented reperfusion-induced myocardial dysfunction in rats [48]. In addition, both Anxa1$_{2-26}$ and ƒMLF induced antinociceptive effects in mice [49]. The FPR2 agonist CGEN-855A (21-amino acid peptide) displayed anti-inflammatory activity in a mouse air pouch model and provided protection against ischemia-reperfusion-mediated injury to the myocardium in both murine and rat models [50]. It has also been suggested that FPR agonists could be utilized as anti-HIV therapeutics/immunoregulators to mobilize phagocytic leukocytes in HIV/AIDS patients [51, 52]. One of most potent mixed-type FPR agonists, a D-methionine-containing hexapeptide WKYMVm, potently inhibited HIV-1 Env-mediated fusion and viral infection through heterologous desensitization of C-X-C chemokine receptor 4 (CXCR4) and C-C chemokine receptor 5 (CCR5), suggesting a novel approach to the development of anti-HIV-1 therapeutics [53]. WKYMVm also increased neutrophil bactericidal activity in chemotherapy-treated cancer patients [54], protected the host by enhancing bactericidal activity and inhibiting vital organ inflammation and apoptosis in a sepsis mouse model [55], and enhanced endogenous tumor necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL) gene expression with tumoricidal activity [56]. Furthermore, airway activation of FPRs with WKYMVm effectively prevented the development of allergic inflammation induced by inhalation of LPS-containing allergens. This effect was mediated by the inhibition of dendritic cell infiltration, maturation, and migration, as well as inhibition of both Th1 and Th17 polarization [57]. Based on localization of FPRs in leukocytes and in the central nervous system, these receptors have also emerged as promising therapeutic targets for the treatment of neurodegenerative diseases [58]. In addition, peptide agonists of FPR1 and FPR2 (i.e., ƒMLF and MMK-1, respectively) prevented alopecia in neonatal rats induced by the anticancer agent etoposide [59].

The most potent and receptor specific FPR1 antagonists described so far are the fungal hydrophobic cyclic peptides, cyclosporines A and H [60]. Although cyclosporine H attenuated the acute inflammatory response evoked by cigarette smoke [61] and blocked ƒMLF-induced analgesia [62], *in vivo* studies of cyclosporines should be interpreted carefully because their main therapeutic effects appear to involve signaling pathways unrelated to FPR1 [63]. Indeed, cyclosporin A, a relatively large molecule (1.2 kDa), inhibited the T-cell receptor signal transduction pathway via the formation of a cyclosporin A-cyclophilin complex, which in turn bound to and inhibited the Ca^{2+}-calmodulin dependent phosphatase calcineurin [64]. Cyclosporin A also inhibited formation and opening of the mitochondrial permeability transition pore [65]. Although cyclosporine H does not bind to immunophilin, this peptide is a potent inhibitor of the Ca^{2+}-calmodulin-dependent phosphorylation of elongation factor 2 (EF-2) [66].

Other known peptide FPR antagonists are Boc-MLF (also termed Boc-1), and Boc-FLFLFL (also termed Boc-2), and there are several reports of *in vivo* application of Boc-2 [46, 48, 67, 68]. For example, Anxa1$_{2-26}$-induced cardioprotection was abolished by Boc-2 [48]. Similarly, Boc-2 prevented the inhibitory effect of Anxa1$_{2-26}$ on neutrophil extravasation [68]. Recently, tryptophan containing dipeptide derivatives of Boc-2 were reported as FPR1 antagonists [69].

The number of novel synthetic peptide FPR ligands continues to increase, and there are a couple of excellent reviews in the past few years summarizing these molecules [11, 43, 58, 70-73]. However, peptides are difficult to make and administer as therapeutic agents, making small-molecule chemical compounds a better choice for future clinical development. Growing evidence supporting the anti-inflammatory and tissue-protective effects of FPR agonists and antagonists prompted us and other research groups to search for novel small-molecule ligands for these receptors. As result of these efforts, a great number of synthetic non-peptide FPR agonists and antagonists with a wide range of chemical diversity were found using different high-throughput platforms in screening of commercial libraries and/or by structure–activity relationship (SAR)-directed design and synthesis (e.g., [74-87]). These have great potential for development of clinically useful anti-inflammatory and immunomodulatory drugs [85]. The availability of structurally defined non-peptide small-molecule FPR ligands is clearly of substantial benefit in drug development and facilitating SAR analysis to model ligand binding features, which is somewhat difficult with peptide ligands.

In this review, we provide an overview of the current literature, perspectives regarding therapeutic potential of various FPR ligands, details on the discovery and design of novel small-molecule non-peptide FPR agonists and antagonists. Because there have been ongoing efforts in several laboratories to study "FPR–ligand" interaction, questions regarding molecular modeling of FPR recognition are also discussed.

3. SMALL-MOLECULE FPR AGONISTS AND THEIR MODELING

Although using the chemical structure of endogenous ligands is one strategy for design of synthetic GPCR agonists and antagonists, this strategy has not been exploited in the development of non-peptide FPR ligands. Indeed, only lipoxin A_4 (LXA_4) and bile acids have been reported to date as endogenous non-peptide FPR ligands [88, 89]. Although LXA_4 has been described as an anti-inflammatory mediator that exerts its effects through FPR2, the LXA_4 target has been a matter of debate, as LXA_4 analogues have been reported to be unable to signal through FPR2 [90-93]. In any case, most primary strategies for identifying new FPR agonists have been high-throughput screening (HTS), SAR analysis, and computer-aid drug design.

3.1. Benzimidazole Derivatives

HTS of a chemical library of synthetic small-molecule compounds identified two FPR1-specific agonists **1** and **2**, which have a common 2-(benzimidazol-2-ylsulfanyl)-*N*-phenyl-acetamide scaffold [79]. Both compounds activated chemotaxis in human neutrophils, and SAR analysis of 52 related derivatives revealed 17 additional FPR1-specific agonists and 16 mixed FPR1/FPR2 agonists [79, 82]. Selected FPR agonists **1-9** with the benzimidazole scaffold are shown in (Table **1**). It should be noted that all active derivatives contained either a 5-methoxy or 5-ethoxy group in the benzene moiety of the benzimidazole heterocycle, which was an essential feature for activity. Modification of

benzene ring **A** also had effects on activity and receptor specificity, although a wider range of modifications was tolerated in this ring, including such substituents in the *para* position as nitro (**1**), ethoxy (**2**), methoxy (**3** and **4**), chlorine (**5**), bromine (**6**), methylthio (**7**), and methylcarboxyl (**8**) (Table **1**). However, if the alkoxy chain on benzene ring **A** in **3** was elongated to four carbons, activity was lost. Introduction of an additional chlorine in compound **5** at the *meta* position resulted in complete loss of activity. Likewise, substitution of the *para* methoxy group in compounds **3** and **4** with trifluoromethoxy led to partial or complete loss of FPR1 agonist activity. All tested derivatives where benzene ring **A** contained fused 1,3-dioxolane or 1,4-dioxane rings were FPR agonists, although only compound **9** was specific for FPR1, and the other compounds with this feature were mixed FPR1/FPR2 agonists [82].

3.1.1. Molecular Docking of Benzimidazole Derivatives

In the absence of an experimentally determined structure of FPR1, homology modeling can provide a rational alternative to a reasonable 3D structure. The FPR1 homology model was created using the crystal structure of bovine rhodopsin, which has a sequence identity of 20% for 348 aligned residues that correspond to the seven transmembrane domains [82, 94]. The position of the ligand binding site in the homology model, based on cross-linking and mutagenesis studies, was found to be located in the upper region of a bundle comprising transmembrane helices 2, 5, 6, and 7 [95, 96] and was confirmed by docking studies with tetrapeptide Ac-QAWF, which is the shortest core structure of the annexin AI-derived peptide [94]. Since pre-docking studies indicated that this region is coincident with the ligand binding site, it was proposed that this feature is relevant to the modeling process [97] and justified use of the rhodopsin-based model as a template for the docking of novel small-molecule FPR1 agonists *vs.* the other known GPCR crystal structures currently available.

Key sub-areas of the FPR1 binding site include two channels (**A** and **C**), two cavities (**B** and **E**), and the bottom (**D**) [82] (see arrows in Fig. **1A**). Docking studies [82] showed that, most active FPR1-specific agonists **7** and **8** both had very similar benzimidazole orientations with their methoxy substituents H-bonded to Thr199 in channel **A** of the FPR1 binding site (Fig. **1B**). Compound **8** forms a H-bond of 1.5 kcal/mol with a key residue (Arg205), and this interaction was weaker than the H-bond formed between Arg205 and *f*MLF. Thirty seven of 43 related alkoxy-substituted benzimidazoles had methoxy or ethoxy oxygen atoms embedded in channel **A** of the FPR1 binding site or in cavity **B**, which is located behind the hydrophobic ledge formed by the isobutyl group of Leu198. Thirty-four of these benzimidazole compounds were active FPR1 agonists, demonstrating the importance of the ligand–receptor interactions in regions **A** and **B** for FPR1 agonist activity. As examples, positions of alkoxy groups in the binding site are shown in Fig. **1A** for FPR1 agonists **1**, **7**, and **8**.

3.2. Pyrazolones

Using a Ca^{2+} flux-based assay in $G_{\alpha15}$ and FPR1/FPR2 co-transfected CHO cells for HTS of a small-molecule

Table 1.   Agonist Activity of Benzimidazoles 1-9 [79, 82]
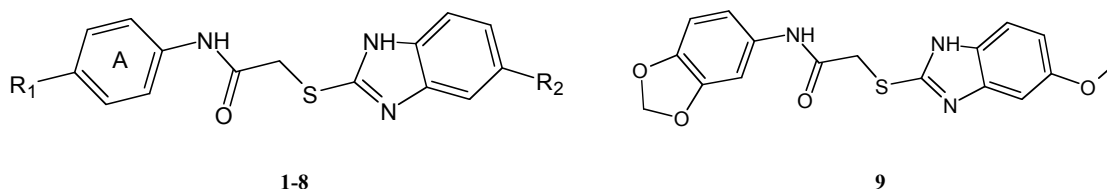
#	R₁	R₂	EC₅₀ (µM)ᵃ		
			FPR1	FPR2	PMN
1	NO₂	OCH₃	3.4	N.A.	0.4
2	OCH₂CH₃	OCH₃	21.5	N.A.	5.8
3	OCH₃	OCH₂CH₃	19.1	N.A.	0.6
4	OCH₃	OCH₃	1.7	5.1	0.3
5	Cl	OCH₃	1.6	6.0	0.7
6	Br	OCH₃	3.3	N.A.	1.8
7	SCH₃	OCH₃	2.0	N.A.	0.5
8	COOCH₃	OCH₃	1.5	N.A.	0.9
9			2.2	N.A.	2.6

ᵃEC₅₀ values were determined by measurement of Ca²⁺ flux in FPR1- and FPR2-transfected HL-60 cells or in human polymorphonuclear neutrophils (PMN). N.A., no activity observed.

chemical library, researchers from Amgen identified pyrazolone **10** as a potent FPR2 agonist [98]. Replacement of the iodine atom in position 4 with other halogens resulted in decreased potency, which correlated with the size of the halo-substituent (compounds **11** and **12**) (Table **2**). However, the analog with an unsubstituted phenyl urea moiety was completely inactive. The 4-methyl and 4-ethyl derivatives were active at FPR2. In contrast, the sterically more demanding 4-isopropyl analog lost activity. A more detailed survey of substituent changes at the phenyl urea moiety demonstrated that the steric and electronic nature of the *para*-substituent on the phenyl group had important effects on FPR2 agonist activity [98].

Modification of substituents at C(5) of pyrazolone analogs revealed that the potency of compounds with bulkier substituents was consistently enhanced (Me<Et<*i*-Pr<*t*-Bu). As examples, structures and activities of compounds **13** and **14** with *i*-Pr and *t*-Bu C(5)-substituents are shown in (Table **2**). Agonist **13** (designated in most of publications as "Compound 43") was rediscovered in independent HTS as a mixed FPR1/FPR2 agonist with EC₅₀ ~4 nM at FPR2 [81]. This compound also induced a respiratory burst in mouse and human neutrophils and activated C3 receptor (CR3) mobilization to the surface of human neutrophils [81, 91]. A substitution of the pyrazolone core at N(2) position showed that modifications within this portion of the molecule were relatively well tolerated. Indeed, the pyrimidines and quinolines were roughly equal or more potent than the corresponding phenyl derivatives, while thiazoles showed somewhat reduced activity [98].
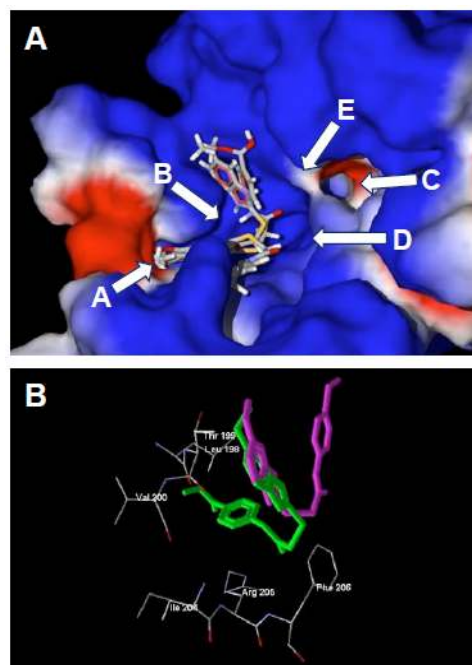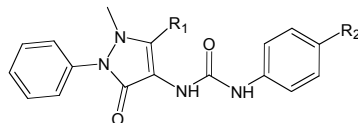

Fig. (1). Panel A. Poses of agonists **1**, **7**, and **8** relative to the surface of the FPR1 binding site. Key sub-areas of the FPR1 binding site are indicated with arrows and include two channels (**A** and **C**), two cavities (**B** and **E**), and the bottom (**D**), as described previously [82]. Surface coloring was made according to electrostatic properties, whereby negatively and positively charged areas are shown in red and blue, respectively. **Panel B**. Docking poses of benzimidazoles **7** (purple) and **8** (green) in FPR1. H-bonds are indicated with dashed lines.

Table 2.   Agonist Activity of Pyrazolones 10-14 [98, 100]

#	R₁	R₂	EC₅₀ (μM)ᵃ	
			FPR1	**FPR2**
10	CH₃	I	N.A.	0.03
11	CH₃	Br	N.A.	0.09
12	CH₃	Cl	N.A.	0.49
13	*i*-Pr	Cl	N.A. (0.065)ᵇ	0.044 (0.022)ᵇ
14	*t*-Bu	Cl	N.A.	0.023

ᵃEC₅₀ values were determined by measurement of Ca²⁺ flux in FPR1- and FPR2-transfected CHO cells; ᵇEC₅₀ values reported [100]. N.A., no activity observed.

Although all 28 pyrazolone-derived FPR2 agonists were reported to have no FPR1 agonist activity up to a concentration of 10 μM [98], Sogawa *et al.* [99, 100] and Forsman *et al.* [91] demonstrated that pyrazolone **13** has dual FPR agonist activity in HL-60 and CHO-K1 cells co-transfected with $G_{\alpha 16}$ and FPR1/FPR2 and suggested that this discrepancy might be due to the different types of G-proteins used in the cell-based screening assays ($G_{\alpha 16}$ *vs.* $G_{\alpha 15}$) [99]. Indeed, compound **13** significantly inhibited the binding of [³H]*f*MLF and [¹²⁵I]WKYMVM to FPR1 and FPR2, respectively [100]. Moreover, the FPR1-specific antagonist cyclosporine H completely abolished the neutrophil response to compound **13** [91]. Compound **13** had agonist activity for murine Fpr1 and Fpr2, with EC₅₀ values of 0.35 and 0.89 μM, respectively [100]. Using RBL-2H3 cells expressing mFpr1, mFpr2, and mFpr-rs1, He *et al.* [21] demonstrated that compound **13** induced Ca²⁺ mobilization and degranulation via both mFpr1 and mFpr2, but not mFpr-rs1. This agonist induced a rapid extracellular signal-regulated kinase (ERK) phosphorylation in murine peritoneal macrophages [101] and stimulated interleukin (IL)-6 secretion in 50% human blood [76]. Compound **13** also activated chemotactic responses in both human and mouse neutrophils, with a typical bell-shaped dose–response curve, and induced internalization of both FPR1 and FPR2 [81, 99, 100].

The most potent pyrazolone FPR2 agonists **10** and **13** inhibited human neutrophil chemotaxis induced by *f*MLF and IL-8, probably via homo- and cross-desensitization [98]. Incubation of human neutrophils with compound **13** diminished the expression of C-X-C chemokine receptor types 1/2 (CXCR1/2), complement receptor C5aR, and leukotriene B₄ (LTB₄) receptor BLT1 [100]. Similarly, pretreatment with compound **13** dose-dependently inhibited Ca²⁺ flux and the chemotactic response of murine neutrophils stimulated with mouse C5a, LTB₄, or keratinocyte chemoattractant (KC/CXCL1), the murine homolog of human IL-8 [100, 102].

Lead pyrazolones also demonstrated anti-inflammatory activity *in vivo*. Pyrazolone **10** caused reduction of ear edema in mice treated topically or orally prior to induction of edema [98]. Compound **13**, administered *i.v.* prior to IL-1β injection into 6-day-old air pouches, produced 50–75% inhibition of cell recruitment in wild-type mice but were ineffective in Fpr2⁻ᐟ⁻ animals [101]. In addition, compound **13** inhibited neutrophil migration into the airway in LPS-exposed mice, as well as zymosan-induced neutrophil accumulation in the peritoneal cavity, possibly through cross-desensitization [100].

3.3. N-Substituted Benzimidazoles

In the next route of screening by researchers from Amgen, the N-substituted benzimidazole **15** was identified as an FPR2-specific agonist, and subsequent SAR studies identified 15 additional FPR2-specific agonists [76]. The authors found that benzimidazoles with small alkyl substituents, such as ethyl at C(2) (**16**), exhibited submicromolar FPR2 activity (Table **3**), and further modification revealed that contraction of the piperidine ring in **16** to pyrrolidine *R*-enantiomer **17** resulted in a 20-fold increase in potency. It should be noted that *R*-enantiomer **17** was significantly more potent than its *S*-counterpart **18** (Table **3**). A brief survey centered around the nature of the C(5)-substituent in the indole fragment revealed that OMe is optimal for FPR2 activity. Indeed, derivatives with F, Cl, Br, O-CF₃, and Et substituents at C(5) of the indole ring were less active than OMe in compound **17**. The most potent N-substituted benzimidazole **17** inhibited human neutrophil chemotaxis induced by *f*MLF and IL-8, probably via cross-desensitization. In addition, compound **17**, in the presence of IL-1β, dose-dependently stimulated IL-6 secretion in 50% human blood above levels induced by IL-1β alone [76].

3.4. Pyridazin-3(2*H*)-ones

In the past six years, our laboratories have been involved in the SAR directed design, synthesis, biological evaluation, and molecular modeling of pyridazin-3(2*H*)-ones with FPR1/FPR2 agonist activities. These aromatic compounds were screened using Ca²⁺ flux assay in FPR-transfected human promyelocytic leukemia HL-60 cells. By starting with

the known pyrazolone scaffold [98] for FPR agonists (Table **2**), we first modified this scaffold but found that related pyridazine derivatives failed to exhibit FPR agonist activity [78]. We next focused on analogues with a substituted benzyl group at position 4 of the pyridazinone moiety and a similar functionalized chain at N-2. This approach led to the identification of compound **19** with medium activity at FPR1/FPR2 (Table **4**). Thus this compound was selected as a lead, and extensive SAR studies were performed (Fig. **2**).

Table 3. Agonist Activity of N-substituted Benzimidazoles 15-18 [76]

#	Structure	EC$_{50}$ (μM)^a	
		FPR1	FPR2
15		N.A.	6.4
16		N.A.	0.69
17		N.A.	0.034
18		N.A.	3.5

^{a}EC$_{50}$ values were determined by measurement of Ca^{2+} flux in FPR1- and FPR2-transfected CHO cells. N.A., no activity observed.

Elongation of the hydrocarbon chain at the acetamide spacer (e.g., compound **20**) reduced potency at FPR1/FPR2 (Table **4**), and other modifications of the functionalized chain resulted in non-active compounds [78, 103]. However, introduction of different substituted aryl groups at the nitrogen atom of the acetamide fragment was more successful. Among compounds with a halogen-substituted phenyl ring, the 4-Cl and 4-I analogues exhibited the same profile as the 4-Br substituted compound (**19**), but the 4-F derivative was specific for FPR1. In contrast, moving Br to positions *meta* or *ortho* resulted in a complete loss of FPR1/FPR2 activity. The elimination or replacement of 4-Br with substituents having similar steric properties, such as *t*-Bu, OCF$_3$, and CN also led to loss of FPR agonist activity. The 4-

trifluoromethyl, the 4-nitro, 4-methyl, 4-methoxy, and 3,4-dimethoxy analogues had relatively low activity at FPR1/FPR2, whereas the 3,4-methylendioxy derivative **21** was specific for FPR1.

The methyl group at position C-6 of the pyridazinone ring was modified to introduce a cyclohexyl group, a 2-thienyl group, (substituted)aryl groups, and a benzyl group. None of these modifications led to more active FPR1/FPR2 agonist compared to reference compound **19** [104]. SAR analysis based on substituents at position C-4 of the pyridazinone scaffold was also performed [104]. Moving OCH$_3$ from the *meta* to the *para* position resulted in compound **22**, an FPR2-selective agonist. Substitution of OCH$_3$ in compound **22** with SCH$_3$ resulted loss of activity for all FPRs [103]. Introduction of fluorine in the *meta* position gave compound **23**, which was an FPR1-specific agonist, and a similar selective activity was evident for its chloro-analogue. Replacement of the methoxyphenyl group in compound **19** with 5- and 6-membered heterocycles (e.g., compound **24**), including 3-furyl, 3-thienyl, 2-thienyl, and 3-pyridyl groups resulted in mixed FPR1/FPR2 agonists. Introduction of a carbonyl group as spacer in place of CH$_2$ in the benzyl group at position C-4 resulted in compound **25**, which is a relatively potent mixed FPR1/FPR2 agonist. Substitution of CH$_2$ with an amidic group was detrimental for FPR1, but not FPR2 activity (compound **26**). In addition, compounds **19-26** also activated Ca^{2+} mobilization and chemotaxis in human neutrophils [78, 104].

Taken together, SAR analysis suggested that the position C-6 of the pyridazinone ring was not readily tolerant to modifications. In contrast, position C-4 was more amenable to chemical manipulation. Indeed, substituted benzyl groups and heterocycles, as well as functionalized spacers (e.g., CO, NH), can be productively introduced at this level, retaining good agonist activity. Regarding the substituted phenyl ring attached to the acetamide fragment, the presence of a lipophilic and/or electronegative substituent, such as F, Br, Cl or CH$_3$, in the *para* position is an essential requirement for FPR1/FPR2 agonist activity. Likewise, the presence of an acetamide spacer at pyridazine N-2 also plays a critical role in specificity and potency. The optimal length of the spacer is four chemical bonds. The importance of both CO and NH in the spacer seems to indicate that a H-bond donor neighboring a H-bond acceptor system is also an essential requirement for binding at FPRs. This is consistent with the structures of other reported FPR1/FPR2 agonists, where the presence of an urea is a common structural element. Moreover, this H-bond donor/acceptor system must be placed at an appropriate distance from both the aromatic and the heterocyclic scaffold (see below).

3.4.1. Molecular Docking of Pyridazin-3(2H)-ones

Molecular docking of selected pyridazin-3(2*H*)-ones into the binding sites of FPR1 and FPR2 was performed in order to evaluate how the presence of different substituents and atoms influences the binding modes of the molecules [103, 104]. Molecular skeletons within the binding site of FPR1 were located mainly along cavity **B** and directed to channels **A** and **C** or to cavity **E**, in accordance with binding modes for 2-arylacetamide pyridazin-3(2*H*)-ones (Figs. **1A** and **3A**).

Table 4.   Agonist Activity of Pyridazin-3(2*H*)-ones 19-26 [78, 103, 104]

#	Structure	EC$_{50}$ (μM)[a]		
		FPR1	**FPR2**	**PMN**
19		3.4	3.8	2.6
20		9.7	5.4	11.3
21		2.3	NA	3.2
22		N.A.	2.4	4.3
23		6.6	N.A.	4.2
24		9.3	2.8	4.9
25		3.0	1.0	2.3
26		9.3	2.8	2.4

[a]EC$_{50}$ values were determined by measurement of Ca^{2+} flux in FPR1- and FPR2-transfected HL-60 cells or in human polymorphonuclear neutrophils (PMN). N.A., no activity observed.

Noticeably, bromine-substituted compounds, in their best poses, had bulky and highly hydrophobic *p*-bromophenyl groups located in the vicinity of channel **A** and directed outside the binding site (for example, see overlapped docking poses of *f*MLF and compound **23** in Fig. **3A**). Additionally, H-bonding interactions of Thr265 with the pyridazine nitrogen atom are evident in agonists **19** and **25**, as are interactions with the carbonyl group of the pyridazinone moiety in compound **24** (Fig. **3B**). For compound **25**, this carbonyl is also H-bonded to both Thr199 and Asn192. Compound **21**, which contains a benzodioxolane moiety instead of a *p*-bromophenyl group, had the opposite binding mode, with the benzodioxolane protruding into channel **C**. In its docking pose, this compound formed a H-bond between one of its endocyclic oxygen atoms and the hydroxyl group of Tyr257 (Fig. **3C**).

The FPR2 model was constructed by homology modeling using the Phyre^2 server. The rhodopsin-based model of FPR2 was selected as the most predictive structure from 18 other

homology models based on 8 dissolved crystal structures of GPCRs [105]. Although the CXCR4 structure has a higher sequence identity with FPR2 (28%), this structure has a low resolution (3.2 Å) for the template, as compared to the rhodopsin structure (2.2 Å). The ligand binding site of FPR2 has a non-symmetric dumb-bell shape with two cavities different in size, where the smaller cavity lies deeply in the binding site and is surrounded by residues Val105, Asp106, Leu109, Phe110, Arg201, Trp254, and Gln258 [105]. FPR2-specific peptide agonist WKYMVM in its best docking pose occupies this cavity with an indole moiety near the N-terminus of the peptide. A narrow channel connecting the two cavities is bordered by residues Phe257, Val260, Ala261, Thr177, Phe178, and Phe180. The larger cavity of the docking site opens outside the receptor and has a complex shape.
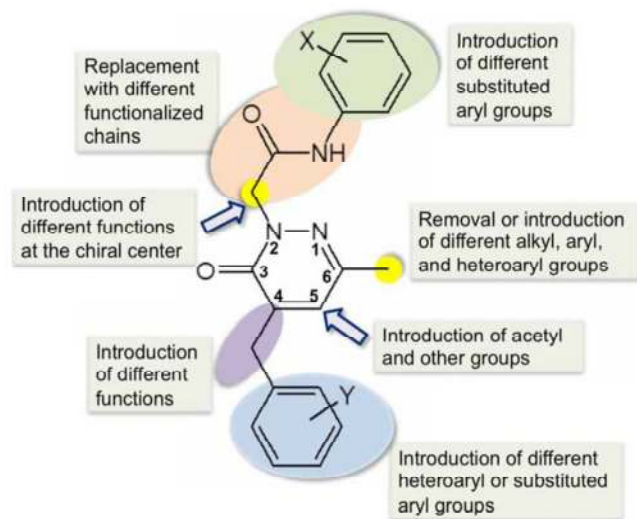
Fig. (2). SAR directed design of FPR agonists with pyridazin-3(2*H*)-one scaffold.

Docking of FPR2 agonists **19**, **22**, and **24-26** to FPR2 showed that they adopt conformations that overlap well with the docking pose of WKYMVM. Characteristically, the bromo-substituted phenyl rings of these molecules lie within the smaller cavity found deep within the binding site (Fig. **4A**). The narrow channel contains an amide fragment adjacent to the *p*-bromophenyl groups of the molecules. In addition, the pyridazinone moieties are oriented similarly in the binding site with their carbonyl and methyl groups overlaid in the same positions. Such an orientation is conditioned by the possibility of H-bonding of the nitrogen atom in the pyridazine ring, as well as an oxygen or nitrogen atom in the amide moiety, with the hydroxyl group of Thr177. As an example, specific interactions of agonist **25** with Thr177 and Ala261 are shown in (Fig. **4B**).

As discussed above, Arg205 is one of the key residues important for FPR1 agonist activity [82, 96]. Indeed, active pyridazinone **19** forms a H-bond with Arg205 in FPR1, with total interaction energy of 32.9 kcal/mol with this residue. However, the sulfur-containing analogue with a thio-acetamide fragment had a much weaker non-bonded attractive interaction with Arg205 (8.82 kcal/mol). Another thio-analogue of compound **22** containing a *p*-methylthio group instead of the *p*-methoxy substituent was not H-bonded to any FPR1 residue [103]. Docking studies with the FPR2 homology model showed that the binding modes of oxygen-containing derivatives were also quite different from their thio-analogues [103]. The inactive sulfur-containing derivatives contain bulky groups that extend outside the cavity, which caused steric hindrance and prevented effective binding of the ligands with FPR2. Hence, these molecules cannot adopt the more suitable conformations that are possible for the corresponding oxygen-containing derivatives. For example, the best docking pose of the *p*-methylthio analogue of compound **22** had significant repulsive interactions with Tyr277 and Ile280 of FPR2. Despite H-bonding with Asn171 and Asp173, this docking pose was energetically unfavorable, as compared to that of the active methoxy-derivative **22**. For the best pose of compound **22**, the closest non-valent contact of 2.48 Å occurs between the methoxy oxygen atom in molecule **22** and Thr168. An analogous pose would be impossible for the corresponding compound with a *p*-methylthio group, which is more bulky than the methoxy substituent.

3.5. Chiral Pyridazines

Based on the pyridazine-3(2*H*)-one scaffold, two series of chiral derivatives were synthesized and evaluated [77, 106]. While we found that orientation of the chiral C5-methyl substituent in *N*-(4-bromophenyl)-2-[5-methyl-6-oxo-3-phenyl-5,6-dihydropyridazin-1(4*H*)-yl]acetamide and its analogues had little effect on agonist activity, orientation of the chiral center attached to nitrogen atom in position 2 of pyridazinone heterocycle had significant effects [77]. For these compounds, the *S*-(+) enantiomers lacked FPR agonist activity, whereas the *R*-(-) counterparts **27-29** had high activity in the micromolar or even nanomolar range (Table **5**). In general, elongation of the carbon chain at the chiral center in *R*-enantiomers increased agonist activity ($CH_3 < C_2H_5 = $n-$C_3H_7 < $n-$C_4H_9 = C_6H_5$) at FPR1/FPR2, suggesting the importance of considering this molecular feature in further development of these analogues.

3.6. N-Phenylurea Derivatives

HTS of a large chemolibrary resulted in the identification of FPR2-specific agonist **30** with an N′-phenylurea scaffold [75]. This compound activated reactive oxygen species (ROS) production by murine neutrophils and induced Ca^{2+} mobilization and chemotaxis in human neutrophils [79]. SAR analysis of related derivatives revealed three additional FPR2-specific agonists **31-33** (Table **6**). All active derivatives contained a *para* methoxy group in benzene ring **B**, which seems to be an essential feature for activity of these derivatives. However, introduction of additional methoxy groups to ring **B** resulted in total loss of activity. Most active derivatives contained a halogen atom in the *para* position of benzene ring **A**. However, the presence of the halogen atom was not absolutely essential for biological activity, as compound **31** was also an active FPR2 agonist. Moving the halogen atom from the *para* position to the *meta* and then *ortho* positions resulted in decreased or completely lost activity, respectively.

Branching of the hydrocarbon chain in N-phenyl-N'-(2-phenylethyl)urea derivatives resulted in a series of analogs with a chiral sp^3 carbon near the carbamide nitrogen atom. The resulting benzyl-containing moiety is structurally related to the phenylalanine derivatives. Our screening demonstrated

that nine Phe-based analogs and nine other related analogs were potent FPR agonists [80], and structures of selected compounds **34-47** are shown in (Tables **7** and **8**). Although most of the compounds were mixed FPR1/FPR2 agonists, many displayed much higher selectivity for FPR2. It should be noted, that both enantiomers of racemic mixture **35** were reported previously in independent screenings as FPR2 agonists Acadia C5 and Acadia C6 [45], and their reported EC_{50} at this receptor was ~30-35 nM [81], which is pretty close to the racemic mixture (Table **7**). The *S*-enantiomer has been shown to dose-dependently prevent hyperalgesia induced by carrageenan in rats [45].
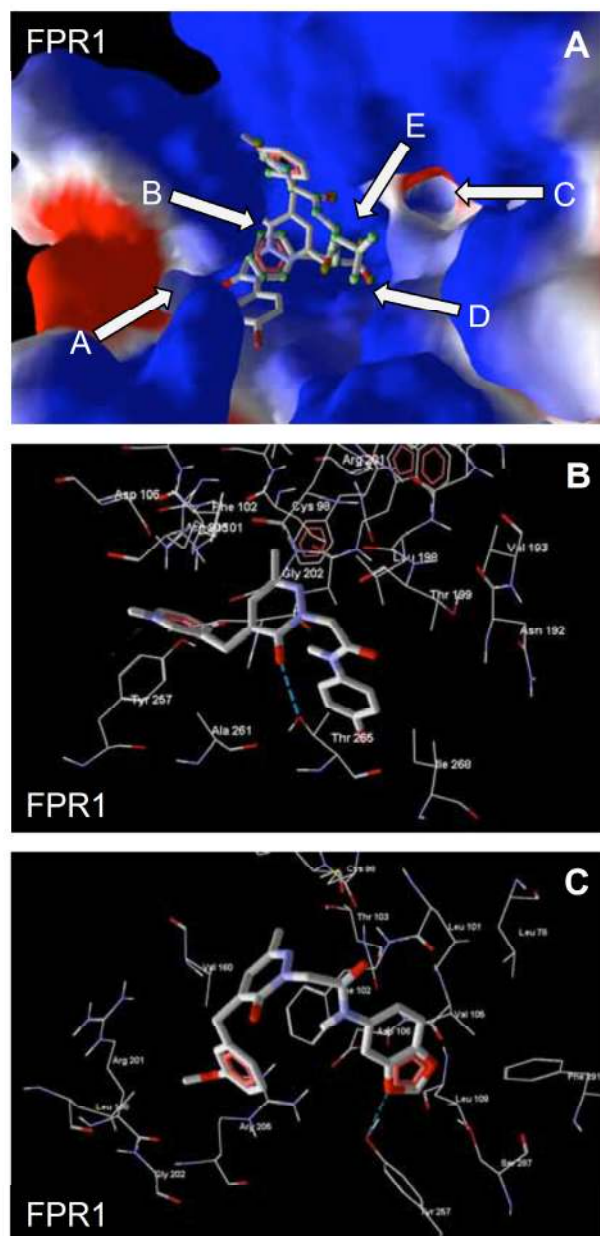
Fig. (3). Panel A. Docking poses of *f*MLF (atoms are highlighted by green spheres) and pyridazin-3(2*H*)-one **23** (atoms are not highlighted). Key sub-areas of the FPR1 binding site are indicated with arrows as in (Fig. **1B**). **Panel B**. Interactions between Thr265 of FPR1 and molecule **24**. H-bond is indicated with a dashed line. **Panel C**. Specific interaction between Tyr257 of FPR1 and compound **21**. H-bond is indicated with a dashed line.
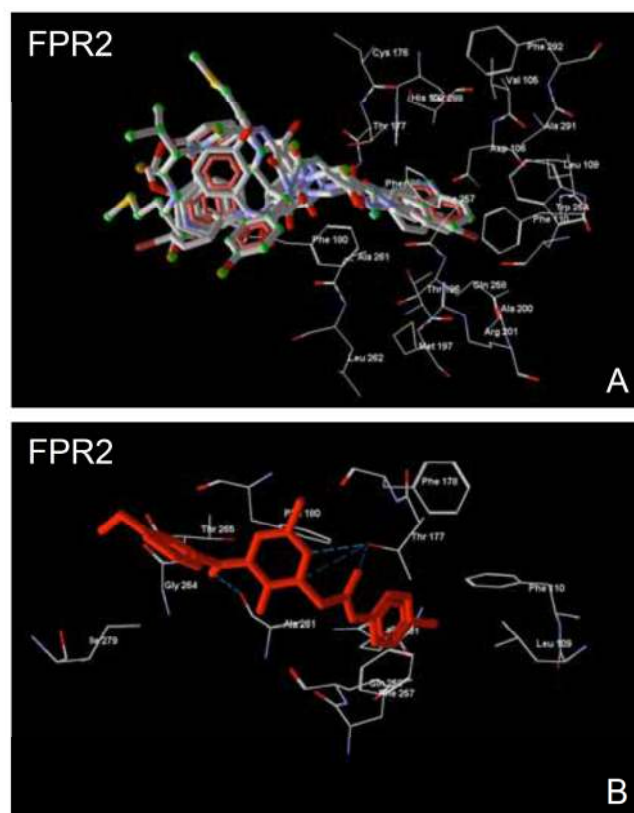

Fig. (4). Panel A. Overlapping docking poses of WKYMVM (atoms are indicated with green spheres) and pyridazin-3(2*H*)-ones **19**, **22**, and **24-26**. FPR2 residues within 6 Å around the smaller cavity are shown. **Panel B.** Compound **25** docked into the FPR2 binding site. Residues lying within 3.5 Å of the pose are shown. H-bonds are indicated with dashed lines.

Table 5.   **Agonist Activity of Chiral Pyridazin-3(2*H*)-ones 27-29 [77]**
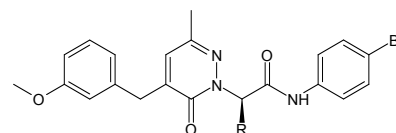
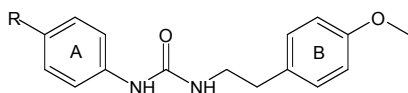| #	R	EC_{50} (μM)[a]		
		FPR1	**FPR2**	**PMN**
27	n-C_3H_7	3.0	0.84	0.93
28	i-C_3H_7	9.4	5.4	2.3
29	n-C_4H_9	0.5	0.089	0.073

[a]EC_{50} values were determined by measurement of Ca^{2+} flux in FPR1- and FPR2-transfected HL-60 cells or in human polymorphonuclear neutrophils (PMN).

3.7. Chiral 3-(1*H*-indol-3-yl)-2-[3-(4-nitrophenyl)ureido]propanamides

Screening of a small library of 32 low-molecular-weight ligands of 24 different GPCRs led to the identification of two bombesin receptor BB_1/BB_2 antagonists, PD176252 (compound **48**) and PD168368 (compound **49**), as potent mixed

FPR1/FPR2 agonists [80]. Although several potent FPR1/ FPR2 agonists were found through secondary screening of Trp-based analogs from commercial chemical libraries, subsequent SAR analysis was completed by synthesis of related enantiomers using stereospecific methods starting from the enantiomerically pure N-Boc-*R*-Trp or N-Boc-*S*-Trp [105]. From this approach, several potent FPR agonists, including FPR2-specific agonists **50-53**, were identified. Unexpectedly, the majority of compounds found to induce Ca^{2+} mobilization in FPR-transfected HL-60 cells failed to stimulate this response in human neutrophils. This finding is supported by our previous findings that some chiral FPR agonists and their closely related achiral derivatives are much (up to 600-fold) less active for activation of Ca^{2+} mobilization in human neutrophils than in the FPR-transfected cells [80]. Pretreatment of human neutrophils with probenecid restored the Ca^{2+} flux response in neutrophils treated with most of these derivatives. Structures of selected FPR agonists **48-53** are shown in (Table **9**). Because substitution of OCH_3, CF_3, Br, and CH_3 in the *para* position of the phenyl ring with CN or NO_2 and removing CH_3 at the chiral center of compounds **48** and **49** resulted in loss of ability to activate neutrophil Ca^{2+} flux without probenecid pretreatment, it appears that the requirement for probenecid is somehow related to compound structure. We suggest that compounds **48** and **49** have more flexible structures than the parent compounds, where an intramolecular H-bond between an amino group and the carbamide carbonyl atom could significantly restrict conformational freedom of these molecules. Thus, increased flexibility of the chiral agonists could be analogous to conformation changes in FPR2 [105]. Alternatively, because OCH_3, CF_3, Br, and CH_3 in the *para*-position of the phenyl ring of FPR2 agonists are less electronegative than NO_2 and CN groups [107], potency of electrostatic and H-bond interactions in FPR2 subpockets could be an important characteristic for activation of G-protein coupling and Ca^{2+} flux in human neutrophils.

**Table 6.   Agonist Activity of N-phenylurea Derivatives 30-33 [75, 79]**

#	R	EC$_{50}$ (μM)[a]		
		FPR1	**FPR2**	**PMN**
30	Cl	N.A.	0.4	0.7
31	H	N.A.	3.0	4.8
32	F	N.A.	0.9	1.2
33	Br	N.A.	0.1	1.2

[a]EC$_{50}$ values were determined by measurement of Ca^{2+} flux in FPR1- and FPR2-transfected HL-60 cells or in human polymorphonuclear neutrophils (PMN). N.A., no activity observed.

Analysis of the literature indicates that probenecid is a non-specific inhibitor of multidrug resistance-associated proteins and can have different effects on several other cellular targets. For example, probenecid is able to activate transient

receptor potential V2 (TRPV2), Ca^{2+}-permeable nonselective cation channel [108], and transient receptor potential channel subtype A member 1 (TRPA1), another nonselective cation channel [109], and it has recently been reported that probenecid can directly modulate interaction of GPCR and G-proteins [110]. In addition, Prossnitz *et al.* [111] proposed that primary myeloid cells maintain a subpopulation of FPR in a low-affinity, possibly G protein-free state, which is not a feature of FPR-transfected HL-60 cells. Because allosteric communication between the ligand-binding orthosteric site and the cytoplasmic G-protein-binding surface is a fundamental feature of GPCRs [112], it is possible that certain FPR2 agonists, such as the ureidopropanamides **50-53**, could stabilize this receptor in a G-protein-free state, and additional agents (e.g., probenecid) may be required to reactivate G-protein coupling.

Table 7.   Agonist Activity of Chiral N-phenylurea Derivatives 34-38 [80]
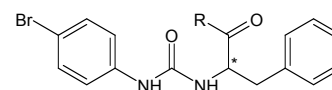
#	R	EC$_{50}$ (μM)[a]			
		FPR1	**FPR2**	**FPR3**	**PMN**
34		4.5	0.14	11.5	3.2
35		1.8	0.04	6.5	1.2
36		0.3	0.004	0.1	0.7
37		0.08	0.007	0.5	0.5
38		N.A.	0.16	N.A.	4.4

[a]EC$_{50}$ values were determined by measurement of Ca^{2+} flux in FPR1-, FPR2-, and FPR3-transfected

HL-60 cells or in human polymorphonuclear neutrophils (PMN). N.A., no activity observed.

### 3.8. Molecular Modeling of Chiral Recognition at FPR2

To investigate the enantiomer preference observed for FPR2 agonists with different scaffolds and chiral center substituents, we created a pharmacophore model for FPR2 using field point methodology [113-115] based on five potent small-molecule non-peptide FPR2 agonists, including FPR agonist **42** and four chiral molecules (both *S*- and *R*- forms) **17**, **35**, **36**, and **49** [80]. The hydrophobic field surface of the 5-molecule FPR2 template consists of three regions (H$_1$, H$_2$, and H$_3$), which correlate with

subpockets I, II, and III in the FPR2 binding site, respectively (Fig. **5**). FPR2 agonists and their inactive enantiomers were overlaid in the three-subpocket model. The similarity values depend equally on geometric and field similarity of a molecule and template. For most chiral pyridazin-3(2*H*)-ones [77], the similarity between aligned molecule and the template for *R*-enantiomers was higher than that of their *S*-enantiomer counterparts. Moreover, more active enantiomers with a ureidopropanamide scaffold had better alignments than the corresponding inactive enantiomers [105]. A visual inspection of the molecule overlays on the 5-molecule FPR2 template showed that in most cases the active enantiomers had alignment modes with non-polar molecular fragments located in subpocket II, while bromo- or nitro-substituted phenyl rings were always positioned in subpocket I. In particular, moieties without polar atoms occupied subpocket II, while polar substructures (methoxy in benzene rings or indole NH groups) were located in subpocket III for these alignments [105].

Table 8.   Agonist Activity of Benzodioxole Derivatives of N-phenylureas 39-47 [80]
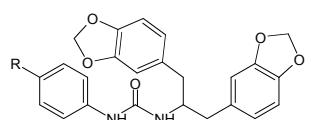
39-43
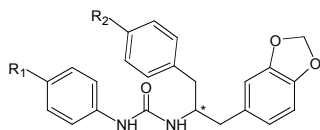
44-47

#	R	EC$_{50}$ (µM)^a			
		FPR1	**FPR2**	**FPR3**	**PMN**
39	H	N.A.	0.006	3.3	5.9
40	F	1.7	0.004	0.7	0.7
41	Cl	3.7	0.002	0.2	0.06
42	Br	2.7	0.004	1.7	0.1
43	Me	5.1	0.07	10.8	4.5

#	R$_1$	R$_2$	EC$_{50}$ (µM)^a			
			FPR1	**FPR2**	**FPR3**	**PMN**
44	H	F	N.A.	0.12	1.3	1.2
45	F	F	7.5	0.02	1.2	0.14
46	Me	F	N.A.	0.5	N.A.	10.1
47	Cl	O-Me	0.11	0.0002	0.05	0.013

^{a}EC$_{50}$ values were determined by measurement of Ca^{2+} flux in FPR1-, FPR2-, and FPR3-transfected

HL-60 cells or in human polymorphonuclear neutrophils (PMN). N.A., no activity observed.

According to docking studies with the FPR2 homology model [105], the pharmacophore subpocket I is surrounded by His102, Val105, Asp106, Leu109, Trp254, Phe257, Ser288, and Phe292 and lies in the smaller cavity. Residues His102, Val105, Asp106, Leu109, and Trp254 were also identified by Fujita *et al.* [116] as critical for the FPR2 binding site. Residues surrounding subpockets II and III were also identified [105]. The FPR2-specific peptide agonist WKYMVM, in its best docking pose, occupies all three subpockets, with the N-terminal indole moiety located in subpocket I. Subsequent modeling with FPR agonists showed that the geometric configuration of the FPR2 binding site fits well with the shape of the hydrophobic field obtained for the FPR2 agonist pharmacophore model, and extrema of negative and positive fields correspond well to areas of the ligand binding site of the FPR2 homology model (Fig. **5**). Thus, this correspondence seems to be important for proper orientation of an agonist molecule for penetration into the binding site.

3.9. 2-(*N*-Piperazinyl)acetamide Derivatives

Eight FPR2-specific agonists **54-61** with a 2-(*N*-piperazinyl)acetamide scaffold were discovered while screening a chemical library using the Ca^{2+} flux assay in FPR1/FPR2 RBL cells as readout (Table **10**). All active derivatives contained Br in the *para* position of benzene ring **A**, which was required for activity. Furthermore, moving Br from the *para* position to the *ortho* or *meta* positions resulted in loss of activity. Finally, replacement of *para* Br in ring **A** with a variety of other substituents resulted in loss of activity [79]. It is noteworthy that related piperazines were reported as selective agonists of the dopamine D$_4$ receptor, which is also a GPCR [117]. Whether our FPR2 agonists are also D$_4$ receptor agonists has not been evaluated.

3.10. Quinazolinones

Quinazolinone **62** (designated in most of publications as Quin-C1) was described as one of first small-molecule non-peptide FPR agonists [74]. This compound selectively activated FPR2 *vs.* FPR1 (EC$_{50}$ ~1.4 µM), induced ROS production, degranulation, and chemotaxis in human neutrophils and stimulated internalization of FPR2 and ERK phosphorylation [74, 81]. Compound **62** activated both mFpr1/mFpr2 [21] and demonstrated anti-inflammatory properties in a mouse model of lung injury [118]. Furthermore, HTS and SAR-directed design and synthesis identified analogs **63-66** [79, 119], including FPR2-specific agonists containing methyl (**63**), nitro (**64**), and 3,4-methylenedioxy (**66**) groups in the *para*-position of benzene ring **A** (Table **11**). Substitution with bulky groups, such as isobutoxy or butoxy, at this position resulted in loss of agonist activity, and activity was also lost when the nitro group in compound **64** was changed to amino or dimethylamino groups. Elimination of the methoxy group in compound **62** or introduction of an additional methoxy group in the *meta* position of **62** also resulted in inactive compounds [119]. Our recent screening identified related quinazolinone **65** as a potent FPR agonist [79].

3.11. Miscellaneous FPR Agonists

Structures of FPR agonists with varying scaffolds but with no clear SAR emerging from evaluation of their analogs

Table 9.   Agonist Activity of Chiral 3-(1*H*-indol-3-yl)-2-[3-(4-nitrophenyl)ureido]propanamides 48-53 [105]

48 (PD176252)   **49** (PD168368)

50   **51**

52   **53**
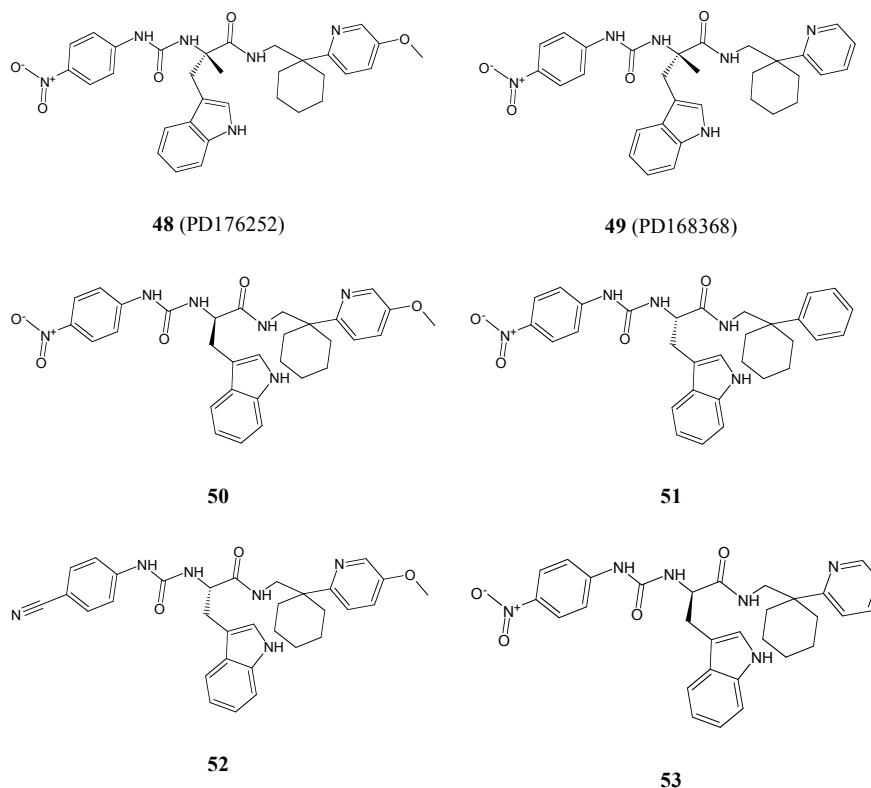
#	EC$_{50}$ (μM)[a]			
	FPR1	**FPR2**	**PMN**	
			w/o Prob.	**with Prob.**
48	0.33	1.3	0.72	0.21
49	0.57	0.62	0.91	0.19
50	N.A.	0.023	N.A.	0.0032
51	N.A.	0.7	N.A.	0.05
52	N.A.	0.36	N.A.	0.022
53	N.A.	0.19	N.A.	0.46

[a]EC$_{50}$ values were determined by measurement of Ca^{2+} flux in FPR1- and FPR2-transfected HL-60 cells or in human polymorphonuclear neutrophils (PMN) analyzed without (w/o) or in the presence of 2.5 mM probenecid (Prob.). N.A., no activity observed.

are discussed here (Table **12**). Five acetohydrazides, including chiral compound **67**, dibenzoylhydrazine **68**, and thienyl-pentanamide **69** were identified as FPR2-specific agonists in library screening [79]. Derivatives of 2-(indol-3-yl)-1,3-thiazolidin-4-one **70**, N,N′-diphenylurea **71**, and (3-thienyl)methylene acetylhydrazide **72** were found to be mixed FPR1/FPR2 agonists, and compounds **68-72** activated chemotaxis in human neutrophils [79]. Two other phenyl-substituted ureas **73** and **74** have been reported as potent FPR2-specific agonists [81]. Compounds **75** and **76** [81] are unique from other described FPR agonists because these compounds have carboxyl/hydroxyl groups. It should be noted that compounds **75** and **76** activated intracellular Ca^{2+} mobilization in CHO cells expressing FPR1 as well as FPR2,

but the EC$_{50}$ for FPR1 agonist activity was not reported [81]. Compound **77**, with a unique 2-(4-phenyl-5-((phenylamino)methyl)-1,2,4-triazol-3-ylthio)acetamide scaffold, and its closely related derivatives were patented as the first small-molecule non-peptide FPR2 agonists, but their activities (EC$_{50}$ values) at this receptor were not reported [45]. Compound **77** was further rediscovered in independent screening as a potent FPR2-specific agonist with nanomolar activity [81]. Compounds **78** [81] and **79** [120] each have identical groups at the *sp^3* carbon atom, resembling structures of other FPR agonists **39-43** [80]. It should be noted, that the low activity FPR1 agonist **79** was found using computer-aided prioritization and subsequent physical screening [120].
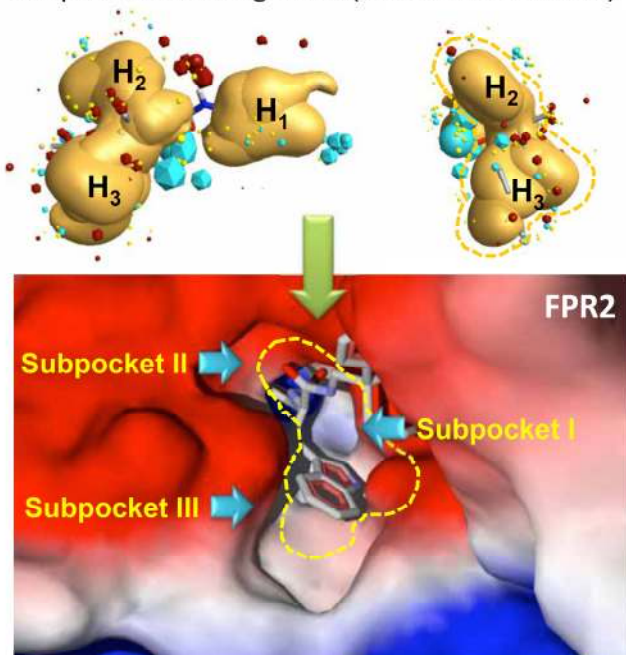
Fig. (5). Model of chiral compound docking to FPR2. Geometry of the hydrophobic field surface of the pharmacophore model matches to the binding site geometry of FPR2. An FPR2 agonist can approach the FPR2 binding site from the top ("mouth") of the cavity, shown by dashed yellow line around the agonist template (hydrophobic regions H_2 and H_3) and around the cavity mouth, which includes subpockets II and III. Field points are colored as follows: blue, electron-rich (negative); red, electron-deficient (positive); yellow, van der Waals attractive (steric). Hydrophobic region H_1 (usually associated with 4-nitrophenyl or 4-bromophenyl groups in FPR2 agonists) should properly fit into subpocket I of the FPR2 ligand-binding site. The cavity of the FPR2 binding site shows the position of side chain tails of compound **53** in subpockets II and III. Surface coloring was made according to electrostatic properties, whereby negatively and positively charged areas are shown in red and blue, respectively. It should be noted, that blue (positively charged) surface areas of the receptor correspond to blue field points obtained with positive probe atom and red (negatively charged) surface areas of the receptor correspond to red field points obtained with negative probe atom. Areas of subpockets are indicated with light-blue arrows. Numeration of subpockets and the hydrophobic surface of the FPR2 pharmacophore model are as reported in [80, 105].

Compounds **80-82** containing an arylcarboxylic acid hydrazide core structure potently induced TNF production in macrophages, presumably via FPR activation [121, 122]. Compound **80** is an FPR1-specific agonist, whereas compounds **81** and **82** are low activity FPR2-specific agonists (Table **12**). Compounds **80-82** stimulated intracellular Ca^{2+} mobilization, chemotaxis, and ROS production in murine and human neutrophils [75, 121]. Currently, compound **80** is sold by Tocris Bioscience as an FPR1 agonist designated as FPRA14.

Recently, polyphenylure **83** and pyrrolidine bis-diketopiperazine **84** were found to be specific high-affinity FPR1 and FPR2 agonists, respectively, using mixture-based

combinatorial libraries [123]. However, activity of these potent agonists in neutrophils was not evaluated.

Two non-peptide calpain inhibitors that are α-mercapto-acrylic acid derivatives, PD150606 (compound **85**) and PD151746 (compound **86**), were reported to induce Ca^{2+} mobilization in FPR2-transfected HEK-293 cells [116, 124]. These compounds have atypical chemical structures, as compared with most reported FPR agonists. Indeed, a visual inspection of molecules **1-84** shows that a typical FPR agonist contains at least two heterocycles separated by a chemical linker with >2 bonds (see also [79]). We evaluated ability of the calpain inhibitors **85** and **86** to stimulate Ca^{2+} mobilization in FPR1/FPR2 transfected HL-60 cells, but both compounds were inactive in our hands at concentrations up to 30 μM (unpublished data). The explanation for this discrepancy might be due to the different types of G-proteins used in the cell-based screening assays. Although docking simulations demonstrated several low-energy poses of compound **85** in the orthosteric binding site of FPR2 [116], pepducin-like allosteric interaction of these calpain inhibitors with allosteric sites, including the FPR2–G-protein interface, or even direct effects on G-proteins could not be excluded.

Two methionine-derived benzimidazoles were recently identified as neutrophil agonists in a Ca^{2+} mobilization assay by Unitt *et al.* [84] during HTS and subsequent SAR analysis [84]. However, FPR subtype specificity for these compounds was not reported.

4. SMALL-MOLECULE FPR ANTAGONISTS AND THEIR MODELING

4.1. Diamides

Using HTS for compound inhibition of Alexa647-labeled *f*MLFK-specific binding to HEL-293 cells expressing FPR1 and $G_{\alpha16}$ and subsequent analysis for inhibition of *f*MLF-stimulated intracellular Ca^{2+} mobilization in human neutrophils, Unitt *et al.* [84] identified diamide **87**, which antagonized FPR1 function in human neutrophils (Table **13**). The most potent diamide analog identified (compound **88**) possessed a more lipophilic substitent R, as compared to compounds **89-92**, which contain 4-chlorophenyl, benzyl, cyclohexyl, and 1-methylimidazolyl substituents, respectively. For the benzoyl moiety, an *ortho* hydroxy group was essential to maintain FPR1 antagonist activity, and replacing the hydroxyl in compound **89** with OCH_3 or CH_3 led to inactive compounds. In addition, the nature of the antagonism exhibited by these diamides (i.e., competitive *vs.* non-competitive) was not evaluated. Initial SAR for the diamides and several of their analogs suggested that in order to generate a good FPR1 antagonist profile, compounds would require a number of parameters that would be challenging to successfully modify in latter phases of drug development. As result, further work, including testing enantiomers, was not undertaken [84].

4.2. Methionine-derived Benzimidazoles

Another FPR1 antagonist discovered by Unitt *et al.* [84] was the methionine-derived benzimidazole **93** (Table **14**). Compound **93** demonstrated low antagonism at rat Fpr1 ($IC_{50} = 10$ μM), but was inactive at mouse Fpr1. Modifica-

Table 10.   Agonist Activity of 2-(*N*-piperazinyl)acetamides 54-61 [79]
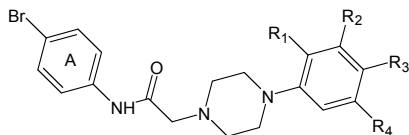
#	R₁	R₂	R₃	R₄	EC₅₀ (µM)ᵃ		
					FPR1	FPR2	PMN
54	H	H	F	H	N.A.	19.3	10.5
55	H	Cl	H	H	N.A.	15.1	16.4
56	H	H	H	H	N.A.	8.7	2.3
57	H	H	Cl	H	N.A.	2.1	2.0
58	H	Cl	CH₃	H	N.A.	4.3	1.0
59	CH₃	Cl	H	H	N.A.	4.1	1.8
60	CH₃	H	H	Cl	N.A.	9.4	0.4
61	H	OCH₃	H	H	N.A.	11.0	7.9

ᵃEC₅₀ values were determined by measurement of Ca^{2+} flux in FPR1- and FPR2-transfected RBL cells or in human polymorphonuclear neutrophils (PMN). N.A., no activity observed.

tion of the benzofuran group in **93**, including removal of the ethoxy group (compound **94**) or fused benzene ring (compound **95**), reduced activity. Compound **96**, with a cyclohexyl moiety, was more active in comparison with compound **97**, which contained a phenyl substituent. Derivative **98** with a 3-chloro-2-thienyl group was very close in activity to cyclohexyl-containing compound **96**. Modification of the benzimidazole group by introduction of a benzyl group reduced activity (compound **99**), although subsequent introduction of a cyano group in the *para* position of the benzyl moiety increased antagonist activity (compound **100**). Incorporation of heteroatoms into the phenyl ring of the benzimidazole had variable effects, depending on the substitution pattern. Purine (compound **101**) and 4-azabenzimidazole (compound **102**) derivatives were less active than reference compound **93**. Moreover, substitution of the benzimidazole group in compound **93** with 5-azabenzimidazole led to the appearance of FPR agonist activity, although FPR subtype specificity for this compound was not reported. *S*-enantiomer **103** with an ethylthiomethyl group was equiactive to compound **93**, although its *R*-counterpart **104** had a lower antagonistic activity.

4.3. Pyrazole-4-carboxamides

A series of pyrazole-based FPR1 antagonists have been identified from HTS and subsequent optimization [86, 87] (Table **15**). Compound **105** was first identified by HTS [87], although attempts to obtain more potent antagonists by modification or replacement of the sulphonamide and amide motif were unsuccessful, suggesting that the amidic group is necessary for FPR1 agonist activity. However, conformational effects of these changes cannot be excluded. Introduction of a methyl substituent at the 3 position of the pyrazole scaffold resulted in a modest increase in potency (compound

105 *vs.* **106**), and modification of the carboxamide moiety led to *S*-enantiomer **107**, which was preferentially active over the *R*-counterpart **108** by ~6-fold. Introduction of strongly electron-withdrawing fluorine and cyano groups into both phenyl rings of the *S*-enantiomer led to compound **109**, which possessed a substantially higher antagonist activity than the initial pyrazole **107**. During subsequent optimization, the alkyl pyrazole substituent was varied in compound **107**, with the most potent analogs **110-112** bearing cyclohexyl, tetrahydrothiopyran-4-yl, and 4-methoxycyclohexyl groups, respectively [86]. It is interesting to note that the *trans*-diastereoisomer of compound **112** was completely inactive, highlighting specificity of the interaction of the methoxy motif with FPR1. Compound **112** has good pharmacokinetic properties and is the most potent FPR1 antagonist among the known synthetic small-molecule FPR antagonists. Note, however, that the nature of the antagonist activity (i.e., competitive *vs.* non-competitive) was not evaluated for these methionine-derived benzimidazoles and pyrazole-4-carboxamides, so allosteric inhibition cannot be excluded.

4.4. Miscellaneous FPR Antagonists

Sulfinpyrazone **113** (Table **16**) and its related derivative 1,2-diphenyl-4-(3-(1-naphthyl)-propyl)-3,5-pyrazolidinedione (DNP) were reported as the first competitive FPR1 antagonists [125, 126]. The low affinity of sulfinpyrazone at FPR1 (Kᵢ=14 µM) was later supported by Young *et al.* [127]. It should be noted that sulfinpyrazone is a non-steroidal anti-inflammatory drug (NSAID) that alters platelet function by inhibiting cyclooxygenase activity [128]. In addition, this drug acts as a general inhibitor of organic anion transporters [129]. Other NSAIDs, including diclofenac, piroxicam (compound **114**), and its close analog tenoxicam were found

to be low activity FPR1 antagonists [130, 131]. Losartan, a selective antagonist of AT1 receptor activation by angiotensin II and sulfasalazine, a drug useful in the therapy of inflammatory bowel disease [132], also decreased the binding of [^{3}H]*f*MLF to neutrophils [133]. Recently, propofol, a widely used *i.v.* anesthetic drug, was reported to exhibit FPR1 antagonist activity [134]. Propofol and its halogenated analogs are also high-affinity inhibitors of voltage-operated sodium channels [135]. Because NSAIDs, losartan, sulfasalazine, and propofol exhibit various pharmacological properties, these drugs are not suitable for *in vivo* studies designed to probe the physiological role of FPR.

Table 11.   Agonist Activity of Quinazolinone Derivatives 62-66 [74, 79, 119]

62-65   **66**
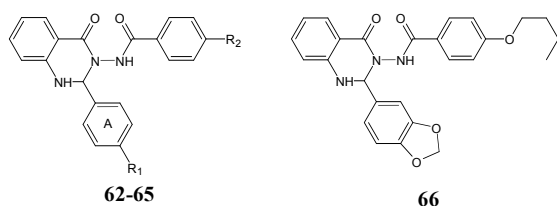
#	R$_1$	R$_2$	EC$_{50}$ (μM)		
			FPR1	FPR2	PMN
62	OCH$_3$	butoxy	N.A.	1.4	N.D.
63	CH$_3$	butoxy	N.D.	≥1.4	N.D.
64	NO$_2$	butoxy	N.D.	>1.4	N.D.
65	OCH$_3$	NO$_2$	N.A.	0.3	1.4
66			N.D.	>1.4	N.D.

N.D., EC$_{50}$ was not reported. N.A., no activity observed.

Several new scaffolds for competitive FPR1 antagonists were discovered by Edwards *et al.* [120] using a flow cytometry-based competition assay (Table **16**). These scaffolds included phenyl-1,4,6,7,8,9-hexahydro-5*H*-pyrazolo[3,4-b]quinolin-5-one (compound **115**), 5-oxo-4-phenyl-1,4,5,6,7,8-hexahydroquinoline (compound **116**), (Z)-5-(2-oxoindolin-3-ylidene)-2-thioxothiazolidin-4-one (compound **117**), [(3-cyclohexylpropanoyl)amino]-4-thiophene-3-carboxylate (compound **118**), benzenesulfonamide (compound **119**), 4-anilino-1,2,3,4-tetrahydroquinoline (compound **120**), 4*H*-1-benzopyran-4-one (compound **121**), and 4-benzoyl-3-hydroxy-5-phenyl-1*H*-pyrrol-2(5*H*)-one (compound **122**). Although seven compounds with a 2,2'-(phenylmethanediyl)bis(3-hydroxy-5,5-dimethylcyclohex-2-en-1-one) scaffold were reported as relatively low activity FPR1 antagonists with K$_i$ values in the 1 to 32 μM range [120], these compounds were also identified to be partial agonists, with most the potent being compound **79** (Table **12**). Thus, it appears that these partial agonists may still be able to desensitize cells but are probably not receptor antagonists, because they can directly induce a Ca^{2+} flux.

Further HTS efforts supported two of the chemotypes described above as FPR1 antagonists, including 4*H*-1-benzopyran-4-one and 4-benzoyl-3-hydroxy-5-phenyl-1*H*-

pyrrol-2(5*H*)-one [83], with compounds **123** and **124** as examples, respectively. Although nine FPR1-specific antagonists with the same 4*H*-1-benzopyran-4-one scaffold were reported in both publications [83, 120], SAR analysis of the substituents attached to the 4*H*-pyran-4-one and benzyl rings or via the carboxyl bridge is limited, and further evaluation will be necessary. Another FPR1 antagonist identified in the screening by Young *et al.* [83] is pyrazolo[1,5-a]pyrimidin-7(1*H*)-one **125**. Pyrrolidine bis-diketopiperazine **126** was recently described as potent and selective FPR1 antagonist by screening 37 different combinatorial libraries and totaling more than five million small molecules [123, 136].

Using of a flow-cytometry-based competition assay in "duplex" format, Edwards *et al.* [137] and Strouse *et al.* [138] identified three FPR2-specific antagonists with an 2-phenylimidazo[1,2-a]pyrimidine scaffold, the most potent being compound **127**. Other less potent FPR2 antagonists include anthrone derivative **128** and 2-(piperazin-1-yl)pyrimidine **129**. It should be noted, that the assay detected active structures, which blocked the binding of a fluorescent ligand to FPR on the surface of intact cells, thus detecting both agonists and antagonists [127, 139]. However, testing of possible agonist effects was not reported by Young *et al.* [83]. To evaluate if these antagonists could have agonist effects and whether receptor desensitization could explain the reported antagonism, we evaluated their activity in HL-60 cells transfected with FPR1/FPR2. However, no direct agonist effects were found for the most potent compounds **123** and **127** in the Ca^{2+} flux assay (unpublished), indicating they are likely true competitive antagonists.

Quinazolinone **130** with a hydroxyl group in the *para* position of benzene ring **A** was described as an FPR2 antagonist (see Tables **11** and **16**). This compound did not activate Ca^{2+} flux in FPR2 transfected cells, but inhibited WKYMVm-stimulated Ca^{2+} flux, chemotaxis, and ERK1/ERK2 phosphorylation in FPR2 transfected RBL cells. Moreover, compound **130** inhibited arachidonic acid-induced ear edema [119].

Several pyrrolidine bis-diketopiperazine-based FPR2 antagonists, including compound **131**, were recently identified by screening combinatorial libraries [123, 136]. Similar to quinazolinone derivatives **62**/**130**, modification of the propyl functionality of FPR2 agonist **84** (see Table **12**) to an isopropyl yielded FPR2 antagonist **131**, which is the most potent non-peptide FPR2 antagonist identified to date.

Compound **132** (BVT173187; 3,5-dichloro-N-(2-chloro-5-methyl-phenyl)-2-hydroxy-benzamide) was reported as an inhibitor of FPR1-dependent signals, but without effect on an agonist binding [85]. Although this compound did not inhibit FPR2-dependent responses, neutrophil responses to C5a and IL-8 were attenuated by this molecule, suggesting a broader specificity and/or interaction with various intracellular domains [85]. Indeed, the chemical scaffold of this compound has similarity with other bioactive molecules, including a potent NF-κB inhibitor IMD-0354 (N-(3,5-bis-trifluoromethyl-phenyl)-5-chloro-2-hydroxy-benzamide) [140], naphtol AS-E and its derivatives, which are inhibitors of cyclic AMP-response element binding (CREB)-mediated gene transcription [141], and *m*-3M3FBS, which is a putative phospholipase C activator [142], as well as an inhibitor of Kv7 (KCNQ) voltage-activated potassium current [143].

Table 12.   Agonist Activity of Miscellaneous Derivatives 67-84 [45, 75, 79, 81, 116, 121, 123, 124]
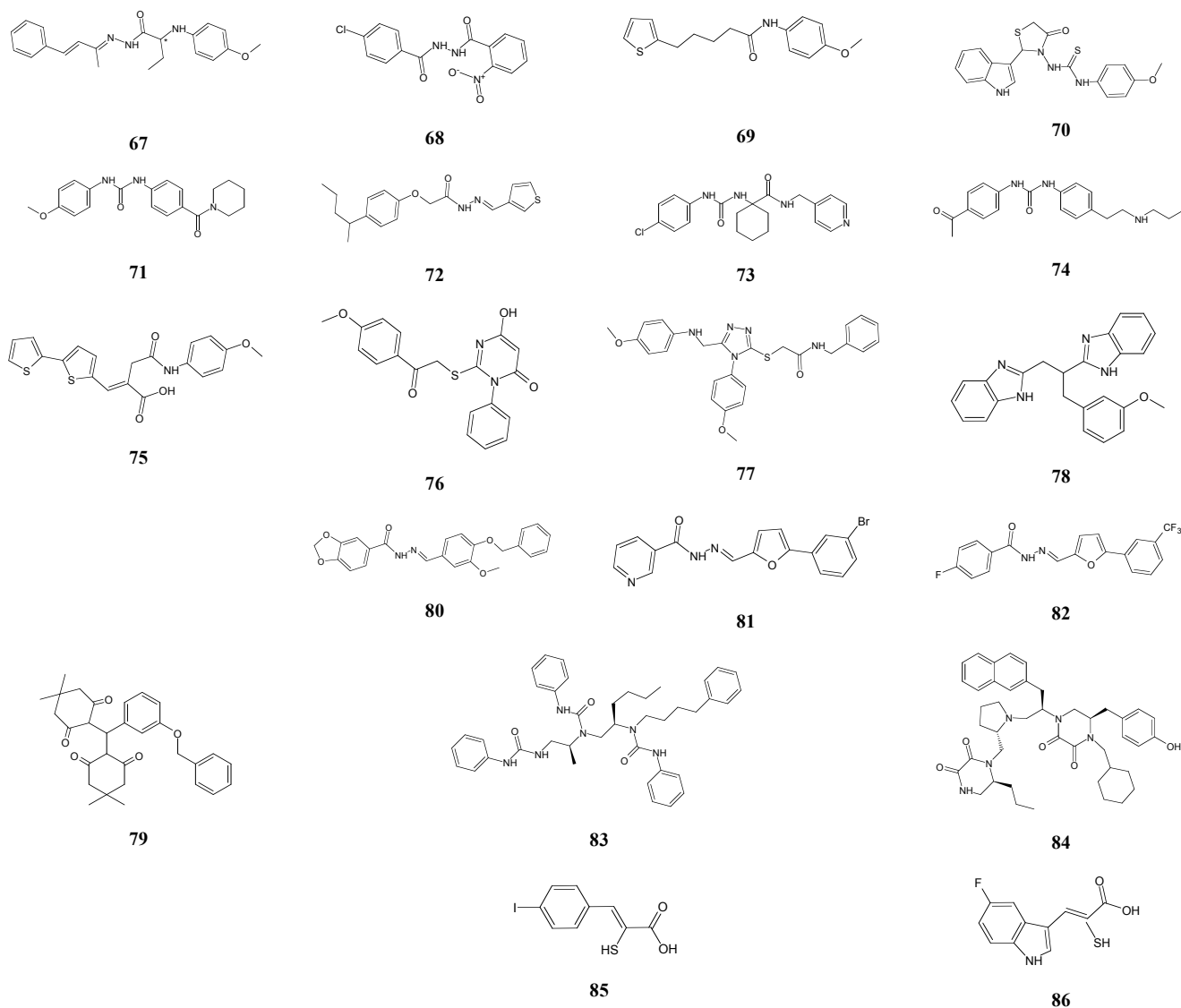
#	EC$_{50}$ (µM)			#	EC$_{50}$ (µM)[a]		
	FPR1	**FPR2**	**PMN**		**FPR1**	**FPR2**	**PMN**
67	N.A.	3.9	1.1	**77**	N.D.	0.045	N.D.
68	N.A.	12.6	7.0	**78**	N.D.	0.2	N.D.
69	N.A.	9.7	28.8	**79**	~20.0	N.D.	N.D.
70	N.A.	10.8	8.2	**80**	6.6	N.A.	0.63
71	18.6	11.1	1.9	**81**	N.A.	19.1	0.3
72	19.7	15.0	23.6	**82**	N.A.	18.3	0.6
73	N.D.[b]	0.04	N.D.	**83**	0.13	N.A.	N.D.
74	N.D.	0.1	N.D.	**84**	N.A.	0.14	N.D.
75	N.D.	0.006	N.D.	**85**	N.A.	~1.0	N.D.
76	N.D.	0.006	N.D.	**86**	N.A.	N.D.	N.D.

[a]EC$_{50}$ values were determined by measurement of Ca^{2+} flux in FPR1- and FPR2-transfected RBL cells (compounds **67-72** and **80-82**), CHO cells (compounds **73-78**), FPR1-transfected U937 cells (compound **79**), or HEK-293 cells (compounds **83-84**). [b]N.D., no data or EC$_{50}$ was not reported. N.A., no activity observed.

Table 13.   FPR1 Antagonist Activity of Diamides 87-92 [84]
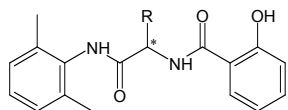
#	R	IC$_{50}$ (µM)^a
87		0.3
88		0.08
89		0.8
90		1.3
91		0.8
92		1.6

^{a}Inhibition of *f*MLF-stimulated intracellular Ca^{2+} flux in human neutrophils; IC$_{50}$ values were recalculated from reported pIC$_{50}$ values.

Bile acids, such as deoxycholic acid (DCA) and chenodeoxycholic acid (CDCA), were reported to antagonize FPR1 at high concentrations (>100 µM) [88, 89]. It should be noted that bile acids have multiple physiological functions, including activation of the farnesoid X receptor (FXR) [144] and Takeda G-protein-coupled receptor (TGR5), a G protein-coupled bile acid receptor (GPBAR1) [145]. Both FXR and TGR5 demonstrate pleiotropic functions, including immune modulation.

4.5. Molecular Modeling of FPR Antagonists and their Receptor Binding

Docking studies of low-activity non-peptide FPR1 antagonists, including sulfasalazine, losartan, phenylbutazone, sulpninpyrazone, several FPR1 ligands, and bile acids DCA and CDCA have been performed [120, 146]. These studies suggest that FPR1 antagonists could block the access of agonists to the receptor by binding at the outer side of the transmembrane helices, between loops E2 and E3 [146]. The authors concluded that while the interaction with Tyr257 is crucial for anchoring the carboxylic group of the bile acids to the receptor, H-bonding with Thr177 and Thr265 is important to determine the potency of bile acids.

Both research groups that described docking studies of FPR1 antagonists also reported pharmacophore models for these antagonists. The pharmacophore model developed by Edwards *et al.* [120] was based on best docking poses of four FPR1 antagonists, including cyclosporin H, phenylbutazone, and 2 peptide FPR1 antagonists [147, 148], into a rhodopsin-based FPR1 homology structure. This pharmacophore model has three points: two acceptors for H-bonding and one hydrophobic point. Using this model, structures of several FPR1 ligands were prioritized, including FPR1 agonist **79**. Moreover, our further pharmacophore modeling also showed that this model is not specific for FPR1 antagonists, because FPR1 agonists (e.g., compound **80**) also fit this model [75, 121]. Ferrari *et al.* [146] described two pharmacophore models for FPR1 antagonists that contain either two hydrophobic centers, one H-bonding donor site, and one H-bond acceptor/negative site (**model I**) or two H-bond acceptor sites and three hydrophobic centers (**model II**).

The present overview of FPR ligands can provide some general observations concerning differences between structures of agonists and antagonists. Indeed, many FPR1 antagonists investigated contain OH groups, which can serve as H-bond donors and/or acceptors upon binding to the receptor. This feature is much more characteristic for antagonists than of agonists. For example, FPR1 antagonists **112**, **113**, **115**, **116**, **118**, **120**, **122**, **128**, all diamides (Table **13**), and FPR2 antagonist **127** contain hydroxyl substituents, while there are no OH-containing FPR1 agonists and only a couple OH-containing FPR1/FPR2 agonists reported (compounds **75**, and **76**). It should be noted that substitution of methoxy, methyl, or nitro groups with a hydroxyl group in FPR1 agonists **62-64** converted them to FPR1 antagonists (e.g., compound **130**) [119]. The presence of OH groups in the structures of known FPR1 antagonists is in agreement with models of Ferrari *et al.* [146], which contain pharmacophore points with H-bond donor and acceptor nature. To date, there are no reports describing modeling of FPR2 antagonists. Because several potent FPR1/FPR2 antagonists were recently described, further molecular modeling should be conducted for determination of peculiarities of their ligand–receptor interactions.

5. COMPUTATIONAL MODELS FOR VIRTUAL SCREENING AND DESIGN OF FPR LIGANDS

Computational drug discovery is an effective strategy for accelerating and economizing the drug discovery and development process. Over the past decades, computational drug discovery methods, such as virtual screening, pharmacophore modeling, and molecular docking have been greatly improved [149]. Since the 3D crystal structures of FPRs have not yet been determined experimentally, ligand-based virtual screening represents an alternative approach for developing new structurally diverse FPR ligands. Among ligand-based virtual screening technologies, pharmacophore modeling and (quantitative) structure-activity relationship [(Q)SAR] analysis are methods for estimating properties of a chemical from its molecular structure. These methods have been used extensively in drug discovery research (reviewed in [150]). The pharmacophore and (Q)SAR functions can be useful for predicting the biological properties of virtual hits or untested compounds obtained from ligand-based virtual screening.

5.1. (Q)SAR Models

While a variety of molecular parameters can be used in the computational methods for (Q)SAR analysis [151], some of these parameters are complex physicochemical or

Table 14.   FPR1 Antagonist Activity of Methionine-derived Benzimidazoles 93-104 [84]
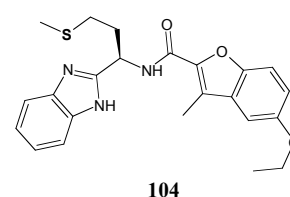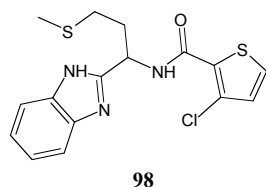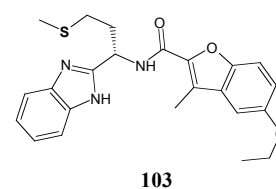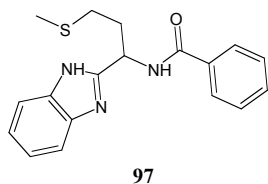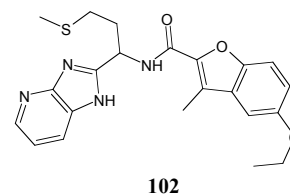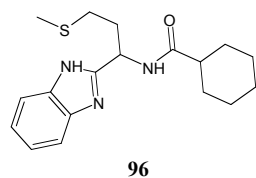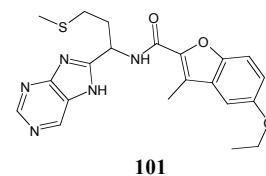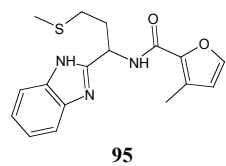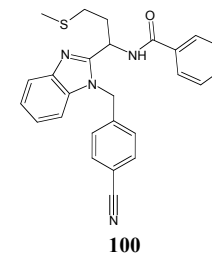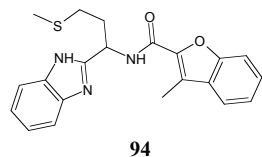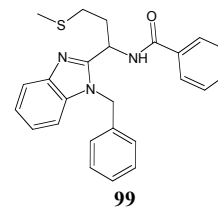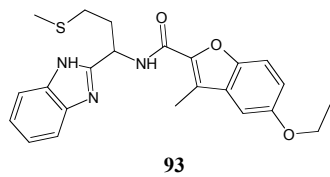
#	IC$_{50}$ (μM)^a	#	IC$_{50}$ (μM)
93	0.5	**99**	2.5
94	4.0	**100**	0.32
95	4.0	**101**	5.0
96	2.5	**102**	3.2
97	5.0	**103**	0.63
98	2.0	**104**	<25

^{a}Inhibition of fMLF-stimulated intracellular Ca^{2+} flux in human neutrophils; IC$_{50}$ values were recalculated from reported pIC$_{50}$ values.

geometrical 3D descriptors whose calculation is associated with difficulties resulting from molecular flexibility. Conversely, topological 2D descriptors, obtainable from the structural formula of a compound are very attractive because of their simplicity. A reasonable compromise between ease of interpretation and ease of computation was reported by Carhart *et al.* [152], who introduced atom pair descriptors as features of the environments of all atoms in the 2D representation of a chemical structure. This methodology has been widely used in the context of fragment-based similarity searches, ligand-based *in silico* drug screening, and database mining [153, 154].

Table 15.   FPR1 Antagonist Activity of Pyrazole-4-carboxamides 105-112 [86, 87]
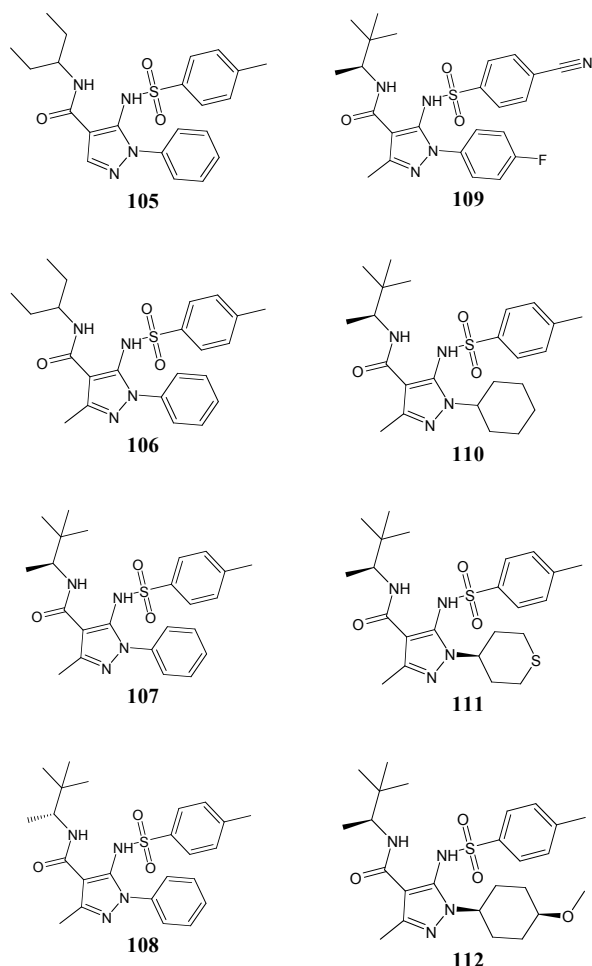
#	IC$_{50}$ (µM)^a	#	IC$_{50}$ (µM)
105	2.0	**109**	0.025
106	0.5	**110**	0.032
107	0.08	**111**	0.04
108	0.5	**112**	0.004

^{a}Inhibition of *f*MLF-stimulated intracellular Ca^{2+} flux in human neutrophils or HEK cells expressing recombinant human FPR1; IC$_{50}$ values were recalculated from reported pIC$_{50}$ values.

Recently we applied atom pair descriptors to represent selected set of FPR1/FPR2 agonists and obtained SAR rules, which were based on six atom pair descriptors [155]. Using binary classification tree methodology, we found that FPR1 agonists in the series investigated could be characterized by simultaneously satisfying certain conditions, as described [155]. Good quality and high predictive ability of the SAR model, as well as simplicity and rapidity of calculations associated with the binary tree algorithm, suggest promise in using the classification tree approach for large database mining and virtual screening of FPR agonists. This application of simple classification rules is especially attractive with the appearance of very large compound databases. However, virtual screening with highly diverse databases should be preceded by development of more sophisticated SAR rules based on large training sets consisting of compounds with various chemical types.

Within a series of molecules with a common scaffold, deriving QSAR models is useful for effective drug design. So far, QSAR models have not been published for FPR agonists or antagonists, and further efforts are necessary to develop such models.

5.2. FPR Pharmacophore Models

A pharmacophore is a model which represents the key physicochemical interactions that mediate biological activity [156]. A pharmacophore model can be used for ligand-based virtual screening and to characterize molecular features of ligands and their structural requirements for biological interaction [157]. Moreover, during virtual screening based on GPCR structure, the data set could be filtered with a simple pharmacophore model representative of the desired receptor ligands in order to exclude compounds considered to be unable to bind [158].

Several pharmacophore models of FPR1/FPR2 ligands have been reported to date [75, 79, 120, 121, 146]. We built a pharmacophore model of FPR1 agonists based on field point methodology developed by Cheeseright *et al.* [113-115]. This approach allowed us to compare diverse molecules in terms of their field similarity and create an alignment of their bioactive conformations [159]. Although the results of our modeling [79] are in agreement with the three-centered pharmacophore model obtained by Edwards *et al.* [120], our model also elucidates features not evident in the Edwards model. For example, the compact group of red spheres in the lower part of (Fig. **6**) is considered a potentially important characteristic of the template, likely representing interaction with electronegative features of the ligand-binding site. Investigation of a wider series of highly active FPR agonists in the future will generate more information about the significance of these field points.

Another useful approach to the construction of pharmacophore models consists of applying comparative molecular field analysis (CoMFA) [160], comparative molecular similarity indices analysis (CoMSIA) [161], and related ligand-based methodologies. This approach allows one to obtain a QSAR model along with spatial arrangement of pharmacologically important areas or points. As an example, QSAR based on CoMFA, CoMSIA, and molecular descriptors was built for ligands of P2Y1, an ADP-activated GPCR [162]. Hence, further is needed to derive such models within series of structurally related FPR agonists or antagonists.

**Table 16.   Antagonist Activity of Miscellaneous Derivatives at FPR1 (Compounds 113-126, and 132) and FPR2 (Compounds 127-131)
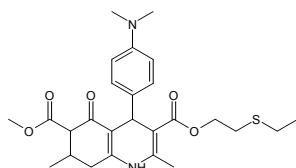[83, 120, 123, 127]**
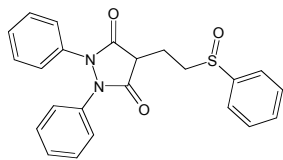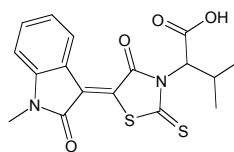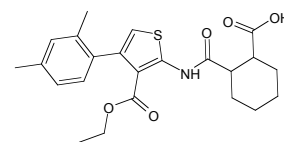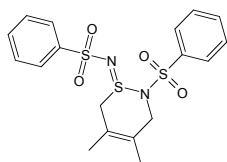

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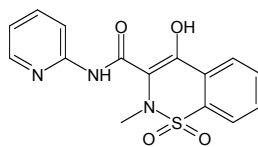
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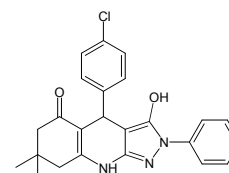
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116

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118

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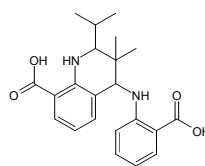
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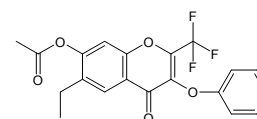
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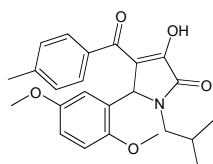
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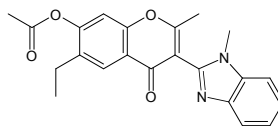
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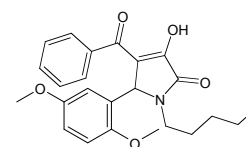
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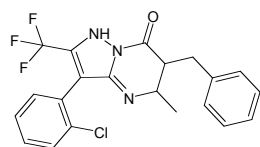
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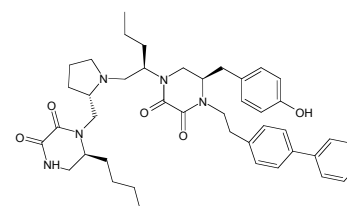
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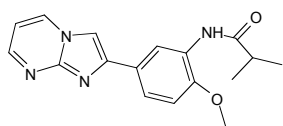
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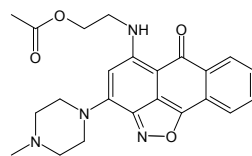
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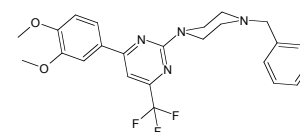
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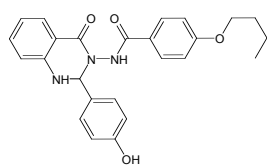
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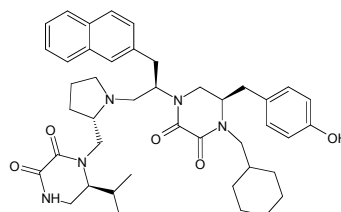
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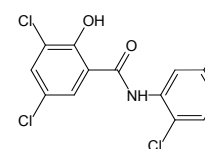
132

#	K_i (µM)	#	K_i (µM)	#	K_i (µM)
113	14.0	**120**	12.0[a]	**127**	0.27
114	18.0	**121**	2.0[a]	**128**	1.8
115	4.0[a]	**122**	4.0	**129**	3.2
116	7.0[a]	**123**	0.095	**130**	6.7[b]
117	4.0[a]	**124**	0.55	**131**	0.001[a]
118	11.0[a]	**125**	0.75	**132**	0.1
119	3.0[a]	**126**	0.002[a]		

[a]Inhibition of fluorescent ligand (WKYMVm-FITC) binding in U937 (FPR1) or RBL (FPR2) cells were used. [b]Binding ability (IC$_{50}$) was found in competition assay [^{125}I]-WKYMVm with membranes prepared from RBL-FPR2 cells.
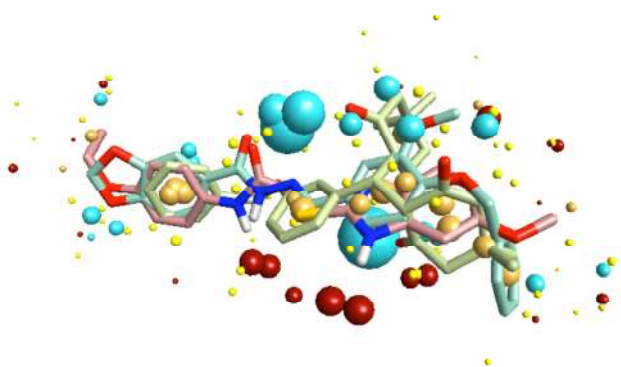
Fig. (6). Multi-molecule template for FPR1 developed from compounds **2**, **79**, and **81**.

5.3. Homology Models and Molecular Docking

Molecular docking is becoming a routine technique during the last decade because of the great success in establishing 3D structures of ligand-receptor complexes and in homology modeling. Although docking is hardly applicable now to large database mining because of high computational demands, its use for small data sets of FPR agonists and other compounds is very helpful for understanding peculiarities of interaction between ligands and receptors. Successful homology models of GPCRs can provide a structural basis for understanding ligand binding and receptor activation of GPCRs, and have been used for determining and comparing specificity profiles of related receptors, guiding drug design, virtual screening, and enriching the rate of ligand hits relative to a random collection of small-molecule compounds [163-166]. Moreover, induced fit docking (IFD) recently was introduced as a method that combines flexible ligand docking with receptor structure prediction and side chain refinement and could be considered as an approach for ligand-based protein structure optimization and homology modeling of GPCR [158, 167]. For drug design, it is important to understand the extent to which crystal structures or homology models can be used to best predict the binding mode of compounds. Thus, the set of active FPR ligands described in this review could be useful for selection of the best FPR homology model and/or for ligand-based FPR structure optimization.

For the identification of ligands based on novel chemotypes, a proven technique is virtual screening through molecular docking of chemically diverse libraries that bind to various GPCRs [168]. Although several homology models of FPR1/FPR2 have been reported to date [82, 105, 116, 120, 146, 169], most of them were used to explain the binding of FPR1/FPR2 agonists. One exception is the use of a combination of the FPR1 homology model and its pharmacophore model [120]. The combined model includes two electron acceptors, one hydrophobic point, and 23 sterically forbidden zones (i.e., exclusion spheres). This computational model was used for *in silico* screening of ~480,000 drug-like small molecules and improved the physical screening hit rate by 12-fold (1.2% vs. 0.1% hit-rate in a random compound collection).

6. CONCLUSION AND PERSPECTIVES

Although FPRs have great potential as pharmacologic targets for treatment of a variety of inflammatory diseases [9, 12, 13], a key question in the field is whether FPR agonists or antagonists have the most therapeutic potential. An additional question is whether FPR agonists/antagonists could represent more specific and/or effective therapeutics than currently available treatments for these processes and pathologies. Indeed, studies indicate that FPRs have a number of functions outside of the immune system and are involved in a variety of signaling systems. Thus, the off-target effects of FPR ligands *in vivo* may be unpredictable. Clearly, further studies are required to understand the complex role of FPRs *in vivo* and how they might serve as therapeutic targets. Although detailed pharmacological characterization of rodent FPRs is clearly interesting as a model for human diseases and determination of the biological roles of FPRs, rodent FPRs are distinct from their human counterparts and many agonists of human FPRs do not activate murine FPRs. Thus, the selection of appropriate *in vivo* models is also important to consider.

Current small-molecule FPR ligands have been discovered as result of HTS efforts and/or synthesis of new structures based on discovered hits and subsequent SAR-directed drug design. Because a key question in drug discovery is how to best prioritize and select hits for further evaluation from the many weakly active compounds, SAR information is the next step in attempts to estimate the chemical optimization potential of hits [170]. Note, however, that SAR

analysis of small-molecule ligands for murine counterparts of the human FPRs has not been performed and is clearly necessary if these compounds are being developed as therapeutics in murine models.

Despite the increased number of FPR agonists discovered in recent years, pharmacokinetic analysis has only been reported for one FPR2 agonist (compound **13**) [98] and all 3 known series of FPR1 antagonists [84, 86, 87]. This may reflect relatively weak interest from pharmaceutical companies for FPRs as perspective therapeutic targets. Indeed, only three companies have reported interest in development of FPR ligands, including Acadia Pharmaceuticals, Inc. (FPR2 agonists) [45], Amgen, Inc. (FPR2 agonists) [76, 98], and AstraZeneca, R&D, Charnwood (FPR1 antagonists) [84, 86, 87]. Furthermore, there are still no therapeutic drugs targeting FPRs in preclinical or clinical trials. Another possibility to apply such non-peptidic FPR ligands in clinical medicine is in the development of imaging agents. Indeed, several imaging conjugates based on the peptide FPR1 antagonist cFLFLFK have been reported, including a ^{64}Cu conjugate for a positron emission tomography (PET) [171], a ^{99m}Tc conjugate for a single photon emission computed tomography (SPECT) [172], a cyanine-7 conjugate for noninvasive near infrared fluorescence imaging [173], and a Gd(III) contrast agent for magnetic resonance imaging (MRI) [174]. Thus, imaging agents based on small-molecule FPR agonists could be desirable agents imaging neutrophils at sites of inflammation.

CONFLICT OF INTEREST

The author(s) confirm that this article content has no conflicts of interest.

ACKNOWLEDGEMENTS

ABBREVIATIONS

Anxa1$_{2–26}$	=	Annexin 1 fragment 2-26
CoMFA	=	Comparative molecular field analysis
CXCR	=	C-X-C chemokine receptor
DCA	=	Deoxycholic acid
FPR	=	Formyl peptide receptor
GPCR	=	G protein-coupled receptor
HIV	=	Human immunodeficiency virus
HTS	=	High-throughput screening
IL	=	Interleukin
LPS	=	Lipopolysaccharide
LTB	=	Leukotriene B4
LXA4	=	Lipoxin A4

NSAID	=	Non-steroidal anti-inflammatory drug
QSAR	=	Quantitative structure-activity relationship
SAA	=	Serum amyloid A
SAR	=	Structure–activity relationship
TNF	=	Tumor necrosis factor

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