

Conformation-Specific Effects of Raf Kinase Inhibitors

Miniperspective

Xiaolun Wang^{*,†} and Joseph Kim[‡][†]Takeda California, 10410 Science Center Drive, San Diego, California 92121, United States[‡]Blueprint Medicines, 215 First Street, Cambridge, Massachusetts 02142, United States

■ INTRODUCTION

The elucidation of signal-transduction networks that regulate most aspects of cell function has led to targeted cancer therapeutics¹ that focus on specific molecular drivers. Kinases have been one of the most intensively studied drug targets in cancer over the past decade,² and 14 small molecule kinase inhibitors (Figure 1) have been approved since 2001 as a result of extensive drug discovery efforts in this area. Coincident with this, a significant amount of structural information on human kinases and their interactions with small molecule inhibitors has accumulated. A recent survey³ revealed that crystal structures of 155 individual kinases among the 518 human protein kinases have been solved, many of them under multiple conformations and/or with numerous distinct inhibitors. This growing database of information has not only expanded our knowledge of kinase structural biology but also facilitated the design of potent and selective kinase inhibitors.

It has been well documented that protein kinases can adopt either active or inactive conformations, which can be targeted by inhibitors classified respectively as type I or type II.^{4–6} Kinase inactive conformations can be further divided into two major subclasses based on the position of the DFG-motif or α C-helix, with further inhibitor classification as type IIA and type IIB.⁷ Each of these kinase domain conformations has proven to be druggable as is summarized in Table 1 for all currently approved kinase inhibitors. Even for the same disease-relevant kinase, targeting disparate conformations has similarly produced clinically efficacious agents. For example, imatinib (type IIA)^{34–36} and dasatinib (type I)²⁶ bind to the inactive and active conformations of BCR-ABL, respectively, and both are effective against BCR-ABL-driven chronic myeloid leukemia. A second example is the pair of VEGFR inhibitors I (sorafenib)⁵⁰ and pazopanib,²⁸ antiangiogenesis agents used for the treatment of renal cell carcinoma. Targeting the inactive conformation has been touted as an approach toward obtaining more selective kinase inhibitors,^{8,9} although this has not been borne out for most type II inhibitors.⁶ Nevertheless, the ability to target different kinase conformations has provided opportunities^{4,6} to medicinal chemists for exploring kinase inhibitor chemical space, modifying inhibitor physical properties, overcoming resistance mutations,¹⁰ and increasing drug–target residence time.^{11,42}

B-Raf has been recognized as a promising drug target since the seminal paper “Mutations of the BRAF Gene in Human Cancer” was published by Davies et al. in 2002.¹² Since then, a number of B-Raf inhibitors have been described,^{13–15} and recently two novel and selective B-Raf inhibitors, **2** (vemurafenib, PLX4032)^{16,17} and *N*-{3-[5-(2-aminopyrimidin-

4-yl)-2-(1,1-dimethylethyl)thiazol-4-yl]-2-fluorophenyl}-2,6-difluorobenzenesulfonamide (dabrafenib, GSK2118436),^{15,18} have shown impressive results in clinical trials against metastatic melanoma harboring the B-Raf^{V600E} mutant kinase. More recently **2** was approved¹⁹ for unresectable or metastatic melanoma with the BRAF^{V600E} mutation. **2** is well-tolerated both clinically and preclinically,²⁰ while other B-Raf inhibitors have suffered from toxicities due to proliferative effects in preclinical studies. Recent studies^{21–23} suggest that B-Raf inhibitors can activate the RAF-MEK-ERK signaling pathway in cells containing wild type B-Raf through Raf dimerization, producing undesired proliferative effects. Moreover, it has been shown that Raf dimerization and resultant pathway activation are dependent on specific conformations that the inhibitors induce upon binding. This perspective focuses on conformational effects of inhibitor binding to Raf kinase and consequences on MAPK pathway activation in B-Raf^{WT} cells. These conformationally driven effects are highly relevant to the successful clinical path of **2** compared to other potent and selective B-Raf inhibitors.

■ RAF CRYSTAL STRUCTURES (KINASE DOMAIN)

As of June 2012, there were 25 B-Raf and 1 C-Raf X-ray crystal structures (Table 2, Figure 2) available in the PDB. The crystallographic results to date all reveal Raf as a dimer with a consistent interface, and this is unlikely driven solely by crystal packing. These structures also demonstrate that B-Raf can adopt all three commonly observed ATP binding site conformations (active, DFG-out, and α C-helix out) with various bound inhibitors. Type I inhibitors bind to a Raf active conformation, while type IIA inhibitors bind to the DFG-out conformation. Type IIB inhibitors bind to an α C-helix-out Raf conformation in which the highly conserved salt bridge between Lys483 and Glu501 is broken. Differences in these conformations are illustrated in Figure 3a, an overlay of three crystal structures of B-Raf with a type I (**3**, SB-590885),^{45,46} type IIA (**13**),^{47,48} and type IIB (**2**)⁴³ inhibitor. Compound **3** binds to the B-Raf active conformation featuring DFG-in and α C-helix-in configurations and a preserved ATP binding pocket, including the Lys483-Glu501 salt bridge. Figure 3b shows key H-bond interactions in the B-Raf/**3** complex. Compound **13** binds to and stabilizes B-Raf in a DFG-out, inactive conformation in which the ATP pocket is partially filled by Phe595 and Gly596 from the DFG motif. Repositioning of the DFG triad creates a hydrophobic pocket that is occupied by

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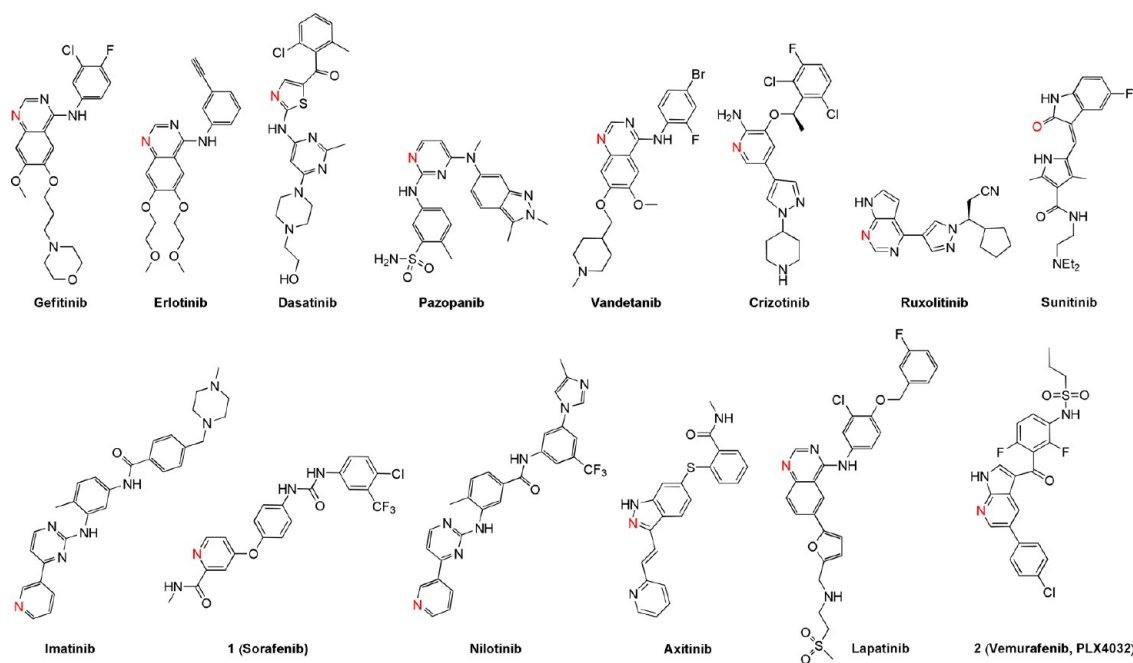


Figure 1. Approved kinase inhibitor drugs.

Table 1. Classification of Marketed Kinase Inhibitors

| name | targets | targeted conformation | type | crystal structure of kinase (PDB code) | ref |
|-------------|-----------------------------|------------------------------------|----------------|--|--------|
| gefitinib | EGFR | DFG-in/ α C-in | I | EGFR (2ITY) | 24 |
| erlotinib | EGFR | DFG-in/ α C-in | I | EGFR (1M17) | 25 |
| dasatinib | BCR-ABL, SRC | DFG-in/ α C-in | I | ABL (2GQG), SRC (3G5D) | 26, 27 |
| pazopanib | VEGFRs | DFG-in/ α C-in | I | two close analogs: VEGFR2 (3CJF, 3CJG) | 28 |
| vandetanib | VEGFRs, RET, EGFR | DFG-in/ α C-in | I | RET (2IVU) | 29 |
| crizotinib | c-MET, ALK | DFG-in/ α C-in | I | c-MET (2WGJ), ALK (2XP2) | 30 |
| ruxolitinib | JAK1, JAK2 | DFG-in/ α C-in ^a | I ^a | has not been reported | 31 |
| sunitinib | PDGFRs, VEGFRs, c-KIT, etc. | DFG-in or -out/ α C-in | I or IIA | I: ITK (3MIY). IIA: KIT(3G0E), KIT ^{D816H} (3G0F) | 32, 33 |
| imatinib | BCR-ABL, c-KIT, PDGFRs | DFG-out/ α C-in | IIA | ABL (1IEP/2HYI/1OPJ/3K5V), KIT (1T46), ABL2 (3GVU) | 34–38 |
| sorafenib | VEGFRs, PDGFRs, c-KIT, Raf | DFG-out/ α C-in | IIA | B-Raf (1UWH), B-Raf ^{V600E} (1UWJ) | 39 |
| nilotinib | BCR-ABL | DFG-out/ α C-in | IIA | ABL (3CS9) | 40 |
| axitinib | VEGFRs | DFG-out/ α C-in | IIA | structure with a close analogue has been reported | 41 |
| lapatinib | EGFR, HER2 | DFG-in/ α C-out | IIB | EGFR (1XKK) | 42 |
| vemurafenib | B-Raf | DFG-in/ α C-out | IIB | B-Raf (3OG7) | 43 |

^aRuxolitinib is structurally similar to tofacitinib, which binds to the active conformations⁴⁴ of JAK1 (3EYG) and JAK2 (3FUP).

Table 2. Conformations of Inhibitor-Bound B-Raf Kinases

| PDB | ligand | inhibitor type | protein conformation | key H-bonding residues | related PDB ^a |
|-------------------|--------|----------------|------------------------------|------------------------|---|
| 2FB8 | 3 | I | DFG-in, α C-helix-in | K483, E501, C532, D594 | 3D4Q, 3PPJ, 3PPK, 3PRF, 3PRI, 3PSB, 3Q4C, 3PSD, 3OMV(C-Raf), 4E26 |
| 3IDP ^b | 13 | IIA | DFG-out, α C-helix-in | K483, E501, C532, D594 | 1UWH, 1UWJ, ^b 3II5, 3Q96, 4DBN |
| 3OG7 ^b | 2 | IIB | DFG-in, α C-helix-out | Q530, C532, D594, G596 | 3C4C, 3C4D, ^b 3SKC, 3TV4, 3TV6, 4E4X, 4EHG, 4EHE |

^aReferences are available at <http://www.rcsb.org/>. ^bB-Raf^{V600E}.

the inhibitor *p*-chlorophenyl group (Figure 3c). As is typical for type IIA binders, the Lys-Glu salt bridge remains intact. **2** binds to a DFG-in, α C-helix-out, inactive B-Raf conformation, similar to binding of the type IIB EGFR/HER2 kinase inhibitor lapatinib to EGFR. The key salt bridge between Lys483 and Glu501 in B-Raf is broken, and the propyl group of **2** inserts into a newly formed hydrophobic pocket between the α C-helix and the N-lobe β -sheets (Figure 3d). Interestingly, one protomer of the B-Raf/**2** dimer is unoccupied and exists in

an active conformation, which may have relevance to models described recently for inhibitor driven, activated Raf dimers.

ENZYME ACTIVITY AND SELECTIVITY OF B-RAF INHIBITORS

Enzyme potencies and kinase selectivity profiles for a set of representative B-Raf inhibitors are summarized in Table 3. This set of inhibitors exhibits high potency against all Raf isoforms (A-Raf data not shown). Both type I inhibitors of the

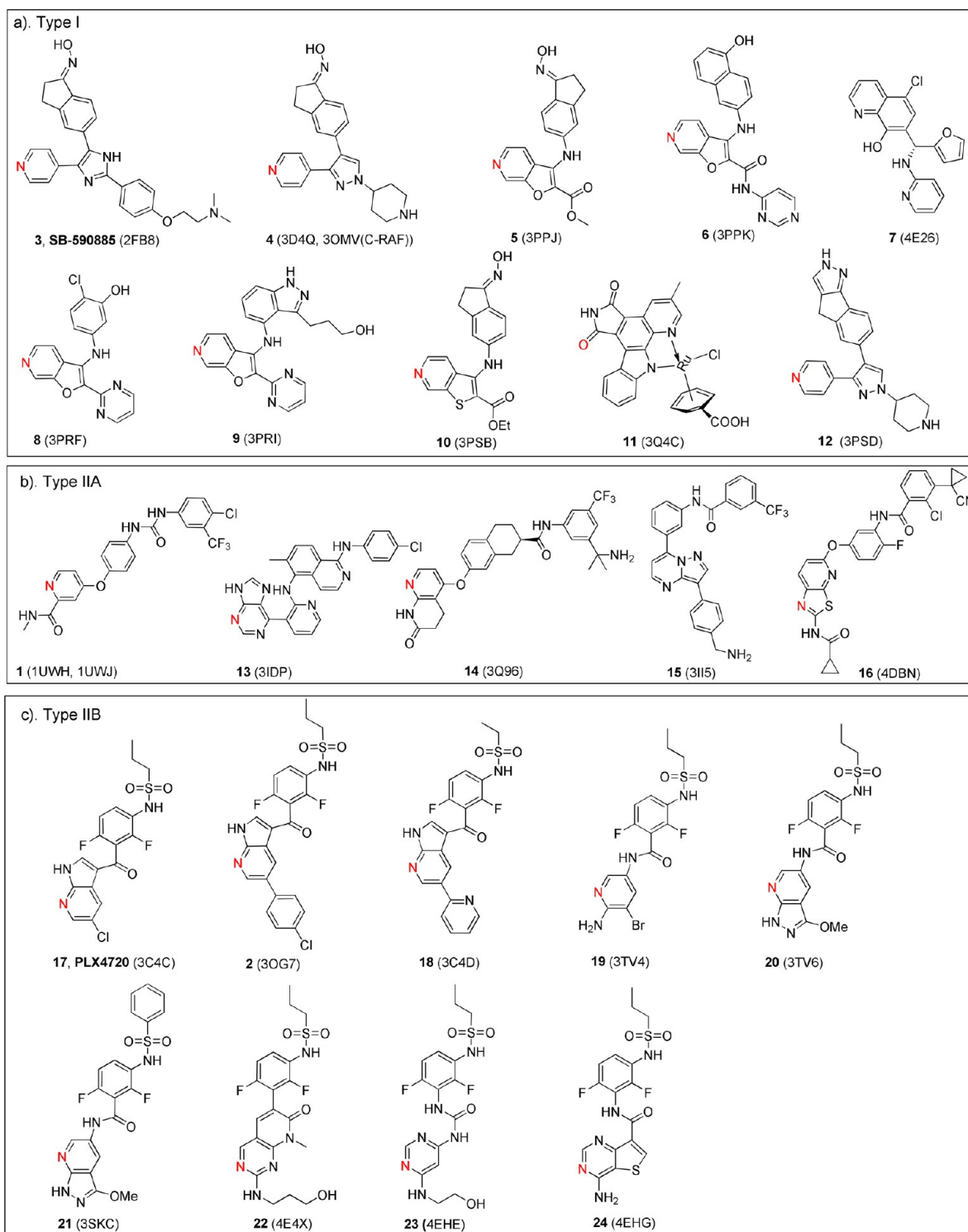


Figure 2. B-Raf inhibitors with X-ray crystal structures.

imidazole/pyrazole class and the type IIB inhibitors show a high degree of kinase selectivity, while the type IIA examples appear less selective, harboring some degree of tyrosine kinase activities. Nevertheless, all three classes of inhibitors show similar affinities for V600E and wild type B-Raf and minimal selectivity against C-Raf. A recent publication²² revealed that the $K_{M,ATP(app)}$ of full length B-Raf^{V600E} is 13-fold higher than that of wild type full length B-Raf. Therefore, while IC_{50} values of some inhibitors suggest varying degrees of selectivity⁴³ for B-

Raf^{V600E}, their K_i values do not support this (Table 3). For example, the affinities (K_i) of compound 17 (PLX4720)^{22,52} for B-Raf^{WT} and B-Raf^{V600E} are roughly equal, although the IC_{50} against B-Raf^{V600E} is 12-fold lower than that against B-Raf^{WT}. Thus, selectivity for mutant B-Raf over wild type as measured at the enzyme level is unlikely the major reason for the relatively benign toxicity profile exhibited by 2 (K_i values for 2 have not been reported).

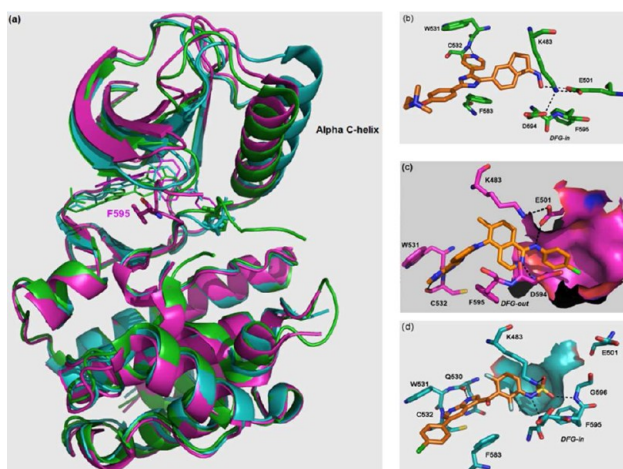


Figure 3. (a) Overlay of three inhibitor-bound conformations: DFG-in and α C-helix-in (green, 2FB8); DFG-out and α C-helix-in (purple, 3IDP, F595 as shown); DFG-in and α C-helix-out (cyan, 3OG7). (b) Binding site of 2FB8. (c) Binding site of 3IDP. (d) Binding site of 3OG7.

CELL SELECTIVITY/ACTIVITY AND TOXICITY

Type I and type IIB B-Raf inhibitors show high apparent selectivity (Table 4a) toward cell lines harboring B-Raf^{V600E}, as measured by viability and by inhibition of ERK phosphorylation. Type IIA inhibitors such as **1** and **13** additionally exhibit low micromolar inhibition against wild type B-Raf cell lines, which may be due to off-target kinase activities or alternatively to pan-Raf inhibition, including Raf dimers. A number of these inhibitors have demonstrated efficacy in B-Raf^{V600E} tumor models with commensurate inhibition of ERK phosphorylation in tumor tissue (Table 4a). While selective B-Raf inhibitors possess no or minimal growth inhibitory activity against cell lines containing wild type B-Raf, many have been shown to activate the RAF-MEK-ERK pathway in such lines, as was first reported for a Raf inhibitor in 1999.⁵³ The former feature of B-Raf inhibitors distinguishes them significantly from MEK inhibitors, which largely suppress MAPK pathway signaling in normal cells and may thereby provide B-Raf inhibitors with a larger therapeutic window relative to MEK inhibitors.^{23,46} The latter property, however, is likely the cause of undesired proliferative effects that have been associated with B-Raf inhibitors preclinically. For example, the type I selective inhibitor **25** (GDC-0879, Figure 4)^{22,49} induces skin acanthosis and hyperkeratosis in mice while another type I B-Raf inhibitor causes epithelial inflammation and hyperplasia in dogs.^{54,55} Similarly, the type IIA inhibitor **13** induced proliferation and

Table 4. Activity, Selectivity, And Effects of B-Raf Inhibitors

| inhibitor (type) | cell IC ₅₀ (μ M) | | | in vivo tumor growth inhibition model ^c | ref |
|----------------------|----------------------------------|-----------------|------------------------------------|--|------------|
| | A375 ^a proliferation | A375 p-ERK | HCT-116 ^b proliferation | | |
| 3 (type I) | 0.37 | 0.29 | 4.6 | A375 | 46 |
| 25 (type I) | <0.5 | <1 | >20 | A375 | 22, 49 |
| 1 (type IIA) | 2.4 | na ^d | 2–4 | Colo205, ^a A549 ^b | 50, 58 |
| 13 (type IIA) | 0.31 | 0.002 | 0.72 | A375, M24met ^e | 47, 48 |
| 17 (type IIB) | 0.5 | 0.046 | 27 | Colo205 | 52 |
| 2 (type IIB) | 0.31 | na ^d | >2 | A375 | 20, 59, 60 |

| inhibitor (type) | (b) Effects of B-Raf Inhibitors on B-Raf ^{WT} Tumors | | | ref |
|---|---|--|---|------------|
| | cell lines with p-ERK enhancement (pathway activation) | in vitro cell growth promotion | in vivo tumor growth promotion | |
| 26 (885-A) ^f (type I) | MM415, ^g WM852 ^g | not reported | not reported | 21 |
| 25 (type I) | H2122, ^b MeWo ^b | H226, ^h CaCo-2 ^h | LXFA983, ^b LXFA1041 ^b | 22 |
| 1 (type IIA) | less common: Calu-6, ^g MIA PaCa-2 ^f | not reported | not reported | 23, 48 |
| 13 (type IIA) | MIA PaCa-2 ^b | MIA PaCa-2 | MIA PaCa-2 | 48 |
| 17 (type IIB) | Calu-6, H2122, MeWo, | SW48 ^h | not reported | 22, 23, 61 |
| 2 (type IIB) | HCT-116, SkMel-31 ^h | WM1382, ^h YULOVY ^g | not reported | 60, 62 |

^aB-Raf^{V600E}; RAS^{WT}. ^bB-Raf^{WT}, KRAS^{MT}. ^cAll were correlated with pERK inhibition except **1** against A549. ^dNot available. ^eB-Raf^{WT}, NRAS^{MT}. ^fA close analogue of **3** (Figure 4). ^gB-Raf^{WT}, NRAS^{MT}. ^hB-Raf^{WT}, RAS^{WT}.

hyperplasia in normal tissues of mice.^{48,56} Moreover, both type I and type IIA inhibitors can promote wild type B-Raf tumor growth correlated with enhanced ERK phosphorylation in mouse xenograft models (Table 4b). Conversely, the closely related type IIB inhibitors **2** and **17** are well tolerated in animal models⁴⁵ and demonstrate no measurable in vivo growth enhancement of B-Raf^{WT} tumors, although increases in ERK phosphorylation have been observed in in vitro studies (Table 4b).

Table 3. Enzymatic Activity and Selectivity of Representative B-Raf Inhibitors

| inhibitor (type) | K _i /IC ₅₀ (nM) | | | kinase selectivity profile | | ref |
|----------------------|---------------------------------------|-------------------------------------|--------------------------------------|---|---|--------|
| | B-Raf ^{WT} | B-Raf ^{V600E} | C-Raf | other kinase hits | S (1 μ M) ^c /panel size ^d | |
| 3 (type I) | 0.3 ^a | 0.16 ^a | 1.72 ^a | clean | 0.00/46 | 45, 46 |
| 25 (type I) | 0.17 ^a | 0.19 ^a | 0.54 ^a | clean (only slightly hits CK1- δ) | 0.01/139 | 22, 49 |
| 1 (type IIA) | 22 ^{b,e} | 38 ^{b,e} | 6 ^{b,e} | RET, KIT, VEGFRs, PDGFRs, TIE1, etc. | 0.14/314 | 50, 51 |
| 13 (type IIA) | 1.0 ^a | 1.0 ^a | 0.3 ^a | LCK, TIE1/2, VEGFRs, JAK2, KIT, etc. | 0.10/350 | 47, 48 |
| 17 (type IIB) | 2.6 ^a /160 ^{b,f} | 4.0 ^a /13 ^{b,f} | 3.3 ^a /6.5 ^{b,f} | BRK | 0.02/65 | 22, 52 |
| 2 (type IIB) | 100 ^{b,f} | 31 ^{b,f} | 48 ^{b,f} | SRMS, ACK1, FGR, LCK, BRK, etc. | 0.04/289 | 43 |

^aK_i. ^bIC₅₀. ^cSelectivity score defined as the number (IC₅₀ < 1 μ M) of hits divided by the panel size. ^dRaf kinases are excluded. ^e[ATP] = 5 μ M. ^f[ATP] = 100 μ M.

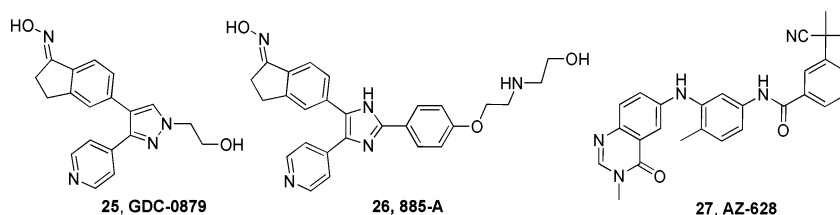


Figure 4. Structures of other B-Raf inhibitors.

2 was the first selective B-Raf inhibitor advanced to clinical trials. In the phase III clinical trial for metastatic melanoma patients with B-Raf^{V600E} mutation, **2** gave an impressive response rate of 48% with corresponding MAPK pathway inhibition.^{16,17} While **2** was generally well tolerated, 18–31% of the patients developed skin squamous-cell carcinoma with “very low invasive potential and no metastatic potential”.^{16,17} This proliferative effect is very likely related to the MAPK pathway activation potential of Raf inhibitors in B-Raf^{WT} cells. Table 5

Table 5. Cell Selectivity and Preclinical Toxicities of Three Types of B-Raf Inhibitors

| type | selective toward B-Raf mutant cells | activation of MAP pathway | toxicity in animal models |
|------|-------------------------------------|---------------------------|---|
| I | yes | yes | hyperkeratosis, acanthosis, hyperplasia, inflammation |
| IIA | dependent on the kinase selectivity | yes | hyperplasia |
| IIB | yes | yes but weak | no proliferative effects observed |

summarizes the cell selectivity and preclinical toxicities for three types of selective B-Raf inhibitors. Type IIB B-Raf inhibitors appear to have a unique ability to inhibit B-Raf^{V600E} driven disease while minimizing adverse proliferative effects. Recent publications^{21–23,57} shed light on why this is so.

■ DIMERIZATION OF RAF KINASES

In 1996, back-to-back publications revealed that homodimerization of two molecules of C-Raf leads to their functional activation.^{63,64} Five years later the heterodimerization of C-Raf and B-Raf in cells harboring activated Ras was discovered⁶⁵ and elevated activity of this B-Raf/C-Raf heterodimer was confirmed.^{66,67} Recently, Rajakulendran et al.⁵⁷ proposed a C2 symmetric, side-by-side model for Raf kinase dimers, recognizing that all six known B-Raf crystal structures published at that time displayed a common dimer interface. Their proposal that this dimer interface was indeed a biologically relevant interface was supported by site-directed mutagenesis studies of Raf kinase in *Drosophila* Schneider S2 cells. Figure 5 shows the overlay of three representative B-Raf and one C-Raf homodimers, illustrating a conserved juxtapositioning between two Raf protomers. As mentioned earlier, this structural feature exists in all known Raf crystal structures and, relevant to binding modes of type IIB inhibitors, involves part of the α C-helix. The Raf dimer interface is highlighted in Figure 6.^{22,57} Hydrophobic and hydrogen binding interactions are formed throughout the interface. Arg509 (B-Raf numbering), located near the center of the interface, plays a critical role in dimerization, interacting with Thr508, Arg506, and Phe516 from the associated protomer. Mutation of this residue to histidine (R509H) or mutation of the analogous residue in C-Raf (R401A/H) abolishes the formation of Raf dimers,

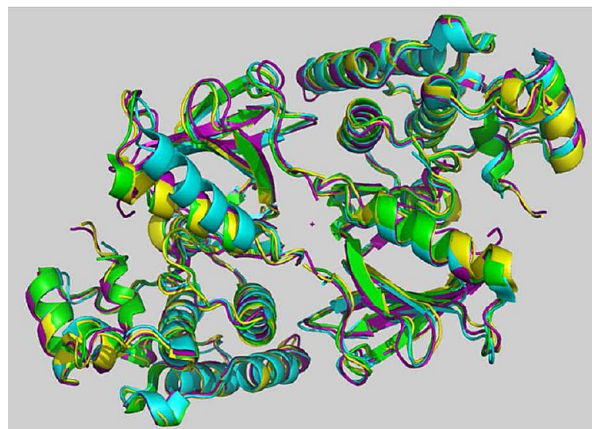


Figure 5. Overlay of B-Raf crystal structures (green, 2FB8; purple 3IDP; cyan 3OG7) and C-Raf crystal structure (yellow, 3OMV).

confirming the importance of this residue and the crystallographically observed interface in Raf dimerization and activation.^{22,23}

While the studies of Rajakulendran et al. demonstrated the association between Raf dimerization and Raf activation, no inhibitor was involved in their work. It was not until 2010 that Heidorn et al.²¹ first described inhibitor-induced Raf dimerization and ERK activation in B-Raf^{WT} cells. Shortly thereafter, papers by Hatzivassiliou et al.²² and Poulikakos et al.²³ reported detailed studies regarding Raf inhibitor induced activation of MAPK pathway signaling. Figure 7 shows a simplified version of their mechanisms.²³ Inhibitor binding to a Raf monomer can induce homo/heterodimerization with a second Raf protomer in the presence of Ras-GTP. Alternatively, inhibitor binding may stabilize pre-existing Raf homo/heterodimers. The paired Raf protomer appears to have considerably lower affinity for inhibitor (or much higher affinity for ATP) and significantly elevated kinase activity, activating MEK and downstream effectors until a second inhibitor can bind, typically at much higher concentration. All three papers^{21–23} revealed that inhibitor-induced Raf dimerization is reliant on the presence of activated Ras and that B-Raf^{V600E} cells maintain low levels of activated Ras, an important distinction between the two genotypes. Low Ras-GTP levels in B-Raf^{V600E} cells disfavor dimer mediated MAPK pathway activation and, coupled with the high $K_{m,ATP}$ of B-Raf^{V600E}, render these lines more sensitive to B-Raf inhibitors. Consequently, tumor growth driven by B-Raf^{V600E} is effectively thwarted by B-Raf inhibitors.

All three classes of B-Raf inhibitors can induce Raf dimerization and MAPK activation in B-Raf^{WT} cells, but there are notable differences among them (Table 6). Type I B-Raf inhibitors such as compound **25** are potent activators of the MAPK pathway. **25** promotes not only C-Raf homodimerization but also B-Raf/C-Raf heterodimerization.²² In animal studies, hyperplasia and inflammation have been linked to type

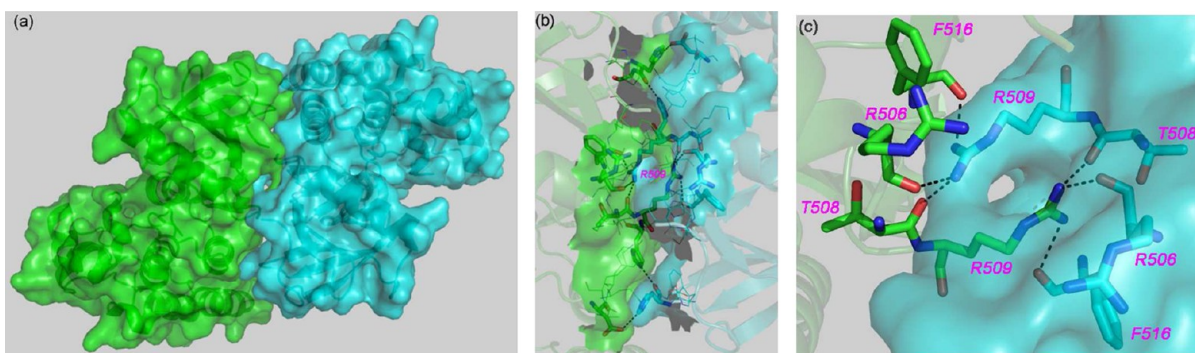


Figure 6. Interactions between two B-Raf protomers in 2FB8.

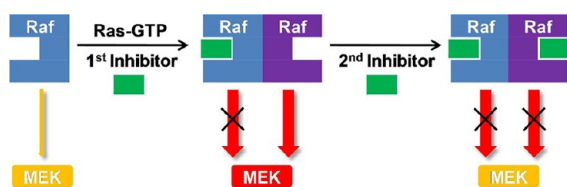


Figure 7. Mechanism of Raf activation in B-Raf^{WT} cells.

Table 6. Raf Dimerization Induced by Three Types of Inhibitors

| type | example | B- and C-Raf heterodimer ^a | C-Raf homodimer | MAPK pathway activation | ref |
|------|---------|---------------------------------------|-----------------|-------------------------|--------|
| I | 25, 26 | yes | yes | yes, significant | 22, 23 |
| IIA | 1, 27 | yes | yes | mixed results | 21–23 |
| IIB | 2, 17 | weak | yes | yes, moderate | 22, 23 |

^aIt has been reported that the Raf heterodimer possesses a higher kinase activity than the homodimer.⁶⁷

I inhibitors, accompanied by sustained levels of phosphorylated ERK.^{22,55} Results for type IIA inhibitors are less consistent among different chemotypes. It has been shown that compound 27 (AZ628)²² strongly induces Raf dimerization but does not elicit the enhanced phosphorylation of MEK and ERK characteristic of inhibitor-induced dimerization. The authors proposed that tight binding and a slow off rate help 27 occupy both ATP binding pockets of the dimer and prevent signal transduction. Unfortunately no preclinical toxicity studies for 27 have been reported to determine if the observed lack of MAPK pathway activation by this agent limits proliferative effects in vivo. Raf dimerization induced by 1 has also been reported.²³ While Heidorn et al.²¹ reported no MAPK activation in cells treated with 10 μ M 1, Poulidakos et al.²³ found that 1 at lower concentrations can activate the MAPK pathway. In line with this finding, cutaneous squamous cell carcinoma is an observed side effect in patients taking 1.⁶⁸

Finally, hyperplasia in a mouse model has been reported for the potent and selective type IIA inhibitor 13.^{48,56}

In contrast, type IIB inhibitors only weakly induce Raf dimerization and do not readily promote the translocation of Raf kinases to the membrane, steps considered important in Raf activation.²² Some B-Raf crystal structures with type IIB inhibitors show two protomers existing in different conformations, with one protomer lacking ligand or being only partially occupied (Table 7).⁶⁹ Movement of the α C-helix to an out position by type IIB inhibitor binding appears to disfavor Raf dimerization,²³ consistent with the α C-helix forming part of the dimerization interface (Figure 8). This conformational effect of

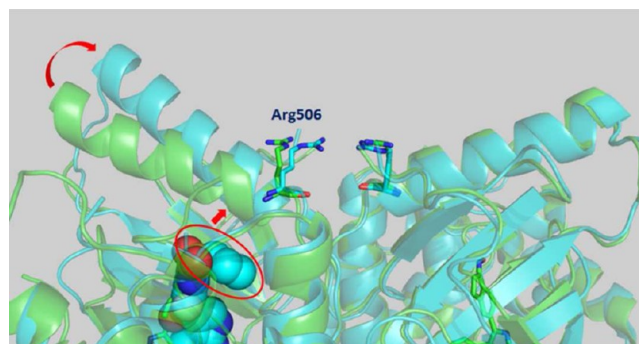


Figure 8. Effect of α C-helix-out conformation on the Raf dimerization (green, 2FB8; cyan, 3OG7). The positively charged side chain of the Arg506 from the α C-helix-out protomer is pushed close to that of the Arg506 from the other protomer.

type IIB inhibitors on Raf binding likely explains their minimal proliferative and favorable toxicity profile in preclinical studies, which allowed their progression into clinical trials. Lack of significant MAPK activation or inhibition in B-Raf^{WT} cells seemingly allows for dosing to greater target coverage in B-Raf mutant tumor without significant proliferative or antiproliferative effects in normal tissues, much to the benefit of large numbers of patients.

Table 7. Conformations of Protomers for Type IIB Inhibitors

| PDB code | protomer 1 | | | protomer 2 | | |
|----------|------------|------------------------------|--------------------------|--------------------------------|------------------------------|-------------|
| | ligand | conformation | salt bridge ^a | ligand | conformation | salt bridge |
| 3OG7 | 2 | DFG-in, α C-helix-out | no | none | DFG-in, α C-helix-in | yes |
| 3C4C | 17 | DFG-in, α C-helix-out | no | 17, 60% occupancy ^b | DFG-out, α C-helix-in | yes |
| 3C4D | 18 | DFG-in, α C-helix-out | no | none | DFG-out, α C-helix-in | yes |

^aIf the salt bridge between Lys483 and Glu501 is maintained. ^bThis suggests 17 is a weak type IIA inhibitor.

CONCLUSION AND PERSPECTIVES

The drug discovery industry has made significant progress toward agents targeting B-Raf since recognizing its important role in cancer progression.^{13,14} These drug candidates have proven to be critical tools in unraveling previously underappreciated intricacies of the MAPK signaling pathway.^{70–72} Recent publications^{21–23} have disclosed a novel mechanism for Raf inhibitor-induced activation of the MAPK pathway in B-Raf wild type cells. Inhibitors binding to different Raf kinase conformations display differential abilities in promoting Raf dimerization and MAPK activation and now provide a guide for designing the next generation of B-Raf inhibitors that may mitigate the adverse effects linked to pathway activation. Also, it was recently shown that combination of a Raf and MEK inhibitor can eliminate undesired proliferative effects in mouse models⁴⁸ and preliminary results from a phase I/II clinical trial combining a B-Raf inhibitor and a MEK inhibitor indicated no cutaneous squamous cell carcinoma incidences while producing a high objective response rate.⁷³ This combination not only may alleviate proliferative side effects but also might also address some of the resistance mechanisms emerging in patients treated with **2**.⁷⁴ For example, Poulikakos et al.⁷⁵ recently found that melanoma patients treated with **2** develop a variant of B-Raf^{V600E} lacking the Ras binding domain, which can form constitutive dimers, reactivate the MAPK pathway absent Ras-GTP, and escape inhibition by **2**. The authors suggested that a combination of a B-Raf inhibitor with a MEK inhibitor might delay the onset of this resistance, since they did not observe this B-Raf^{V600E} variant at a detectable level in **2** naive patients and because these **2** resistant cells are still sensitive to MEK inhibition. As more details of MAPK signaling biology are being elucidated,^{76,77} the desired profile for a B-Raf inhibitor will also evolve, eventually leading to better therapeutics for the treatment of B-Raf mutant cancers, including possible combinations with other mechanism-based agents.

AUTHOR INFORMATION

Corresponding Author

*Phone: (858) 731-8983. E-mail: xxw104@gmail.com.

Notes

The authors declare no competing financial interest.

Biographies

Xiaolun Wang obtained his Ph.D. in Organic Chemistry from Columbia University, NY, under the supervision of Prof. James Leighton and then joined Wyeth at Pearl River in 2005. He moved to the Cambridge site after the acquisition of Wyeth by Pfizer. In 2011, he joined Takeda California. He has led the chemistry teams for multiple projects in the immunology and oncology therapeutic areas. His main areas of expertise are structure based drug design, kinase inhibitor design, and fragment based drug discovery.

Joseph Kim obtained his Ph.D. in Biophysical Chemistry at Yale University, CT, and undertook postdoctoral studies in X-ray crystallography at The Rockefeller University, NY, under the direction of Dr. Stephen Burley. Dr. Kim joined Vertex Pharmaceuticals in 1995, where his accomplishments included solving the crystal structures of three novel proteins. In 1998 he joined Kinetix Pharmaceuticals and commenced work on structure-based design and optimization of protein kinase inhibitors. Upon acquisition of Kinetix by Amgen, he joined the Amgen Massachusetts site, continuing structure-based inhibitor efforts around numerous kinase targets, including VEGFR-2, Tie-2, and B-Raf. In 2011 Dr. Kim joined Blueprint Medicines, a company discovering selective agents against genetic drivers of cancer.

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ABBREVIATION USED

ACK1, activated CDC42 kinase 1; ALK, anaplastic lymphoma kinase; BCR-ABL, breakpoint cluster region Abelson kinase; BRK, breast tumor kinase; CK1- δ , casein kinase I isoform δ ; c-MET, MNNG HOS transforming gene; EGFR, epidermal growth factor receptor; ERK, extracellular signal-regulated kinase; HER2, human epidermal growth factor receptor 2; LCK, lymphocyte-specific protein tyrosine kinase; MEK, mitogen activated protein kinase kinase; PDGFR, platelet derived growth factor receptor; RET, rearranged during transfection; SRMS, src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites; VEGFR, vascular endothelial growth factor receptor

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