Electronic Supporting Information

Discovery of N-Substituted-2-Oxoindolin Benzoylhydrazines as c-MET/SMO Modulators in EGFRi-Resistant Non-Small Cell Lung Cancer

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Figure S1. Predicted binding mode of **3** in complex with DFG-in (A) and DFG-out (B) conformation of c-MET, respectively. The ligand and receptor are in green sticks and purple sticks and ribbons, respectively. H-bonds are represented as dashed yellow lines.



Figure S2. RMSD (Å) plot over simulation time (ns) of **3** in complex with DFG in (blue line) and DFG out (orange line) conformation of c-MET.



Figure S3. Histogram of protein-ligand interactions fraction of the 500 ns long MD simulation for **3** in complex with DFG in (A) and DFG out (B) conformations of c-MET, respectively. H-bonds are in green, hydrophobic contacts are in purple, and water-mediated interactions are in blue.

	Table S1.	Description	of the em	ployed 2	0 kinases.
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ТК	Description
ABL(ABL1)	Full-length human ABL [2-1130(end) amino acids of accession number
	NP_005148.2] wasexpressed as N-terminal His-tagged protein (126 kDa)
	using baculovirus expressionsystem. His-tagged ABL was purified by
	using Ni-NTA affinity chromatography.
CSK	Full-length human CSK [1-450(end) amino acids of accession number
	NP_004374.1] wasexpressed as N-terminal GST-fusion protein (78 kDa)
	using baculovirus expressionsystem. GST-CSK was purified by using
	glutathione sepharose chromatography.
EGFR	Human EGFR, cytoplasmic domain [669-1210(end) amino acids of
	accession numberNP_005219.2] was expressed as N-terminal GST-fusion
	protein (89 kDa) usingbaculovirus expression system. GST-EGFR was
	purified by using glutathione sepharosechromatography.
EPHA2	Human EPHB4, cytoplasmic domain [577-987(end) amino acids of
	accession numberNP_004435.3] was expressed as N-terminal GST-
	protein (73 kDa) using baculovirusexpression system. GST-EPHB4 was
	purified by using glutathione sepharosechromatography.
FGFR1	Human FGFR1, cytoplasmic domain [398-822(end) amino acids of
	accession numberNP_075598.2] was expressed as N-terminal GST-fusion
	protein (75 kDa) usingbaculovirus expression system. GST-FGFR1 was

	purified by using glutathione sepharosechromatography.
FLT3	Human FLT3, cytoplasmic domain [564-993(end) amino acids of
	accession numberNP_004110.2] was expressed as N-terminal GST-fusion
	protein (77 kDa) usingbaculovirus expression system. GST-FLT3 was
	purified by using glutathione sepharosechromatography.
IGF1R	Human IGF1R, cytoplasmic domain [959-1367(end) amino acids of
	accession numberNP 000866.1] was expressed as N-terminal GST-fusion
	protein (73 kDa) usingbaculovirus expression system. GST-IGF1R was
	purified by using glutathione sepharosechromatography.
ІТК	Full-length human ITK [2-620(end) amino acids of accession number
	NP_005537.3] wasexpressed as N-terminal GST-fusion protein (99 kDa)
	using baculovirus expressionsystem. GST-ITK was purified by using
	glutathione sepharose chromatography.
ТАКЗ	Human IAK3, catalytic domain [795-1124(end) amino acids of accession
57 113	numberNP_000206 2] was expressed as N-terminal His-tagged protein
	(41 kDa) using haculovirusexpression system. His-tagged IAK3 was
	nurified by using Ni-NTA affinitychromatography and gel filtration
	chromatography
KDB	Human KDR cytoplasmic domain [790-1356/end) amino acids of
KUK	accession number NP_002244_1] was expressed as N-terminal GST-fusion
	protein (90 kDa) usingbaculovirus expression system GST-KDB was
	purified by using glutathione senharosechromatography
	Full longth human LCK [1 E00(and) aming acids of accession number
	ND 005247.21 wasovproceed as N terminal CCT fusion protoin (85 kDa)
	NP_003347.2] wasexpressed as N-terminal GST-rusion protein (85 kDa)
	duing baculovirus expressionsystem. GST-LCK was purified by using
	giutatinone sepharose cirromatography.
	Human Well, cytoplasmic domain [956-1390(end) amino acids of
	accession numbering_000236.2] was expressed as N-terminal GST-rusion
	protein (76 kDa) usingbaculovirus expression system. GST-IVET was
	purmed by using glutatione septiarosechromatography.
PDGFRα(PDGFRA)	Human PDGFRQ, cytoplasmic domain [550-1089(end) amino acids of
	accession numbering_006197.1] was expressed as N-terminal GS1-fusion
	protein(89 kDa) using baculovirusexpression system. GSI-PDGFRα was
	purified by using glutathione sepharosechromatography.
PYK2(PTK2B)	Full-length numan PYK2 [1-967(end) amino acids of accession number
	NP_//526/.1] wasexpressed as N-terminal GS1-fusion protein (138 kDa)
	using baculovirus expressionsystem. GST-PYK2 was purified by using
	glutathione sepharose chromatography.
SRC	Full-length human SRC [1-536(end) amino acids of accession number
	NP_005408.1] wasexpressed as N-terminal GS1-fusion protein (87 kDa)
	using baculovirus expressionsystem. GSI-SRC was purified by using
	glutathione sepharose chromatography.
SYK	Full-length human SYK [1-635(end) amino acids of accession number
	NP_003168.2] wasexpressed as N-terminal GST-fusion protein (99 kDa)
	using baculovirus expressionsystem. GST-SYK was purified by using
	glutathione sepharose chromatography.
ТІЕ2(ТЕК)	Human TIE2, cytoplasmic domain [771-1124(end) amino acids of
	accession numberNP_000450.1] was expressed as N-terminal GST-fusion
	protein (68 kDa) usingbaculovirus expression system. GST-TIE2 was
	purified by using glutathione sepharosechromatography.
TRKA(NTRK1)	Human TRKA, cytoplasmic domain [436-790(end) amino acids of

	accession numberNP_001012331.1] was expressed as N- terminal GST-
	fusion protein (67 kDa) usingbaculovirus expression system. GST-TRKA
	was purified by using glutathione sepharosechromatography
TYRO3	Human TYRO3, cytoplasmic domain of [453-890(end) amino acids of
	accession numberNP_006284.2] was expressed as N-terminal GST fusion
	protein (76 kDa) usingbaculovirus expression system. GST-TYRO3 was
	purified by using glutathione sepharosechromatography

Compound (3) ¹H NMR (400 MHz, DMSO-d₆)







Compound (3) ¹³C NMR (101 MHz, DMSO-d₆)



Compound (6) ¹H NMR (400 MHz, DMSO-d₆)





Compound (6) ¹³C NMR (101 MHz, DMSO-*d*₆)





00 190 180 170 160 150 140 130 120 110 100 90 80 70 60 50 40 30 20 10 f1 (ppm)

Compound (10) ¹H NMR (400 MHz, DMSO-*d*₆)







Compound (10) ¹³C NMR (101 MHz, DMSO-*d*₆)





Compound (25) ¹H NMR (400 MHz, DMSO-d₆)





Compound (25) ¹³C NMR (101 MHz, DMSO-*d*₆)





Figure S4. SMO binding curves of compounds 3, 6, 10, and 25.



Figure S5. MTT Cell viability Assay with increasing concentrations of respective TKI (gefitinib for HCC827-GR and osimertinib for PC9-OR). Table shows the IC_{50} values for parental versus resistant NSCLC cell lines. Data are presented as mean of three biological replicates and four technical replicates ± SD. Statistical significance**p<0.01, ***p< 0.001 and ****p<0.0001.



Figure S6. MTT Cell viability Assay with increasing concentrations of compounds (**3**, **6**, **10**, **25**) in combination with IC_{50} value dose for respective TKI (gefitinib for HCC827-GR and osimertinib for PC9-OR). Table shows the IC_{50} values of the compound in combination with gefitinib or osimertinib for HCC827-GR and PC9-OR cell lines, respectively. Data are presented as mean of three biological replicates and four technical replicates ± SD. Statistical significance**p<0.01, ***p< 0.001 and ****p<0.0001.



Figure S7. Western Blot raw gels for Figure 4 in the main text.



Figure S8. Western Blot raw gels using HCC827-GR cell lines for Figure 6 in the main text.



Figure S9. Western Blot raw gels using PC9-OR cell lines for Figure 6 in the main text.



Figure S10. Annexin V/Propidium Iodide Apoptosis assay of Figure 7 in the main text.



Figure S11. Western Blot raw gels using PC9-OR cell lines for Figure 7 in the main text.



Figure S12. Western Blot raw gels using HCC827-GR cell lines for Figure 7 in the main text.