# **Supporting Information**

# **Optimization of 3-Pyrimidin-4-yl-oxazolidin-2-ones as Allosteric and Mutant Specific Inhibitors of IDH1**

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# **Contents**



# **General Comment on Synthesis for Compounds 1c-f**

An interesting analytical observation of the <sup>1</sup>H-NMR spectra for **1c-f** was a peak broadening and shift of ~0.4 ppm for the isopropyl (iPr) signals in the *R,R*- and *S,S*isomers, relative to the *R,S*- and *S,R*-isomers (Figure SI-1a vs. b for **IDH125** vs. **1e**). Smallmolecule X-ray crystallography of **IDH125** (Figure SI-1c) shows the molecule undergoes hydrophobic collapse to place the iPr and phenyl on the same side of the plane within van-der-Waals contact with each other, which could explain both the broadening (restricted rotation) as well as the upfield shift (shielding) of the iPr signals. The conformation is the same for the enantiomer (**1c)**, albeit with both phenyl and iPr on the opposite side of the plane of the pyrimidine. However, both the R,S (**1e**) and S,R (**1d**) have one substituent on each side of the plane leading to sharp iPr signals in the  ${}^{1}$ H-NMR





#### **Experimental details for the synthetic procedures and characterization data**

All starting materials were commercially available from Sigma Aldrich, VWR, Oakwood, Chembridge, Ryan Scientific and Anichem. All chiral ethylamines were commercially available as racemates, and were either used as such (with separation of the final compounds), separated prior to the final coupling reactions, or synthesized as pure enantiomers using Ellman chiral sulfinamides as chiral auxiliaries. Commerically available chiral building blocks were purchased as >97% ee, and assumed to have the chiral identity and purity as claimed; for example (R)-(+)-4 isopropyl-2-oxazolidinone was purchased from Aldrich (Cat #339946), with ee: 99% (GLC) and (S)-(−)-4-isopropyl-2-oxazolidinone was purchased from Aldrich (Cat # 298883), with ee: 98% (GLC).

(*S*)-3-(2-chloropyrimidin-4-yl)-4-isopropyloxazolidin-2-one

A solution of 2,4-dichloropyrimidine (3.86g, 25.9mmol) and (S)-4-isopropyloxazolidin-2-one (3.03g, 23.46mmol) in DMF (30mL) was stirred at room temperature and treated slowly with NaH. The resulting reaction mixture was stirred at room temperature for 2 h, diluted with EtOAc (200 mL), washed with 4% aqueous NaCl (3 x 75 mL), dried over Na2SO4, filtered and concentrated to dryness. The crude product was purified on silica gel with gradient dilution of ethyl acetate/heptane from 5 to 70% to give (S)-3-(2-chloropyrimidin-4-yl)-4-isopropyloxazolidin-2-one (3.507g, 14.5mmol, 62%). 1H-NMR (400 MHz, CD3OD) δ8.50 (d, J = 5.9 Hz, 1 H), 8.17 (d, J = 5.8 Hz, 1 H), 4.83 – 4.76 (m, 1 H), 4.48 – 4.43 (m, 2 H), 2.56 (dtd, J = 14, 7.0, 3.8 Hz, 1 H), 0.99 (d, J = 7.1 Hz, 3 H), 0.87 (d, J = 7.1 Hz, 3 H); LCMS  $m/z$  242.6 (M+H)<sup>+</sup>.

#### (S)-3-(2-fluoropyrimidin-4-yl)-4-isopropyloxazolidin-2-one

A solution of 2,4-difluoropyrimidine (3.5 mL, 41 mmol) and (S)-4-isopropyloxazolidin-2-one (5.3 g 41 mmol) in 30 mL DMF was cooled to 0 °C under N<sub>2</sub> atmosphere. NaH (2.1 g of 60% suspension, 53 mmol) was slowly added. A bubbling exotherm was observed. Internal temp was kept below 5 °C. After 5 minutes, the cold bath was removed. Reaction mixture (a sandy suspension) was allowed to warm to room temp and stir for 18 h. The reaction mixture was diluted with water (100 mL) and extracted with (3 x 75 mL) EtOAc. Organic layer was washed with water (50mL), and brine (50mL). Dried over Na<sub>2</sub>SO<sub>4</sub>, and concentrated on silica gel in vacuo. Column chromatography (EtOAc/heptane 10 to 100% gradient) gave 3.1 g (S)-3-(2-fluoropyrimidin-4-yl)- 4-isopropyloxazolidin-2-one (IV) as a crystalline white solid (33%). <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ

8.50 (dd, J = 5.8, 2.2 Hz, 1H), 8.19 (dd, J = 5.8, 3.8 Hz, 1H), 4.79 (dt, J = 8.1, 3.5 Hz, 1H), 4.48 – 4.34 (m, 2H), 2.64 (heptd, J = 7.0, 3.6 Hz, 1H), 1.01 (d, J = 7.0 Hz, 3H), 0.90 (d, J = 6.9 Hz, 3H). MS  $m/z$  471.8 and 471.8 (M + H)+. [CAUTION : HF byproduct]

#### 1-(5-(4-fluoro-3-methylphenyl)pyrimidin-2-yl)ethanone

1-(5-Bromopyrimidin-2-yl)ethanone (200 mg, 0.995 mmol), 4-fluoro-3-methylphenylboronic acid (306 mg, 1.99 mmol), K<sub>3</sub>PO<sub>4</sub> (634 mg, 2.98 mmol), and [2-(Di-tert-butylphosphino)-2',4',6'triisopropyl-1,1′-biphenyl][2-(2-aminoethyl)phenyl)]palladium (II) chloride (34 mg, 0.05 mmol) in toluene (6mL) was heated at 110ºC for 1 h. The reaction mixture was cooled to room temperature, and filtered through Celite. Filter cake was rinsed with EtOAc (30mL). The filtrate was poured into water (30mL). Layers were separated, and the aqueous was further extracted with EtOAc (2x20 mL). Combined organics were washed with water (20mL) and brine (20mL), dried over Na<sub>2</sub>SO<sub>4</sub>, filtered and concentrated directly onto silica gel. Column chromatography (10 - 50% EtOAc/heptane) gave 1-(5-(4-fluoro-3-methylphenyl)pyrimidin-2-yl)ethanone (68mg, 30%) as white solid. <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 9.09 (s, 2H), 7.52 – 7.41 (m, 2H), 7.24 – 7.16 (m, 1H), 2.85 (s, 3H), 2.41 (d, J = 2.0 Hz, 3H). MS m/z 231.0 (M+H)+.

## 1-(5-(4-fluoro-3-methylphenyl)pyrimidin-2-yl)ethanamine

1-(5-(4-fluoro-3-methylphenyl)pyrimidin-2-yl)ethanone (65 mg, 0.282 mmol), NH4OAc (0.326 g, 4.23 mmol), and NaBH3CN (71 mg, 1.13 mmol) were taken up in 200 proof EtOH (6mL), and heated at 130ºC for 3 minutes in a microwave apparatus. The mixture was concentrated to remove the EtOH. Crude was taken up in water (30mL) + EtOAc (25mL). 6N NaOH was added until aqueous pH was ~10. Separated layers, and extracted aqueous with EtOAc (25 mL). The combined organic layer was washed with brine (25mL) and dried with Na<sub>2</sub>SO<sub>4</sub>. Filtered and concentrated with reduced pressure to give crude product as a colorless oil (60mg), which was carried forward without further purification. MS m/z 231.9 (M+H)+.

## (*S*)-3-(2-chloropyrimidin-4-yl)-4-phenyloxazolidin-2-one

A solution of (*S*)-4-phenyloxazolidin-2-one (2.99 g, 18.3 mmol) and 2,4-dichloropyrimidine (3 g, 20.2 mmol, 1.1 equiv) in DMF (30 mL) was treated with NaH (95 %, 0.48 g, 19 mmol, 1.04 equiv), and the resulting mixture (yellow to red cloudy) was stirred at room temperature for 4 h. The reaction mixture was diluted with EtOAc (200 mL), washed with sat.  $NH_4Cl$  (75 mL) and 4% aqueous NaCl (2 x 100 mL), dried over Na<sub>2</sub>SO<sub>4</sub>, filtered and concentrated. Silica gel column chromatography (EtOAc/Heptane 0 to 50%) provided (*S*)-3-(2-chloropyrimidin-4-yl)-4phenyloxazolidin-2-one as a tacky white solid (2 g, 39%). <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>)  $\delta$  8.48 (d, J = 6.1 Hz, 1 H), 8.18 (d, J = 5.7 Hz, 1 H), 7.39 – 7.27 (m, 5 H), 5.80 (dd, J = 8.6, 3.5 Hz, 1 H), 4.87 (t, J = 8.8 Hz, 1 H), 4.37 (dd, J = 8.8, 3.8 Hz, 1 H); MS  $m/z$  276.5 (M + H)<sup>+</sup>.

**Table SI-1:** Chemical name, NMR chemical shifts and LCMS signal for each compound synthesized by the same methods as described for (S)-3-(2-fluoropyrimidin-4-yl)-4 isopropyloxazolidin-2-one, (*S*)-3-(2-chloropyrimidin-4-yl)-4-isopropyloxazolidin-2-one or (*S*)-3-(2 chloropyrimidin-4-yl)-4-phenyloxazolidin-2-one



#### (S)-3-(2-chloropyrimidin-4-yl)-4-ethyloxazolidin-2-one

Step 1: A solution of 2,4-dichloropyrimidine (500mg, 3.36mmol) and (S)-2-aminobutan-1-ol (299mg, 3.36mmol) was dissolved in DMF (6mL), heated at 65°C for 2h, cooled to rt and poured into water (30mL). Extracted with EtOAc (2x25mL), washed organics with water and brine, dried over Na<sub>2</sub>SO<sub>4</sub>, and concentrated onto silica. Silica-gel column chromatography (EtOAc / heptane, 10-100%) gave (S)-2-((2-chloropyrimidin-4-yl)amino)butan-1-ol (310mg, 46%). MS m/z 202.4 (M  $+ H$ )+.

Step 2: (S)-2-((2-chloropyrimidin-4-yl)amino)butan-1-ol (200mg, 0.992mmol) was dissolved in THF (6mL) and added *N,N*-diisopropylethylamine (260µL, 1.488mmol, 1.5eq). Triphosgene (300mg, 1mmol) was added and rm heated at 50°C for 4h. Added water (30mL), extracted into EtOAc (2x30mL), washed organics with water and brine, dried over Na<sub>2</sub>SO<sub>4</sub>, and concentrated onto silica. Silica-gel column chromatography (EtOAc / heptane, 10-100%) gave (S)-3-(2 chloropyrimidin-4-yl)-4-ethyloxazolidin-2-one

(155mg, 69%) as a white solid. <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>)  $\delta$  8.61 (d, H), 8.07 (d, H), 4.68-4.74 (m, H), 4,53 (t, H), 4,32 (dd, H), 1.79-1.86 (m, 2H), 0.85 (t, 3H). MS m/z 228.0 (M + H)+.

### 1-(5-(4-fluorophenoxy)pyrimidin-2-yl)ethanamine

Step 1: A solution of 1-(5-fluoropyrimidin-2-yl)ethanone (700 mg, 5.0 mmol) and 4-fluorophenol (616 mg, 5.50 mmol) in DMF (6mL) was treated with potassium carbonate (829 mg, 6.0 mmol) and heated to 50ºC for 3.5 h. The reaction mixture was poured into water (20mL), and extracted with EtOAc (2 x 20 mL). Organics were washed with water (20mL), brine (20mL), and dried over Na<sub>2</sub>SO<sub>4</sub>, filtered and concentrated on silica gel. Column chromatography (10-100% EtOAc / heptane) gave 1-(5-(4-fluorophenoxy) pyrimidin-2-yl)ethanone (295mg, 25%) as a white solid used directly in the following step. MS m/z 233.2 (M + H)+.  $^{1}$ H NMR (400 MHz, CDCl<sub>3</sub>)  $\delta$  8.55 (s, 2H), 7.23 – 7.07 (m, 4H), 2.78 (s, 3H).

Step 2: 1-(5-(4-fluorophenoxy)pyrimidin-2-yl)ethanone (290 mg, 1.25 mmol), NH<sub>4</sub>OAc (1.9 g, 24.6 mmol), and NaBH<sub>3</sub>CN (314 mg, 5.00 mmol) were taken up in 200 proof EtOH (20mL), and heated at 130°C for 3 minutes in a microwave apparatus. The mixture was concentrated to remove the EtOH. Crude was taken up in water (30mL) + EtOAc (25 mL). 6N NaOH was added until aqueous pH was ~10. Separated layers, and extracted aqueous with EtOAc (25 mL). The combined organic layer was washed with brine (25 mL) and dried with Na<sub>2</sub>SO<sub>4</sub>. Filtered and concentrated with reduced pressure to give 275 mg crude tan oil, which was carried forward without further purification. MS m/z 234.1 (M+H)+.

(*S*)-4-isopropyl-3-(2-((*R*)-1-phenylethylamino)pyrimidin-4-yl)oxazolidin-2-one (**1e**)

A solution of (S)-3-(2-chloropyrimidin-4-yl)-4-isopropyloxazolidin-2-one (96 mg, 0.395 mmol) and (*R*)-(-)-1-phenylethanamine (0.3 mL, 2.4 mmol, 6 equiv) in DMSO (1.5 mL) was heated at 110 °C for 2 hours. The reaction mixture was diluted with EtOAc (8 mL) and washed with water (30 mL). After separation, the aqueous phase was extracted with EtOAc (3 x 8 mL). Combined organics

were dried over Na<sub>2</sub>SO<sub>4</sub>, filtered and concentrated. Silica gel column chromatography (EtOAc/Heptane 10 to 50%) provided (*S*)-4-isopropyl-3-(2-((*R*)-1-phenylethylamino)pyrimidin-4 yl)oxazolidin-2-one (98 mg, 76%) as a white solid. <sup>1</sup>H NMR (400 MHz, CD<sub>3</sub>OD) δ 8.10 (d, J = 5.8 Hz, 1 H), 7.35 – 7.27 (m, 5 H), 7.23 – 7.15 (m, 1 H), 4.96 (q, J = 6.9 Hz, 1 H), 4.44 (br s, 1 H), 4.34 – 4.23 (m, 2 H), 2.72 – 2.58 (m, 1 H), 1.51 (d, J = 6.6 Hz, 3 H), 0.99 (d, J = 7.1 Hz, 3 H), 0.85 (d, J = 7.1 Hz, 3 H); HRMS  $m/z$  326.1746 M<sup>+</sup>.

1c, 1d, and 1f were synthesized by the same method described for 1e above, but using the appropriate chiral starting materials. 1a and 1b were also synthesized using the same methodology but using a racemic mixture of 1-phenylethanamine with the chirally pure oxazolidinone starting material. Chiral analysis with SFC chromatography on chiralpak IA 4.6 x 100mm 5µm column, 5-55% MeOH with 10mM NH4OH/CO2 at 5mL/min flow rate gave the following analysis:



(*S*)-3-(2-((*S*)-1-(biphenyl-4-yl)ethylamino)pyrimidin-4-yl)-4-isopropyloxazolidin-2-one (**5r**) A solution of (*S*)-3-(2-chloropyrimidin-4-yl)-4-isopropyloxazolidin-2-one (90 mg, 0.37 mmol), *N,N*diisopropylethylamine (0.455 mL, 2.61 mmol, 7.0 equiv) and racemic 1-(biphenyl-4 yl)ethanamine hydrochloride (87 mg, 0.37 mmol) in DMSO (1 mL) was heated at 110 °C for 2 h. The reaction mixture was diluted with EtOAc (8 mL) and washed with water (30 mL). After separation, the aqueous phase was extracted with EtOAc (3 x 8 mL). Combined organics were dried over Na2 SO4 , filtered and concentrated. Silica gel column chromatography (EtOAc/Heptane 10 to 50%) provided (*S*)-3-(2-((*S*)-1-(biphenyl-4-yl)ethylamino)pyrimidin-4-yl)-4 isopropyloxazolidin-2-one as the second eluted product (21 mg,  $14\%$ ) <sup>1</sup>H NMR (400 MHz, CD<sub>3</sub>OD)  $\delta$  8.14 (d, J = 5.8 Hz, 1 H), 7.58 – 7.52 (m, 4 H), 7.42 – 7.28 (m, 6 H), 5.06 (q, J = 7.1 Hz, 1 H), 4.63

(br s, 1 H), 4.34 – 4.25 (m, 2 H), 1.79 (br s, 1 H), 1.55 (d, J = 7.1 Hz, 3 H), 0.65 (br s, 3 H), 0.53 (br s, 3 H); HRMS  $m/z$  403.2139 (M + H)<sup>+</sup>.

(S)-3-(2-((S)-1-(5-(4-fluoro-3-methylphenyl)pyrimidin-2-yl)ethylamino)pyrimidin-4-yl)-4 isopropyloxazolidin-2-one (**IDH889, 5x**).

A solution of (*S*)-3-(2-fluoropyrimidin-4-yl)-4-isopropyloxazolidin-2-one (1055 mg, 4.68 mmol), 1- (5-(4-fluoro-3-methylphenyl)pyrimidin-2-yl)ethanamine (1300 mg, 5.62 mmol, 1.2 equiv) and diisopropylethylamine (908mg, 7.03mmol, 1.5 equiv) in DMSO (20 mL) was heated at 110 °C for 1 h. The reaction mixture was poured into water (60 mL) and extracted with EtOAc (2x50 mL). Combined organics were washed with water (40mL), brine (40mL), dried over Na<sub>2</sub>SO<sub>4</sub>, filtered and concentrated directly onto silica gel. Silica gel chromatography provided the mixed distereomers of (S)-3-(2-(1-(5-(4-fluoro-3-methylphenyl)pyrimidin-2-yl)ethylamino) pyrimidin-4 yl)-4-isopropyloxazolidin-2-one (560mg). Chiral separation was carried out with SFC (ID, 5µm, 20 x 250 mm) using 35% MeOH in CO2 to give (S)-3-(2-((S)-1-(5-(4-fluoro-3-methylphenyl)pyrimidin-2-yl)ethylamino)pyrimidin-4-yl)-4-isopropyloxazolidin-2-one as the first eluted product (302 mg, 15%) <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 8.87 (s, 2H), 8.23 (d, J = 5.8 Hz, 1H), 7.49 (d, J = 5.7 Hz, 1H), 7.43 – 7.30 (m, 2H), 7.21 – 7.11 (m, 1H), 6.26 (br s, 1H), 5.31 (br s, 1H), 4.75 (dt, J = 7.9, 3.3 Hz, 1H), 4.39 – 4.24 (m, 2H), 2.38 (s, 3H), 2.09 (br s, 1H), 1.66-1.62 (m, 3H), 0.90 (dd, J = 9.8, 6.0 Hz, 3H), 0.78 (br s, 3H). HRMS  $m/z$  437.2093 (M + H)+. [CAUTION : HF byproduct]

Chiral analysis with SFC chromatography on chiralpak IA 4.6 x 100mm 5µm column, 5-55% MeOH with 20mM NH4OH/CO2 at 5mL/min flow rate gave the following analysis:



**Table SI-2** . Chemical name, NMR chemical shifts and LCMS signal for each compound synthesized by the same methods as described for (*S*)-4-isopropyl-3-(2-((*R*)-1 phenylethylamino)pyrimidin-4-yl)oxazolidin-2-one (**1e**) and (*S*)-3-(2-((*S*)-1-(biphenyl-4 yl)ethylamino)pyrimidin-4-yl)-4-isopropyloxazolidin-2-one (**5r**)









**Table SI-3**. Chemical name, NMR chemical shifts and LCMS signal for each compound synthesized by the same method as described for (S)-3-(2-((S)-1-(5-(4-fluoro-3 methylphenyl)pyrimidin-2-yl)ethylamino)pyrimidin-4-yl)-4-isopropyloxazolidin-2-one (**5x**)



# (S)-3-(2-bromopyridin-4-yl)-4-isopropyloxazolidin-2-one

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To a solution of 2-bromo-4-fluoropyridine (0.79 mL, 7.3 mmol) and (S)-4-isopropyloxazolidin-2 one (2.38 g, 18.2 mmol) in DMF (15 mL) was added potassium carbonate (3.0 g, 21.9 mmol). The mixture was heated by microwave apparatus to 110 °C for 3 hours, then diluted with ethyl acetate (100 mL) and washed with water (2 x 50 mL). The organic phase was dried over sodium

sulfate, filtered and concentrated under reduced pressure. DCM (30 mL) was added to the crude residue and the precipitate was collected by filtration. The resulting filtrate was then concentrated under reduced pressure, acetonitrile (20 mL) was added and the predipitate was filtered again through the same filter to obtain 494 mg as a white solid which was carried forward without further purification. MS m/z 285.3 (M+H)+.

#### [(S)-3-(6-fluoropyridin-2-yl)-4-isopropyloxazolidin-2-one

To a 20 mL microwave reactor vial containing 2-bromo-6-fluoropyridine (1.67 g, 9.49 mmol), (S)- 4-isopropyloxazolidin-2-one (1.96 g, 15.18 mmol) and trans-N,N'-dimethyl-1,2 cyclohexanediamine (1.52 mL, 9.49 mmol) in 1,4-dioxane (10 mL), was added copper (I) iodide (1.81 g, 9.49 mmol) and potassium carbonate (3.95 g, 28.6 mmol). The vial was capped and heated by microwave apparatus to 130 °C for 1 hour. The reaction mixture was diluted with ethyl acetate (200mL) and vacuum filtered to remove a precipitate. The filtrate was washed with 3% aq ammonia (4 x 40 mL) followed by brine, then the organic portion was dried over sodium sulfate, filtered and concentrated with reduced pressure to a yellow oil. Silica-gel column chromatography (EtOAc / heptane, 0-10%) gave 991 mg as a white powder, which was carried forward without further purification. MS m/z 225.4 (M + H)+.

## (S)-4-isopropyl-3-(2-(((S)-1-phenylethyl)amino)pyridin-4-yl)oxazolidin-2-one (**4b**)

To a 10 mL microwave reactor vial containing a nitrogen purged mixture of (S)-3-(2 bromopyridin-4-yl)-4-isopropyloxazolidin-2-one (485 mg, 1.70 mmol), (S)-1-phenylethan-1-amine (0.439 mL, 3.40 mmol) and dioxane (5 mL), added sodium t-butoxide (327 mg, 3.40 mmol) and bis(tri-t-butylphosphine)palladium(0) (87 mg, 0.17 mmol). The vial was capped and heated by microwave apparatus to 130 °C for 20 minutes. The mixture was then diluted with ethyl acetate (100 mL), sonicated and vacuum filtered to remove a precipitate. The filtrate was purified by silica gel column chromatography (EtOAc/Heptane 0 to 50%) to obtain (S)-4-isopropyl-3-(2-(((S)- 1- phenylethyl)amino)pyridin-4-yl)oxazolidin-2-one as an off-white powder (117 mg, 20%). 1H NMR (400 MHz, DMSO-d6) δ 7.84 (d, J = 5.9 Hz, 1H), 7.37 – 7.33 (m, 2H), 7.31 – 7.25 (m, 2H), 7.20 – 7.14 (m, 1H), 7.09 (d, J = 7.7 Hz, 1H), 6.79 (dd, J = 5.8, 1.6 Hz, 1H), 6.60 (s, 1H), 5.00 – 4.90 (m, 1H), 4.48 – 4.42 (m, 1H), 4.35 (t, J = 8.7 Hz, 1H), 4.29 (dd, J = 9.0, 3.4 Hz, 1H), 1.98 – 1.85 (m, 1H), 1.40 (d, J = 6.9 Hz, 3H), 0.82 (d, J = 7.0 Hz, 3H), 0.66 (d, J = 6.8 Hz, 3H); HRMS *m/z* 326.1866

 $(M + H)^{+}$ .

(S)-4-isopropyl-3-(6-(((S)-1-phenylethyl)amino)pyridin-2-yl)oxazolidin-2-one (**4c**)

To a 5mL microwave reactor vial containing [(S)-3-(6-fluoropyridin-2-yl)-4-isopropyloxazolidin-2 one (310 mg, 1.38 mmol) in NMP (2 mL) was added ((S)-1-phenylethan-1-amine (0.356 mL, 2.76 mmol). The vial was capped and heated by microwave apparatus to 200 °C for 20 minutes. Further (S)-(-)-α-methylbenzylamine (0.710 mL, 5.52 mmol) was added and heating again to 200 °C for 20 minutes. The reaction mixture was diluted with EtOAc (20 mL), then washed with a saturated solution of sodium bicarbonate (2 x 10 mL) followed by water, then brine. Dried organic portion over sodium sulfate, filtered and concentrated under reduced pressure. Silica gel column chromatography (0-30% EtOAc in heptane) gave (S)-4-isopropyl-3-(6-(((S)-1 phenylethyl)amino)pyridin-2-yl)oxazolidin-2-one (55 mg, 12%). <sup>1</sup>H NMR (400 MHz, DMSO-d<sub>6</sub>) δ 7.37 (t, *J* = 8.0 Hz, 1H), 7.32 – 7.23 (m, 4H), 7.20 – 7.13 (m, 2H), 7.04 (d, *J* = 7.8 Hz, 1H), 6.29 (d, *J* = 8.1 Hz, 1H), 5.02 – 4.93 (m, 1H), 4.60 – 4.53 (m, 1H), 4.29 (t, *J* = 8.8 Hz, 1H), 4.19 (dd, *J* = 9.0, 3.3 Hz, 1H), 1.80 – 1.67 (m, 1H), 1.40 (d, *J* = 7.0 Hz, 3H), 0.61 (d, *J* = 7.0 Hz, 3H), 0.48 (d, *J* = 6.9 Hz, 3H); HRMS  $m/z$  326.1874 (M + H)<sup>+</sup>. [CAUTION : HF byproduct]

# **Biochemical IDH1R132H+/+ 2-HG LCMS assay protocol**

IDH enzyme assays were run in the following buffer: 50 mM HEPES, pH 7.3, 10 mM MgCl2, 50 mM KCl, 0.02% BSA, and 1mM DTT. Compounds were diluted in DMSO. IDH $^{R132H}$  was added to a final concentration of 500 pM. Spin down for 1min. NADPH (5 µM final concentration) and αKG (200 µM final concentration) were added as a premixed solution to start the reaction. Reactions were incubated for 60mins then quenched using formic acid (4.4% final concentration). 20 µL of quenched sample was added to 100 uL of acetonitrile, and samples were centrifuged before injection onto the LC/MS/MS system. Quantitation of 2-HG was performed using Agilent 1260 LC systems coupled to an Applied Biosystems API 4000 mass spectrometer.

## **Biochemical mutant (R132H and R132C) and wild type IDH1 fluorescence assay protocol**

Biochemical assays were run in the following reaction buffer: 50mM HEPES pH7.5, 50mM KCl, 1mM dithiothreitol (DTT), 10mM MgCl<sub>2</sub>, and 0.02% bovine serum albumin (BSA). IDH1 WT assays used 30 μM isocitrate and 30 μM NADP. IDH1 mutant assays used 100μM  $\alpha$ -ketoglutarate and 10 µM NADPH. Reactions were initiated through addition IDH1 protein, and monitored for the production (WT) or consumption (MUT) of NADPH through measuring the fluorescence of NADPH (excitation wavelength=355 nm, emission wavelength=520 nm). WT assay was run for 2h, R132H for 90mins, R132C for 45mins. No preincubation time prior to initiation of the reaction by addition of protein.

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## **Cellular mutant IDH1R132H assay**

Parental and IDH1<sup>R132H</sup> heterozygous mutant HCT116 cells (Horizon Discovery) were cultured in McCoy's 5A Modified medium with 10% fetal bovine serum. For assessing cellular 2-HG inhibition, cells were plated at 3,500 cells/well in 384-well plates (Corning) and incubated overnight at 37°C prior to compound addition. Compounds were added to wells in order to allow 10-point 3-fold dilutions in triplicate, starting at 10 µM. Cells were incubated with compounds for an additional 48 hours. To extract 2-HG, media was removed and 70 µL of 90% methanol was added to each well. Plates were then covered with foil seals and shaken for 30 seconds at high frequency, then incubated on dry ice for 15 minutes, spun at 2000 RPM for 15 minutes, and 30 µL of supernatant was used to measure 2-HG. 2-HG quantification was performed by LC-MS/MS analysis using an AB Sciex 4000 triple quadrupole mass spectrometer equipped with an Agilent 1200 series HPLC system, as previously described (Grassian, A.R.; Lin, F.; Barrett, R.; Liu, Y.; Jiang, W.; Korpal, M.; Astley, H.; Gitterman, D.; Henley, T.; Howes, R.; Levell, J.; Korn, J.M.; Pagliarini, R. Isocitrate dehydrogenase (IDH) mutations promote a reversible ZEB1/microRNA (miR)-200 dependent epithelial-mesenchymal transition (EMT). *J Biol Chem* **2012**, *287 (50)*, 42180-94.)

# **Proliferation assay of MCF10A-IDH1R132H cells**

IDH1<sup>R132H/+</sup> heterozygous mutant cells (Horizon Discovery) were cultured in DMEM/F12 media with hydrocortisone (0.5 mg/ml), cholera toxin (100 ng/ml), insulin (10 ug/ml), and 2% horse serum. Cells were plated for growth assays similarly to HCT116 cells as above, with the following exceptions. Compounds were incubated for 5 days, and cell proliferation was measured by the addition of Cell Titer Glo (Promega) according to manufacturer's instructions.

#### **Cell Culture and Sample Preparation for DNA Methylation Studies**

Parental, IDH1 wild type HCT116 human cell line, 2 isogenic mutant IDH1 cell lines (IDH1- R132C/+ 2A9 clone & IDH1-R132H/+ 2H1 clone) were grown in DMEM with 10% FCS and 1% Non-Essential Amino Acids and treated with DMSO (0.05%), IDH889 (3µM in DMSO) for 3, 7, 14 or 28 days. Cells were kept in culture with regular splitting and compound was replaced twice weekly. Genomic DNA was also obtained from Xenograft tumor samples from IDH889 pharmacology studies. Compound addition was as noted in the main text. Genomic DNA was extracted according to manufacturer's instructions (Qiagen AllPrep kit). Samples were analyzed according to manufacturer's instructions using the Illumina Infinium 450K BeadChip Array platform, which interrogates the methylation status of 485,000 potential methylation sites

across the genome. Infinium methylation data were pre-processed with the R/Bioconductor (Bioconductor.org) package 'minfi' to produce normalized beta (β) values, which range between 0 for unmethylated and 1 for fully methylated (0.5 being heterozygous methylation, assuming a diploid cell).

For cell-line samples, heatmaps were calculated with the R/Bioconductor packages 'fastcluster' and 'heatmap2' using Ward's clustering method.

For tumor tissue samples, hypermethylated and hypomethylated sites in xenograft tumors were heuristically selected by examining the minimum b-value difference at a site between replicates of a control and test sample. For example to select sites that were hypomethylated in IDH1 $R132H$ mutant tumors in relation to wild type tumors the minimum b-value at a site of the wild type pair was subtracted from the maximum b-value of the mutant pair to get the methylation difference in the direction of hypomethylation. If the b-value difference was less than -0.3 then the site was declared hypomethylated. A similar comparison using the same cutoff was performed with for the hypermethylation and for the treated vs. vehicle comparison. Methylation sites that were not able to be categorized by this method where declared ambiguous. Due to the heuristic nature of this categorization, it is likely that the ambiguous site sets could contain, and seem to, sites that are significantly perturbed by IDH $1^{R132H}$  mutation. Fisher's Exact test was used to confirm the methylation status of sites in the mutant are converted by **IDH889** to that similar to the WT.For example, a test for conversion from hypermethylated to hypomethylated was performed. This is represented in the first row (Hypermethylated vs. hypomethylated) of Table SI4. 'Common Sites' is the count of those sites that were declared hypermethylated in the mutant vs. WT context and hypomethylated in the vehicle vs. treatment comparison. 'Sites perturbed by mutation' are the sites that were classified as hypermethylated in the untreated mutant and 'Sites post treatment' are the sites that were classified as hypomethylated post treatment. The 'Total sites' is the number of sites that were assayed. The p-value was calculated by converting these numbers to a truth table and applying the fisher exact function from the the SciPy Stats package

(http://docs.scipy.org/doc/scipy/reference/stats.html).

All methylation data is available in the Gene Expression Omnibus (GEO: http://www.ncbi.nlm.nih.gov) under accession number GSE85571.

Table SI-4. Statistical comparisons of the methylation state of sites perturbed by IDH1<sup>R132H</sup> mutation vs. their status upon treatment with **IDH889**.





Table SI-5. IDH1<sup>R132H</sup> biochemical activity of initial analogs of IDH125 exploring tolerance for oxazolidinone, pyrimidine and α-methyl substitutions.







 $2a-d$ 

 $3a-f$ 



*\*-racemic at alpha-methyl benzylamine, not pure S-enantiomer as shown* 

#### **Small molecule crystallography for IDH125 and 1e**

#### Crystallization, data collection and structure determination

Crystals of compounds **IDH125** and **1e** were obtained by dissolving in a minimum amount of solvents from which the solvent was allowed to slowly evaporate at room temperature: for compound **IDH125** acetone was used, for compound **1e** a solvent mixture of acetone, heptane and diisopropyl ether.

Diffraction data were collected at 100 K on a Bruker AXS MicroStar diffractometer using a SMART 6000 CCD detector on a three-circle platform goniometer with Cu(K<sub>a</sub>) radiation ( $\lambda$  = 1.54178 Å) from a microfocus sealed tube generator equipped with Incoatec multilayer optics (QUAZAR focussing mirror system). 16 ω-scans at different φ-positions were performed to ensure appropriate data redundancy (5.6 in the monoclinic space group P21 for **IDH125** and 11.5 in the orthorhombic space group P212121 for **1e**, Friedel pairs not merged, respectively).The use of Cu radiation enables the absolute structure determination of **IDH125** and **1e** based on the anomalous scatterers present (O and N). For the C3*S*, C15*S* the Flack *x* parameter refined to 0.00(16) for **IDH125** and for C5*S*, C17*R* (C35*S*, C47*R* in molecule 2) the Flack *x* parameter refined to 0.04(13) for **1e** (Flack HD (1983)).

Crystal data, data collection and structure refinement details are summarized in supplemental data tables 1-7, respectively. The crystal structures were solved by dual space-recycling methods and refined based on full-matrix least-squares on  $F^2$  using the SHELXTL program suite (Sheldrick GM (2001)). The structure of **IDH125** consists of one independent molecule, the structure of **1e** consists of two independent molecules. In molecule 2, all numbers used for molecule 1 have been increased by 30. Data will be deposited at the Cambridge Crystallographic Data Centre CCDC.

Reference Citation (SHEXLTL and PLATON)

- 1. Sheldrick, G.M. **SHELXTL** Version 6.14, Bruker Analytical Instruments Inc. Madison, WI, USA, (2001).
- 2. Flack, H.D. On Enantiomorph-Polarity Estimation. *Acta Crystallogr.* **A39**, 876-881 (1983).
- 3. Spek, A.L. (2003) Single-crystal structure validation with the program PLATON. J. Appl. Cryst.; 36: 7-13.



**Figure SI-2**. ORTEP representation for the small-molecule structure of **IDH125**

![](_page_18_Picture_91.jpeg)

![](_page_19_Picture_126.jpeg)

Table SI-7. Atomic coordinates ( x 10<sup>4</sup>) and equivalent isotropic displacement parameters (Å<sup>2</sup>x  $10^3$ 

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![](_page_19_Picture_127.jpeg)

for IDH125. U(eq) is defined as one third of the trace of the orthogonalized U<sup>ij</sup> tensor.

![](_page_20_Picture_119.jpeg)

**Table SI-8**. Bond lengths [Å] and angles [°] for IDH125.

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![](_page_20_Picture_120.jpeg)

![](_page_21_Picture_118.jpeg)

![](_page_22_Picture_121.jpeg)

![](_page_23_Picture_127.jpeg)

Symmetry transformations used to generate equivalent atoms:

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**Table SI-9**. Anisotropic displacement parameters (Å2x 103) for IDH125. The anisotropic displacement factor exponent takes the form:  $-2\pi^2$ [ h<sup>2</sup> a<sup>\*2</sup>U<sup>11</sup> + ... + 2 h k a<sup>\*</sup> b<sup>\*</sup> U<sup>12</sup>]

	$U^{11}$	U <sup>22</sup>	U <sup>33</sup>	$U^{23}$	$U^{13}$	$U^{12}$	
C(1)	34(1)	22(1)	22(1)	$-1(1)$	8(1)	0(1)	
C(2)	24(1)	20(1)	21(1)	$-2(1)$	3(1)	$-2(1)$	
C(3)	18(1)	17(1)	19(1)	1(1)	4(1)	0(1)	
C(4)	23(1)	18(1)	25(1)	$-1(1)$	7(1)	$-2(1)$	

![](_page_24_Picture_126.jpeg)

**Table SI-10.** Hydrogen coordinates ( $x 10<sup>4</sup>$ ) and isotropic displacement parameters ( $\AA$ <sup>2</sup> $x 10$ <sup>3</sup>) for IDH125.

![](_page_24_Picture_127.jpeg)

![](_page_25_Picture_119.jpeg)

**Table SI-11.** Torsion angles [°] for IDH125.

![](_page_25_Picture_120.jpeg)

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![](_page_26_Picture_120.jpeg)

Symmetry transformations used to generate equivalent atoms:

# **Table SI-12.** Hydrogen bonds for IDH125 [Å and °].

![](_page_26_Picture_121.jpeg)

Symmetry transformations used to generate equivalent atoms: #1 -x+1,y-1/2,-z+1

**Figure SI-3.** ORTEP representation for the small-molecule structure of **1e**

![](_page_27_Figure_0.jpeg)

![](_page_27_Picture_100.jpeg)

![](_page_27_Picture_101.jpeg)

![](_page_28_Picture_147.jpeg)

**Table SI-14.** Atomic coordinates ( $\times$  10<sup>4</sup>) and equivalent isotropic displacement parameters ( $A^2x$  $10^3$ 

for 1a. U(eq) is defined as one third of the trace of the orthogonalized  $U^{ij}$  tensor.

![](_page_28_Picture_148.jpeg)

![](_page_29_Picture_118.jpeg)

**Table SI-15.** Bond lengths [Å] and angles [°] for 1a.

![](_page_29_Picture_119.jpeg)

![](_page_30_Picture_121.jpeg)

![](_page_31_Picture_121.jpeg)

![](_page_32_Picture_118.jpeg)

![](_page_33_Picture_121.jpeg)

![](_page_34_Picture_121.jpeg)

![](_page_35_Picture_121.jpeg)

$C(47)$ -C $(48)$ -H $(48A)$	109.5
$C(47)$ - $C(48)$ -H(48B)	109.5
H(48A)-C(48)-H(48B)	109.5
$C(47)$ -C $(48)$ -H $(48C)$	109.5
H(48A)-C(48)-H(48C)	109.5
H(48B)-C(48)-H(48C)	109.5
$C(54)-C(49)-C(50)$	118.32(15)
$C(54)-C(49)-C(47)$	121.56(15)
$C(50)$ -C(49)-C(47)	120.11(12)
$C(51)$ -C $(50)$ -C $(49)$	121.07(17)
$C(51)-C(50)-H(50)$	119.5
$C(49)$ -C $(50)$ -H $(50)$	119.5
$C(52)$ -C $(51)$ -C $(50)$	120.2(2)
$C(52)-C(51)-H(51)$	119.9
$C(50)-C(51)-H(51)$	119.9
$C(51)-C(52)-C(53)$	119.84(18)
$C(51)-C(52)-H(52)$	120.1
$C(53)-C(52)-H(52)$	120.1
$C(52)$ -C $(53)$ -C $(54)$	120.44(17)
$C(52)$ -C $(53)$ -H $(53)$	119.8
$C(54)-C(53)-H(53)$	119.8
$C(49)$ -C $(54)$ -C $(53)$	120.16(19)
$C(49)$ -C $(54)$ -H $(54)$	119.9
$C(53)-C(54)-H(54)$	119.9

Symmetry transformations used to generate equivalent atoms:

![](_page_36_Picture_160.jpeg)

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![](_page_36_Picture_161.jpeg)

 $\_$  , and the set of th

![](_page_37_Picture_121.jpeg)

C(51)	51(1)	40(1)	114(2)	30(1)	$-31(1)$	$-12(1)$
C(52)	38(1)	74(1)	107(2)	60(1)	$-17(1)$	$-16(1)$
C(53)	24(1)	131(2)	49(1)	53(1)	$-5(1)$	$-6(1)$
C(54)	21(1)	88(1)	30(1)	16(1)	$-1(1)$	$-9(1)$

**Table SI-17.** Hydrogen coordinates ( $\times$  10<sup>4</sup>) and isotropic displacement parameters ( $\AA^2$  $\times$  10<sup>3</sup>) for 1a.

![](_page_38_Picture_133.jpeg)

![](_page_39_Picture_118.jpeg)

**Table SI-18.** Torsion angles [°] for 1a.

![](_page_39_Picture_119.jpeg)

![](_page_40_Picture_121.jpeg)

![](_page_41_Picture_121.jpeg)

Symmetry transformations used to generate equivalent atoms:

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![](_page_42_Picture_44.jpeg)

**Table SI-19.** Hydrogen bonds for 1a [Å and °].

Symmetry transformations used to generate equivalent atoms:

#1 x-1/2,-y+1/2,-z+1 #2 x+1/2,-y+1/2,-z+1

![](_page_43_Figure_0.jpeg)

**ATYPICAL** 

**MUTANT** 

![](_page_43_Figure_3.jpeg)

# **Table SI-20:** %control values for IDH125 at 10µM vs DiscoverX kinase panel

![](_page_43_Picture_70.jpeg)

![](_page_44_Picture_115.jpeg)

![](_page_45_Picture_115.jpeg)

![](_page_46_Picture_115.jpeg)

![](_page_47_Picture_115.jpeg)

![](_page_48_Picture_115.jpeg)

![](_page_49_Picture_115.jpeg)

![](_page_50_Picture_115.jpeg)

![](_page_51_Picture_115.jpeg)

![](_page_52_Picture_115.jpeg)

![](_page_53_Picture_115.jpeg)

![](_page_54_Picture_115.jpeg)

![](_page_55_Picture_115.jpeg)

![](_page_56_Picture_155.jpeg)

# **Crystallography for IDH889 with IDH1R132H+/+ [PDB ID: 5TQH]**

### Protein expression and purification

The R132H mutant IDH1 was expressed in *E. coli* cells using a construct expressing human IDH1 bearing the R132H mutation with N-terminal 6xHis tag and PreScission protease cleavage site. *E. coli* strain Rosetta™2(DE3) (Novagen) transformed with the IDH1<sup>R132H</sup> expression construct was grown at 37<sup>°</sup>C in shaker flasks to an OD<sub>600</sub> of 0.8 in Terrific Broth (Teknova) with 50 $\mu$ g/ml of Kanamycin and 34 $\mu$ g/mL of chloramphenicol, then cooled down to below 18°C. IDH1<sup>R132H</sup> protein expression was induced by addition of Isopropyl-*β*-D-thiogalactopyranoside (IPTG) to 0.2 mM for 18 hours at 18° C. The harvested cells were resuspended in lysis buffer (50mM Tris pH=7.4, 500mM NaCl, 20mM Imidazole, 0.5mM DTT) containing DNAse I and protease inhibitors (complete EDTA-free protease inhibitor tablets (1 tablet per 50mL of buffer) and 200uM PMSF), and lysed on ice using a microfluidizer (M-110L, Microfluidics). After lysis, Trition X-100 was added to 0.1% and stirred at 4°C for 30 minutes. The cleared lysate containing His-tagged IDH1<sup>R132H</sup> fusion protein was then loaded onto 2x 5mL HisTrap FF crude columns (GE Healthcare), and the His-tagged protein eluted with Ni Elution Buffer (50mM Tris pH=7.4, 150mM NaCl, 200mM Imidazole, 0.5mM DTT). Peak eluted fractions were concentrated to 30mL, EDTA was added to 1mM and GST-PreScission protease (*in house*) was added to 3U/100µg of protein. The sample was dialyzed against 2L Dialysis Buffer I (20mM Tris pH=7.4, 150mM NaCl, 0.5mM DTT, 50mM Imidazole) for 6 hours at 4° C, then dialyzed against 2L of Dialysis Buffer II (20mM Tris pH=7.4, 150mM NaCl, 0.5mM DTT) at 4°C for at least 6 more hours. GST-PreScission cleaved sample was rocked with Glutathione Agarose Beads, spun down and then the supernatant was loaded through a 5mL HisTrap HP column (GE Healthcare) and the flow through was collected. The collected flow through was then diluted with 20mM Tris pH 7.4 and 0.5mM DTT until the conductivity dropped to less than 5 mS/cm and loaded onto a HiTrap Q column (GE Healthcare). The tag-free IDH1 $R132H$  protein was then collected from the flow through of HiTrapQ column (GE Healthcare) and further purified by size exclusion chromatography (HiLoad 26/60 Superdex 200,

GE Healthcare). The purified IDH1<sup>R132H</sup> was concentration to 5 mg/ml in buffer (20 mM Tris pH7.5, 150mM NaCl), and frozen in liquid N2 for storage at -80°C.

## Crystallization, data collection and structure determination

To obtained crystals of IDH1 $R132H$ :compound complex, IDH1 $R132H$  was diluted to 1mg/mL in storage buffer then incubated with compound at 2-5x molar excess of protein concentration. The mixture was concentrated 10 fold prior to crystallization. The complexes were crystallized using sitting drop vapor diffusion method at 20 °C by mixing equal volumes (2  $\mu$ L + 2  $\mu$ L) of protein:compound mixture and crystallization solution (0.1 M Bis-Tris pH5.5-6.5 and 1.45-1.7 M Trisodium citrate dehydrate). In all cases, the crystals were directly looped from their mother liquor and flash frozen in liquid nitrogen for diffraction experiment.

Crystals of all three IDH1 $R132H$ : compound complexes were determined to have the orthorhombic space group  $P2_12_12_1$  with two complexes in the asymmetric unit. Each complex comprises a dimer of IDH1 $R132H$ , with each protein in complex with one NADPH molecule (co-purified with protein) and one compound molecule. A citrate molecule is also modeled at the substrate binding site for each protein, as a result of presence of high concentration of trisodium citrate dihydrate in the crystallization solution.

All diffraction data were collected at the X-ray Operations and Research beamline 17-ID at the Advanced Photon Source, Argonne National Laboratory, with the crystal kept at 100K and wavelength of X-ray beam at 1.0 Å. The diffraction data from all crystals were integrated and scaled using autoPROC (6). The structures were solved by molecular replacement with Phaser (1) using another IDH1<sup>R132H</sup> structure<sup>6</sup> as a starting model. Model building and refinement was performed using COOT (5) and PHENIX (2). Statistics for the collected data and refined model are summarized in Table SI-21. PDB coordinates and accompanying structure factors will be deposed to protein data bank.

#### Reference Citation (PHENIX and COOT)

- 4. McCoy AJ, Grosse-Kunstleve RW, Adams PD, Winn MD, Storoni LC, et al. (2007) **Phaser** crystallographic software. J Appl Crystallogr 40: 658–674. doi: 10.1107/s0021889807021206
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Richardson JS, Terwilliger TC, and Zwart PH. **PHENIX**: a comprehensive Python-based system for macromolecular structure solution. Acta Cryst. D66, 213-221 (2010).

- 6. Afonine PV, Grosse-Kunstleve RW, Echols N, Headd JJ, Moriarty NW, Mustyakimov M, Terwilliger TC, Urzhumtsev A, Zwart PH, and Adams PD. Towards automated crystallographic structure refinement with **phenix.refine**. Acta Cryst. D68, 352-367 (2012).
- 7. Chen VB, Arendall WB, Headd JJ, Keedy DA, Kapral GL, Murry LW, Richardson JS, and Richardson DC. **MolProbity**: all-atom structure validation for macromolecular crystallography. Acta Cryst. D66, 16-21 (2010)
- 8. P. Emsley, B. Lohkamp, W. G. Scott, K. Cowtan, Features and development of **Coot**. Acta Crystallogr. D Biol. Crystallogr. 66, 486 (2010).
- 9. Vonrhein, C., Flensburg, C., Keller, P., Sharff, A., Smart, O., Paciorek, W., Womack, T. & Bricogne, G. (2011).Data processing and analysis with the **autoPROC** toolbox. Acta Cryst. D67, 293-302.

[full dataset will be deposited to the PDB upon publication].

![](_page_58_Picture_220.jpeg)

# **Table SI-21:** IDH1-R132H:NADPH:IDH889

![](_page_59_Picture_144.jpeg)

\* Values in parentheses are for highest-resolution shell.

#### **Determination of plasma protein and brain homogenate binding**

*In vitro* plasma and brain protein binding of IDH662 and IDH889 were assessed in triplicate using an equilibrium dialysis method (Rapid Equilibrium Dialysis (RED) System; Thermo Fisher Scientific, Inc., Waltham MA). For plasma protein binding, compound was added to mouse or human plasma at a final concentration of 1  $\mu$ M (in 1% DMSO). For brain protein binding, brain tissue was homogenized in 4 volumes (w/v) of phosphate-buffered saline (PBS) (dilution factor D = 5). Compound was then added to brain homogenate at a final concentration of 1  $\mu$ M (in 1%) DMSO). The plasma or brain homogenate were incubated at 37°C under 5% CO<sub>2</sub> for 4 h in the rapid equilibrium dialysis (RED) Device. Parent compound concentrations in the plasma or brain homogenate and phosphate-buffered saline (PBS) compartments were measured at time 0 and 4 h by LC/MS/MS.

A fraction unbound (fu) of compound in plasma was calculated as:

*fu = [PBS]4 h/[Plasma]4 h*

A fraction unbound ( $f_{\text{U}}(n_{\text{train}})$  of compound in brain tissue (undiluted) was calculated as: *fubrain = (1/D) / (((1/fu)-1)+1/D)* 

reference for the RED assay for PPB: J Pharm Sci. 2008 Oct;97(10):4586-95. doi: 10.1002/jps.21317.

#### **Pharmacokinetics in Mice**

#### Naive mouse PK study

Mouse pharmacokinetics (PK) studies were performed with male C57BL/6 mice weighing 25-30g that are approximately 6-8 weeks old, obtained from Harlan Research Laboratories (South Easton, MA; now Envigo). For this study, PK in mice was assessed at doses of 10 and 100 mg/kg with n=3 mice per dose level. The oral dose for compound **IDH662** was prepared at 1 and 10 mg/mL in a solution containing 3% 0.2N HCl, 20% PEG400, 50% of (20% Crem El) in Water for Injection. Each animal received 10 mL of the dosing solution per kg of body weight by oral gavage of the 1 and 10 mg/mL solution for the 10 and 100 mg/kg dose groups, respectively. For PK determination, approximately 50 µl of whole blood was collected from the tail of each animal using microvette EDTA tube at 0.25, 0.5, 1, 2, 4, and 7 h post-dose and transferred to a EDTA tube. The blood was centrifuged at 3000 rpm and plasma was transferred to PCR-96-AB-C WELL plate, capped with PCR strip cap and stored frozen (-20 °C) for parent compound analysis.

#### Bioanalysis for determination of plasma drug levels from PK and PK/PD studies

For determination of **IDH662** and **IDH889** plasma concentrations, blood was collected via tail nick (non-terminal) or cardiac puncture (terminal), collected into EDTA-lined microtainers (BD Microtainer®, Cat No. 365973), centrifuged at 13,200 rpm for 5 minutes and the plasma supernatant placed in a 1 mL 96 well collection plate and stored at -20°C until analysis. Plasma concentrations were determined by LC-MS/MS. Acetonitrile protein precipitation was employed to extract plasma samples, which were processed using a Freedom EVO® 150 and a Freedom EVO® from TECAN. Test samples were diluted with blank mouse plasma 2 to 10 fold and 25 µL of each undiluted or diluted test sample were transferred to a 96-well plate. A 150 µL volume of acetonitrile with 100 ng/mL glyburide (internal standard) was added to each well containing test sample, or calibration standard, vortexed, then centrifuged at 4,000 rpm for 10 minutes. 125 µL of each supernatant were transferred to a clean 1 mL 96-well plate, followed by the addition of 50 µL of water. For each sample, a 10 µL aliquot was injected into the LC-MS/MS system. Chromatographic separation was achieved with an ACE C18 column (3  $\mu$ m, 2.1 × 30 mm) from MAC-MOD Analytical, Inc. (Chadds Ford, PA), using 0.1% formic acid in water (A) and 0.1% formic acid in acetonitrile (B) as solvents in a multistep gradient. Data were acquired and processed using Sciex Analyst 1.4.2 software. All pharmacokinetic (PK) parameters were derived from concentration-time data by noncompartmental analyses (Thermo Watson 7, Thermo Fisher Scientific, Inc., Philadelphia, PA). The peak concentrations ( $C_{\text{max}}$ ) and times they occurred ( $T_{\text{max}}$ ) were recorded. The area under the concentration-time curve  $(AUC<sub>last</sub>)$  was calculated using the linear trapezoidal rule. The area under the concentration-time curve from time 0 to infinity

( $AUC<sub>inf</sub>$  was calculated using the following equation,

*z*  $\frac{C_{last}}{2}$  $AUC_{\text{int}} = AUC_{\text{int}} + \frac{C}{\sqrt{2}}$  $\delta_{\text{inf}} = AUC_{\text{last}} + \frac{U_{\text{last}}}{\lambda}$ 

terminal elimination rate constant  $(\lambda_z)$  for the unchanged compound was the slope of the log linear line from at least the last three data points. Results are expressed as mean ± SD when are applicable. No further statistical analysis was performed.

# **HCT116IDH1 R132H/+ xenograft model**

#### Cell culture

HCT116 cells expressing the R132H mutant form of IDH1 (HCT116<sup>IDH1 R132H/+</sup> Clone 2H1, HCHZ2H1) were purchased from Horizon (Cat#: HD 115-002, clone 2H1), expanded for 5 passages, then stored in liquid Nitrogen. Cells were tested free of Mycoplasma and viral contamination (MAP Impact panel VIII testing, Radil). Cells used for subcutaneous implantation were cultured in

McCoy's 5A medium (Corning, Cat #: 10-050-CV) supplemented with 10% FBS (High Clone cat#sh30071) and split 1:3 twice weekly. Cells were cultured for 7-10 passages prior to implantation.

# Generation of HCHZ2H1 xenografts

All studies were performed in accordance with Novartis Institutes for Biomedical Research (NIBR) Animal Care and Use Committee. Outbred athymic (*nu/nu*) female mice ("HSD: Athymic Nude-nu") weighing 19-32 grams (Envigo, Indianapolis) were allowed to acclimate in the NIBR animal facility with access to food and water *ad libitum* for minimum of 3 days prior to manipulation. All studies were performed in accordance with Novartis Institutes for Biomedical Research Animal Care and Use Committee. HCHZ2H1 cells were harvested at 80-90% confluency, washed once with Hank's Balanced Salt Solutions (HBSS, Cat No. 14175, Invitrogen Corporation, Gibco, Grand Island, NY), and suspended in 100% HBSS at  $5 \times 10^7$  cells/mL for implantation. For tumor cell implantation, mice were anesthetized with continuous flow of 2-4% isoflurane/oxygen mixture using the Integrated Multi Patient Anesthesia Center (IMPAC6) and induction chamber (Vetequip, Inc., Pleasanton, CA). Female nude mice were injected subcutaneously (dorsal right supra-axillary region) with 5 x  $10^6$  HCHZ2H1 tumor cells suspended in 100% HBSS in a total volume of 100  $\mu$ L. Mice were monitored for tumor growth, and once palpable, tumors were measured by caliper. 14-22 days post implant mice with tumors ranging from 100-300 mm<sup>3</sup> were selected for enrollment on study and randomized to experimental groups.

#### PK/PD experiment

![](_page_61_Picture_186.jpeg)

**Table SI-22.** Plasma concentration, normalized tumor 2-HG concentration and percent tumor 2-HG inhibition by **IDH889** following a single oral dose at 200 mg/kg dose in HCHZ2H1 xenograft model.

![](_page_62_Picture_151.jpeg)

**Table SI-22 notes:** The LLOQ for IDH889 was 10 nM; ND (not determined); fu (fraction unbound) in mouse plasma: 0.02

**Table SI-23.** Normalized tumor 2-HG concentration and percent tumor 2-HG inhibition by **IDH889** following a four consecutive oral doses at 25 mg/kg (12:12) dose in HCHZ2H1 xenograft model.

![](_page_62_Picture_152.jpeg)

Female nude mice bearing HCHZ2H1 tumors were administered either a single dose of 200 mg/kg or four consecutive doses (every 12 hours) of 25 mg/kg of IDH889 in 25% PEG300; 10% Cremophor EL; 10% Solutol; 3% 0.2N HCl, and 52% WFI, pH=3.5, by oral gavage. Mice that were treated with a single, 200 mg/kg dose of IDH889 were euthaized by carbon dioxide inhalation at 0 (untreated), 2, 4, 8, 12, 16, 20, 24, and 36 hours following treatment (n=3/time-point). Blood was collected by cardiac puncture into EDTA-lined microtainers (BD Microtainer Tubes, Cat No 365974, BD Diatnostics, Franklin Lakes, NJ), placed on wet ice and centrifuged at 13,200 rpm at 4° C within 30 minutes of collection. Plasma supernatant was collected into a 96 well plate and stored at -80° C until PK analysis. Tumors were collected into 15 ml geno/grinder tube (Pre-Cleaned 5 mL Polycarbonate Vial Set, SPEX SamplePrep LLC, 15 Liberty Street, Metuchen, NJ, USA, Catalog# 2240-PC) , snap-frozen in liquid nitrogen and stored at -80° C until 2-HG analysis. For the 25 mg/kg multi-dose study, five (n=5) mice were treated with 25 mg/kg IDH889 in 25% PEG300; 10% Cremophor EL; 10% Solutol; 3% 0.2N HCl, and 52% WFI, pH=3.5, by oral gavage every 12 hours. Just prior to first treatment and 24 (just prior to 3<sup>rd</sup> dose), 36 (just prior to 4<sup>th</sup> , final, dose), 46, 48, 54 and 72 hours following first dose animals were anesthetized with

continuous flow of 2-4% isoflurane/oxygen mixture using the Integrated Multi Patient Anesthesia Center (IMPAC6) and induction chamber (Vetequip, Inc., Pleasanton, CA). After disinfecting the tumor area with 70% ethanol, fine needle aspirate biopsies (FNA) were collected by inserting a 22 G needle attached to a 20ml syringe into the tumor mass and gently drawing back on syringe. FNA biopsies were flushed from needle with 270 µl of 80% methanol and were snap-frozen in liquid nitrogen and stored at -80° C until 2-HG analysis.

Tumors 2-HG levels were normalized to amount of pulverized tumor used for extraction; FNA levels were normalized to total protein as determined by bicinchoninic acid detection (Pierce BCA Protein Assay Kit, Cat No 23227, Thermo Fisher Scientific, Waltham, MA). Percent 2-HG inhibition was calculated relative to untreated or pre-treated controls.

## Determination of tumor 2-HG level

Tumor fragments of approximately 50 mg were placed into 15 ml geno/grinder tube (Pre-Cleaned 5 mL Polycarbonate Vial Set, SPEX SamplePrep LLC, 15 Liberty Street, Metuchen, NJ, USA, Catalog# 2240-PC), snap frozen in liquid nitrogen, then transferred to -80°C until extraction. For extraction, geno/grinder tubes with tumor were placed on dry ice. The geno/grinder adaptor and cover was chilled on dry ice, then adaptor was loaded with sample tubes, placed in the geno/grinder (SPEX SamplePrep LLC, Catalog# 2010-geno/grinder) and homogenized for 30 seconds. Samples were then removed from the adaptor and set on dry ice. 2-10 mg of pulverized tumor sample was weighed out and transferred to a fresh 2 ml screw-top tube on dry ice. Twohundred microliters (200 µl) of 80% cold methanol for every mg of tumor powder was added, then tubes vortexed until sample fully resuspended. Samples were sonicated for 10 minutes in an ice-water bath, then incubated on dry ice for a minimum of 30 minutes. Samples were then centrifuged for 10 minutes at 13,200 rpm at 4ºC. Supernatants were diluted 1:25 in 80% methanol and were transferred to a 96 well plate, sealed using LC-MS/MS plate sealer and stored at -80C until LC-MS/MS analysis**.**

FNA biopsies were vortexed, incubated on dry ice for 30 minutes and centrifuged at 13,200 rpm at 4 C for 10 minutes. Supernatants were diluted 1:25 in 80% methanol and were transferred to a 96 well plate, sealed using LC-MS/MS plate sealer and stored at -80C until LC-MS/MS analysis. Pelleted material was reserved for total protein concentration determination.

The growth of the HCT116<sup>IDH1 R132H/+</sup> cell lines used in our in vitro and in vivo studies are not dependent upon mutant IDH1, and therefore the in vitro and in vivo growth is not impacted by selective mutant IDH1 inhibitors.

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Compound	IDH $1^{R132C}$ IC <sub>50</sub> / $\mu$ M	IDH $1^{WT}$ IC <sub>50</sub> / $\mu$ M
1f / IDH125	0.150	>50
2a	11.3	$>25$
2 <sub>b</sub>	4.6	$>25$
2c	8.5	$>25$
$\overline{2d}$	$\overline{ND}$	$>25$
3 <sub>b</sub>	$\overline{2.4}$	$>25$
3 <sub>c</sub>	1.5	>25
5a	0.618	>25
5f	0.184	$\overline{13}$
5g	0.083	2.9
5h	0.353	$>25$
5n	1.567	$>25$
5r	0.324	24.6
5s / IDH662	0.041	1.03
5۷	0.056	3.65
5w	<b>ND</b>	12.3
5x / IDH889	0.072	1.375

Table SI-24. IDH1<sup>R132C</sup> and IDH1<sup>WT</sup> biochemical activity