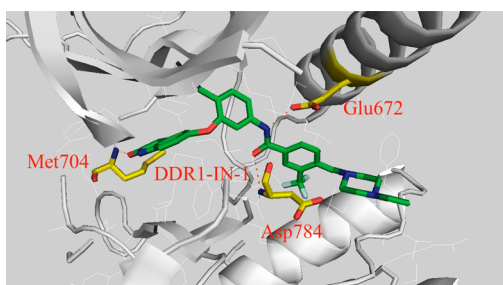


## Correction to Discovery of a Potent and Selective DDR1 Receptor Tyrosine Kinase Inhibitor

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In the reported X-ray cocrystal structure of the DDR1 kinase domain in complex with the inhibitor DDR1-IN-1 (PDB code 4BKI), the indolin-2-one moiety was modeled with two hydrogen bonds to the kinase hinge residues Met704 and Asp702. Subsequent analysis of the electron density has revealed that the indolin-2-one group is flipped allowing only a single hydrogen bond to Met704. The amended coordinates have been released with the new PDB code 4CKR. The corrected Figure 2A is shown, together with the



**Figure 2.** Binding information of DDR1-IN-1/2 against DDR1. (A) X-ray cocrystal structure of DDR1-IN-1 with DDR1 kinase.

updated refinement statistics (Table 5) reported in Supporting Information Table 5 of the original paper. This change does not otherwise affect the scientific integrity of the article. We thank Oliver Smart, Global Phasing Ltd., for drawing our attention to the error.

**Table 5.** Data Processing and Refinement Statistics. Values in Parentheses Refer to the Highest Resolution Shell

DDR1 with DDR1-IN-1	
Data	
wavelength (Å)	0.9795
resolution range (Å)	49.44–2.2 (2.278–2.199)
space group	P4 <sub>1</sub> 2 <sub>1</sub> 2
unit cell (Å)	59.3, 59.3, 178.5
unit cell (deg)	90, 90, 90
total reflections	183798 (14101)
unique reflections	17062 (1526)
multiplicity	11 (9.2)
completeness (%)	100 (100.00)
I/σ(I)	17.5 (2.4)
Wilson B-factor (Å <sup>2</sup> )	36.2
R-merge	0.1 (0.956)
R-meas	0.109 (1.071)
CC <sub>1/2</sub>	0.999 (0.720)
Refinement	
R-work/R-free	0.1982/0.2470
no. of atoms	2422
macromolecules	2324
ligands	60
water	38
protein residues	301
RMS(bonds) (Å)	0.01
RMS(angles) (°)	1.3
Ramachandran favored (%)	96.2
Ramachandran outliers (%)	0.34
Clashscore	1.49
avg B-factor (Å <sup>2</sup> )	48.3
macromolecules	48.8
ligands	33.1
solvent	37.3
PDB ID	4CKR