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Correction: Identification of selective protein–protein interaction inhibitors using efficient *in silico* peptide-directed ligand design†

Andrew M. Beekman,^{*a} Marco M. D. Cominetti,^a Samuel J. Walpole,^a Saurabh Prabhu,^a Maria A. O’Connell,^a Jesus Angulo^a and Mark Searcey^{*ab}

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Correction for ‘Identification of selective protein–protein interaction inhibitors using efficient *in silico* peptide-directed ligand design’ by Andrew M. Beekman *et al.*, *Chem. Sci.*, 2019, DOI: 10.1039/c9sc00059c.

The authors regret that the structures of compounds 2, 3, 10 and 11 are incorrect in the original article. The correct structures are presented in the updated version of Table 1 below.

The original ESI was replaced by a correspondingly revised version on 1st May 2019 to reflect these changes.

^aSchool of Pharmacy, University of East Anglia, Norwich Research Park, Norwich, Norfolk, NR47TJ, UK. E-mail: A.Beekman@uea.ac.uk; M.Searcey@uea.ac.uk

^bSchool of Chemistry, University of East Anglia, Norwich Research Park, Norwich, Norfolk, NR47TJ, UK

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Table 1 IC₅₀ values for inhibition of the binding of FAM-p4 to hDM2 and hDMX of small molecules.^a A green background indicates the compound was designed for and was selective to the same protein. Yellow indicates the compound is a dual inhibitor. A red background indicates the compound was designed for one protein but was selective for the other protein

Structure	hDMX		hDM2		Structure	hDMX		hDM2	
	FA IC ₅₀ (μM)	[95% CI]	FA IC ₅₀ (μM)	[95% CI]		FA IC ₅₀ (μM)	[95% CI]	FA IC ₅₀ (μM)	[95% CI]
	0.013	[0.003, 0.046]	0.24	[0.16, 0.36]		>100		2.46	[1.01, 4.70]
	0.019	[0.005, 0.071]	0.10	[0.03, 0.76]		>100		5.77	[4.00, 8.37]
	1.28	[0.64, 2.52]	8.00	[6.12, 20.06]		>100		12.42	[8.61, 21.23]
	1.49	[1.06, 2.10]	>100			10.97	[8.28, 19.66]	22.44	[17.92, 29.60]
	0.97	[0.79, 1.44]	1.74	[0.89, 3.38]		1.17	[1.02, 4.20]	>100	

^a IC₅₀ values determined by non-linear regression of at least three independent experiments (see ESI, pg 10). Errors are 95% confidence intervals (CI). Fmoc, 9-fluorenylmethylcarbonyl.

The Royal Society of Chemistry apologises for these errors and any consequent inconvenience to authors and readers.

