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CORRECTION

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

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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.

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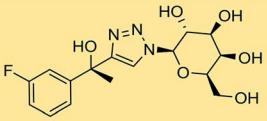
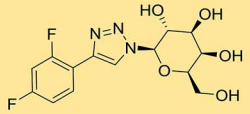
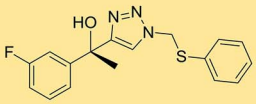
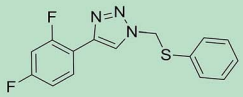
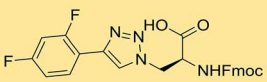
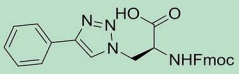
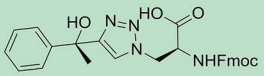
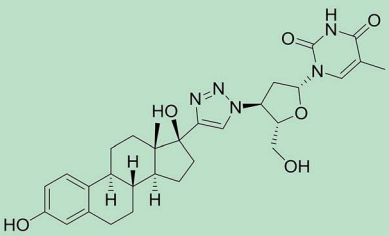
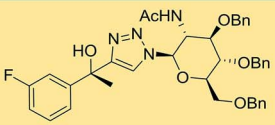
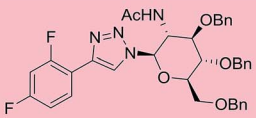
Table 1 IC_{50} values for inhibition of the binding of FAM-p4 to *h*DM2 and *h*DMX of small molecules.[a] A green background indicates the compound was designed for and was selective to the same protein. Yellow indicates the compound is a dual inhibitor. A red background indicates the compound was designed for one protein but was selective for the other protein

	Structure	*h*DMX FA IC_{50} (μM) [95% CI]	*h*DM2 FA IC_{50} (μM) [95% CI]
2		0.013 [0.003, 0.046]	0.24 [0.16, 0.36]
3		0.019 [0.005, 0.071]	0.10 [0.03, 0.76]
4		1.28 [0.64, 2.52]	8.00 [6.12, 20.06]
5		1.49 [1.06, 2.10]	>100
6		0.97 [0.79, 1.44]	1.74 [0.89, 3.38]
7		>100	2.46 [1.01, 4.70]
8		>100	5.77 [4.00, 8.37]
9		>100	12.42 [8.61, 21.23]
10		10.97 [8.28, 19.66]	22.44 [17.92, 29.60]
11		1.17 [1.02, 4.20]	>100

[a] IC_{50} 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.