

CORRECTION

Correction: Data-Driven Prediction and Design of bZIP Coiled-Coil Interactions

The *PLOS Computational Biology* Staff

An error was introduced during the production process. A fixed-width font should have been used for the sequences in [Table 3](#). The publisher apologizes for the error.

Please view the corrected table here:



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Table 3. Binding of designed peptides to their bZIP targets

Design	Target	K _d at 37 °C (nM)	Designed sequence
XBP1-d1 ¹	XBP1	172 ± 65	EREAQLENRVVAHLKEKNQELKAQNLHLKEALSEAQNRRNQELKNDA
XBP1-d2	XBP1	≥ 5,000	AETDQLENRVKDLKKNESLKEEKRQASNKYKALLTNNRSLKVKKA
XBP1-d2* ²	XBP1	≥ 5,000 (269 at 23 °C)	AETDQLENRVKDLKKNESLKEEKRQAKNKLKALLTNNRSLKVKKA
JUN-d1 ¹	JUN	5.8 ± 0.7	SIAATLEKEEANLEKMNKLAEEIESLLKEKDKLESVLYNHE
JUN-d2	JUN	1	QRALQLQKEKERLEKMNKLAEEIESLLEERERLESVLYNHE
ATF3-d1	ATF3	~1,000	NDLARLENKAEELKVQNRILVDERKYLQREISELHDELAHAHE
ATF3-d2	ATF3	564	NLVAQLEKKNEALKAENAALEIERIQLQDKIEELKYELAAIE
ATF3-d3	ATF3	≥ 5,000 (117 at 4 °C)	KDAASLENKKEELKVQNRILVDERKYLQMMNSELKDELAHAHE
ATF4-d1 ¹	ATF4	9.3 ± 2.3	NQIKTLRTRLSKLRKDNLQLEKDIANLERKAKDLRAEKEQLEYEL
ATF5-d1 ¹	ATF5	1680 ± 1050	KRIAYLRQRIAE LRNENHVLESRIQRMEKEKDALQQDRDHLEYEL
ATF5-d1 ³	ATF4	4.9 ± 1.0	(same as above)

¹ These four designs were chosen for further characterization.

² A double mutant of XBP1-d2, in which serine at position 4e and tyrosine at position 5a were mutated to lysine and leucine, respectively.

³ Although ATF5 was used in the computational design, binding was tighter to ATF4, which shares 69.2% sequence identity with ATF5 in **a**, **d**, **e** and **g** positions.

doi:10.1371/journal.pcbi.1004243.t001

Reference

1. Potapov V, Kaplan JB, Keating AE (2015) Data-Driven Prediction and Design of bZIP Coiled-Coil Interactions. PLoS Comput Biol 11(2): e1004046. doi: [10.1371/journal.pcbi.1004046](https://doi.org/10.1371/journal.pcbi.1004046) PMID: [25695764](https://pubmed.ncbi.nlm.nih.gov/25695764/)