Corrections

The p73 DNA Binding Domain Displays Enhanced Stability Relative to Its Homologue, the Tumor Suppressor p53, and Exhibits Cooperative DNA Binding, by Seema Patel, Tam T. T. Bui, Alex F. Drake, Franca Fraternali, and Penka V. Nikolova,* Volume 47, Number 10, 2008, pages 3235–3244.

Page 3238. Table 2 appears in its correct form here, with several rows of data shown in bold as noted in the footnote.

Page 3242. The correct version of Figure 8 appears here.

All CD data reported in the paper were made using 100 mM NaCl and not 150 mM as originally stated.

Table 2: Buried Solvent Accessible Surface Areas for p73 DBD and p53 DBD upon Dimerization[a]

residue	phobic (%)	philic (%)	total (%)
	(A) p53 DBD Chain C		
CYS 176	1.3	0.0	1.3
PRO 177	**41.6**	**1.2**	**42.8**
HIS 178*	**43.8**	**20.7**	**64.5**
HIS 179	4.2	3.2	7.4
ARG 181	14.7	30.5	45.2
CYS 242	2.8	0.1	2.9
MET 243*	**128.8**	**4.7**	**133.4**
GLY 244	11.7	3.7	15.4
	(B) p53 DBD 180° Rotated Chain D		
CYS 176	1.4	0.0	1.4
PRO 177	**46.9**	**1.2**	**48.0**
HIS 178*	**43.5**	**20.9**	**64.4**
HIS 179	4.7	3.5	8.2
ARG 181	15.1	29.8	44.9
CYS 242	2.2	0.1	2.3
MET 243*	**127.7**	**4.7**	**132.3**
GLY 244	11.1	3.4	14.5
	(C) p73 DBD Chain C		
CYS 194	2.5	0.1	2.6
PRO 195	**60.8**	**1.7**	**62.4**
ASN 196*	**25.0**	**77.0**	**101.9**
HIS 197	0.9	0.4	1.3
GLU 198*	0.0	0.5	0.5
LEU 199*	11.6	0.0	11.6
CYS 262	0.2	0.0	0.2
VAL 263*	**29.1**	**4.5**	**33.6**
GLY 264	7.6	3.6	11.3
GLY 265*	0.2	0.3	0.5
	(D) p73 DBD 180° Rotated Chain D		
CYS 194	2.5	0.2	2.7
PRO 195	**61.6**	**1.8**	**63.3**
ASN 196*	**25.0**	**76.7**	**101.8**
HIS 197	1.0	0.3	1.4
GLU 198*	0.0	0.5	0.5
LEU 199*	13.7	0.0	13.7
CYS 262	0.2	0.0	0.2
VAL 263*	**24.5**	**4.1**	**28.5**
GLY 264	7.3	3.6	10.9
GLY 265*	0.1	0.3	0.4

[a] Surface areas are reported in angstroms. The most significant differences between p53 and p73 residues at the interface are highlighted in bold. Asterisks (*) indicate the residues that differ in the two structures upon DNA binding (see sequence alignment).

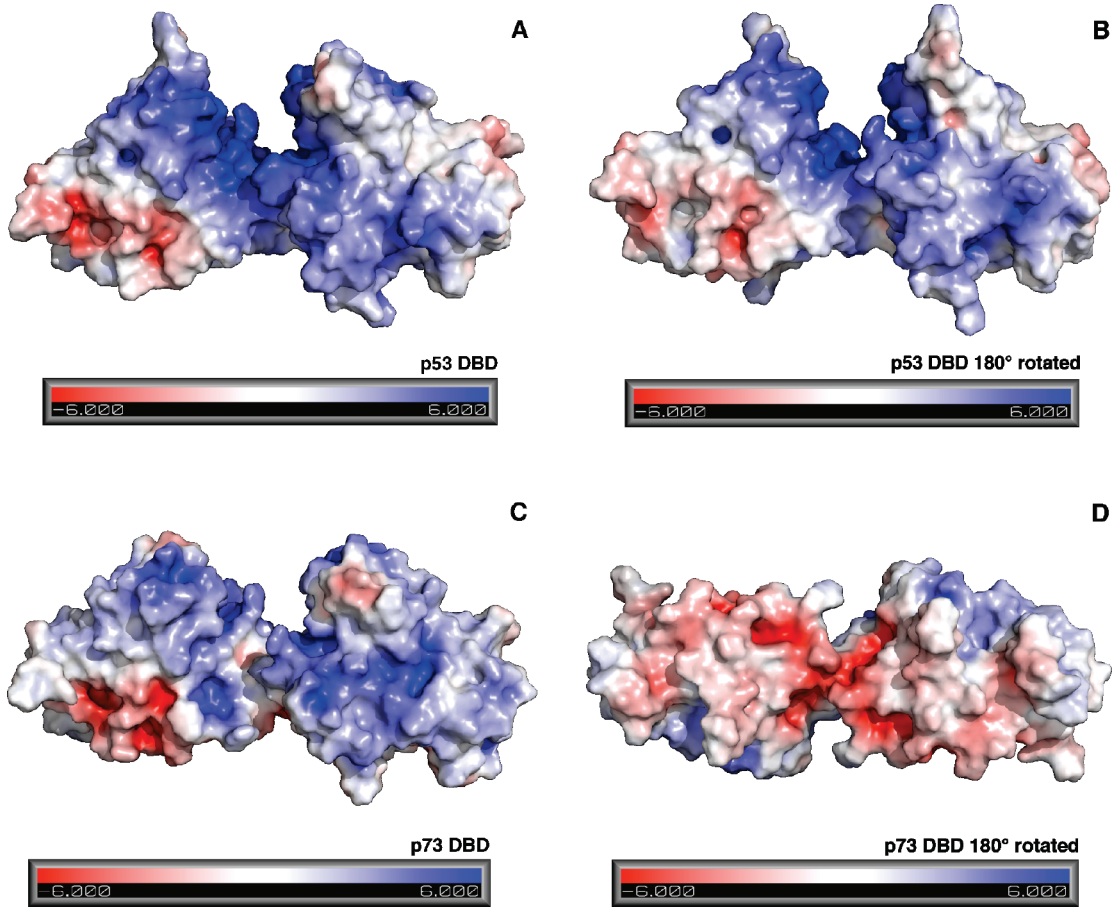

FIGURE 8: Structure-based homology modelling of the dimeric p73 DBD-DNA complex based on the p53 DBD−DNA complex. Comparison of the electrostatic potential of the p53 DBD based on 2aco dimer (A and B) and the predicted model of p73 DBD dimer (C and D). The potential ranges from the negative value –6*k*T (red) to the positive value +6*k*T (blue). For each complex, two views are presented: a front view along the DNA axis and the opposite face view obtained by rotation of 180°.

BI8003439

10.1021/bi8003439
Published on Web 04/24/2008