corrections

Structure of the *Bacillus subtilis* D-aminopeptidase DppA reveals a novel self-compartmentalizing protease

Han Remaut, Coralie Bompard-Gilles, Colette Goffin, Jean-Maire Frère and Jozef Van Beeumen

Nature Struct. Biol. **8**, 674–678 (2001).

Part of the reference list was incorrectly printed in this paper. The first ref. 12 in the list should be renumbered as ref. 11; the original ref. 11 in the list should be deleted. The citation of these references in the text corresponds to the corrected numbering scheme. Citations for MLPHARE and DM in footnotes 2 and 3 of Table 1 were also incorrectly printed. The correct citation for both is ref. 27. We apologize for any confusion these may have caused.

Structural insights into the hydrolysis of cellular nitric oxide synthase inhibitors by dimethylarginine dimethylaminohydrolase

Judith Murray-Rust, James Leiper, Mark McAlister, John Phelan, Sarah Tilley, Jo Santa Maria, Patrick Vallance and Neil McDonald

Nature Struct. Biol. **8**, 679–683 (2001).

The genus name for the organism from which dimethylarginine dimethylaminohydrolase is derived was printed incorrectly in this paper. The correct name of the organism is *Pseudomonas aeroginosa*. We apologize for any confusion this may have caused.

erratum

Structural basis for substrate specificities of cellular deoxyribosenucleoside kinases

Kenneth Johansson, S. Ramaswamy, Catarina Ljungcrantz, Wolfgang Knecht, Jure Piškur, Birgitte Munch-Petersen, Staffan Eriksson and Hans Eklund

Nature Struct. Biol. **8**, 616–620 (2001).

A production error resulted in several mistakes in the Tables of this paper. In Table 1, the amino acid type of several residues was incorrectly printed; one table heading was incorrectly aligned. For clarity, the corrected Table 1 is reprinted on the next page. The dimension of the a-axis for the native dNK crystal is incorrectly printed in Table 2. The correct value is a = 119.5 Å. We apologize for any confusion these may have caused.

erratum

Table 1 Substrate interactions[1]

Interactions	dNK	TK2	dGK	dCK	HSV1-TK
Hydrogen bonds to substrate base	Gln 81	Gln 79	Gln 111	Gln 97	Gln 125
In plane	Glu 52	Glu 50	Glu 70	Glu 53	Glu 83
	Met 69	Met 67	Met 99	Met 85	Ile100
	Tyr 70	Tyr 68	Tyr 100	Tyr 86	Tyr 101
	Val 84	Val 82	Ser 114	Ala 100	Met 128
	Met 88	Met 86	Arg 118	Arg 104	Tyr 132
	Ala 110	Ala 108	Asp 147	Asp 133	Ala 168
	Met 118	Leu 116	Leu 155	Leu 141	Arg 176
Stacking	Trp 57	Trp 55	Trp 75	Trp 58	Trp 88
	Phe 80	Leu 78	Phe 110	Phe 96	Ala 124
	Phe 114	Phe 112	Phe 151	Phe 137	Tyr 172
	Val 84	Val 82	Ser 114	Ala 100	Met 128[2]
O3′ hydrogen bonds	Tyr 70	Tyr 68	Tyr 100	Tyr 86	Tyr 101
	Glu 172	Glu 170	Glu 211	Glu 197	Glu 225
O3′ surroundings[3]	Ile 29	Ile 28	Ile 47	Ile 30	His 58
	Leu 66	Leu 64	Leu 96	Leu 82	Ile 97
O5′	Glu 52	Glu 50	Glu 70	Glu 53	Glu 83
	Arg 105	Arg 103	Arg 142	Arg 128	Arg 163
	Arg 169	Arg 167	Arg 208	Arg 194	Arg 222
Phosphates	Ser 31	Ser 30	Val 49	Ala 32	Met 60
	Lys 33	Lys 32	Lys 51	Lys 34	Lys 62
	Thr 34	Thr 33	Ser 52	Ser 35	Thr 63
	Thr 35	Thr 34	Thr 53	Thr 36	Thr 64
	Arg 167	Arg 165	Arg 206	Arg 192	Arg 220
	Arg 169	Arg 167	Arg 208	Arg 194	Arg 222

[1] Amino acid residues at equivalent positions in the enzymes are listed in each row.

[2] The position of the Sδ and Cε of the side chain of Met 128 is the same as Phe 80, Leu 78, Phe 110 and Phe 96 and forms stacking interactions to the base in HSV1-TK, but the position of Cα of Met 128 is equivalent to that of Val 84, Val 82, Ser 114 and Ala 100.

[3] Residues in van der Waals or hydrogen bond contacts.