Erratum

Two Mutations Convert Mammalian Xanthine Oxidoreductase to Highly Superoxide-productive Xanthine Oxidase

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The publishers wish to apologize for errors which occurred in Figures 2 and 3 legends. The corrected legends for these figures are published below.

Fig 2. Changes of the absorption spectra of DTT-treated W335A/F336L mutant after mixing with NADH under anaerobic conditions. (A) A $4.63\,\mu\text{M}$ DTT-treated double mutant in $50\,\text{mM}$ KP buffer (pH 7.8) containing $0.4\,\text{mM}$ EDTA was anaerobically mixed with 1/39 volume of NADH ($5.08\,\text{mM}$) in the same buffer, and the absorption spectra were recorded before mixing and at several times after mixing ($20\,\text{s}$, $30\,\text{s}$, $60\,\text{s}$, $5\,\text{min}$ and $60\,\text{min}$). (B) Time courses of absorption at 450, $520\,\text{and}$ $630\,\text{nm}$ of the mutant after mixing with $60\,\mu\text{M}$ NADH using a stopped-flow apparatus. (C) Observed rate constants (k_{obs}) for the first phase of the reaction are plotted against substrate concentration to obtain the dissociation constant (K_{d}).

Fig. 3. Structural consequences of the W335A/F336L mutation of rat XOR. (A) Overall structure of the rat W335A/F336L mutant. Subunit A is shown in green and subunit B in blue. Red boxes mark the regions of each subunit shown in higher magnification in Fig. 4A and B. (B) In the XO form (e.g. subunit B of the W335A/F336L mutant), the cluster has disintegrated and opened up another access route (red arrow) to the flavin ring from the opposite side of the molecule. At the same time, the NAD⁺-binding site has been partially filled-in, preventing access of this substrate. The residues 334, 335 and 426 are shown in space-filling representation; FAD is shown in stick representation; the active site loop (A-loop) is in space-filling representation (green). (C) In the XDH form (e.g. in the C535A/C992R/C1324S triple mutant), the enzyme molecule displays the elongated cleft (red arrow) necessary for binding of the substrate NAD⁺. Note the compactness of the cluster. The cluster consisting of residues 334, 335, 426 and 549 is shown in space-filling representation; FAD is shown in stick representation; the active site loop (A-loop) is in space-filling representation (green).