Int J Biochem Mol Biol 2026;17(4):35-37
www.ijbmb.org /ISSN:2152-4114/IJBMB0156401

Erratum

Structural evidence for the order of preference of inorganic substrates in mammalian heme peroxidases: crystal structure of the complex of lactoperoxidase with four inorganic substrates, SCN^-, I^-, Br^- and Cl^-: Int J Biochem Mol Biol. 2011; 2(4): 328-339

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Received March 7, 2024; Accepted October 25, 2026; Epub October 25, 2026; Published October 30, 2026

Some errors have been found in **Table 1** and **Figure 3**. This corrects **Table 1** on page 330. The results in **Table 1** are based on the refinement of the structure using new data set and the new PDB ID is 8Y9X. This also corrects **Figure 3** on page 334 where the orientation of SCN is different from that reported earlier in **Figure 3**. The refinement was carried out using a better-quality data to improve the results. The Erratum is required to make new PDB, new **Table 1** and new **Figure 3** available to the readers. It will be helpful, please consider and do the needful. We sincerely apologize for this oversight and any confusion it may have caused. The corrected **Table 1** and **Figure 3** are shown below.

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https://doi.org/10.62347/WWSQ1379

Table 1. Data collection and refinement statistics

Data collection	
Space group	$P2_1$
Unit-cell parameters	a = 53.4 Å, b = 80.3 Å, c = 73.4 Å, β = 103.94°
No of molecules in the unit cell	2
V_m (Å^3/Da)	1.9
Solvent Content (%)	35.0
Resolution range (Å)	43.52-1.99
Total number of measured reflections	240622
Number of unique reflections	39294
Completeness of data (%)	96.7 (77.0)
R_{sym} (%)	8.2 (31.0)
I/σ(I)	29.8 (4.3)
Redundancy	6.2 (3.2)
Refinement	
R_{cryst} (%)	15.1
R_{free} (%)	19.5
Protein atoms	4758
Calcium ion	1
Heme (1)	43
Water oxygen atoms	408
NAG atoms (6)	84
Polyethylene glycol atoms (7)	49
Thiocyanate atoms (5)	15
Iodide atoms	17
Bromide atom	1
Chloride atom	1
RMS Deviation	
Bond length (Å)	0.01
Bond angles (°)	1.68
Dihedral angles (°)	13.04
Mean B-Factor	
Wilson B-factor (Å^2)	21.9
Main Chain atoms (Å^2)	25.1
Side Chain atoms (Å^2)	32.9
Water oxygen atoms (Å^2)	24.3
Overall (Å^2)	32.0
Ramachandran Plot	
Most favoured region (%)	89.6
Additional allowed region (%)	8.8
Generously allowed region (%)	1.4
Disallowed regions (%)	0.2 (Cys167)
PDB code	8Y9X

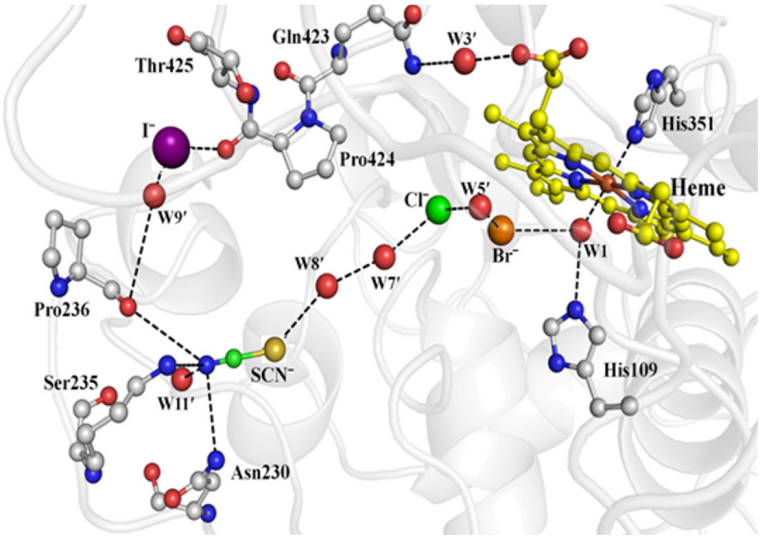


Figure 3. The hydrogen bonded interactions involving Br^-, Cl^-, I^-, SCN^-, W1 (B14), W3' (A892), W5' (A1055), W7' (A1053), W8' (B13), W9' (A941) and W11' (B2) are shown by dashed lines. The names in the parentheses correspond to the names in the PDB file, 8Y9X. The hydrogen bonded residues to halides and water molecules are also indicated.