## Supporting information

## Unexpected In Crystallo Reactivity of the Potential Drug Bis(maltolato)oxidovanadium(IV) with Lysozyme

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**Figure S1** Anomalous difference electron density map (at 3.0  $\sigma$  level) of the (bis)V-containing fragment. Atoms from a symmetry related molecule are highlighted with the asterisk (\*) and coloured in grey.



**Figure S2** Interaction of the (bis)V-containing fragment bound to the side chain of Lys1. Atoms from a symmetry related molecule are highlighted with the asterisk (\*) and coloured in grey. The side chain of Ser86\* adopts two difference conformations.



Figure S3 Proposed reactions of pyrylium ions.<sup>1</sup>



**Figure S4** Maltol cleavage by diketone cleaving enzyme via molecular oxygen and subsequent hydrolytic decomposition of the products.<sup>2</sup>



Figure S5 Oxidation products of maltol: A) lactic acid and B) 3-hydroxyacrylic acid.<sup>3</sup>



**Figure S6** Structure of the cross-linked HEWL dimer formed in the crystals of the protein exposed to BMOV. The symmetry related molecule is coloured in grey. Asp87 from the symmetry-related molecule is highlighted with the asterisk (\*).



**Figure S7** MALDI MS spectra of the peptide mixture obtained from *in situ* hydrolysis of non-metalated HEWL (band 1.1 in Figure 4 of the main text): magnification of 1110-1150 (A) and 2600-2800 (B) m/z ranges.



**Figure S8** MALDI MS spectra of the peptide mixture obtained from *in situ* hydrolysis of cross-linked HEWL dimer (band 2.1 in Figure 4 of the main text): magnification of 1110-1150 m/z range. The signals present in the reference (not metalated HEWL, band 1.1 in Figure 4 of the main text) are marked with asterisks (\*).



**Figure S9** MALDI MS spectra of the peptide mixture obtained from *in situ* hydrolysis of metalated monomeric HEWL (band 2.2 in Figure 4 of the main text) (A) and cross-linked HEWL dimer (band 2.1 in Figure 4 of the main text) (B): magnification of 3000-3100 m/z range.

 Table S1 Data collection and refinement statistics.

Data collection						
PDB code	9FMY					
Crystallization condition	1.1 M NaCl					
	0.1M sodium acetate at pH 4.0					
Soaking time	21 days					
Space group	P4 <sub>3</sub> 2 <sub>1</sub> 2					
a (Å)	78.11					
b (Å)	78.11					
c (Å)	37.21					
α/β/γ (°)	90.0/90.0/90.0					
Molecules for asymmetric unit	1					
Resolution range (Å)	55.23-1.09 (1.11-1.09)					
Observations	1112770 (44263)					
Unique reflections	48619 (2359)					
Completeness (%)	99.9 (99.1)					
Redundancy         22.9 (18.8)						
Rmerge (%)	0.056 (1.455)					
Average I/σ(I)	29.0 (2.2)					
CC <sub>1/2</sub>	0.999 (0.822)					
Anom. completeness (%)	100.0 (99.5)					
Anom. Multiplicity	12.1 (9.7)					
Refiner	nent					
Resolution (Å)	55.23-1.09					
N° reflections	45192					
N° reflections in working set	2841					
Rfactor/Rfree	0.129/0.152					
N° non-H atoms in the refinement	1272					
B-factor overall (Å <sup>2</sup> )	19.11					
Estimated occupancy of V (1)	0.30					
Estimated occupancy of V (2)	0.60					
Estimated occupancy of [VO(H <sub>2</sub> O) <sub>5</sub> ] <sup>2+</sup>	0.50					
Estimated occupancy of (bis)V-containing fragment	0.60					
B-factor of V (1) (Å <sup>2</sup> )	27.47					
B-factor of V (2) (Å <sup>2</sup> )	33.43					
B-factor of V [VO(H₂O)₅] <sup>2+</sup> (Å <sup>2</sup> )	22.86					
B-factor of (bis)V-containing fragment (Å <sup>2</sup> )	15.4±2.7					
Ramachandran values (%)						
Most favoured/Additional allowed	96.52/3.48					
Outliers 0.00						
R.m.s.d. from ideality						
R.m.s.d. bonds (Å)	1111					
R.m.s.d. angles (°)	1515					

**Table S2** Anomalous difference electron density peaks interpreted as V centers.

Assignment	Occupancy of the V center in the model	Anomalous difference e.d. map peaks σ level	
V (1) of bis(V)-containing fragment	0.60	21.96	
V (2) of bis(V)-containing fragment	0.60	16.90	
V (1)	0.30	8.31	
V (2)	0.60	4.61	
V of [VO(H <sub>2</sub> O) <sub>5</sub> ] <sup>2+</sup>	0.50	11.23	

**Table S3** Specific m/z of signals recorded in MALDI-MS and ESI-LC-MSMS analysis of metalated monomeric HEWL (band 2.2 of SDS-PAGE reported in Figure 4 of the main text) and of cross-linked HEWL dimer (band 2.1 of SDS-PAGE reported in Figure 4 of the main text). Signals are due to peptide mixtures deriving from hydrolysis with Asp-N protease followed by trypsin. Expected Molecular Weight (MW, Da) values are also

Experimental m/z (MALDI- MS) - Metalated monomeric HEWL	Experimental m/z (ESI- LCMSMS) - Metalated monomeric HEWL	Experimental m/z (MALDI- MS) - Cross-linked HEWL dimer	Experimental m/z (ESI- LCMSMS) - Cross-linked HEWL dimer	Expected MW (Da)	Interpretation
1111.61	555.76	1111.66	-	1110.39	[62-68] + V + V=O
1127.60	-	1127.66	-	1126.39	[62-68] + 2V=O
2699.31	—	-	-	2699.28	[74-97] K <sub>96</sub> Ac, (Na <sup>+</sup> )
2713.43	-	-	-	2713.28	[74-97] K <sub>96</sub> Ac (C- propionamide), (Na⁺)
2742.37	1371.70, 915.10	-	-	2744.28	[74-97] K <sub>96</sub> Ac + V=O
2756.36	-	-	-	2575.28	[74-97] K <sub>96</sub> Ac (C- propionamide) + V=O
2776.35	1389.14 <i>,</i> 926.43	-	-	2776.35	[22-45] K <sub>33</sub> Ac
-	-	4974.19	-	4974.22	<pre>[1-17] + [74-96] + (bis)V-containing fragment + VO<sub>3</sub></pre>

reported.

## Notes and references

- 1 V. A. Yaylayan and S. Mandeville, J. Agric. Food Chem., 1994, 42, 771–775.
- 2 C. M. L. Di Giuro, D. Buongiorno, E. Leitner and G. D. Straganz, J. Inorg. Biochem., 2011, 105, 1204–1211.
- 3 C. Kanzler, P. T. Haase, H. Schestkowa and L. W. Kroh, J. Agric. Food Chem., 2016, 64, 7829–7837.