Supplementary information

Oxaliplatin vs Cisplatin: competition experiments in the binding to Lysozyme

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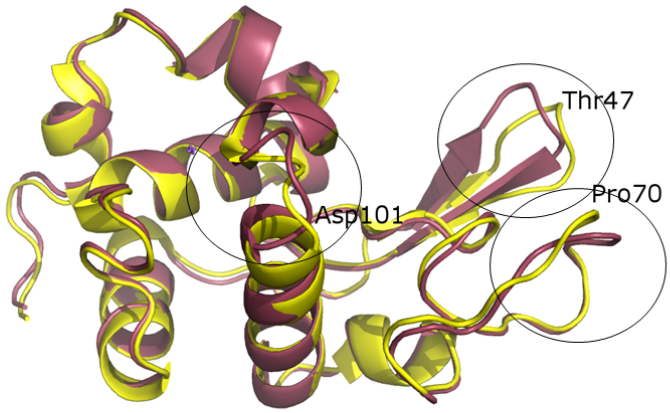
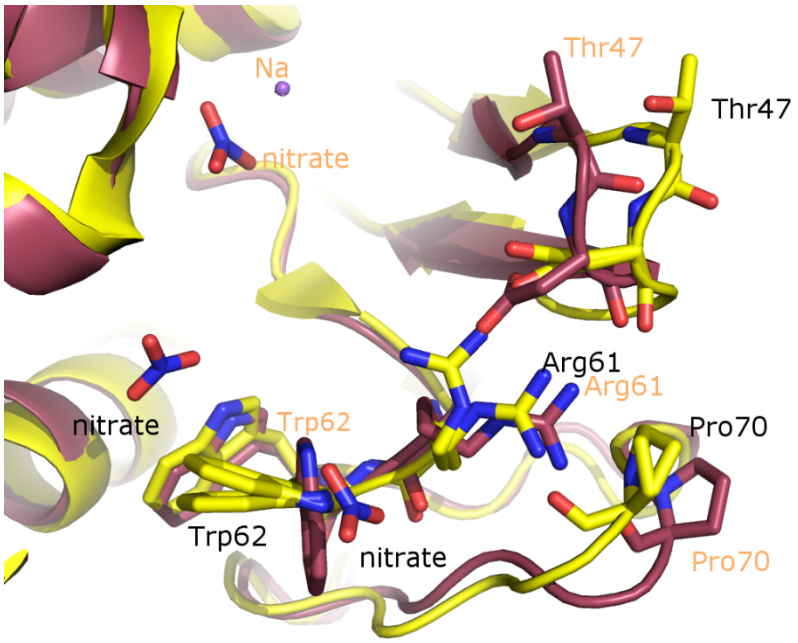
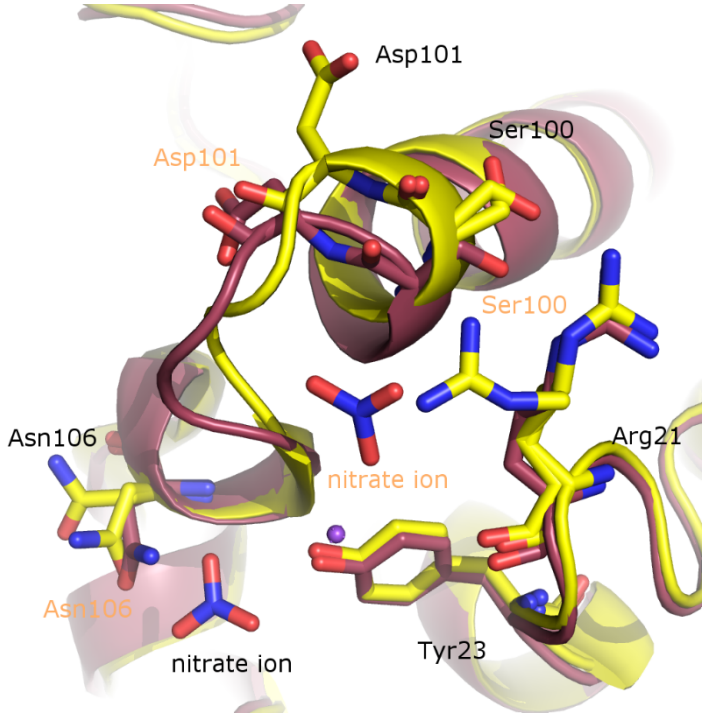


Figure S1. Superposition of bis-adduct (brown) and atomic resolution structure of HEWL (PDB code 2VB1, yellow).



A



B

Figure S2. Details of the comparison of the HEWL structure in the bis-adduct (brown) and in the and atomic resolution structure (yellow, PDB code 2VB1). Major differences are observed at the end of helix constituted by residues 88-101 and in the loop regions corresponding to residues 44-51 and 69-73. These structural variations are probably related to the differences in the position of nitrate ions on the protein surface.

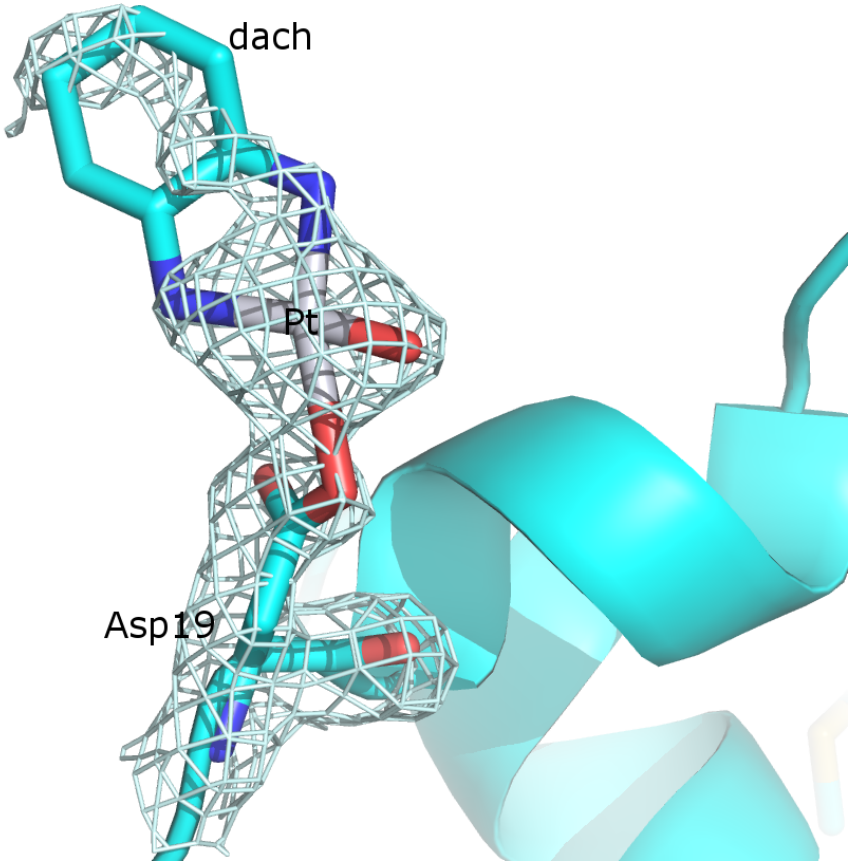


Figure. S3. Oxaliplatin binding site in the second structure of bis-adduct (PDB code 4ZEE). 2Fo-Fc electron density maps are contoured at 1σ (grey) level.

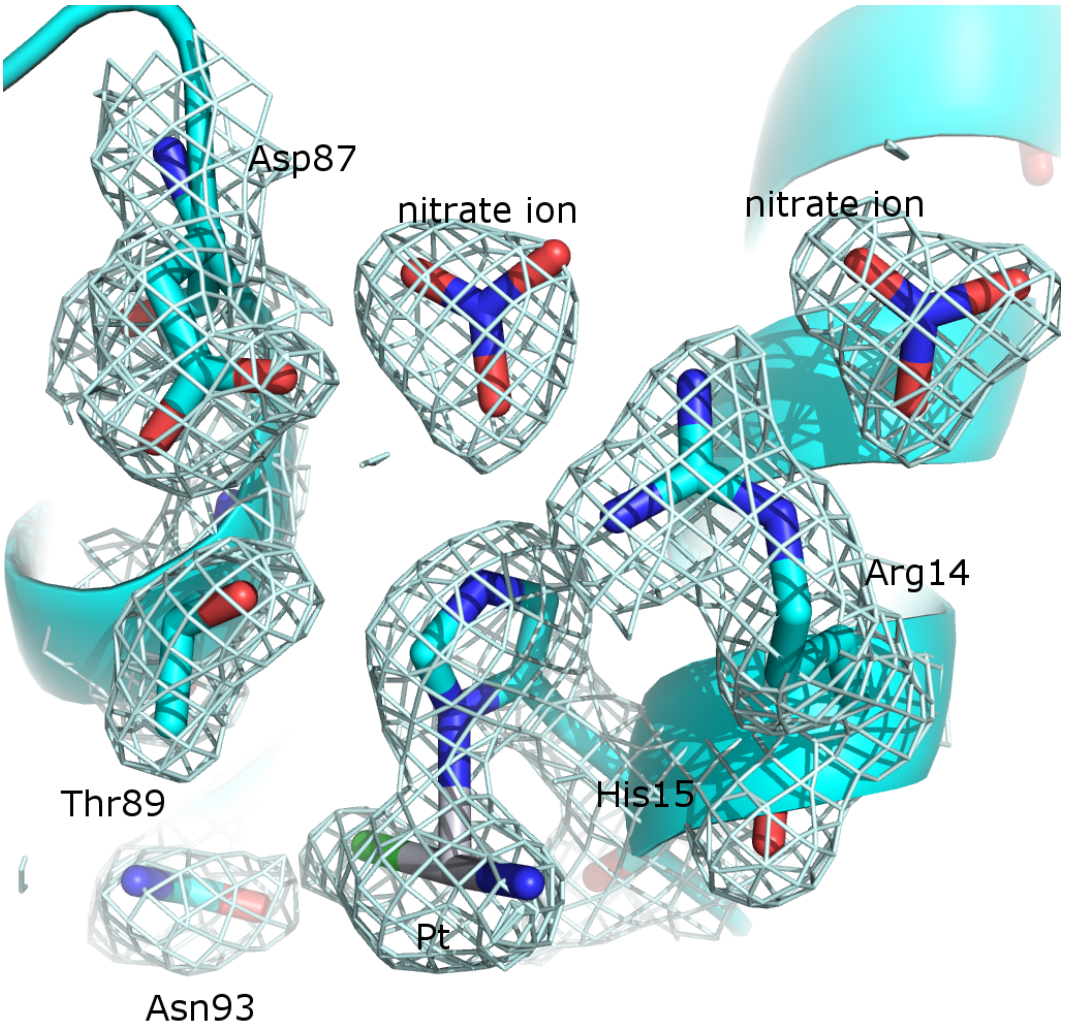


Figure S4. Cisplatin binding site in the second structure of bis-adduct (PDB code 4ZEE). 2Fo-Fc electron density maps are contoured at 1σ (grey) level.

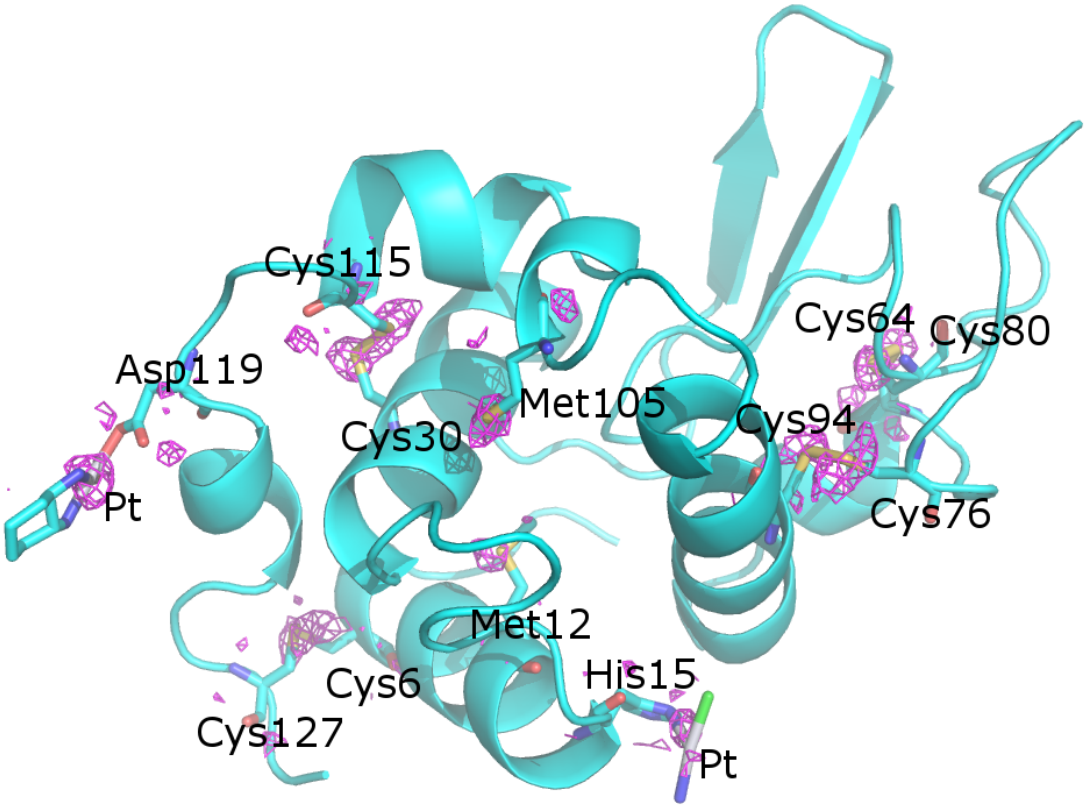


Figure S5. Anomalous difference map calculated from anomalous data collected for the second bis-adduct crystal (PDB code 4ZEE). The anomalous map is rendered in violet and contoured at 2.0 σ. The inspection of the map allows the identification of the positions of Pt and of sulphur atoms of Cys6, Met12, Cys30, Cys64, Cys76, Cys80, Cys94, Met105, Cys115 and Cys127.

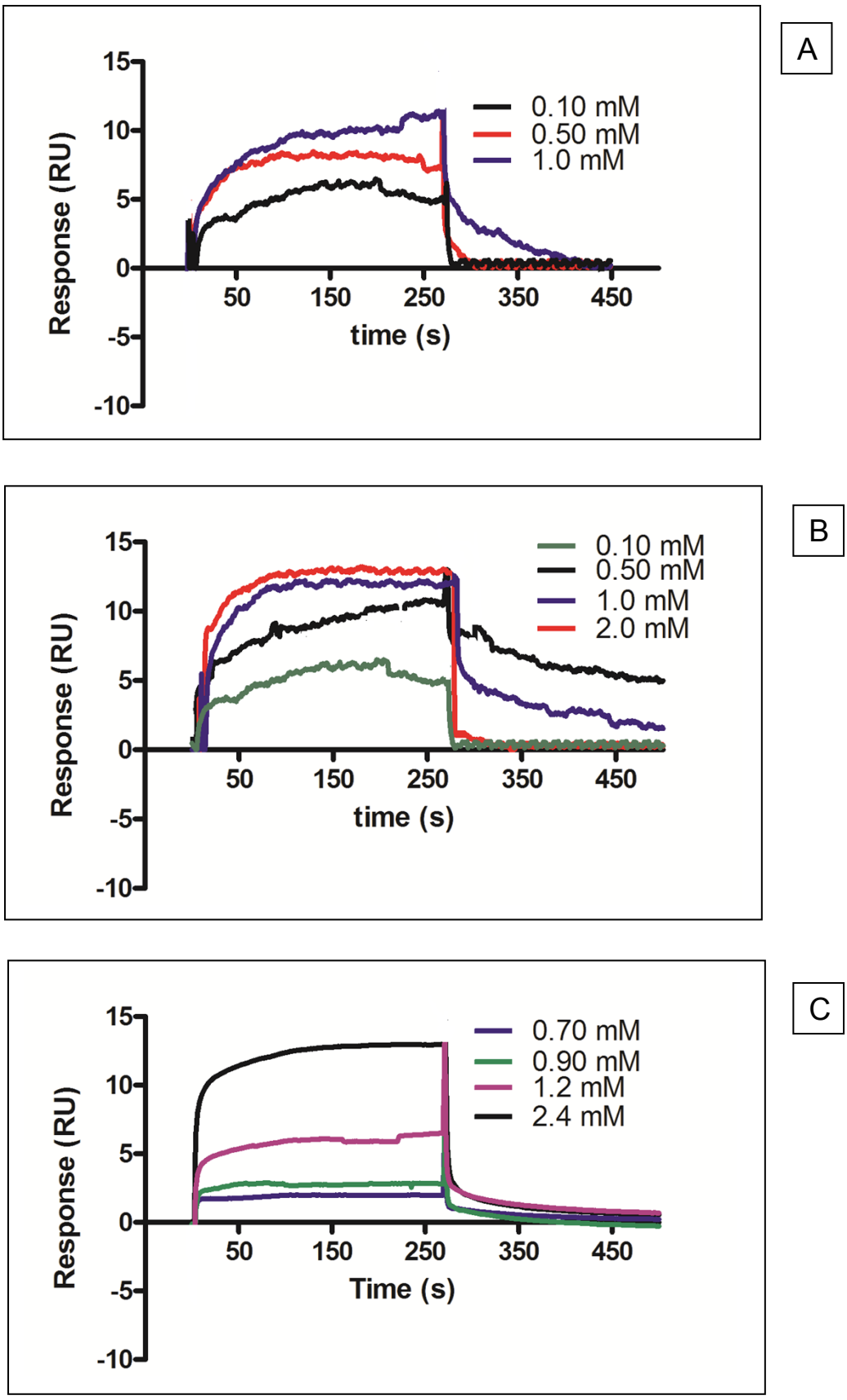


Figure S6: Overlay of sensorgrams for the interaction between Oxaliplatin (A) and Cisplatin (B) and HEWL. Experiments have been carried out at room temperature using 20 mM sodium citrate at pH 4.4 as running-buffers. In panel C, the interaction between HEWL and Cisplatin has been evaluated at room temperature using HBS (10 mM Hepes, 150 mM NaCl, 3 mM EDTA, pH 7.4) as running buffer.

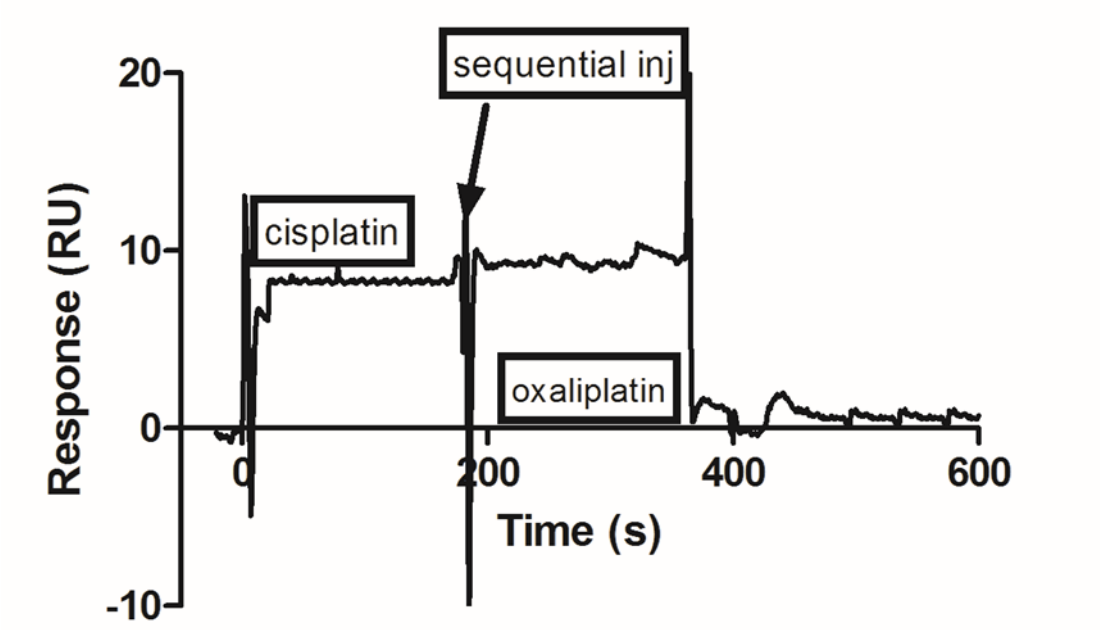


Figure S7. SPR Sensorgram for the sequential injection of Cisplatin and (then) Oxaliplatin, both at 1 mM, to immobilized HEWL in the presence of 20 mM sodium citrate buffer at pH 4.4. In the time of this experiment Oxaliplatin does not bind the preformed HEWL-Cisplatin adduct

Table S1. Data collection and refinement statistics

	Bis-adduct 1	Bis-adduct 2
PDB code	4ZEE	4Z46
Data Collection		
Space group	$P4_32_12$	$P4_32_12$
Unit-cell parameters		
a, b, c (Å)	77.377, 77.377, 37.600	77.318, 77.318, 37.325
Molecules per a. u.	1	1
Resolution (Å)	54.71-1.95 (1.98-1.95)	54.67-1.85 (1.88-1.85)
Observed reflections	47779	58591
Unique reflections	8452	10100
Completeness (%)	95.8 (83.2)	99.4 (92.2)
Rmerge†	0.113 (0.611)	0.095 (0.471)
I/σ(I)	11.7 (2.3)	13.8 (2.2)
Multiplicity	5.7 (4.3)	5.8 (3.1)
Refinement		
Resolution (Å)	54.71-1.95 (1.98-1.95)	54.67-1.85 (1.88-1.85)
number of reflections in working set	8023	9585
number of reflections in test set	403	482
R factor/Rfree (%)	15.8/23.0	15.5/21.8
Number of non-H atoms used in the refinement	1209	1210
Occupancy of Pt ions	0.40, 0.35	0.40, 0.35
B-factor of Pt ions ($Å^2$)	55.8, 63.6	52.5, 67.0
Overall B-factor	27.6	26.8
Deviations from ideality values		
R.m.s.d. bonds (Å)	0.019	0.019
R.m.s.d. angles (Å)	1.94	1.94
Estimated overall coordinate errors (Å)	0.148	0.196