Electronic Supplementary Material

Addressing the Presence of Biogenic Selenium Nanoparticles in Yeast Cells: Analytical Strategies Based on ICP-TQ-MS

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Parameter		
RF Power [W]	1550	
Coolant gas flow [L min ⁻¹]	14.0	
Auxiliary gas flow [L min-1]	0.8	
Carrier gas flow [L min-1]	0.8	
Sheath gas flow [L min-1]	0.31	
Cell gas flow [mL min-1]	0.31	
Q1 bias [V]	0	
Q _{cell} bias [V]	-5.94	
Q3 bias [V]	-12.0	
Q1 masses [u]	31 (³¹ P ⁺) or 80 (⁸⁰ Se ⁺)	
Q3 masses [u]	47 (³¹ P ¹⁶ O ⁺) or 96 (⁸⁰ Se ¹⁶ O ⁺)	
Single cell / single particle modes		
Dwell time [ms]	5 (0.1)	
Sample flow rate [mL min-1]	0.01	
Run time [s]	120	
HPLC-ICP-MS		
Dwell time [ms]	100	
Sample flow rate [mL min-1]	0.5	
Run time [s]	480	

 Table S1
 Operating conditions of the iCAP TQ ICP-MS in the different measurement modes.

Figure S1: Time-resolved measurements of yeast 1 monitoring phosphorous as ³¹P¹⁶O⁺ and selenium as ⁸⁰Se¹⁶O⁺ before (a) and after adding (b) selenomethionine and (c) sodium selenite. (The final concentration of total added Se was 2000 mg kg⁻¹ in yeast, equivalent to the Se content of SELM-1, (2031 ± 70) mg kg⁻¹.)



Figure S2: Single particle analysis of a standard suspension of Se nanoparticles (a) before and (b) after the mechanical treatment with the used glass.



Figure S3: The obtained size distribution in Se-yeast 1 by single particle ICP-MS (bin size: 10 nm).



Figure S4: The EDX spectrum corresponding to the HR-TEM image shown in Figure 3 indicating the presence of selenium.



Figure S5: Single particle ICP-MS experiments on Se-yeast 1 after lysis (a) before and (b) after the reaction with sodium sulphite with a dwell time of 5 ms.

