MATRIX-ASSISTED LASER DESORPTION/IONIZATION TIME-OF-FLIGHT (MALDI-TOF) MASS SPECTROMETRY APPLIED TO VIRUS IDENTIFICATION

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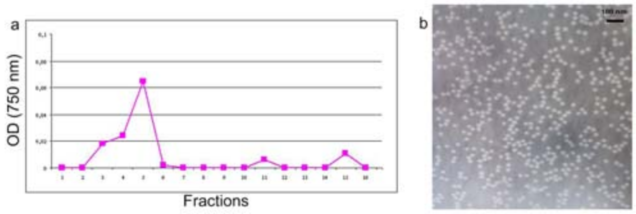
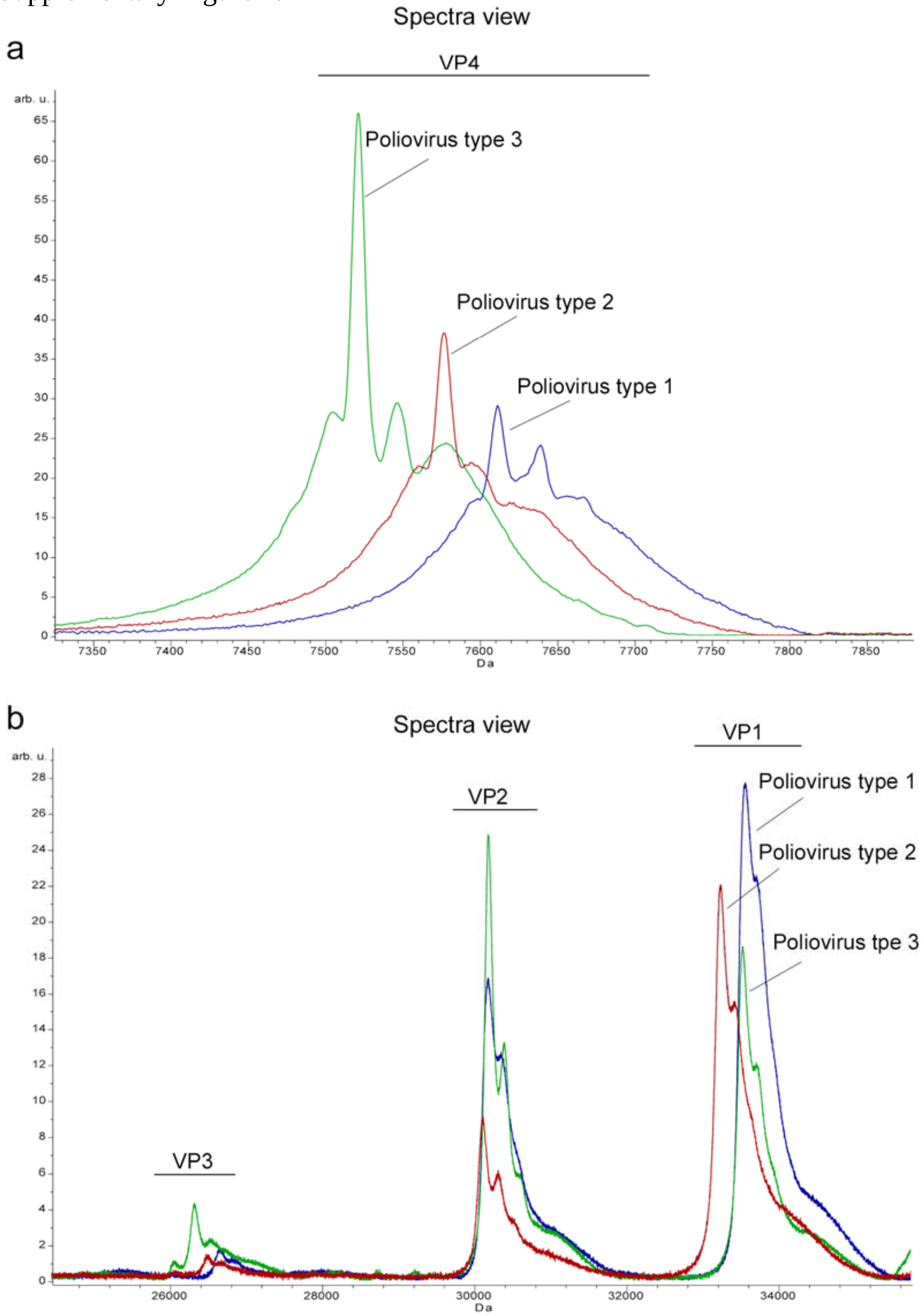
Supplementary Figure 1.



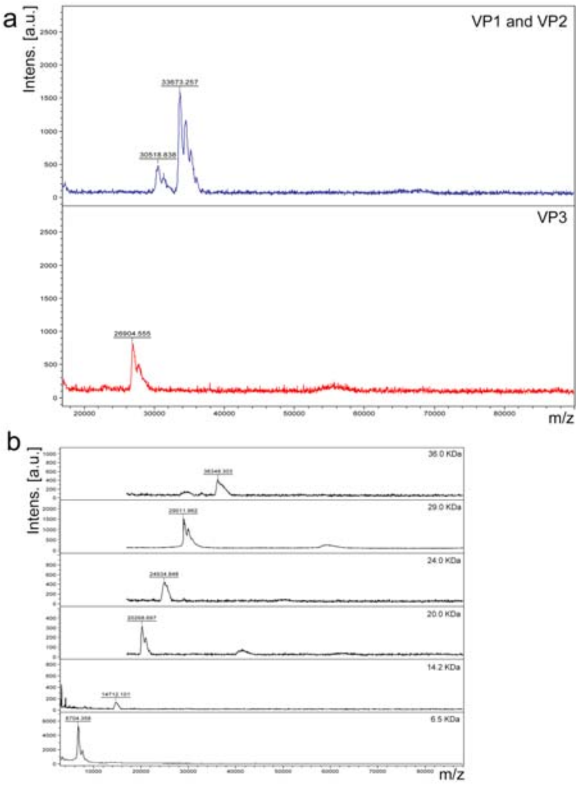
Supplementary Figure 1 legend: Purification of poliovirus type 1 Sabin reference strain. **(a)** Linear sucrose gradient (15% - 45%) distribution of viral particles as determined by protein analysis following Lowry assay; sedimentation is from right to left. **(b)** Electron micrograph of an aliquot of the pool corresponding to gradient fractions 2 to 6 (negative staining; 44,000 X).

Supplementary Figure 2.



Supplementary Figure 2 legend. Details of the “Spectra view” of the three purified poliovirus Sabin reference strains in the low and high mass range. The “Spectra view” displays, in the mass range 7,400 to 7,900 Da **(a)** and 26,000 to 35,000 Da **(b)**, the three average spectra obtained from all the imported replicates for poliovirus type 1, 2 and 3, showing differences in the main poliovirus structural protein VP4 **(a)** and VP3, VP2 and VP1 **(b)**.

Supplementary Figure 3



Supplementary Figure 3 legend. MALDI-TOF MS analysis in the mass range 2 – 20 KDa and 17 – 90 KDa of purified Sabin poliovirus type 1 protein bands excised from Coomassie blue stained polyacrylamide gel. (a) Mass spectra of purified poliovirus type 1 protein gel bands corresponding to VP1 and VP2, of about 33,000 and 30,000 m/z, and VP3 of about 26,400 m/z. (b) Protein mass spectra of molecular weight marker bands in the range of interest, corresponding to: glyceraldehyde-3-phosphate¬dehydrogenase from rabbit muscle (36.0 KDa), carbonic anhydrase from bovine erythrocytes (29.0 KDa), trypsinogen from bovine pancreas (24.0 KDa), trypsin inhibitor from soybean (20.0 KDa), alpha-¬lactalbumin from bovine milk (14.2 KDa) and aprotinin from bovine lung (6.5 KDa) obtained by MALDI-TOF MS analysis.