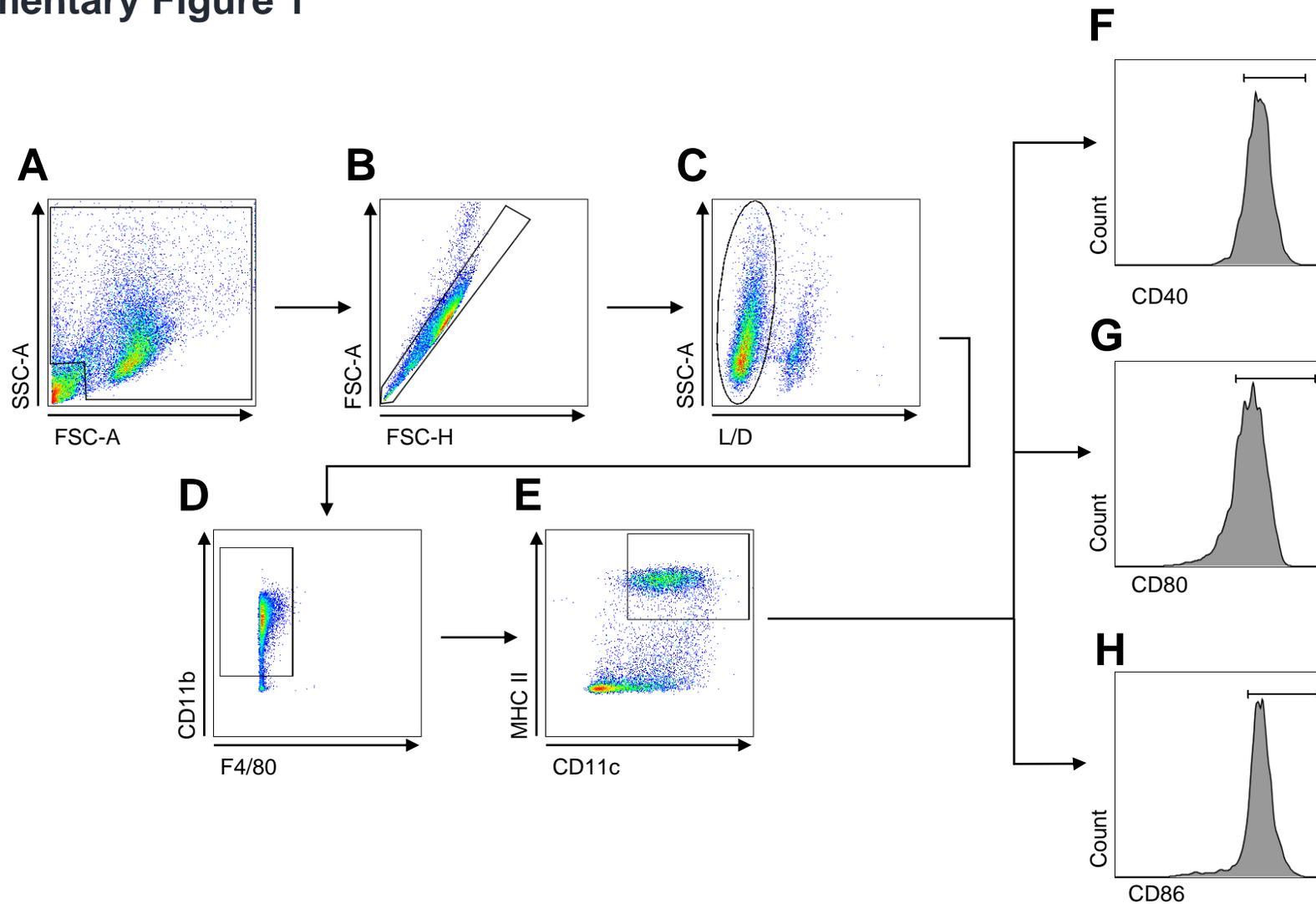
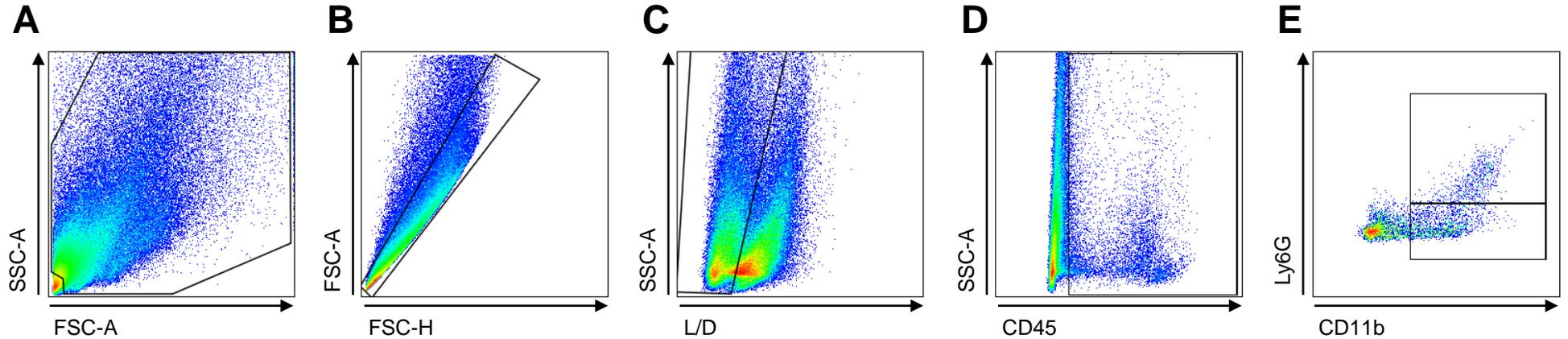


Supplementary Figure 1



Supplementary Figure 1. Gating strategy for the analysis of accessory/costimulatory molecules expressed by DCs. (A) Small-sized events and debris exclusion based on forward scatter (FSC) and side scatter (SSC) parameters. (B) Doublets exclusion using the area (FSC-A) and height (FSC-H) parameters. (C) Exclusion of dead cells, identified as Live/Dead-positive events. (D and E) Selection of CD11b⁺F4/80⁻CD11c⁺MHC^{high} cells (considered DCs). From the DC population, the percentage of CD40⁺ (F), CD80⁺ (G), and CD86⁺ (H) cells was assessed and the median fluorescence intensity (MFI) calculated.

Supplementary Figure 2

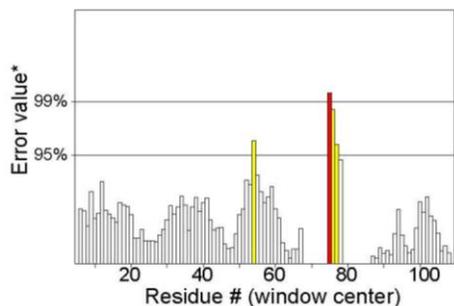


Supplementary Figure 2. Gating strategy for the analysis of cell infiltrate in carrageenan-induced paw edema. (A) Small-sized events and debris exclusion based on FSC and SSC parameters. (B) Exclusion of doublets using FSC-A and FSC-H parameters. (C) Exclusion of dead cells, identified as exclusion Live/Dead-positive events. (D and E) Selection of CD45⁺CD11b⁺Ly6G⁺ cells (neutrophils) and CD45⁺CD11b⁺Ly6G⁻ cells (other myeloid cells).

Supplementary Figure 3

A

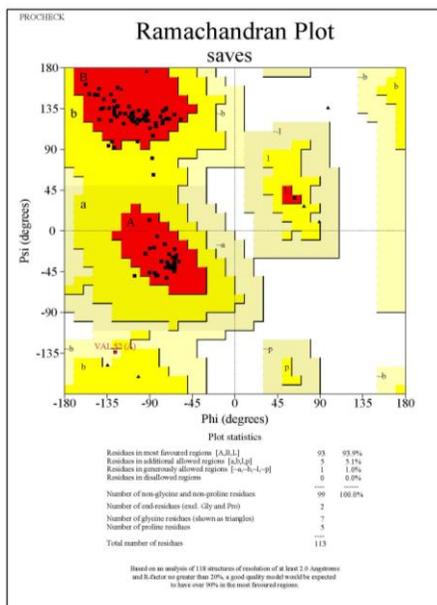
Program: ERRAT2
File: model_2.pdb
Chain#:A
Overall quality factor**: 95.455



*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

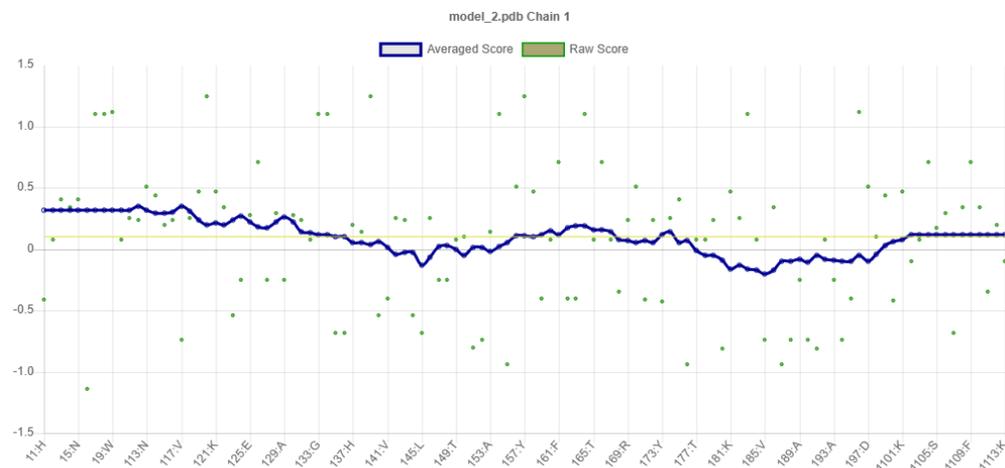
**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

B



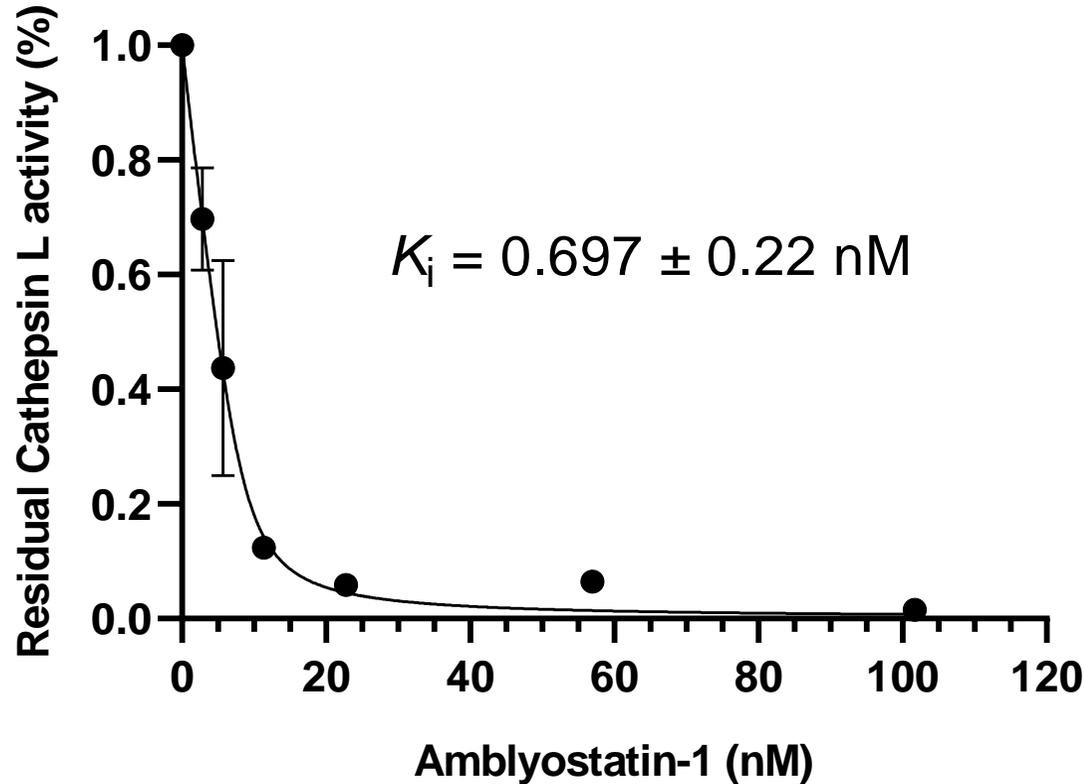
saves_01.pse

C



Supplementary Figure 3. SAVES validation output. (A) ERRAT2 analysis showing an overall quality factor of 95.455, indicating a high-quality model. (B) Ramachandran plot with 93.9% of residues in the most favored regions, supporting good stereochemical quality. (C) Verify3D results indicating that 54.87% of the residues have an averaged 3D-1D score ≥ 0.1 , suggesting moderate compatibility between the 3D model and its amino acid sequence.

Supplementary Figure 4



Supplementary Figure 4. Residual cathepsin L activity in the presence of Amblyostatin-1. Active cathepsin L (6 nM) was incubated with varying concentrations of Amblyostatin-1 followed by addition of the fluorogenic substrate Z-Phe-Arg-AMC. Fluorescence readings were taken at 30 °C over a 15 minutes period, and enzyme activity was estimated by their V_{max} . Residual activity was calculated as V_{max} of enzyme activity in the presence of the inhibitor divided by the V_{max} of the control enzyme (without inhibitor). The dissociation constant (K_i) was calculated through nonlinear regression analysis using the Morrison equation for tight-binding inhibition.

Supplementary Table 1

Supplementary Table 1. Tested human cathepsins with its respective substrates and reaction buffers.

Enzyme	Final enzyme concentration	Substrate	Final substrate concentration	Reaction butter
Cathepsin L	250 nM	Z-LR-AMC	250 μ M	100 mM Na-acetate, 100 mM NaCl, 1 mM EDTA, 0.01 % Triton X-100, 100 μ g/ml cysteine, pH 5.5
Cathepsin B	85.5 nM	Z-LR-AMC	250 μ M	
Cathepsin H	286 nM	Z-LR-AMC	250 μ M	
Cathepsin S	169 nM	VVR-AMC	250 μ M	
Cathepsin C	50 nM	H-GR-AMC	250 μ M	50 mM Na-acetate, 50 mM NaCl, 5 mM DTT, pH 5.5