Algorithm SMC method for protein segment construction

$x_0^{(j)} = \emptyset, j = 1, 2, \ldots, N$
for i from 1 to $l - 3$ **do**
  for j from 1 to N **do**
    Construct list $L_i^{(j)}$ of possible pairs (ϕ', ψ') for amino acid i
    for n from 1 to 100 **do**
      Propagate $x_{i-1}^{(j)} \to x_i^{(j,n)}$ as follows:
      Draw one (ϕ_i, ψ_i) pair from $L_i^{(j)}$ and $\omega_i \sim p(\omega_i)$, and sample up to n_s side chain positions for χ_i.
      if $i = 1$ **then**
        Let $\{s_{i,j,n}^{(k)}\}_{k=1}^{N_s}$ contain the n_s positions for χ_1
      else
        Propagate $\{s_{i-1,j,n}^{(k)}\}_{k=1}^{N_s} \to \{s_{i,j,n}^{(k)}\}_{k=1}^{N_s}$ using embedded side chain filter: set $\{s_{i,j,n}^{(k)}\}_{k=1}^{N_s}$ to be the N_s vectors of $\chi_{1:i}$ with the lowest energies among the $N_s \times n_s$ combinations of $\chi_{1:i-1}$ with χ_i.
      end if
    end for
  end for
  Sample N particles from $\{x_i^{(j,1)}, \ldots, x_i^{(j,100)}\}_{j=1}^{N}$ to be $x_i^{(1)}, \ldots, x_i^{(N)}$
end for
Do final processing (including analytical closure for last three amino acid positions) and output conformations.