

**Front Cover:**

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The Role of Spike Protein Mutations in the Infectious Power of SARS-CoV-2 Variants: A Molecular Interaction Perspective

## Classical

$$V(R) = \sum_{\text{ALL BONDS}} K_b (b - b_0)^2$$

$$+ \sum_{\text{ALL ANGLES}} K_\theta (\theta - \theta_0)^2$$

$$+ \sum_{\text{ALL TORSION ANGLES}} \sum_n K_\phi \cos(n\phi - \gamma)$$

$$+ \sum_{\text{ALL NONBONDED PAIRS}} \left( \frac{A}{r_{ij}^{\alpha}} - \frac{B}{r_{ij}^{\beta}} \right)$$

$$+ \sum_{\text{ALL PARTIAL CHARGES}} \left( \frac{q_i q_j}{\epsilon_D r_{ij}} \right)$$



## Quantum

$$i\hbar \frac{\partial}{\partial t} |\Psi_n(\vec{r}, t)\rangle = \mathcal{H} |\Psi_n(\vec{r}, t)\rangle$$

$$\mathcal{H} |\Psi_n(\vec{r}, t)\rangle = E_n |\Psi_n(\vec{r}, t)\rangle$$

$$f(\vec{r}_c), \frac{\mathcal{H}(\vec{r}_c)}{f(\vec{r}_c)}, \frac{|V(\vec{r}_c)|}{g(\vec{r}_c)}$$

$$E_{d \rightarrow a}^{(2)} = -q_d \frac{|\langle \Psi_d | \mathcal{F} | \Psi_a \rangle|^2}{\epsilon_a - \epsilon_d}$$

$$R_O: \omega_T = 2.5, \alpha = 4.7, \beta = 4.8, \gamma = 4.9$$