

# Exploring Amino Acid Peptide Bond Formation/Break in Presence of Clay Surface: An *Ab Initio* Study

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The fundamental understanding of biomolecule-clay interaction and peptide bond formation or break is of great relevance to the biotechnology industry.<sup>1-4</sup> To this end, we use density functional theory (DFT) to examine the relationship between the two simple alanine amino acids and the most common type of clay mineral, montmorillonite (MMT).<sup>5</sup> Five model systems were investigated in order to gain a better knowledge of peptide bond formation/break catalyzed by inorganic substrate: (1) no substrate as a reference point, (2) a clay surface without defects, (3) a clay surface with a missing oxygen atom, (4) a clay surface with a missing silicon atom, (5) an iron-doped clay surface. To trace the system's total energy as a function of the reaction coordinate, the transition state (TS) search approach is ultimately used for each of the model systems. In accordance with the findings, only the fifth system has positive binding energy while the other models all have negative binding energies. The lowest binding energy occurs in the fourth system, and the binding energies of the oxygen-defective and pristine models are nearly equal. Furthermore, studies from heating and molecular dynamics (MD) demonstrate that the original system's (#1) peptide bond breaks at 500 K. The results of this work pave the way for the specifically tailored design of clay-based materials in the realms of biotechnology and prebiotic chemistry.

## References

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