

DOI: 10.21767/2172-0479.100072

A Translational Biomedical Approach to Structural Arrangement of Amino Acids' Complexes: A Combined Theoretical and Computational Study

A Heidari

Faculty of Chemistry, California South University, 14731 Comet St. Irvine, CA 92604, USA

Corresponding author: A Heidari, Faculty of Chemistry, California South University (CSU), 14731 Comet St. Irvine, CA 92604, USA, Tel: +1 (775) 410-4974; E-mail: Scholar.Researcher.Scientist@gmail.com**Received:** May 23, 2016; **Accepted:** May 30, 2016; **Published:** Jun 07, 2016**Citation:** A Heidari. A Translational Biomedical Approach to Structural Arrangement of Amino Acids' Complexes: A Combined Theoretical and Computational Study. *Transl Biomed.* 2016, 7:2.

Short Communication

In this short communication, respectively bonding among Boron (B^{3+}), Aluminum (Al^{3+}), Gallium (Ga^{3+}), Indium (In^{3+}) and Thallium (Tl^{3+}) cations and Alanine, Arginine, Asparagine, Aspartic Acid, Cysteine, Glutamic Acid, Glutamine, Glycine, Proline, Selenocysteine, Serine, Tyrosine, Histidine, Isoleucine, Leucine, Lysine, Methionine, Phenylalanine, Threonine, Tryptophan and Valine ligands and also structural arrangement of the present compounds were studied, theoretically and computationally [1-16]. Calculations were done via HF, PM3, MM2, MM3, AM1, MP2, MP3, MP4, CCSD, CCSD(T), LDA, BVWN, BLYP and B3LYP computational methods with 31G, 6-31G*, 6-31+G*, 6-31G(3df,3pd), 6-311G, 6-311G* and 6-311+G* basis sets, respectively. Alanine, Arginine, Asparagine, Aspartic Acid, Cysteine, Glutamic Acid, Glutamine, Glycine, Proline, Selenocysteine, Serine, Tyrosine, Histidine, Isoleucine, Leucine, Lysine, Methionine, Phenylalanine, Threonine, Tryptophan and Valine ligands are bonded to Boron (B^{3+}), Aluminum (Al^{3+}), Gallium (Ga^{3+}), Indium (In^{3+}) and Thallium (Tl^{3+}) cations via Oxygen (O) and Nitrogen (N) atoms. It is evident that if Alanine, Arginine, Asparagine, Aspartic Acid, Cysteine, Glutamic Acid, Glutamine, Glycine, Proline, Selenocysteine, Serine, Tyrosine, Histidine, Isoleucine, Leucine, Lysine, Methionine, Phenylalanine, Threonine, Tryptophan and Valine ligands form complexes with Boron (B^{3+}), Aluminum (Al^{3+}), Gallium (Ga^{3+}), Indium (In^{3+}) and Thallium (Tl^{3+}) cations, different isomers will be obtained. Energy of each of the isomers was optimized via HF, PM3, MM2, MM3, AM1, MP2, MP3, MP4, CCSD, CCSD(T), LDA, BVWN, BLYP and B3LYP computational methods with 31G, 6-31G*, 6-31+G*, 6-31G(3df,3pd), 6-311G, 6-311G* and 6-311+G* basis sets, respectively. The most stabilized isomers are complexes in which Boron (B^{3+}), Aluminum (Al^{3+}), Gallium (Ga^{3+}), Indium (In^{3+}) and Thallium (Tl^{3+}) cations are bonded to Oxygen (O) in Carbonyl (C=O) group and Nitrogen (N) in Amide (R-CO-NR'R'') group in Alanine, Arginine, Asparagine, Aspartic Acid, Cysteine, Glutamic Acid, Glutamine, Glycine, Proline, Selenocysteine, Serine, Tyrosine, Histidine, Isoleucine, Leucine, Lysine, Methionine, Phenylalanine, Threonine, Tryptophan and Valine ligands. Then, numbers of Alanine, Arginine, Asparagine, Aspartic Acid, Cysteine, Glutamic Acid, Glutamine, Glycine, Proline, Selenocysteine, Serine, Tyrosine, Histidine, Isoleucine, Leucine, Lysine, Methionine, Phenylalanine, Threonine, Tryptophan and Valine ligands surrounding Boron (B^{3+}),

Aluminum (Al^{3+}), Gallium (Ga^{3+}), Indium (In^{3+}) and Thallium (Tl^{3+}) cations are increased. Energy of each of the resulting complexes was optimized via HF, PM3, MM2, MM3, AM1, MP2, MP3, MP4, CCSD, CCSD(T), LDA, BVWN, BLYP and B3LYP computational methods with 31G, 6-1G*, 6-31+G*, 6-31G(3df, 3pd), 6-311G, 6-311G* and 6-311+G* basis sets as mentioned above, respectively. Furthermore, stability energy of the complexes, bond lengths and also bond angles were investigated.

References

- Andrew SM, Nagaraju A, Malena BR, Vassilios P (2015) Computational modeling and biological validation of novel non-steroidal ligands for the cholesterol recognition/interaction amino acid consensus (CRAC) motif of the mitochondrial translocator protein (TSPO), *Pharmacological Research* 99: 393-403.
- Daniel Garcez SQ, Glaucio BF, Leonardo M da Costa, José Walkimar de MC (2016) DFT studies of the interactions between the $[Ca(H_2O)_5]^{2+}$ cation and monofunctional oxo, aza, sulfur and phosphorous ligands, *Computational and Theoretical Chemistry* 1075: 104-110.
- Marcos VMM, Daniel GS Quattrocchio, Leonardo M Da Costa, Glaucio BF, José W de MC (2015) Computational study of the interaction between the $[Pb(H_2O)_3]^{2+}$ cation and ligands containing oxygen, nitrogen and sulfur donor atoms, *Polyhedron* 102: 193-200.
- Bigler DJ, Peterson LW, Cafiero M (2015) Effects of implicit solvent and relaxed amino acid side chains on the MP2 and DFT calculations of ligand-protein structure and electronic interaction energies of dopaminergic ligands in the SULT1A3 enzyme active site, *Computational and Theoretical Chemistry* 1051: 79-92.
- Hellal A, Chafaa S, Chafai N (2016) Synthesis, characterization and computational studies of three α -amino-phosphonic acids derivatives from Meta, Ortho and Para aminophenol, *Journal of Molecular Structure* 1103: 110-124.
- Sardella R, Macchiarulo A, Carotti A, Ianni F, Rubiño MEG, et al. (2012) Chiral mobile phase in ligand-exchange chromatography of amino acids: Exploring the copper(II) salt anion effect with a computational approach, *Journal of Chromatography A* 1269: 316-324.
- Suncica ZB, Srdan DS (2013) Halogen bonding in complexes of proteins and non-natural amino acids, *Computational Biology and Chemistry* 47: 231-239.

8. Cao H, Chen H, Cui Y, Tian H, Chen J (2016) Structure-based design and confirmation of peptide ligands for neuronal polo-like kinase to promote neuroregeneration, *Computational Biology and Chemistry* 61: 238-244.
9. Katherine HA, Mallory Morris, Larryn WP, Cafiero M (2016) Ab initio study of electronic interaction energies and desolvation energies for dopaminergic ligands in the catechol-O-methyltransferase active site, *Computational and Theoretical Chemistry* 1078: 146-162.
10. Natalini B, Marinozzi M, Sardella R, Macchiarulo A, Pellicciari R (2004) Evaluation of the enantiomeric selectivity in the chiral ligand-exchange chromatography of amino acids by a computational model, *Journal of Chromatography A* 1033: 363-367.
11. Qin P, Zhang W, Lu W (2013) Theoretical study of hydrated Ca²⁺-amino acids (glycine, threonine and phenylalanine) clusters, *Computational and Theoretical Chemistry* 1021: 164-170.
12. Philips A, Lach G, MBujnicki J (2015) Chapter Eleven-Computational Methods for Prediction of RNA Interactions with Metal Ions and Small Organic Ligands, In: Shi-Jie Chen and Donald H. Burke-Aguero, Editor(s), *Methods in Enzymology*, Academic Press 553: 261-285.
13. Natalini B, Giacche N, Sardella R, Ianni F, Macchiarulo A (2010) Computational studies for the elucidation of the enantiomer elution order of amino acids in chiral ligand-exchange chromatography, *Journal of Chromatography A* 1217: 7523-7527.
14. Anighoro A, Graziani D, Bettinelli I, Cilia A, De Toma C, et al. (2015) Insights into the interaction of negative allosteric modulators with the metabotropic glutamate receptor 5: Discovery and computational modeling of a new series of ligands with nanomolar affinity, *Bioorganic & Medicinal Chemistry* 23: 3040-3058.
15. Diana JB, Larryn WP, Mauricio Cafiero (2015) DFT and MP2 study of the effects of mutations on the binding of ligands within the SULT1A3 active site, *Computational and Theoretical Chemistry* 1068: 63-71.
16. Santos HFD (2014) Reactivity of auranofin with S-, Se- and N-containing amino acids, *Computational and Theoretical Chemistry* 1048: 95-101.