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Theoretical calculation of electronic parameters, UV spectra and Thermodynamic properties of Benzotriazoles

Abstract

In present communication we have calculated geometry optimization, electronic properties and UV spectra biological and thermodynamical properties of Benzotriazoles by using combination of DFT/B3LYP and 6-311G base (d, p). The Highest occupied molecular orbital (HOMO), Lowest unoccupied molecular orbital (LUMO), Molecular electronic surface plot (MESP) are used to obtain electronic property of Benzotriazole molecule. Several thermodynamical properties are also obtained by means of same level theory. The time dependent density functional theory (TDDFT) of concerned molecule is also obtained by using same theory. Many biological activities are calculated by the program PASS. Swiss Dock is online server which is used for docking of Benzotiazole with 6LU7 protein The calculated value full fitness score and ΔG shows that Benzotriazoles dock well with 6LU7 protein.

Key word: HOMO, LUMO, TDDFT, DFT, 6LU7 protein

D V Shukla[1], Vijay Narayan Mishra[2], Atul Tiwari[3], Apoorva Dwivedi*

Author Affiliations
[1]Department of applied science G.L.A. University Mathura (India)
[2] Department of applied science S.R.M.G.P.C. Lucknow (India)
[3]Deptt of Zoology, Dr. B. S. Porte Govt. College, Pendra, Gaurela, C.G. (India)

***Corresponding Author**
Apoorva Dwivedi
[*]Deptt of Physics, Marwar Business School, Gorakhpur (India)
E- mail: apporvahri@gmail.com
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1. Introduction:

Benzotriazoles (BT) such as 1H-benzotriazole (1H-BT), commonly utilized as corrosion inhibitors in aircraft de-icing/anti-icing fluids , dish washer detergents, brake fluids, metal-cutting fluids, automotive antifreeze materials, liquids for industrial cooling systems, and in solid cooling fluids (Kiss A, Fries E. 2009). BTA can highly enhance the tribiological actions of ionic liquids carrying hexafluoro phosphate anions for Steel/Cu–Sn alloy sliding pair primarily for the corrosion relief (Liu X, et.al. 2006). Benzotriazole and its derivatives have vital application in the field of pharmaceutical industry. It may also be used as agonists in reference of some of very crucial proteins. Its esters derivative may act as in activators for severe acute respiratory syndrome (SARS). It may act as an acid or base, can have capability to attach outer species by using its lone pair electron properties. The BTA can be used as antifreezer in vapor phase inhibitors etc. as well (Sease C. 1978). A complete quantum chemical study may lead to asses every energetic as well as significant mechanistic insight within its formulation periphery.

In the current programme, the investigation of the structural, electronic biological properties of benzotriazoles (BT) have been undertaken. The structure and numbers of harmonic waves were determined and analyzed at the level of density functional theory (DFT) using the set of bases 6-311 G (d, p). A number of studied have been carried out on chemical compounds which proves reliability of our method(Pandey A K, Siddiqui SA,.Misra N. 2012,2013, Dwivedi A, Kumar A.2019, Das S, Bharanidharan S, and Dhandapani A. 2018, Aljuboori S, Mahmood A. 2019. Our study on title molecule helps for researchers to understand new reactive sites for chemical reaction e.g. oxidation/reduction on polyfunctional bioactive compounds. We have docked our molecule with 6LU7 protease which is related to novel COVID 19.The optimized geometry of title molecule and its molecular properties (equilibrium energy, frontier orbital energy gap, molecular electrostatic potential (MESP) energy map) were calculated and discussed. PASS analysis may significantly support its bio-utility.

2.Experimental:

We have modeled initial structure of title molecule by using GassVew3.0 (Frisch MJ et.al.2003). The geometry of concerned molecule is optimized with grouping of DFT/B3LYP method and 6-311G (d, p) basis set without any symmetry constrains. Entire calculations are done on G03 program (Frisch A et.al. 2000), on our personal laptop. The electronic parameters are calculated by means of same level theory. The Ultravoilet of concerned molecule is calculated by means of TDDFT .The HOMO, LUMO, MESP of molecule is plotted by means of of Gauss View3.0.

3. Results and Discussion

3.1. Molecular Structure

The optimized geometry of Benzotriazole molecule is shown is **Fig.1**.The optimized geometry of title shows C_1 symmetry with ground state energy 395.96 a.u. The title molecule has benzene fused with pentene ring. In pentene ring three carbon atoms are replaced by nitrogen. The C-C bond length of benzene ring is $1.42A^0$-$1.38A^0$ however C-N and N-N bond length in pentene ring are$1.34\ A^0$ and $1.32\ A^0$ correspondingly.

3.2. MESP and $HOMO - LUMO$ Plots

The chemical reactivity of title molecule are described by $\boldsymbol{HOMO}$ is known as highest occupied molecular orbitals and $\boldsymbol{LUMO}$ is known as lowest unoccupied molecular are frontier molecular orbital. The frontier orbital gap gives important result about chemical reactivity and stability of molecule. The energy gap is inversely

related with polarization and reactivity of molecule (Fleming I.1976, Murray JS and Sen K.1996). The calculated gap for title molecule is 4.89eV is comparable with carbon so title molecule shows less reactivity. The calculated, $\boldsymbol{LUMO}$ and MESP Plot of molecule are given in Fig. 2. The $\boldsymbol{HOMO}$ of title molecule distributed over whole molecule except N8 however $\boldsymbol{LUMO}$ share out throghout whole molecule. The transition $\boldsymbol{HOMO} \rightarrow \boldsymbol{LUMO}$ shows that charge transfer to N8 atom to benzene ring. The MESP plays important role to develop relationship in between molecular structure with its physiochemical property (Sponer J. and Hobza P. 1996, Kohn W**,** Sham LJ.**1965**).

3.3. Electronic and Thermodynamic properties

Pearson established relation in between hardness and HOMO-LUMO gap. The negative Eigen value HOMO and LUMO is known as ionization potential and electronegativity.

$$IP=-\varepsilon_{HOMO}\ EA=-\ \varepsilon_{LUMO}$$

Several electronic parameters are calculated and collected (Parr RG, Pearson RG.1983, Geerlings P et.al.2003**,** Parr RG, Szentpály L, Liu S.1999, P.W. Ayers and R.G. Parr.2000, Erdogdu Y, Unsalan O, Gulluoglu MT..2010) in Table-2 by given formula:

$$\text{Energy band gap} = \varepsilon LUMO - \varepsilon HOMO)$$

$$\text{Electronegativity } (\chi) = -\tfrac{1}{2}\ \varepsilon LUMO + \varepsilon HOMO) \text{ ----(1)}$$

$$\text{Chemical potential } \mu = -\ \chi,$$

$$\text{Global hardness } \eta = \tfrac{1}{2}\ \varepsilon LUMO - \varepsilon HOMO) \text{ ----} \quad (2)$$

$$\text{Global softness } S = \frac{1}{2\eta} \quad \text{----------} \quad (3)$$

$$\text{Global electrophilicity index } \omega = \frac{\mu 2}{2\eta} \text{ --------} \quad (4)$$

Several thermodynamically parameter are obtained by grouping of DFT/B3LYP method and 6-311G base (d, p) and collected in **Table-1**. The vibrational energy plays important role in entropy specific heat capacity contributes.

3.4. UV spectral analysis

The UV spectrum (Fig-3) of Benzotriazole is obtained by TDDFT calculation by using unchanged level theory. The optimized structure of title molecule is used for TDDFT calculation. The Calculated electronic transitions: E (eV), oscillatory strength (f), λ_{max} (nm) are listed in table-3.The Ultravoilet spectra of title molecule shows two prominent peak corresponds to 271nm and 217 nm. These peaks are originated by $HOMO \rightarrow LUMO$ (97%) and $HOMO - 1 \rightarrow LUMO$ (80%), $HOMO \rightarrow LUMO + 1$(20%) respectively.

Biological Activity

Some biological activities of title molecule for Pa>70% are listed in table-4. These biological activities are intended by using PASS software which determined 900 pharmacological activities (Tetko IV et.al.2001) . The title molecule shows good activities against TGF beta receptor type-I kinaseinhibitor(0.991), Renal disease treatment(0.975), Aspulvinone dimethylallyltransferase inhibitor(0.842), Chymosin inhibitor(0.830).

Swiss dock(Grosdidier A et.al.2011) is online server which predicts and performs docking with suitable protein. Swiss dock predicts 6LU7 protein suitable for docking. The 6LU7 protein is responsible for new epidemic COVID19. The calculations of molecular docking have been undertaken as blind not covered any specific area to avoid sampling. In docking process we upload coordinate file of optimized parameter and PDB file of 6LU7 protein (Liu X et.al.2020). The full fitness score (FF) and binding affinity are used to determine strength of docking of title molecule with 6LU7 protein. The more negative of FF means protein bind well with drugs. In this docking process calculated value of FF score (-1186.93kcal/mol) and binding affinity (-5.80 kcal/mol) shows that of title molecule bind well with 6LU7 protein. The docking picture of concerned molecule with 6LU7 protein is presented in fig-7. The N8 atom of title molecule bind with hydrophobic surface amphipathic amino acid Methionine (MET17) residue at 2.39A^0.

4. Conclusions

In this paper DFT calculations B3LYP/6-311 G (d, p) on Benzotriazoles. The calculated HOMO-LUMO gap (4.41eV) shows that Benzotriazoles is chemically stable. The calculated MESP plot shows that N8 atom is suitable for nucleophilic attack. The UV spectra of Benzotriazoles have two prominent peaks. The Full fitness score and ΔG shows that N8 atom of Benzotriazoles bind with hydrophobic surface amphipathic amino acid Methionine (MET17) residue at 2.39A^0. The Benzotriazoles shows good potential against in the search of potential inhibitors for novel corona virus, COVID-19 protease. This study only based on theoretical assumption of docking so we have not considered other side effects.

Table 1: Calculated thermodynamic properties of Benzotriazole by B3LYP/ 6-311 G(d,p) level.

	E (kcal/mol) Benzotriazole	C_v (cal/K-mol) Benzotriazole	S (cal/K-mol) Benzotriazole
Total	70.633	23.452	77.233
Translational	0.878	2.893	40.238
Rotational	0.891	2.979	28.076
Vibrational	68.855	17.491	8.920

Table 2: Calculated Electronic properties of Benzotriazole by B3LYP/ 6-311 G(d,p) level .

Electronic Parameters	I.P (eV)	EA (eV)	η (eV)	χ (eV)	S (eV)	ω (eV)	E_g (eV)
Pyrozine	8.57	0.39	4.09	4.48	0.12	4.91	4.89

Table3: Calculated electronic transitions: E (eV), oscillatory strength (f), λ_{max} (nm) using TDDFT/B3LYP/6–311G (d, p) method.

S. N.	Electronic Transitions	E (eV)	Oscillatory strength (f)	Calculated (λmax)	% Contribution
1	$HOMO \rightarrow LUMO$	4.56	0.114	271.07	97%
2	$HOMO1 \rightarrow LUMO$	5.02	0.119	247.09	80%
	$HOMO \rightarrow LUMO + 1$				20%

Table-4 Several Biological Activity (Pa>70%) calculated by PASS

S.N.	Biological Activity	Pa	Pi
1	TGF beta receptor type I kinase inhibitor	0,991	0,001
2	Signal transduction pathways inhibitor	0,977	0,004
3	Renal disease treatment	0,975	0,002
4	NADPH peroxidase inhibitor	0,840	0,007
5	MAP kinase inhibitor	0,826	0,003
6	5-O-(4-coumaroyl)-D-quinate 3'-monooxygenase inhibitor	0,827	0,005
7	Glycosylphosphatidylinositol phospholipase D inhibitor	0,829	0,009
8	Aspulvinone dimethylallyltransferase inhibitor	0,842	0,022
9	Saccharopepsin inhibitor	0,830	0,014
10	Chymosin inhibitor	0,830	0,014
11	Acrocylindropepsin inhibitor	0,830	0,014
12	Phobic disorders treatment	0,829	0,023
13	Nicotinic alpha2beta2 receptor antagonist	0,811	0,009
14	Arylacetonitrilase inhibitor	0,804	0,010
15	Complement factor D (inhibitor)	0,794	0,007
16	Taurine dehydrogenase inhibitor	0,799	0,013
17	Testosterone 17beta-dehydrogenase (NADP+)(inhibitor)	0,806	0,024
18	Glutamyl endopeptidase II(inhibitor)	0,790	0,011

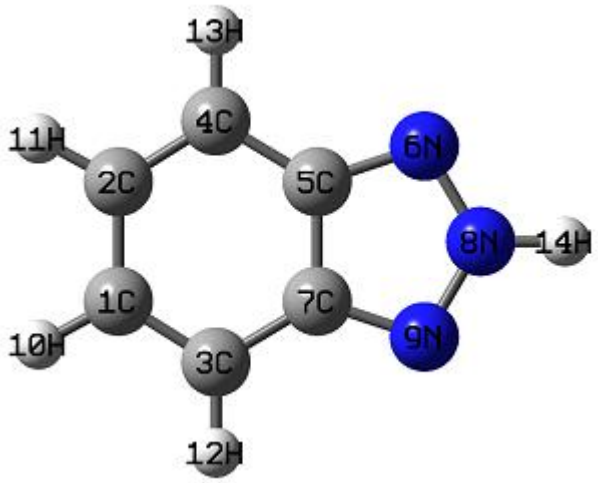

Figure 1. Molecular structure of Benzotriazole by B3LYP/ 6-311 G(d,p) level.

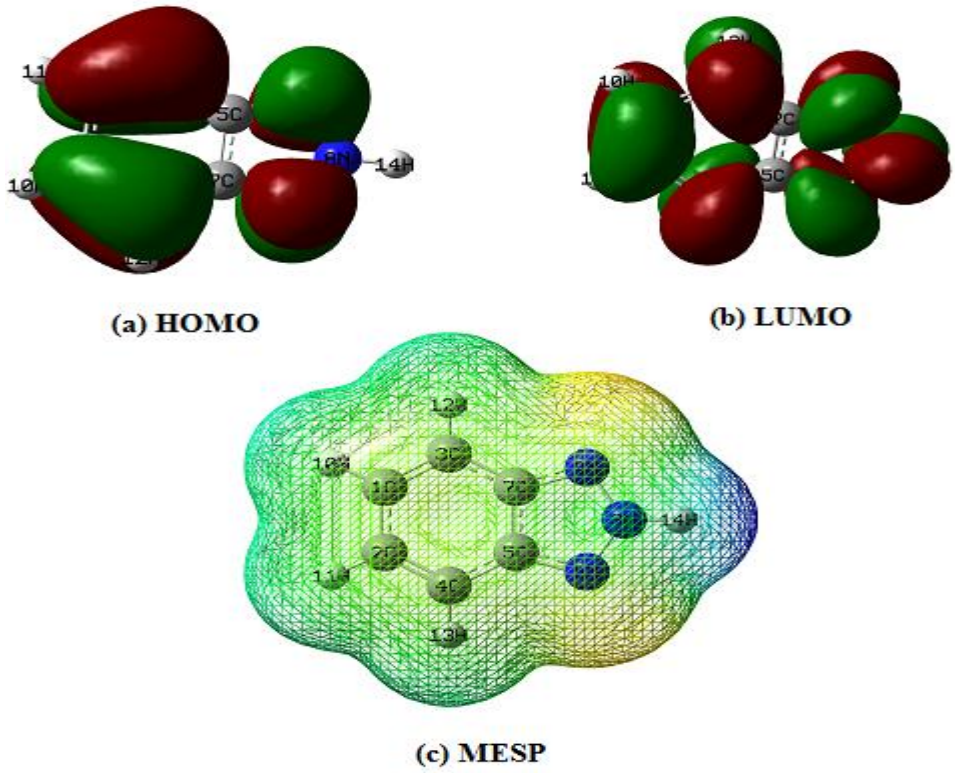

Figure2: HOMO, LUMO and MESP surfaces of Benzotriazole.

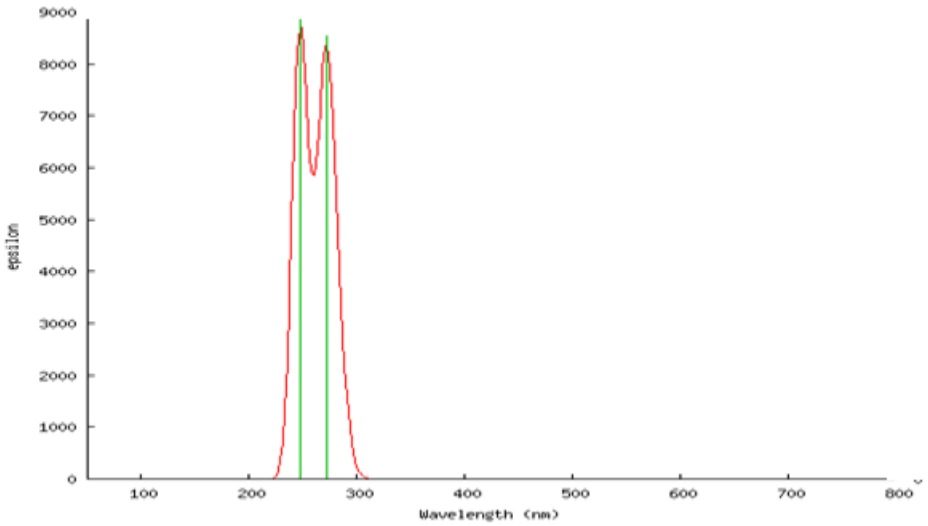

Figure 3. The Benzotriazole observed UV-vis spectrum calculated by TDDFT method at B3LYP/6-311G (d,p) level.

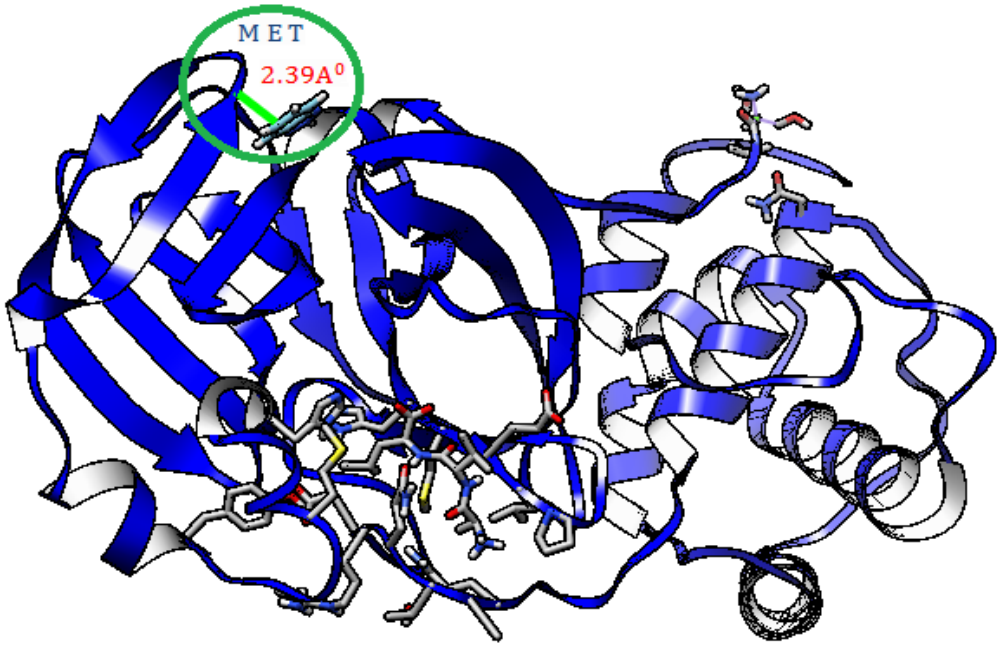

Fig-4 Molecular docking figure of title molecule with 6LU7 protein

4. References:

Ayers PW, Parr RG.2000. Variational Principles for Describing Chemical Reactions: The Fukui Function and Chemical Hardness Revisited.*Journal of the American Chemical Society*, 122(9), 2010–2018**.**

Aljuboori S, Mahmood A. 2019. Synthesis, antimicrobial evaluation, density functional theory and docking studies of some new 2 mercapto pyrimidine Schiff bases. Asian J Pharm Clin. Res. 12(2): 496-502.

Frisch MJ, Trucks GW, Schlegel HB, et al. 2003. *Gaussian 03 Revision C.02*, Gaussian Inc., Pittsburgh, PA. 2003.

Frisch A, Nelson AB and Holder A.J. 2000.*GAUSSVIEW Inc.*user manual. Pittsburgh PA.

Fleming I.1976. frontier Orbitals and Organic Chemical Reactions, John Wiley & Sons, New York, NY, USA..

Das S, Bharanidharan S, and Dhandapani A. 2018. Molecular Spectroscopy and Molecular Docking Studies on (E)-1-(4-Bromobenzylidene) Thiourea. Journal of New Developments in Chemistry 1(3): 62-81 .

Dwivedi A, Kumar A.2019. Molecular Docking and Comparative Vibrational Spectroscopic Analysis, HOMO-LUMO, Polarizabilities, and Hyperpolarizabilities of N-(4-Bromophenyl)-4-Nitrobenzamide by Different DFT (B3LYP, B3PW91, and MPW1PW91) Methods, Polycyclic Aromatic Compounds. https://doi.org/10.1080/10406638.2019.1591466.

Dwivedi A., Pandey A. K., Misra N. (2012)., Comparative Study of Vibrational Spectra of Two Bioactive Natural Products Lupeol and Lupenone Using MM/QM Method, *Spectroscopy: An International Journal*,27(3), 155–166.

Erdogdu Y, Unsalan O, Gulluoglu MT..2010. FT- Raman, FT- IR spectral and DFT studies on 6, 8- dichloroflavone and 6, 8- dibromoflavone.

*J. Raman Spectrosc.***41,** 820-828(2010).

Geerlings P, Proft FD. 18.Geerlings P, Proft FD. Langenaeker W.2003. Conceptual density functional theory . *Chem. Rev.*103, 1793–1873.

Grosdidier A, Zoete V., Michielin O. 2011. SwissDock, a protein-small molecule docking web service based on EADock DSS.Nucleic Acids Res. 39 W270 –W277.

Grosdidier A, Zoete V, Michielin O. 2011. Fast docking using the CHARMM force field with EADock DSS, J. Comput. Chem. 32: 2149 –2159.

Liu X, Zhang B, Jin Z, Yang H, Rao, Z.2020. The crystal structure of COVID-19 main protease in complex with an inhibitor N3. http://www.rcsb.org/structure/6LU7.

Kiss A, Fries E. 2009. Occurrence of benzotriazoles in the rivers Main, Hengstbach, and Hegbach (Germany) .Environmental Science and Pollution Research international. 16:702–710.

Liu X, Zhou F, Liang Y & Liu W. 2006. Benzotriazole as the additive for ionic liquid lubricant: one pathway towards actual application of ionic liquids.Tribology Letters. 23(3):191–196.

Murray JS and Sen K.1996. Molecular Electrostatic Potential, Concepts and Applications, Elsevier, Amsterdam, The Netherlands.

Pandey A K, Siddiqui SA,.Misra N. 2013. Vibrational Spectra of Two Narcotics-A DFT Study.*Chinese Journal of Physics* 51(3):473-499.

Pandey A.K, Dwivedi A, Misra N.2013. Quantum Mechanical Study on the Structure and Vibrational Spectra of Cyclobutanone and 1,2-Cyclobutanedione,Spectroscopy, 2013 Article ID 937915, 11 pages.

Pandey A. K., Dwivedi A., Misra N.2013. Quantum Mechanical Study on the Structure and Vibrational Spectra of Cyclobutanone and 1,2-Cyclobutanedione, Spectroscopy, Volume 2013, Article ID 937915, 11 pages(open access).

Kohn W, Sham LJ.1965. Self-Consistent Equations Including Exchange and Correlation Effects,Phys. Rev. A 140: 1133.

Parr RG, Pearson RG.1983. Absolute hardness: companion parameter to absolute electronegativity. *J. Am. Chem. Soc.* 105, 7512–7516.

Parr RG, Szentpály L, Liu S.1999. Electrophilicity Index.*J. Am. Chem. Soc.*121, 1922–1924.

Sease C. 1978. Benzotriazole: a review for conservators.Studies in Conservation, 23, No. 2 : 76-85.

Sponer J. and Hobza P. 1996. DNA base amino groups and their role in molecular interactions: Ab initio and preliminary density functional theory calculations. International Journal of Quantum Chemistry. 57(5): 959-970.

Tetko IV, Tanchuk VY,Kasheva TN, Villa AEP.2001. Internet software for the calculation of the lipophilicity and aqueous solubility of chemical compounds . *J. Chem. Inf. Comput. Sci.*, *41*(2):*246*-52 .