## ORIGINAL PAPER

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# **Cross section calculations for electron scattering** from DNA and RNA bases

Received: 17 February 2003 / Accepted: 30 July 2003 / Published online: 11 September 2003 © Springer-Verlag 2003

**Abstract** Differential and integral cross sections for elastic electron collisions with uracil, cytosine, guanine, adenine and thymine have been calculated using the independent atom method with a static-polarization model potential for incident energies ranging from 50 to 4000 eV. Total cross sections for single electron-impact ionization of selected DNA and RNA bases have also been calculated with the binary-encounter-Bethe model from the ionization threshold up to 5000 eV. Cross sections within the investigated energy range, can be related to the molecular symmetry, the number of target electrons and molecular size; elastic and ionization processes are most efficient for guanine and adenine molecules, while the lowest cross sections were obtained for the uracil molecule. The ionization cross sections for cytosine, thymine, adenine and guanine are compared with those recently obtained with a semi-classical and binary-encounter-Bethe formalisms. No theoretical and experimental data for elastic electron scattering from DNA and RNA bases are available, but comparisons with calculations for molecules of similar size and geometry allows the validity of the theoretical approach to be verified.

## Introduction

Uracil  $(C_4H_4N_2O_2)$ , thymine  $(C_5H_6N_2O_2)$  and cytosine (C<sub>4</sub>H<sub>5</sub>N<sub>3</sub>O), as well as adenine (C<sub>5</sub>H<sub>5</sub>N<sub>5</sub>) and guanine (C<sub>5</sub>H<sub>5</sub>N<sub>5</sub>O) molecules are some of the simplest pyrimidine and purine bases, respectively, and are components of deoxyribonucleic (DNA) and ribonucleic (RNA) acids. These nucleic acids whose function is the storage and

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transfer of genetic information [1], are essential components of all living cells.

The interaction of ionizing radiation (i.e.  $\beta$ -rays, x-rays, or  $\gamma$ -rays) with living cells induces different types of damage in DNA and RNA such as single-strand breaks, double-strand breaks, base deletions etc. [2, 3, 4]. Such modifications of cellular DNA and RNA promote cytotoxic, mutagenic and carcinogenic lesions and are the result of energy transfers that occur via a variety of excitation and ionization processes producing large quantities of radicals, ions and secondary electrons [4, 5, 6, 7, 8, 9].

The process of DNA damage induced along ionization radiation tracks is usually modeled with Monte Carlo simulations [4, 5, 6, 7, 8, 9, 10] for which a complete set of cross sections for the interaction of the primary and secondary fast particles with target molecules is needed. Usually, in these simulations a simplified linear segment of DNA or structured higher ordered DNA target (e.g. a nucleosome core particle or a piece of chromatin fiber [10]) occupies a given volume within the irradiated medium, e.g., in the form of a cylinder [8]. Using liquid water as the irradiated medium containing DNA, a Monte Carlo track structure simulation code (e.g. CPA100 [11], OREC [12], PARTRAC [13, 14]) provides the history of electron interactions in the solvent with that portion of the energy which is deposited in the DNA. From this information the damage induced in the DNA can be evaluated [6]. The input data sets for such simulations include mainly cross sections for primary and secondary electron interactions with liquid and/or gaseous water (e.g. [9]).

It has been demonstrated that not only high-energy projectiles but also electrons of lower energies can induce DNA damage [3, 15, 16, 17, 18, 19, 20]. Electrons with energies below 15 eV, which are produced in large quantities by ionizing radiation ( $\sim 4 \times 10^4$  per MeV [21, 22]), can induce single-strand and double-strand breaks in DNA [15, 16] via electron resonances (i.e. the formation of transient anions) [19, 23, 24, 25, 26, 27] with a substantial cross section [16]. Similar cross sections are found at higher energies [16]. Hence it appears that in order to refine theoretical modeling of radiation damage

to cellular DNA and RNA, more input data on the action of electrons on DNA are needed, particularly on the interaction of secondary electrons of low energy with the basic components of these acids (e.g., the bases).

In this paper, we report elastic and ionization cross section calculations for 50–3000 eV electron scattering from DNA and RNA bases. These two processes dominate the scattering of electrons from atoms and molecules in this energy range. In elastic collisions, the impinging electron,  $e^-$ , does not change its kinetic energy,  $E_i$ , and a scattering molecule remains at the same energetic state:

$$(AB)_i + e^-(E_i) \to (AB)_i + e^-(E_i)$$

where i denotes initial energetic state of a hypothetical diatomic molecule AB.

In the electron-impact ionization process in which a positive ion  $AB^+$  is produced, the scattered electron  $e^-(E_i)$  loses part of its initial kinetic energy and an additional electron,  $e^-(E_i-E_{\text{ion}}-E_f)$  is ejected from molecule AB:

$$(AB)_i + e^-(E_i) \to (AB)_f^+ + e^-(E_f) + e^-(E_i - E_{\text{ion}} - E_f)$$

where  $E_{\text{ion}}$  and  $E_f$  are the binding energy of the electron within the AB molecule and final energy of the primary electron, respectively. While elastic scattering dominates in electron collisions with atoms and molecules, above 70 eV electron impact ionization is the most efficient inelastic process.

Since low energy electron (LEE) interaction with DNA and RNA is a complex process, there is a need to develop a relatively simple theoretical approach to calculate LEE scattering cross sections from these molecules. As a starting point, such a simple approach can be tested on basic components of DNA and later be extended to include larger portions of the DNA molecule. Since cross sections are also presently being generated experimentally for the DNA bases [28], it should become possible to check in which energy range the present simplified theoretical approach, namely the independent particle model can be employed in calculations.

To our knowledge this is the first attempt to generate elastic cross sections for DNA and RNA bases within the intermediate energy range (50–4000 eV). Very recently, electron impact ionization cross sections for constituents of DNA, namely cytosine, thymine, adenine, guanine and the sugar-phosphate backbone, over the energy range from the ionization threshold to 1000 eV have been obtained with the Deutsch-Mark semi-classical formalism and the binary-encounter-Bethe method by Bernhardt and Paretzke [29]. Ionization and fragmentation of the uracil molecule by electron impact have been studied experimentally by Coupier et al. [30]. In the two following sections we describe the theoretical approaches and give the results.

## Theory and computational methods

In the present work, we employed two relatively simple calculation methods to generate these cross sections: differential (DCS) as well

as integral cross sections (ICS) for elastic electron scattering have been obtained with the independent atom method, while electron-impact ionization cross sections has been calculated with the binary-encounter-Bethe method.

Independent atom method

In this subsection, for convenience, we adopted atomic units in which  $e=m_e=\hbar=1$ , but the final results of calculations are given in the SI units.

Calculations of elastic cross sections have been carried out using the independent-atom method (IAM) [31, 32, 33] with a static-polarization model potential. In this approximation, an electron-molecule collision is reduced to the problem of collision with individual atoms: it is assumed that each atom of the molecule scatters independently, any redistribution of atomic electrons due to the molecular binding is unimportant, and multiple scattering within the molecule is negligible [31]. This approach offers reasonable approximations to elastic, momentum transfer and total cross sections for intermediate energy and high energy electrons and/or positron scattering from many polyatomic molecular targets [32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45].

In the simple form of the independent atom approximation, the DCS for elastic electron scattering on molecules, taking into account all possible orientations of the intermolecular axis in the space, is given by:

$$\frac{d\sigma}{d\Omega} = \sum_{i=1}^{N} \frac{d\sigma^{A}}{d\Omega_{j}} + \sum_{i \neq i=1}^{N} f_{i}(\theta, k) f_{j}^{*}(\theta, k) \frac{\sin(sr_{ij})}{sr_{ij}}$$
(1)

where N is the number of atoms within molecule,  $\theta$  the scattering angle,  $\frac{d\sigma^A}{d\Omega_i}$  the elastic differential cross section of the j-th atom, and  $f_i(\theta,k)$  and  $f_i^*(\theta,k)$  the complex scattering amplitudes due to the *i*-th and j-th atom of the molecule, respectively. In Eq. 1, k denotes the incident electron wave number and  $s=2k\sin(\theta/2)$  the magnitude of the momentum transfer during the collision. The internuclear distance between the i-th and j-th atom of the target molecule is represented by  $r_{ij}$ . The internuclear distances  $r_{ij}$  for guanine, adenine, thymine, cytosine and uracil were obtained using a geometry optimization procedure with the ab initio quantum chemistry package GAMESS (General Atomic Molecular Electronic Structure System) [46] with a built in "triple-split" Gaussian basis set (6-311G) [47] and by choosing the framework symmetry group as C<sub>1</sub>. Geometrically optimized structures of the investigated molecules are very close to those published previously [48, 49], with discrepancies in bond lengths and bond angles less than 0.01 Å and 1°, respectively. The small discrepancies are mainly due to different basis sets and methods used in optimization procedures.

It follows from the optical theorem that the ICS for electron elastic scattering on the molecule in the IAM approximation is given by:

$$\sigma(E) = \frac{4\pi}{k} \operatorname{Im} f(s = 0, k) = \frac{4\pi}{k} \sum_{i=1}^{N} \operatorname{Im} f_i(\theta = 0, k)$$
$$= \sum_{i=1}^{N} \sigma_i(E)$$
(2)

where  $\sigma_i(E)$  is the ICS of the *i*-th atom of the molecule at energy  $E=k^2/2$ .

To obtain the atomic scattering amplitudes and elastic electronatom cross sections, we employed partial wave analysis [50] and solved numerically with the Numerov method [51] (for details see Appendix A) the radial Schrödinger equation:

$$\[ \frac{d^2}{dr^2} - \frac{l(l+1)}{r^2} + k^2 - 2(V_{stat}(r) + V_{polar}(r)) \] u_l(r) = 0$$
(3)

under the boundary conditions:

$$u_l(0) = 0, \ u_l(r) \xrightarrow{r \to \infty} A_l \hat{j}_l(kr) - B_l \hat{n}_l(kr) \tag{4}$$

where  $\hat{j}_l(kr)$  and  $\hat{n}_l(kr)$  are the spherical Bessel-Riccati and Neumann-Riccati functions [52] (for basic definition see Appendix B), respectively.  $V_{\text{stat}}(r)$  is the static potential of the atom expressed in the form proposed by Salvat et al. [53]:

$$V_{stat}(r) = -\frac{Z}{r} \sum_{n=1}^{3} a_n \exp\left(-\beta_n r\right)$$
 (5)

where Z is the nuclear charge, and  $a_n$  and  $\beta_n$  are the parameters determined by an analytical fitting procedure to Dirac-Hartree-Fock-Slater self-consistent data [53]. For this formulation, it has been shown [53] that n=1,...,3 is sufficient to obtain a reliable static potential (i.e. comparable to that obtained directly from the Dirac-Hartree-Fock-Slater functions). The polarization potential  $V_{\text{polar}}(r)$  was expressed in the form proposed by Padial and Norcross [54]:

$$V_{polar}(r) = \begin{cases} v(r) & r \leq r_c \\ -\alpha/2r^4 & r > r_c \end{cases}$$
 (6)

where v(r) is the free-electron-gas correlation energy [55] and  $\alpha$  is the static electric dipole polarizability of an atom. The distance  $r_c$  is that of the first crossing point of the v(r) and  $-\alpha/2r^4$  curves [56]. In the present study, we neglected exchange effects as these have been found to be negligible at high incident energies. Furthermore, our previous work [33] has shown that the IAM method, with static and polarization potentials only, can reproduce very well experimental elastic DCS and ICS even for low (~20 eV) collision energies.

The scattering amplitudes for electron scattering on atom were obtained using the following equation:

$$f(\theta, k) = \frac{1}{2ik} \sum_{l=0}^{l_{\text{max}}} (2l+1) (e^{2i\delta_l} - 1) P_l(\cos \theta) + \pi \alpha k \left( \frac{1}{3} - \frac{1}{2} \sin \frac{\theta}{2} - \sum_{l=1}^{l_{\text{max}}} \frac{P_l(\cos \theta)}{(2l-1)(2l+3)} \right)$$
(7)

where  $P_l(\cos\theta)$  are Legendre polynomials and the second term in Eq. 7 is the Born scattering amplitude (i.e. the scattering amplitude generated within the Born approximation) for a potential of the form from Eq. 6 [57]. In the present calculations, we obtained for the first  $l_{\text{max}}$ =50, the exact phase shifts and the contribution of those remaining (from  $l_{\text{max}+1}$  to  $\infty$ ) is included through the Born approximation. The phase shifts  $\delta_l$  are connected with the asymptotic form of the wave function,  $u_l(r)$ , by:

$$\tan \delta_l = \frac{B_l}{A_l} \tag{8}$$

**Table 1** Selected ionization potentials<sup>3</sup> of DNA and RNA bases obtained from different theoretical methods and experiments

The DCS for elastic electron scattering from a particular atom,  $\frac{d\sigma^A}{d\Omega}$ , was calculated according to:

$$\frac{d\sigma^{A}}{d\Omega} = |f(\theta, k)|^{2} \tag{9}$$

while the atomic elastic ICS cross section,  $\sigma^A$ , was derived from the following expression:

$$\sigma^{A} = \frac{4\pi}{k^{2}} \left( \sum_{l=0}^{l_{\max}} (2l+1) \sin \delta_{l} + \sum_{l=l_{\max}}^{\infty} (2l+1) \sin \delta_{l}^{(B)} \right)$$
(10)

Since the above theoretical and numerical approaches have yielded encouraging results for polyatomic molecular targets like  $XY_4$  (X=C, Si, Ge; Y=H, F, Cl) and for  $C_2F_6$  [33, 58], it is expected that the differential cross sections and integral cross sections for electron elastic scattering by more complex molecules, such as those presented here may also be fairly reliable.

#### Binary-encounter-Bethe (BEB) method

Electron-impact ionization cross sections have been calculated using the binary-encounter-Bethe model [59, 60], which is a simplified version of the binary-encounter-dipole model [59]. This method is based on a combination of two earlier theories, the Mott theory [61] and the Bethe [62, 63] theory and has been successfully employed for calculation of total electron-impact ionization cross sections of a variety of molecules of atmospheric [64] and industrial interest [65, 66]. In this approximation the electron-impact ionization cross section per molecular orbital is given by:

$$\sigma_{BEB} = \frac{S}{t+u+1} \left[ \frac{\ln t}{2} \left( 1 - \frac{1}{t^2} \right) + 1 - \frac{1}{t} - \frac{\ln t}{t+1} \right]$$
 (11)

where u=U/B, t=T/B,  $S=4\pi a_0^2 NR^2/B^2$ ,  $a_0=0.5292$  Å, R=13.61 eV, and T is the energy of impinging electrons. Finally, the total cross section for electron-impact ionization was obtained as the sum of  $\sigma_{\rm BEB}$  for all molecular orbitals.

The electron binding energy B, kinetic energy of the orbital, U, and orbital occupation number, N, were obtained for the ground states of the investigated molecules with the Hartree-Fock method using the GAMESS code [46] and the Gaussian 6-311G basis set. Because the valence orbital energies obtained in this way differ slightly from those obtained with other theories [67, 68, 69] and experimental ones [70, 71, 72], we also performed outer valence Green function calculations of correlated electron affinities and ionization potentials [73, 74, 75, 76] with the GAUSSIAN code [77]. The experimental values [70, 71] of the first ionization potential were inserted in the calculation, instead of those obtained theoretically, to fix the threshold behavior of the ionization cross section at the experimental value. In Table 1, we compare the values of the first ionization potential obtained in the different theoretical calculations and experiments. The values of B, U, and Nfor uracil, thymine, cytosine, adenine and guanine, incorporated in

Method	Ionization potential (eV)					
	Uracil	Cytosine	Thymine	Adenine	Guanine	Reference
B3LYP/6-311++G**	9.25	8.59	8.76	8.12	7.68	[67]
B3PW91/6-311++G**	9.33	8.66	8.85	8.14	7.69	[67]
BP/6-311++G**	9.27	8.79	8.79	8.10	7.68	[67]
$MP2/6-31+G^*$	-	8.74	8.85	8.18	7.66	[67]
B3LYP/6-311G(2df,p)	9.21	8.57	8.74	8.09	7.64	[68]
RHF/3-21G	-	9.01	9.48	8.48	8.05	[29]
RHF/6-311 G (GAMESS)	10.16	9.34	9.75	8.72	8.35	Present theory
ROVGF/6-311 G	8.97	8.12	8.53	8.02	7.44	Present theory
(GAUSSIAN)						•
Experimental	-	8.68	8.87	8.26	7.77	[70]
Experimental	$8.35 \pm 0.01$	-	-	-	-	[71]
Experimental	-	-	-	8.55±0.10	-	[72]

Table 2 Molecular orbitals, electron binding energy and kinetic energy for uracil, cytosine, thymine, adenine and guanine

МО	Uracil	Uracil		Cytosine		Thymine		Adenine		Guanine	
	В	U	В	U	В	U	В	U	В	U	
1	559.3	794.1	558.0	794.0	559.3	794.1	425.6	601.4	558.6	794.0	
2	559.3	794.1	425.4	601.5	559.1	794.1	424.1	601.7	425.6	601.4	
3	426.0	601.5	424.4	601.4	425.8	601.5	424.0	601.3	425.5	601.5	
2 3 4	425.6	601.5	423.2	601.6	425.5	601.5	423.8	601.6	424.9	601.4	
5	311.4	435.9	310.0	435.9	311.3	435.9	423.5	601.6	423.9	601.6	
6	310.4	435.9	309.5	435.9	310.3	435.9	309.1	435.8	423.8	601.7	
6 7	308.9	435.8	308.7	435.8	308.6	435.8	308.6	435.7	310.8	435.9	
8	306.7	435.7	306.5	435.6	306.9	435.7	308.5	435.7	309.0	435.9	
9	39.76	61.89	38.34	61.13	306.0	435.8	308.2	435.8	308.7	435.8	
10	38.76	69.71	35.88	56.41	39.64	61.64	306.8	435.6	308.0	435.8	
11	36.18	59.11	34.83	54.68	38.71	69.65	37.99	47.59	306.5	435.6	
12	34.41	57.75	32.40	55.07	36.01	59.36	36.13	49.59	38.67	57.80	
13	30.19	47.89	29.57	47.79	34.31	57.56	34.46	52.34	37.70	55.30	
14	25.82	43.50	24.94	44.77	30.65	45.68	32.79	56.05	37.03	54.12	
15	24.99	52.31	24.41	48.31	26.78	41.79	31.82	56.88	33.77	52.96	
16	22.42	39.72	21.26	37.51	25.38	41.68	28.90	49.55	33.64	57.37	
17	21.35	44.20	21.13	40.57	24.83	50.42	24.89	46.04	32.48	56.46	
18	17.47	39.71	20.03	46.17	21.43	42.88	24.30	46.23	28.77	50.67	
19	16.25	35.30	16.85	41.45	21.40	43.51	23.33	45.31	25.14	45.95	
20	16.20	54.61	15.20	43.14	17.30	40.10	21.70	41.29	24.69	49.02	
21	15.55	55.06	15.11	33.17	16.17	34.63	20.51	42.55	23.18	45.39	
22	14.56	59.57	14.65	42.36	16.14	55.42	17.23	40.27	22.44	40.13	
23	14.45	45.68	13.86	60.95	15.12	60.01	16.52	47.58	20.75	43.27	
24	13.85	43.18	13.06	38.13	14.88	53.86	15.60	30.26	20.52	47.56	
25	12.66	40.97	11.76	41.54	14.82	30.57	15.52	44.28	17.45	43.93	
26	11.12	63.08	9.56	61.60	13.63	42.69	15.13	45.43	16.56	46.47	
27	10.18	65.30	9.38	54.81	13.43	40.10	14.31	42.48	15.78	31.80	
28	10.05	65.30	8.91	43.66	13.47	33.43	13.60	34.70	15.26	49.35	
29	8.35	49.96	8.68	45.78	12.31	41.94	12.14	35.98	14.48	44.63	
30	0.55	17.70	0.00	13.70	10.98	62.66	11.02	51.76	14.34	63.78	
31					10.14	64.81	10.23	42.73	14.33	35.03	
32					9.97	55.67	9.98	51.48	13.23	41.05	
33					8.87	41.52	9.28	39.90	10.88	51.10	
34					0.07	71.52	8.99	52.12	10.63	41.58	
35							8.26	39.89	9.99	48.79	
36							0.20	37.07	9.99	63.50	
37									9.80	54.22	
38									9.38 9.71	54.22 43.57	
38 39									9.71 7.77		
39									1.11	41.75	

the computation of electron-impact ionization cross sections are presented in Table  $2. \,$ 

#### **Results and discussion**

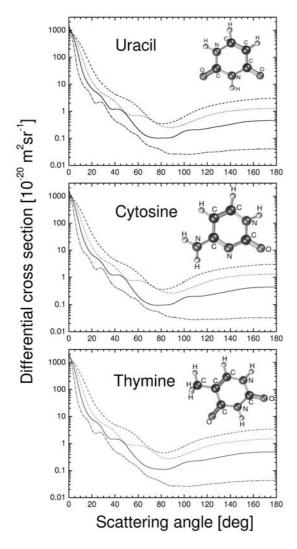
Differential and integral cross sections

Differential cross sections for elastic electron scattering from uracil, thymine, cytosine, adenine and guanine are presented in Figs. 1 and 2 for electron energies of 50 (short dashed line), 100 (dotted line), 200 (solid line) and 500 eV (dotted and dashed line). There is no elastic measurement and calculation to be compared with these results.

The angular dependence of DCS values is very similar for all investigated pyrimidine bases, which reflects the similarity in molecular structure, especially the molecular geometry of uracil, cytosine and thymine. Comparison of the angular distributions of scattered electrons for adenine and guanine also shows a large similarity in the cross

sections for the purine bases related to similarity in the geometry. Although the difference in geometry of purine and pyrimidine bases is significant, the shape of the DCSs for pyrimidine bases differs only slightly from those of the purine bases. This means that the main contribution to DCS in Eq. 1 comes from terms with i=j, i.e. the contribution from interference terms  $(i\neq j)$  is rather small so that the cross section depends mainly on the molecular size and numbers of atoms. For scattering angles ranging from  $3^{\circ}$  to  $180^{\circ}$  the cross section value for each molecule studied decreases with increasing electron energy. Only for forward scattering angles (i.e. scattering within  $0-3^{\circ}$ ) does the contribution to the elastic DCS increase with collision energy (see comparison in Table 3).

Generally, the calculated DCSs for elastic electron scattering from DNA and RNA bases are typical for elastic differential cross sections of other polyatomic molecules [33, 40, 42, 58]. The highest values of the elastic DCSs are obtained for the largest molecule (i.e. guanine) and the lowest for uracil which is the smallest



**Fig. 1** Differential cross section for 50 eV (*short dashed line*), 100 eV (*dotted line*), 200 eV (*solid line*), and 500 eV (*dotted and dashed line*) elastic electron scattering from uracil, cytosine, and thymine

investigated molecule. Thus, the elastic DCS value appears to be essentially connected with number of electrons in the molecule and molecular size, while angular dependence of the elastic DCSs is related to molecular geometry.

The incident electron energy dependence of the ICSs for the investigated molecular targets are presented in Fig. 3 and the values of the ICSs at selected energies are listed in Table 4.

In each case, the integral elastic cross sections are monotonically decreasing functions of impact energy and also dependent on molecular size. The integral elastic cross section values are highest for guanine and adenine molecules and lowest for cytosine and uracil over the entire energy range investigated.

In Fig. 4, we compared elastic ICS for the uracil molecule with cross sections obtained previously [58] for benzene ( $C_6H_6$ ), hexafluorobenzene ( $C_6F_6$ ), chloroben-

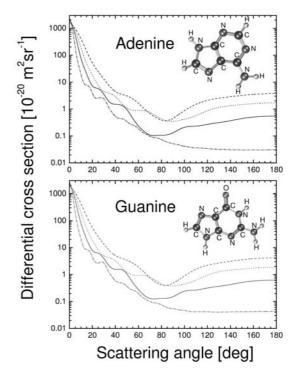


Fig. 2 Differential cross section for 50 eV (short dashed line), 100 eV (dotted line), 200 eV (solid line), and 500 eV (dotted and dashed line) elastic electron scattering from adenine and guanine

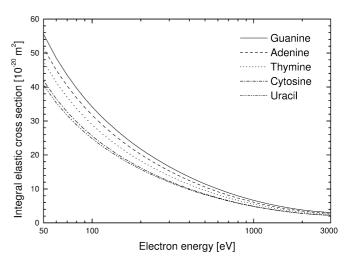


Fig. 3 Energy dependence of integral elastic cross sections for electron collisions with guanine, adenine, thymine, cytosine and uracil

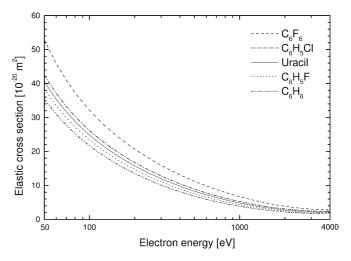
zene  $(C_6H_5Cl)$  and fluorobenzene  $(C_6H_5F)$  with the same method. It is evident that the energy dependence of the ICS for uracil is similar to other ring molecules of similar size. Its value is higher than the cross sections values for benzene and fluorobenzene molecules and lower than the corresponding values for chlorobenzene and hexafluorobenzene. Thus, in this case ICS values strongly depend on the molecular size and on the nature of the outermost atoms.

**Table 3** Differential cross sections (DCS) for elastic electron scattering in the forward direction from uracil, cytosine, thymine, adenine and guanine in units of  $10^{-20}$  m<sup>2</sup> sr<sup>-1</sup>

	Energy (eV)	Scattering angle (deg)						
		0	1	2	3	4	5	
Uracil	50	1007	932	850	766	689	613	
	100	1113	998	870	743	628	522	
	200	1270	1089	889	697	534	396	
	500	1450	1128	778	487	288	160	
Cytosine	50	1144	1058	961	863	771	682	
•	100	1259	1126	977	828	693	568	
	200	1438	1230	995	769	579	421	
	500	1621	1252	847	515	269	162	
Thymine	50	1497	1382	1252	1120	996	875	
,	100	1652	1474	1273	1070	887	719	
	200	1871	1594	1276	971	718	509	
	500	2121	1623	1072	628	346	181	
Adenine	50	1665	1537	1392	1242	1102	965	
	100	1840	1641	1414	1185	978	788	
	200	2127	1812	1448	1097	806	568	
	500	2383	1824	1201	698	382	202	
Guanine	50	1861	1718	1553	1382	1220	1063	
	100	2051	1829	1570	1306	1068	851	
	200	2369	2015	1597	1192	860	596	
	500	2678	2037	1311	739	395	207	

**Table 4** Cross sections for elastic electron scattering from guanine, adenine, thymine, cytosine and uracil at selected energies

Energy	Integral elastic cross section (10 <sup>-20</sup> m <sup>2</sup> )							
(eV)	Guanine	Adenine	Thymine	Cytosine	Uracil			
50	55.56	51.48	47.43	41.84	40.55			
60	48.53	45.01	41.34	36.50	35.36			
70	43.49	40.36	36.97	32.67	31.65			
80	39.67	36.83	33.67	29.76	28.85			
90	36.65	34.03	31.05	27.47	26.63			
100	34.18	31.73	28.92	25.59	24.82			
110	32.11	29.81	27.13	24.02	23.30			
120	30.34	28.16	25.61	22.67	22.01			
140	27.45	25.47	23.12	20.49	19.90			
160	25.17	23.35	21.17	18.76	18.24			
180	23.31	21.61	19.58	17.36	16.89			
200	21.75	20.16	18.25	16.19	15.76			
220	20.42	18.92	17.12	15.18	14.79			
250	18.75	17.35	15.69	13.92	13.58			
300	16.55	15.30	13.83	12.28	11.99			
350	14.86	13.73	12.40	11.01	10.76			
400	13.51	12.46	11.26	10.00	9.784			
450	12.39	11.43	10.33	9.170	8.980			
500	11.46	10.56	9.544	8.475	8.306			
600	9.977	9.182	8.302	7.372	7.234			
700	8.848	8.135	7.357	6.533	6.418			
800	7.958	7.310	6.614	5.873	5.775			
900	7.238	6.644	6.013	5.340	5.254			
1000	6.644	6.095	5.518	4.900	4.824			
1100	6.146	5.635	5.103	4.532	4.463			
1200	5.723	5.245	4.750	4.219	4.156			
1400	5.045	4.621	4.186	3.718	3.664			
1600	4.530	4.148	3.758	3.339	3.290			
1800	4.132	3.783	3.427	3.045	3.000			
2000	3.819	3.497	3.168	2.816	2.772			
2200	3.574	3.273	2.964	2.636	2.592			
2500	3.303	3.028	2.742	2.440	2.394			
3000	3.052	2.803	2.541	2.263	2.209			
3500	2.997	2.760	2.511	2.235	2.168			
4000	3.114	2.876	2.633	2.342	2.255			



**Fig. 4** Comparison of the energy dependence of integral elastic cross sections for electron scattering from hexafluorobenzene ( $C_6F_6$ ), chlorobenzene ( $C_6H_5Cl$ ), uracil ( $C_4H_4N_2O_2$ ), fluorobenzene ( $C_6H_5F$ ) and benzene ( $C_6H_6$ ). The results for  $C_6F_6$  and benzene were calculated by Możejko et al. [58]. The other were generated in the present investigation

It is worth noting that in mathematical form the main assumptions of the independent atom method can be expressed by kR >> 1, where k is the momentum of the incident electron (in a.u.) and R the typical internuclear distance (in a.u.) in the target molecule. In the present study, at the lowest energies, the kR value is greater than 1 for all investigated molecules. However, below 50 eV, the approximation can give values too high for the elastic ICS. Usually, elastic cross sections obtained with IAM for electron scattering from polyatomic molecules, exceed the total (elastic + inelastic) cross section values for collision energies lower than 10 eV. Such disagreements

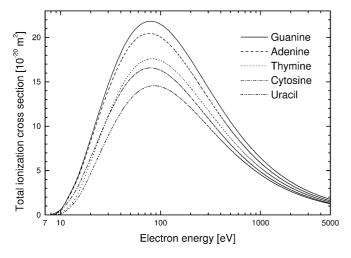


Fig. 5 Energy dependence of total cross sections for electronimpact ionization of guanine, adenine, thymine, cytosine and uracil

[33, 58] can be due to neglect of the bond distortion and multiple scattering at impact energies, corresponding to electron wavelengths comparable to internuclear distances. However, it should be noted that even at collision energies as low as 20 eV, for some small molecules (e.g., SiH<sub>4</sub> and GeH<sub>4</sub>), the IAM method yields elastic ICS in very good agreement with experimental findings [33].

## Total cross section for electron impact ionization

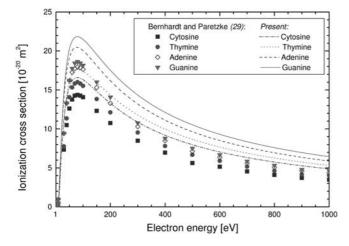
Figure 5 shows the calculated total cross sections for single electron-impact ionization of uracil, cytosine, thymine, adenine and guanine. They are listed at selected energies in numerical form in Table 5. For each molecule the cross section maximum is located near 80 eV. Ionization processes are most efficient for guanine and adenine with a cross section maximum exceeding  $2\times10^{-19}$  m<sup>2</sup>. Ionization cross sections for thymine and cytosine are very similar especially at the threshold and uracil has the lowest ionization cross section.

Recently, ionization of uracil induced by proton and electron impact has been reported within the 20-150 keV and 8–16 eV ranges, respectively [30]. No cross section data for electron impact ionization were published, but it was shown that the most abundant species are the parent ion C<sub>4</sub>H<sub>4</sub>N<sub>2</sub>O<sub>2</sub><sup>+</sup> and two fragment ions C<sub>3</sub>H<sub>3</sub>NO<sup>+</sup> and CNO+. More recently, total cross sections for electron impact ionization of cytosine, thymine, adenine, and guanine have been calculated by Bernhard and Paretzke [29] with the Deutsch-Mark (DM) and BEB formalisms for energies ranging from the ionization threshold to 1000 eV. They observed that both algorithms yield very similar total electron impact ionization cross sections; only for higher impact energies is there a smaller decrease of the cross section with energy in the case of the BEB theory. In Fig. 6, the present ionization cross sections are compared with those obtained by Bernhardt and Paretzke [29] with the DM formalism. Qualitative behavior of both

**Table 5** Total cross section for electron impact ionization of guanine, adenine, thymine, cytosine and uracil at selected energies

Energy	Ionization cross section (10 <sup>-20</sup> m <sup>2</sup> )							
(eV)	Guanine	Adenine	Thymine	Cytosine	Uracil			
10	0.575	0.545	0.171	0.457	0.0739			
11	1.238	1.177	0.487	0.965	0.334			
12	2.032	1.902	0.883	1.483	0.677			
13	2.803	2.670	1.319	2.036	1.047			
14	3.579	3.435	1.844	2.623	1.456			
15	4.402	4.223	2.454	3.232	1.931			
16	5.268	5.050	3.145	3.911	2.445			
17	6.145	5.898	3.873	4.576	3.009			
18	7.007	6.738	4.604	5.232	3.582			
19	7.834	7.539	5.310	5.851	4.146			
20	8.610	8.290	5.979	6.433	4.682			
25	12.02	11.54	8.897	9.059	7.042			
30	14.70	14.04	11.20	11.11	8.943			
35	16.70	15.91	12.95	12.65	10.40			
40	18.23	17.33	14.29	13.83	11.53			
45	19.38	18.37	15.30	14.71	12.41			
50	20.23	19.13	16.06	15.36	13.07			
55	20.84	19.67	16.61	15.83	13.56			
60	21.27	20.03	17.01	16.15	13.93			
65	21.55	20.27	17.28	16.37	14.19			
70	21.73	20.40	17.46	16.50	14.36			
75	21.81	20.46	17.57	16.57	14.48			
80	21.84	20.45	17.61	16.58	14.54			
85	21.80	20.40	17.61	16.56	14.57			
90	21.73	20.31	17.57	16.50	14.56			
95	21.62	20.19	17.51	16.42	14.52			
100	21.49	20.05	17.41	16.31	14.46			
110	21.16	19.71	17.18	16.06	14.30			
125	20.59	19.14	16.75	15.62	13.98			
150	19.54	18.12	15.94	14.83	13.36			
175	18.50	17.12	15.12	14.03	12.71			
200	17.52	16.18	14.34	13.29	12.08			
250	15.79	14.54	12.95	11.97	10.94			
300	14.35	13.19	11.78	10.87	9.980			
350	13.14	12.07	10.80	9.957	9.169			
400	12.13	11.12	9.979	9.187	8.481			
450	11.27	10.32	9.275	8.532	7.891			
500	10.52	9.634	8.667	7.968	7.381			
600	9.308	8.513	7.674	7.047	6.544			
700	8.358	7.639	6.895	6.327	5.886			
800	7.594	6.936	6.268	5.748	5.355			
900	6.966	6.359	5.751	5.272	4.917			
1000	6.439	5.876	5.318	4.873	4.549			
1500	4.710	4.293	3.895	3.563	3.337			
2000	3.743	3.409	3.097	2.831	2.656			
2500	3.121	2.841	2.583	2.360	2.216			
3000	2.684	2.443	2.222	2.030	1.907			
3500	2.360	2.443	1.954	1.785	1.678			
4000	2.300	1.919	1.934	1.785	1.500			
4500	1.910	1.737	1.582	1.444	1.358			
5000	1.746	1.737	1.362	1.320	1.242			
5000	1./40	1.300	1.740	1.540	1.242			

data sets is almost the same, although some discrepancies exist mainly in the magnitude of the cross section (up to 10%) and threshold energies. Since in both calculations the same structural codes (GAUSSIAN and GAMESS) have been used, we can assume that the computational uncertainties in both ionization cross sections are very similar and therefore the observed discrepancies cannot be due to them. They can be correlated to the different computational approaches and especially to the *ab initio* 



**Fig. 6** Comparison between the present cross sections for ionization of the DNA bases calculated with the BEB model and the ionization cross sections for the same molecules obtained with the DM formalism by Bernhardt and Paretzke [29]

calculation of the binding energy of the first ionization potentials and the highest occupied molecular orbitals (HOMO). In the present work, the first ionization potentials (here it is assumed, according to the Koopman theorem that the calculated electron binding energy of the HOMO is the first ionization potential) were taken from experimental data [70, 71], which are in very close agreement with the values obtained theoretically [68] from the density functional theory (see Table 1). They are slightly lower (by about 0.3 eV for cytosine and thymine, 0.2 eV for adenine and 0.5 eV for guanine) than those of Bernhardt and Paretzke [29]. Moreover, in their calculations Bernhardt and Paretzke [29] took the binding energies of the HOMO generated at the Hartee-Fock level without any energy correlation of the electrons. These energies are about 1 eV higher than those used in the present work and may therefore account for differences between the two sets of data. It is worth noting that ionization potentials are lower in solution. For example calculations of the threshold of ionization for uracil and thymine molecules in water solution give values of 7.02 eV and 6.74 eV, respectively [78]. This means that according to the BEB formalism employed in the present work, the cross sections for electron impact ionization of DNA and RNA bases in water will be higher than in the gas phase. In such calculations the binding energies of higher occupied orbitals for DNA and RNA bases in the water solution should be taken into account but these are not presently available.

In summary, using simple computational models, the cross sections for elastic electron scattering and electron impact ionization of uracil, cytosine, thymine, adenine and guanine have been calculated at low and intermediate collision energies. It was found that the magnitude of the differential as well as integral elastic cross sections essentially depends on the number of electrons in the target and the molecular size. Similarly, the ionization cross sections strongly depend on the molecular size for

energies ranging from 70 eV to 5000 eV. The results obtained can be useful for comparison with experimental results and in further studies of electron collisions with more complicated DNA and RNA components as well as with DNA and RNA. Such cross sections are also needed to describe in more details ionizing radiation damage to DNA and RNA via Monte Carlo simulations.

**Acknowledgments** This work was supported by the Canadian Institutes of Health Research.

# Appendix A

The Schrödinger Eq. 3 is a differential equation of the following form:

$$\frac{d^2}{dr^2}u_l(r) = F_l(r)u_l(r) \tag{12}$$

where

$$F_l(r) = -2\left(E - V(r) - \frac{l(l+1)}{2r^2}\right) \tag{13}$$

In our caclulations, we integrated Eq. 12 using the Numerov method [51], in which:

$$\left[1 - \frac{1}{12} (\Delta r)^{2} F_{l}(r_{j+1})\right] u_{l}(r_{j+1})$$

$$-2 \left[1 + \frac{5}{6} (\Delta r)^{2} F_{l}(r_{j})\right] u_{l}(r_{j})$$

$$+ \left[1 - \frac{1}{12} (\Delta r)^{2} F_{l}(r_{j-1})\right] u_{l}(r_{j-1}) = 0$$
(14)

where  $\Delta r$  is the increment in the method and in the presented calculations  $\Delta r$ =0.01.

## Appendix B

The Bessel-Riccati and Neumann-Riccati functions [52] obey the following relationships:

$$\frac{d}{dx}\hat{z}_{l}(x) + \frac{l}{x}\hat{z}_{l}(x) - \hat{z}_{l-1}(x) = 0$$
(15)

and

$$\frac{d}{dx}\hat{z}_{l}(x) - \left(\frac{l+1}{x}\right)\hat{z}_{l}(x) + \hat{z}_{l+1}(x) = 0$$
(16)

where x=kr, and  $\hat{z}_l(x)$  represents Bessel-Riccati,  $\hat{j}_l(x)$ , and Neumann-Riccati,  $\hat{n}_l(x)$ , functions, respectively. It follows from Eqs. 15 and 16 that:

$$\hat{z}_{l+1}(x) = \frac{2l+1}{r}\hat{z}_l(x) - \hat{z}_{l-1}(x)$$
(17)

Using Eq. 17 it is possible to generate any Bessel-Riccati and Neuman-Riccati function for l>2.

For l=0 and l=1, the Bessel-Riccati and Neumann-Riccati functions have the following form:

$$\hat{j}_0(x) = \sin x \tag{18}$$

$$\hat{j}_1(x) = -\cos x + \frac{\sin x}{x} \tag{19}$$

$$\hat{n}_0(x) = -\cos x \tag{20}$$

and

$$\hat{n}_1(x) = -\sin x - \frac{\cos x}{x} \tag{21}$$

Since in the present calculations, the argument x=kr can reach large values, we generated Bessel-Riccati and Neumann-Riccati functions from the following relationships:

$$\hat{j}_{l}(x) = \left[ P\left(l + \frac{1}{2}, x\right) \sin\left(x - \frac{1}{2}l\pi\right) + Q\left(l + \frac{1}{2}, x\right) \cos\left(x - \frac{1}{2}l\pi\right) \right]$$
(22)

and

$$\hat{n}_l(x) = (-1)^{l+1} \left[ P\left(l + \frac{1}{2}, x\right) \cos\left(x + \frac{1}{2}l\pi\right) - Q\left(l + \frac{1}{2}, x\right) \sin\left(x + \frac{1}{2}l\pi\right) \right]$$
(23)

where

$$P\left(l + \frac{1}{2}, x\right) = \sum_{i=0}^{[l/2]} (-1)^{i} \left(l + \frac{1}{2}, 2i\right) (2x)^{-2i}$$
 (24)

and

$$Q\left(l+\frac{1}{2},x\right) = \sum_{i=0}^{\left[(l-1)/2\right]} (-1)^{i} \left(l+\frac{1}{2},2i+1\right) (2x)^{-2i-1}$$
(25)

In the above equations

$$\left(l + \frac{1}{2}, i\right) = \frac{(l+i)!}{l!\Gamma(l-i+1)} \tag{26}$$

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