2013
international year of crystallography

File conversion and processing

Tony Weight

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When a Co-editor accepts a paper

- An email is sent to the contact author of the paper
- An email is sent to the technical editor in Chester
- Files are transferred from the submission area to the paper directory for editing
- The IUCr database is updated
- The paper submission URL is closed to the author

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What files are transferred?

- Source file of the text
- Figures
- Supplementary material
- Review PDF

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Converting to SGML

- SGML = standard generalized markup language
- Structured ASCII document
- Conforms to our document type definition (DTD)
- Is an archival format
- Used for typesetting
- Used to create metadata
- Easily converted to HTML for online journals

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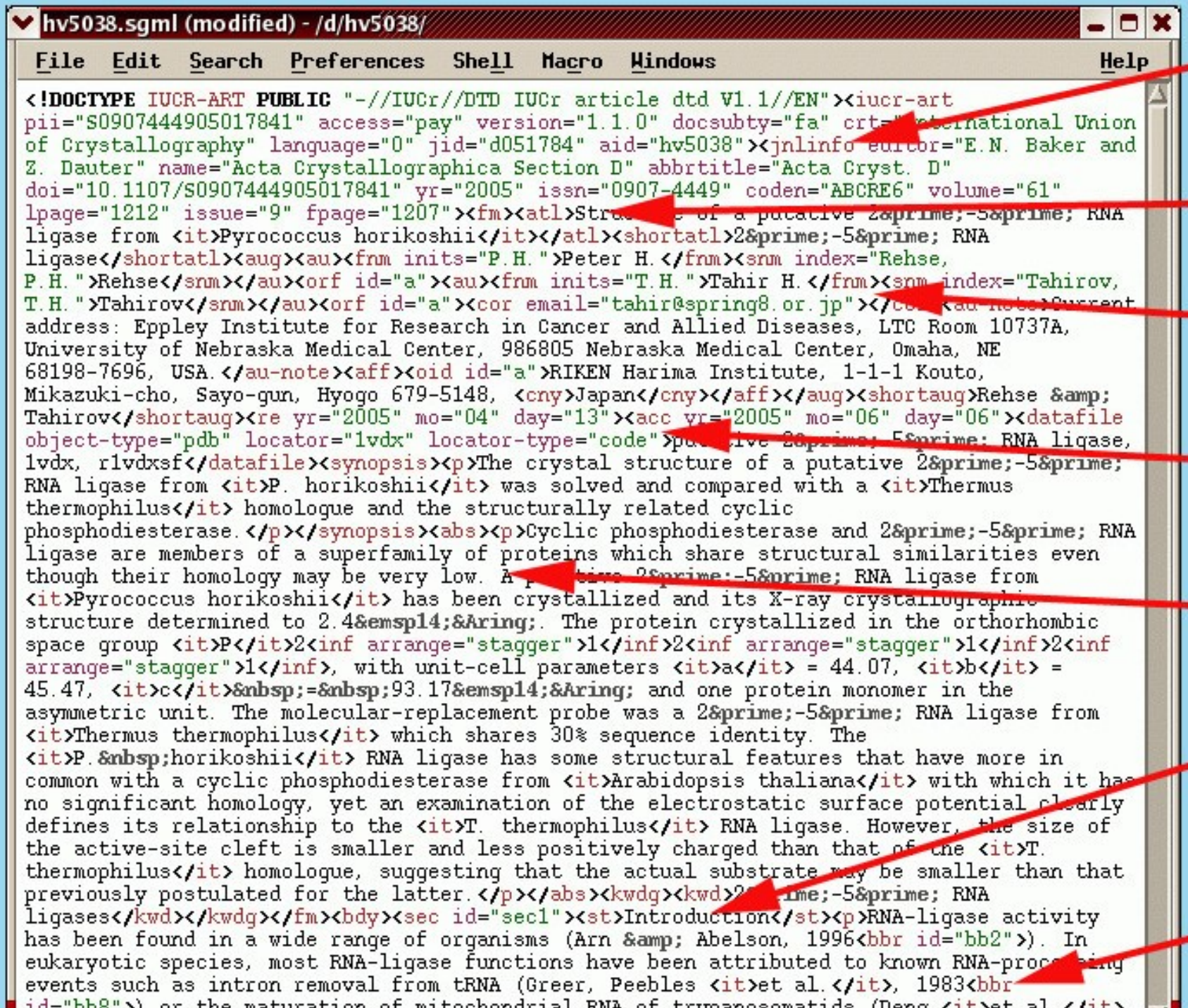
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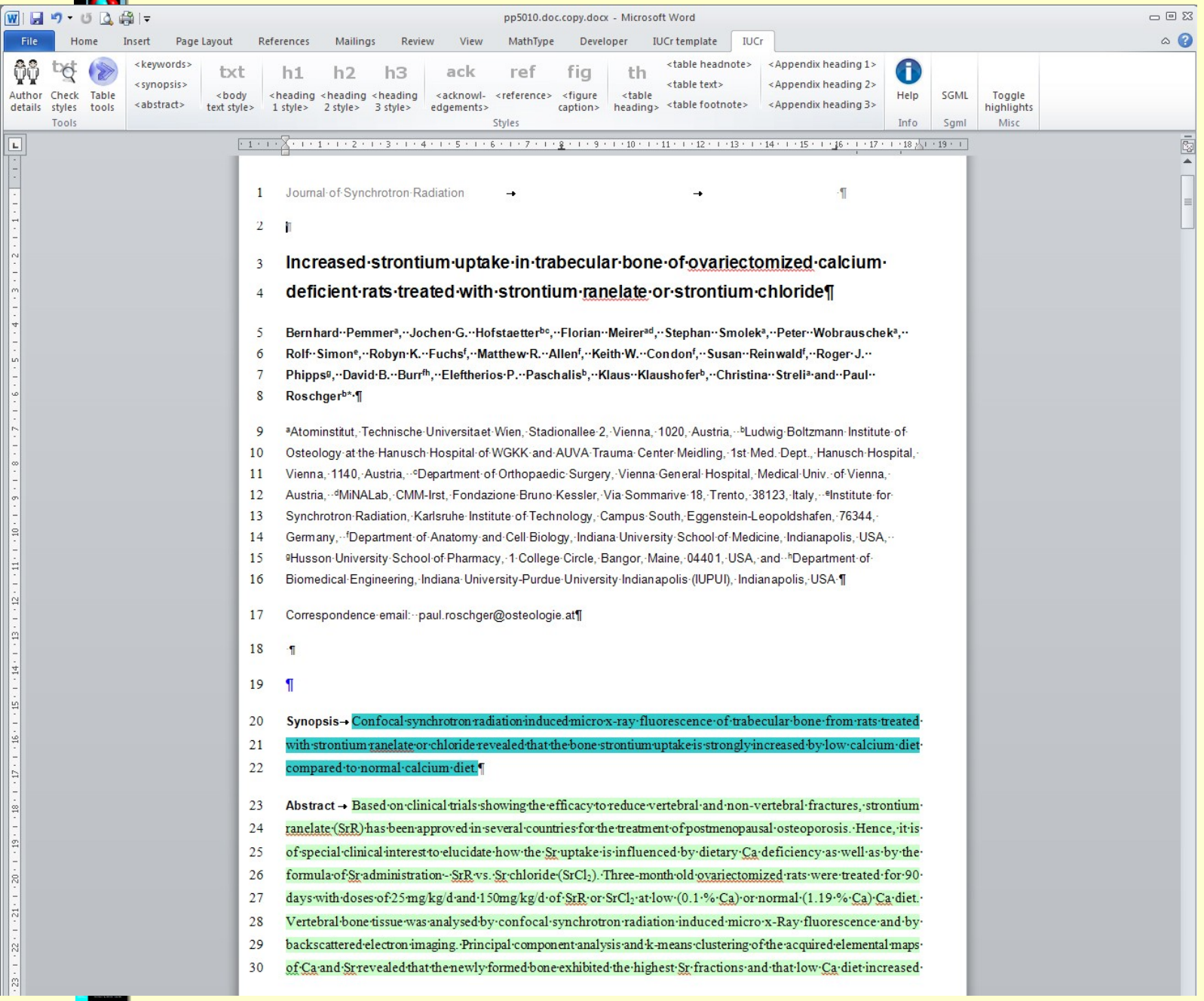
Z. Dauter" name="Acta Crystallographica Section D" abbrtitle="Acta Cryst. D"
doi="10.1107/S0907444905017841" yr="2005" issn="0907-4449" coden="ABCRE6" volume="61"
lpage="1212" issue="9" fpage="1207"><fm><atl>Structure of a putative 2′-5′ RNA
ligase from <it>Pyrococcus horikoshii</it></atl><shortatl>2′-5′ RNA
ligase</shortatl><aug><au><fnm inits="P.H.">Peter H.</fnm><snm index="Rehse,
P.H.">Rehse</snm></au><orf id="a"><au><fnm inits="T.H.">Tahir H.</fnm><snm index="Tahirov,
T.H.">Tahirov</snm></au><orf id="a"><cor email="tahir@spring8.or.jp"></cor><au-note>Current
address: Eppley Institute for Research in Cancer and Allied Diseases, LTC Room 10737A,
University of Nebraska Medical Center, 986805 Nebraska Medical Center, Omaha, NE
68198-7696, USA.</au-note><aff><oid id="a">RIKEN Harima Institute, 1-1-1 Kouto,
Mikazuki-cho, Sayo-gun, Hyogo 679-5148, <cny>Japan</cny></aff></aug><shortaug>Rehse &
Tahirov</shortaug><re yr="2005" mo="04" day="13"><acc yr="2005" mo="06" day="06"><datafile
object-type="pdb" locator="1vdx" locator-type="code">putative 2′-5′ RNA ligase,
1vdx, r1vdxsf</datafile><synopsis> The crystal structure of a putative 2′-5′
RNA ligase from <it>P. horikoshii</it> was solved and compared with a <it>Thermus
thermophilus</it> homologue and the structurally related cyclic
phosphodiesterase. </synopsis><abs> Cyclic phosphodiesterase and 2′-5′ RNA
ligase are members of a superfamily of proteins which share structural similarities even
though their homology may be very low. A putative 2′-5′ RNA ligase from
<it>Pyrococcus horikoshii</it> has been crystallized and its X-ray crystallographic
structure determined to 2.4 Å. The protein crystallized in the orthorhombic
space group <it>P</it>2<inf arrange="stagger">1</inf>2<inf arrange="stagger">1</inf>2<inf
arrange="stagger">1</inf>, with unit-cell parameters <it>a</it> = 44.07, <it>b</it> =
45.47, <it>c</it> = 93.17 Å and one protein monomer in the
asymmetric unit. The molecular-replacement probe was a 2′-5′ RNA ligase from
<it>Thermus thermophilus</it> which shares 30% sequence identity. The
<it>P. horikoshii</it> RNA ligase has some structural features that have more in
common with a cyclic phosphodiesterase from <it>Arabidopsis thaliana</it> with which it has
no significant homology, yet an examination of the electrostatic surface potential clearly
defines its relationship to the <it>T. thermophilus</it> RNA ligase. However, the size of
the active-site cleft is smaller and less positively charged than that of the <it>T.
thermophilus</it> homologue, suggesting that the actual substrate may be smaller than that
previously postulated for the latter. </abs><kwdg><kwd>2′-5′ RNA
ligases</kwd></kwdg></fm><bdy><sec id="sec1"><st>Introduction</st> RNA-ligase activity
has been found in a wide range of organisms (Arn & Abelson, 1996<bbr id="bb2">). In
eukaryotic species, most RNA-ligase functions have been attributed to known RNA-processing
events such as intron removal from tRNA (Greer, Peebles <it>et al.</it>, 1983<bbr
Journal details
Article details
Author details
Database details
Synopsis and Abstract
Start of text
Cross references

In-house Word template

Synopsis and Abstract automatically recognised and highlighted



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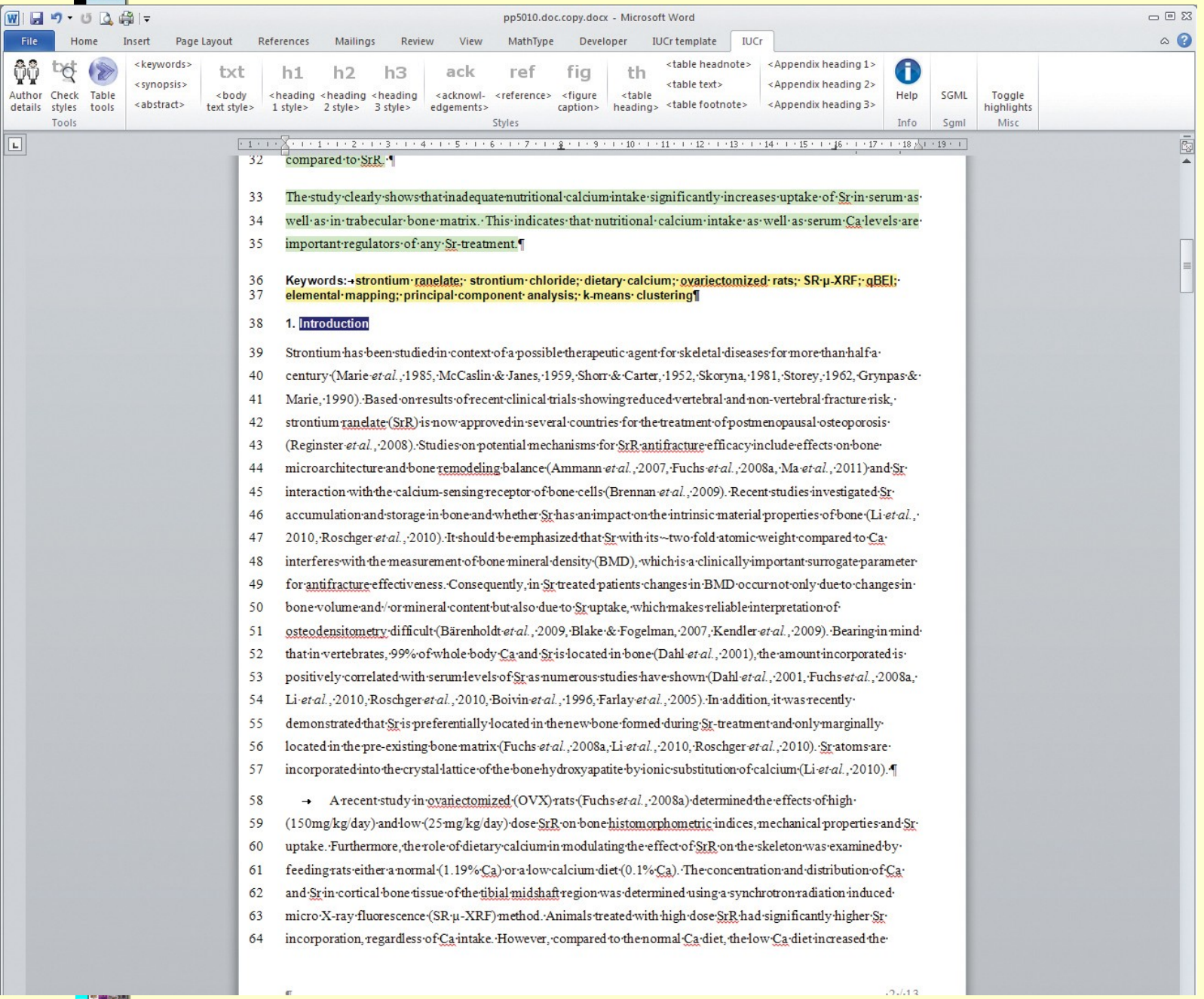

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Keywords and a first-level heading automatically recognised and highlighted

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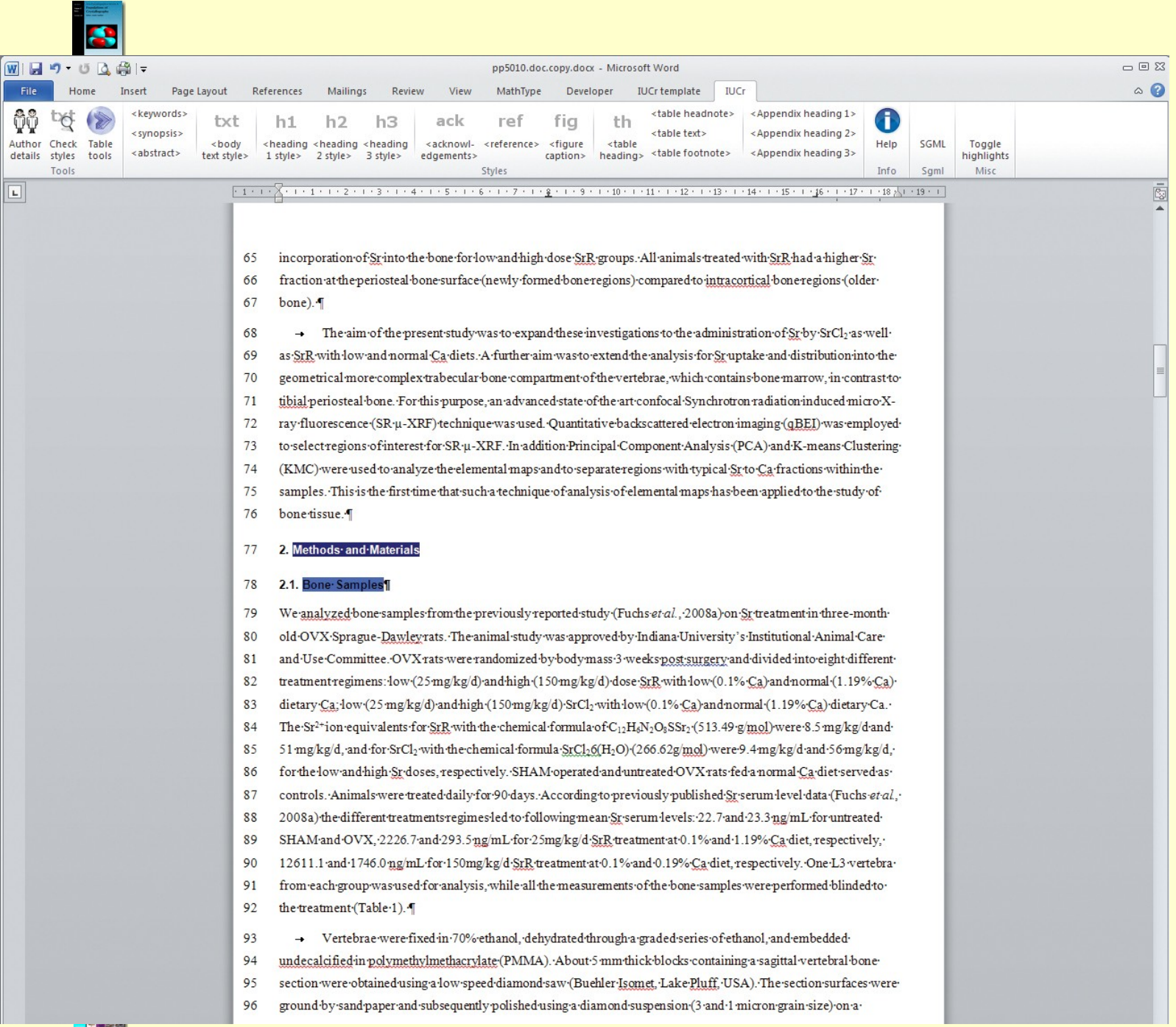

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First and second heading levels automatically recognised and highlighted

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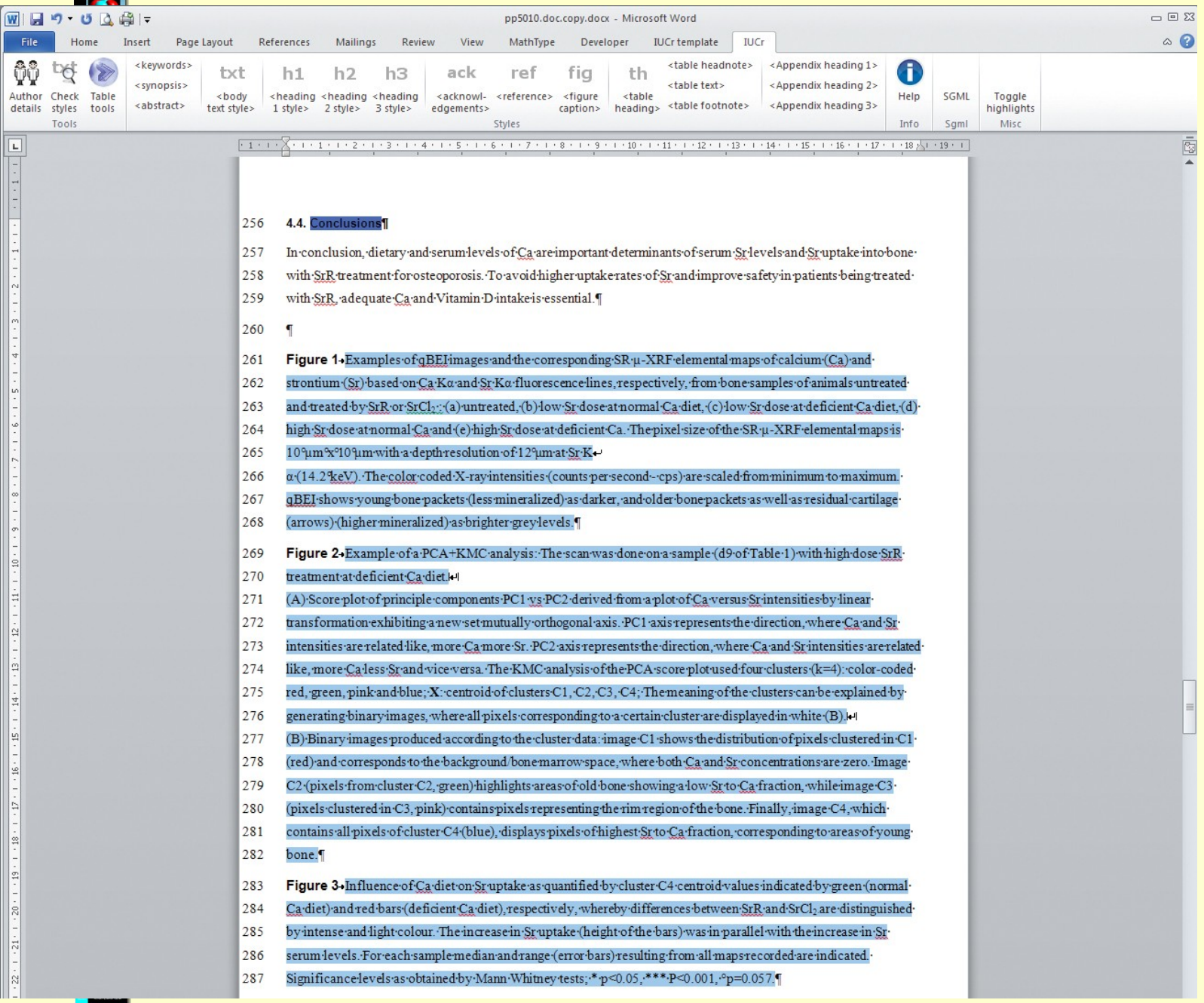

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Figure captions automatically recognised and highlighted

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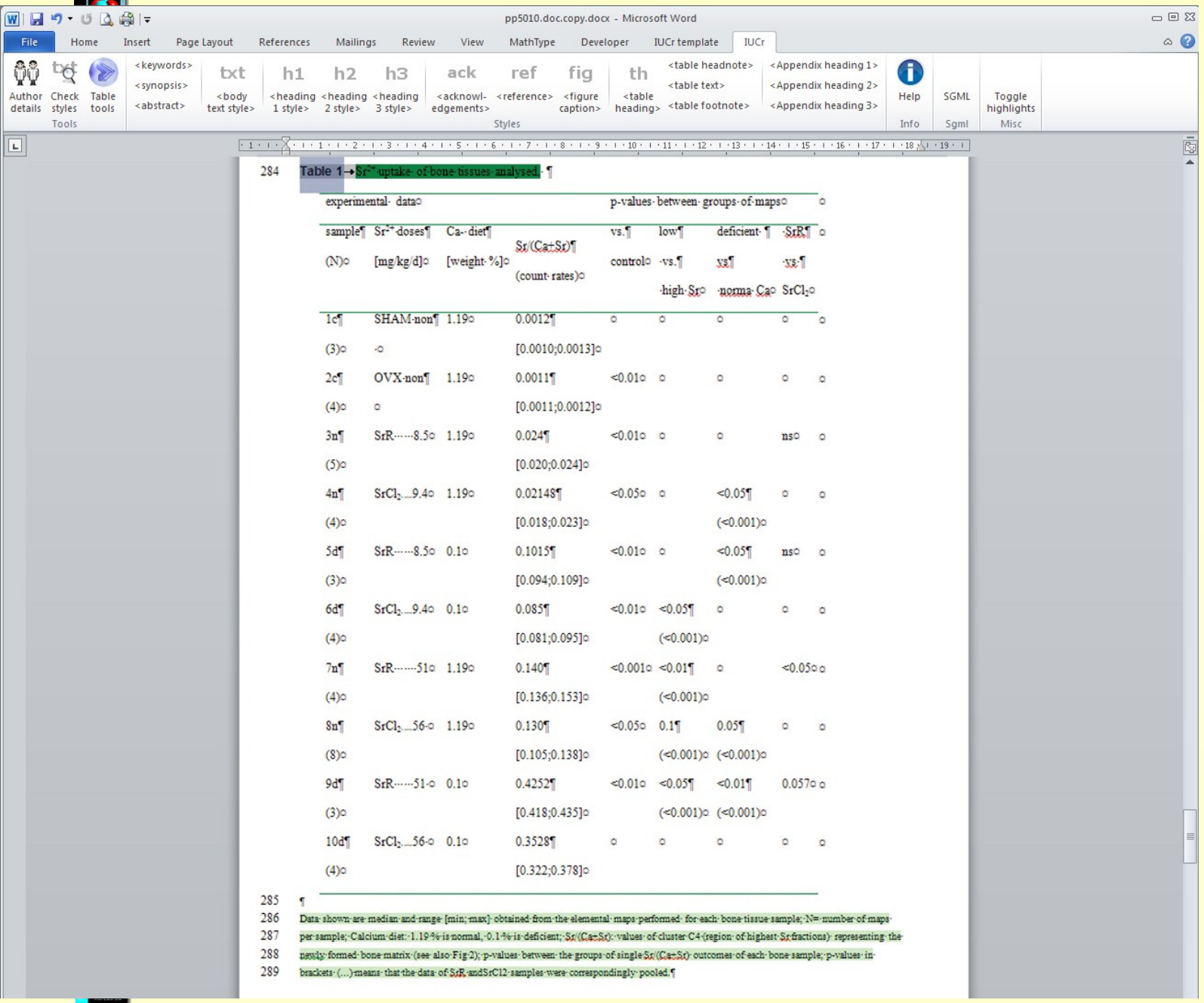


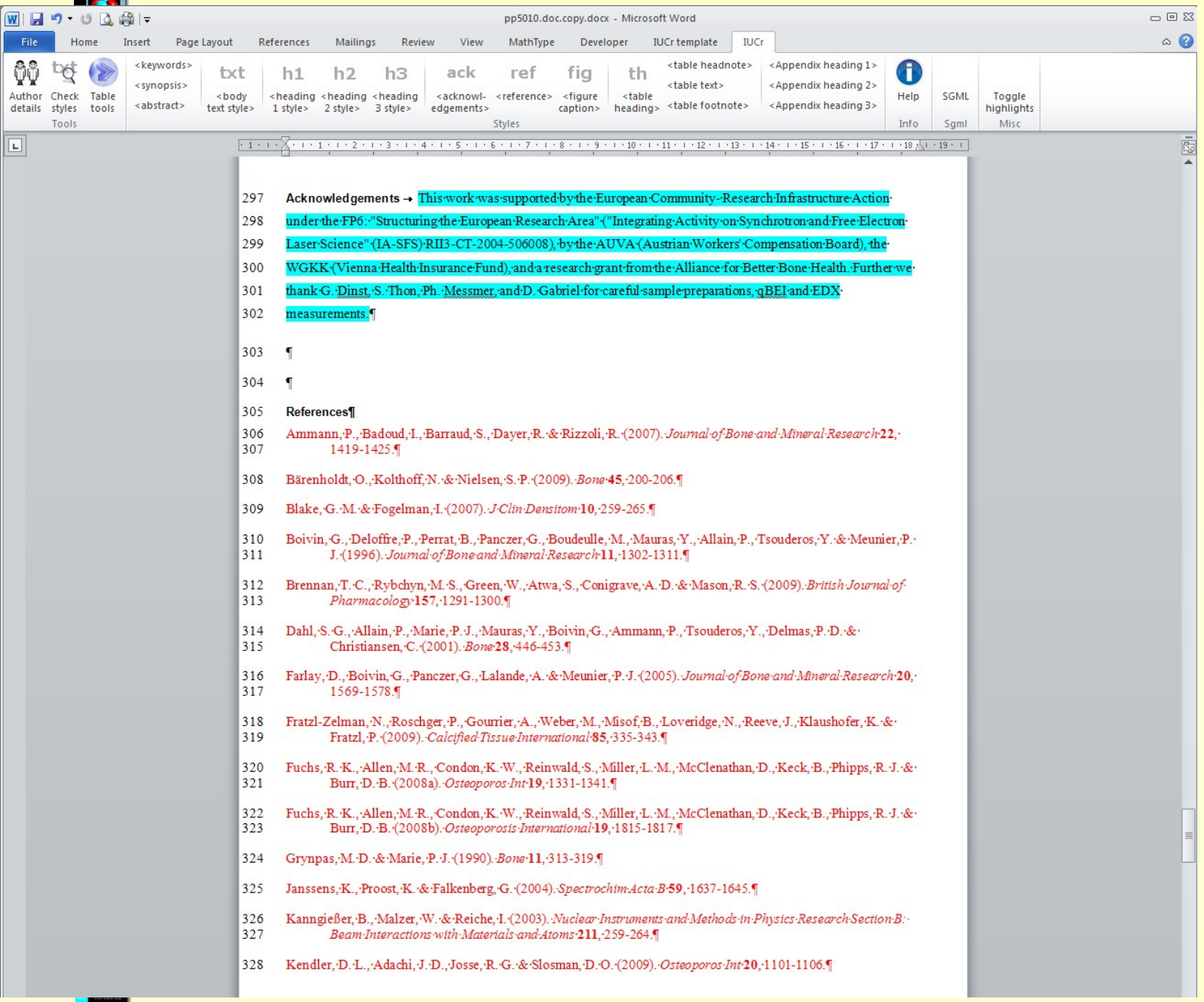
284 **Table 1** Sr^{2+} uptake of bone tissues analysed. ¶

experimental data				p-values between groups of maps				
sample (N)	Sr^{2+} doses [mg/kg/d]	Ca-diet [weight %]	Sr/(Ca+Sr) (count rates)	vs. control	low vs. high Sr	deficient vs. norma Ca	SrR vs. $SrCl_2$	
1c (3)	SHAM-non	1.19	0.0012 [0.0010;0.0013]					
2c (4)	OVX-non	1.19	0.0011 [0.0011;0.0012]	<0.01				
3n (5)	SrR-8.5	1.19	0.024 [0.020;0.024]	<0.01			ns	
4n (4)	$SrCl_2$-9.4	1.19	0.02148 [0.018;0.023]	<0.05		<0.05 (<0.001)		
5d (3)	SrR-8.5	0.1	0.1015 [0.094;0.109]	<0.01		<0.05 (<0.001)	ns	
6d (4)	$SrCl_2$-9.4	0.1	0.085 [0.081;0.095]	<0.01	<0.05 (<0.001)			
7n (4)	SrR-51	1.19	0.140 [0.136;0.153]	<0.001	<0.01 (<0.001)		<0.05	
8n (8)	$SrCl_2$-56	1.19	0.130 [0.105;0.138]	<0.05	0.1 (<0.001)	0.05 (<0.001)		
9d (3)	SrR-51	0.1	0.4252 [0.418;0.435]	<0.01	<0.05 (<0.001)	<0.01 (<0.001)	0.057	
10d (4)	$SrCl_2$-56	0.1	0.3528 [0.322;0.378]					

285 ¶

286 Data shown are median and range [min;max] obtained from the elemental maps performed for each bone tissue sample; N= number of maps
287 per sample; Calcium diet: 1.19 % is normal, 0.1 % is deficient; Sr/(Ca+Sr) values of cluster C4 (region of highest Sr fractions) representing the
288 newly formed bone matrix (see also Fig 2); p-values between the groups of single Sr/(Ca+Sr) outcomes of each bone sample; p-values in
289 brackets (…) means that the data of SrR and SrCl2 samples were correspondingly pooled. ¶

Table caption and table footnote automatically recognised and highlighted



In-house Word template

Acknowledgements and References automatically recognised and highlighted

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Conversion of Word file to SGML

- Text is converted to SGML
- Mathematical equations are converted to TeX format using MathType
- References are checked against databases
  e.g. Crystallography Journals Online, PubMed
- Resulting SGML file is saved in the paper directory

Crystallography Journals Online

Conversion of LaTeX file to SGML

- SGML conversion starts automatically once paper is accepted
- References are checked against databases
  e.g. Crystallography Journals Online, PubMed
- Resulting SGML file is saved in the paper directory

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Filtering the SGML

- Adds fixed spaces between possible units and values
- Double spaces are removed
- Unit symbols are altered, *e.g.* seconds becomes s
- Table attributes are changed, *e.g.* entries are aligned left
- Sections, figures and tables are numbered
- Cross references citations to figures, tables, schemes, equations and footnotes
- Checks for uncited figures, tables, schemes, equations and footnotes

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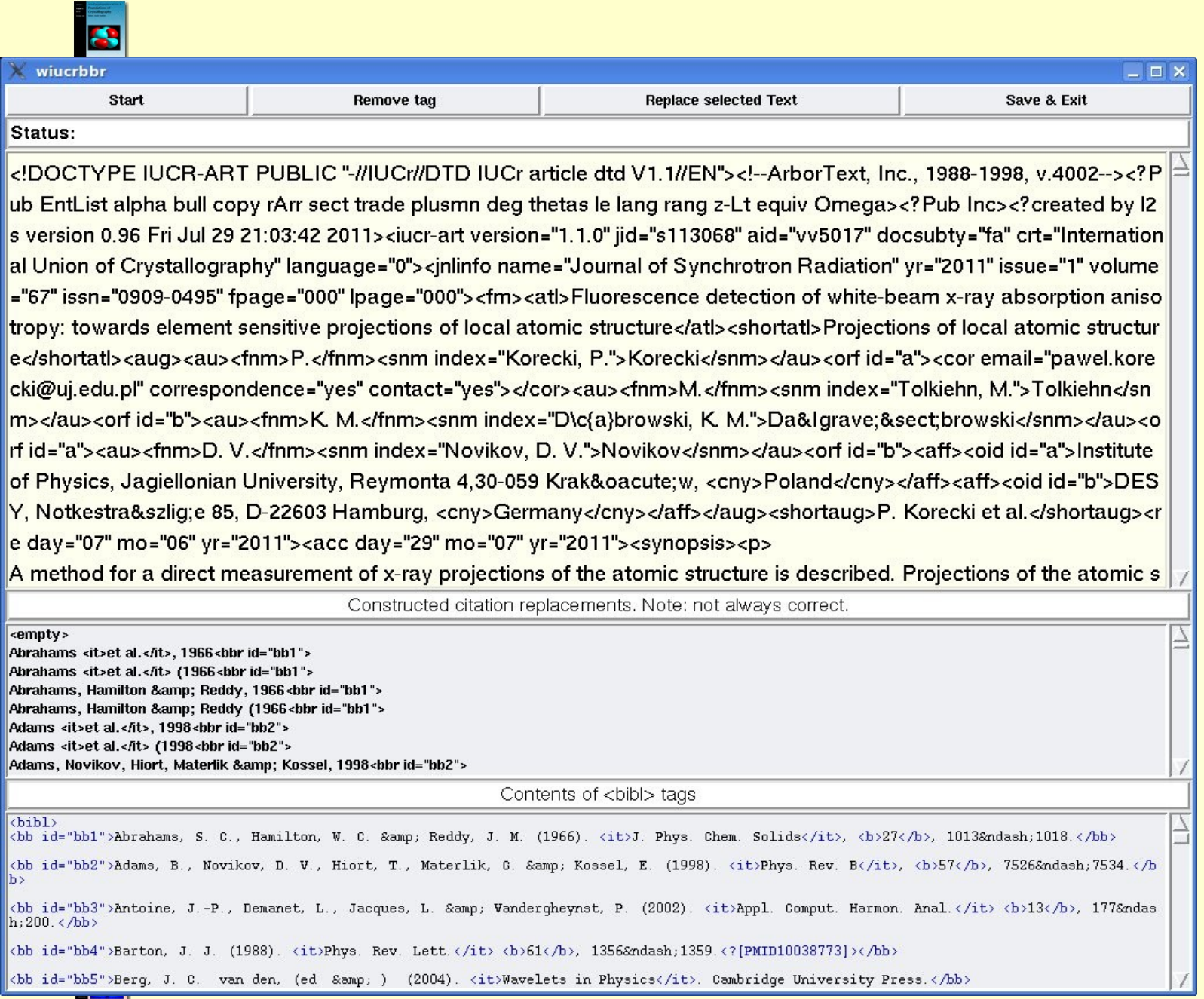
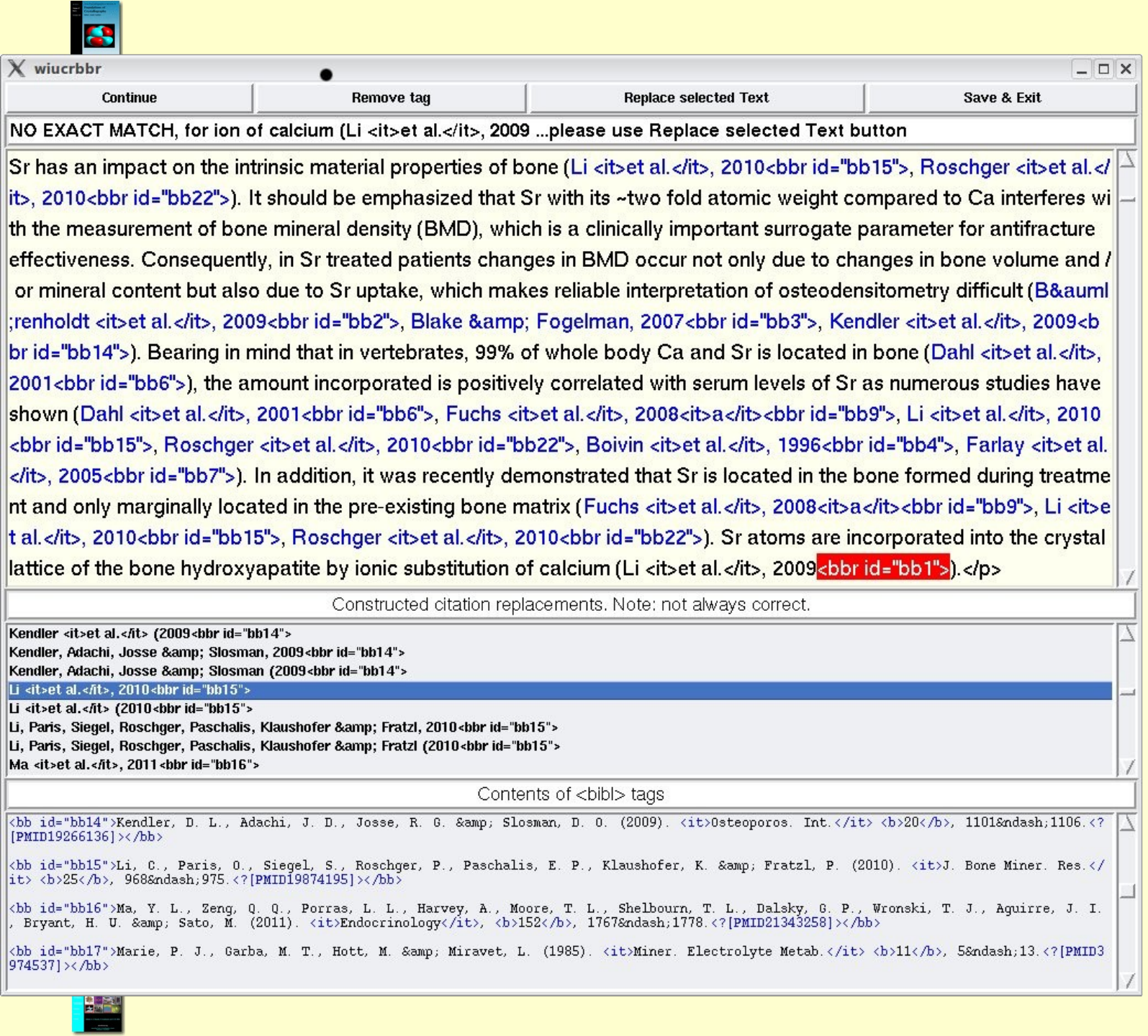


Reference filter program

Checks citations
In text against
references

Crystallography Journals Online



Reference filter program

If a citation cannot be matched it is highlighted

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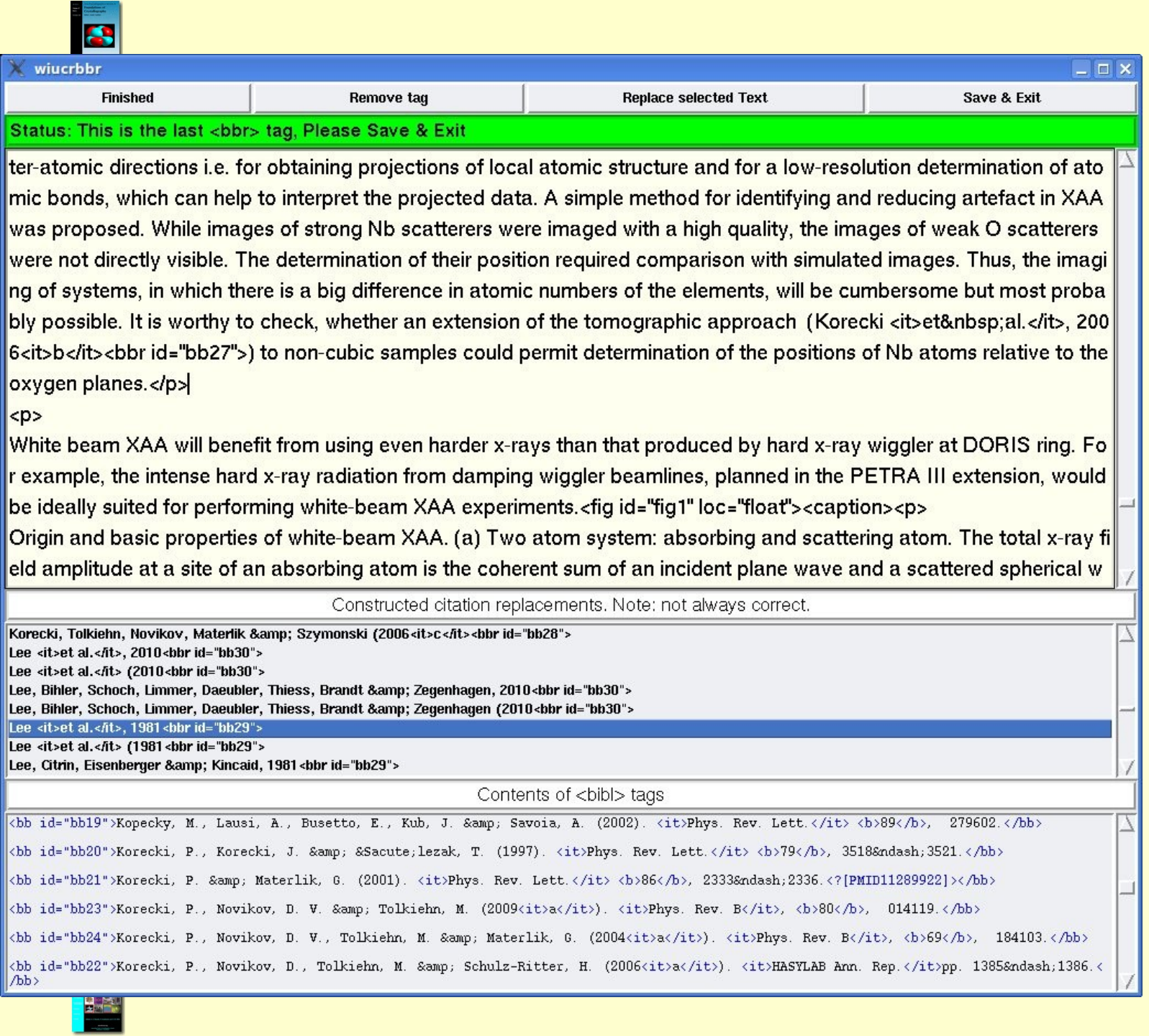

Reference filter program

All citations have been checked

File is saved and is ready for editing

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