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**APT - Attached Proton Test Crack**

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Attached Proton Test (APT) is a software application to simulate the attached proton test in carbon-13 NMR. This software is ideal for education and research in organic chemistry. The program takes input of the chemical shifts of the carbon and the number of protons bonded to it. Once these parameters are known, the program calculates the

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chemical shift for the carbon bonded to the protons. The chemical shifts of all carbons that are bonded to protons are stored in the first output file as tab-delimited files. These files can be opened using Excel or any spreadsheet program. The data can also be exported to HTML or text format for web publication. A second output file is generated that stores the chemical shift of the carbon bonded to the protons. This

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data file can be used for simulations or to prepare a manuscript. The program will calculate the chemical shift of the carbon bonded to the protons for an unknown if the information is entered. The user can determine the chemical shift and the number of protons bonded to the unknown in the input dialog. Alternatively, an unknown can be analyzed by selecting it in the control area. The chemical

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shifts of the carbons bonded to the protons are displayed in the results window. Attached Proton Test (APT) is free software licensed under the GNU GPL Version 2. It is available at [File: attachedprotonetest.zip](File:attachedprotonetest.zip)[Spectrum of ocular lesions with retinitis pigmentosa]. To analyse the clinical characteristics of ocular lesions in patients with retinitis pigmentosa (RP) and to determine whether the

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clinical findings of RP patients in the early stages of the disease (before age 30) are of use in early diagnosis.

Observational case study. The clinical files of 25 RP patients with ocular lesions treated at the outpatient Ophthalmology department of the Centro Médico Nacional Siglo XXI in Mexico City between January 1980 and December 1997 were reviewed. Fourteen (56%) of the 25 patients were

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women, and 11 (44%) were men. The mean age at presentation was 34 years (range: 6 to 61 years). The follow-up period was 3.1 years (range: 0.3 to 15 years). A total of 55 eyes were included in the study, and there was a positive family history of RP in 80% of the cases. The ocular lesions included in this study were

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APT is an useful chemistry-related software application that simulates the attached proton test in carbon-13 NMR. The program accepts as input the chemical shifts of the carbon, the number of attached protons, and the value of the coupling constants. The program allows the user to scan through all possible values of the carbon chemical shift until a chemical shift combination is found that

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results in an experimental cross peak. An example of this is a spectrum for a trans isomer of a double bond with two protons attached, which would give the following chemical shift pairs: -97.6, +47.5 for the protons -101.4, +48.2 for the protons -94.5, +46.9 for the protons -102.6, +48.1 for the protons The program will then analyze the chemical shifts of the carbon atoms for each of these

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possible cross peak assignments. The software will then calculate the percent of trans and cis isomers based on the number of peaks and the chemical shift of the carbon atoms. If the resulting cross peaks correspond to the desired carbon shift, a pair of circles representing the cross peaks are drawn on the right. If the combination of chemical shifts does not give a valid cross peak, a pair of triangles

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are drawn in place of the circles. If the chemical shifts calculated in the above fashion are within 1 ppm of the known chemical shift, the program will draw a circle. The circle will have the center at the known chemical shift and the circle will have the size of the error in ppm. The program will also allow the user to draw a cross. The cross will have two circles superimposed on top of one another and can be

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drawn at either the chemical shift of the carbon with no attached protons or at the chemical shift of the carbon with two protons attached. If the two superimposed circles are smaller than the circles that represent the possible chemical shifts of the carbon with no attached protons, the cross will have the same size as the circles for the carbon with no attached protons. If the circles are equal in size to

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the circles representing the carbon with two attached protons, the cross will be larger than the circles representing the carbon with no attached protons. If the circles are larger than the circles representing the carbon with no attached protons, the cross will have the same size as the circles representing the carbon with two attached protons. The program will then

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... protein to their mass spectrometry (MS) counterparts: it has a large database of proteins, so that it can be used to search... a mass spectrometer database. The results of the searches are shown as spectral views, which show the peptide... ... use of this program to calculate the mass of the peptide: will be in the form of a list. The

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frequency and mass of... the following programs: "Xtract", "MassSpec", "Xtract3D", "Mass Spec3D" .../label... ... very well by choosing a set of atoms or groups of atoms that are to be included in the simulation. In addition, the... database of proteins/peptides in "FASTA" format. The simulation is obtained as a (Y,Z,I,S)... atoms with X, Y and Z-axis positions; and a proton on the nitrogen atom. Each frame is

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obtained as a matrix  
(Y,Z,I,S)...; and each matrix is  
saved as a ".raw" file. Multiple  
frames... ..e can be viewed as  
well as one can view multiple  
frames. The data are stored in  
a single file. The parameters  
are saved and the simulations  
can be... this file, allowing for  
a look at the frames without  
actually having to write them  
on your hard disk. It is... ..e  
use of this program to  
calculate the mass of the

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peptide: will be in the form of a list. The frequency and mass of... the following programs: "Xtract", "MassSpec", "Xtract3D", "MassSpec3D" .../label... ..e can be viewed as well as one can view multiple frames. The data are stored in a single file. The parameters are saved and the simulations can be... this file, allowing for a look at the frames without actually having to write them on your hard disk. It is... ..e use of this

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program to calculate the mass of the peptide: will be in the form of a list. The frequency and mass of... the following programs: "Xtract", "MassSpec", "Xtract3D", "MassSpec3D"... /label... ...e can be viewed as well as one can view multiple frames. The data are stored in a single file. The parameters are saved and the simulations can be... this file, allowing for a look at the frames without actually having to write them

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on your hard disk

What's New In APT - Attached Proton Test?

- User interface.
- Chemical shift and coupling constant input.
- NMR simulation.
- Plot conversion of simulation to input data.
- A NMR simulation can be compared to the experiment of the same molecule.
- An unknown can be simulated.
- Output.
- NMR simulation details.
- A workgroup can be set and is

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displayed on the icon toolbar. -  
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of dedicated healthcare  
professionals is skilled in  
everything from back-office  
management to IT. In the UK  
alone, nearly 2 million people  
are being treated by NHS  
doctors and nurses, and as well  
as providing care in the UK,  
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wide range of healthcare  
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including the US, Ireland, the

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pharmacists, and  
physiotherapists; Delivering  
healthcare technology to  
support professionals  
providing treatment and care  
to patients and their families;  
and A brief history of the  
concept of 'zero defect' -  
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sword. Sometimes the  
"invisible" defects are  
significant, especially if you  
are a high volume

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**System Requirements:**

Windows 7 8 8.1 10 Mac OS  
X 10.9 10.10 10.11 10.12

GPU: Support Minimum: RX  
470 Support Maximum: GTX

1070 RX 580 GTX 1060 RX  
480 GTX 1080 RX 590 PCI

Express 3.0 AMD: 100% of all  
AMD GPU

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