

REFERENCES

- Altschul, S. F., Gish, W., Miller, W., Myers, E. W., Lipman, D. J. (1990) Basic local alignment search tool. *J. Mol. Biol.* 215: 403-410.
- Arias, C. F., Preugschat, F., Strauss, J. H. (1993) Dengue 2 virus NS2B and NS3 form a stable complex that can cleave NS3 within the helicase domain. *Virology* 193: 888–899.
- Bartelma, G., and Padmanabhan, R. (2002) Expression, purification, and characterization of the RNA 5'-triphosphatase activity of dengue virus type 2 nonstructural protein 3. *Virology* 299: 122-132.
- Bartenschlager, R., V. Lohman, T. Wilkinson, and J. O. Koch. (1995) Complex formation between the NS3 serine-type proteinase of the hepatitis C virus and NS4A and its importance for polyprotein maturation. *J. Virol.* 69: 7519–7528.
- Baxeavanis, A. D. (1998) Practical aspects of multiple sequence alignment. *Methods Biochem Anal.* 39: 172-188.
- Bazan, J. F., and Fletterick, R. J. (1989) Detection of a trypsin-like serine protease domain in flaviviruses and pestiviruses. *Virology* 171: 637–639.
- Belew, R. K. and Mitchell, M. (1996) Adaptive Individuals in Evolving Populations: Models and Algorithms. Santa Fe Institute Studies in the Science of Complexity, XXVI, Addison-Wesley, Reading, MA.
- Bergman, E. D., Ginsburg, D., Pappo, R. (1959) The Michael reaction. *Org. React.* 10: 179–556.
- Bianchi, E. and Pessi, A. (2002) Inhibiting viral proteases: challenges and opportunities. *Biopolymers* 66: 101–114.
- Blundell, T. L., Sibanda, B. L., Sternberg, M. J., Thornton, J. M. (1987) Knowledge-based prediction of protein structures and the design of novel molecules. *Nature*, 326: 347-352.
- Bowie, J. U., Luthy, R., Eisenberg, D. (1991) A method to identify protein sequences that fold into a known three-dimensional structure. *Science* 253: 164–170.
- Brenner, C. and Fuller, R. S. (1992) Structural and enzymatic characterization of a purified prohormone-processing enzyme: secreted, soluble Kex2 protease. *Proc. Natl Acad. Sci. USA*, 89: 922–926.
- Briffeuil, P., Baudoux, G., Lambert, C., De, B. X., Vinals, C., Feytmans, E., Depiereux, E. (1998) Comparative analysis of seven multiple protein sequence alignment servers: clues to enhance reliability of predictions. *Bioinformatics* 14: 357-366.
- Brinkworth, R. I., Fairlie, D. P., Leung, D., Young, P. R. (1999) Homology model of the dengue 2 virus NS3 protease: putative interactions with both substrate and NS2B cofactor. *J. Gen. Virol.* 80: 1167–1177.

- Brooks, B. R., Bruccoleri, R. E., Olafson, B. D., States, D. J., Swaminathan, S. and Karplus, M. (1983) CHARMM: A program for macromolecular energy, minimization, and dynamics calculations. *J. Comput. Chem.* 4: 187–217.
- Browne, W. J., North, A. C. T., Phillips, D. C., Brew, K., Vanaman, T.C., Hill, R.C. (1969) A possible threedimensional structure of bovine lactalbumin based on that of hen's egg-white lysozyme. *J. Mol. Biol.* 42: 65-86.
- Buckley, S. M. (1961) Serial propagation of types 1, 2, 3 and 4 dengue virus in HeLa cells with concomitant cytopathic effect. *Nature* 192 (4804): 778-779.
- Chambers, T. J., Grakoui, A., Rice, C. M., (1991) Processing of the yellow fever virus nonstructural polyprotein: a catalytically active NS3 proteinase domain and NS2B are required for cleavages at dibasic sites. *J. Virol.* 65: 6042–6050.
- Chambers, T. J., Nestorowicz, A., Amberg, S. M., Rice, C. M. (1993) Mutagenesis of the yellow fever virus NS2B protein: effects on proteolytic processing, NS2B-NS3 complex formation, and viral replication. *J. Virol.* 67: 6797–6807.
- Chanprapaph, S., Saparpakorn, P., Sangma, C., Niyomrattanakit, P., Hannongbua, S., Angsuthanasombat, C., Katzenmeier, G. (2005) Competitive inhibition of the dengue virus NS3 serine protease by synthetic peptides representing polyprotein cleavage sites. *Biochem. Biophys. Res. Commun.* 330: 1237-1246.
- Claessens, M., Van Cutsem, E., Lasters, I., Wodak, S. (1989) Modelling the polypeptide backbone with 'spare parts' from known protein structures. *Prot. Eng.* 2: 335-345.
- Cleaves, G. R. (1985) Identification of dengue type 2 virus-specific high molecular weight proteins in virus-infected BHK cells. *J. Gen. Virol.* 66 (12): 2767-2771.
- Colovos, C. and Yeates, T. O. (1993) Verification of protein structures: Patterns of non-bonded atomic interactions. *Protein Sci.* 2: 1511-1519.
- Cornell, W. D., Cieplak, P., Bayly, C. I., Gould, I. R., Merz, K. M., Ferguson, D.M., Spellmeyer, D.C., Fox, T., Caldwell, J.W. and Kollman, P. A. (1995) A second generation force field for the simulation of proteins, nucleic acids and organic molecules. *J. Am. Chem. Soc.* 117: 5179–5197.
- Corner, L. C. and Ng, M. L. (1987) The influence of higher temperature on Dengue-2 virus infected C6/36 mosquito cell line. *Can. J. of Microbiol.* 33 (10): 863-869.
- Corpet, F. (1988) Multiple sequence alignment with hierarchical clustering. *Nucleic Acids Res.* 16: 10881-10890.
- Crooks, A. J., Lee, J. M., Easterbrook, L. M., Timofeev, A. V. & Stephenson, J. R. (1994) The NS1 protein of tick-borne encephalitis virus forms multimeric species upon secretion from the host cell. *J. Gen. Virol.* 75: 3453–3460.
- Dodd, D. S. and A. C. Oehlschlager (1992) Synthesis of Inhibitors of 2,3-oxidosqualene-lanosterol cyclase: Conjugate Addition of Organocuprate to N-

(Carbobenzyloxy)-3-carbomethoxy-5,6-dihydro-4-pyridone. *J. Org. Chem.* 57: 2794-2803.

- Dunsdon, R. M., Greening, J. R., Jones, P. S., Jordan, S., Wilson, F.X. (2000) Solid phase synthesis of aminoboronic acids: potent inhibitors of the hepatitis C virus NS3 proteinase. *Bioorg. Med. Chem. Lett.* 10: 1577-1579.
- Durdagi, S.; Supuran, C. T.; Strom, T. A.; Doostdar, N.; Kumar, M. K.; Barron, A. R.; Mavromoustakos, T.; Papadopoulos, M. G. (2009) In Silico Drug Screening Approach for the Design of Magic Bullets: A Successful Example with Anti-HIV Fullerene Derivatized Amino Acids. *J. Chem. Inf. Model.* 49: 1139– 1143.
- Egloff, M.P., Benarroch, D., Selisko, B., Romette, J.L., Canard, B. (2002) An RNA cap (nucleoside-2'-*O*-)-methyltransferase in the flavivirus RNA polymerase NS5: crystal structure and functional characterization, *EMBO J.* 21: 2757–2768.
- Eishner, U. and Kuthan, J. (1972) The Chemistry of Dihydropyridines. *Chem. Rev.* 72 (1): 1-42.
- Eldridge, M. D., Murray, C. W., Auton, T. R., Paolini, G.V. and Mee, R.P. (1997) Empirical scoring functions: I. The development of a fast empirical scoring function to estimate the binding affinity of ligands in receptor complexes. *J. Comput. Aid. Mol. Des.* 11: 425–445.
- Falgout, B., Pethel, M., Zhang, Y. M., Lai, C. J., (1991) Both nonstructural proteins NS2B and NS3 are required for the proteolytic processing of dengue virus nonstructural proteins. *J. Virol.* 65: 2467–2475.
- Falgout, B. and Markoff, L. (1995) Evidence that flavivirus NS1-NS2A cleavage is mediated by a membrane-bound host protease in the endoplasmic reticulum, *J. Virol.* 69: 7232–7243.
- Fiser, A. and Sali, A. (2003) Modeller: generation and refinement of homology-based protein structure models. *Methods Enzymol.* 374: 461-491.
- Fiser, A., Feig, M., III Brooks, C.L., Sali, A. (2002) Evolution and Physics in Comparative Protein Structure Modeling. *Acc. Chem. Res.*, 35: 413-421.
- Flamand, M., Chevalier, M., Henchal, E., Girard, M., Deubel, V. (1995) Purification and renaturation of Japanese encephalitis virus nonstructural glycoprotein NS1 overproduced by insect cells. *Prot. Expr. Purif.* 6 (4): 519-527.
- Ganesh, V. K., Muller, N., Judge, K., Luan, C. H., Padmanabhan, R., Murthy, K.H. (2005) Identification and characterization of nonsubstrate-based inhibitors of the essential dengue and West Nile virus proteases. *Bioorg. Med. Chem.* 13: 257-264.
- Gorbalenya, A. E., Donchenko, A. P., Koonin, E. V., and Blinov, V. M. (1989) N-terminal domains of putative helicases of flavi- and pestiviruses may be serine proteases. *Nucleic Acids Res.* 17 (10): 3889–3897.

- Greer, J. (1990) Comparative modeling methods: application to the family of the mammalian serine proteases. *Proteins* 7: 317-334.
- Gubler, D. J. (1996) World distribution of dengue. *Dengue Bulletin* 20: 1-12.
- Hantzsch, A. (1882) Ueber die Synthese Pyridinartiger Verbindungen aus Acetessigather und Aldehydammoniak. *Justus Liebigs Ann. Chem.* 215: 1-82.
- Hart, W. E., Kammeyer, T. E., Belew, R. K. (1994) In *Foundations of Genetic Algorithms III*, D. Whitley and M. Vose, Eds., Morgan Kaufman, San Francisco, CA.
- Hedstrom, L. (2002) Serine protease mechanism and specificity. *Chem. Rev.* 102: 4501-4524.
- Henikoff, S., Henikoff, J. G., Alford, W. J., Pietrokovski S. (1995) Automated construction and graphical presentation of protein blocks from unaligned sequences. *Gene* 163: GC17-GC26.
- Hetényi, C. and van der Spoel, D. (2002) Efficient docking of peptides to proteins without prior knowledge of the binding site, *Protein Sci.* 11: 1729–1737.
- Higgins, D. G., Thompson, J. D., Gibson, T.J. (1996) Using CLUSTAL for multiple sequence alignments. *Methods Enzymol.* 266: 383-402.
- Hilgeroth, A. and Baumeister, U. (2000) The First Functionalized 6,12-Diazatetrakisomocubanes. *Angew. Chem. Int. Ed.*, 39 (3): 576-578.
- Hilgeroth, A., Heinemann, F. W., and Baumeister, U. (2002) First Rotameric *Anti* Dimers and 3,9-Diazatetraasteranes from Unsymmetrically Substituted *N*-Acyl- and *N*-Acyloxy-4-Aryl-1,4-Dihydropyridines. *Heterocycles* 57 (6): 1003-1016.
- Holland, J. H (1975) *Adaptation in Natural and Artificial Systems*, University of Michigan Press, Ann Arbor, MI.
- Hooft, R. W., Sander, C., Vriend, G. (1996) Positioning hydrogen atoms by optimizing hydrogen bond networks in protein structures. *Proteins* 26: 363-376.
- Hotta, S. (1957) Some immunological properties of dengue virus cultivated in tissue culture. *Ann. Trop. Med. Parasitol.* 51: 249-255.
- http://merops.sanger.ac.uk/cgi-bin/statistics_index?type=P, 15 May 2010
- <http://nihserver.mbi.ucla.edu/SAVES/>, 16 April 2005
- http://www.cdc.gov/dengue/resources/Dengue&DHF%20Information%20for%20Health%20Care%20Practitioners_2009.pdf, 15 May 2010
- <http://www.moh.gov.my/MohPortal/newsFull.jsp?action=load&id=432>, 14 March 2010

<http://www.searo.who.int/EN/Section10/Section332/Section1631.htm>, 4 August 2006

http://www.searo.who.int/en/Section10/Section332_1103.htm, 14 August 2006

<http://www.who.int/mediacentre/factsheets/fs117/en/>, 13 March 2009

Institute of Medicine. (1986) New vaccine development: Establishing priorities, Volume II, *Diseases of Importance in Developing Countries*, Washington DC: National Academy Press: 170-177.

Irie, K., Mohan, P.M., Sasaguri, Y., Putnak, R., and Padmanabhan, R. (1989) Sequence analysis of cloned dengue virus type 2 genome (New Guinea-C strain). *Gene* 75 (2): 197–211.

Jacobs, S. C., Stephenson, J. R., Wilkinson, G.W. (1992) High-level expression of the tick-borne encephalitis virus NS1 protein by using an adenovirus-based vector: protection elicited in a murine model. *J Virol.* 66 (4):2086–2095.

Jahn, R., Lang, T., and Sudhof, T.C. (2003) Membrane fusion. *Cell* 112 (4): 519-533.

Jan, L. R., Yang, C. S., Trent, D. W., Falgout, B., Lai, C. J. (1995) Processing of Japanese encephalitis virus non-structural proteins: NS2B-NS3 complex and heterologous proteases. *J. Gen. Virol.* 76: 573–580.

Jones, T. A. and Thirup, S. (1986) Using known substructures in protein model building and crystallography. *EMBO J.* 5: 819-822.

Jorgensen, W. L. and Tirado-Rives, J. (1988) The OPLS Potential Functions for Proteins. Energy Minimization for Crystals of Cyclic Peptides and Crambin. *J. Am. Chem. Soc.* 110: 1657–1666.

Kapoor, M., Zhang, L., Ramachandra, M., Kusukawa, J., Ebner, K.E., Padmanabhan, R. (1995) Association between NS3 and NS5 proteins of dengue virus type 2 in the putative RNA replicase is linked to differential phosphorylation of NS5. *J. Biol. Chem.* 270: 19100–19106.

Kautner, I., Robinson, M. J., and Kuhnle, U. (1997) Dengue virus infection: epidemiology, pathogenesis, clinical presentation, diagnosis, and prevention. *J. Pediatr.* 131 (4): 516–524.

Khumthong, R., Angsuthanasombat, C., Panyim, S., and Katzenmeier, G. (2002) In vitro determination of dengue virus type 2 NS2B-NS3 protease activity with fluorescent peptide substrates. *J. Biochem. Mol. Biol.* 35 (2): 206–212.

Khumthong, R., Niyomrattanakit, P., Chanprapaph, S., Angsuthanasombat, C., Panyim, S., and Katzenmeier, G. (2003) Steady-state cleavage kinetics for dengue virus type 2 NS2B-NS3(pro) serine protease with synthetic peptides. *Protein Peptide Lett.* 10 (1): 19–26.

Kim, J. L., Morgenstern, K. A., Lin, C., Fox, T., Dwyer, M. D., Landro, J. A., Chambers, S. P., Markland, W., Lepre, C. A., O'Malley, E. T., Harbeson, S. L., Rice, C. M., Murcko, M. A., Caron, P. R., and Thomson, J. A. (1996)

- Crystal structure of the hepatitis C virus NS3 protease domain complexed with a synthetic NS4A cofactor peptide. *Cell* 87 (2): 343–355.
- Klasse, P. J., Born, R. and Marsh, M. (1998) Mechanism of enveloped virus entry into animal cells. *Adv. Drug Deliv. Rev.* 1 (34): 65-69.
- Klix, R. C., Cain, M. H., Bhatia, A.V. (1995) Synthesis of 5,6-methylenedioxy-1-tetralone. An aryl Grignard approach from guaiacol, *Tet. Lett.* 36: 6413-6414.
- Kuntz, I. D., Blaney, J. M., Oatley, S. J., Langridge, R. and Ferrin, T. E. (1982) A geometric approach to macromolecular-ligand interactions *J. Mol. Biol.* 161: 269-288.
- Lamarck, J. B (1914) *Zoological Philosophy*, Macmillan, London.
- Laskowski, R. A., MacArthur, M.W., Thornton, J. M. (1998) Validation of protein models derived from experiment. *Curr. Opin. Struct. Biol.* 8: 631-639.
- Laskowski, R. A., Rullmann, J. A., MacArthur, M. W., Kaptein, R., Thornton, J. M. (1996) AQUA and PROCHECK-NMR: programs for checking the quality of protein structures solved by NMR. *J. Biomol. NMR* 8: 477-486.
- Lavilla, R. (2002) Recent developments in the Chemistry of Dihydropyridines. *J. Chem. Soc., Perkin Trans.*, 1: 1141-1156.
- Leach, A.R. (2001) *Molecular Modelling: Principles and Applications*. 2nd Edition, Pearson Education Limited, U.K.
- Lescar, J., Roussel A., Wien, M. W., Navaza, J., Fuller, S.D., Wengler, G., Wengler, G., Rey, F.A. (2001) The fusion glycoprotein shell of Semliki Forest virus: an icosahedral assembly primed for fusogenic activation of endosomal pH. *Cell*, 105 (1): 137-148.
- Lesk, A. M. and Chothia, C. (1980) How different amino acid sequences determine similar protein structures: the structure and evolutionary dynamics of the globins. *J Mol Biol.* 136: 225-270.
- Leung, D., Schroeder, K., White, H., Fang, N. X., Stoermer, M. J., Abbenante, G., Martin, J. L., Young, P. R., and Fairlie, D. P. (2001) Activity of recombinant dengue 2 virus NS3 protease in the presence of a truncated NS2B co-factor, small peptide substrates, and inhibitors. *J. Biol. Chem.* 276 (49): 45762–45771.
- Levitt, M. (1992) Accurate modeling of protein conformation by automatic segment matching. *J. Mol. Biol.* 226:507-533.
- Li, H., Clum, S. You, S., Ebner, K. E. and Padmanabhan, R. (1999) The serine protease and RNA-stimulated nucleoside triphosphatase and RNA helicase functional domains of dengue virus type 2 NS3 converge within a region of 20 amino acids. *J. Virol.* 73 (4): 3108–3116.
- Luthy, R., Bowie, J. U., Eisenberg, D. (1992) Assessment of protein models with three-dimensional profiles. *Nature* 356: 83-85.

- Mackenzie, J.M., Jones, M.K. and Young, P.R. (1996) Immunolocalization of the dengue virus nonstructural glycoprotein NS1 suggests a role in viral RNA replication. *Virology* 220 (1): 232-240.
- Mandl, C.W., Heinz, F.X. and Kunz, C. (1988) Sequence of the structural proteins of tick-borne encephalitis virus (western subtype) and comparative analysis with other flaviviruses, *Virology* 166 (1): 197–205.
- Marianneau, P., Steffan, A. M., Royer, C., Drouet, M. T., Kirn, A., Deubel, V. (1998) Differing infection patterns of dengue and yellow fever viruses in a human hepatoma cell line. *J. Infect. Dis.* 178: 1270-1278.
- Marti-Renom, M. A., Madhusudhan, M. S., Fiser, A., Rost, B., Sali, A. (2002) Reliability of assessment of protein structure prediction methods. *Structure (Camb)* 10: 435-440.
- Mehler, E. L. and Solmajer, T. (1991) Electrostatic effects in proteins: comparison of dielectric and charge models. *Prot. Eng.* 4: 903-910.
- Melo, F. and Feytmans, E. (1998) Assessing protein structures with a non-local atomic interaction energy. *J. Mol. Biol.* 277: 1141-1152.
- Mentzel, M. and Hoffmann, H. M. R. (1997) *N*-Methoxy-*N*-methylamides (Weinreb Amides) in Modern Organic Synthesis. *J. Prakt. Chem.* 39: 517-524.
- Modis, Y., Ogata, S., Clements, D., Harrison, S. C. (2003) A ligand-binding pocket in the dengue virus envelope glycoprotein. *Proc. Natl. Acad. Sci. U. S. A.* 100: 6986-6991.
- Monath, T. P. (1994) Dengue: the risk to developed and developing countries. *Proc. Natl. Acad. Sci. U. S. A.* 91(7): 2395–2400.
- Morris, G. M., Goodshell, D. S., Huey, R., Olson, A. J. (2001) Autodock's User's Guide: Automated Docking of Flexible Ligands to Receptors. Version 3.0.5. Scripps Research Institute, Department of Molecular Biology, USA.
- Morris, G. M., Goodshell, D. S., Haliday, R. S., Huey, R., Hart, W. E., Belew, R. K., Olson, A.J. (1998) Automated docking using Lamarckian Genetic Algorithm and an empirical binding free energy function. *J. Comput. Chem.* 19 (14): 1639-1662.
- Muegge, I. and Martin, Y. C. (1999) A General and Fast Scoring Function for Protein-Ligand Interactions: A Simplified Potential Approach. *J. Med. Chem.* 42: 791–804.
- Mudiana, M. (2010) Mechanism of inhibition by *Boesenbergia rotunda* plant extract on Dengue Virus Type 2 (DENV2) replication. PhD thesis.
- Murray, R. K., Granner, D. K., Mayes, P. A., Rodwell, V. M. (2003) Harper's Illustrated Biochemistry, 26th Ed. McGraw-Hill Co., Columbus, OH.
- Murthy, H., Clum, S., Padmanabhan, R. (1999) Dengue virus NS3 serine protease.

- Crystal structure and insights into interaction of the active site with substrates by molecular modeling and structural analysis of mutational effects. *J. Biol. Chem.* 274: 5573-5580.
- Muylaert, I.R, Galler, R., and Rice, C.M. (1997) Genetic analysis of the yellow fever virus NS1 protein: identification of a temperature-sensitive mutation which block RNA accumulation. *J. Virol.* 71 (1): 291-298.
- Nahm, S. and Weinreb, S. M. (1981) *N*-methoxy-*N*-methylamides as effective acylating agents. *Tet. Lett.* 22: 3815-3818.
- Nestorowicz, A., Chambers, T. J., Rice, C. M. (1994) Mutagenesis of the yellow fever virus NS2A/2B cleavage site: effects on proteolytic processing, viral replication, and evidence for alternative processing of the NS2A protein. *Virology* 199: 114–123.
- Oldfield, T. J. (1992) SQUID: a program for the analysis and display of data from crystallography and molecular dynamics. *J. Mol. Graph.* 10: 247-252.
- Oscarsson, K., Lahmann, M., Lindberg, J., Kangasmetsä, J., Unge, T., Oscarson, S., Hallberg, A., Samuelsson, B. (2003) Design and synthesis of HIV-1 protease inhibitors. Novel tetrahydrofuran P2/P2'-groups interacting with Asp29/30 of the HIV-1 protease. Determination of binding from X-ray crystal structure of inhibitor protease complex. *Bioorg. Med. Chem.* 11 (6): 1107-15.
- Pearson, W. R. (1990) Rapid and sensitive sequence comparison with FASTP and FASTA. *Methods Enzymol.* 183: 63-98.
- Phoolcharoen, W. and Smith, D. R. (2004) Internalization of the dengue virus is cell cycle modulated in HepG2, but not Vero cells. *J. Med Virol.* 74 (3): 434-441.
- Rawlings, N. D., Barrett, A. J., Bateman, A. (2010). "MEROPS: the peptidase database". *Nucleic Acids Res.* 38 (Database issue): D227–33.
- Read, R. J., and James, M. N. G. (1986) in *Introduction to Protein Inhibitors: X-ray Crystallography*, Barrett, A. J., and Salvesen, G., eds.. pp. 301–336, Elsevier Science Publishers, Amsterdam.
- Rey, F. A., Heinz, F. X., Mandl, C., Kunz, C., Harrison, S. C. (1995) The envelope glycoprotein from tick-borne encephalitis virus at 2Å resolution. *Nature* 375: 291-298.
- Rost B. (1999) Twilight zone of protein sequence alignments. *Prot. Eng.* 12: 85–94.
- Sabin, A. B., and Schlesinger, R. W. (1945) Production of immunity to dengue with virus modified by propagation in mice. *Science* 101: 640-642.
- Sali, A. and Blundell, T. L. (1993) Comparative protein modelling by satisfaction of spatial restraints. *J Mol Biol.* 234: 779-815.

- Sambrook, M. R., Beer, P. D., Wisner, J. A., Paul, R. L., Cowley, A. R., Szemes, F., Drew, M. B. (2005) Anion-Templated Assembly of Pseudorotaxanes: Importance of Anion Template, Strength of Ion-Pair Thread Association, and Macrocyclic Ring Size. *J. Am. Chem. Soc.* 127 (7): 2292-2302.
- Sanchez, R. and Sali A. (1998) Large-scale protein structure modeling of the *Saccharomyces cerevisiae* genome. *Proc. Natl. Acad. Sci. U. S. A.* 95: 13597–13602.
- Sanchez, R. and Sali, A. (1997) Advances in comparative protein-structure modelling. *Curr. Opin. Struct. Biol.* 7: 206-214.
- Saqi, M. A. S., Russell, R. B. and Sternberg, M. J. E. (1998) Misleading local sequence alignments: implications for comparative protein modeling. *Prot. Eng.*, 11: 627–630.
- Schlesinger, R. W., Gordon, I., Frankel, J. W., Winter, J. N., Patterson, P. R., Dorrance, W. R. (1956) Clinical and serological response of man to immunization with attenuated dengue and yellow fever viruses. *J. Immunol.* 77: 352-364.
- Seife, C. (1997) Blunting nature's Swiss army knife. *Science* 277: 1602-1603.
- Shoichet, B. K. and Kuntz, I. D. (1993) Matching chemistry and shape in molecular docking. *Prot. Eng.* 6: 723-732.
- Sippl, M. J. (1990) Calculation of conformational ensembles from potentials of mean force. An approach to the knowledge based prediction of local structures in globular proteins. *J. Mol. Biol.* 213: 859–883.
- Sippl, M. J. (1993) Recognition of errors in three-dimensional structures of proteins. *Proteins* 17: 355-62.
- Smith, R. F., Wiese, B. A., Wojzynski, M. K., Davison, D. B., Worley, K. C. (1996) BCM Search Launcher-an integrated interface to molecular biology data base search and analysis services available on the World Wide Web. *Genome Res.* 6: 454-462.
- Smith, T. F. (1999) The art of matchmaking: sequence alignment methods and their structural implications. *Structure Fold Des.* 7: R7-R12.
- Solis, F. J. and Wets, J. B. (1981) Minimization by Random Search Techniques, *Math. Oper. Res.* 6 (1): 19–30.
- Srinivasan, N. and Blundell, T. L. (1993) An evaluation of the performance of an automated procedure for comparative modelling of protein tertiary structure. *Protein Eng.* 6: 501-512.
- Stout, D. M. and Meyers, A. I. (1982) Recent Advances in the Chemistry of Dihydropyridines. *Chem. Rev.*, 82 (2): 223-243.

- Tan, S. K., Phippen, R., Yusof, R. Ibrahim, H. Khalid, N. and Abd Rahman, N. (2006) Inhibitory activity of cyclohexenyl chalcone derivatives and flavonoids of fingerroot, *Boesenbergia rotunda* (L.) towards dengue-2 Virus NS3 protease. *Bioorg. Med. Chem. Lett.* 16 (12): 3337-3340.
- Taylor, R. D., Jewsbury, P. J., Essex, J. W. (2002) A review of protein-small molecule docking methods. *J. Comp. Aided Mol. Design* 16: 151–166.
- Thompson, J. D., Higgins, D. G., Gibson, T. J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* 22: 4673-4680.
- Topham, C. M., Srinivasan, N., Thorpe, C. J., Overington, J. P., Kalsheker, N. A. (1994) Comparative modelling of major house dust mite allergen Der p I: structure validation using an extended environmental amino acid propensity table. *Protein Eng* 7: 869-894.
- Valle, R. P. C., and Falgout, B. (1998) Mutagenesis of the NS3 protease of dengue virus type 2. *J. Virol.* 72 (1): 624–632.
- Wahab, H. A., Yusof, R., Rahman, N.A. (2007) A Search for Vaccines and Therapeutics for Dengue: A Review. *Current Computer Aided Drug Design*, 3(2): 101-112.
- Wani, M., Taylor, H., Wall, M., Coggon, P., McPhail, A. (1971) Plant antitumor agents. VI. The isolation and structure of taxol, a novel antileukemic and antitumor agent from *Taxus brevifolia*. *J. Am. Chem. Soc.* 93 (9): 2325–2327.
- Wesson, L. and Eisenberg, D. (1992) Atomic solvation parameters applied to molecular dynamics of proteins in solution. *Prot. Sci.* 1: 227-235.
- West, M. L. and Fairlie, D. P. (1995) Targeting HIV-protease: a test of drug design methodologies. *Trens Pharmacol. Sci.* 16: 67-75.
- Westbrook, J., Feng, Z., Jain, S., T. N. Bhat, Thanki, N., Ravichandran, V., Gilliland, G. L., Bluhm, W. F., Weissig, H., Greer, D. S., Bourne, P. E., Berman, H. M. (2002) The protein data bank: unifying the archive. *Nucleic Acids Research* 30(1): 245–248.
- WHO, 1997: Dengue Haemorrhagic Fever: Diagnosis, treatment, prevention and control. 2nd edition.
- Winkler G., Maxwell, S. E., Ruemmler, C., Stollar, V. (1989) Newly synthesized dengue-2 virus nonstructural protein NS1 is a soluble protein but becomes partially hydrophobic and membrane-associated after dimerization. *Virology* 171(1): 302–305.
- Wissemann, C. L., Jr., Sweet, B. H. and Rosenzweig, E. C. (1963) Attenuated living type 1 dengue vaccines. *Am. J. Trop. Med. Hyg.* 12: 620-623.

- Xu, T., Sampath, A., Chao, A., Wen, D., Nanao, M., Chene, P., Vasudevan, S.G., Lescar, J. (2005) Structure of the Dengue virus helicase/nucleoside triphosphatase catalytic domain at a resolution of 2.4 Å. *J. Virol.* 79: 10278–10288.
- Yan, Y., Y. Li, S. Munshi, V. Sardana, J. L. Cole, M. Sardana, C. Steinkuehler, L. Tomei, R. De Francesco, L. C. Kuo, and Z. Chen. (1998) Complex of NS3 protease and NS4A peptide of BK strain hepatitis C virus: a 2.2 Å resolution structure in a hexagonal crystal form. *Protein Sci.* 7(4): 837–847.
- Yon, C., Teramoto, T., Mueller, N., Phelan, J., Ganesh, V. K., Murthy, K. H., Padmanabhan, R. (2005) Modulation of the nucleoside triphosphatase/RNA helicase and 5'-RNA triphosphatase activities of dengue virus type 2 nonstructural protein 3 (NS3) by interaction with NS5, the RNA-dependent RNA polymerase. *J. Biol. Chem.* 280: 27412-27419.
- Yusof, R., Clum, S., Wetzel, M., Murthy, H. M., Padmanabhan, R. (2000) Purified NS2B/NS3 serine protease of dengue virus type 2 exhibits cofactor NS2B dependence for cleavage of substrates with dibasic amino acids in vitro. *J. Biol. Chem.* 275: 9963–9969.

APPENDIX 1

DOCKING OUTPUT FILES

4-OH Panduratin A Docking Output file (extracted from *.dlg file)

Number of distinct conformational clusters found = 6, out of 100 runs,
Using an rmsd-tolerance of 0.5 A

CLUSTERING HISTOGRAM

Clus- -ter Rank	Lowest Docked Energy	Run	Mean Docked Energy	Num in Clus	Histogram						
					5	10	15	20	25	30	35
1	-10.23	9	-10.16	9	#####						
2	-10.13	93	-10.02	30	#####						
3	-10.02	63	-9.93	9	#####						
4	-9.99	21	-9.91	7	#####						
5	-9.88	96	-9.84	8	#####						
6	-9.54	18	-9.48	37	#####						

```

MODEL          9
USER          Run = 9
USER          Cluster Rank = 1
USER          Number of conformations in this cluster = 9
USER
USER          RMSD from reference structure      = 2.977 A
USER
USER          Estimated Free Energy of Binding   = -7.38 kcal/mol  [(1)+(3)]
USER          Estimated Inhibition Constant, Ki = +3.86e-06    [Temperature = 298.15 K]
USER
USER          Final Docked Energy              = -10.23 kcal/mol  [(1)+(2)]
USER
USER          (1) Final Intermolecular Energy   = -8.94 kcal/mol
USER          (2) Final Internal Energy of Ligand = -1.29 kcal/mol
USER          (3) Torsional Free Energy        = +1.56 kcal/mol
USER
USER
USER          DPF = 10-4-oh-panduratin-ns2b3-b4-1-606060box-r.dpf
USER          NEWDPF move      10-4-oh-panduratin.pdbq
USER          NEWDPF about     21.343000 70.076698 35.802601
USER          NEWDPF tran0     22.738017 69.630442 37.963966
USER          NEWDPF quat0     0.155462 0.220579 -0.962900 -156.276329
USER          NEWDPF ndihe     8
USER          NEWDPF dihe0     -61.70 98.59 15.25 24.50 -32.20 -14.34 151.47 -25.14
USER
USER
USER          x      y      z      vdW      Elec      q      RMS
ATOM      1  C1_____ <1> d      22.625 66.413 34.750 -0.68 +0.01 +0.043 2.977
ATOM      2  C13_____ <1> d      21.767 69.250 37.301 -0.36 -0.00 +0.078 2.977
ATOM      3  C14_____ <1> d      20.532 69.874 36.583 -0.24 +0.00 +0.034 2.977
ATOM      4  C20_____ <1> d      22.694 68.557 36.251 -0.52 +0.00 +0.029 2.977
ATOM      5  C21_____ <1> d      21.896 67.556 35.424 -0.64 -0.01 -0.082 2.977
ATOM      6  C22_____ <1> d      20.566 67.683 35.237 -0.38 +0.00 -0.023 2.977
ATOM      7  C23_____ <1> d      19.716 68.758 35.875 -0.38 +0.00 +0.037 2.977
ATOM      8  C11_____ <1> d      22.539 70.236 38.164 -0.27 -0.01 +0.170 2.977
ATOM      9  O12_____ <1> d      22.926 71.311 37.703 +0.16 +0.00 -0.292 2.977
ATOM     10  A6_____ <1> d      23.007 69.846 39.505 -0.27 -0.01 +0.076 2.977
ATOM     11  A5_____ <1> d      24.145 69.138 39.664 -0.39 -0.03 +0.085 2.977
ATOM     12  A7_____ <1> d      22.216 70.232 40.692 -0.23 -0.01 +0.085 2.977
ATOM     13  A4_____ <1> d      24.598 68.767 41.015 -0.09 -0.03 +0.074 2.977
ATOM     14  A8_____ <1> d      23.882 69.125 42.097 -0.35 -0.03 +0.071 2.977
ATOM     15  A3_____ <1> d      22.639 69.889 41.924 -0.28 -0.01 +0.074 2.977
ATOM     16  O2_____ <1> d      24.279 68.796 43.351 -0.11 +0.17 -0.361 2.977
ATOM     17  H32_____ <1> d      24.365 67.899 43.622 -0.18 -0.23 +0.217 2.977
ATOM     18  O10_____ <1> d      21.066 70.936 40.531 +0.13 +0.02 -0.360 2.977
ATOM     19  H31_____ <1> d      21.071 71.868 40.398 +0.11 -0.01 +0.217 2.977
ATOM     20  O9_____ <1> d      24.871 68.750 38.586 -0.44 +0.05 -0.360 2.977
ATOM     21  H30_____ <1> d      25.534 68.086 38.653 -0.21 -0.05 +0.217 2.977
ATOM     22  C19_____ <1> d      23.428 69.558 35.300 -0.34 +0.01 +0.037 2.977
ATOM     23  C18_____ <1> d      24.925 69.566 35.521 -0.67 -0.01 -0.024 2.977
ATOM     24  C16_____ <1> d      25.669 70.687 35.618 -0.60 -0.01 -0.091 2.977
ATOM     25  C15_____ <1> d      25.091 72.081 35.500 -0.41 +0.00 +0.042 2.977
ATOM     26  C17_____ <1> d      27.154 70.572 35.890 -0.62 +0.00 +0.042 2.977
ATOM     27  A27_____ <1> d      19.634 70.657 37.532 -0.11 -0.00 -0.053 2.977
ATOM     28  A26_____ <1> d      19.581 72.003 37.460 -0.04 +0.00 +0.007 2.977
ATOM     29  A28_____ <1> d      18.821 69.965 38.555 -0.19 -0.00 +0.007 2.977
ATOM     30  A24_____ <1> d      18.736 72.769 38.387 -0.02 +0.00 +0.001 2.977
ATOM     31  A25_____ <1> d      18.007 72.132 39.320 -0.03 +0.00 +0.000 2.977
ATOM     32  A29_____ <1> d      18.052 70.667 39.407 -0.11 -0.00 +0.001 2.977
TER
ENDMDL

```

Panduratin A Docking Output file (extracted from *.dlg file)

Number of distinct conformational clusters found = 9, out of 100 runs,
Using an rmsd-tolerance of 0.5 A

CLUSTERING HISTOGRAM

Clus -ter Rank	Lowest Docked Energy	Run	Mean Docked Energy	Num in Clus	Histogram						
					5	10	15	20	25	30	35
1	-10.20	32	-10.16	3	###						
2	-10.11	14	-10.04	34	#####						
3	-10.03	46	-9.95	27	#####						
4	-10.01	9	-9.96	7	#####						
5	-9.94	80	-9.85	4	####						
6	-9.90	82	-9.86	2	##						
7	-9.87	13	-9.86	2	##						
8	-9.77	73	-9.77	1	#						
9	-9.59	96	-9.52	20	#####						

```

MODEL          14
USER          Run = 14
USER          Cluster Rank = 2
USER          Number of conformations in this cluster = 34
USER
USER          RMSD from reference structure          = 3.674 A
USER
USER          Estimated Free Energy of Binding      = -7.70 kcal/mol  [(1)+(3)]
USER          Estimated Inhibition Constant, Ki    = +2.28e-06      [Temperature = 298.15 K]
USER
USER          Final Docked Energy                  = -10.11 kcal/mol [(1)+(2)]
USER
USER          (1) Final Intermolecular Energy     = -9.56 kcal/mol
USER          (2) Final Internal Energy of Ligand = -0.55 kcal/mol
USER          (3) Torsional Free Energy           = +1.87 kcal/mol
USER
USER          DPF = 10-panduratin-a-ns2b3-b4-1-606060box-r.dpf
USER          NEWDPF move          10-panduratin-a.pdbq
USER          NEWDPF about         21.245399 70.046204 35.711201
USER          NEWDPF tran0         24.146369 70.570682 38.992737
USER          NEWDPF quat0         0.188694 0.368220 -0.910389 176.863752
USER          NEWDPF ndihe         8
USER          NEWDPF dihe0         63.19 -88.38 65.15 -31.17 -0.94 -10.82 122.24 -51.81
USER
USER          x          y          z          vdW          Elec          q          RMS
ATOM          1 C1_____ <1> d          26.036 68.609 35.407 -0.68 +0.01 +0.043 3.674
ATOM          2 C2_____ <1> d          23.513 69.966 38.073 -0.38 -0.00 +0.078 3.674
ATOM          3 C3_____ <1> d          22.281 70.214 37.150 -0.26 +0.00 +0.034 3.674
ATOM          4 C4_____ <1> d          24.827 70.049 37.227 -0.49 +0.00 +0.029 3.674
ATOM          5 C5_____ <1> d          24.750 69.101 36.037 -0.63 -0.02 -0.082 3.674
ATOM          6 C6_____ <1> d          23.572 68.723 35.500 -0.55 -0.01 -0.023 3.674
ATOM          7 C7_____ <1> d          22.220 69.118 36.049 -0.44 +0.00 +0.037 3.674
ATOM          8 C8_____ <1> d          23.570 70.881 39.287 -0.29 -0.02 +0.170 3.674
ATOM          9 O9_____ <1> d          23.912 72.060 39.170 +0.13 +0.03 -0.292 3.674
ATOM          10 A10_____ <1> d         23.449 70.320 40.644 -0.31 -0.02 +0.076 3.674
ATOM          11 A11_____ <1> d         24.317 69.295 41.070 -0.32 -0.03 +0.085 3.674
ATOM          12 A12_____ <1> d         22.463 70.805 41.528 -0.22 -0.01 +0.085 3.674
ATOM          13 A13_____ <1> d         24.208 68.776 42.372 -0.23 -0.03 +0.074 3.674
ATOM          14 A14_____ <1> d         23.236 69.265 43.261 -0.34 -0.02 +0.073 3.674
ATOM          15 A15_____ <1> d         22.363 70.280 42.829 -0.24 -0.01 +0.074 3.674
ATOM          16 O16_____ <1> d         23.188 68.716 44.507 -0.05 +0.17 -0.356 3.674
ATOM          17 C17_____ <1> d         22.126 68.000 45.058 -0.41 -0.11 +0.210 3.674
ATOM          18 O18_____ <1> d         21.616 71.786 41.131 +0.18 +0.02 -0.360 3.674
ATOM          19 H19_____ <1> d         20.781 71.592 40.743 +0.11 -0.01 +0.217 3.674
ATOM          20 O20_____ <1> d         25.246 68.794 40.216 -0.12 +0.16 -0.360 3.674
ATOM          21 H21_____ <1> d         25.210 67.904 39.914 -0.24 -0.21 +0.217 3.674
ATOM          22 C28_____ <1> d         25.161 71.492 36.729 -0.39 +0.00 +0.037 3.674
ATOM          23 C29_____ <1> d         26.651 71.766 36.729 -0.56 -0.00 -0.024 3.674
ATOM          24 C30_____ <1> d         27.222 72.834 36.134 -0.59 -0.01 -0.091 3.674
ATOM          25 C32_____ <1> d         28.720 73.031 36.241 -0.70 +0.01 +0.042 3.674
ATOM          26 C31_____ <1> d         26.437 73.884 35.376 -0.49 +0.00 +0.042 3.674
ATOM          27 A22_____ <1> d         20.967 70.258 37.916 -0.16 +0.00 -0.053 3.674
ATOM          28 A23_____ <1> d         20.218 71.452 37.947 -0.06 +0.00 +0.007 3.674
ATOM          29 A24_____ <1> d         20.467 69.125 38.591 -0.21 -0.00 +0.007 3.674
ATOM          30 A25_____ <1> d         19.003 71.517 38.651 -0.06 +0.00 +0.001 3.674
ATOM          31 A26_____ <1> d         18.521 70.386 39.328 -0.15 -0.00 +0.000 3.674
ATOM          32 A27_____ <1> d         19.255 69.189 39.296 -0.31 -0.00 +0.001 3.674
TER
ENDMDL

```

Ester 3 Docking Output file (extracted from *.dlg file)

Number of distinct conformational clusters found = 10, out of 100 runs,
Using an rmsd-tolerance of 1.5 A

CLUSTERING HISTOGRAM

Clus- ter Rank	Lowest Docked Energy	Run	Mean Docked Energy	Num in Clus	Histogram							
					5	10	15	20	25	30	35	
1	-9.23	63	-8.90	55	#####							
2	-9.13	2	-8.67	33	#####							
3	-8.33	5	-8.31	2	##							
4	-8.22	25	-7.98	3	###							
5	-8.22	36	-8.22	1	#							
6	-8.20	15	-8.20	1	#							
7	-8.17	32	-8.17	1	#							
8	-8.16	81	-8.15	2	##							
9	-7.85	59	-7.85	1	#							
10	-7.68	97	-7.68	1	#							

```

MODEL          63
USER          Run = 63
USER          Cluster Rank = 1
USER          Number of conformations in this cluster = 7
USER
USER          RMSD from reference structure          = 4.493 A
USER
USER          Estimated Free Energy of Binding      = -6.10 kcal/mol  [(1)+(3)]
USER          Estimated Inhibition Constant, Ki    = +3.36e-05   [Temperature = 298.15 K]
USER
USER          Final Docked Energy                  = -9.23 kcal/mol  [(1)+(2)]
USER
USER          (1) Final Intermolecular Energy      = -8.90 kcal/mol
USER          (2) Final Internal Energy of Ligand = -0.32 kcal/mol
USER          (3) Torsional Free Energy           = +2.80 kcal/mol
USER
USER          DPF = 7-compound4-12-757-ns2b3-b4-1.dpf
USER          NEWDPF move          7-compound4-12-757-rigid.pdbq
USER          NEWDPF about         23.575300 70.044998 37.007500
USER          NEWDPF tran0         26.786331 70.847130 37.669288
USER          NEWDPF quat0         0.645909 0.660907 0.382103 -166.895328
USER          NEWDPF ndihe         10
USER          NEWDPF dihe0         -53.71 -81.71 -47.56 -70.73 54.04 168.06 -4.25 -131.79 120.60 84.73
USER
USER          x          y          z          vdW      Elec          q          RMS
ATOM      1  A7_____ <1> d      27.254  72.065  36.108 -0.52 +0.01      +0.102  4.493
ATOM      2  A8_____ <1> d      26.489  72.346  37.336 -0.37 -0.00      +0.104  4.493
ATOM      3  A9_____ <1> d      25.663  71.403  37.830 -0.33 -0.01      +0.076  4.493
ATOM      4  A10_____ <1> d     25.531  70.087  37.180 -0.47 +0.00      +0.114  4.493
ATOM      5  A11_____ <1> d     26.234  69.828  36.057 -0.61 +0.00      +0.001  4.493
ATOM      6  A12_____ <1> d     27.124  70.867  35.504 -0.44 +0.01      +0.051  4.493
ATOM      7  O13_____ <1> d     26.696  73.558  37.924 +0.02 +0.00      -0.348  4.493
ATOM      8  C22_____ <1> d     27.672  73.931  38.853 -0.39 -0.01      +0.185  4.493
ATOM      9  C1_____ <1> d     27.142  75.028  39.813 -0.35 -0.00      +0.138  4.493
ATOM     10  C2_____ <1> d     27.970  75.120  41.068 -0.31 -0.02      +0.260  4.493
ATOM     11  O3_____ <1> d     27.607  74.521  42.083 -0.27 -0.03      -0.265  4.493
ATOM     12  O4_____ <1> d     29.100  75.875  41.065 -0.30 -0.01      -0.322  4.493
ATOM     13  C5_____ <1> d     29.285  77.027  41.834 -0.38 +0.00      +0.174  4.493
ATOM     14  C6_____ <1> d     30.382  76.774  42.891 -0.37 +0.00      +0.034  4.493
ATOM     15  O14_____ <1> d     28.075  73.048  35.643 -0.19 -0.02      -0.353  4.493
ATOM     16  C15_____ <1> d     29.443  73.181  35.878 -0.72 +0.04      +0.210  4.493
ATOM     17  N16_____ <1> d     24.679  69.125  37.780 -0.39 +0.00      -0.115  4.493
ATOM     18  O18_____ <1> d     25.010  68.576  38.885 -0.47 +0.12      -0.532  4.493
ATOM     19  O17_____ <1> d     23.455  69.047  37.424 -0.03 -0.01      -0.532  4.493
ATOM     20  C19_____ <1> d     26.139  68.508  35.325 -0.56 +0.05      +0.205  4.493
ATOM     21  O20_____ <1> d     24.963  68.505  34.506 -0.49 -0.24      -0.396  4.493
ATOM     22  H21_____ <1> d     25.250  68.181  33.625 -0.97 +0.11      +0.209  4.493
TER
ENDMDL

```

CP14 Docking Output file (extracted from *.dlg file)

Number of distinct conformational clusters found = 6, out of 100 runs,
Using an rmsd-tolerance of 0.5 A

CLUSTERING HISTOGRAM

Clus -ter Rank	Lowest Docked Energy	Run	Mean Docked Energy	Num in Clus	Histogram						
					5	10	15	20	25	30	35
1	-11.44	21	-11.30	92	:	:	:	:	:	:	:
2	-11.08	11	-10.95	4	#####						
3	-10.93	85	-10.93	1	#						
4	-10.86	52	-10.86	1	#						
5	-10.71	56	-10.71	1	#						
6	-10.66	9	-10.66	1	#						

```

MODEL          21
USER          Run = 21
USER          Cluster Rank = 1
USER          Number of conformations in this cluster = 92
USER
USER          RMSD from reference structure          = 1.231 A
USER
USER          Estimated Free Energy of Binding      = -8.70 kcal/mol  [(1)+(3)]
USER          Estimated Inhibition Constant, Ki    = +4.21e-07      [Temperature = 298.15 K]
USER
USER          Final Docked Energy                  = -11.44 kcal/mol  [(1)+(2)]
USER
USER          (1) Final Intermolecular Energy      = -10.57 kcal/mol
USER          (2) Final Internal Energy of Ligand = -0.87 kcal/mol
USER          (3) Torsional Free Energy           = +1.87 kcal/mol
USER
USER          DPF = 46-ns2b3-b4-1-606060box-r.dpf
USER          NEWDPF move                          46.pdbq
USER          NEWDPF about                          22.728701 69.597504 38.105499
USER          NEWDPF tran0                          23.590250 69.499526 37.958079
USER          NEWDPF quat0                          -0.638436 -0.758282 -0.131936 13.346826
USER          NEWDPF ndihe                           8
USER          NEWDPF dihe0                          45.14 73.40 -110.44 -61.43 166.03 -7.51 29.08 2.59
USER
USER          x          y          z          vdW      Elec      q          RMS
ATOM          1  C1_____ <1> d      23.104  69.135  36.942 -0.45 +0.01  +0.102  1.231
ATOM          2  C2_____ <1> d      21.726  69.276  36.217 -0.37 +0.00  +0.034  1.231
ATOM          3  C3_____ <1> d      24.235  68.751  35.920 -0.52 +0.07  +0.232  1.231
ATOM          4  N4_____ <1> d      23.684  67.993  34.758 -0.59 +0.06  +0.088  1.231
ATOM          5  C5_____ <1> d      22.567  67.098  35.125 -0.68 +0.06  +0.271  1.231
ATOM          6  C6_____ <1> d      21.326  67.935  35.530 -0.50 +0.00  +0.040  1.231
ATOM          7  H31_____ <1> d      24.436  67.413  34.376 -0.46 +0.36  +0.316  1.231
ATOM          8  C7_____ <1> d      23.422  70.355  37.794 -0.31 -0.00  +0.169  1.231
ATOM          9  O8_____ <1> d      23.397  71.471  37.269 +0.15 -0.00  -0.292  1.231
ATOM         10  A9_____ <1> d      23.289  70.289  39.263 -0.28 -0.01  +0.046  1.231
ATOM         11  A11_____ <1> d      22.347  71.210  39.931 -0.15 -0.00  +0.018  1.231
ATOM         12  A10_____ <1> d      23.995  69.409  40.005 -0.37 -0.04  +0.112  1.231
ATOM         13  A14_____ <1> d      22.180  71.165  41.263 -0.17 -0.00  +0.004  1.231
ATOM         14  A13_____ <1> d      22.943  70.205  42.067 -0.29 -0.01  +0.039  1.231
ATOM         15  A12_____ <1> d      23.813  69.366  41.472 -0.35 -0.03  +0.099  1.231
ATOM         16  O15_____ <1> d      24.881  68.573  39.409 -0.44 +0.14  -0.357  1.231
ATOM         17  H16_____ <1> d      24.929  67.659  39.626 -0.52 -0.17  +0.217  1.231
ATOM         18  O35_____ <1> d      24.525  68.476  42.207 -0.06 +0.17  -0.358  1.231
ATOM         19  H51_____ <1> d      24.126  67.710  42.581 -0.44 -0.21  +0.217  1.231
ATOM         20  A22_____ <1> d      20.622  69.735  37.159 -0.20 -0.00  -0.053  1.231
ATOM         21  A23_____ <1> d      20.049  70.945  36.999 -0.09 +0.00  +0.007  1.231
ATOM         22  A24_____ <1> d      20.188  68.885  38.290 -0.19 -0.00  +0.007  1.231
ATOM         23  A25_____ <1> d      19.014  71.414  37.932 -0.06 +0.00  +0.001  1.231
ATOM         24  A26_____ <1> d      18.634  70.639  38.961 -0.12 -0.00  +0.000  1.231
ATOM         25  A27_____ <1> d      19.247  69.318  39.148 -0.30 -0.00  +0.001  1.231
ATOM         26  C17_____ <1> d      25.033  69.950  35.316 -0.55 +0.01  +0.039  1.231
ATOM         27  C18_____ <1> d      26.521  70.033  35.769 -0.73 +0.00  +0.033  1.231
ATOM         28  C19_____ <1> d      26.774  71.002  36.959 -0.62 -0.00  +0.114  1.231
ATOM         29  C20_____ <1> d      27.903  72.028  36.677 -0.63 +0.00  +0.039  1.231
TER
ENDMDL

```


Blind Docking of CP14 Docking Output file (extracted from *.dlg file)

Number of distinct conformational clusters found = 5, out of 100 runs,
Using an rmsd-tolerance of 2.0 A

CLUSTERING HISTOGRAM

Clus- ter Rank	Lowest Docked Energy	Run	Mean Docked Energy	Num in Clus	Histogram						
					5	10	15	20	25	30	35
1	-8.92	56	-8.92	65	_____	_____	_____	_____	_____	_____	_____
2	-8.48	99	-8.48	5	#####						
3	-8.31	27	-8.30	6	#####						
4	-7.98	43	-7.98	11	#####						
5	-7.62	36	-7.62	13	#####						

Number of multi-member conformational clusters found = 5, out of 100 runs.

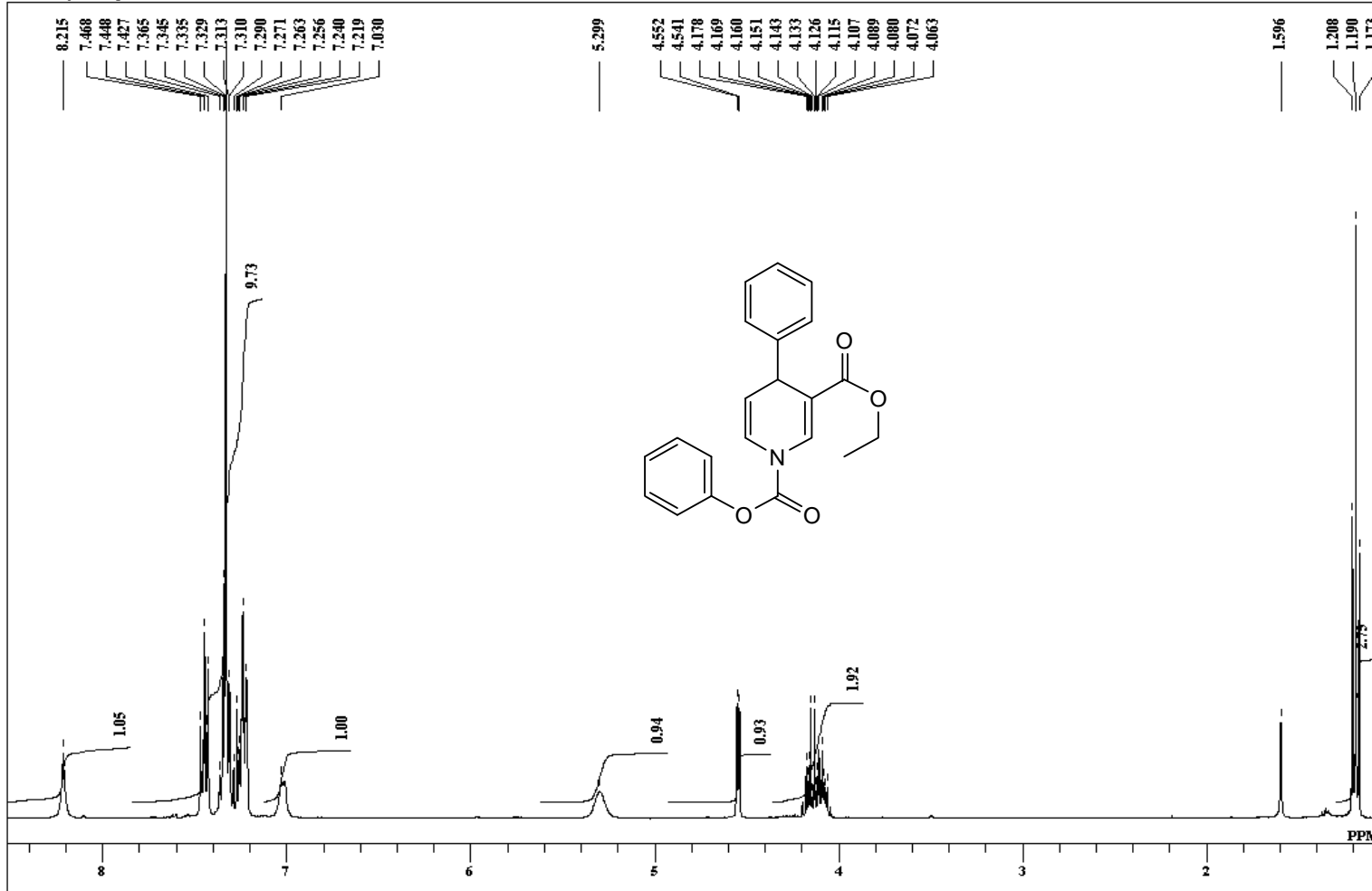
-

APPENDIX 2

^1H and ^{13}C NMR SPECTRUM OF SYNTHESISED MOLECULES

single_pulse-yk25

D:\ECA1\yk25-4.jdf

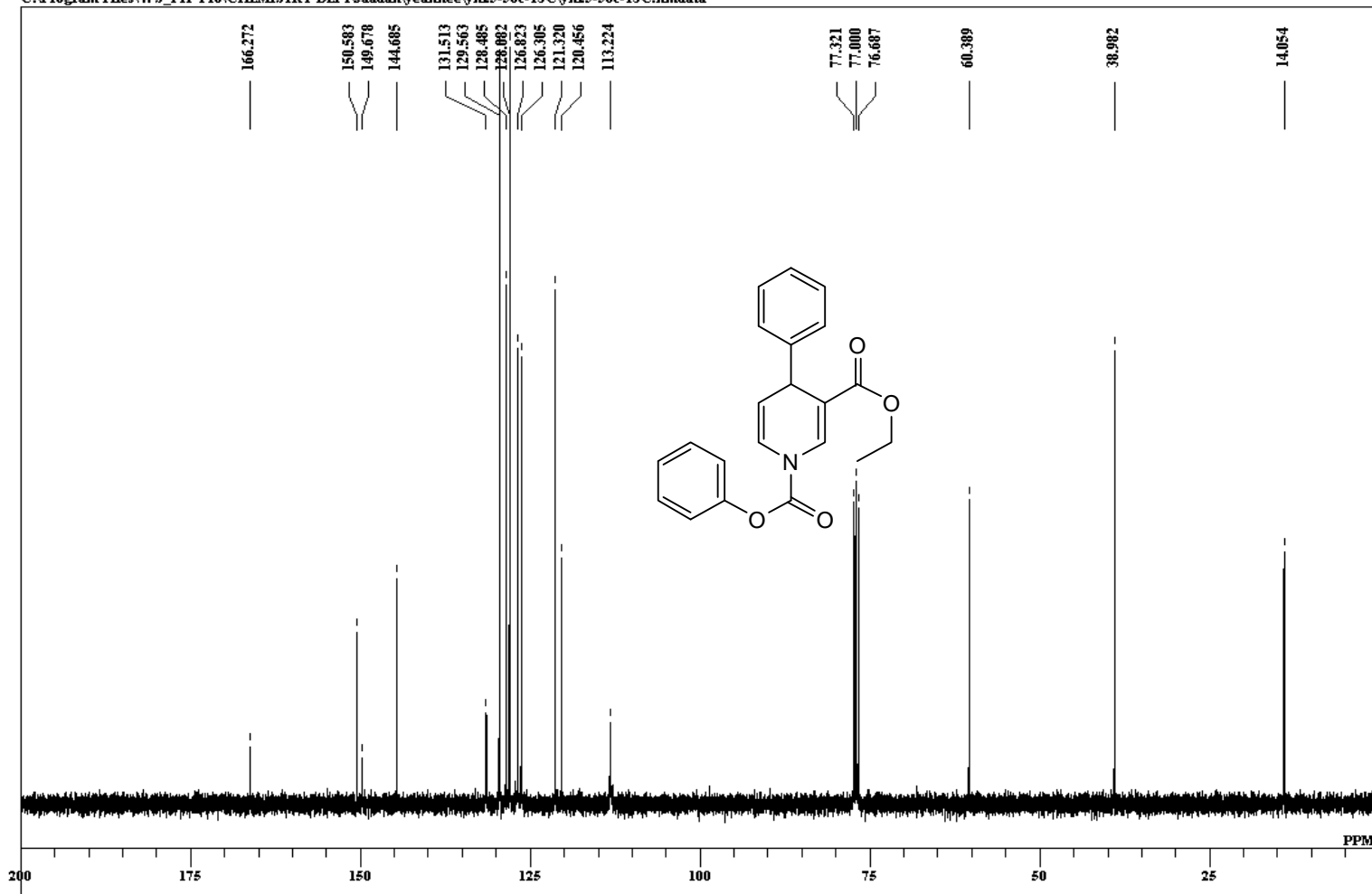


D:\ECA1\yk25-4.jdf
COMNT single_pulse-yk25
DATIM 09-04-2007 16:37
OBNUC 1H
EXMOD single_pulse.ex2
OBFRQ 395.88 MHz
OBSET 6.28 KHz
OBFIN 0.87 Hz
POINT 16400
FREQU 7422.80 Hz
SCANS 8
ACQIM 2.2073 sec
PD 5.0000 sec
PW1 5.25 usec
IRNUC 1H
CTEMP 22.1 c
SLVNT CDCL3
EXREF 7.24 ppm
BF 0.12 Hz
RGAIN 32

IH-yk25-50c-13C

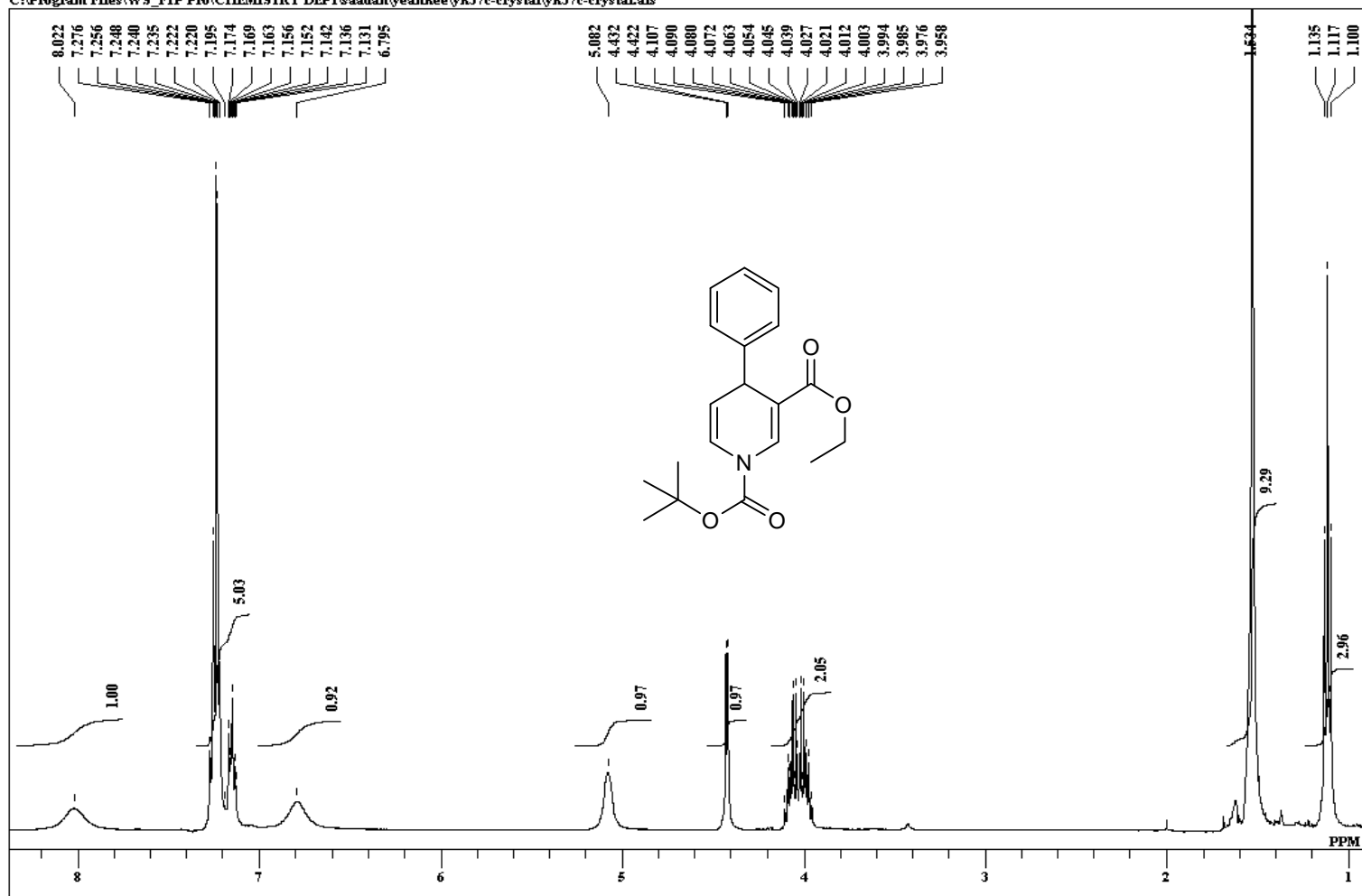
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeankeeyk25-50c-13C\yk25-50c-13C.nmdata

DFILE yk25-50c-13C.nm
COMNT IH-yk25-50c-13C
DATIM Mon Apr 23 14:5
OBNUC 13C
EXMOD bcm
OBFRQ 100.40 MHz
OBSET 130.00 KHz
OBFIN 5500.00 Hz
POINT 32768
FREQU 27100.27 Hz
SCANS 400
ACQTM 1.2091 sec
PD 1.7909 sec
PW1 6.50 usec
IRNUC IH
CTEMP 50.0 c
SLVNT CDCL3
EXREF 77.00 ppm
BF 0.12 Hz
RGAIN 30



1H-yk37c-crystal

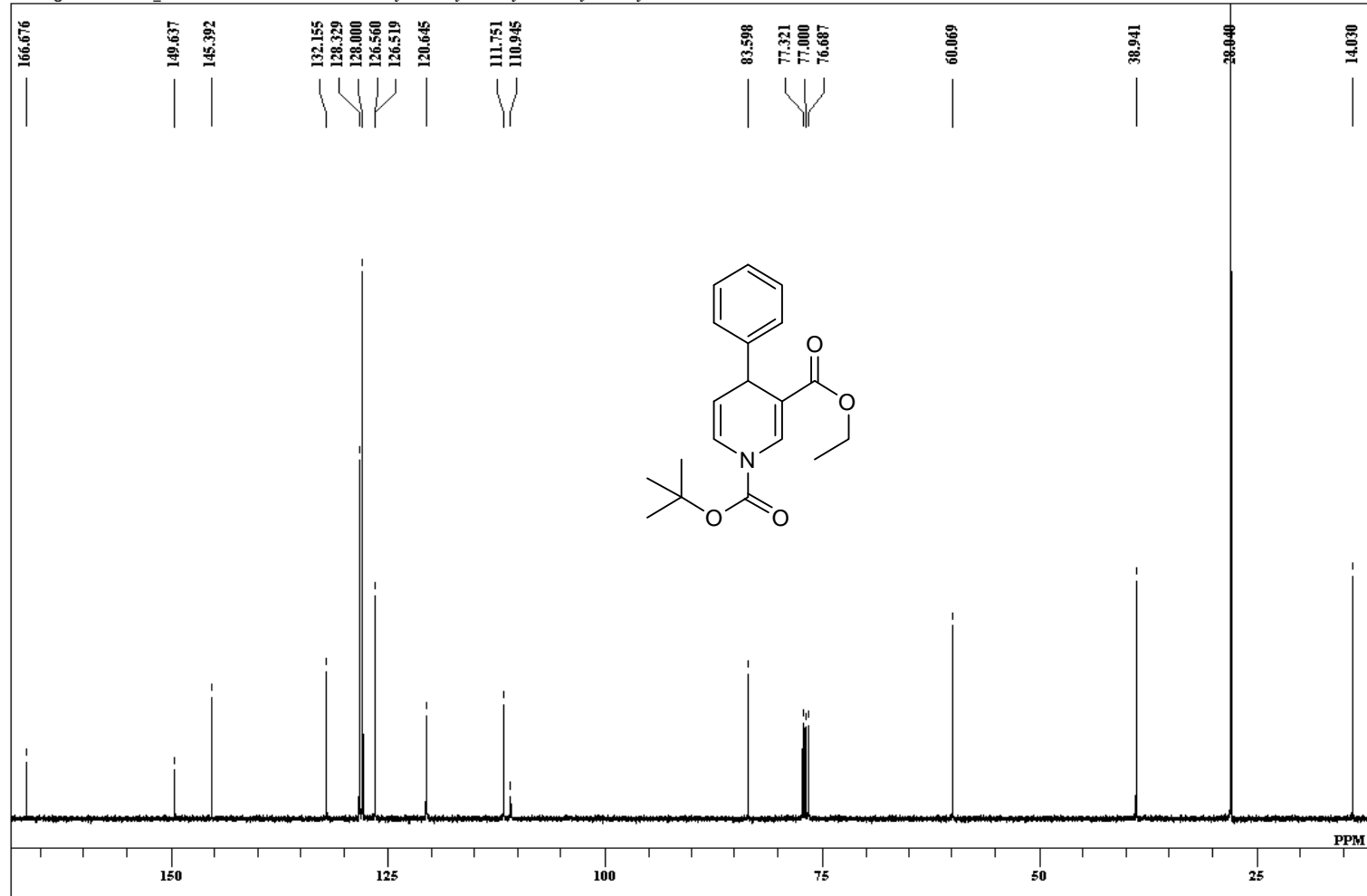
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeanhee\yk37c-crystal\yk37c-crystal.lals



DFILE yk37c-crystal.lals
COMNT 1H-yk37c-crystal
DATIM Fri May 4 15:09:
1H
OBNUC 1H
EXMOD non
OBFRQ 399.65 MHz
OBSET 130.00 KHz
OBFIN 4300.00 Hz
POINT 32768
FREQU 7993.60 Hz
SCANS 8
ACQTM 4.0993 sec
PD 2.9007 sec
PW1 6.95 usec
IRNUC 1H
CTEMP 24.3 c
SLVNT CDCL3
EXREF 7.24 ppm
BF 0.12 Hz
RGAIN 15

13C-yk37c-crystal

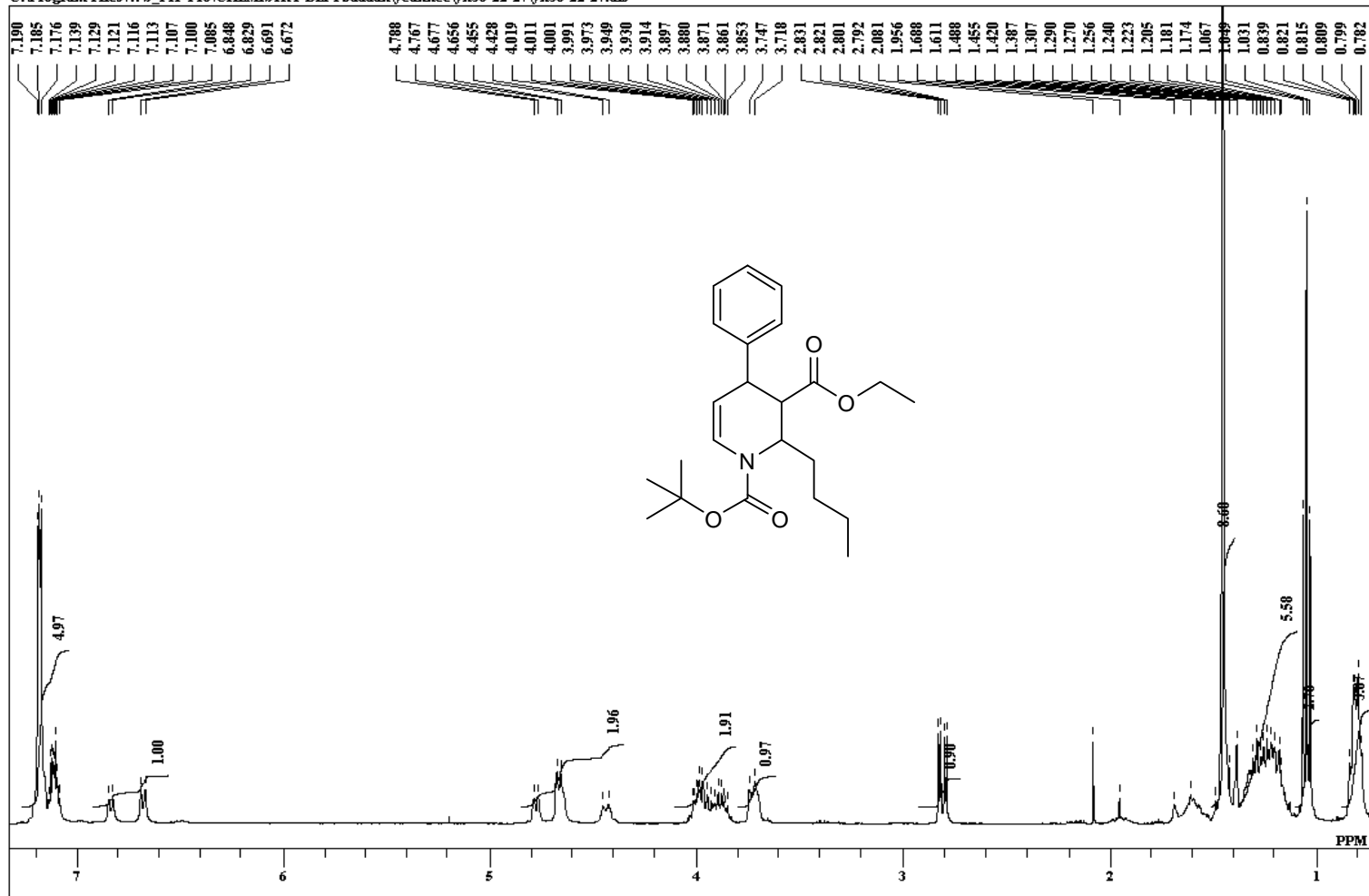
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeankeeyk37c-crystal-13C\yk37c-crystal-13C.nmdata



DFILE yk37c-crystal-13
COMNT 13C-yk37c-cryst
DATIM Fri May 4 16:01:
OBNUC 13C
EXMOD bcm
OBFRQ 100.40 MHz
OBSET 130.00 KHz
OBFIN 5500.00 Hz
POINT 32768
FREQU 27100.27 Hz
SCANS 881
ACQTM 1.2091 sec
PD 1.7909 sec
PWI 6.50 usec
IRNUC 1H
CTEMP 50.0 c
SLVNT CDCL3
EXREF 77.00 ppm
BF 0.12 Hz
RGAIN 30

IH-yk38-22-27

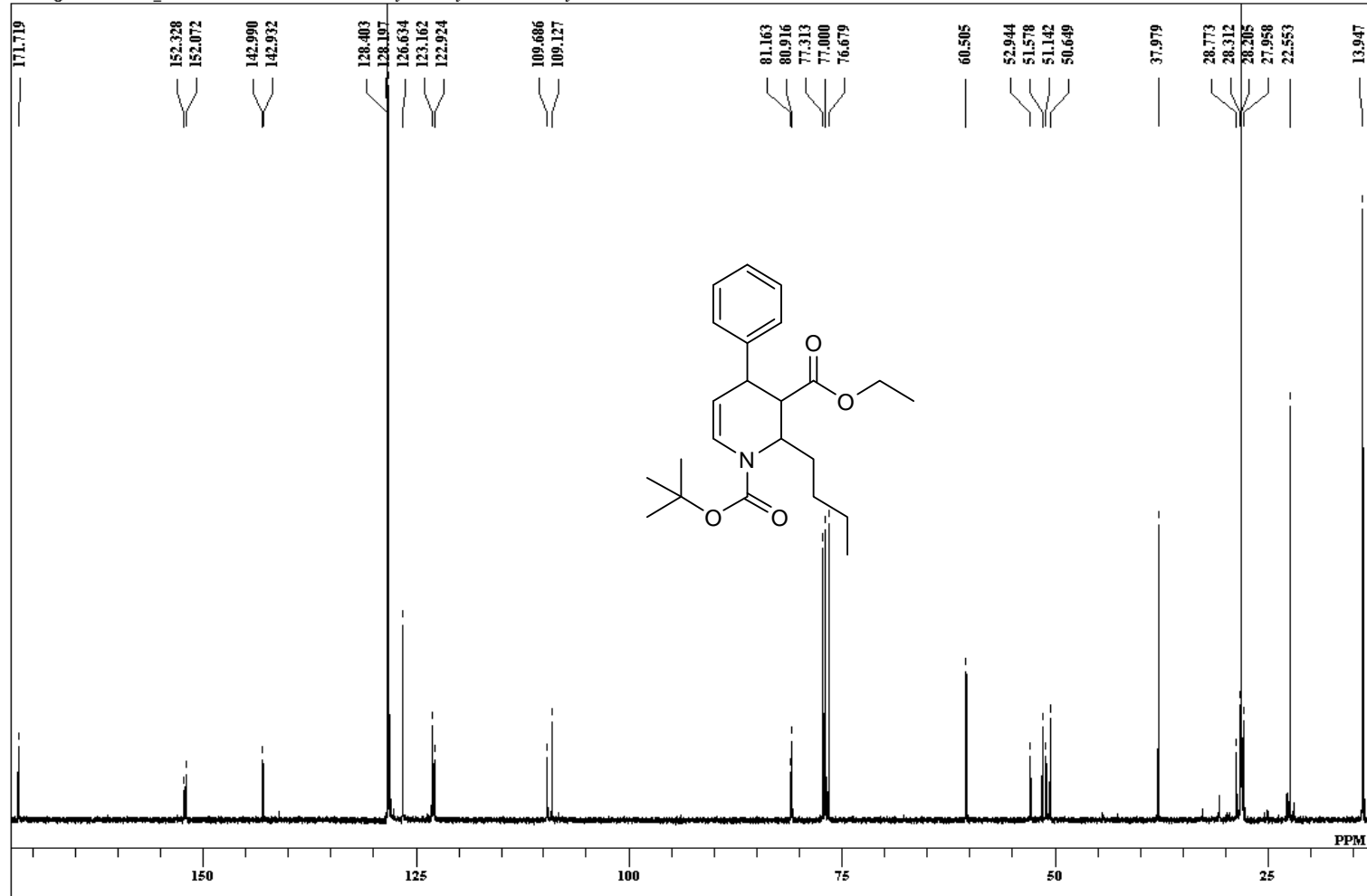
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeankeeyk38-22-27\yk38-22-27.als



DFILE yk38-22-27.als
COMNT IH-yk38-22-27
DATIM Tue Jan 16 17:30
OBNUC 1H
EXMOD non
OBFRQ 399.65 MHz
OBSEI 130.00 KHz
OBFIN 4300.00 Hz
POINT 32768
FREQU 8000.00 Hz
SCANS 8
ACQIM 4.0960 sec
PD 5.0000 sec
PWI 5.00 usec
IRNUC 1H
CTEMP 23.6 c
SLVNT CDCL3
EXREF 0.00 ppm
BF 0.12 Hz
RGAIN 13

13C-yk38-22-27

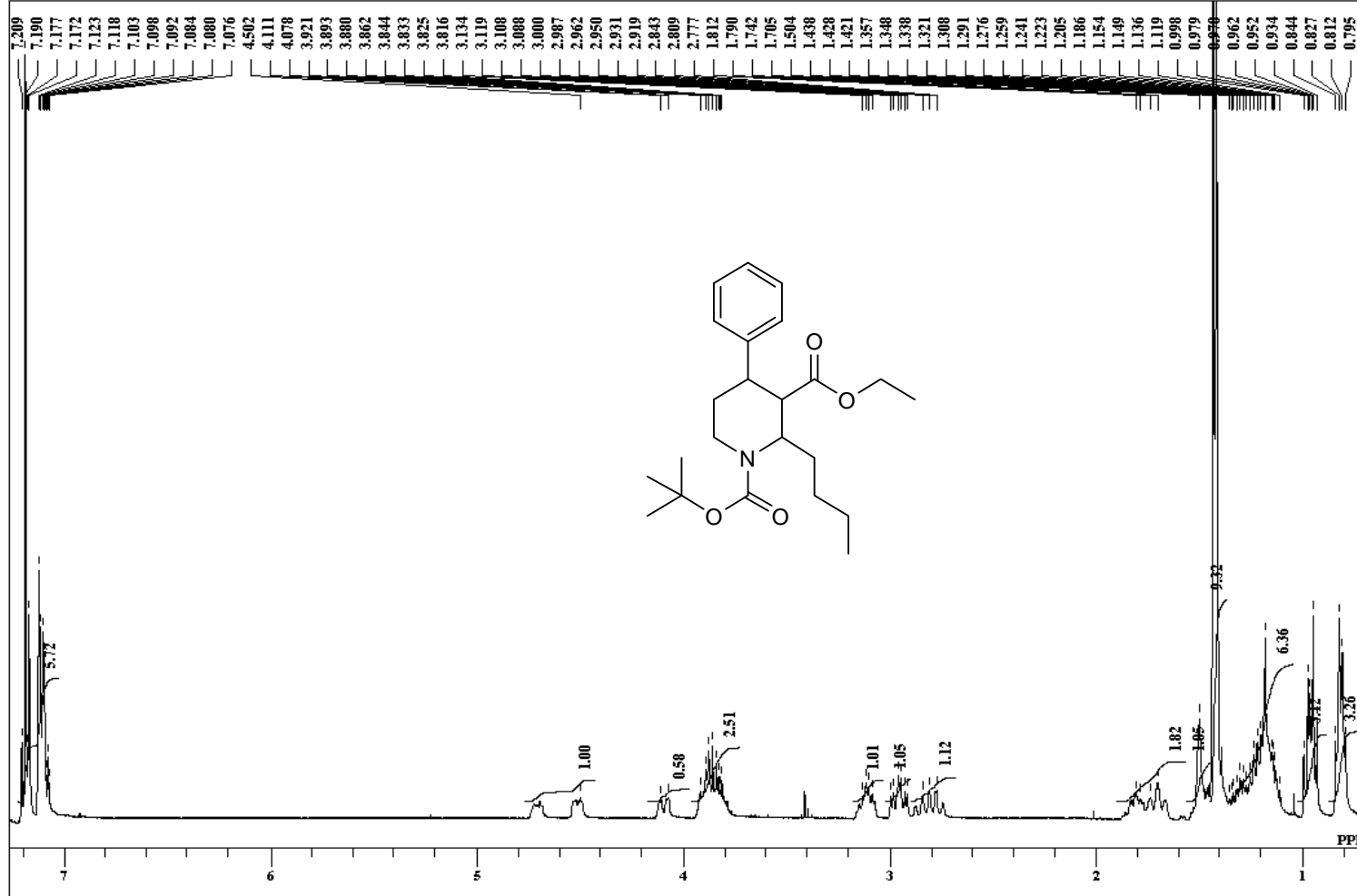
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeanhee\yk38-22-27-13C\yk38-22-27-13C.als



DFILE yk38-22-27-13C.
COMNT 13C-yk38-22-27
DATIM Tue Jan 16 20:52
13C
EXMOD bcm
OBFRQ 100.40 MHz
OBSET 130.00 KHz
OBFIN 5500.00 Hz
POINT 32768
FREQU 27100.27 Hz
SCANS 4000
ACQTM 1.2091 sec
PD 1.7909 sec
PW1 6.50 usec
IRNUC 1H
CTEMP 25.0 c
SLVNT CDCL3
EXREF 77.00 ppm
BF 0.12 Hz
RGAIN 29

IH-yk51-r

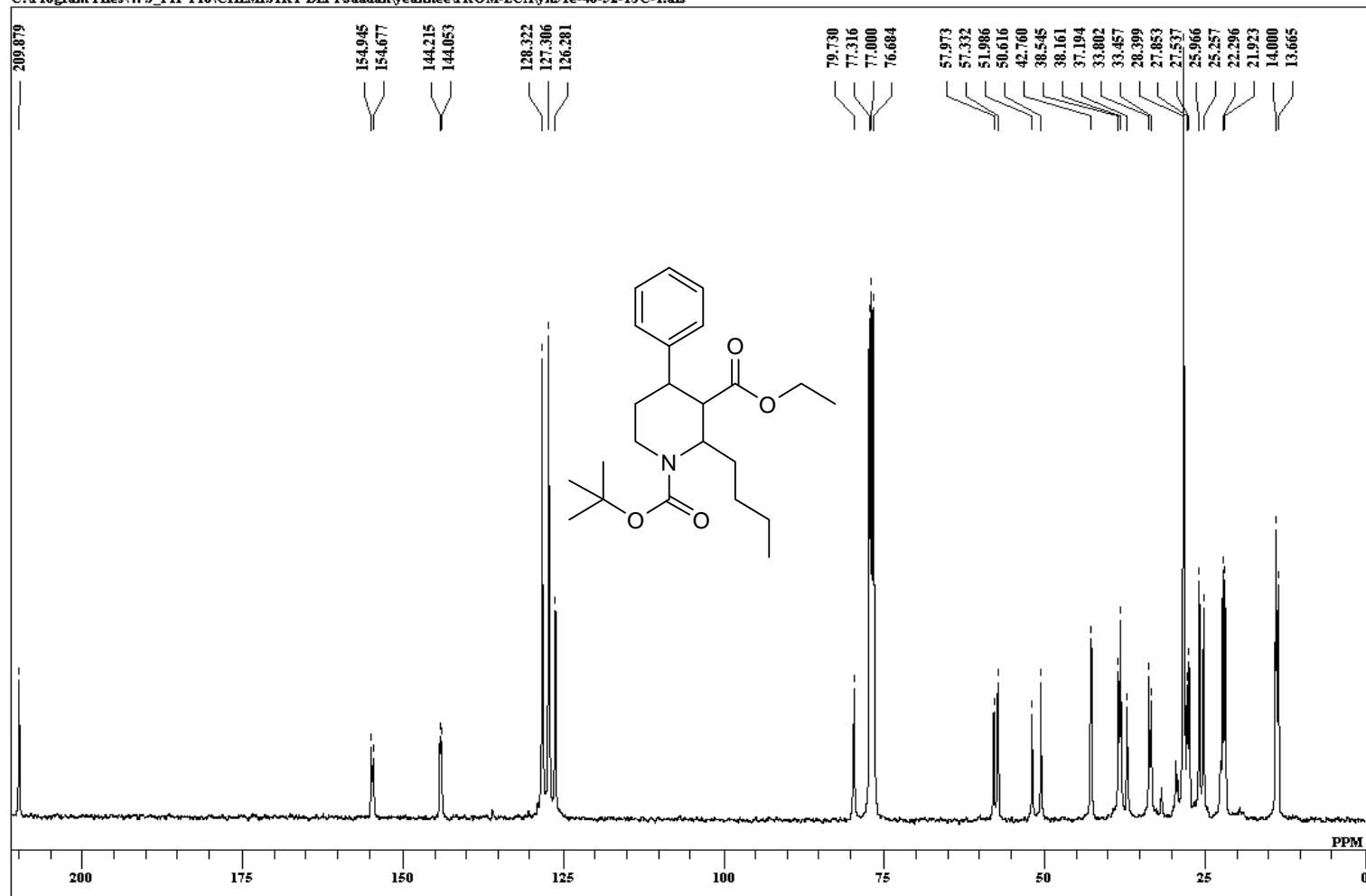
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DFILE	yk51-r.nmdata
COMNT	IH-yk51-r
DATEM	Thu Aug 7 17:22
OBNUC	IH
EXMOD	non
OBFRQ	399.65 MHz
OBSET	130.00 KHz
OBFIN	4300.00 Hz
POINT	32768
FREQU	7993.60 Hz
SCANS	8
ACQTM	4.0993 sec
PD	2.9007 sec
PW1	7.50 usec
IRNUC	IH
CTEMP	30.0 c
SLVNT	CDCL3
EXREF	0.00 ppm
BF	0.12 Hz
RGAIN	19

single pulse decoupled gated NOE-yk51e-46-52-13C

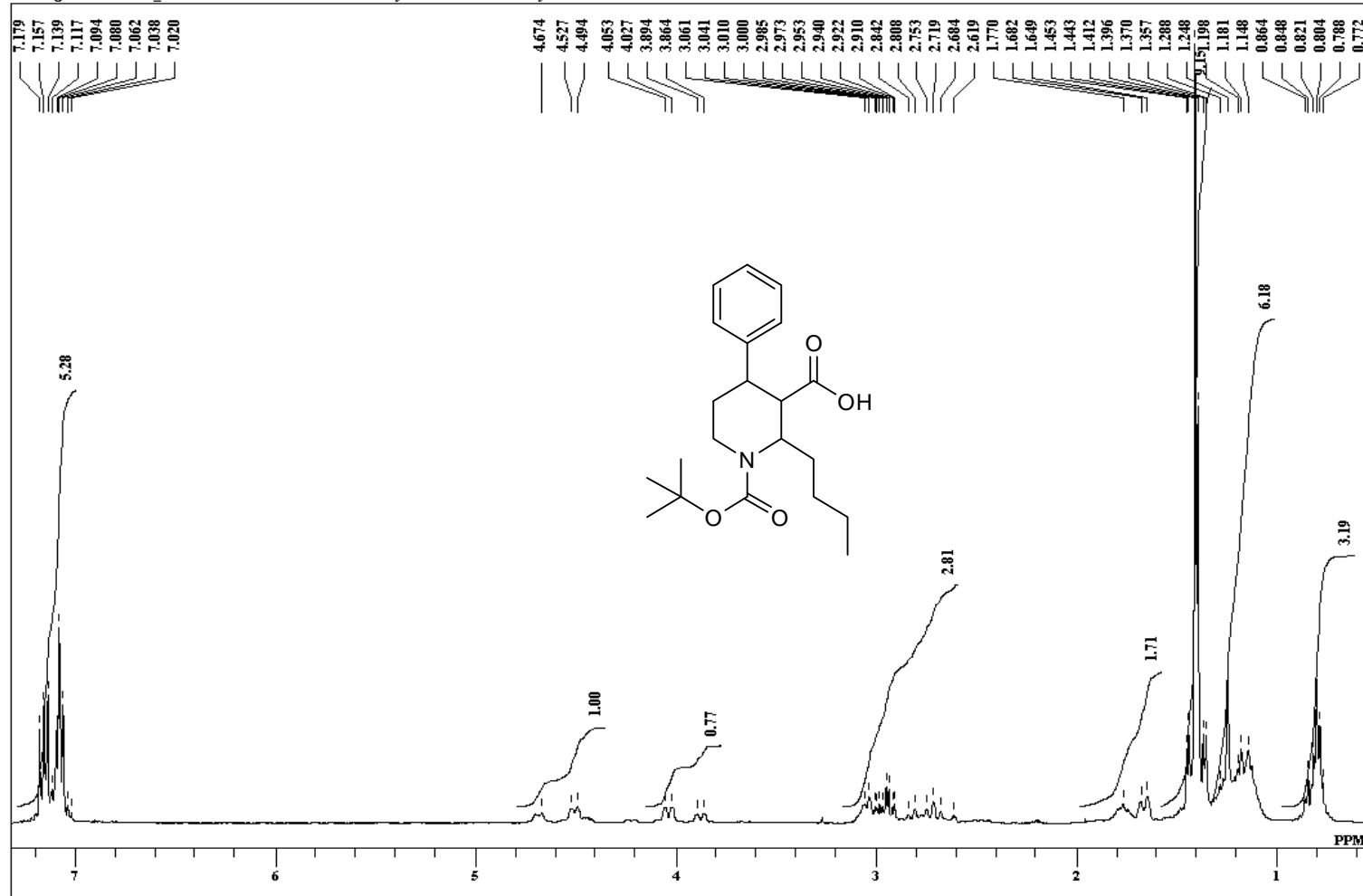
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeahee\FROM-ECA\yk51e-46-52-13C-1.als



DFILE yk51e-46-52-13C
COMNT single pulse dec
DATIM 22-12-2007 01:49
OBNUC 13C
EXMOD single_pulse_de
OBFRQ 99.55 MHz
OBSET 5.13 KHz
OBFIN 0.98 Hz
POINT 26214
FREQU 24999.62 Hz
SCANS 3000
ACQTM 1.0486 sec
PD 2.0000 sec
PW1 3.07 usec
IRNUC 1H
CTEMP 20.9 c
SLVNT CDCL3
EXREF 77.00 ppm
BF 10.00 Hz
RGAIN 54

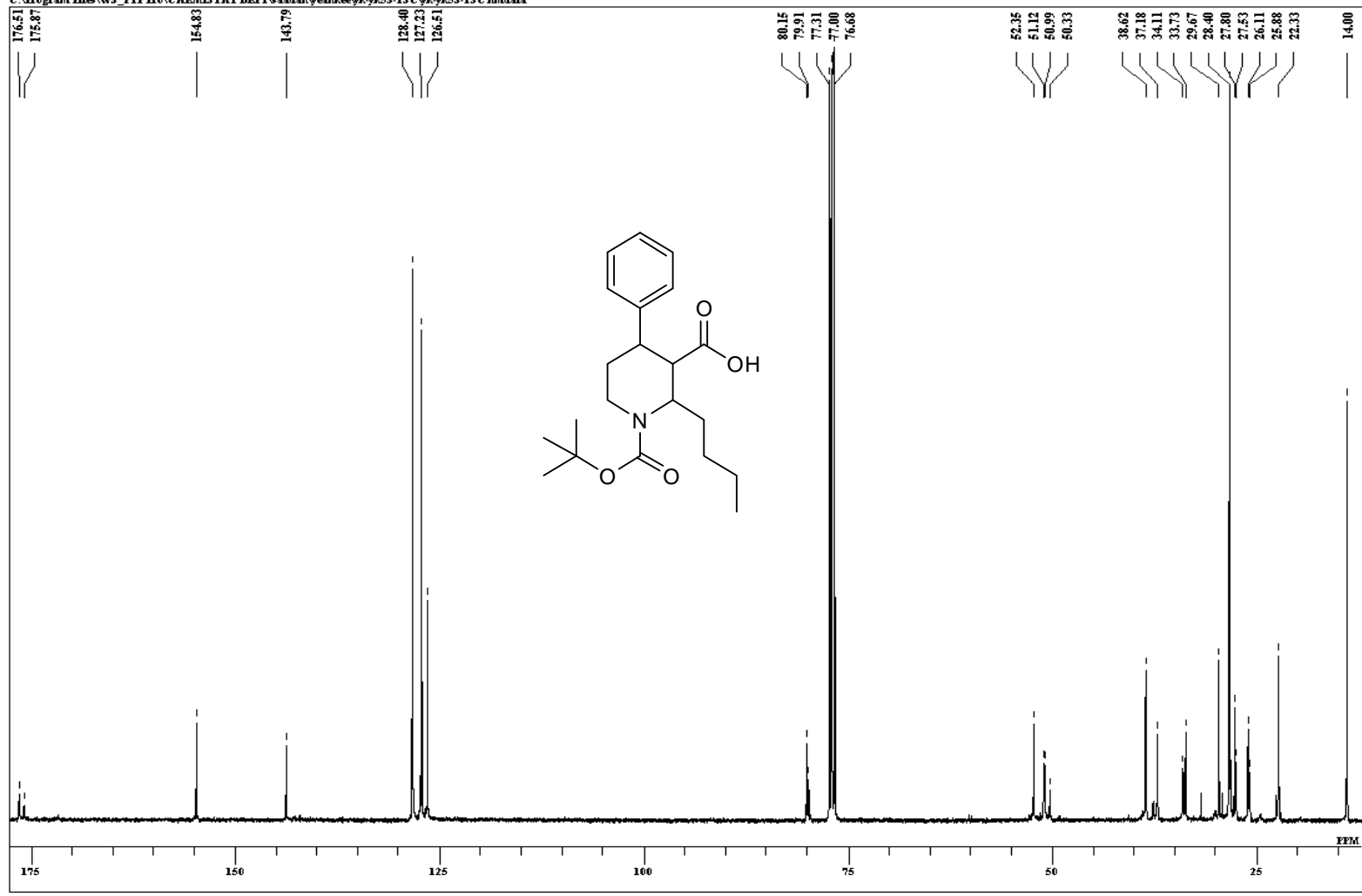
single_pulse-ylk53h-acid

C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeanke\FROM-ECA\ylk53h-acid-3.als



DFILE ylk53h-acid-3.als
COMNT single_pulse-ylk
DATIM 04-12-2007 13:32
OBNUC 1H
EXMOD single_pulse.ex2
OBFRQ 395.88 MHz
OBSEI 6.28 KHz
OBFIN 0.87 Hz
POINT 16400
FREQU 7422.80 Hz
SCANS 8
ACQTM 2.2073 sec
PD 5.0000 sec
PW1 5.75 usec
IRNUC 1H
CTEMP 21.0 c
SLVNT CDCL3
EXREF 0.00 ppm
BF 10.00 Hz
RGAIN 26

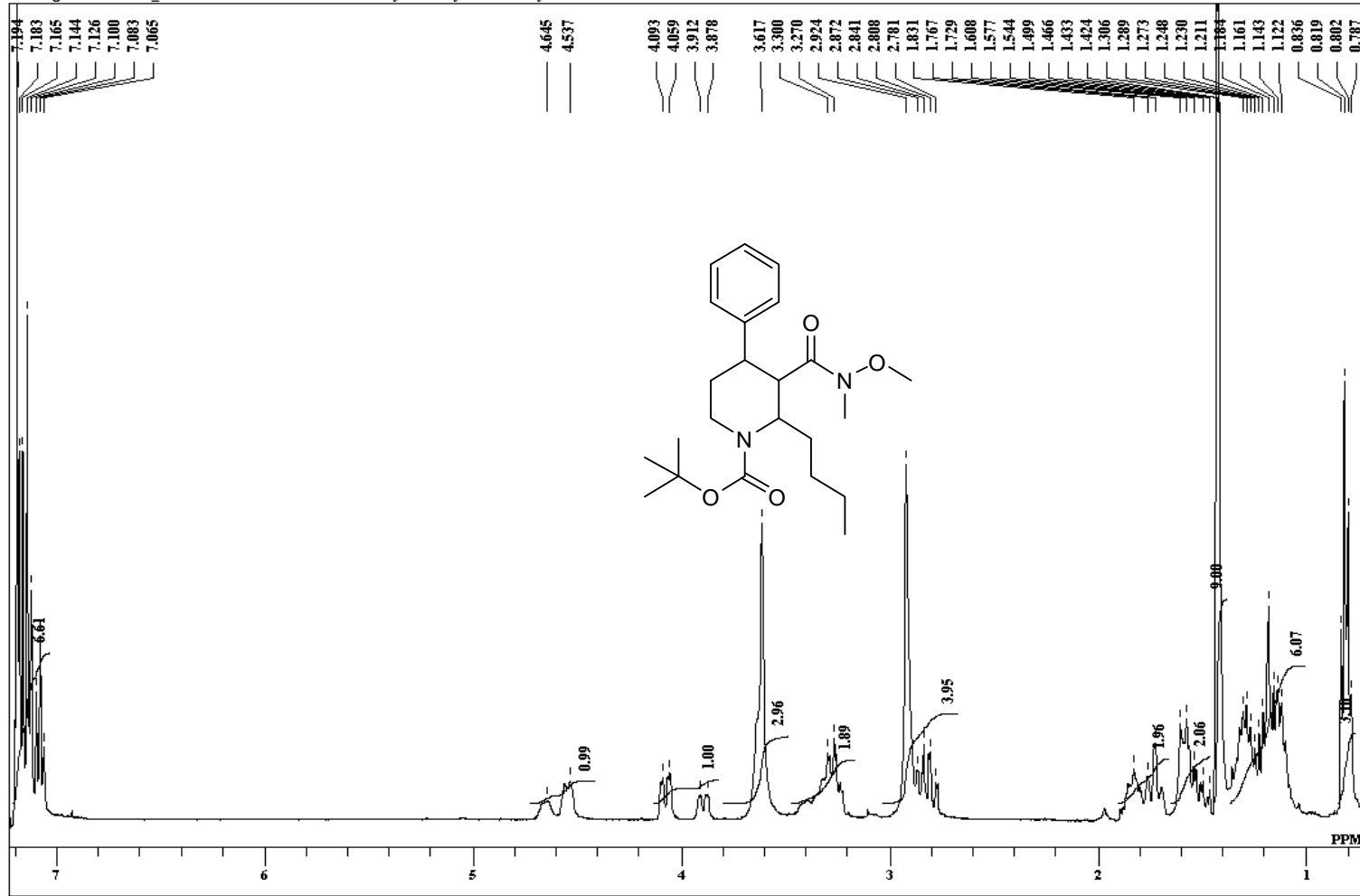
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DFILE y53-13 C\data
COMNT y53-13 C
DATIM Thu Nov 11 08:19:
ORNUC 13C
EXMOD hca
OBFREQ 100.40 MHz
OBSET 130.00 KHz
OBFIN 5500.00 Hz
POINT 32768
FREQU 27100.27 Hz
SCANS 18000
ACQTM 1.2091 sec
PD 1.7909 sec
PWI 4.65 usec
IRNUC 1H
CTEMP 0.0 c
SLVNT CDCL3
EXREF 77.00 ppm
BF 1.20 Hz
RGAIN 31

IH-yk73c-26-34

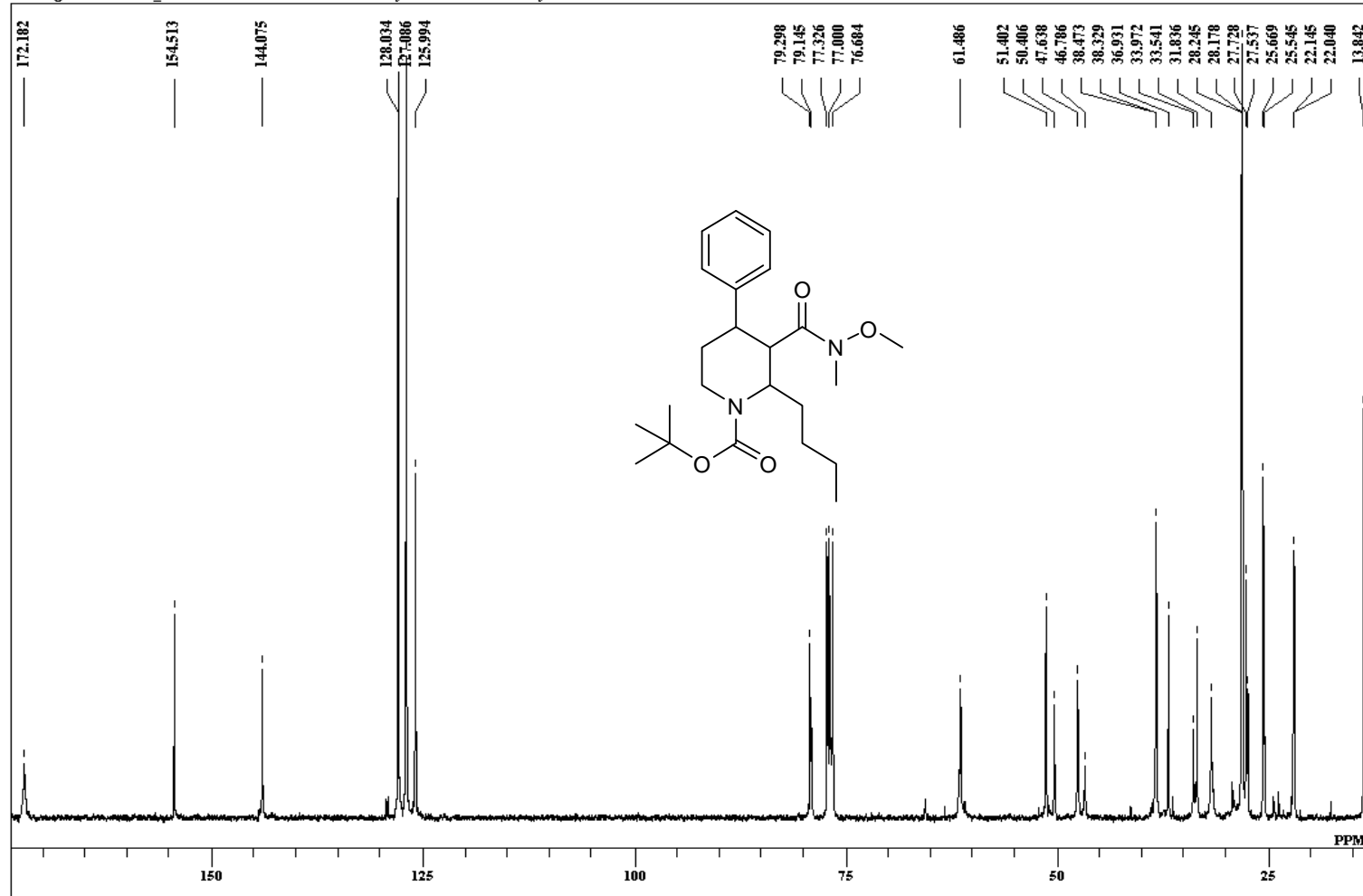
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeankeeyk73c-26-34\yk73c-26-34.als



DFILE yk73c-26-34.als
COMNT IH-yk73c-26-34
DATIM Wed Jun 6 12:4
OBNUC IH
EXMOD non
OBFRQ 399.65 MHz
OBSET 130.00 KHz
OBFIN 4300.00 Hz
POINT 32768
FREQU 7993.60 Hz
SCANS 8
ACQTM 4.0993 sec
PD 2.9007 sec
PW1 6.95 usec
IRNUC IH
CTEMP 22.8 c
SLVNT CDCL3
EXREF 0.00 ppm
BF 10.00 Hz
RGAIN 18

single pulse decoupled gated NOE-yk73d-56-69-13C

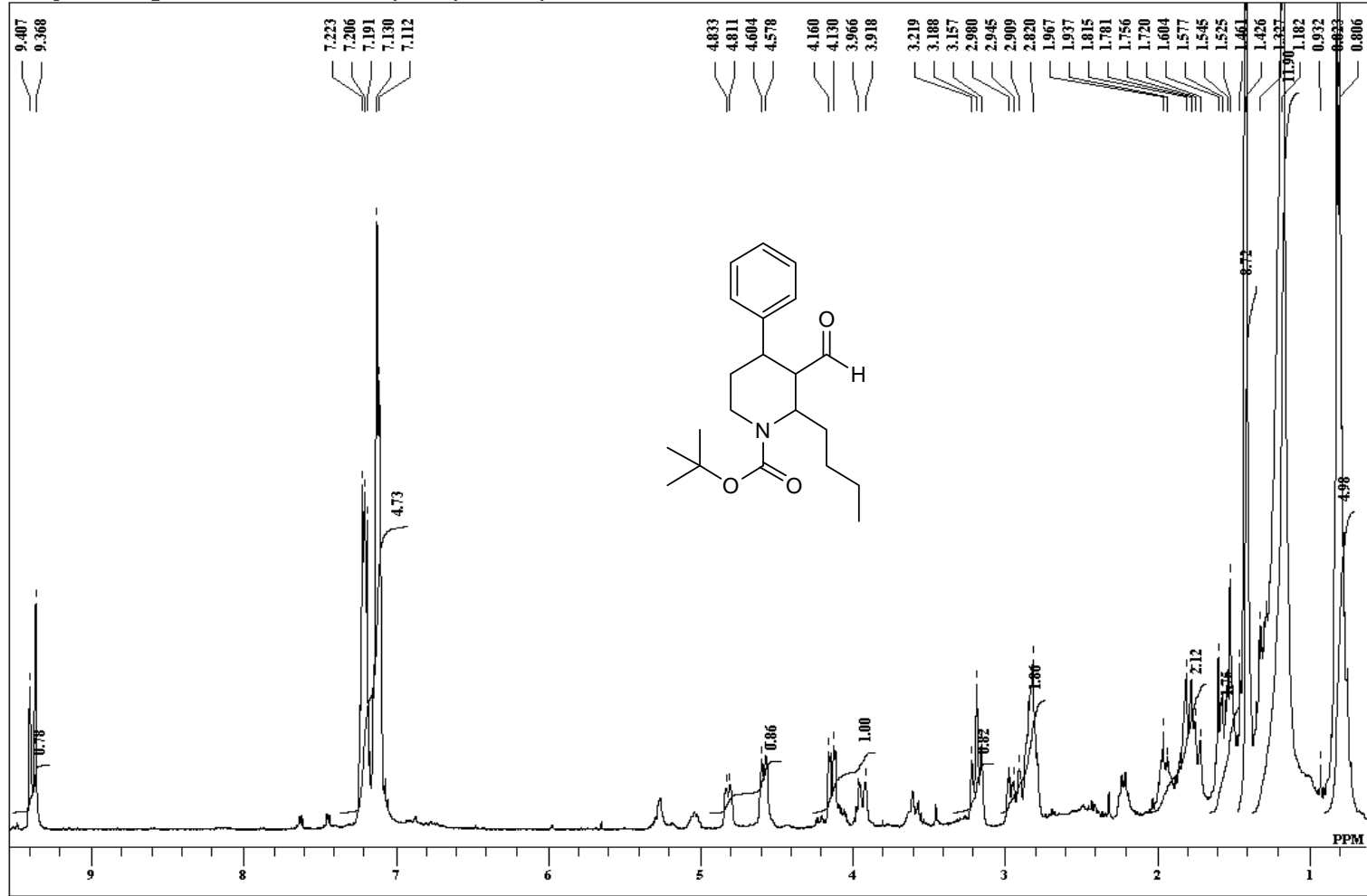
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeanhoo\FROM-ECA\yk73d-56-69-13C-5.als



DFILE yk73d-56-69-13C
COMNT single pulse dec
DATIM 28-06-2007 03:29
OBNUC 13C
EXMOD single_pulse_dec
OBFRQ 99.55 MHz
OBSET 5.13 KHz
OBFIN 0.98 Hz
POINT 32781
FREQU 31250.00 Hz
SCANS 2000
ACQTM 1.0486 sec
PD 2.0000 sec
PW1 2.92 usec
IRNUC 1H
CTEMP 23.0 c
SLVNT CDCL3
EXREF 77.00 ppm
BF 1.20 Hz
RGAIN 50

1H-yk92b-crude

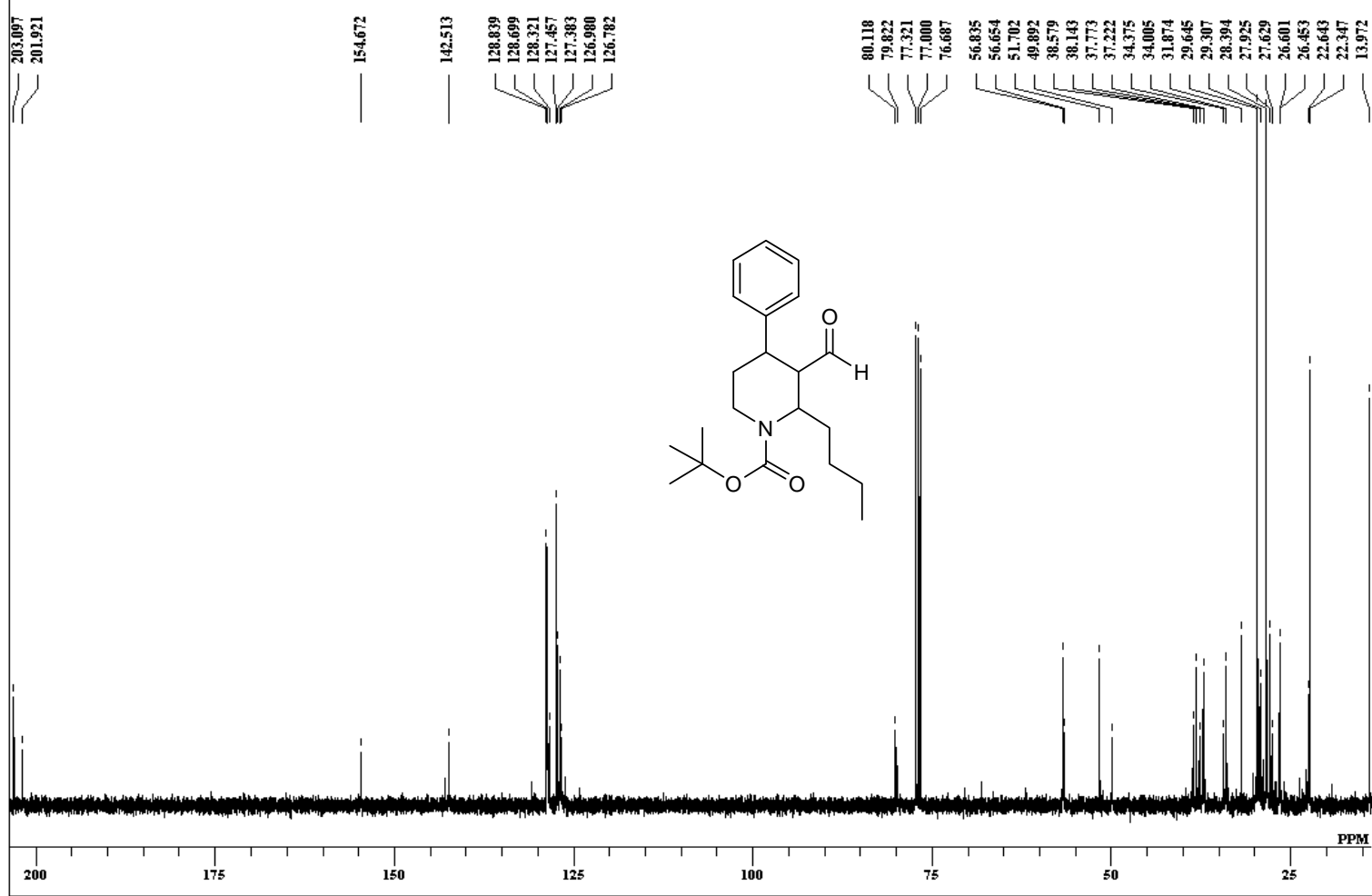
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeankeeyk92b-crude\yk92b-crude.als



DFILE yk92b-crude.als
COMNT 1H-yk92b-crude
DATIM Fri Jan 11 11:13:
IH
OBNUC non
EXMOD non
OBFRQ 399.65 MHz
OBSET 130.00 KHz
OBFIN 4300.00 Hz
POINT 32768
FREQU 7993.60 Hz
SCANS 8
ACQTM 4.0993 sec
PD 2.9007 sec
PW1 6.95 usec
IRNUC IH
CTEMP 22.7 c
SLVNT CDCL3
EXREF 0.00 ppm
BF 1.00 Hz
RGAIN 13

13C-yk92b-crude

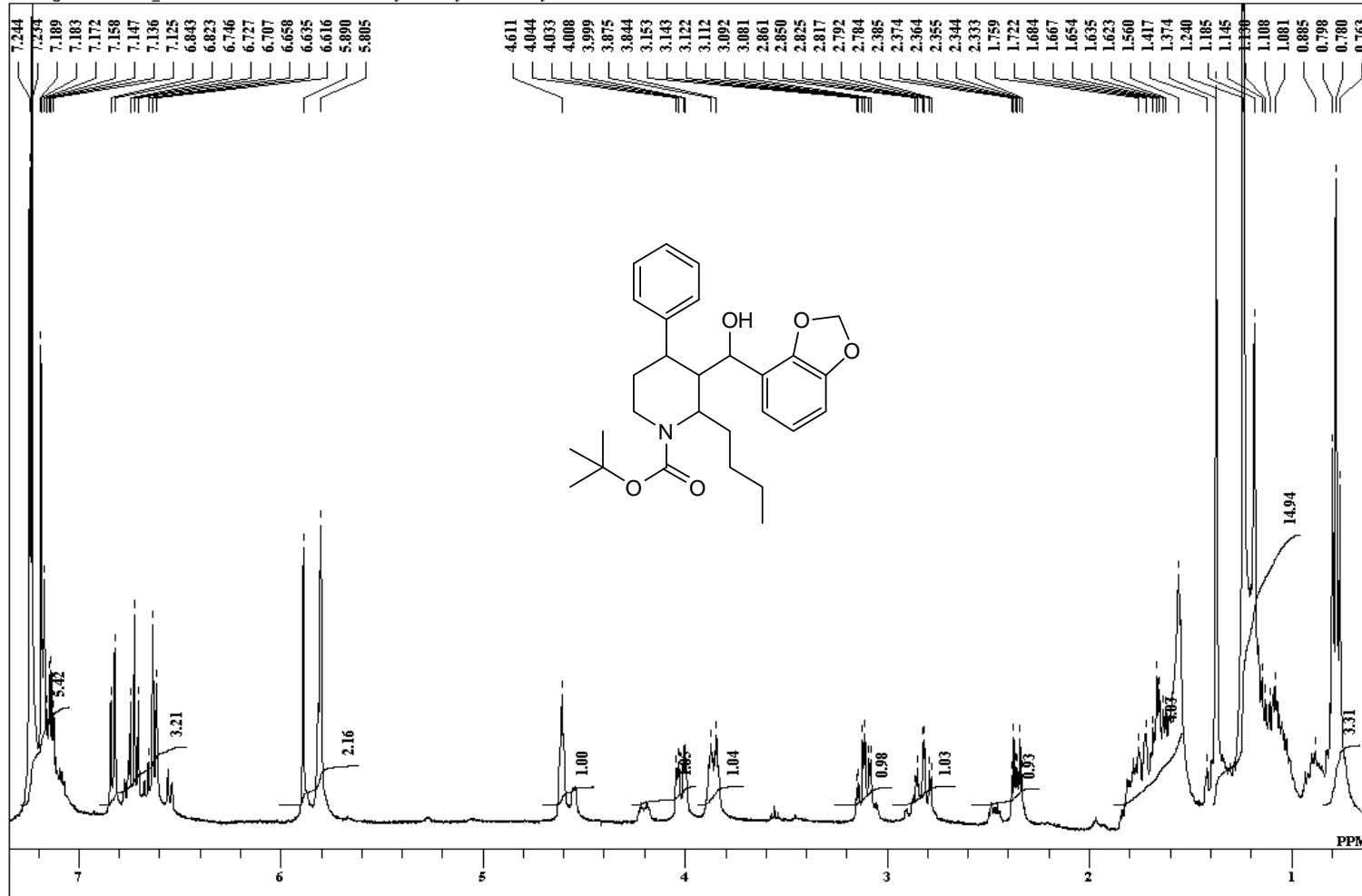
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeankeeyk92b-crude-13C\yk92b-crude-13C.nmdata



DFILE yk92b-crude-13C
COMNT 13C-yk92b-crude
DATIM Fri Jan 11 14:13:
OBNUC 13C
EXMOD bcm
OBFRQ 100.40 MHz
OBSET 130.00 KHz
OBFIN 5500.00 Hz
POINT 32768
FREQU 27100.27 Hz
SCANS 1442
ACQTM 1.2091 sec
PD 1.7909 sec
PW1 6.50 usec
IRNUC 1H
CTEMP 24.5 c
SLVNT CDCL3
XREF 77.00 ppm
BF 1.00 Hz
RGAIN 30

IH-yk94a-18-20

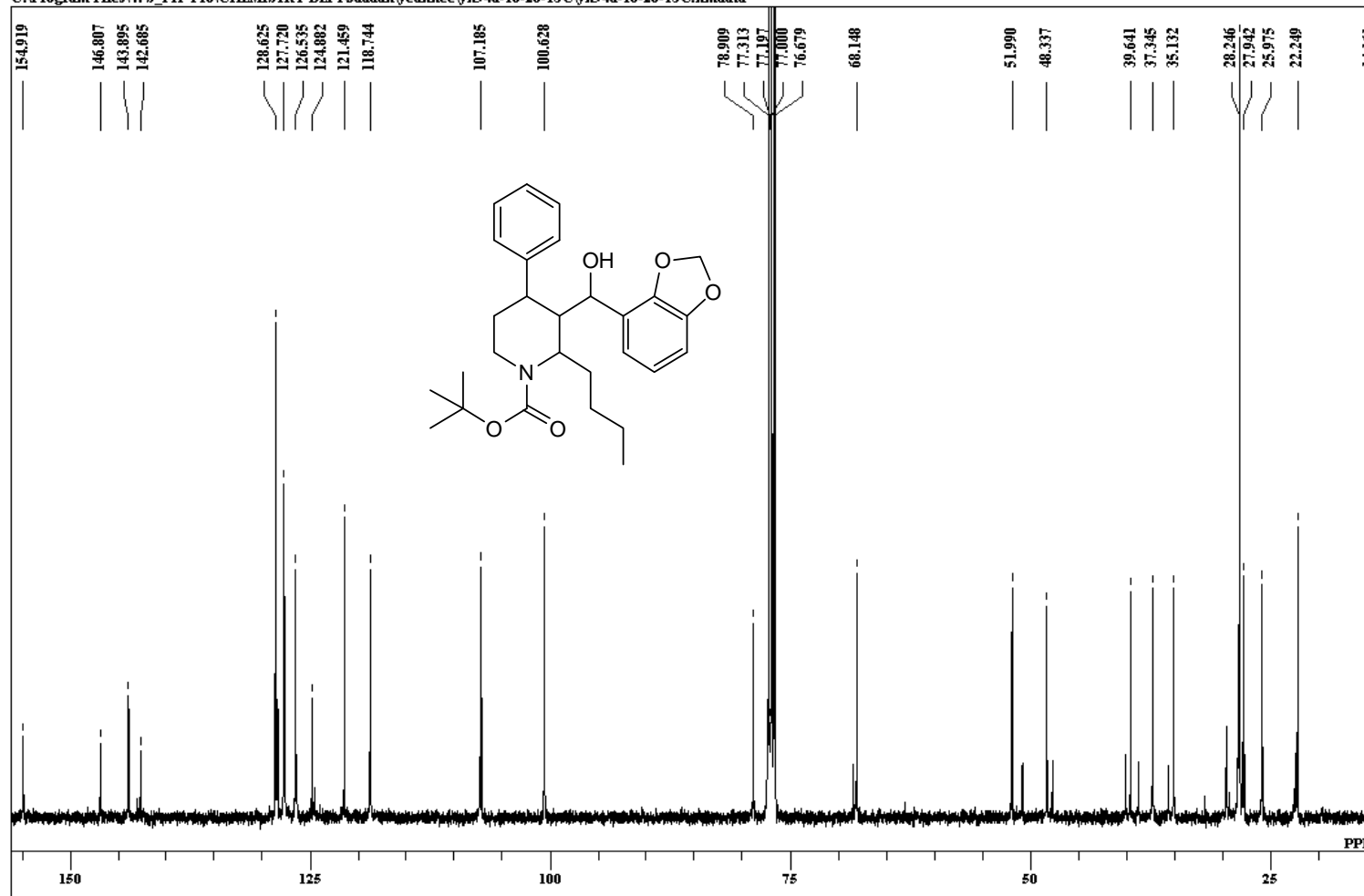
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DFILE	yk94a-18-20.als
COMNT	IH-yk94a-18-20
DATIM	Wed Jan 30 17:1
OBNUC	IH
EXMOD	non
OBFRQ	399.65 MHz
OBSET	130.00 KHz
OBFIN	4300.00 Hz
POINT	32768
FREQU	7993.60 Hz
SCANS	4
ACQTM	4.0993 sec
PD	2.9007 sec
PW1	6.95 usec
IRNUC	IH
CTEMP	23.9 c
SLVNT	CDCL3
EXREF	0.00 ppm
BF	1.00 Hz
RGAIN	18

13C-yl94a-18-20

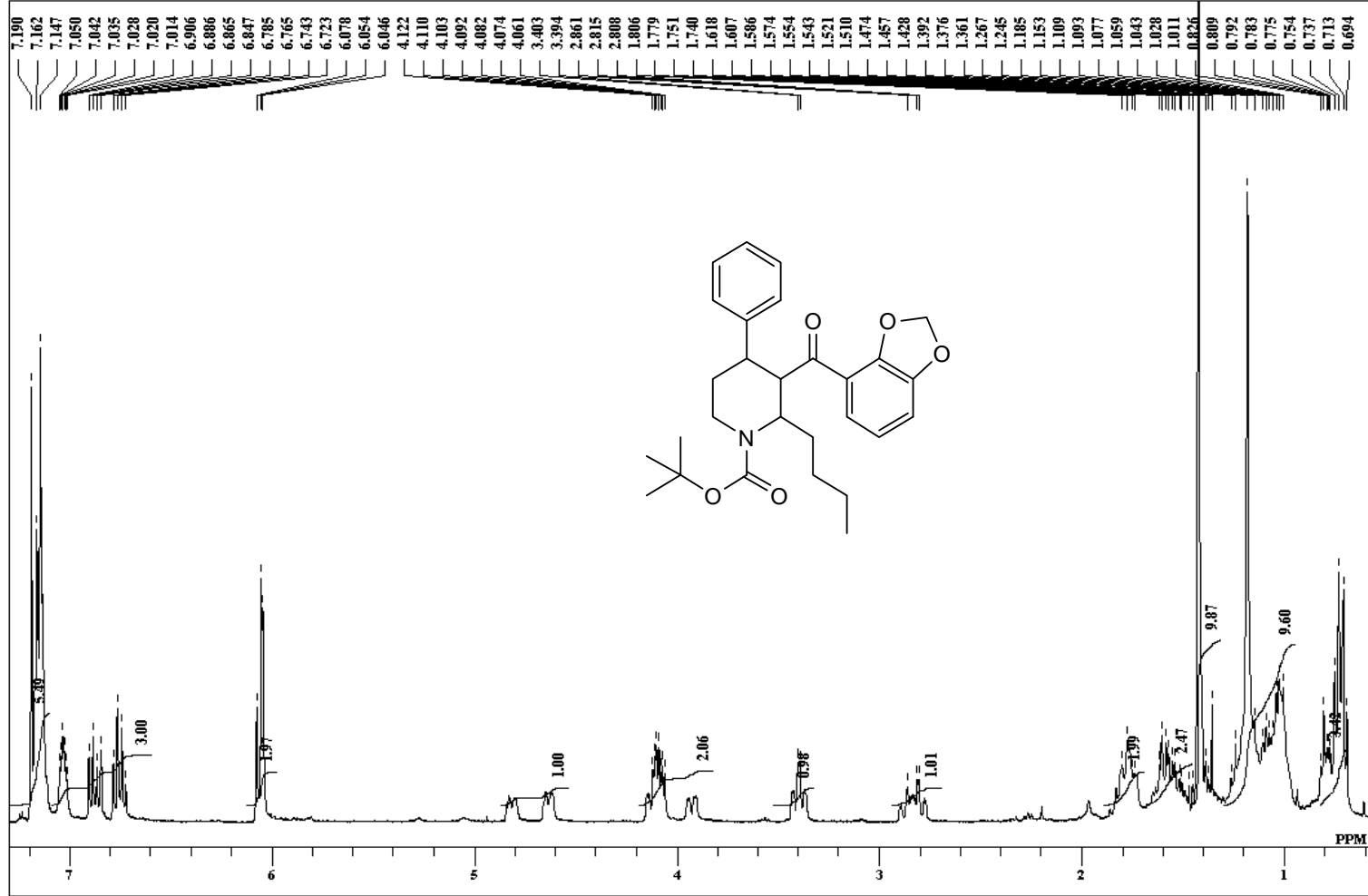
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeankeeyk94a-18-20-13C\yk94a-18-20-13C.nmdata



DFILE	yk94a-18-20-13C
COMNT	13C-yl94a-18-20
DATIM	Thu Jan 31 08:48
OBNUC	13C
EXMOD	bcm
OBFRQ	100.40 MHz
OBSET	130.00 KHz
OBFIN	5500.00 Hz
POINT	32768
FREQU	27100.27 Hz
SCANS	7000
ACQTM	1.2091 sec
PD	1.7909 sec
PW1	6.90 usec
IRNUC	1H
CTEMP	25.4 c
SLVNT	CDCL3
EXREF	77.00 ppm
BF	1.00 Hz
RGAIN	29

1H-yk96a-crude

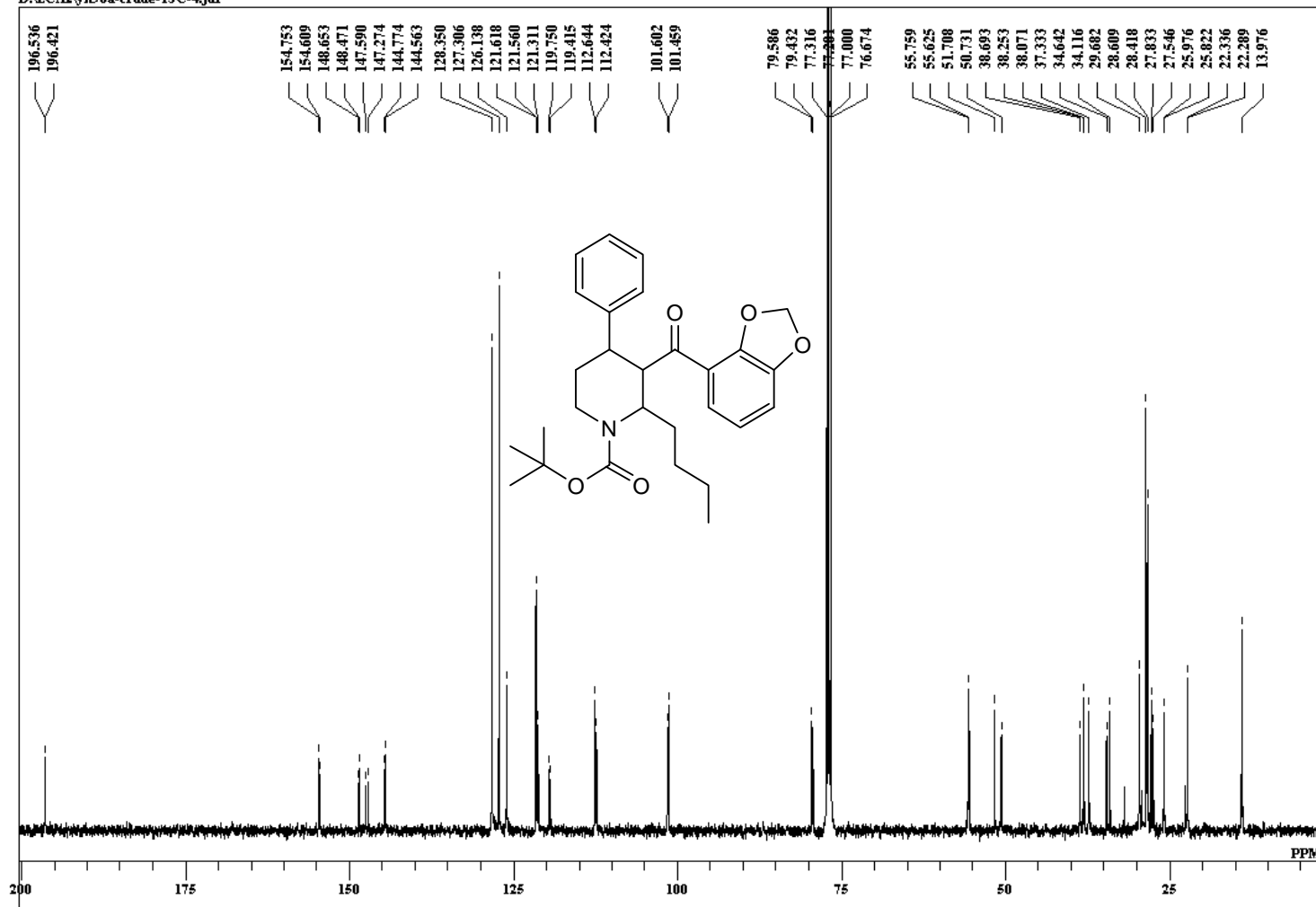
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeanhee\yk96a-crude\yk96a-crude.nmdata



DFILE yk96a-crude.nm
COMNT 1H-yk96a-crude
DATIM Fri Feb 22 10:43:
OBNUC 1H
EXMOD non
OBFRQ 399.65 MHz
OBSET 130.00 KHz
OBFIN 4300.00 Hz
POINT 32768
FREQU 7993.60 Hz
SCANS 8
ACQTM 4.0993 sec
PD 2.9007 sec
PW1 6.95 usec
IRNUC 1H
CTEMP 24.2 c
SLVNT CDCL3
EXREF 0.00 ppm
BF 1.20 Hz
RGAIN 18

single pulse decoupled gated NOE-yl96a-crude-13C

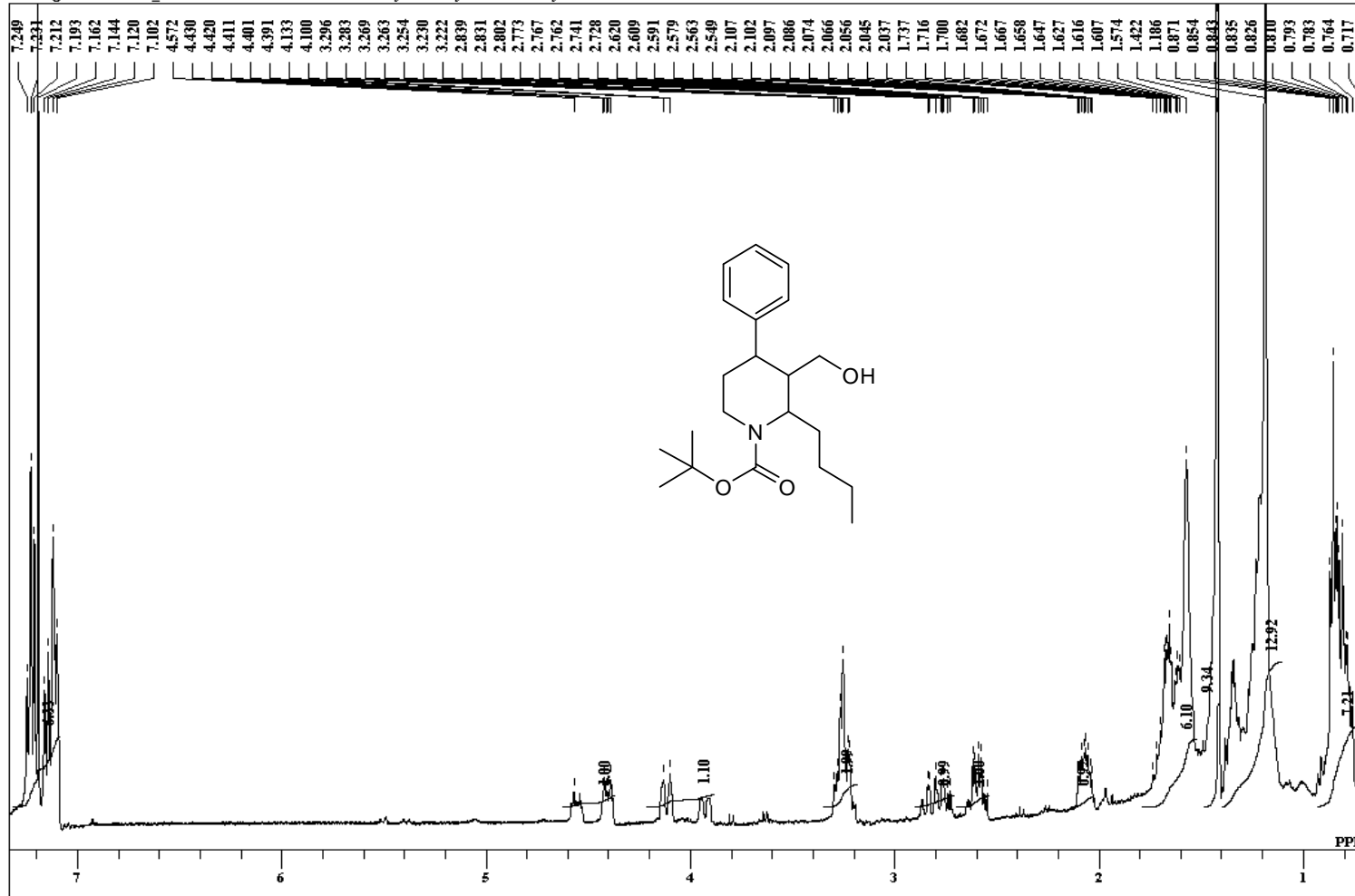
D:\ECA2\yl96a-crude-13C-4.jdf



DFILE yl96a-crude-13C
COMNT single pulse decc
DATIM 02-03-2008 04:08
OBNUC 13C
EXMOD single_pulse_de
OBFRQ 99.55 MHz
OBSET 5.13 KHz
OBFIN 0.98 Hz
POINT 32781
FREQU 31250.00 Hz
SCANS 5000
ACQIM 1.0486 sec
PD 2.0000 sec
PW1 3.07 usec
IRNUC 1H
CTEMP 21.0 c
SLVNT CDCL3
EXREF 77.00 ppm
BF 1.20 Hz
RGAIN 56

1H-yk97a-37-47-r

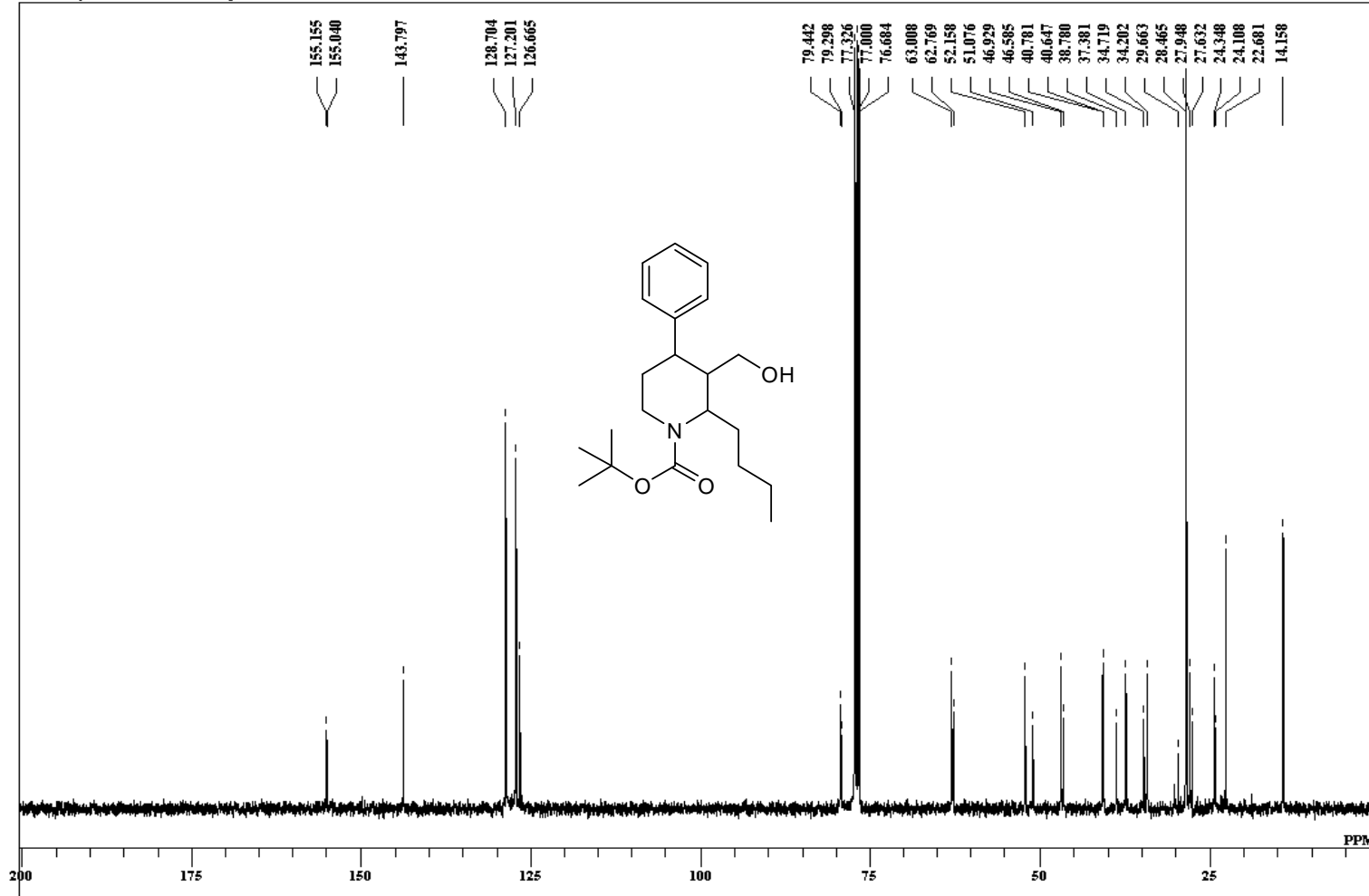
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\aadah\yeankeeyk97a-37-47-r\yk97a-37-47-r.nmdata



DFILE yk97a-37-47-r.nr
COMNT 1H-yk97a-37-47-
DATIM Fri Mar 14 10:59
OBNUC 1H
EXMOD non
OBFRQ 399.65 MHz
OBSET 130.00 KHz
OBFIN 4300.00 Hz
POINT 32768
FREQU 7993.60 Hz
SCANS 8
ACQTM 4.0993 sec
PD 2.9007 sec
PW1 6.95 usec
IRNUC 1H
CTEMP 23.1 c
SLVNT CDCL3
EXREF 0.00 ppm
BF 1.20 Hz
RGAIN 19

single pulse decoupled gated NOE-yl97b-crude-r3-13C

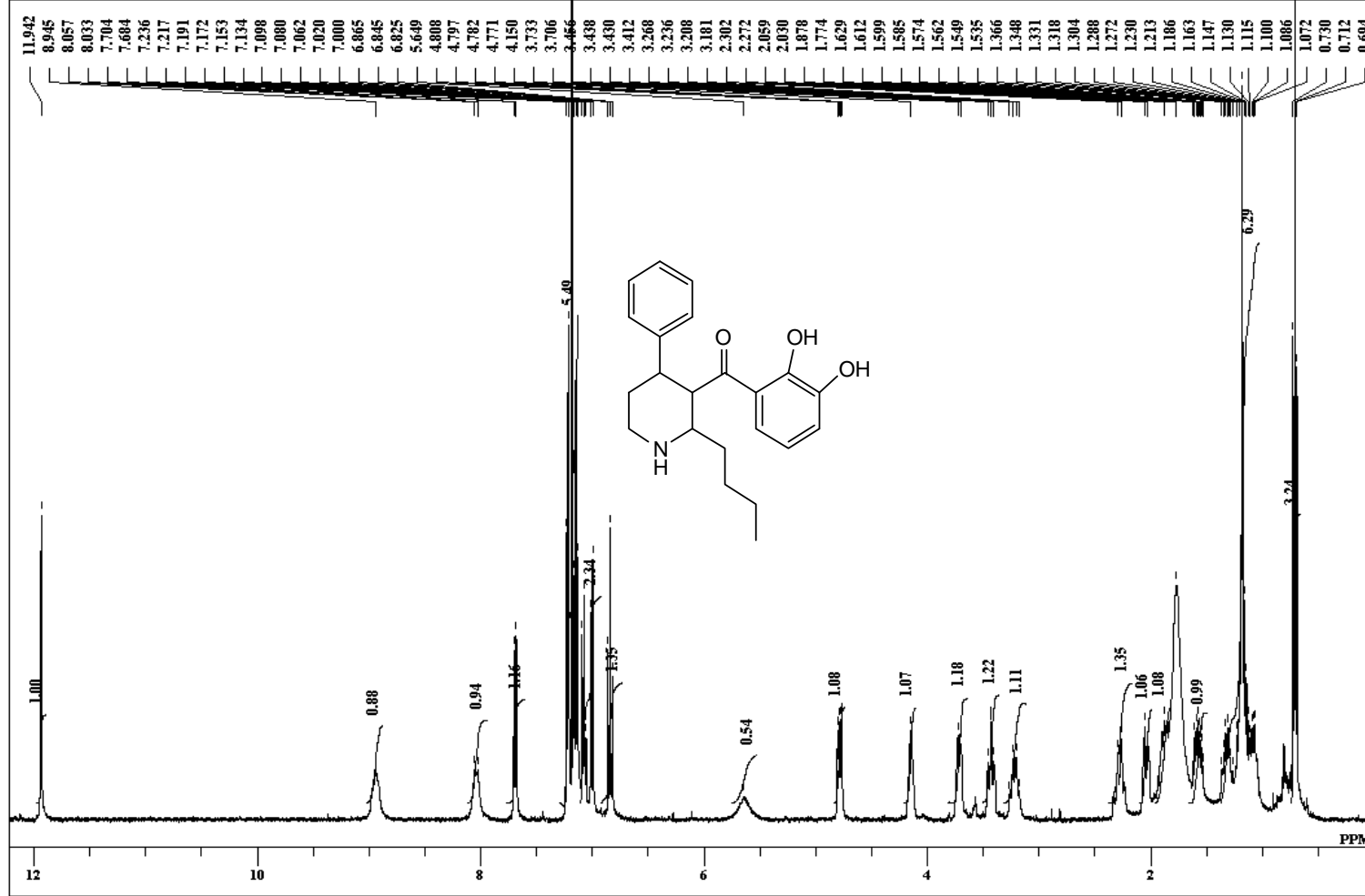
D:\ECA2\yl97b-crude-r3-13C-4.jdf



DFILE yl97b-crude-r3-1
COMNT single pulse dec
DATIM 18-03-2008 20:09
OBNUC 13C
EXMOD single_pulse_de
OBFRQ 99.55 MHz
OBSET 5.13 KHz
OBFIN 0.98 Hz
POINT 32781
FREQU 31250.00 Hz
SCANS 2000
ACQTM 1.0486 sec
PD 2.0000 sec
PW1 4.42 usec
IRNUC 1H
CTEMP 21.8 c
SLVNT CDCL3
EXREF 77.00 ppm
BF 1.20 Hz
RGAIN 54

1H-yk101

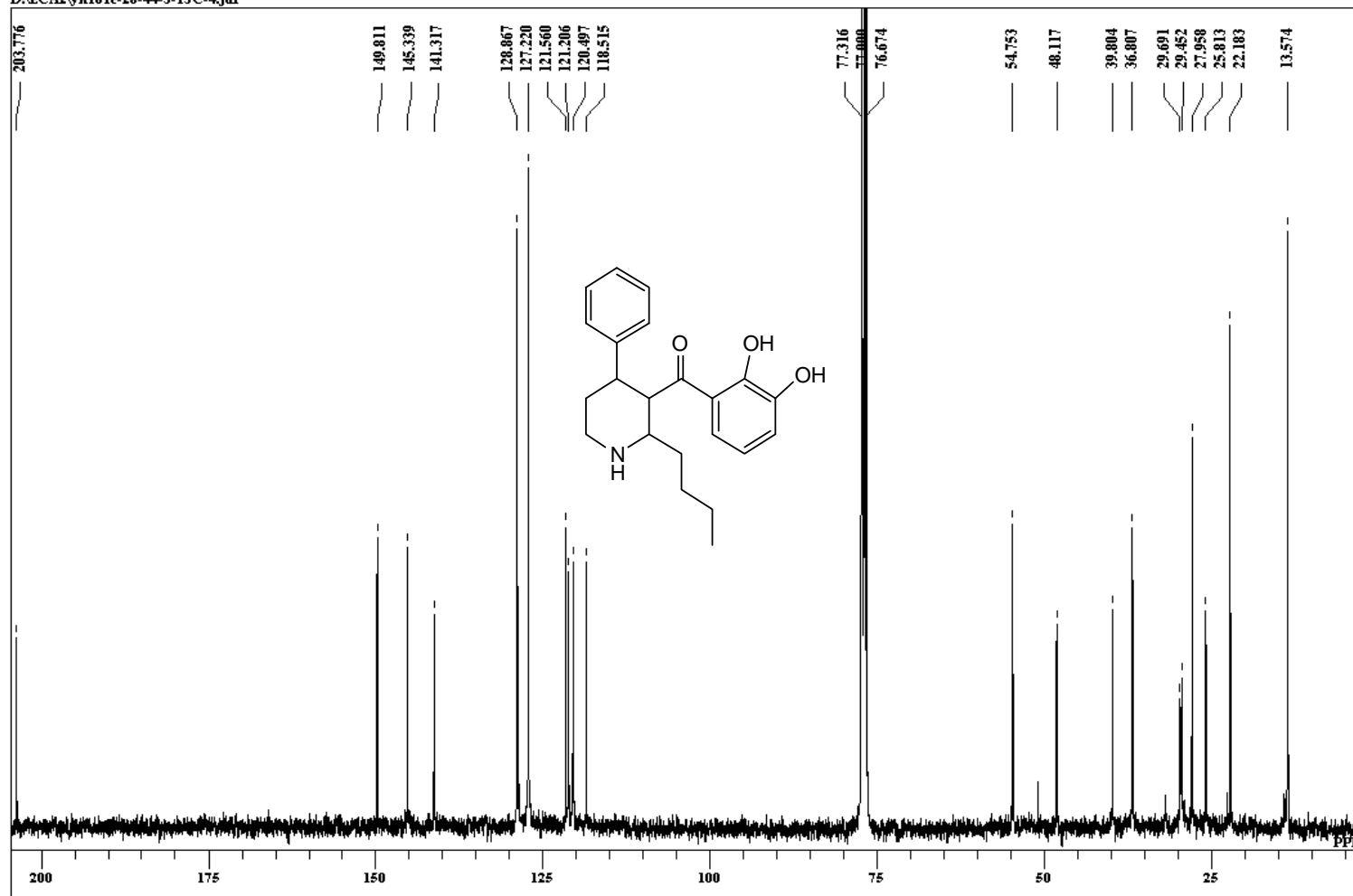
C:\Program Files\WS_FTP Pro\CHEMISTRY DEPT\saadah\yeankeeyk101\yk101.nmdata



DFILE yk101.nmdata
COMNT 1H-yk101
DATIM Mon Jun 16 15:3
OBNUC 1H
EXMOD non
OBFRQ 399.65 MHz
OBSET 130.00 KHz
OBFIN 4300.00 Hz
POINT 32768
FREQU 7993.60 Hz
SCANS 4
ACQTM 4.0993 sec
PD 1.0500 sec
PW1 13.00 usec
IRNUC 1H
CTEMP 30.0 c
SLVNT CDCL3
EXREF 0.00 ppm
BF 1.00 Hz
RGAIN 21

single pulse decoupled gated NOE-yk101c-28-44-3-13C

D:\ECA2\yk101c-28-44-3-13C-4.jdf



DFILE	yk101c-28-44-3-1
COMNT	single pulse dec
DATE	27-04-2008 02:23
OBNUC	13C
EXMOD	single_pulse_dec
OBFRQ	99.55 MHz
OBSET	5.13 KHz
OBFIN	0.98 Hz
POINT	32781
FREQU	31250.00 Hz
SCANS	10000
ACQTM	1.0486 sec
PD	2.0000 sec
PW1	3.07 usec
IRNUC	1H
CTEMP	20.1 c
SLVNT	CDCL3
EXREF	77.00 ppm
BF	1.00 Hz
RGAIN	60