coding sequence of Zymomonas mobilis QC (ZmQC) was cloned and expressed. The recombinant ZmQC shows QC activity and its 1.7Å resolution crystal structure confirmed its close relationship to the plant QC enzymes. The bacterial ZmQC protein exhibits a five β-propeller fold with a cation, presumably calcium, in its core. The β-propeller consists of a five-fold repetition of four stranded antiparallel β-sheets arranged around a central axis to form a central tunnel connecting both sides of the molecule. The propeller is stabilized through a ¨ Velcro ¨ motif that tethers the toroidal structure but lacks any disulfide bridges present in the related plant enzymes. The putative active center of ZmQC, occupied in the crystal by a glycerol molecule, is lined by the residues E46, E90, W104, W130, W175, N175 and K244. The three trytophans form a square pocket juxtaposed by the other catalytically relevant residues E46, E90 and K244.

Keywords: Alzheimer disease, bacterial glutaminyl cyclase, pyroglutamate

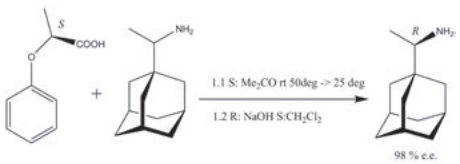
P05.02.01

Acta Cryst. (2008). A**64**, C380

Optical separation of rimantadine and *in silico* prediction of chiral selectivity of M2 protein

Isao Fujii[1], Taichi Akimoto[2], Tetsuro Watadani[2], Shigeki Nunomura[2], Yukio Takahashi[2]
[1]Tokai University, Department of Biological Sci. and Tech., Nishino 317, Numazu, Shizuoka, 410-0321, Japan, [2]Daito Chemical, Suka 2700, Hiratuka, Kanagawa, 254-0022 Japan, E-mail：fujii@wing.ncc.u-tokai.ac.jp

Racemic rimantadine possesses some N-methyl-D-aspartate (NMDA) antagonistic properties and is used as an antiparkinsonic drug. Rimantadine is also an orally administered antiviral drug used to treat and prevent influenza A infection. Genetic studies suggest that the virus M2 protein, a proton channel, plays an important role in the susceptibility of influenza A virus to inhibition by rimantadine. The production of chiral amines has great importance in the pharmaceutical industry, such as chiral switch. An aqueous solution of racemic compound and optically pure 2-phenoxypropionic acid [PPA] has been applied in the diastereomer salt separation.[1)] In this study, we focus on synthesis of chiral rimantadine, and clarify the inherent structures of R-rimantadine HCl and its diastereomer salt with R-PPA by X-ray analysis. From in silico prediction study of the enantiomers, it reveals that R-rimantadine has the higher inhibition activity of M2 protein than S-rimantadine and its derivative, adamantadine.



1) T Watadani, S Nunomura, Y. Takahashi and I Fujii, Jpn. Kokai Tokkyo Koho, 2008024666.

Keywords: molecular mechanics dynamics, chiral drugs, single-crystal X-ray analysis

P05.03.02

Acta Cryst. (2008). A**64**, C380

Validation of charge density refinements and application to molecules of biological interest

Julian J. Holstein[1], Peter Luger[2], Carsten Paulmann[3], Birger Dittrich[4]
[1]Georg-August-University, Inorganic Chemistry, jholste@gwdg.de, Goettingen, Niedersachsen, 37073, Germany, [2]Georg-August-University, Tammanstr.4, 37073 Goettingen, Germany, [3]Free University, Fabeckstr. 36a, 14195 Berlin, Germany, [4]DESY/HASYLAB, Notkestr. 85, 22607 Hamburg, Germany, E-mail：jholste@gwdg.de

The electronic properties of the macrolide antibiotic roxithromycin (1) that interacts with the nucleotides of the peptidyl transferase cavity of the bacterial ribosome [1] are investigated. A high resolution dataset of (1) was collected with synchrotron radiation. The experimental charge density was determined by least-squares refinements (program XD [2]) using the rigid pseudoatom formalism of Hansen and Coppens [3]. The multipole model was based on one generated by the program INVARIOMTOOL [5]. Differences between experimental- and invariom model [4] electron density were calculated on a grid. The refined multipole parameters model the electron density in the crystal (including packing effects and hydrogen bonding), but can also model disorder. (1) provides a good example that minor disorder can easily escape the attention of the examiner. However, slight differences in the electronic density tend to result in pronounced differences in the electrostatic potential. Since we hope to shed light on biological function of the molecule on the electronic level, the calculated difference density is used to validate the experimental charge density. A closely related problem in charge density refinements is over-parametrisation, which can be indicated by RFree. Results for both validation procedures are reported.

[1] F. Schluenzen, R. Zarivach, J. Harms, A. Bashan, A. Tocilj, R. Albrecht, A. Yonath, F. Franceschi, Nature, 2001, 413, 814-821.
[2] XD2006, A. Volkov, P. Macchi, L. J. Farrugia, C. Gatti, P. Mallinson, T. Richter, T. Koritsanszky, 2006.
[3] N. K. Hansen, P. Coppens, Acta Cryst. A, 1978, 34, 909-921.
[4] B. Dittrich, T. Koritsanszky, P. Luger, Angew. Chem., 2004, 116, 2773-2776.
[5] C. B. Huebschle, P. Luger, B. Dittrich, J. Appl. Cryst., 2007, 40, 623-627.

Keywords: charge density analysis, electrostatic properties, disorder

P05.03.03

Acta Cryst. (2008). A**64**, C380–381

High-pressure crystallisation of antibiotic molecules

Francesca P. A. Fabbiani, Heidrun Sowa, Werner F Kuhs
Universitaet Goettingen, GZG, Abteilung Kristallographie, Goldschmidtstr. 1, Goettingen, Niedersachsen, 37077, Germany, E-mail：ffabbia@gwdg.de

The application of high pressure is a powerful method for exploring the polymorphic behaviour of simple molecular compounds.[1, 2] Direct compression of either single crystals or powders, and crystal growth from the melt are two methods that have been successfully used to prepare new polymorphs.[3] The recent development of the experimental technique for in situ high-pressure growth of single crystals from solution has allowed a wider range of compounds to be studied including small-molecule pharmaceuticals and energetic materials, and has enabled the preparation of new solvates and hydrates.[2] We have tested and extended the technique to the study of larger, more complex compounds of biological importance, namely antibiotics, with chemical formulae comprising more than 15 non-H atoms. Materials crystallised in the 0.1 - 2.0 GPa pressure range have been identified and characterised by in situ X-ray diffraction. Monitoring and understanding the effects of pressure on antibiotics is an important step towards understanding the phenomenon of polymorphism in terms of observed and favourable intermolecular