Paper

Retinal Location and Structure in Squid Rhodopsin

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Abstract: In order to understand retinal we calculated the dihedral angles around carbon axis ^{10}C–^{12}C, since two different carbon sequences ^{9}C–^{10}C–^{11}C–^{12}C and ^{10}C–^{11}C–^{12}C–^{13}C exist. We also calculated the distances between two specified carbon pairs. Those results are tabulated. Photon absorption changes the conformation of retinal conformation. This fact is confirmed from dihedral angle changes and distance changes of targeted of retinal carbon atomsa. These matters are discussed in the present paper.

1. Introduction

We have been studying squid rhodopsin. In particular we have concentrated on understanding the conformation of retinal in squid rhodopsin. We have used the PDB identification codes 2Z73, 2ZIY, 3AYM, and 3AYN found in the RCSB protein data bank (URL, www.rcsb.org/pdb/).

Squid retinal consist of twenty carbons (^{1}C– ^{20}C) as shown in Fig. 1 [1]. The squid retinal has the hexa-ring [1] that interacts with ring parts of amino acid residues (phenylalanine : Phe and tryptophan: Trp) in rhodopsin chain A, while the long chain residues of amino acids (arginine: Arg and isoleucine: Ile) are in chain B [2, 3].

The nearest atom contact of retinal to the atoms of the rhodopsin molecules was tabulated [2]. The retinal area in a rhodopsin molecule is estimated in an obscure way. The considered results are shown in references 2 and 3. Our investigations employed viewing procedures created RasMol or RasWin software. The resulting viewings yielded intuitive scope, but those pictures are not quantitative ones [1, 2, 3]. The wave–length of light absorbed is determined by which side of carbon is changed between cis–conformation and trans–conformation [4, 5, 6]. The utilized PDB data denote citations [7, 8, 9].

In section 2, we considered the retinal location within squid rhodopsin to look at what every retinal carbon is contacting with respect to the nearest atom of residue of the amino acids in squid

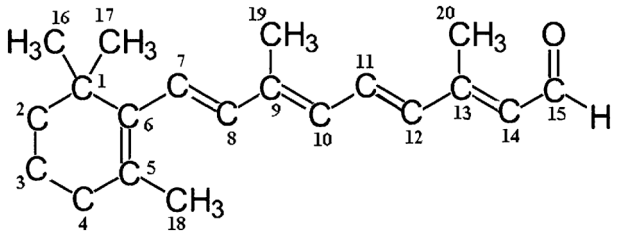

Fig. 1 Carbon numbering of retina

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rhodopsin. Those facts can be seen from the references [2, 3], where we calculated the distances between the retinal carbon and atoms in the amino acid residues of squid rhodopsin.

In squid retinal, carbon eleven (^{11}C) has the advantage for conformation change. Thus we have here calculated the dihedral angle around carbon pair axis ^{10}C–^{12}C. Dihedral angles less than π radians imply that the triangle plane including ^{11}C is located on the upper side with respect to the other triangle plane. On the other hand, dihedral angles over π radian denote that the triangle plane including 11C is located on the lower side with respect to the other triangle plane. Therefore the dihedral angle around ^{10}C–^{12}C line indicates whether the location of carbon ^{11}C is upper or lower. There exist two kinds of the carbon axes for ^{10}C to ^{12}C, namely, the carbon sequences ^{9}C–^{10}C–^{11}C–^{12}C and ^{10}C–^{11}C–^{12}C–^{13}C. We therefore give two dihedral angles for chain A or chain B of the PDB identification of squid rhodopsin. We also calculated carbon pairs to look at the cases of retinal taking the cis- or trans-conformation. If the retinal takes the trans–conformation, the distance between ^{9}C and ^{13}C becomes longer than the distance is given by the cis-conformation.

Section 4 is devoted to ''Discussion'', where we consider what conformation changes occur in squid retinal within squid rhodopsin.

2. Contact residues of rhodopsin for each carbon of retinal

We have reported the contact atoms of the amino acid residues of squid rhodopsin to each retinal carbon [2]. The relevant contact amino acid residues are 112–120, 187–209, 274, and 305 for chain A, and 69, 70, 129–133, 187, 259–274, 305, and 319 for chain B [2]. We placed the data for those retinal twenty carbons for those amino acid residues in name.pdb files. We used RasMol software, to create the ball and stick representation of Fig. 2. The below figure is an example chain A and chain B using PDB 2Z73.

As seen from Fig. 2, It is difficult to image the retinal and amino acid residues of rhodopsin.

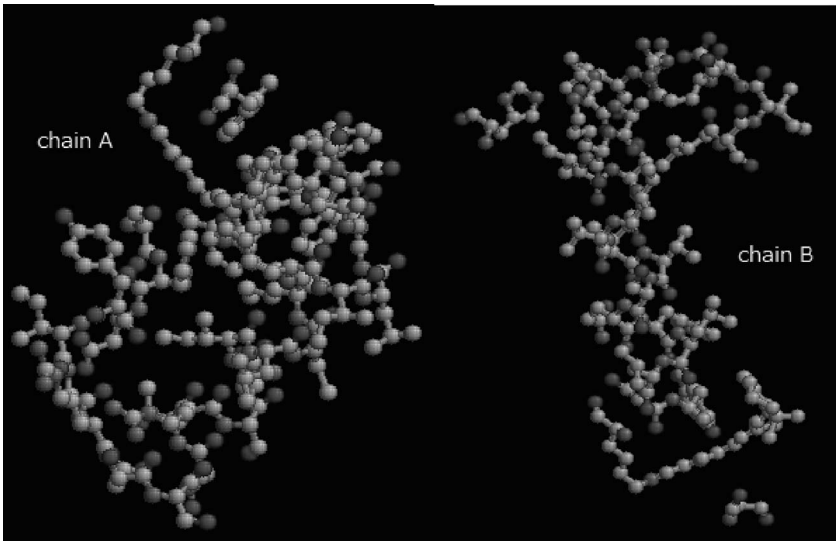

Fig. 2 Ball and stick pictures for chain A and chain B of rhodopsin data from PDB 2Z73

We therefore searched for the nearest atom of amino acid residues to each carbon of squid retinal [2, 7]. Thus we know that the above amino acid residues of rhodopsin should be included with squid retinal to draw figures. We actually calculated the real distances to find what atoms of the amino acid residues contact each retinal carbon. We also quantified the mobility of ^{11}C of retinal. We therefore now calculate the dihedral angles and distances between specified pairs of carbons.

3. Dihedral angles around axis ^{10}C–^{12}C and distances of carbon pairs

We calculated the dihedral angles around the carbon axis that consisted of the carbon pair ^{10}C and ^{12}C. There are two kinds of dihedral angles for the same carbon pair using the two amino acid sequences ^{9}C–^{10}C–^{11}C–^{12}C and ^{10}C–^{11}C–^{12}C–^{13}C. We refer to this dihedral angle as $\theta(^{10}C-^{12}C)$. One can see the relevant two triangle-planes from Fig. 3. We therefore use these two carbon sequences (^{9}C–^{10}C–^{11}C–^{12}C and ^{10}C–^{11}C–^{12}C–^{13}C).

The dihedral angles around carbon axis 10C–12C we are calculated using following formula.

$$\theta(^{10}C-^{12}C)=\frac{(\overrightarrow{^{10}C^{9}C}\times\overrightarrow{^{10}C^{12}C})\cdot(\overrightarrow{^{11}C^{10}C}\times\overrightarrow{^{11}C^{12}C})}{|\overrightarrow{^{10}C^{9}C}\times\overrightarrow{^{10}C^{12}C}|\,|\overrightarrow{^{11}C^{10}C}\times\overrightarrow{^{11}C^{12}C}|}$$

$$\theta(^{10}C-^{12}C)=\frac{(\overrightarrow{^{11}C^{12}C}\times\overrightarrow{^{11}C^{10}C})\cdot(\overrightarrow{^{13}C^{12}C}\times\overrightarrow{^{13}C^{10}C})}{|\overrightarrow{^{11}C^{12}C}\times\overrightarrow{^{11}C^{10}C}|\,|\overrightarrow{^{13}C^{12}C}\times\overrightarrow{^{13}C^{10}C}|}$$

Were the vector denotes $\overrightarrow{^{i}C^{j}C}=(^{j}C_x-{}^{i}C_x,\ ^{j}C_y-{}^{i}C_y,\ ^{j}C_z-{}^{i}C_z)$ and $\times$ indicates the vector product. The dihedral angles calculated are tabulated in Table I. In Table I, values of dihedral angles have radian units, i.e., π is 3.14159265... and it is obvious that unit circle has the length 2π radian.

If two vectors cross orthogonally, the dihedral angle is $\pi/2$ or $3\pi/2$ radian. In the case of the two triangle planes coexisting on a plane, the dihedral angle is π radian, in other words, the two triangle planes are opened on a flat plane. If dihedral angle is zero radian, the two triangle planes take a closed form. We can read Table I from these viewpoints. We can give a discussion in the next section about the obtained dihedral angles.

We tabulate distances between specified carbon pairs of squid retinal to consider the movement of carbon ^{11}C. Quite small deviations were found in carbon pair ^{9}C–^{13}C. Large distance changes were found in carbon pair ^{20}C–^{18}C. Electron movement is the order of 0.1 nm so that 0.4

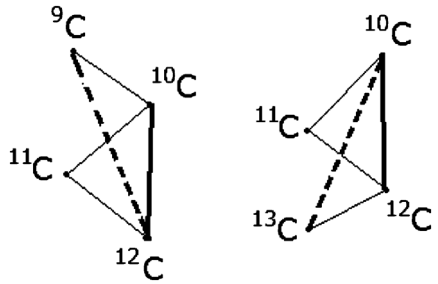

Fig. 3 Two carbon sequences (^{9}C–^{10}C–^{11}C–^{12}C and ^{10}C–^{11}C–^{12}C–^{13}C) of squid retinal

Table I Dihedral angles for chain A and chain B of the PDB data

PDB id	^{9}C–^{10}C–^{11}C–^{12}C		^{10}C–^{11}C–^{12}C–^{13}C	
	chain A	chain B	chain A	chain B
2Z73	3.139705	3.099925	2.919768	2.427132
2ZIY	3.038743	—	2.882382	—
3AYM	2.59887	2.409588	1.222221	1.042949
3AYN	3.019744	3.002237	0.710811	0.126709

Table II Calculated distances for specified carbon pairs to look at the movement of ^{11}C

Distances for paired carbons	2Z73 cahin A	2Z73 cahin B	2ZIY cahin A	3AYM cahin A	3AYM cahin B	3AYN cahin A	3AYN cahin B
^{9}C–^{13}C	4.666776	4.667803	4.609363	4.942753	4.795278	4.935296	4.973205
^{9}C–^{20}C	4.392748	4.37294	4.396047	5.338241	4.969198	5.152009	5.200158
^{19}C–^{20}C	5.713856	5.699356	5.624375	5.655004	4.99673	6.625895	6.672787
^{19}C–^{13}C	5.72009	5.735514	5.541339	5.620504	5.261216	6.273443	6.309689
^{20}C–^{18}C	6.775899	6.821912	4.887197	9.31865	8.78693	6.396053	6.70284

nm is a relatively long distance. The average distance of alpha-carbons of the amino acid residues is 0.38 nm. The distance change can encompass bond rotation or carbon movement.

4. Discussion

Here we discuss the results of Table I and Table II, in particular we can discuss dihedral angle changes and distance changes of carbon pairs. The unit of Table II is Å since location atom is denoted by Å unit.

For Table I, Dihedral angles have values near π except for the 3AYM PDB data for the carbon sequence ^{9}C–^{10}C–^{11}C–^{12}C. This means that for this case the two triangle planes have an open shape. Thus, this means ^{11}C is located on an expand plane. The PDB data 3AYM for this sequence takes a little bit closed but still open shape for both chains. In 3AYM, chain A of the carbon sequence ^{10}C–^{11}C–^{12}C–^{13}C takes a value near $\pi/2 = 1.5707\ldots$ so that the two triangle planes are almost orthogonal to each other. In the chain B of 3AYN the value of the dihedral angle is near 0.127. This might indicate a closed shape for the two triangle planes, namely it is expected that conformation change has occurred from trans to cis. This implies that the distance between ^{20}C and ^{18}C has become shorter. This fact can be seen from Table II.

We can estimate distance changes of the carbon pairs. Large distance change implies rotation of the bond. With the rotation of the bond, the distance between carbon pairs becomes shorter or longer. If the retinal takes the trans-conformation, the distance between carbon pairs becomes longer. As seen from Table II, big changes can be seen at carbon pair ^{20}C–^{18}C. In this sense, the PDB data 3AYM takes the trans-conformation, namely a wavy line of carbons within the sequence ^{9}C–^{10}C–^{11}C–^{12}C–^{13}C is expected. The shape can be visualized using RasMol pictures, and the expectation can be seen. In comparing the distances for carbon pair ^{20}C–^{18}C, big distance changes ap-

peared. Thus we can conclude that rotation of the bonds ^{10}C–^{11}C or ^{11}C–^{12}C should have occurred. In other words, cis and trans conformation change occurrs by this rotation of the bond. Light absorption should have occurred creating the retinal change of conformation [4–9].

References

[1] Y. Nagai, K. Kito, H. Kagawa, T. Maddess, A quantum chemistry of retinal of squid rhodopsin, *Mem. Kokushikan U Cent. Inf. Sci.* **32** (2011) 20–31.

[2] Y. Nagai, K. Kito, T. Maddess, Spacing between retinal and amino acid residues in squid rhodopsin, *Mem. Kokushikan U Cent. Inf. Sci.* **33** (2012) 1–7.

[3] Y. Nagai, K. Kito, T. Maddess, Atomic configuration around retinal in squid rhodopsin, *Mem. Kokushikan U Cent. Inf. Sci.* **34** (2013) 1–8.

[4] O. P. Ernst* and F. J. Bartl, Active States of Rhodopsin, *Chem. Bio. Chem.* **3** (2002) 968–974.

[5] M. V. Altaisky, V. N. Gorbachev, and F. Pichierri, Coherent Signal Amplification in Rhodopsin Media, *Physics of Particles and Nuclei Letters*, **4** (2007) 150–153.

[6] W. D. Hoff, K. H.H. Jung, and J. L. Spudich, Molecular mechanism of photosignaling by archaeal sensory rhodopsins, *Annu. Rev. Biophys. Biomol. Struct.* **26** (1997) 223–258.

[7] M. Murakami, T. Kouyama, Crystal structure of squid rhodopsin, *Nature* **453** (2008) 363–367.

[8] M. Miyano, T. Shimamura, Crystal structure of squid rhodopsin with intracellularly extended cytoplasmic region, *J. Biol. Chem.* **283** (2008) 17753–17756.

[9] M. Murakami, T. Kouyama, Crystallographic Analysis of the Primary Photochemical Reaction of Squid Rhodopsin, *J. Mol. Biol.* **413** (2011) 615–627.