Paper

Estimation for Energy Transformation from Retinal to Rhodopsin in Squid

Yoshinori NAGAI[1], Masashi KITO[1], and Ted MADDESS[2]

(Received 5 January 2016, revised 15 January 2016)

Abstract: Squid retinal will yield energy during the conformational change from the 11-cis-retinal to all-trans-retinal. The retinal that we investigate here, 4WW3, accepts light near 500 nm. Using the Planck-Einstein relationship $E=hv$, the absorption energy is about 4×10^{-19} J. The identification in the Protein Data Bank (PDB) of 4WW3 is appeared in the last year. The analyses of 4WW3 here are the same as our previous analysis for 2Z73, 2ZIY, 3AYM, and 3AYN.

Key words: photon absorption energy, chemical bond, contacted residues, chemical reaction

1. Introduction

We examined the crystal structure of squid rhodopsin in the lumi-intermediate state, referred to as PDB id 4WW3. We analyzed this data found no major difference compared to our previous PDB data for 2Z73, 2ZIY, 3AYM, and 3AYN [1,2,3]. Following the TABLE I of reference [4], PDB id 2Z73 and 2ZIY attach 11-cis-retinal. This means retinal gives its absorbed photon energy by the conformation change of 11-cis-retinal to all-trans-retinal. This implies that photochemical energy is transmitted to the residues of rhodopsin, namely to the nearest atom composed the side group of the amino acid. This point is considered in section 2. We show Tables for the contact atoms of the amino acid residues of squid rhodopsin to the retinal carbons (C1 to C20). The conformation change from 11-cis-retinal to all-trans-retinal can be understood [4]. In chain A, rings contact with retinal carbons, while the long side chain for the amino acid arginine is observed in chain B [2]. We recognize the distances of second atoms of rhodopsin residues are shorter than the first for retinal carbons C10 and C11. The other distances are longer than those of first atoms. These facts are summarized in section 2.

Photo-chemical energy transformation is a rapid conformation change around a time of 330 fs, in other words, it is the sub-picosecond order [5]. Thus the excitation period is in the order of sub-picoseconds ($<$ps), in other words the process time order smaller than 10^{-12} seconds [5]. The wavelength of the absorbed photon is around 500 nm [5]. This gives rough estimation of absorbed energy and discussed in the section 3. The absorption energy is much smaller than with the covalent bond energy in organic chemistry. The estimated absorption energy by retinal is discussed in section 4.

[1] Faculty of Business, Kokushikan University, 4–28–1 Setagaya, Tokyo 154–8515, Japan.
[2] Eccels Institute for Neuroscience, John Curtin School of Medical Research, Australian National University, Canberra 2601, Australia.

2. Atoms around the retinal in squid rhodopsin

We used our established program to find the proximal atoms of each carbon of the squid retinal. As a result we know that the proximal atoms of each retinal carbon are the same as previous retinal as we reported for 2Z73, 2ZIY, 3AYM, and 3AYN. The proximal atoms of retinal carbons are tabulated in Table I for chain A of 4WW3 and Table II for the chain B of 4WW3. PDB id 4WW3 is the new found squid rhodopsin. One can see a similar table for 2Z73 in the reference [2].

Here we concentrate on retinal carbons C10 and C11 because of retinal takes 11-cis-conformation [5]. As seen tables we can see that that C10 and C11 have much more space compared to other retinal carbons. The spacing is also different between retinal of chain A and that of chain B. The retinal carbons of chain A have the space of over 3 angstroms while C10 has a spacing near 3.5 angstroms relative to chain B. PDB id 4WW3 includes the lumi-intermediate retinal, in other words 11-cis-retinal. In that sense we examine the contact atom of the rhodopsin residue to retinal carbons C10 and C11. We noted that the spacing between C10 and the atoms of the rhodopsin residues is relatively different. The spacing between C11 and atom rhodopsin residues is not so far since there can be observed much longer distances to the atoms of the rhodopsin residues. As mentioned in our previous work [2], the retinal of chain A contacts with the rings of residues of the amino acids phenylalanine or tryptophan. In the chain B, the side chains of arginine or aspartic acid contact to retinal carbons. The chemical energy transport occurs at the conformation change of 11-cis-retinal to all-trans-retinal. The conformation change requires more space. Thus, we understand that retinal carbon C10 has relatively large volume available for conformational change that occurs by rotation of retinal carbons.

We note again that amino acid residues around the retinal are: in chain A; phenylalanine (120, 188, 205, 209), tryptophan (274), cysteine (186), serine (187), lysine (305), and in chain B; arginine (133).isoleucine (129), alanine (69), asparagine (70), aspartic acid (132), histidine (319), lysine (305). We know ^{305}Lys is the same in chain A and chain B, but that otherwise the other residues are different to each other in chain A and B. The distance for C10-Trp274 is 3.743 angstroms, and that for C11-Ser187 is 3.422 angstroms in chain A. For chain B, the distances are 3.476 angstroms against C10-Ala69 and 2.533 angstroms against C11-Asn70. The distances become a little bit shorter for the second distances for these two pairs, but other pairs are more separated for the second order distances in chain B. The shape of side chain of the amino acid plays an important role if they are simple short structures. We haven't captured the information about hydrogen bonding in this analysis.

3. Absorption energy by retinal in the light field

Light absorption by retinal has been investigated [6]. The absorption speed was considered relative to thinking on photochemical reactions [5]. Their conclusion is that the faster conformational change was around 330 fs [5]. We can understand the transition scheme 11-cis-retinal to all-trans-retinal from this reference [5]. It is difficult to determine the exact absorption wave length from the data [5,7,8]. So we have roughly estimated that wavelength absorbed by retinal is around

TABLE I First and second order proximal atoms contact to retinal carbons in chain A of 4WW3

The coordinate (x, y, z) of atom of contacted amino acid residues corresponding to each retinal carbon is represented. The second third and fourth decimals are the same because of checking the values. This value denotes the distance between retinal carbon and atom of contacted residues. In the middle characters denote atom and amino acid residue. The number followed residue name is residue number. Last three blocks of numbers are the coordinate of atom of first and second order.

```
"DISTANCE ORDER : ",1
"C1 ",4.42981,4.42981,4.42981,"CE1","PHE",205,23.337,44.787,59.627
"C2 ",3.57972,3.57972,3.57972,"CG ","PHE",209,21.928,45.781,64.761
"C3 ",3.56126,3.56126,3.56126,"CG ","PHE",209,21.928,45.781,64.761
"C4 ",3.65238,3.65238,3.65238,"CD2","PHE",209,21.401,45.102,65.849
"C5 ",3.60786,3.60786,3.60786,"CE2","PHE",120,16.634,48.201,62.695
"C6 ",3.49056,3.49056,3.49056,"CE2","PHE",120,16.634,48.201,62.695
"C7 ",3.26386,3.26386,3.26386,"CE2","PHE",120,16.634,48.201,62.695
"C8 ",3.80741,3.80741,3.80741,"CZ3","TRP",274,16.034,41.12,60.898
"C9 ",3.54365,3.54365,3.54365,"CD2","PHE",188,16.007,44.976,55.911
"C10",3.74297,3.74297,3.74297,"CH2","TRP",274,14.698,41.039,61.313
"C11",3.42198,3.42198,3.42198,"OG ","SER",187,13.881,42.372,55.32
"C12",3.40562,3.40562,3.40562,"OG ","SER",187,13.881,42.372,55.32
"C13",3.55178,3.55178,3.55178,"O  ","CYS",186,9.941,40.832,54.765
"C14",2.37835,2.37835,2.37835,"NZ ","LYS",305,10.878,37.625,58.055
"C15",1.34314,1.34314,1.34314,"NZ ","LYS",305,10.878,37.625,58.055
"C16",3.64754,3.64754,3.64754,"CG ","PHE",205,22.991,47.178,59.279
"C17",3.93165,3.93165,3.93165,"CE2","PHE",188,17.119,44.238,56.364
"C18",3.36084,3.36084,3.36084,"CD2","PHE",120,16.083,48.155,63.959
"C19",3.50857,3.50857,3.50857,"CD2","PHE",188,16.007,44.976,55.911
"C20",3.09871,3.09871,3.09871,"O  ","CYS",186,9.941,40.832,54.765

"DISTANCE ORDER : ",2
"C1 ",4.44981,4.49901,4.49901,"CE2","PHE",120,16.634,48.201,62.695
"C2 ",3.59972,3.6718,3.6718,"CD1","PHE",209,23.033,45.245,64.113
"C3 ",3.58126,3.61112,3.61112,"CD2","PHE",209,21.401,45.102,65.849
"C4 ",3.67238,3.88948,3.88948,"CG ","PHE",209,21.928,45.781,64.761
"C5 ",3.62786,3.8613,3.8613,"CD2","PHE",120,16.083,48.155,63.959
"C6 ",3.51056,4.18705,4.18705,"CZ ","PHE",120,15.983,48.882,61.667
"C7 ",3.28386,3.45797,3.45797,"CZ ","PHE",120,15.983,48.882,61.667
"C8 ",3.82741,3.92486,3.92486,"CE2","PHE",188,17.119,44.238,56.364
"C9 ",3.56365,3.62429,3.62429,"CA ","GLY",116,11.726,46.109,61.118
"C10",3.76297,3.78391,3.78391,"CA ","GLY",116,11.726,46.109,61.118
"C11",3.44198,3.65503,3.65503,"N  ","GLY",116,10.588,45.34,60.656
"C12",3.42562,3.86206,3.86206,"CH2","TRP",274,14.698,41.039,61.313
"C13",3.57178,3.69962,3.69962,"NZ ","LYS",305,10.878,37.625,58.055
"C14",2.39835,3.75779,3.75779,"O  ","CYS",186,9.941,40.832,54.765
"C15",1.36314,2.49722,2.49722,"CE ","LYS",305,10.087,36.399,58.029
"C16",3.66754,3.72718,3.72718,"CD2","PHE",205,22.455,46.88,58.035
"C17",3.95165,4.03843,4.03843,"CZ ","PHE",205,22.8,44.495,58.384
"C18",3.38084,3.52596,3.52596,"N  ","PHE",120,13.714,46.367,65.719
"C19",3.52857,3.56816,3.56816,"CA ","GLY",116,11.726,46.109,61.118
"C20",3.11871,3.47334,3.47334,"CA ","GLY",112,8.29,44.613,56.05
```

TABLE II First and second order proximal atoms contact to retinal carbons in chain B of 4WW3

The coordinate (x, y, z) of atom of contacted amino acid residues corresponding to each retinal carbon is represented. The second third and fourth decimals are the same because of checking the values. This value denotes the distance between retinal carbon and atom of contacted residues. In the middle characters denote atom and amino acid residue. The number followed residue name is residue number. Last three blocks of numbers are the coordinate of atom of first and second order.

```
"DISTANCE ORDER : ",1
"C1 ",1.64957,1.64957,1.64957,"CB ","ARG",133,19.5,44.085,12.084
"C2 ",1.70237,1.70237,1.70237,"CB ","ARG",133,19.5,44.085,12.084
"C3 ",3.09651,3.09651,3.09651,"CB ","ARG",133,19.5,44.085,12.084
"C4 ",3.34849,3.34849,3.34849,"O  ","ILE",129,22.551,43.767,10.217
"C5 ",2.60321,2.60321,2.60321,"O  ","ILE",129,22.551,43.767,10.217
"C6 ",2.09933,2.09933,2.09933,"O  ","ILE",129,22.551,43.767,10.217
"C7 ",2.61165,2.61165,2.61165,"O  ","ILE",129,22.551,43.767,10.217
"C8 ",2.97801,2.97801,2.97801,"OD1","ASP",132,23.627,42.552,14.004
"C9 ",2.79481,2.79481,2.79481,"CB ","ALA",69,26.3,39.876,13.89
"C10",3.47563,3.47563,3.47563,"CB ","ALA",69,26.3,39.876,13.89
"C11",2.53306,2.53306,2.53306,"ND2","ASN",70,24.825,34.898,13.416
"C12",2.26567,2.26567,2.26567,"ND2","ASN",70,24.825,34.898,13.416
"C13",1.72395,1.72395,1.72395,"ND2","ASN",70,24.825,34.898,13.416
"C14",2.07338,2.07338,2.07338,"NE2","HIS",319,20.685,32.483,13.855
"C15",1.32077,1.32077,1.32077,"NZ ","LYS",305,20.843,31.974,14.236
"C16",1.01023,1.01023,1.01023,"N  ","ARG",133,21.775,44.787,12.597
"C17",.878612,.878612,.878612,"CD ","ARG",133,19.333,41.653,12.75
"C18",3.48807,3.48807,3.48807,"O  ","ILE",129,22.551,43.767,10.217
"C19",1.46501,1.46501,1.46501,"CB ","ALA",69,26.3,39.876,13.89
"C20",1.04823,1.04823,1.04823,"ND2","ASN",70,24.825,34.898,13.416

"DISTANCE ORDER : ",2
"C1 ",1.66957,2.1936,2.1936,"CD ","ARG",133,19.333,41.653,12.75
"C2 ",1.72237,2.25345,2.25345,"CG ","ARG",133,18.578,42.974,12.573
"C3 ",3.11651,3.19914,3.19914,"CG ","ARG",133,18.578,42.974,12.573
"C4 ",3.36849,3.65714,3.65714,"CD2","PHE",209,19.154,44.694,6.291
"C5 ",2.62321,3.68655,3.68655,"CE3","TRP",274,19.09,38.776,10.112
"C6 ",2.11933,3.02689,3.02689,"CD ","ARG",133,19.333,41.653,12.75
"C7 ",2.63165,2.8188,2.8188,"OD1","ASP",132,23.627,42.552,14.004
"C8 ",2.99801,3.36771,3.36771,"NH1","ARG",133,21.318,42.09,14.726
"C9 ",2.81481,3.09301,3.09301,"OD1","ASP",132,23.627,42.552,14.004
"C10",3.49563,3.8227,3.8227,"ND2","ASN",70,24.825,34.898,13.416
"C11",2.55306,3.58515,3.58515,"CG ","ASN",70,25.873,34.283,13.941
"C12",2.28567,3.45917,3.45917,"CG ","ASN",70,25.873,34.283,13.941
"C13",1.74395,2.69846,2.69846,"CG ","ASN",70,25.873,34.283,13.941
"C14",2.09338,2.37678,2.37678,"NZ ","LYS",305,20.843,31.974,14.236
"C15",1.34077,1.41331,1.41331,"NE2","HIS",319,20.685,32.483,13.855
"C16",1.03023,1.52159,1.52159,"CA ","ARG",133,20.446,44.637,13.153
"C17",.898612,1.50295,1.50295,"CG ","ARG",133,18.578,42.974,12.573
"C18",3.50807,3.5655,3.5655,"CD2","PHE",120,25.016,42.908,8.216
"C19",1.48501,2.68944,2.68944,"OD1","ASP",132,23.627,42.552,14.004
"C20",1.06823,1.27628,1.27628,"CG ","ASN",70,25.873,34.283,13.941
```

500 nm. Using famous relationship $E = h\nu$ of energy to wave-frequency and $\lambda\nu = c$ between wavelength and wave-frequency [9], we obtain the following result [9],

$$E = \frac{c}{\lambda}$$

where h is Planck's constant (6.626×10^{-34} Js) and c the speed of light in the empty space (2.9979×10^{8} m/s). Single retinal absorption energy is estimated using wave length 500 nm like as 3.973×10^{-19} J. Changing the wavelength, absorption energy is varied from 3.31×10^{-19} J (600 nm) to 4.97×10^{-19} J (400 nm).

This value can be compared with the chemical bond energy. The chemical energy of a covalent bond will be estimated from 380 kJ/mol to 450 kJ/mol [10]. The one mol is equivalent to Avogadro number so that $1\ \text{mol} = 6.022 \times 10^{23}$. Thus the energy of one covalent-bond is in the range from 6.30×10^{-19} J to 7.45×10^{-19} J [10]. These energies are about twice the absorption energy

4. Discussion

The photon absorption energy is estimated that the conformation change from 11-cis-retinal to all-trans-retinal that wave length around 500 nm using Plank-Einstein relationship $E = h\nu$ between energy and the frequency. This energy value is small compared with the bonding energy of covalent bond in organic chemistry. The energy value is about half the energy of covalent bond. We have concentrated on the retinal carbons C10 and C11 since that is the location of the conformation change from 11-cis-retinal to all-trans-retinal. The structural change of retinal may come from a rotation of the retinal carbon line. The conformation change of retinal contact with squid rhodopsin again, we suppose. The estimated energy by photon absorption sits on the range from 3.31×10^{-19} J to 4.97×10^{-19} J. Squid opsin like many invertebrate opsins and can be driven from rhodopsin to meta-rhodopsin and back again, each conversion being driven by absorption of a photon. In the squid opsin investigated by Hubbard and St George [11] the rhodopsin absorbed at 493 nm, but depending on whether the meta-rhodopsin was in an acid or basic condition the reverse photoisomerisation had peak absorptions at 500 nm or 380 nm. Squids also have a method for regenerating rhodopsin in the dark [12]. The fact that the retinal has to flip easily between two states may account for the relatively large amount of space around C10 and C11. It would be interesting to compare the amount of space around these key carbons in vertebrate opsins, which do not show reverse photoisomerisation [12].

The main phototransduction energy translation is from retinal conformation to a contacted residue of rhodopsin. In this sense, Trp274 and Ser187 are noticed in chain A and Ala69 and Asn70 in chain B. The Trp274 has a ring but Ser187, Ala69, and Asn70 have simple side chain amino acids. Alanine and serine also have the small side residues. So it is expected that the required transfer of absorption energy is very small. We guess that main acceptor of absorption energy may be tryptophan and arginine.

References

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

[2] Yoshinori Nagai, Masashi Kito, and Ted Maddess, Atomic configuration around retinal in squid rhodopsin, *Mem. Kokushikan U Cent. Inf, Sci.*, **34** (2013) 1–8

[3] Yoshinori Nagai, Masashi Kito, and Ted Maddess, Retinal location and structure in squid rhodopsin, *Mem. Kokushikan U Information Science*, **35** (2014) 19–23

[4] Debarshi Mustafi and Krzysztof Palczewski, Topology of class A G protein-coupled receptors: Insights gained from crystal structures of rhodopsin, adrenergic and adenosine receptors. *Mol. Pharmacol.*, **75** (2009) 1–12

[5] Robert S. H. Liu and George Hammond, Photochemical reactivity of polyenes: from dienes to rhodopsin, from microseconds to femtoseconds, *Photochem. Photobiol. Sci.*, **2** (2003) 835–844

[6] H. Kandori, Y; Shichida, and T. Yoshizawa, Photoisomerization in rhodopsin, *Biochemistry*, **66** (2001) 1483–1498

[7] Jay M. Janz, Jonathan F. Fay, and David L. Farrens, Stability of dark state rhodopsin is mediated by a conserved ion pair in intradiscal loop E-2, *J. Biol. Chem.* **278** (2003) 16982–16991

[8] Tomiyuki Hara and Reiko Hara, Distribution of rhodopsin and retinochrome in squid retina, *J, Gen. Physiol.* **67** (1976) 791–806

[9] Arthur Beiser, Concepts of Modern Physics, McGraw-Hill revised edition (1967)

[10] Harold Hart, Leslie E. Craone, and David J. Hart, Organic Chemistry: A Short Course, Cengage Learning, 13-th edition (2012)

[11] Ruth Hubbard, and Robert C Saint George, The rhodopsin system of the squid. *J. Gen. Physiol.* **41** (1958) 501–528.

[12] Trevor D Lamb. Evolution of phototransduction, vertebrate photoreceptors and Retina. Prog Retinal Eye Res **36** (2013) 52–119.