View metadata, citation and similar papers at core.ac.uk

brought to you by CORE

provided by Kanazawa University Repository for Academic Resources

Krafft temperature and enthalpy of solution of N-acyl amino acid surfactants and their racemic modifications: Effect of the counter ion

著者	Ohta Akio, Nakashima Satoru, Matsuyanagi Hiroki, Asakawa Tsuyoshi, Miyagishi Shigeyoshi
journal or publication title	Colloid and Polymer Science
volume	282
number	2
page range	162-169
year	2003-12-01
URL	http://hdl.handle.net/2297/1831

Submitted to Colloid Polymer Sci. 2003

Krafft Temperature and Enthalpy of Solution of *N*-Acyl Amino Acid Surfactants and Their Racemic Modifications: Effect of the Counter Ion

Akio Ohta, Satoru Nakashima, Hiroki Matsuyanagi, Tsuyoshi Asakawa, and Shigeyoshi Miyagishi

Department of Chemistry and Chemical Engineering, Faculty of Engineering, Kanazawa University, Ishikawa 920-8667, Japan

Mailing address:
Akio Ohta
Department of Chemistry and Chemical Engineering, Faculty of Engineering, Kanazawa University, 2-40-20 Kodatsuno, Kanazawa, Ishikawa 920-8667, Japan

e-mail address
akio-o@t.kanazawa-u.ac.jp

1. To whom the correspondence should be addressed.

Abstract

The Krafft temperatures and the enthalpies of solution of *N*-hexadecanoyl alaninate and valinate and *N*-tetradecanoyl phenylalaninate were obtained from differential scanning calorimetry. The Krafft temperature of *N*-acyl amino acid surfactant increased with decreasing size of the counter ion with some exceptions. The enthalpy of solution was endothermic and increased with decreasing size of the counter ion except for the cases of lithium salt. It was found from these results that the L-L interaction in solid state of *N*-hexadecanoyl amino acid surfactant salt was superior to the D-L interaction for both the alanine and valine systems when the counter ion size increased. On the other hand the D-L interaction was still advantageous for the phenylalanine system for the case of Cs^+ as a counter ion. Both FT-IR studies and theoretical calculations suggested that the difference in magnitude of the interaction between peptide and counter ion was a dominant factor for the chiral effect.

Keywords *N*-Acyl amino acid surfactant • Krafft temperature • Enthalpy of solution • Counter ion • Chiral effect

Introduction

N-Acyl amino acid surfactants are useful both from the industrial and the domestic viewpoints because of their biodegradability and low toxicity [1,2]. On the other hand, the concern with chiral discrimination of them has been growing since it has been reported that some amphiphiles containing peptide groups like as *N*-acyl amino acid were self-assembled to the micrometer- and nanometer-scale structures [3-7]. It has been known

that the chiral discrimination of *N*-acyl amino acid surfactants is occurred remarkably in the concentrated molecular organizations like as solid [8-10], liquid crystal [11,12], and condensed interfacial film [13-17]. In previous study [10], we have shown by the measurements of the Krafft temperature (KT) and the enthalpy of solution of sodium *N*-hexadecanoyl amino acid surfactant salt that the heterochiral interaction was superior to the homochiral interaction in the solid state for both the alanine and phenylalanine systems, while the homochiral interaction was advantageous for both the valine and leucine systems. Furthermore we have concluded that both the peptide-peptide hydrogen bonding and the steric hindrance of the amino acid residue govern the chiral effect. There are some studies on crystal structures of *N*-acyl amino acid in which the hydrogen bonds between peptide-peptide groups and between peptide-carboxylic acid groups are suggested [6,18-20]. In the case of *N*-acyl amino acid salt, however, the interaction through the counter ion should be taken into account in addition to the hydrogen bond.

In this study, therefore, the effects of the counter ion size of *N*-acyl amino acid surfactants on the chiral discrimination are investigated through differential scanning calorimetry (DSC) measurement of the KT and the enthalpy of solution. In addition, we also studied their interaction in the solid states by use of FT-IR measurement and theoretical calculations. FT-IR spectroscopy is one of the most powerful methods for analysis of the interaction of the peptide group of *N*-acyl amino acid surfactant [21]. These are discussed from the viewpoint of the interactions between peptide-peptide groups and between peptide group and counter ion.

Experimental

Materials

L-Alanine (Ala), L-valine (Val), L-phenylalanine (Phe) and their racemic mixtures (DL-form) were purchased from Peptide Institute, Inc. and Nacalai Tesque, Inc., and used without further purification. *N*-Acyl amino acids (C*n*-amino acid; n = 14,16) were synthesized by the reaction of an amino acid with hexadecanoyl or tetradecanoyl chlorides as described previously [22] and were re-crystallized from mixtures of either diethyl ether-ethanol or acetone-methanol. Their purities were checked by HPLC and DSC and by observing no minimum on the surface tension vs concentration curves at 298.15 K. *N*-Acyl amino acids were dissolved in 1mM excess aqueous solution of alkali hydroxide (LiOH, NaOH, KOH, and CsOH).

DSC

Differential scanning calorimetry (DSC) experiments were made by using a DSC7 (Perkin-Elmer) thermal analyzer. A sample solution was prepared in the dissolving the *N*-hexadecanoyl amino acids in an aqueous solution of 0.4 M chloride salt, and was sealed in a Large Volume Capsule (Perkin-Elmer) using an O-ring sealed 60 μl stainless steel container. The solutions were kept at 2 ˚C to deposit the solid *N*-hexadecanoyl amino acid salts for a day. The experiments were done on the solutions in the concentration range 10 to 20 mM using about 50 mg of the samples. After the samples were kept at 0 °C for 5 hours, they were heated at a rate of 0.5 K/min. Two runs were performed each system at least.

FT-IR

Infrared absorption spectra were measured on a JASCO 460 Plus spectrometer by the KBr disc method. The salt samples were prepared in the filtering of the salts deposited from the alkali solutions of *N*-hexadecanoyl amino acid at 2˚C, and were dried *in vacuo* at 40 ˚C for a day before the measurement. Sixteen scans were accumulated at a resolution of 1 cm^{-1}.

Results and Discussion

DSC

The thermograms of 15mM aqueous solution of *N*-hexadecanoyl alaninate and valinate surfactants in the presence of the solid deposit are shown in Fig. 1. It can be seen that an endothermic peak accompanies the dissolution of surfactant around the KT. KT can be defined as the temperature corresponding to the onset of the peak and these values are shown in Table 1. It is confirmed that the KT values determined by this method are similar to those obtained from the solubility measurements [10]. The thermograms of 15mM aqueous solutions of *N*-tetradecanoyl phenylalaninate surfactants are shown in Fig. 2. The enthalpy of solution was calculated from the peak area and is shown in Table 2.

Krafft temperature: It is seen that the KT of *N*-acyl amino acid surfactants increased with decreasing the size of the ion radius of counter ion except for the partial cases of Li C16-L-Ala and Li C14-DL-Phe systems. This may be interpreted that the decrease in size of the counter ion makes the molecular packing of surfactant tighten and the salting out effect enlarge. Especially, the gap of KT value of C16-Val between Li and Na salts is

surprisingly large, and it is more than 60 K for the C16-DL-Val case. It is also seen that another peak appeares at lower temperature (269.2 K) than KT in the case of Na C14-DL-Phe. Probably it was caused by a kind of the transition in solid state. The transition enthalpy was 15.4 kJ mol^{-1}.

The chiral effect of the amino acid can be divided into two types: Firstly where the KT of the DL-form is higher than that of the L-form, and secondly where the opposite is the case. In the former case, the heterochiral interaction is favor, while in the latter case the homochiral interaction is favor. An important point to emphasize is the fact that the favorable interaction is shifted from heterochiral to homochiral with increasing the counter ion radius for the both cases of C16-Ala and C16-Val. Figure 3 summarized the trend in chiral interaction between the isomers of *N*-acyl amino acid surfactant with a higher KT in terms of the both sizes of counter ion and residue of amino acid. Here the case of H^+ as a counter ion was judged by the melting point of *N*-acyl amino acid [10]. This result suggests that a formation of the molecular pair between the L-form and the D-form of *N*-acyl amino acid surfactant is very effective at enhancing the molecular packing in the solid state with decreasing the size of hydrophilic moiety. From the viewpoint of counter ion size as well as residue size, phenylalanine, which contains an aromatic ring, can be considered an exceptional case. As mentioned in our previous study [10], the interaction between the benzyl groups is favorable and is enhanced by a combination of the L- and D-forms. It is concluded that the heterochiral interaction in *N*-acyl phenylalanine system is extraordinary strong and then, remains still favorable although the counter ion is replaced by a large one like as Cs^+. For the case of Li C14-Phe system, however, the KT of the L-form was higher than that of the DL-Form.

Enthalpy of solution: The enthalpy of solution Δh_{sol} obtained in this study corresponds to the difference between the enthalpy of surfactant in the micellar state h(micelle) and that in the solid state h(solid).

$$\Delta h_{sol} = h(\text{micelle}) - h(\text{solid}) \qquad [1]$$

There are two effects of the increase in size of the counter ion; one is the loosening of molecular packing in the solid state, another is the reduction of hydration of the counter ion in the micellar state. These effects raise the values of h(solid) and h(micelle), respectively. We see from Table 2 that the Δh_{sol} value of Na salt in C16-Ala systems is the largest irrespective of chirality. Therefore the difference of Δh_{sol} between Na and K salts is principally attributable to h(solid), while that between Na and Li salts is caused by the variance of h(micelle). The Δh_{sol} value of C14-DL-Phe increases with decreasing the counter ion size from Cs^+ to Na^+. This is simply because the molecular packing in solid state is tightened by decrease of counter ion size. In the C16-L-Val and C14-L-Phe systems, however, the Δh_{sol} value is not very affected by the size of counter ion. It is suggested that the counter ion size effect contributes to both h(solid) and h(micelle) equally in those cases.

Next let us examine the chiral effect of the amino acid on the enthalpy of solution. When the KT of the DL-form was higher than that of the L-form, the Δh_{sol} of the DL-form was much larger than that of the L-form. Conversely for the case of Li C14-Phe, the Δh_{sol} value of the DL-form was much larger than that of the L-form, though the KT of the DL-form was lower than that of the L-form. On the other hand, for K C16-Ala and Na C16-Val systems, which are cases that the KT of the DL-form was lower than that of the L-form, there is no remarkable difference between the L- and DL-forms in the value of the Δh_{sol}. Since the racemic effect

was very small in a micelle [22], the enthalpy of formation of racemic compound Δh_{rac} could be evaluated by subtracting the Δh_{sol} value of the DL-form from that of the L-form under the condition that the temperature dependence of enthalpy might be ignored.

$$\begin{aligned}\Delta h_{\mathrm{rac}} &= h_{\mathrm{DL}}(\mathrm{solid}) - \frac{1}{2}\left[h_{\mathrm{L}}(\mathrm{solid}) + h_{\mathrm{D}}(\mathrm{solid})\right] \\ &= h_{\mathrm{DL}}(\mathrm{solid}) - h_{\mathrm{L}}(\mathrm{solid}) = \Delta h_{\mathrm{sol,\ L}} - \Delta h_{\mathrm{sol,\,DL}}\end{aligned} \qquad [2]$$

The values obtained for Δh_{rac} of C16-Ala, Li C16-Val, and C14-Phe were ca. –13 kJ mol^{-1}, -16 kJ mol^{-1}, and –20 ~ -47 kJ mol^{-1}, respectively. These values are much larger than the interaction energies between either methyl or benzyl groups and correspond to the larger interaction energy like as hydrogen bonding or coordination. It is quite likely that the combination of the L- and D-forms in those systems enhances the contribution of coordination of carbonyl or carboxyl groups to alkali metal ion as well as the contribution of hydrogen bonding between adjacent peptide groups as mentioned in our previous study [10]. This is a question to be considered in next chapter. The Δh_{rac} value of Li C16-Ala is almost same with that of Na C16-Ala, while the absolute value of Δh_{rac} of C14-Phe system increases with decreasing the counter ion size form Cs^+ to Na^+. Judging from both the Δh_{rac} and the KT values of Li C14-Phe systems, the solid of Li C14-DL-Phe is a racemic compound and has much smaller entropy compared with that of Li C14-L-Phe.

IR spectroscopy: Figure 4a shows FT-IR spectra of C16-Ala (acid) and Na C16-Ala (salt) in the solid state respectively in the region of 3600-3200 cm^{-1} where the key band is the N-H stretching vibration of the peptide group. Since the absorption band is shifted to lower wave number by

hydrogen bonding, the bands around 3500 cm^{-1} and 3340 cm^{-1} are assigned the free and the hydrogen-bonded N-H stretching vibrations, respectively. It is seen from Fig.4a that the absorption of free N-H is absent for C16-DL-Ala while the absorption is slightly detected for C16-L-Ala. This fact supports the idea that the hydrogen bonding ability is a dominant factor for the difference of physicochemical property between L- and DL-form of *N*-acyl amino acid. For the case of Na-C16-Ala in Fig. 4a, however, there is a rather large absorption of the free N-H in both L- and DL-forms. Then it is difficult to explain the difference between L- and DL-forms of Na-C16-Ala in terms of the hydrogen bonding ability. Figure 4b shows the same FT-IR spectra in the region of 1800-1500 cm^{-1} where the key band is the C=O stretching vibration of peptide or carboxyl groups. The absorption band around 1705 cm^{-1} is assigned the C=O stretching of carboxyl group and it is shifted to around 1580 cm^{-1} by neutralization to sodium carboxylate as shown in Fig. 4b. Without distinction between acid and salt systems, the absorption band of DL-form resembles that of L-form. However the absorption band of the C=O stretching vibration of peptide group (amide I), which corresponds the peak around 1646 cm^{-1}, reflects precisely the distinction of chirality. In the case of the acid form, there is a singlet peak for DL-form in contrast to a doublet peak for L-form. This corresponds to the result in Fig. 4a and suggests that the peptide group of C16-L-Ala has two states; one is hydrogen-bonded state and another is non-hydrogen-bonded state. In the case of Na L-Ala, on the other hand, a new absorption band appeared at 1625 cm^{-1} in addition to the band around 1646 cm^{-1}. Furthermore the band around 1646 cm^{-1} was completely shifted to 1623 cm^{-1} in the case of Na DL-Ala. These bands appeared at lower wave number could be assigned the C=O stretching vibration of the

peptide group interacting with sodium ion. It was found from these results that in the case of Na C16-DL-Ala which has higher KT and Δh_{sol} values, the peptide group interacts with sodium ion more efficiently than in the case of Na C16-L-Ala.

From the facts discussed above, we can conclude that the observation of the C=O stretching vibration of peptide group is the most advantageous way to examine the chiral effect of *N*-acyl amino acid salts. Figure 5 shows FT-IR spectra of other samples in the region of 1800-1500 cm^{-1}. It was interested that in the case of K C16-Ala system, where DL-form was less stable than L-form, the band of the C=O stretching vibration of peptide group of DL-form only remained around 1646 cm^{-1} on contrast to the case of Na C16-Ala (see Fig. 5a). However K C16-DL-Ala was less-stable racemic compound, because the spectrum of K C16-DL-Ala was different with that of K C16-L-Ala. While it is seen from Fig. 5b that the spectrum of Na C16-DL-Val is almost same with Na C16-L-Val; this fact suggests that Na C16-L-Val is not mixed nor combined with Na C16-D-Val in the solid state at all. In Figs. 5b and 5c, there are results of Li C16-Val and K C14-Phe, where the DL-form is more stable than the L-form. It was found that the main band of the C=O stretching vibration of peptide group of DL-form appeared at lower wave length than that of L-form in all systems. It might be concluded form these results that the difference of the interaction between the peptide group and alkali metal ion governed the chiral discrimination. On the other hands, for the Li C14-Phe system where the KT of DL-form was lower than that of L-form, the influence of chirality on the spectra was similar to the case that the DL-form is more stable than the L-form. (see Fig. 5c) This result strongly supports that the solid of Li C14-DL-Phe is a racemic compound. It seems that, the reason

why KT of DL-form of Li C14-Phe is lower than that of L-form is that the free energy of DL-form is higher value compared to L-form owing to smaller entropy.

Theoretical calculation: We had applied *ab initio* calculation to the dimer of sodium *N*-acetyl alaninate (see Fig. 6(a)) as a model compound for simplification of calculation in our previous study [10], and concluded that the difference of the magnitude of the peptide-peptide hydrogen bonding was dominant factor for the chiral effect. From the FT-IR study, however, it is reasonable to suppose that the dominant factor is the difference of the coordination bonding between the peptide group and the alkali metal ion rather than that of the peptide-peptide hydrogen bonding. Therefore let us reconsider the obtained geometries from this standpoint. The optimized geometry were calculated by using the restricted Hartree-Fock (RHF) procedure with the 6-31 + G* basis set. All calculations were performed using Gaussian 98 [23].

The top views of obtained geometries of L-L and D-L dimers are shown in Fig. 6(b). The top view of the two structures seem to be similar to each other, however, the difference is clear from the side view of the structures in Fig. 6(c). In the D-L dimer, each alanine residue is situated in the *trans* position through the bonding between carboxylates, while in the *gauche* position for the L-L dimer. Furthermore, it was found that the dimers could interact with the two adjacent molecules at the two coordination bond lines. It should be noted that one line is parallel to the other in the D-L dimer, whereas the two lines intersect each other in the L-L dimer (Fig. 6[c]). This suggests that the DL form of Na *N*-acyl alaninate can create a sheet structure stabilized by interaction between the

peptide group and sodium ion more effectively than the L-form. To further substantiate this assumption, semi-empirical MO calculation was applied to the dimer of the dimer obtained by *ab initio* calculation. These calculations were performed using MOPAC 2000 with PM3 hamiltonian [24] under the condition that the geometries of dimers by *ab initio* calculation were fixed. Obtained geometries of dimer of the DL- and LL-dimers were shown in Fig. 7: it was seen that the C=O group of peptide did not interacted with the N-H group of peptide but with the sodium ion in the both cases. Furthermore the axes of two dimers intersected each other in the case of LL-dimer, while there were two dimers on the almost identical plane in the case of DL-dimer as expected. Therefore, Na *N*-acyl DL-alaninate becomes a racemic compound in the solid state. This could explain why Na *N*-acyl DL-valinate and K *N*-acyl DL-alaninate are less stable than their L-form counterparts, since the larger hydrophobic residues and counter ions may hinder the stacking in the sheet-like structure. Conversely, in the case of Na *N*-acyl DL-phenylalaninate, contact between the benzyl groups in the sheet structure is an advantageous factor and results in the racemic compound.

Conclusions

The Krafft temperature of *N*-acyl amino acid surfactant increased with decreasing size of the counter ion except for the cases of Li C16-L-Ala and Li C14-DL-Phe. Experimental results showed that the L-L interaction became to be superior to the D-L interaction in the solid state of *N*-acyl amino acid surfactant salt for both the alanine and valine systems when the size of the counter ion size increased. While the D-L interaction was still

advantageous for the phenylalanine system if the counter ion was replaced by a large one like as Cs^+. It was suggested that both the interaction between peptide and counter ion and the steric hindrance of the amino acid residue govern the chiral effect.

References

1. Takehara M (1984) Hyomen(in Japanese) 35: 459
2. Takehara M (1984) Colloids Surf 38: 149
3. Kogiso M, Ohnishi S, Yase K, Masuda M, Shimizu T (1998) Langmuir 14:4978
4. Matsui H, Gologan B (2000) J Phys Chem B 104: 3383
5. Ariga K, Kikuchi J, Naito M, Koyama E, Yamada N (2000) Langmuir 16: 4929
6. Schneider J, Messerschmidt C, Schulz A, Gnade M, Schade B, Luger P, Bombicz P, Hubert V, Fuhrhop J H (2000) Langmuir 16: 8575
7. Matsui H, Douberly Jr G E (2001) Langmuir 17: 7918
8. Miyagishi S, Matsumura S, Murata K, Asakawa T, Nishida M (1985) Bull Chem Soc Jpn 58: 1019
9. Miyagishi S, Matsumura S, Asakawa T, Nishida M (1986) Bull Chem Soc Jpn 59: 557
10. Ohta A, Ozawa N, Nakashima S, Asakawa T, Miyagishi S (2003) Colloid Polym Sci in press
11. Sakamoto K, Hatano M (1980) Bull Chem Soc Jpn 53: 339
12. Sakamoto K (1980) Mol Cryst Liq Cryst 59: 59
13. Harvry N G, Mirajovsky D, Rose P L, Verbiar R, Arnett R M (1989) J Am Chem Soc 111: 1115
14. Stine K J, Uang J Y -J, Dingman S D (1993) Langmuir 9: 2112
15. Gericke A, Hühnerfuss H (1994) Langmuir 10: 3782
16. Parazak D P, Uang J Y -J, Turner B, Stine K J (1994) Langmuir 10: 3787

17. Hoffmann F, Hühnerfuss H, Stine K J (1998) Langmuir 14: 4525
18. Donohue J, Marsh R E (1962) Acta Cryst 15: 941
19. Cole F E (1970) Acta Cryst B26: 622
20. Lovas G, Kalman A, Argay G (1974) Acta Cryst B30: 2882
21. Du X, Liang Y (2000) Langmuir 16: 3422
22. Miyagishi S, Nishida M (1978) J Colloid Interface Sci 65: 380
23. Frisch M J, Trucks G W, Schlegel H B, Scuseria G E, Robb M A, Cheeseman J R, Zakrzewski V G, Montgomery J A, Stratmann R E, Burant J C, Dapprich S, Millam J M, Daniels A D, Kudin K N, Strain M C, Farkas O, Tomasi J, Barone V, Cossi M, Cammi R, Mennucci B, Pomelli C, Adamo C, Clifford S, Ochterski J, Petersson G A, Ayala P Y, Cui Q, Morokuma K, Malick D K, Rabuck A D, Raghavachari K, Foresman J B, Cioslowski J, Ortiz J V, Stefanov B B, Liu G, Liashenko A, Piskorz P, Komaromi I, Gomperts R, Martin R L, Fox D J, Keith T, Al-Laham M A, Peng C Y, Nanayakkara A, Gonzalez C, Challacombe M, Gill P M W, Johnson B G, Chen W, Wong M W, Andres J L, Head-Gordon M, Replogle E S, Pople J A (1998) Gaussian 98 (Revision A.9). Gaussian Inc, Pittsburgh, PA
24. Stewart J J P (1989) J Comp Chem 10: 209

Figure Captions

Fig. 1 Thermograms of the 15mM of the aqueous solutions of *N*-hexadecanoyl alaninate and valinate salts. (solid line) L-form, (dotted line) DL-form.

Fig. 2 Thermograms of the 15mM of the aqueous solutions of *N*-tetradecanoyl phenylalaninate salts. (solid line) L-form, (dotted line) DL-form.

Fig. 3 Schematic diagrams of effects of the sizes of counter ion and of amino acid residue on the chiral discrimination for the KT of *N*-acyl amino acid salts. *Reference 10

Fig. 4 FT-IR spectra of *N*-hexadecanoyl alanine and sodium *N*-hexadecanoyl alaninate. (a) 3600-3200 cm^{-1}, (b) 1800-1500 cm^{-1}; (1) C16-Ala(acid), (2) Na C16-Ala(salt); (solid line) L-form, (dotted line) DL-form.

Fig. 5 FT-IR spectra of *N*-acyl amino acid salts. (a) C16-Ala, (b) C16-Val, (c) C14-Phe; (solid line) L-form, (dotted line) DL-form.

Fig. 6 (a) Chemical structure of dimer of sodium *N*-acetyl alaninate, (b) Top view of optimized dimer geometries, (c) Side view of optimized dimer geometries.

Fig. 7 (a) Top views of optimized geometries of dimer of dimer of sodium *N*-acetyl alaninate, (c) Side views of optimized geometries.

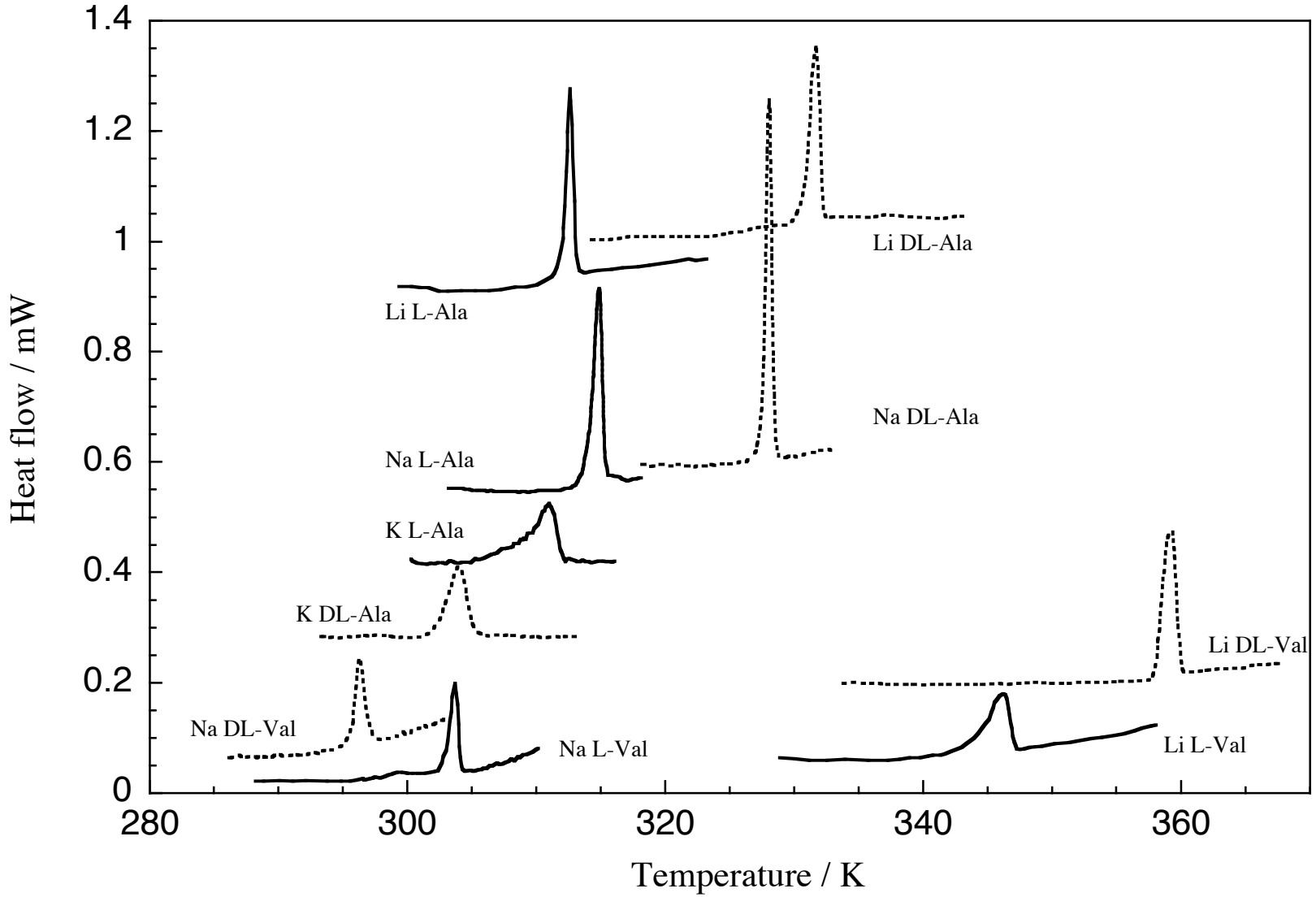


Fig. 1 Ohta et al

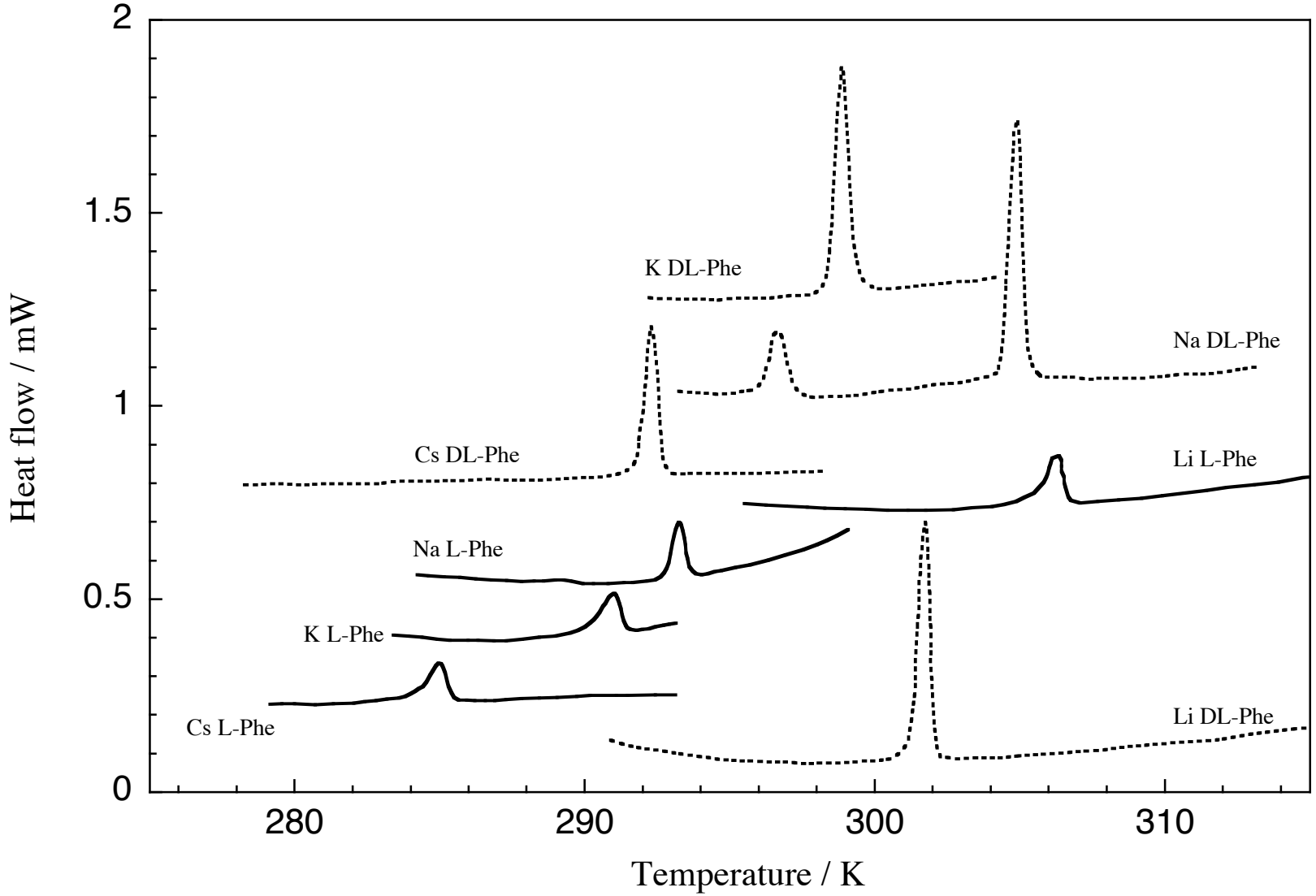


Fig. 2 Ohta et al

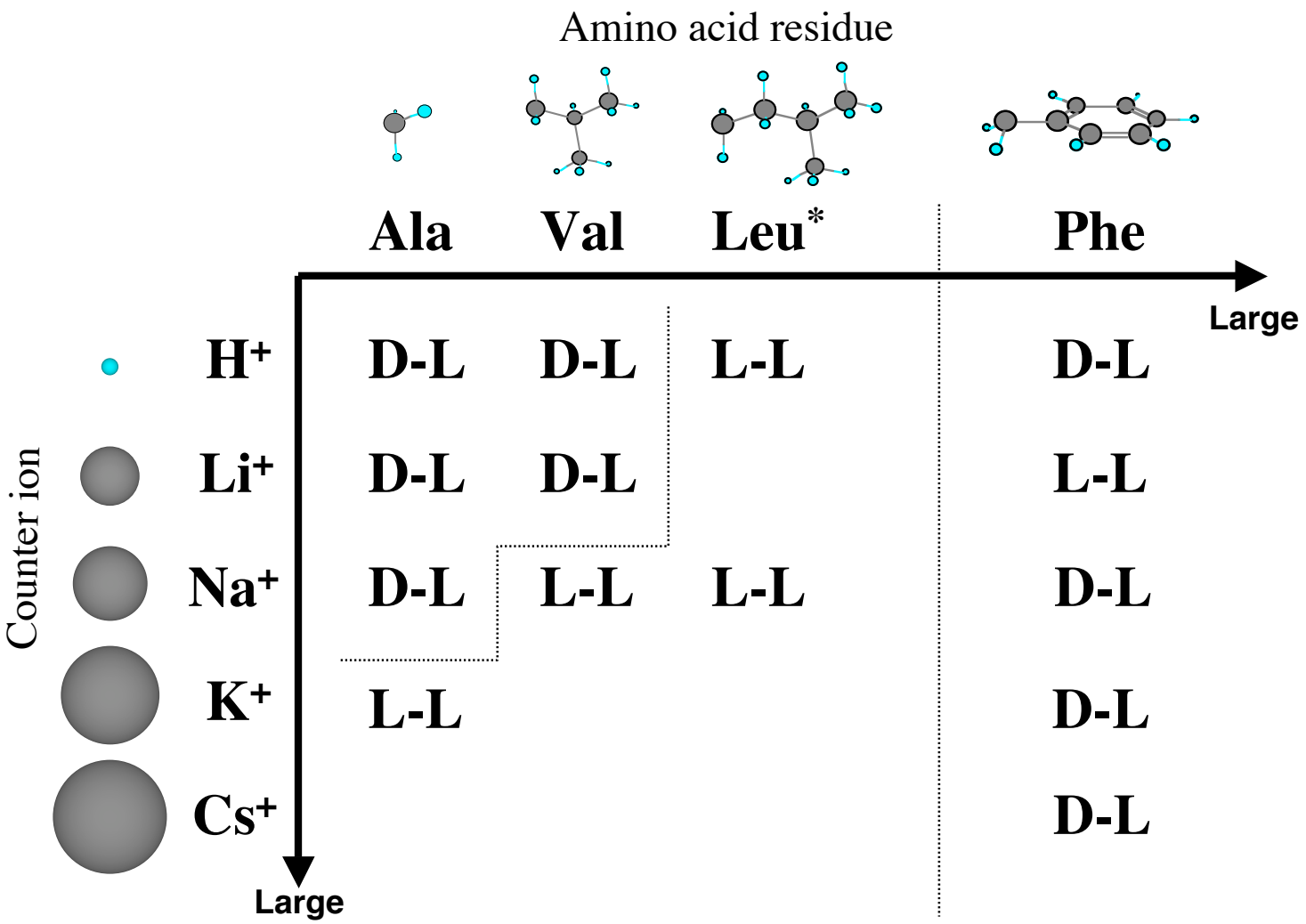


Fig. 3 Ohta et al

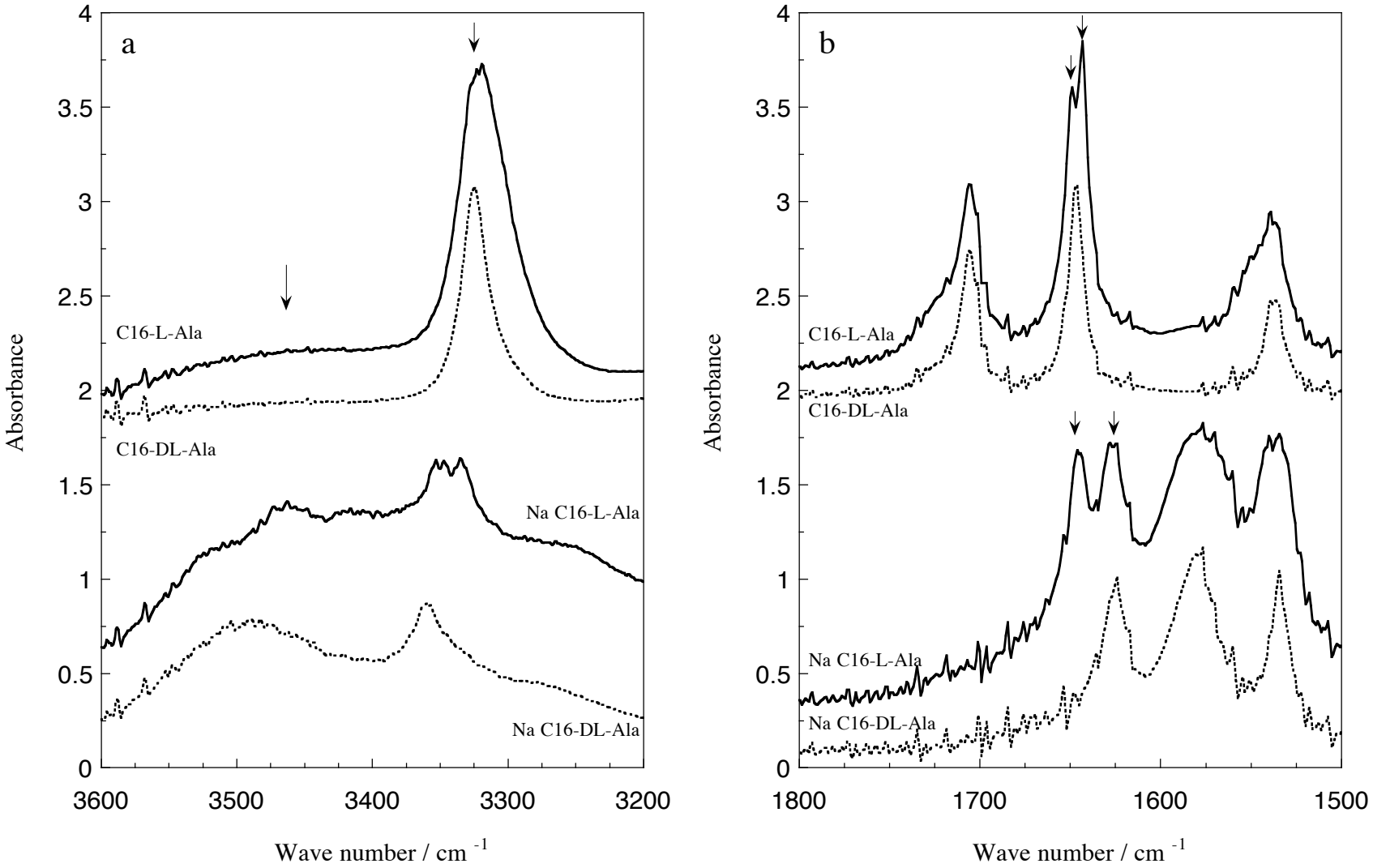


Fig. 4 Ohta et al

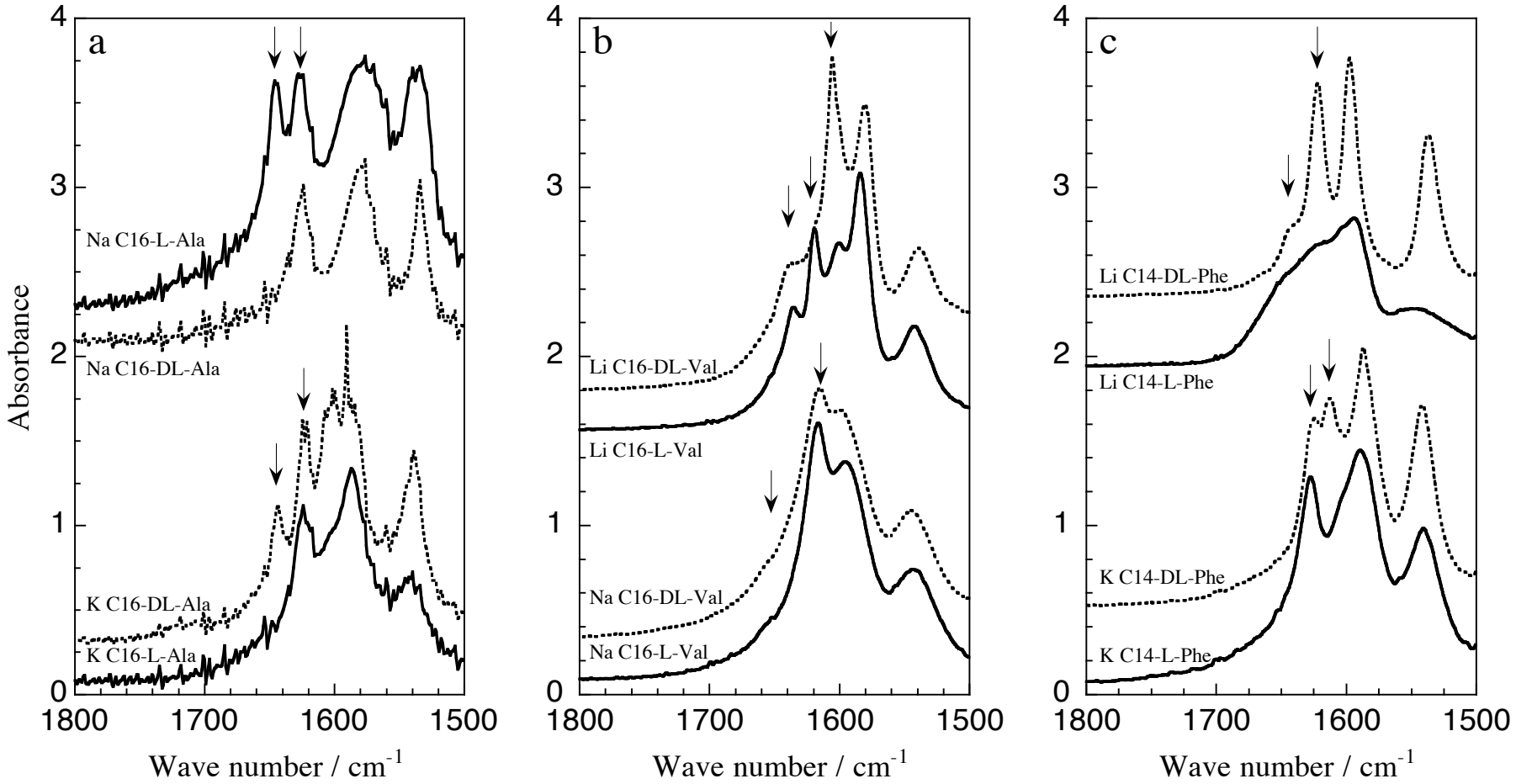


Fig. 5 Ohta et al

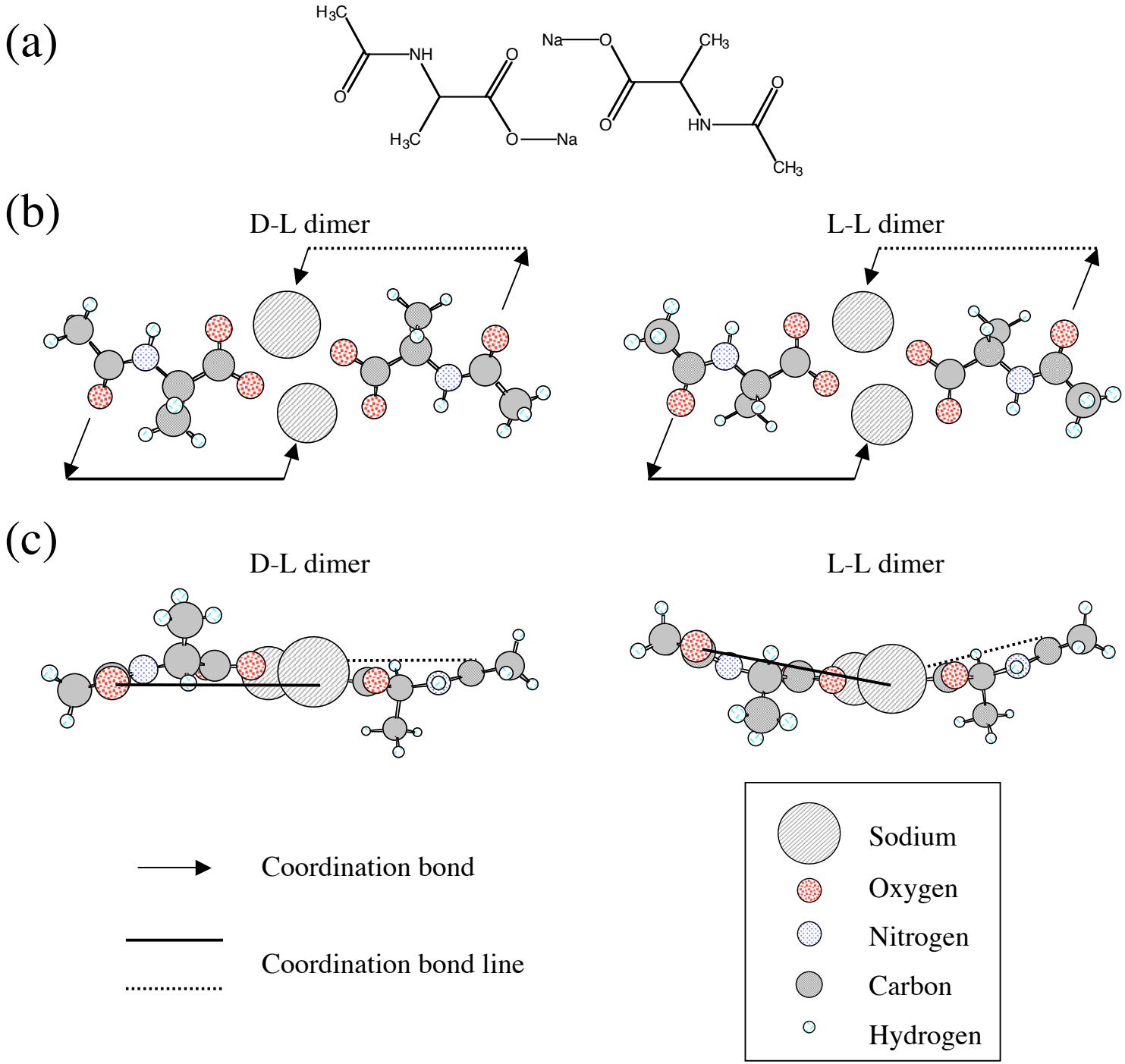
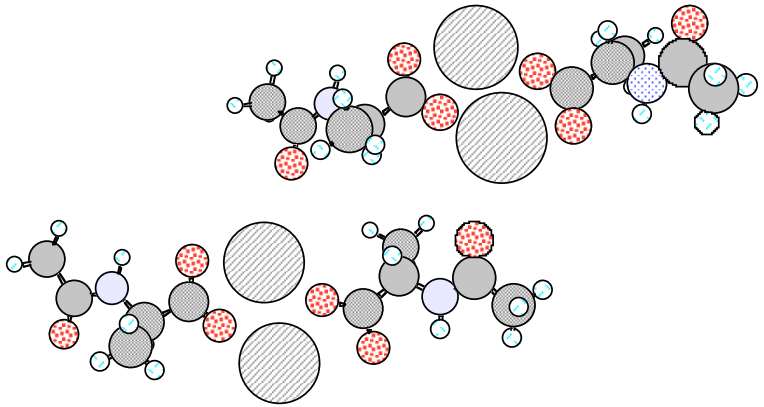


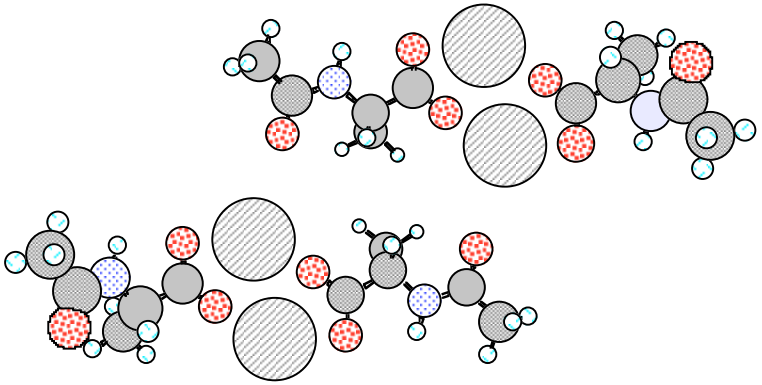
Fig. 6 Ohta et al

(a)

dimer of D-L dimer

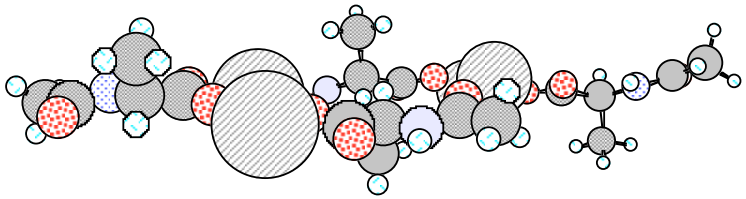


dimer of L-L dimer



(b)

dimer of D-L dimer



dimer of L-L dimer

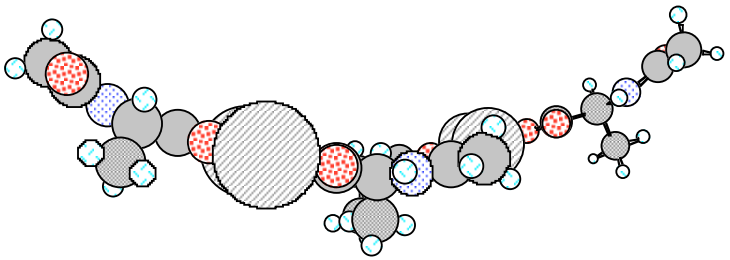


Fig. 7 Ohta et al