Water molecules organization surrounding amphiphilic residues

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1

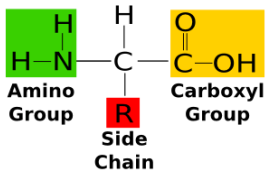
Objective

- How are water molecules arranged around amphiphilic particles?
- Do water molecules form a regular structures (so-called structural water)?

2

Amino acids

Amino acids are organic compounds that contain:
- amine (-NH2) functional groups
- carboxyl (-COOH) functional groups
- side chain (R group) specific to each amino acid.



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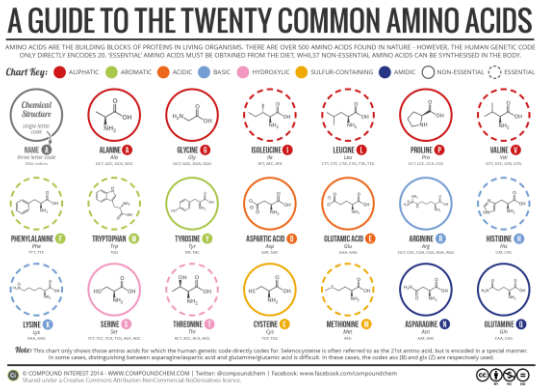

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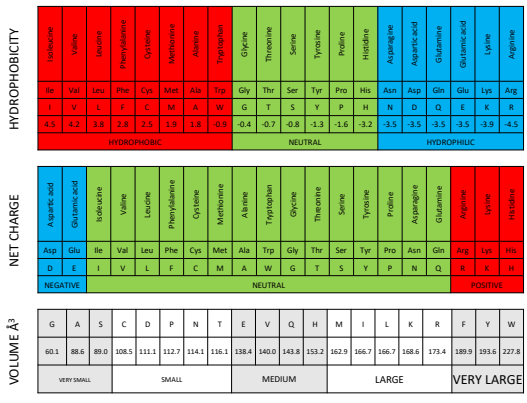


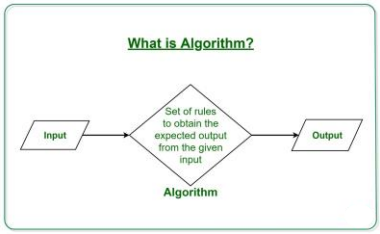
	Isoleucine	Valine	Leucine	Phenylalanine	Cysteine	Methionine	Alanine	Tryptophan	Glycine	Threonine	Serine	Tyrosine	Proline	Histidine	Asparagine	Aspartic acid	Glutamine	Glutamic acid	Lysine	Arginine
	Ile	Val	Leu	Phe	Cys	Met	Ala	Trp	Gly	Thr	Ser	Tyr	Pro	His	Asn	Asp	Gln	Glu	Lys	Arg
	I	V	L	F	C	M	A	W	G	T	S	Y	P	H	N	D	Q	E	K	R
HYDROPHOBICITY	4.5	4.2	3.8	2.8	2.5	1.9	1.8	-0.9	-0.4	-0.7	-0.8	-1.3	-1.6	-3.2	-3.5	-3.5	-3.5	-3.5	-3.9	-4.5
	HYDROPHOBIC								NEUTRAL						HYDROPHILIC					
NET CHARGE	Aspartic acid	Glutamic acid	Isoleucine	Valine	Leucine	Phenylalanine	Cysteine	Methionine	Alanine	Tryptophan	Glycine	Threonine	Serine	Tyrosine	Proline	Asparagine	Glutamine	Arginine	Lysine	Histidine
	Asp	Glu	Ile	Val	Leu	Phe	Cys	Met	Ala	Trp	Gly	Thr	Ser	Tyr	Pro	Asn	Gln	Arg	Lys	His
	D	E	I	V	L	F	C	M	A	W	G	T	S	Y	P	N	Q	R	K	H
	NEGATIVE		NEUTRAL															POSITIVE		
VOLUME Å^3	G	A	S	C	D	P	N	T	E	V	Q	H	M	I	L	K	R	F	Y	W
	60.1	88.6	89.0	108.5	111.1	112.7	114.1	116.1	138.4	140.0	143.8	153.2	162.9	166.7	166.7	168.6	173.4	189.9	193.6	227.8
	VERY SMALL		SMALL						MEDIUM				LARGE					VERY LARGE		

5

	Isoleucine	Valine	Leucine	Phenylalanine	Cysteine	Methionine	Alanine	Tryptophan	Glycine	Threonine	Serine	Tyrosine	Proline	Histidine	Asparagine	Aspartic acid	Glutamine	Glutamic acid	Lysine	Arginine
	Ile	Val	Leu	Phe	Cys	Met	Ala	Trp	Gly	Thr	Ser	Tyr	Pro	His	Asn	Asp	Gln	Glu	Lys	Arg
	I	V	L	F	C	M	A	W	G	T	S	Y	P	H	N	D	Q	E	K	R
HYDROPHOBICITY	4.5	4.2	3.8	2.8	2.5	1.9	1.8	-0.9	-0.4	-0.7	-0.8	-1.3	-1.6	-3.2	-3.5	-3.5	-3.5	-3.5	-3.9	-4.5
	HYDROPHOBIC								NEUTRAL						HYDROPHILIC					
NET CHARGE	Aspartic acid	Glutamic acid	Isoleucine	Valine	Leucine	Phenylalanine	Cysteine	Methionine	Alanine	Tryptophan	Glycine	Threonine	Serine	Tyrosine	Proline	Asparagine	Glutamine	Arginine	Lysine	Histidine
	Asp	Glu	Ile	Val	Leu	Phe	Cys	Met	Ala	Trp	Gly	Thr	Ser	Tyr	Pro	Asn	Gln	Arg	Lys	His
	D	E	I	V	L	F	C	M	A	W	G	T	S	Y	P	N	Q	R	K	H
	NEGATIVE		NEUTRAL															POSITIVE		
VOLUME Å^3	G	A	S	C	D	P	N	T	E	V	Q	H	M	I	L	K	R	F	Y	W
	60.1	88.6	89.0	108.5	111.1	112.7	114.1	116.1	138.4	140.0	143.8	153.2	162.9	166.7	166.7	168.6	173.4	189.9	193.6	227.8
	VERY SMALL		SMALL						MEDIUM				LARGE					VERY LARGE		

6

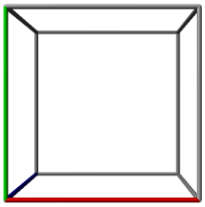
(In silico) Experimental setup



7

(In silico) Experimental setup

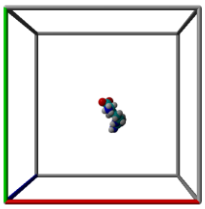
Simulation box: 40Å x 40Å x40Å



8

(In silico) Experimental setup

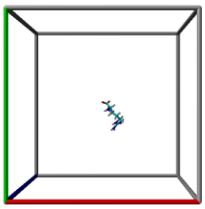
Amino acid molecule (20)



9

(In silico) Experimental setup

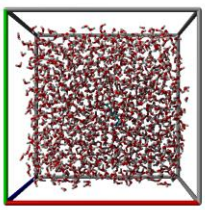
Amino acid molecule (20)



10

(In silico) Experimental setup

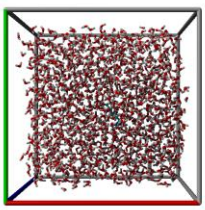
Water: ~1700 molecules (density=0.997 g/ml)



11

(In silico) Experimental setup

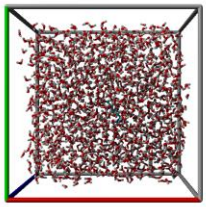
Temperature: 298 K = 25°C



12

(In silico) Experimental setup

Force field: YAMBER3

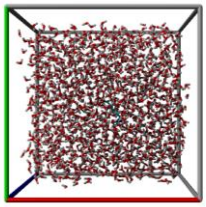


13

(In silico) Experimental setup #1

Procedure:

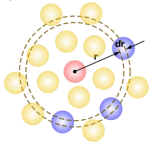
1. Energy minimization
2. Start (short) simulation
3. Collect distance distribution between pairs of atoms/residues
4. Repeat #2-#3 x100
5. **Calculate the radial distribution function**



14

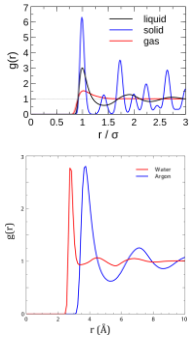
Radial distribution function g(r)

The radial distribution function g(r) defines the probability of finding a particle at a distance r from another tagged particle.
It describes how the density of surrounding matter varies as a function of the distance from a point.



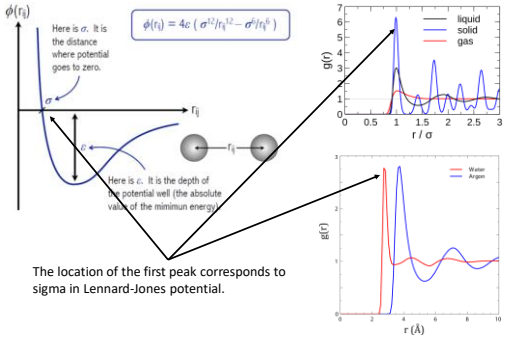
$$g(r) = \frac{dn_r}{4\pi dr * \rho}$$

where dn_r is a function that computes the number of particles within a shell of thickness dr.



15

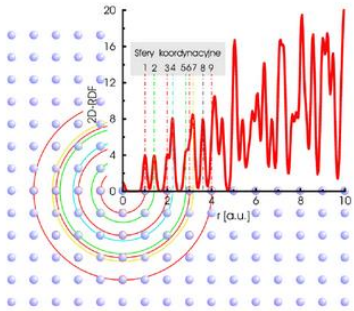
Radial distribution function g(r)



The location of the first peak corresponds to sigma in Lennard-Jones potential.

16

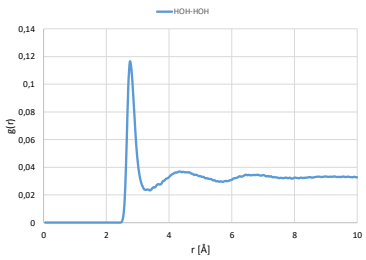
Radial distribution function g(r)



The area under the first peak indicates the number of nearest neighbors

17

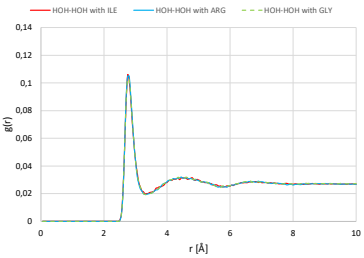
Radial distribution function g(r) of pure water – reference system



HOH = H_2O – water

18

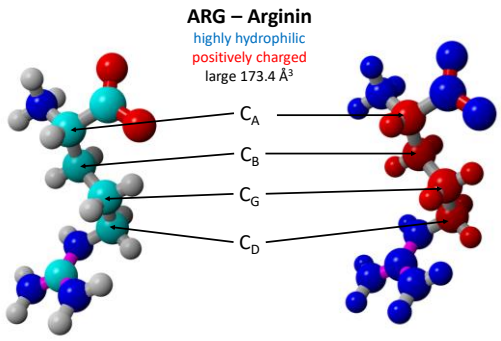
Radial distribution function g(r) of water surrounding amphiphilic residues



ILE – Isoleucine
ARG – Arginine
GLY – Glycine

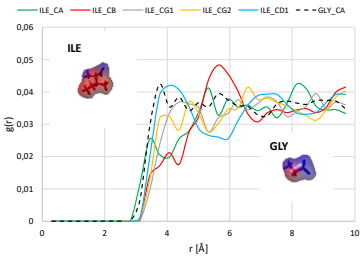
19

Radial distribution function g(r) - atom labeling



20

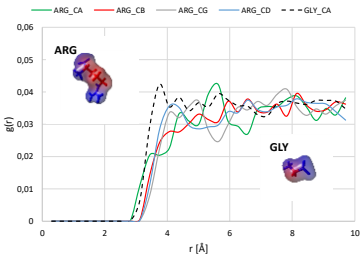
Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
AMPHIPHILIC EFFECT



ILE – Isoleucine - highly hydrophobic
GLY – Glycine - neutral

21

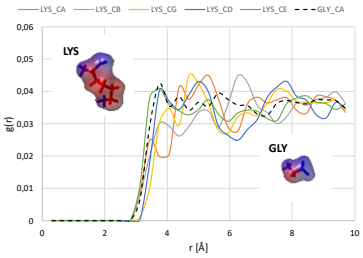
Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
AMPHIPHILIC EFFECT



ARG – Arginine - highly hydrophilic
GLY – Glycine - neutral

22

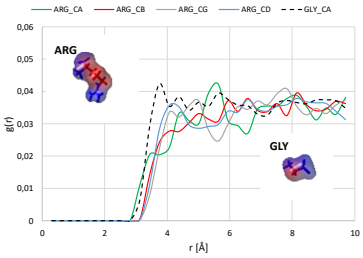
Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
NET CHARGE EFFECT



LYS – Lysine - positive charged
GLY – Glycine - neutral

23

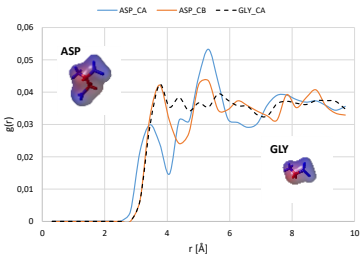
Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
NET CHARGE EFFECT



ARG – Arginine - positive charged
GLY – Glycine - neutral

24

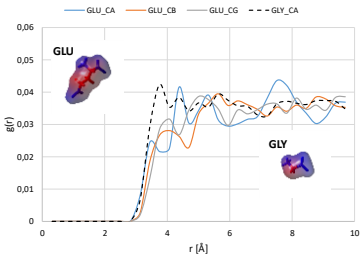
Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
NET CHARGE EFFECT



ASP – Aspartic acid - negative charged
GLY – Glycine - neutral

25

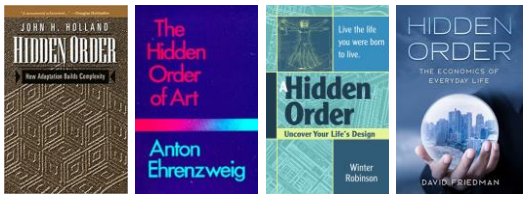
Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
NET CHARGE EFFECT



GLU – Glutamic acid - negative charged
GLY – Glycine - neutral

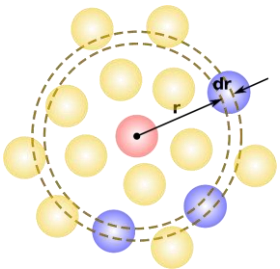
26

Does anyone see any ordered structure?



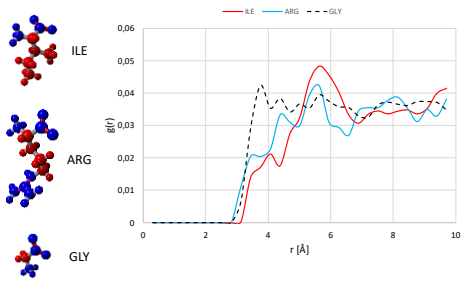
27

Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
THICKNESS OF THE SHELL EFFECT



28

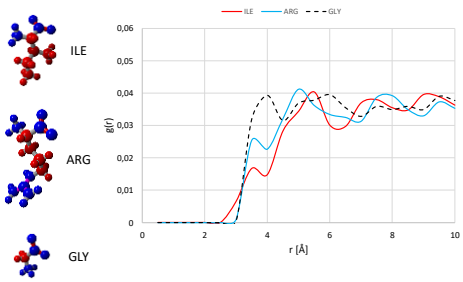
Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
THICKNESS OF THE SHELL EFFECT



dr =0.313 Å

29

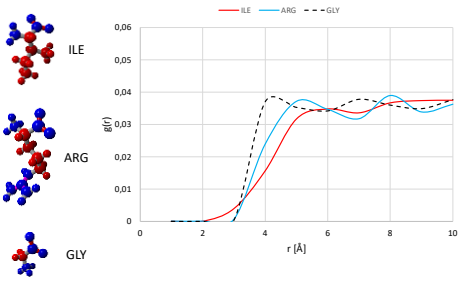
Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
THICKNESS OF THE SHELL EFFECT



dr =0.5 Å

30

Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
THICKNESS OF THE SHELL EFFECT



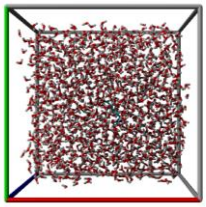
dr =1 Å

31

(In silico) Experimental setup #2

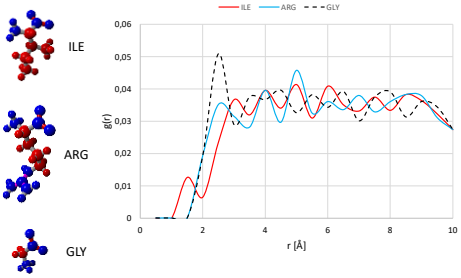
Procedure:

1. Energy minimization
2. Start (short) simulation
3. **Energy minimization**
4. Collect distance distribution between pairs of atoms/residues
5. **Calculate the radial distribution function**



32

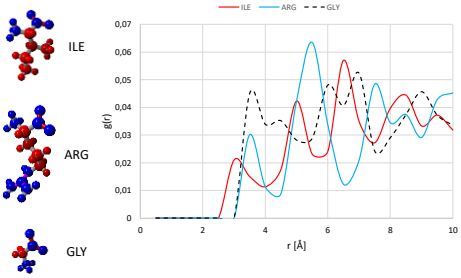
Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
ENERGY MINIMIZATION + STATIONARY STATE + THICKNESS OF THE SHELL EFFECT



Insufficient energy minimization

33

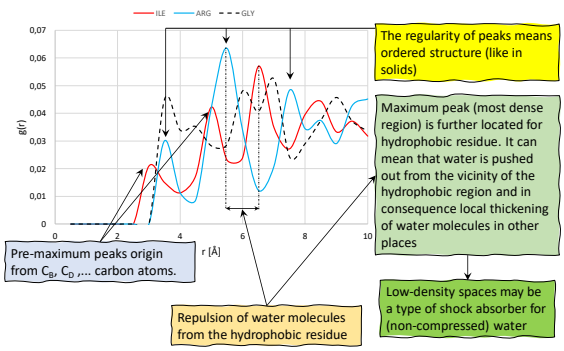
Radial distribution function g(r) of the pair: hydrophobic carbon atom – water
VERY DEEP ENERGY MINIMIZATION + STATIONARY STATE + THICKNESS OF THE SHELL



Very deep minimization means that the energy change ΔE in the next step of the simulation is less than 0.1 kJ/mol

34

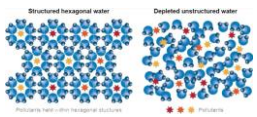
Summary



35

Conclusion

We are far from this state for now



but

there's a light in the tunnel

37