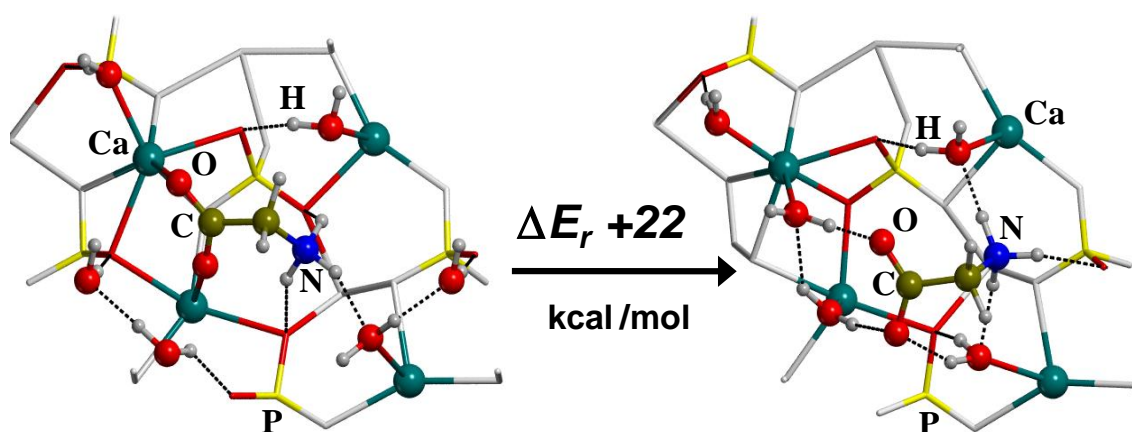


## Supplementary Information

**Title:** Ab initio Modeling of Protein/biomaterial Interactions: Competitive Adsorption between Glycine and Water onto Hydroxyapatite Surfaces

**Authors:** Albert Rimola, Marta Corno, Claudio Marcelo Zicovich-Wilson, and Piero Ugliengo\*



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## Surface Models

The (001) surface of hexagonal hydroxyapatite has been fully optimized using the CRYSTAL06 code at the B3LYP level within the slab approach; *i.e.*, by selective cuts of the optimized bulk<sup>1</sup> ( $[\text{Ca}_{10}(\text{PO}_4)_6(\text{OH})_2]$ , 44 atoms in the unit cell, space group  $P6_3$ ). The considered bare surface exhibits  $P3$  layer group symmetry, is a non-defective (vacancies, steps or kink sites), uncharged, stoichiometric slab of thickness 13.5 Å. To avoid any possible bias, for the present work, the optimization was carried out within the  $PI$  symmetry.

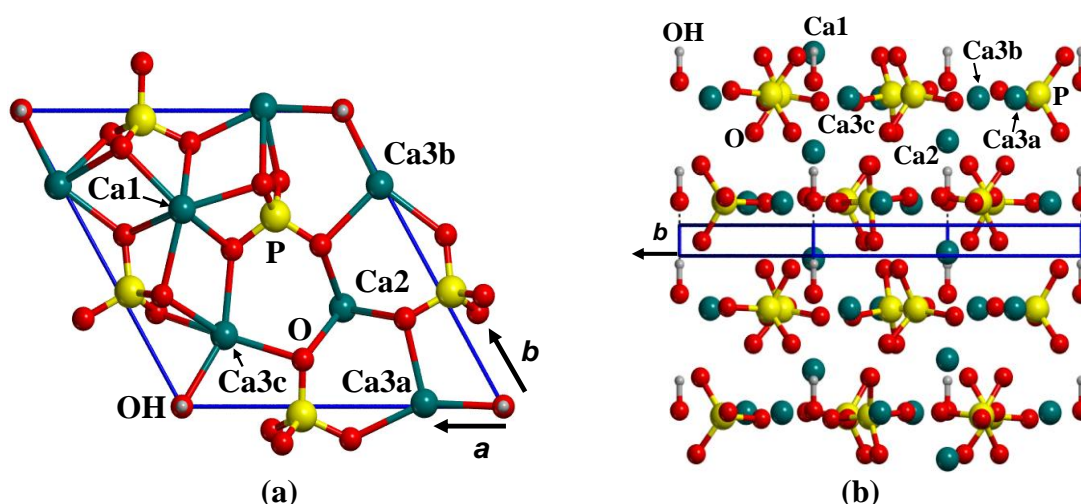
The (001) surface derived from the hexagonal HA (shown in Figure 1) exhibits a dipolar character due to the ferroelectric orientation of the OH groups. In a previous work,<sup>2</sup> the effect of ferroelectricity on the surface energy as a function of the slab thickness was carefully checked. The structural and electronic characterization of these models, in terms of surface energy, geometry relaxation, band gap, field across the slab and electrostatic features in close proximity of the surface, has shown that the OH ferroelectricity does not prevent the formation of a (001) slab of thickness of at least 10 nm. For these reasons and for computational convenience, the HA double-layer slab is considered as a proper model of the HA (001) crystal face to study adsorption processes (see Reference<sup>2</sup> for details). Table 1 reports some significant features of the (001) double-layer model, including the surface energy ( $E_{\text{surf}} = 1.043 \text{ J m}^{-2}$ ), which is defined as

$$E_{\text{surf}} = (E_{sN} - N \cdot E_b) / 2A$$

in which  $E_{sN}$ ,  $N$ ,  $E_b$ , and  $A$  are the energy of the slab unit cell, the number of bulk unit cell present in the considered slab model, the energy of the bulk and the unit cell area, respectively.

**Table 1.** B3LYP lattice parameters (Å), slab thickness (Å), unit cell surface area  $A$  (Å<sup>2</sup>), surface energy  $E_{\text{surf}}$  (J m<sup>-2</sup>) and average geometrical distances (Å) for the hexagonal (001) HA surface. The slab thickness is defined as the perpendicular distance between the most exposed Ca<sup>2+</sup> surface ions.

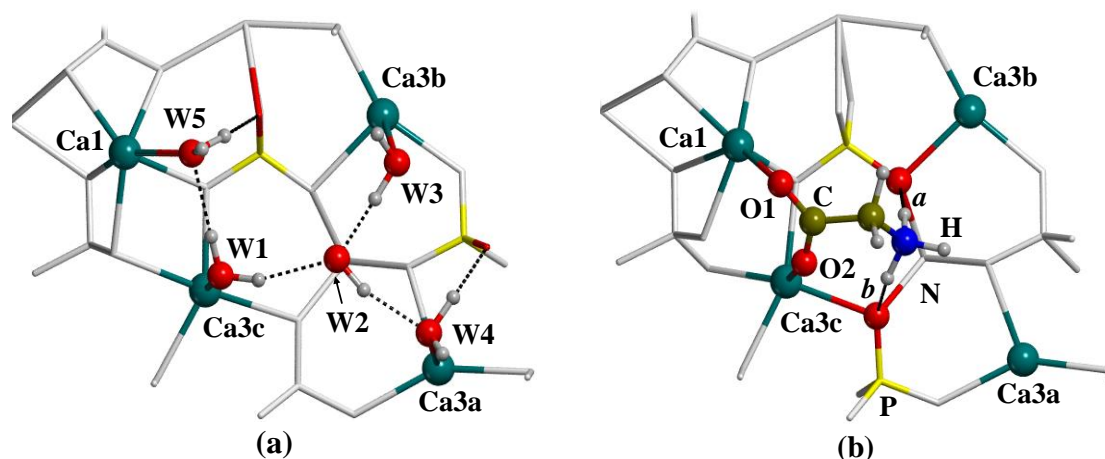
surface	$a$	$b$	thickness	$A$	$E_{\text{surf}}$	<P-O>	<Ca-O>	<O-H>
(001)	9.307	9.307	13.5	75.0	1.043	1.551	2.385	0.9705



**Figure 1.** B3YP-fully optimized structure of the (001) hydroxyapatite surface: (a) top view, (b) lateral view.

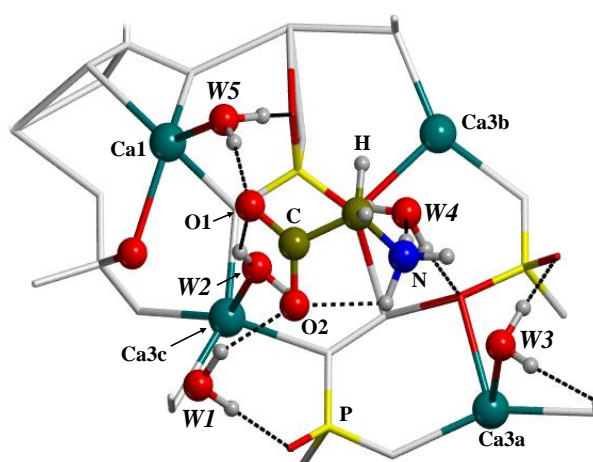
The analysis of the electrostatic potential features was useful to predict the possible adsorption sites. Highly positive values of potential were found on top of the Ca<sup>2+</sup> ions, suggesting compatible sites for the interaction with glycine electron rich groups. Deep negative zones are exhibited in close proximity of PO<sub>4</sub> groups so that it was expected that water and glycine donor hydrogen bond groups could easily interact with the (001) surface by exploiting rather strong H-bonds with the PO<sub>4</sub> groups.

In very recent works, the (001) HA surface's adsorptive capacity towards water<sup>3</sup> and glycine<sup>4</sup> have been investigated with the same computational parameters of the present work, considering Ca<sup>2+</sup> as adsorption sites. In the surface's unit cell, different Ca ions are available to adsorbates and each of them has been investigated in interaction with water and glycine. For the case of water, the effect of increasing molecules loading was considered and the vibrational properties of the models were computed within the harmonic approximation at  $\Gamma$  point. Results showed that H<sub>2</sub>O is molecularly adsorbed on the Ca ions of the (001) slab and, at higher water coverages, an important fraction of the interaction energy is due to inter-water H-bond. The average binding energy resulted about 90 kJ mol<sup>-1</sup> molecule<sup>-1</sup>. No water dissociation occurred; optimization starting from a pre-dissociated water molecule at the HA surface, reforms H<sub>2</sub>O in a barrierless process. For the case of glycine, results showed that the adsorption is given in its zwitterionic state, in which the COO<sup>-</sup> group interacts with two different Ca ions and the NH<sub>3</sub><sup>+</sup> establishes H-bond with the oxygen surface atoms.



**Figure 2.** B3-LYP-fully optimized structure of the (001) hydroxyapatite surface: (a) in interaction with five H<sub>2</sub>O molecules, (b) in interaction with glycine in the gas phase.

Among the various structures considered in this work, of particular relevance is structure [Gly-5w]0w/HA shown in Figure 3 below. It represents one glycine molecule adsorbed on a fully hydrated HA(001) surface originated from Figure 2a. This structure exhibits five H<sub>2</sub>O molecules in contact with HA(001) surface and has been used as a further case in the discussion to prove that glycine prefers to contact HA(001) directly rather than through water molecules. Indeed [Gly-5w]0w/HA structure is 38 kJ/mol higher in energy than the most stable [Gly-1w]4w/HA structure.



**Figure 3.** B3-LYP-fully optimized structure [Gly-5w]0w/HA of the (001) hydroxyapatite surface in direct interaction with five H<sub>2</sub>O molecules and one glycine (zwitterion) only interacting with the water layer.

## Computational Details

All calculations published in the present article have been carried out using a development version of the CRYSTAL06 periodic code,<sup>5</sup> which uses a local Gaussian basis set, allowing us to treat molecules, 1D periodic polymers, 2D periodic surfaces (slabs), and 3D crystals (bulks) with the same level of theory.<sup>6</sup> All calculations have been carried out on standard Linux boxes whereas graphical manipulations and vibration visualizations have been carried out with the molecular graphics program MOLDRAW<sup>7</sup> running on Microsoft Windows.

**Basis Set.** The details of the adopted Gaussian basis set are available on the CRYSTAL web site.<sup>8</sup> Here, the exponents of the outer sp and d shells in Bohr<sup>-2</sup> are explicitly given: H, 31G\* ( $\alpha_s=0.161$ ,  $\alpha_p=1.1$ ); O, 6-31G\* ( $\alpha_{sp}=0.27$ ,  $\alpha_d=0.8$ ); N, 6-31G\* ( $\alpha_{sp}=0.212$ ,  $\alpha_d=0.8$ ); C, 6-31G\* ( $\alpha_{sp}=0.1687$ ,  $\alpha_d=0.8$ ); P, ( $\alpha_{sp}=0.135$ ,  $\alpha_d=0.7458$ ); Ca, quasi-relativistic effective core potential of Hay and Wadt to represent the 10 innermost electrons, whereas a 31\* ( $\alpha_{sp}=0.5$ ) for the 8 outermost electrons and valence orbitals (basis [HAYWSC]-31G).

**Hamiltonian and Computational Parameters.** For systems in which hydrogen bond interactions are present, and in a periodic context, B3LYP has been proven to be rather accurate as far as structure, energetics, and vibrational frequency prediction are concerned.<sup>9,10</sup> It is now well established that standard GGA and hybrid functionals are unable to cope with dispersive interactions (London forces).<sup>11-13</sup> Because of that, the present absolute reaction energies should be considered underestimated by some amount. Because we mainly concern with the comparison between relative energies ( $\Delta E_{rel}$  of Table 1 in the paper) of structures containing the same number of atoms we do not expect this deficiency to affect the general trend. For the same reason, the basis set superposition error BSSE has not been taken into account because, while affecting the absolute values of  $\Delta E_{R1}$   $\Delta E_{R2}$   $\Delta E_{R3}$  it almost cancels out when computing the relative stability of the considered structures ( $\Delta E_{rel}$  of Table 1 in the paper). The Hamiltonian matrix is diagonalized<sup>5,14</sup> in  $10k$  points, corresponding to a shrinking factor of 4. Values of (6, 6, 6, 6, 14) for the tolerances controlling Coulomb and exchange series have been adopted for all calculations. The exchange and correlation functional is integrated numerically on a grid of points. Integration over radial and angular coordinates is performed through Gauss-Legendre and Lebedev schemes, respectively. A pruned grid consisting of 75 radial points and 5 subintervals with (86, 194, 350, 974, 350) angular points has been used for all calculations. This grid reduces the error to  $3 \times 10^{-5}$  electrons per unit cell in the total integrated electron

density (890 electrons). The SCF process was stopped when the energy difference between cycles was smaller than  $10^{-8}$  in the geometry optimizations.

**Geometry Optimization.** A full relaxation of the atomic coordinates within the *PI* symmetry was performed while keeping fix the lattice parameters; *i.e.*, the unit cell is kept fixed to the optimized values of the free HA (001) surface whereas the internal coordinates are relaxed by means of analytical DFT energy gradients.<sup>15,16</sup> The geometry optimization was performed by means of a quasi-Newton algorithm in which the quadratic step (BFGS Hessian updating scheme) is combined with a linear one (parabolic fit) as proposed by Schlegel.<sup>17</sup> Convergence was tested on the rms and the absolute value of the largest component of the gradients and the estimated displacements. The thresholds for the maximum force, the rms force, the maximum atomic displacement, and the rms atomic displacement on all atoms were set to 0.00045, 0.00030, 0.00180, and 0.00120 au, respectively. The optimization was considered to be complete when the four conditions were simultaneously satisfied.<sup>18</sup>

**Adopted strategy.** The procedure adopted to study the micro-solvation of glycine adsorbed on the HA(001) surface is described in detail in the text. Here we would like to expand upon some of the difficulties related to approaches different from the present one which can be adopted to tackle the same problem.

*Classical Molecular Dynamics (MD).* One possibility is to adopt classical MD in order to consider the “bulk water” on top of the HA surface. This approach heavily relies, for the results to be physically meaningful, on a well developed force field. Reasonably accurate force fields exist for amino acids and proteins and bulk water when treated separately. For HA (both bulk and surfaces), far less exists and only quite recently a new force field has been developed by some of us.<sup>19</sup> The point is that there are no force fields which are capable to model the complex interactions between amino acids and the surface of HA in presence of water as this will require to cope with a variety of interactions spanning from electrostatic to H-bond. Indeed, in absence of accurate force fields any results will be almost useless for instance, in assessing the role of “bulk water” when adopting the most accurate B3LYP approach.

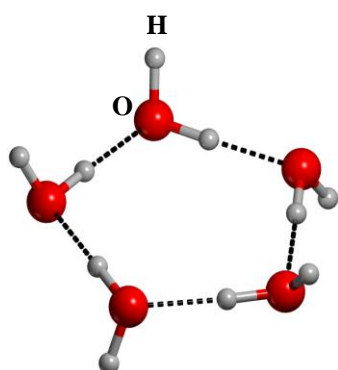
*Ab initio Molecular Dynamics (AIMD).* To study the process of moving glycine from bulk water towards a fully solvated (again in a bulk water) HA (001) surface one can adopt ab-initio molecular dynamics based on pseudo-potentials and plane-waves approach which is free from the points of weakness explained in the previous point. Let us summarize what are the difficulties which in our opinion hamper this straightforward approach. One should simulate a water slab on top of the HA(001) thick enough to be really representative of a

“bulk water”. The interspace between the HA slabs (not needed in our work because Gaussian-type orbitals are adopted) should be large enough to allow glycine to be solvated as in the water bulk when detaching from the HA surface. The problem is then similar to what we got with our simplified microsolvated model: the surrounding of glycine and HA is distorted by the limited amount of water considered but at a much higher computational cost. There is a further drawback in this approach: the MD simulation should run by a very long time to allow glycine to desorb from the HA surface considering the very high energy of interaction (see column  $\Delta E_{RI}$  of Table 1). The size of the system and the need for extremely long simulation time renders this approach at the limit of the top computational resources available in supercomputing centers.

## Optimized Fractionary Coordinates

In the paper it has been adopted the notation [Gly- $X_w$ ] $Y_w$ /HA to refer to a total of  $X+Y$   $H_2O$  molecules of which  $X$  bridge Gly through the HA surface whereas  $Y$  interact only with the HA surface. Optimized fractionary coordinates have been written in the MOLDRAW format (MOLDRAW is freely available at <http://www.moldraw.unito.it>). Each coordinates block starts with a TITLE record and is terminated by a “-1 0 0 0” record. The coordinates of each structure can be copied and pasted in an ASCII editor and saved as a file with .MOL extension.

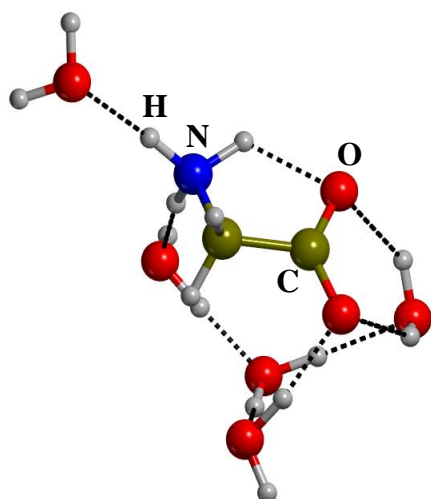
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# Gly/5w



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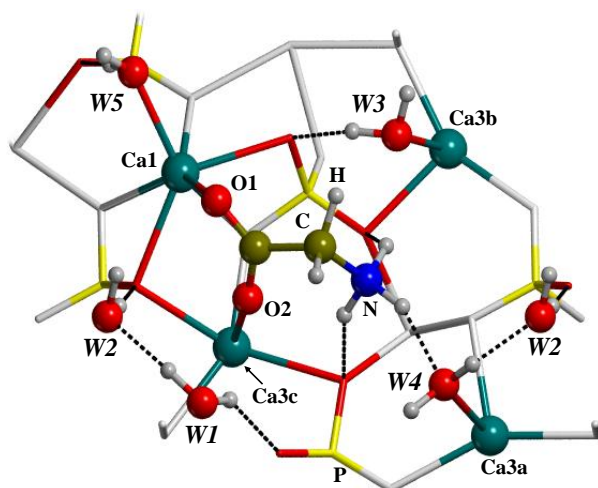
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[Gly-0w]5w/HA



No water molecules bridging the Gly-HA interaction.

Fully direct contact between Gly and HA

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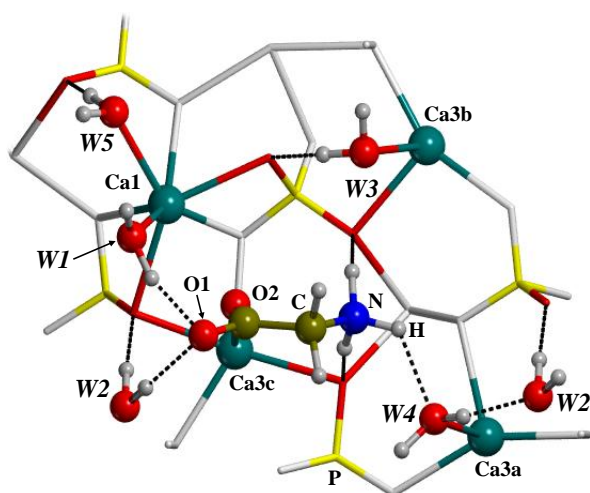
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### [Gly-1w]4w/HA



1 water molecule bridging the Gly-HA interaction.

Contact between Gly and HA through W1, which interferes the O1-Ca1 interaction

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TITLE
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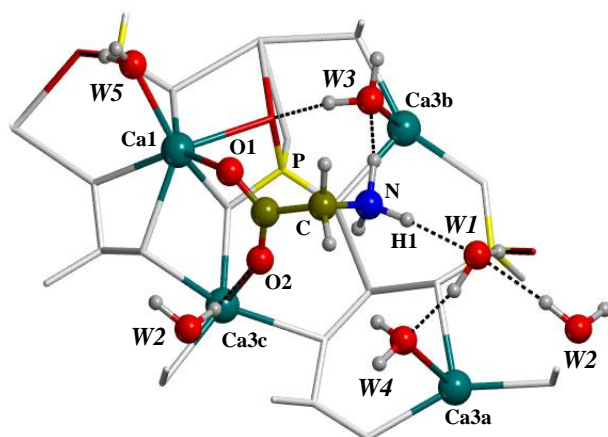
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[Gly-1w]4w-SI1/HA



1 water molecule bridging the Gly-  
HA interaction.  
Contact between Gly and HA  
through W1, which interferes the  
NH1-surface interaction

TITLE

[Gly-1w]4w-SI1/HA

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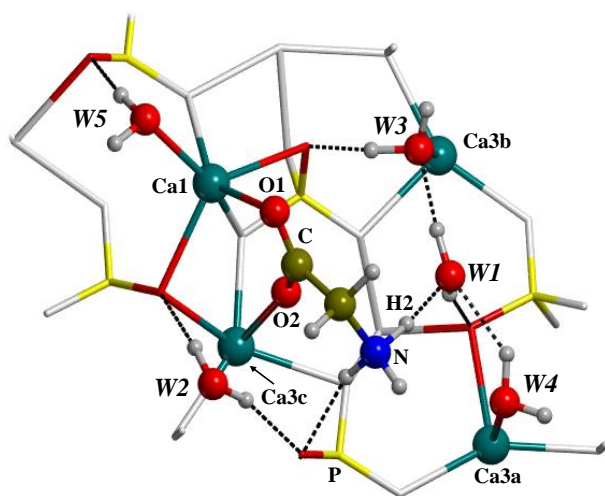
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### [Gly-1w]4w-SI2/HA



1 water molecule bridging the Gly-HA interaction.

Contact between Gly and HA through W1, which interferes the NH<sub>2</sub>-surface interaction

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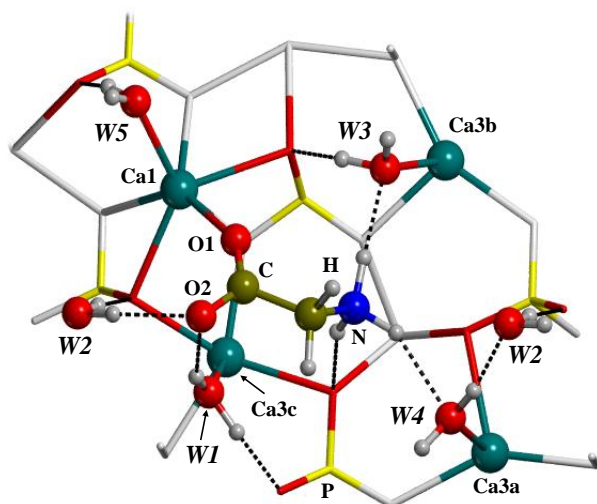
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### [Gly-1w]4w-SI3/HA



1 water molecule bridging the Gly-HA interaction.

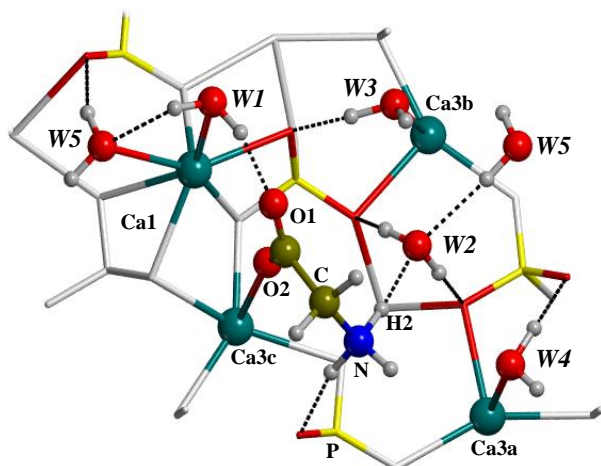
Contact between Gly and HA through W1, which interferes the O2-Ca3c interaction

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[Gly-2w]3w/HA



2 water molecules bridging the Gly-HA interaction.

Contact between Gly and HA through W1 and W2, which interfere the O1-Ca1 and the NH<sub>2</sub>-surface interactions, respectively.

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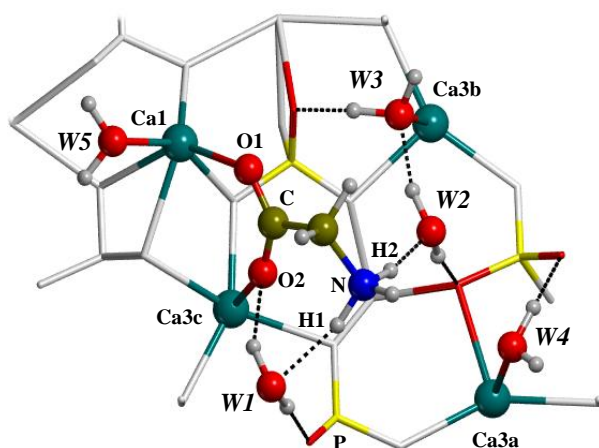
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### [Gly-2w]3w-SI1/HA



2 water molecules bridging the Gly-HA interaction.

Contact between Gly and HA through W1 and W2, which interfere the NH1-surface and NH2-surface interactions, respectively.

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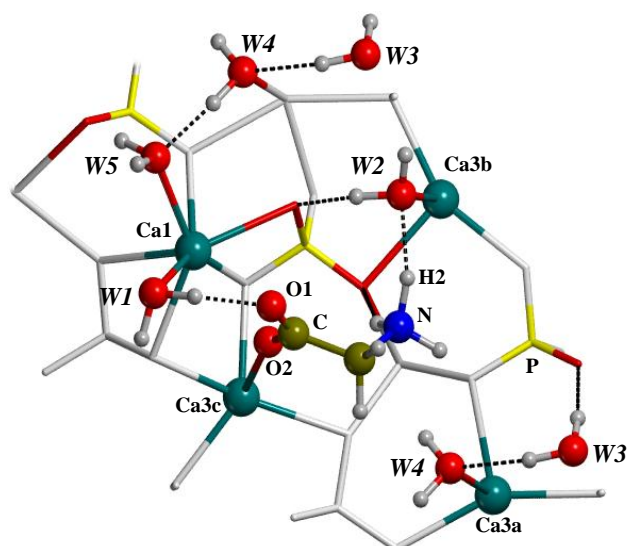
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### [Gly-2w]3w-SI2/HA



2 water molecules bridging the Gly-HA interaction.

Contact between Gly and HA through W1 and W2, which interfere the O1-Ca1 and NH<sub>2</sub>-surface interactions, respectively.

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[Gly-2w]3w-SI2/HA  
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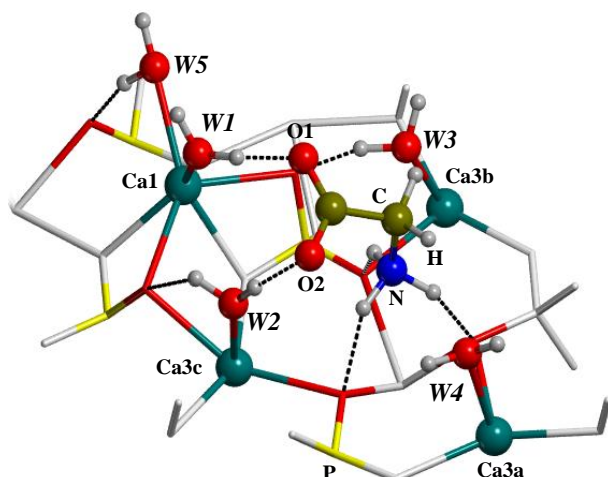
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[Gly-2w]3w-SI3/HA



2 water molecules bridging the Gly-HA interaction.

Contact between Gly and HA through W1 and W2, which interfere the O1-Ca1 and O2-Ca3c surface interactions, respectively.

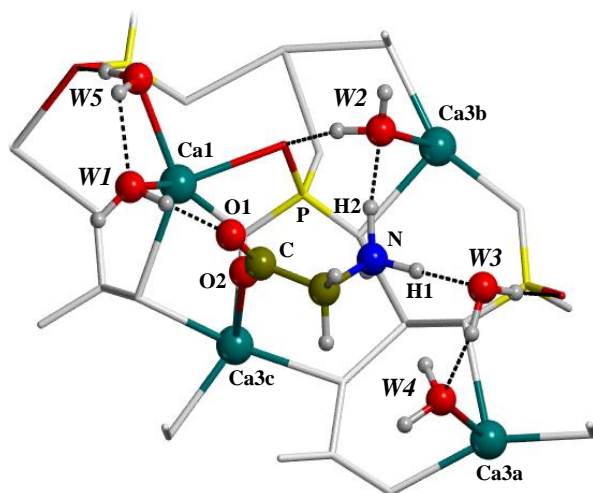
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### [Gly-3w]2w/HA



3 water molecules bridging the Gly-HA interaction.

Contact between Gly and HA through W1, W2 and W3, which interfere the O1-Ca1, NH<sub>2</sub>-surface and NH<sub>1</sub>-surface interactions, respectively.

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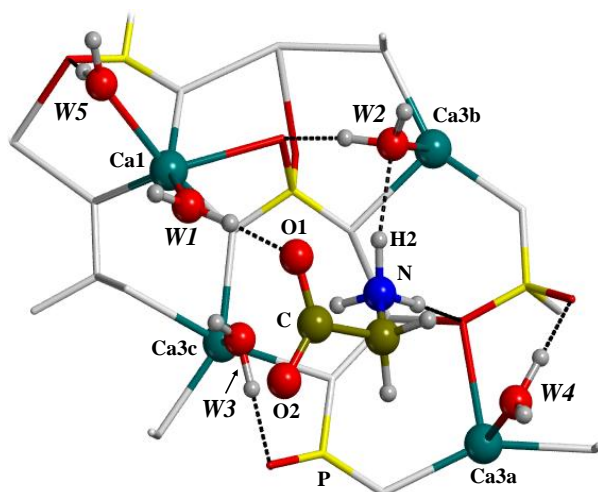
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### [Gly-3w]2w-SI1/HA



3 water molecules bridging the Gly-HA interaction.

Contact between Gly and HA through W1, W2 and W3, which interfere the O1-Ca1, NH<sub>2</sub>-surface and O2-Ca3c interactions, respectively.

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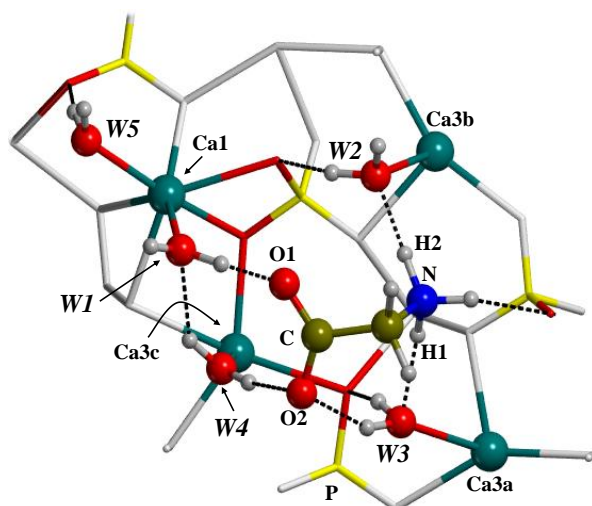
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8	0.263001328551	0.846841223551	8.669750364447
1	0.229740800212	0.896899932334	7.935198641860
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1	0.250809691180	0.287284582496	8.367006754143
1	0.249799707622	0.142544864993	7.499698302061
-1	0	0	0

[Gly-4w]1w/HA



4 water molecules bridging the Gly-HA interaction.

Contact between Gly and HA through W1, W2, W3, and W4, which interfere the O1-Ca1, NH<sub>2</sub>-surface, NH<sub>1</sub>-surface, and O2-Ca3c interactions, respectively.

```

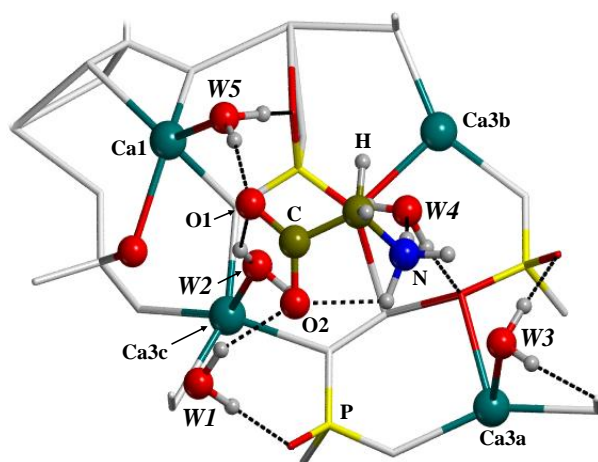
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8	0.847478970885	0.678832828121	0.550783544401
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8	0.564341824997	0.744710587676	-0.310691802385
8	0.201929317997	0.925037175041	-0.399966819724
8	0.041892938454	0.390370822301	-0.322575432567
1	0.947344638283	0.025929288328	-0.206044557588
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8	0.409621723678	0.902999925225	-1.799417810814
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### [Gly-5w]0w/HA



Gly adsorption onto HA-5w  
surface.

5 water molecules bridging the Gly-  
HA interaction.

No contact between Gly and HA

```

TITLE
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8	0.040501956536	0.986172586186	12.633733254120
1	0.421492385509	0.594322036403	13.578031654320
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1	0.095391996883	0.947108603085	12.011479033840
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8	0.333239686988	0.330569201799	11.623747199330
1	0.912711382696	0.229295677543	11.656237360220
1	0.305534146394	0.340248271601	12.543965086170
1	0.854102450073	0.056730289576	12.294021643500
1	0.378259803028	0.256478518096	11.644063543800
8	0.754963219057	0.477209427453	11.613895214610
1	0.671998533372	0.501984763768	11.259607176180
1	0.760154236980	0.407154155498	10.868907006930
-1	0	0	0



**Table 1.** Absolute electronic energies ( $E$ ) of the computed structures, in Hartrees. Relative energies ( $\Delta E_{\text{rel}}$ ), of the structures belonging to the Gly/5w/HA system, in kcal mol<sup>-1</sup>. The notation [Gly- $X$ w]Yw/HA refers to a total of  $X+Y$  H<sub>2</sub>O molecules of which  $X$  bridge Gly through the HA surface whereas  $Y$  interact only with the HA surface.

	structure	$E$ (Hartrees)	$\Delta E_{\text{rel}}$ (kcal mol <sup>-1</sup> )
fragments	5w	-381.99201545	
	Gly	-284.28424845	
	5w/Gly	-666.29052606	
	HA	-8742.20219147	
	5w/HA	-9124.34623291	
	Gly/HA	-9026.47547860	
	0 water at Gly/HA interface	[Gly-0w]5w/HA	-9408.70916978
1 water at Gly/HA interface	[Gly-1w]4w/HA	-9408.70726715	1.2
	[Gly-1w]4w-SI1/HA	-9408.69928672	6.2
	[Gly-1w]4w-SI2/HA	-9408.68988017	12.1
	[Gly-1w]4w-SI3/HA	-9408.68781288	13.4
2 water at Gly/HA interface	[Gly-2w]3w/HA	-9408.69632501	8.1
	[Gly-2w]3w-SI1/HA	-9408.69194824	10.8
	[Gly-2w]3w-SI2/HA	-9408.68869168	12.9
	[Gly-2w]3w-SI3/HA	-9408.67854284	19.2
3 water at Gly/HA interface	[Gly-3w]2w/HA	-9408.69291030	10.2
	[Gly-3w]2w-SI1/HA	-9408.69076107	11.6
4 water at Gly/HA interface	[Gly-4w]1w/HA	-9408.67477203	21.6
5 water at Gly/HA interface	[Gly-5w]0w/HA	-9408.64832359	38.1

**Table 2.** Absolute electronic energies ( $E$ ) of the single-point energy calculations for the extraction of one  $\text{H}_2\text{O}$  molecule, in Hartrees. Reaction energies ( $\Delta E_r$ ) of the water extraction process, in  $\text{kcal mol}^{-1}$ .

[Gly-0w]5w/HA $\rightarrow$ [Gly-0w]4w/HA + W		
Extracted water W	E [Gly-0w]4w/HA (Hartrees)	$\Delta E_r$ ( $\text{kcal mol}^{-1}$ )
W1	-9332.280751	31.1
W2	-9332.270294	37.6
W3	-9332.266350	40.1
W4	-9332.261874	42.9
W5	-9332.253153	48.4
[Gly-1w]4w/HA $\rightarrow$ [Gly-1w]3w/HA + W		
Extracted water W	E [Gly-1w]3w/HA (Hartrees)	$\Delta E_r$ ( $\text{kcal mol}^{-1}$ )
W2	-9332.272848	36.0
W3	-9332.269555	38.1
W4	-9332.269102	38.4
W5	-9332.255208	47.1
[Gly-2w]3w/HA $\rightarrow$ [Gly-2w]2w/HA + W		
Extracted water W	E [Gly-2w]2w/HA (Hartrees)	$\Delta E_r$ ( $\text{kcal mol}^{-1}$ )
W3	-9332.252563	48.7
W4	-9332.247052	52.2
W5	-9332.237212	58.4
[Gly-3w]2w/HA $\rightarrow$ [Gly-3w]1w/HA + W		
Extracted water W	E [Gly-3w]1w/HA (Hartrees)	$\Delta E_r$ ( $\text{kcal mol}^{-1}$ )
W4	-9332.260724	43.6
W5	-9332.235398	59.5

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