

Supplementary Material for

Molecular Simulation of Fibronectin Adsorption onto Polyurethane Surfaces

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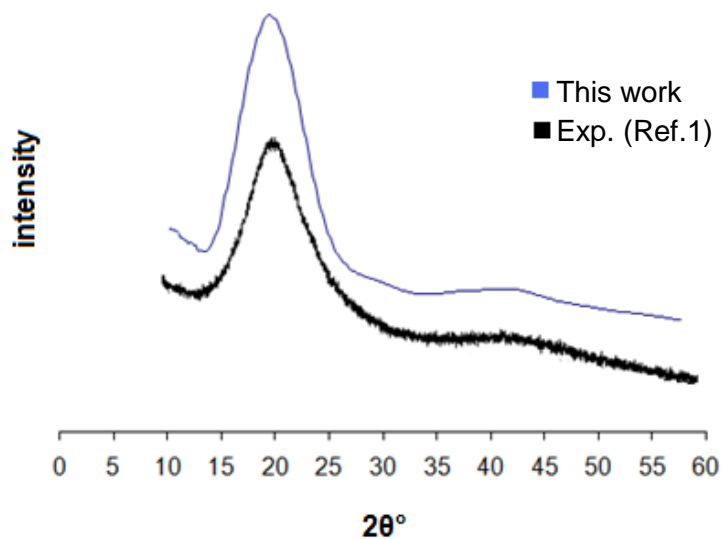


Figure S1. Experimental [1] and simulated x-ray pattern of amorphous CO-HDI polymer

Table S1. Structural and mechanical properties of amorphous PVA and CO-HDI

Property	Method	PVA	CO-HDI
Young modulus (GPa)	This work	5.43	1.76
	Experimental [2]	4.34+/-0.017	
Poisson ratio	This work	0.31	0.37
	Experimental [3]	0.426-0.447	
Radius of gyration (Å)	This work	8.17	16.61
	Experimental [4]	11.4	
Cohesive energy density (cal/cm ³)	This work	138.87	
	Experimental [4]	158-201	
Solubility parameter (cal/cm ³) ^{1/2}	This work	11.78	
	Experimental [4]	12.6-14.2	

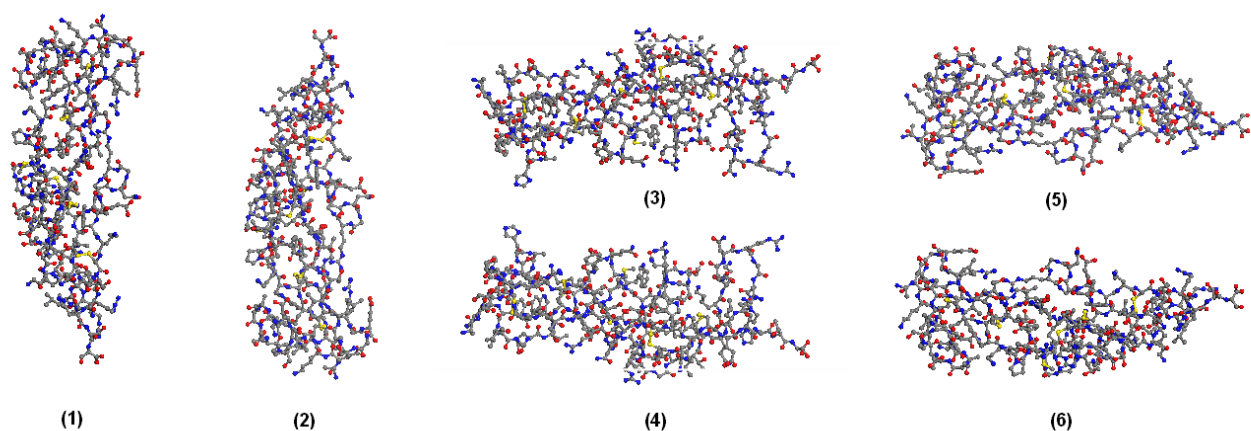


Figure S2 : Fibronectin domain 1FBR in six different initial orientations perpendicular to the polymer surfaces. Hydrogen atoms are omitted for the purpose of clarity.

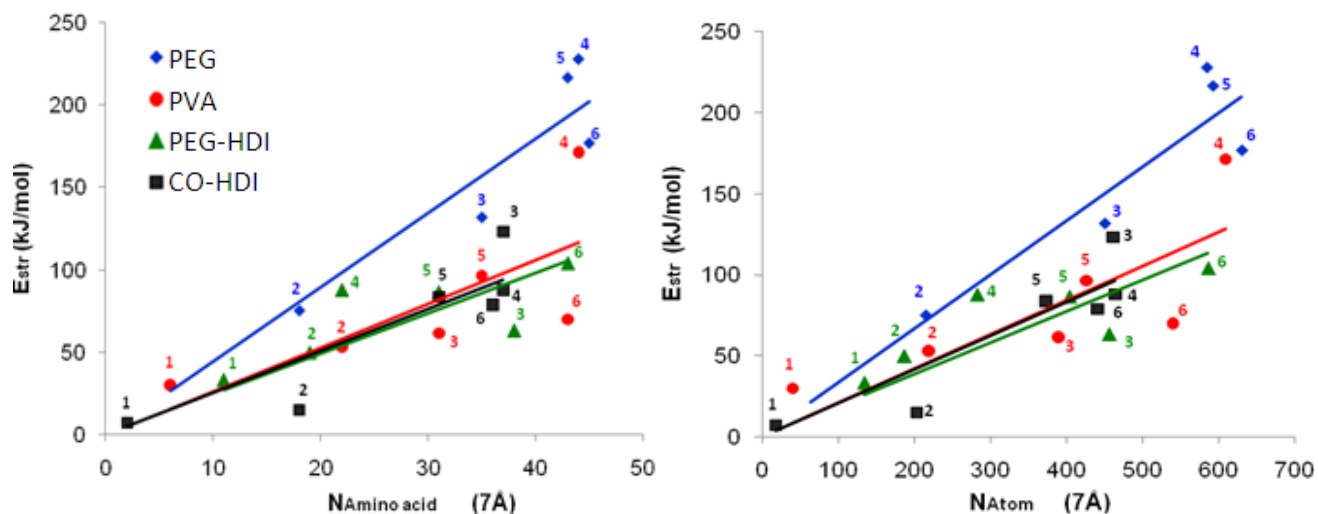


Figure S3. Strain energies with respect to protein amino acids and atoms within an adsorption layer of $\delta = 7\text{\AA}$ on the polymer surface after energy minimization. Numbers next to the data marks indicate the initial orientation of the protein above the surface as defined in Figure S2.

Table S3. Absolute protein-surface interaction energies E_{int} (kJ/mol) and strain energies E_{strain} (kJ/mol) after energy minimization as function of the adsorption layer thickness (δ) based on the number of amino acids (N_{AA}) and on the number of protein atoms (N_{Atom}).

E_{int} (kJ/mol)	N_{AA}			N_{Atom}		
	$\delta = 3 \text{ \AA}$	$\delta = 5 \text{ \AA}$	$\delta = 7 \text{ \AA}$	$\delta = 3 \text{ \AA}$	$\delta = 5 \text{ \AA}$	$\delta = 7 \text{ \AA}$
PEG	25.01	19.66	15.16	5.67	1.70	1.12
PVA	19.73	13.32	10.25	4.84	1.39	0.81
PEG-HDI	28.23	20.10	15.30	6.20	1.94	1.20
CO-HDI	23.93	15.68	11.88	5.93	1.60	0.97

E_{strain} (kJ/mol)	$\delta = 3 \text{ \AA}$	$\delta = 5 \text{ \AA}$	$\delta = 7 \text{ \AA}$	$\delta = 3 \text{ \AA}$	$\delta = 5 \text{ \AA}$	$\delta = 7 \text{ \AA}$
	PEG	7.49	5.84	4.49	1.67	0.51
PVA	5.04	3.50	2.65	1.29	0.37	0.21
PEG-HDI	4.80	3.29	2.46	1.01	0.32	0.19
CO-HDI	4.52	3.38	2.54	1.29	0.35	0.21

Table S4. Number of amino acids (N_{AA}) adsorbed on the polymer surfaces in the most favorable orientation for $\delta = 7 \text{ \AA}$ after energy minimization.

PEG-HDI		CO-HDI		PEG		PVA	
Orientation	N_{AA}	Orientation	N_{AA}	Orientation	N_{AA}	Orientation	N_{AA}
6		3		5		4	
GLY	4	GLY	4	ARG	5	THR	6
SER	4	CYS	3	ASN	4	GLY	4
ASP	3	ASP	3	THR	4	ARG	4
ARG	3	ARG	3	SER	3	SER	4
THR	3	ASN	3	GLU	3	GLU	4
TYR	3	THR	2	GLN	3	LYS	3
TRP	3	TRP	2	CYS	3	CYS	3
GLN	2	GLN	2	LYS	3	TRP	3
ALA	2	ALA	2	GLY	2	ASN	2
GLU	2	GLU	2	ASP	2	ASP	2
LYS	2	LYS	2	LEU	2	LEU	2
HIS	2	HIS	1	TRP	2	ILE	2
MET	2	MET	1	MET	2	GLN	1
CYS	2	TYR	1	ALA	1	ALA	1
ASN	2	SER	1	TYR	1	TYR	1
PHE	1	PHE	1	VAL	1	VAL	1
PRO	1	PRO	1	ILE	1	HIS	1
VAL	1	VAL	1	HIS	1		
LEU	1	LEU	1				
		ILE	1				
Total AA	43		36		43		44
Polar AA	31		20		29		24

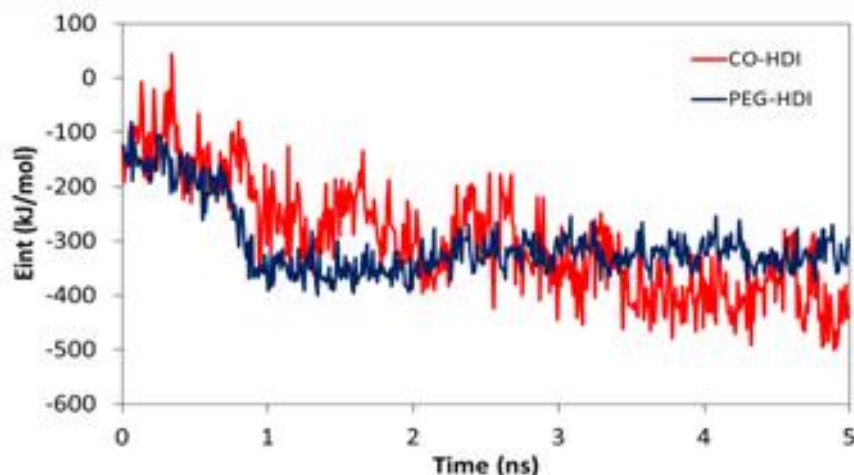


Figure S4. Equilibration of the protein-surface interaction energy on CO-HDI and PEG-HDI surfaces.

References

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