Electronic Supplementary Material (ESI) for New Journal of Chemistry.

Supporting Information for

Computer aided design and NMR characterization of an oligopeptide targeting Ebola virus VP24 protein

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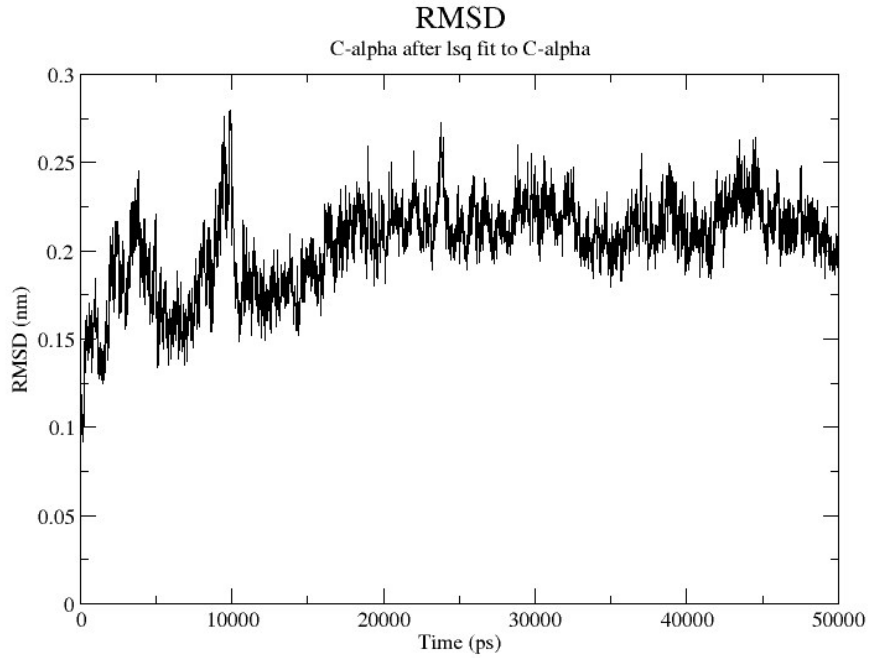

Fig. S1 RMSD versus time for VP24-K complex Cα atoms considering the crystal structure as reference

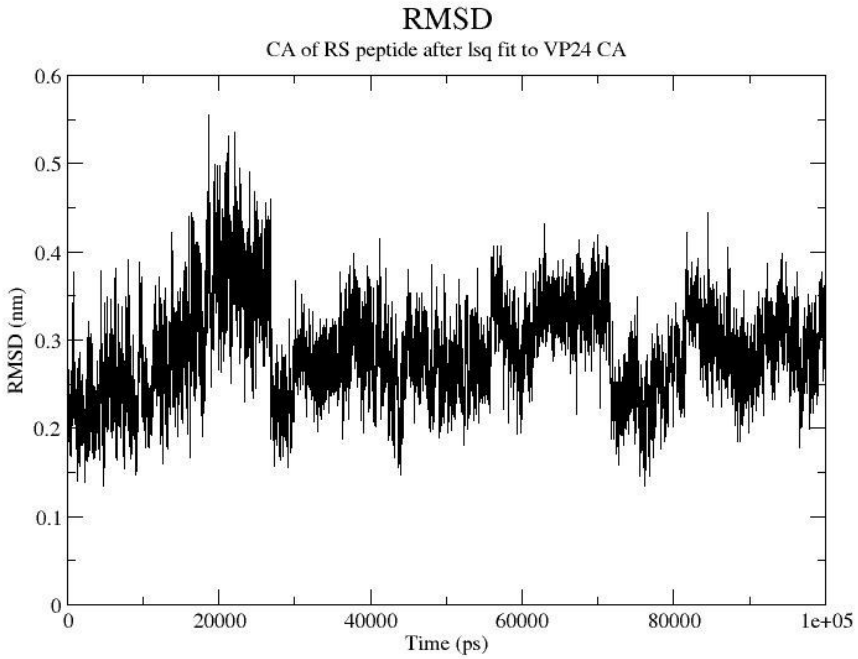

Fig. S2 RMSD versus time for the RS peptide in complex with VP24.

Mutation	$\Delta\Delta G \ / \ kcal\ mol^{-1}$	$err \ / \ kcal\ mol^{-1}$
TYR477’	7.68	0.60
LEU479’	0.76	0.60
ASP480’	18.28	0.57
LYS481’	19.71	0.60
ILE482’	1.67	0.62
GLU483’	10.67	0.55
PHE484’	6.99	0.60

Table S1 Computational alanine scanning results for RS peptide in complex with VP24

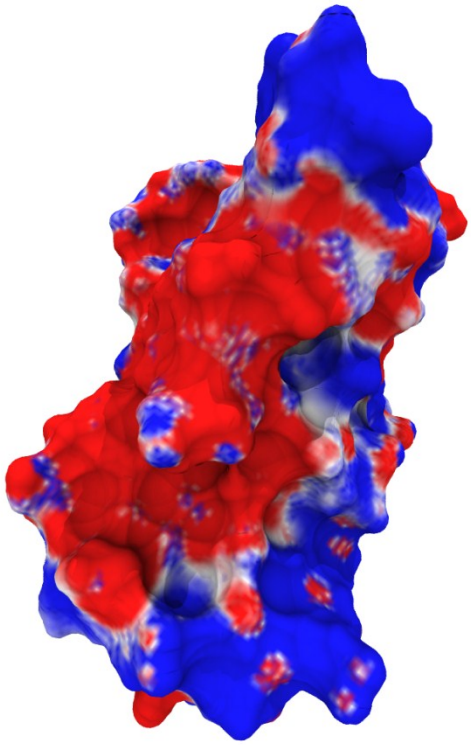

Fig. S3 Electrostatic potential of VP24 at the interface with Karyopherin. Values ranging from -1 k_bT/e (red) to +1 k_bT/e (blue)

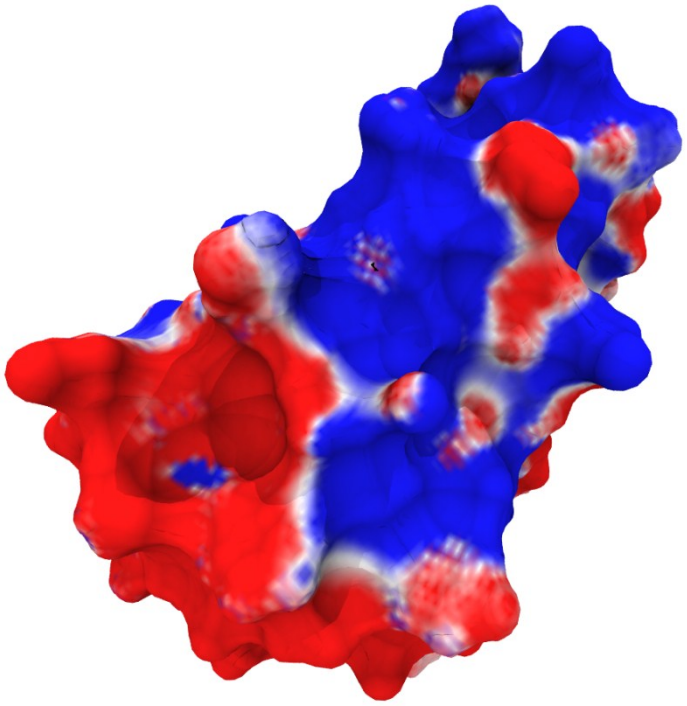

Fig. S4 Electrostatic potential of Karyopherin at the interface with VP24. Values ranging from -1 k_bT/e (red) e to +1 k_bT/e (blue)

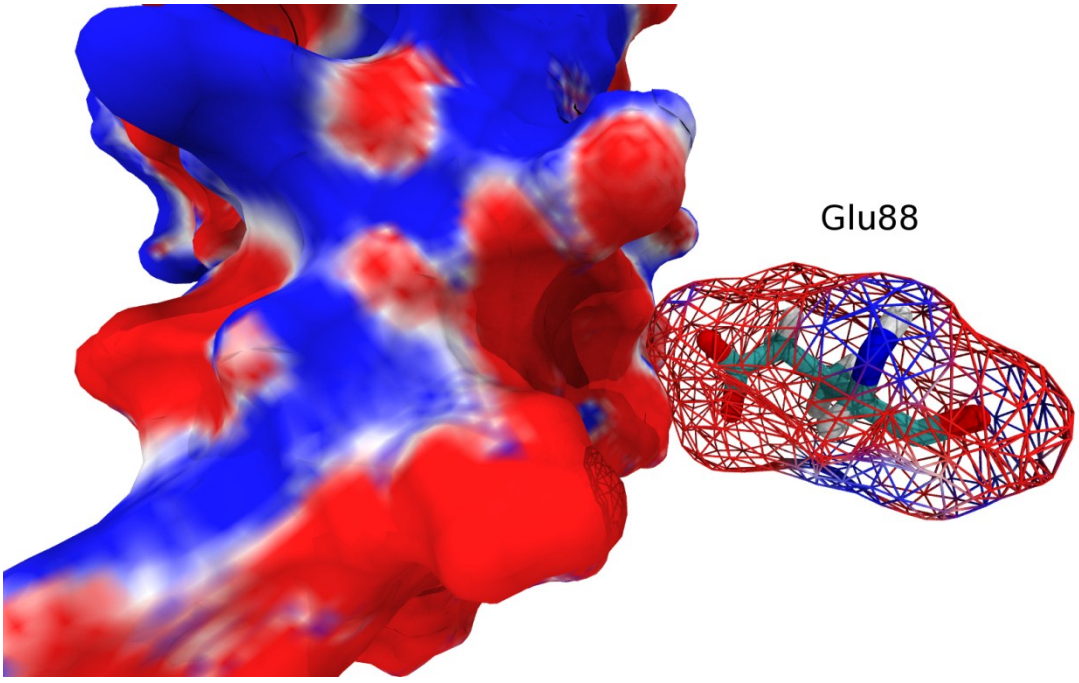

Fig. S5 Electrostatic potential of Glu88 (mesh grid) facing Karyopherin interface (surface representation). Values ranging from -1 k_bT/e (red) e to +1 k_bT/e (blue).

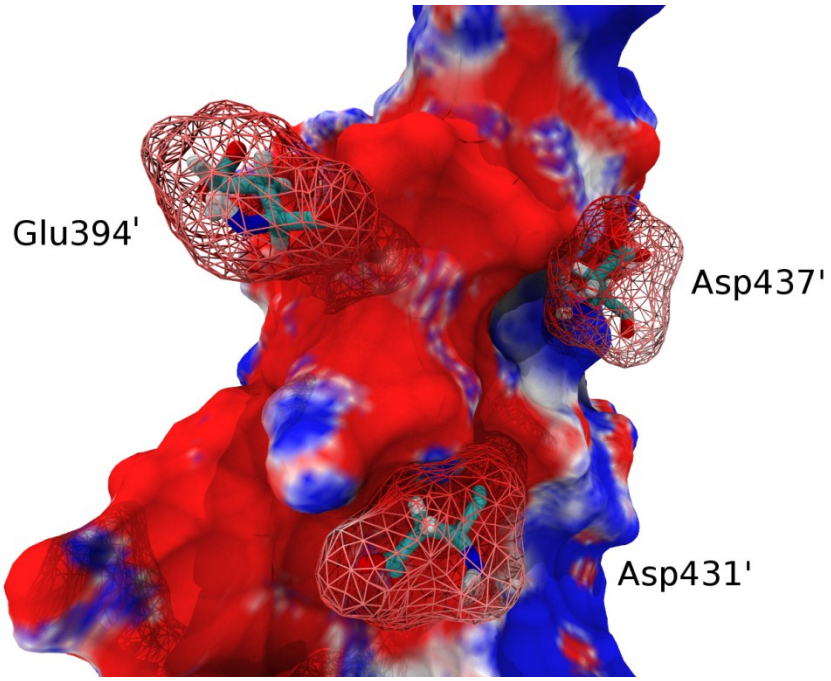

Fig. S6 Electrostatic potentials of Glu394', Asp431' and Asp 437' (mesh grid) facing VP24 interface (surface representation). Values ranging from -1 k_bT/e (red) e to +1 k_bT/e (blue).

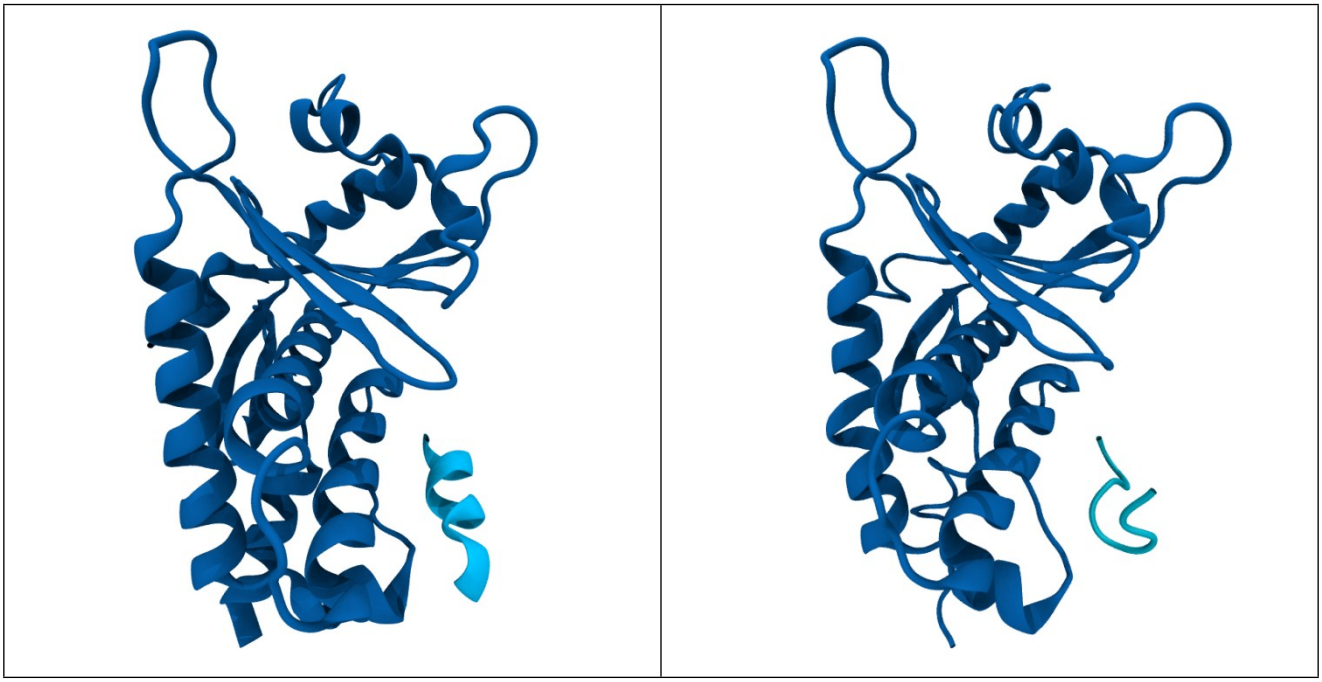

Fig. S7 The RS peptide in complex with VP24. In the left panel the starting complex structure is shown, in the right panel the VP24-RS structure after MS simulation. RS, while keeping its interaction with the protein, loses its helical shape.

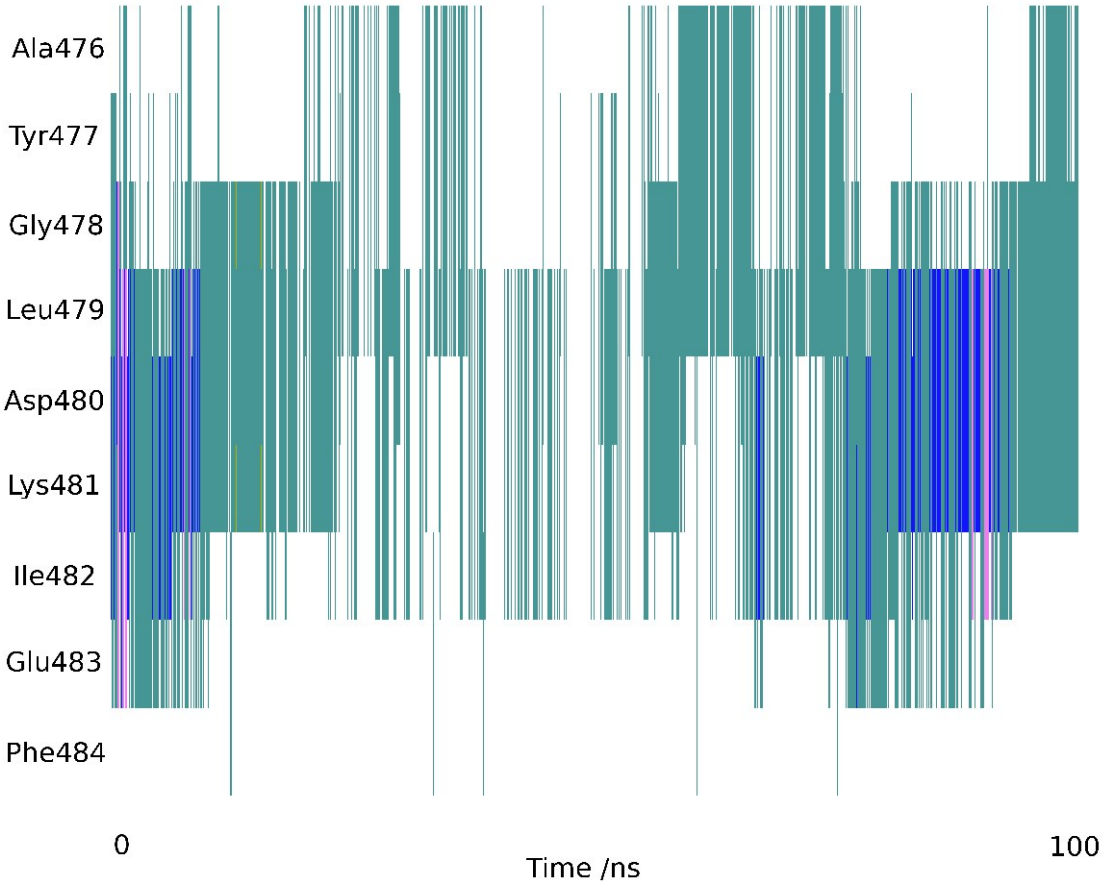

Fig. S8 Time evolution of secondary structure of RS in solution as obtained from MD simulation. Residues belonging to alpha helix are highlighted in pink.

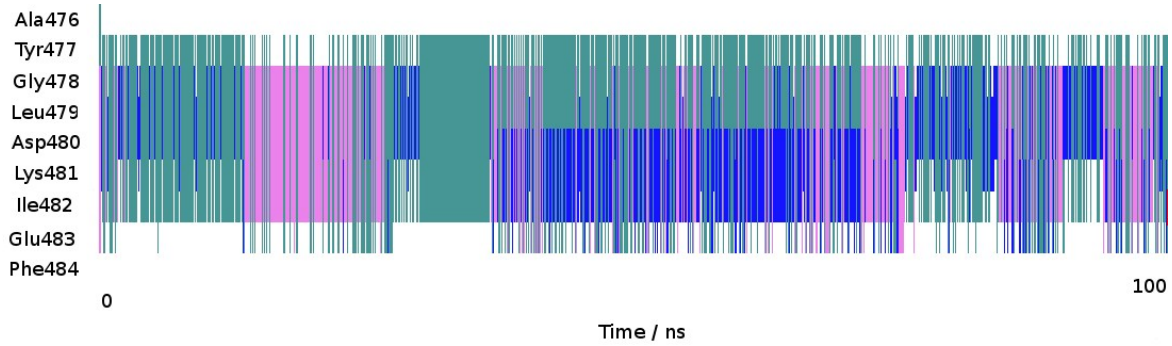

Fig. S9 Time evolution of secondary structure of RS in complex with VP24 as obtained from MD simulation. Residues belonging to alpha helix are highlighted in pink.

a.a.	NH	α	β	γ	δ	ε	Other
Ala476’	8.11	4.17	1.19		COCH3 1.91		
Tyr477’	8.06	4.53	3.05	2.82			7.07, 6.78
Gly478’	8.22	3.98					
Leu479’	7.98	4.26	1.74	1.57	0.85		
Asp480’	8.33	4.51	2.65				
Lys481’	7.98	4.24	1.77	1.67	1.59	1.33	2.91
Ile482’	7.99	4.02	1.75	0.74			
Glu483’	8.30	4.22	2.08	1.80			
Phe484’	8.10	4.54	3.14	2.94			7.30, 7.22, 7.26

Table S2. Chemical shifts of RS peptide in H_2O/D_2O at 298 K in phosphate buffer

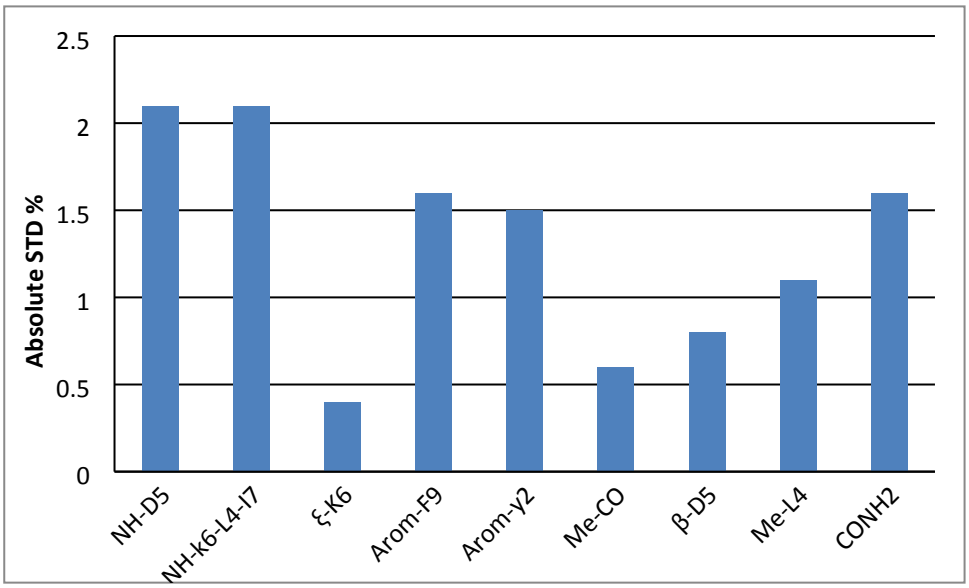

Fig. S10. Absolute STD % obtained for peptide-VP24 complex.

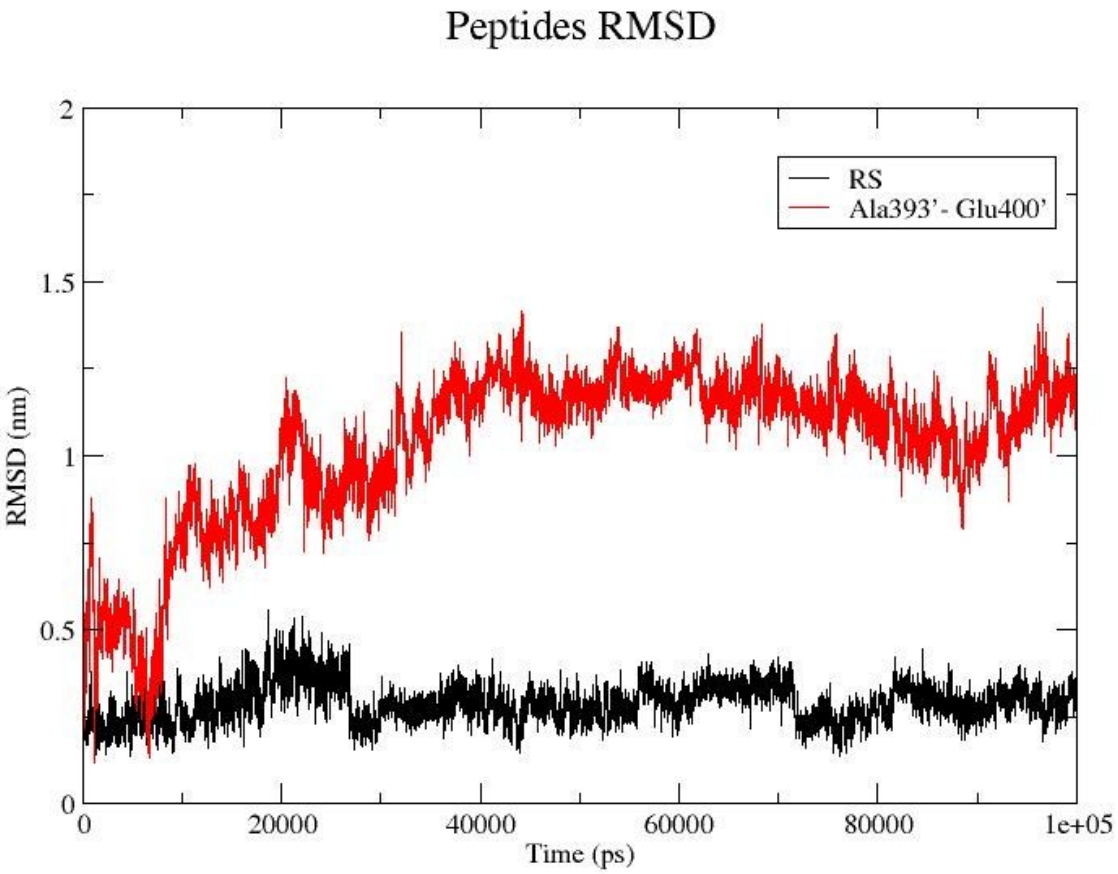

Fig. S11. Comparisons of RMSD between RS (black) and peptide comprising residues ranging from Ala393' to Glu400' (red).

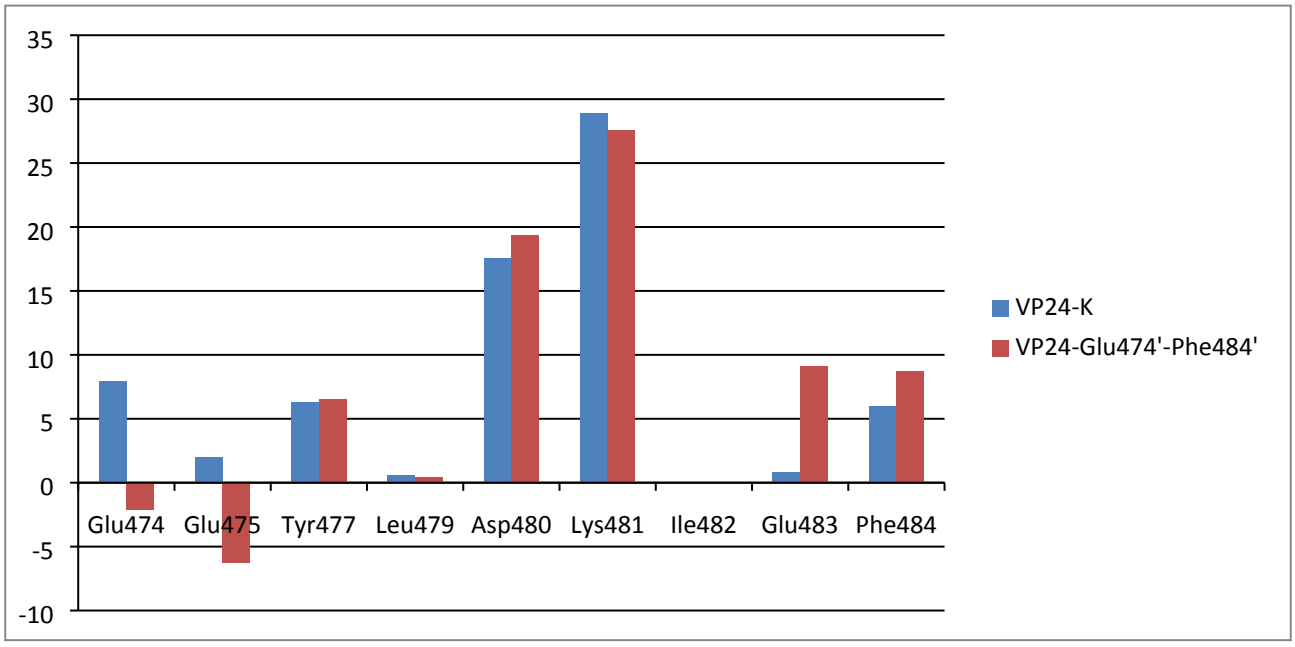

Fig. S12. Computational Alanine Scanning results for residues ranging from Glu 474' to Phe 484' belonging to Karyopherin (blue bars) or to the extracted peptide (red bars).

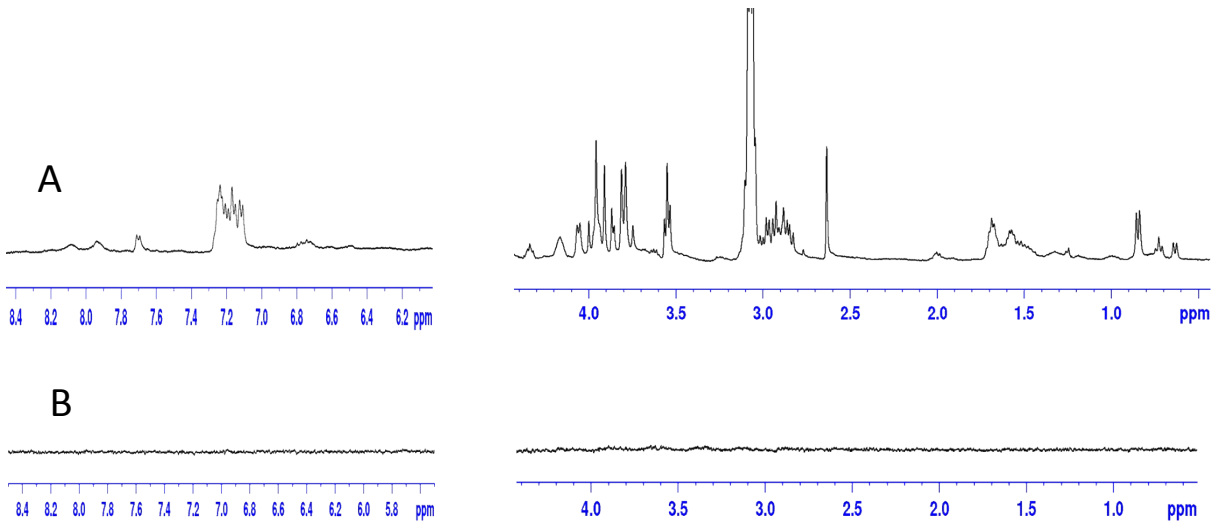

Fig. S13. A) ^{1}H-NMR spectrum of 1 mM peptide A in the presence of 22 µM VP24 protein in phospate buffer. B) STD-NMR spectrum of the same sample. No signals were observed.

	E113	L121	D124	N135	R137	R140	V141	E203	D205	K218	R396	R398	K399	K427	T434	M436	E474	E475	T477	D480	K481	F484
E113																			vdW		vdW	vdW
L121							vdW														SB	
D124															HB							
N135																				HB		
R137																		SB				
R140		vdW																	vdW		vdW	vdW
V141								SB														
E203									SB													
D205																						
K218									SB													
R396																						
R398								SB														
K399																						
K427			HB																			
T434																						
M436																						
E474						SB																
E475					HB																	
T477		vdW					vdW														vdW	vdW
D480					HB																	
K481		vdW	SB				vdW												vdW			vdW
F484		vdW					vdW												vdW		vdW	

Table S3. Interaction table for hot spots of the VP24-KPNA complex. In cyan van der Waals interactions, in orange salt bridges and in green H-bond.