Supplementary Data

Evaluation of *Annona muricata* Acetogenins as Potential Anti-SARS-Cov-2 Agents Through Computational Approaches

SARS-CoV-2 Spike Protein – Crystal structure

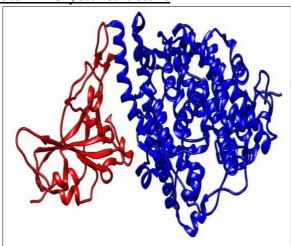
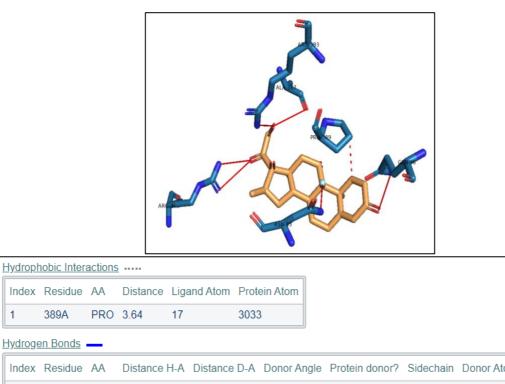


Figure S1: The crystal structure of corona virus spike (S) receptor (blue colored) - binding domain bound with ACE2 receptor (red colored) (PDB ID: 6M0J).

<u>Ligand-Protein Interaction</u>

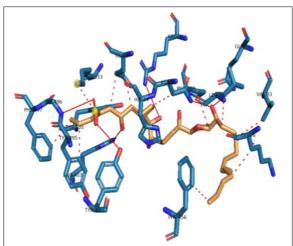
Index Residue AA

389A



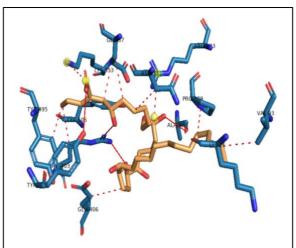
Index	Residue	AA	Distance H	-A Distance	D-A Donor Ang	le Protein do	onor? Sidechain	Donor Atom	Acceptor Aton
1	96A	GLN	2.38	3.24	145.33	✓	✓	670 [Nam]	23 [O2]
2	387A	ALA	2.45	3.33	142.86	×	×	26 [O3]	3017 [O2]
3	393A	ARG	1.89	2.85	162.58	✓	✓	3072 [Ng+]	26 [O3]
4	403E	ARG	2.36	3.31	160.96	✓	✓	5449 [Ng+]	25 [O2]
5	403E	ARG	2.71	3.57	145.33	✓	✓	5448 [Ng+]	25 [O2]
laloger	Bonds -								
Index	Residue	AA	Distance [Donor Angle	Acceptor Angle	Donor Atom	Acceptor Atom		
1	33A	ASN	3.05	135.51	123.49	28 [F]	154 [Nam]		

Figure S2: The detailed interaction of dexamethasone against SARS-CoV-2 spike protein.



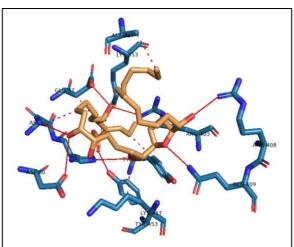
Index	Residue	AA	Distance	Liga	nd Atom	Prot	ein Atom				
1	26A	LYS	3.42	17		107					
2	26A	LYS	3.46	10		108					
3	29A	LEU	3.87	9		134					
4	33A	ASN	3.47	26		170					
5	34A	HIS	3.99	28		178					
6	37A	GLU	3.64	30		203					
7	37A	GLU	3.64	28		202					
8	93A	VAL	3.76	11		663					
9	389A	PRO	3.83	6		3050)				
10	456E	PHE	3.68	20		5885	5				
11	495E	TYR	3.54	34		6188	3				
12	497E	PHE	3.64	35		6206	5				
13	505E	TYR	3.84	30		6264	4				
<u>ydroge</u>	n Bonds	_									
Index	Residue	AA	Distance	H-A	Distance	D-A	Donor Angle	Protein donor?	Sidechain	Donor Atom	Acceptor Atom
1	33A	ASN	1.93		2.80		145.63	~	~	172 [Nam]	37 [O3]
2	96A	GLN	3.30		3.84		116.56	~	~	688 [Nam]	37 [O3]
3	393A	ARG	3.31		4.03		131.57	~	~	3090 [Ng+]	42 [O3]
4	403E	ARG	2.37		2.88		112.00	~	~	5466 [Ng+]	41 [O3]
5	453E	TYR	2.91		3.80		159.87	~	~	5859 [O3]	40 [O.co2]
6	453E	TYR	2.89		3.80		157.23	×	~	40 [O.co2]	5859 [O3]
7	496E	GLY			3.92		126.20	~	×	6194 [Nam]	

Figure S3: The detailed interaction of Annomuricin A against SARS-CoV-2 spike protein.



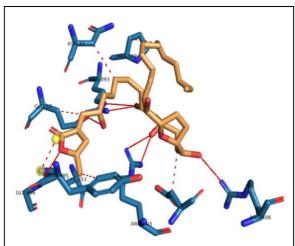
Index	Residue	AA	Distance	Ligand Aton	n Prot	tein Atom				
1	26A	LYS		19	106					
2	33A	ASN	3.97	26	168					
3	37A	GLU	3.65	29	201					
4	37A	GLU	3.97	27	200					
5	93A	VAL	3.62	18	661					
6	389A	PRO	3.81	15	304	8				
7	403E	ARG	3.96	34	546	0				
8	406E	GLU	3.83	5	548	3				
9	495E	TYR	3.75	34	618	6				
10	505E	TYR	3.96	31	626	0				
11	505E	TYR	3.59	29	626	2				
l <u>ydroge</u>	en Bonds									
Index	Residue	AA	Distance	H-A Distanc	e D-A	Donor Angle	Protein donor?	Sidechain	Donor Atom	Accepto
1	387A	ALA	2.22	3.11		151.77	×	×	42 [O3]	3033 [O
2	403E	ARG	2.39	2.91		112.15	~	❤	5464 [Ng+]	41 [O3]
3	403E	ARG	2.68	3.06		103.73	~	❤	5465 [Ng+]	35 [O3]
4	453E	TYR	3 14	4.01		154.74	~	~	5857 [O3]	40 [O.co

Figure S4: The detailed interaction of Annomuricin B against SARS-CoV-2 spike protein.



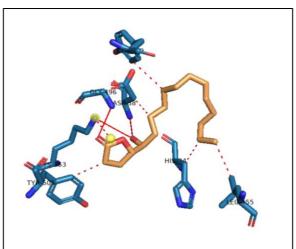
<u>ydroph</u>	nobic Inter	actions	·								
Index	Residue	AA	Distance	Ligan	d Atom	Prote	ein Atom				
1	33A	ASN	3.56	25		170					
2	37A	GLU	3.60	30		202					
3	387A	ALA	3.79	20		3036	3				
4	417E	LYS	3.88	2		5565	5				
5	495E	TYR	3.40	34		6188	3				
<u>ydroge</u>	en Bonds										
ndex	Residue	AA	Distance	H-A [Distance	D-A	Donor Angle	Protein donor?	Sidechain	Donor Atom	1
1	30A	ASP	2.99	3	3.55		117.89	×	~	42 [O3]	
2	33A	ASN	2.04	2	2.95		153.17	~	~	172 [Nam]	
3	34A	HIS	3.44	3	3.96		115.37	×	~	38 [O3]	
4	34A	HIS	3.02	3	3.97		162.71	×	~	43 [O3]	
5	37A	GLU	2.27	2	2.78		111.74	×	~	41 [O3]	
3	403E	ARG	2.47	3	3.09		120.88	~	~	5466 [Ng+]	
7	408E	ARG	2.12	2	2.80		123.90	~	~	5505 [Ng+]	3
3	409E	GLN	2.52	2	2.99		108.85	✓	~	5514 [Nam]	
9	453E	TYR	1.98	2	2.87		158.58	~	~	5859 [O3]	3

Figure S5: The detailed interaction of Annomuricin C against SARS-CoV-2 spike protein.



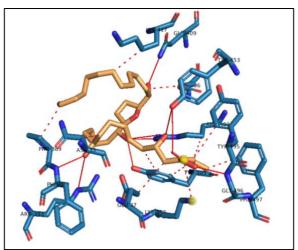
Indev	Residue	ΔΔ	Distance	Ligar	nd Atom	Prote	ein Atom				
							CITACOIII				
1	33A	ASN	3.75	26		169					
2	37A	GLU	3.50	30		201					
3	389A	PRO	3.76	14		3049	9				
4	405E	ASP	3.75	1		5475	5				
5	495E	TYR	3.68	34		6187	7				
	Residue		Distance	H-A [Distance	D-A	Donor Angle	Protein donor?	Sidechain	Donor Atom	Acceptor Ate
							Donor / trigic	i iotelli dolloi :	Sidecitalii	DONO! ALOIN	Acceptor Att
1	37A	GLU			2.97		118.18	×	✓ V	41 [O3]	205 [O.co2]
1 2	37A 393A	GLU ARG	2.39	1					✓ ✓		•
			2.39 1.94	4	2.97		118.18	×	✓	41 [O3]	205 [O.co2]
2	393A	ARG	2.391.943.20	2	2.97		118.18 169.79	× ~	Y	41 [O3] 3089 [Ng+]	205 [O.co2] 42 [O3]
2	393A 393A	ARG ARG	2.39 1.94 3.20 2.04	1	2.97 2.92 3.92		118.18 169.79 132.55	× ×	* * * *	41 [O3] 3089 [Ng+] 42 [O3]	205 [O.co2] 42 [O3] 3086 [Ng+]
2 3 4	393A 393A 403E	ARG ARG ARG	2.39 1.94 3.20 2.04 3.18		2.97 2.92 3.92 2.96		118.18 169.79 132.55 155.37	× × × ×		41 [O3] 3089 [Ng+] 42 [O3] 5466 [Ng+]	205 [O.co2] 42 [O3] 3086 [Ng+] 43 [O3] 43 [O3]

Supplementary Figure 6: The detailed interaction of Muricatocin C against SARS-CoV-2 spike protein.



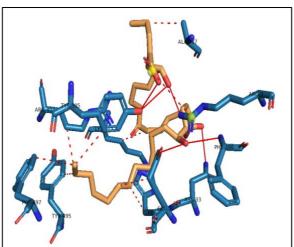
<u>lydroph</u>	obic Inter	actions	<u>s</u>								
Index	Residue	AA	Distance	Liga	and Atom	Prot	ein Atom				
1	34A	HIS	3.71	16		150					
2	38A	ASP	3.42	1		183					
3	449E	TYR	3.89	9		5788	3				
4	455E	LEU	3.81	17		5850)				
5	505E	TYR	3.54	6		6234	1				
<u>lydroge</u>	n Bonds										
Index	Residue	AA	Distance	H-A	Distance	D-A	Donor Angle	Protein donor?	Sidechain	Donor Atom	Acceptor Ato
1	38A	ASP	3.39		3.70		100.03	✓	×	179 [Nam]	20 [O3]
2	353A	LYS	3.23		3.68		108.42	✓	✓	2736 [N3+]	20 [O3]
	496E		1.99		2.86		147.15	~	×	6166 [Nam]	10 [02]

Figure S7: The detailed interaction of Muricatacin against SARS-CoV-2 spike protein.



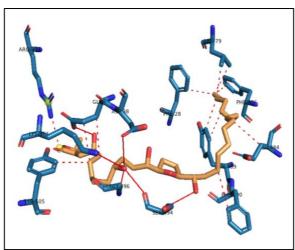
<u>lydroph</u>	nobic Inter	actions								
Index	Residue	AA	Distance	Ligand Atom	Prot	tein Atom				
1	33A	ASN	3.64	24	168					
2	37A	GLU	3.87	30	201					
3	389A	PRO	3.68	18	304	8				
4	403E	ARG	3.90	33	546	0				
5	406E	GLU	3.64	8	548	3				
6	417E	LYS	3.61	13	556	3				
7	495E	TYR	3.90	32	618	6				
8	497E	PHE	3.63	34	620	4				
9	505E	TYR		33	626	0				
10	505E	TYR	3.89	28	626	2				
<u>lydroge</u>	en Bonds									
Index	Residue	AA	Distance	H-A Distance	e D-A	Donor Angle	Protein donor?	Sidechain	Donor Atom	Acceptor At
1										
•	390A	PHE	2.53	3.01		109.66	~	×	3051 [Nam]	
2	390A 393A	PHE ARG		3.01 4.07		109.66 145.99	×	×	3051 [Nam] 42 [O3]	
			3.22							42 [O3]
2	393A	ARG	3.22 2.37	4.07		145.99	×	~	42 [O3]	42 [O3] 3085 [Ng+]
2	393A 403E	ARG ARG	3.22 2.37 2.11	4.07 3.22		145.99 143.29	×	~	42 [O3] 5464 [Ng+]	42 [O3] 3085 [Ng+] 38 [O3] 38 [O3]
2 3 4	393A 403E 403E	ARG ARG ARG	3.22 2.37 2.11 2.34	4.07 3.22 3.02		145.99 143.29 154.52	× ·	~ ~	42 [O3] 5464 [Ng+] 5465 [Ng+]	42 [O3] 3085 [Ng+] 38 [O3] 38 [O3]
2 3 4 5	393A 403E 403E 409E	ARG ARG ARG GLN	3.22 2.37 2.11 2.34 3.11	4.07 3.22 3.02 3.18		145.99 143.29 154.52 142.71	*	~ ~ ~	42 [O3] 5464 [Ng+] 5465 [Ng+] 5512 [Nam]	42 [O3] 3085 [Ng+] 38 [O3] 38 [O3] 37 [O3]
2 3 4 5 6	393A 403E 403E 409E 453E	ARG ARG ARG GLN TYR	3.22 2.37 2.11 2.34 3.11 3.31	4.07 3.22 3.02 3.18 4.01		145.99 143.29 154.52 142.71 162.10	× · · · · · · · · · · · · · · · · · · ·	~ ~ ~	42 [O3] 5464 [Ng+] 5465 [Ng+] 5512 [Nam] 5857 [O3]	42 [O3] 3085 [Ng+] 38 [O3] 38 [O3] 37 [O3] 39 [O.co2] 5857 [O3]

Figure S8: The detailed interaction of cis-Annonacin against SARS-CoV-2 spike protein.



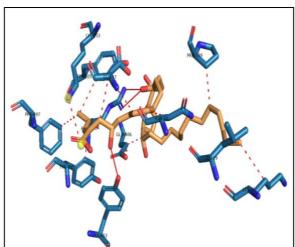
Index	Residue	AA	Distance	Ligar	nd Atom	Prote	ein Atom				
1	34A	HIS	3.93	12		175					
2	37A	GLU	3.68	13		200					
3	387A	ALA	3.57	33		3033	3				
4	403E	ARG	3.86	17		5459	9				
5	417E	LYS	3.93	22		5562	2				
6	495E	TYR	3.44	17		6185	5				
7	497E	PHE	3.92	18		6203	3				
8	505E	TYR	3.67	18		6259	9				
l <u>ydroge</u>	en Bonds										
Index	Residue	AA	Distance	H-A [Distance	D-A	Donor Angle	Protein donor?	Sidechain	Donor Atom	Acceptor Ator
Index 1	Residue 33A	AA ASN			Distance 3.85	D-A	Donor Angle 109.71	Protein donor?	Sidechain	Donor Atom 169 [Nam]	Acceptor Ator
			3.40	;		D-A					
1	33A	ASN	3.40 2.39	;	3.85	D-A	109.71	✓	~	169 [Nam]	42 [O3] 203 [O.co2]
1 2 3	33A 37A	ASN GLU	3.40 2.39 2.76	;	3.85 3.35	D-A	109.71	×	~	169 [Nam] 37 [O3]	42 [O3] 203 [O.co2]
1	33A 37A 390A	ASN GLU PHE	3.40 2.39 2.76 2.24	;	3.85 3.35 3.30	D-A	109.71 166.43 115.12	×	~ ~	169 [Nam] 37 [O3] 3050 [Nam]	42 [O3] 203 [O.co2] 37 [O3]

Figure S9: The detailed interaction of Annonacin-10-one against SARS-CoV-2 spike protein.



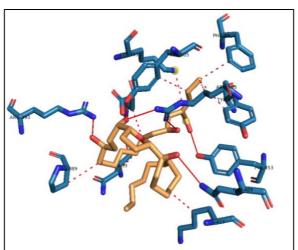
l <u>ydroph</u>	nobic Inter	actions	· · · ·							
Index	Residue	AA	Distance	Ligand Aton	n Prot	tein Atom				
1	28A	PHE	3.37	20	122					
2	37A	GLU	3.90	28	199					
3	37A	GLU	3.86	27	200					
4	79A	LEU	3.43	18	545					
5	79A	LEU	3.50	20	546					
6	484E	GLU	3.96	15	610	1				
7	486E	PHE	3.75	20	611	6				
8	489E	TYR	3.83	16	614	1				
9	489E	TYR	3.45	18	614	3				
10	490E	PHE	3.94	8	615	4				
11	505E	TYR	3.66	27	626	1				
l <u>ydroge</u>	en Bonds									
Index	Residue	AA	Distance	H-A Distand	ce D-A	Donor Angle	Protein donor?	Sidechain	Donor Atom	Acceptor A
1	37A	GLU	1.89	2.70		137.88	×	~	41 [O3]	203 [O.co2
2	38A	ASP	3.56	3.85		100.51	~	~	210 [O3]	42 [O3]
3	353A	LYS	2.54	3.38		138.40	~	~	2761 [N3+]	42 [O3]
4	494E	SER	2.52	3.15		120.11	~	×	6173 [N3]	37 [O3]
5	494E	SER	2.12	3.07		163.62	×	×	42 [O3]	6176 [O2]
			2.54	2.96		105.28	~	×	6191 [Nam]	

Figure S10: The detailed interaction of cis-Goniothalamicin against SARS-CoV-2 spike protein.



lydroph	obic Inter	actions								
Index	Residue	AA	Distance	Ligand	Atom Prot	ein Atom				
1	26A	LYS	3.93	19	106					
2	29A	LEU	3.76	19	132					
3	33A	ASN	3.56	25	168					
4	37A	GLU	3.86	30	201					
5	37A	GLU	3.84	26	200					
6	389A	PRO	3.57	15	304	3				
7	403E	ARG	3.73	34	546	0				
8	406E	GLU	3.93	5	548	3				
9	495E	TYR	3.81	33	618	3				
10	497E	PHE	4.00	34	620	4				
11	505E	TYR	3.79	34	626	0				
lydroge	n Bonds									
Index	Residue	AA	Distance	H-A Di	istance D-A	Donor Angle	Protein donor?	Sidechain	Donor Atom	Acceptor Ato
1	403E	ARG	2.31	3.	15	142.22	✓	❤	5465 [Ng+]	42 [O3]
2	403E	ARG	2.04	2.	95	153.97	✓	✓	5464 [Ng+]	42 [O3]
3	453E	TYR	2.06	2.	85	141.57	~	~	5857 [O3]	41 [O3]

Figure S11: The detailed interaction of Arianacin against SARS-CoV-2 spike protein.

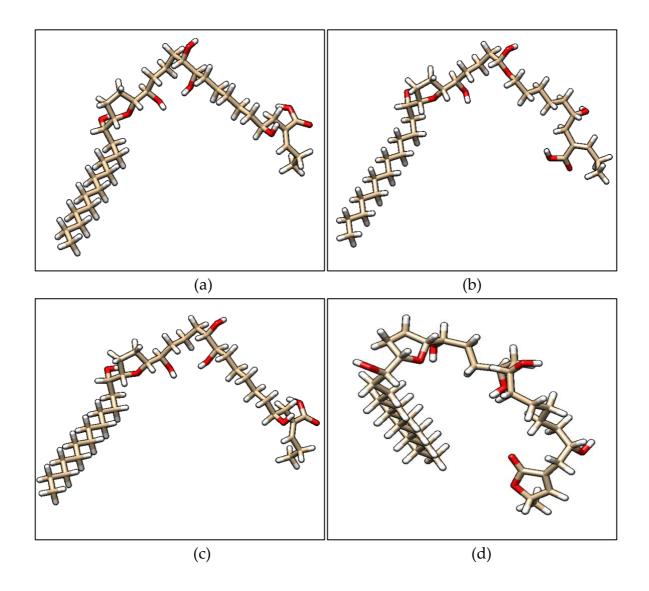


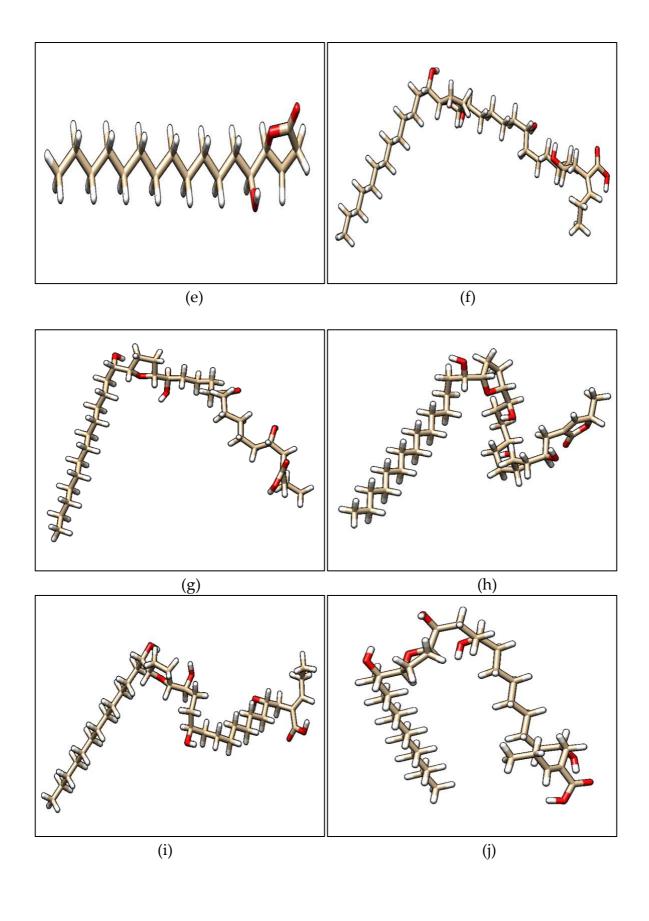
	nobic Inter										
Index	Residue	AA	Distance	Ligan	nd Atom	Prote	ein Atom				
1	33A	ASN	3.63	26		168					
2	37A	GLU	3.91	27		200					
3	389A	PRO	3.96	23		3048	3				
4	403E	ARG	3.88	34		5460)				
5	417E	LYS	3.73	11		5563	3				
6	495E	TYR	3.73	34		6186	3				
7	497E	PHE	3.68	34		6204	4				
	FOFE	TVD	3.78	33		6260)				
8	505E	TIIX	3.70								
lydroge	en Bonds							Destain dama?	Cidaabaia	Danas Atam	0
Index	en Bonds Residue	AA	Distance	H-A [Distance I		Donor Angle	Protein donor?			· · · · · · · · · · · · · · · · · · ·
lydroge	en Bonds		Distance	H-A [Protein donor?	Sidechain	Donor Atom 3088 [Ng+]	Acceptor Ato
l <u>ydroge</u> Index	en Bonds Residue	AA	Distance 2.04	H-A [Distance I		Donor Angle				· · · · · · · · · · · · · · · · · · ·
lydroge Index 1	Residue 393A	AA ARG	Distance 2.04 2.07	H-A [Distance I		Donor Angle 166.55	~	✓	3088 [Ng+]	42 [O3]
Index 1	Residue 393A 403E	AA ARG ARG	Distance 2.04 2.07 1.93	H-A [Distance I 3.00 2.91		Donor Angle 166.55 141.92	Y Y	~	3088 [Ng+] 5464 [Ng+]	42 [O3] 41 [O3] 38 [O3]
Index 1 2 3	Residue 393A 403E 403E	AA ARG ARG	Distance 2.04 2.07 1.93 2.38	H-A [Distance 3.00 2.91 2.87		Donor Angle 166.55 141.92 158.74	* * *	v v v	3088 [Ng+] 5464 [Ng+] 5465 [Ng+]	42 [O3] 41 [O3] 38 [O3]
Index 1 2 3	Residue 393A 403E 403E 409E	AA ARG ARG ARG GLN	Distance 2.04 2.07 1.93 2.38 2.10	H-A [Distance 3.00 2.91 2.87 3.23		Donor Angle 166.55 141.92 158.74 145.13		* * * * * * * * * * * * * * * * * * *	3088 [Ng+] 5464 [Ng+] 5465 [Ng+] 5512 [Nam]	42 [O3] 41 [O3] 38 [O3] 37 [O3]

Figure S12: The detailed interaction of Javoricin against SARS-CoV-2 spike protein.

Optimized Molecular Structures:

Before Docking





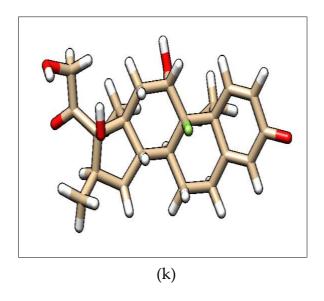
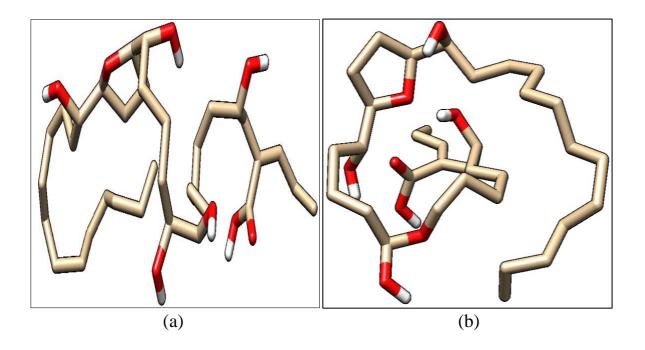
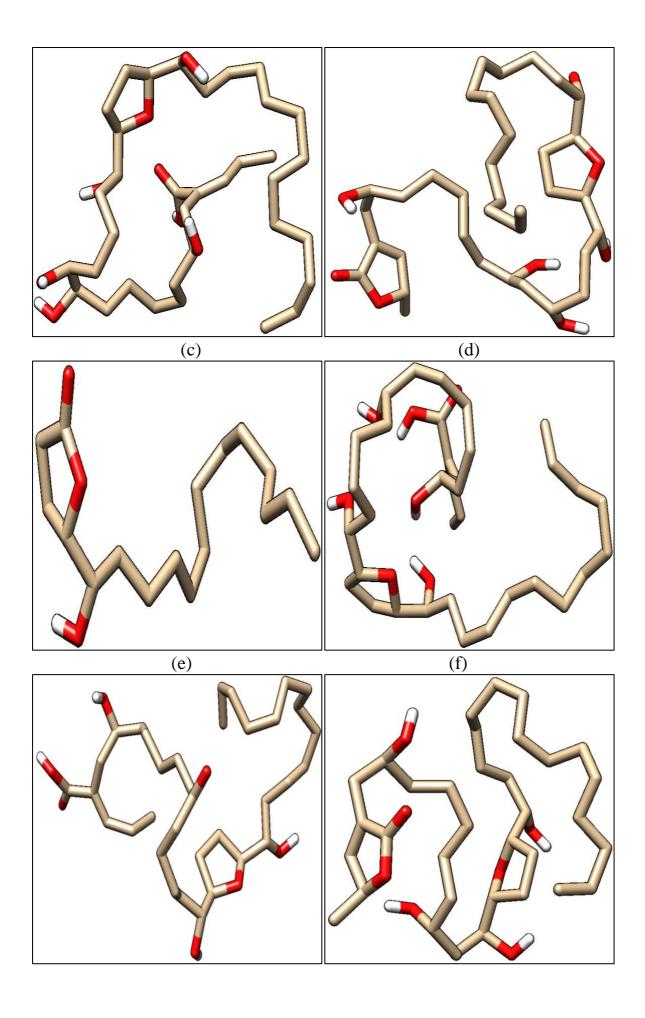


Figure S13: Optimized molecular structures of (a) Annomuricin A, (b) Annomuricin B, (c) Annomuricin C, (d) Muricatocin C, (e) Muricatacin, (f) cis-Annonacin, (g) Annonacin-10-one, (h) cis-Goniothalamicin, (i) Arianacin, (j) Javoricin and (k) Dexamethasone, before docking to the spike protein.

After Docking





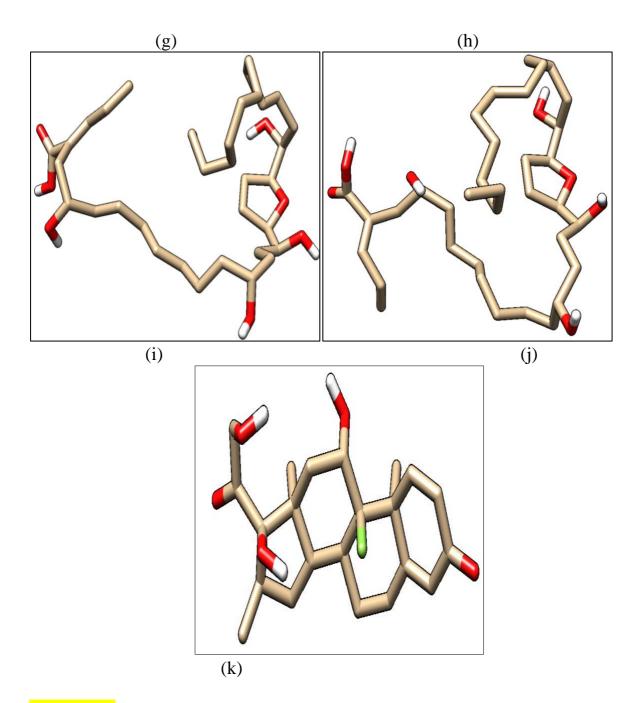


Figure S14: 3-dimensional pictures of the ligands obtained after the Molecular docking interaction studies (a) Annomuricin A, (b) Annomuricin B, (c) Annomuricin C, (d) Muricatocin C, (e) Muricatacin, (f) cis-Annonacin, (g) Annonacin-10-one, (h) cis-Goniothalamicin, (i) Arianacin, (j) Javoricin and (k) Dexamethasone.