Supporting Information

An *in-silico* analysis of ivermectin interaction with potential SARS-CoV-2 targets and host nuclear importin α

Faizul Azam[1,*], Ismail M. Taban[2,3], Eltayeb E M Eid[1], Muzaffar Iqbal[4], Ozair Alam[5], Shamshir Khan[6], Danish Mahmood[7], Md Jamir Anwar[7], Habibullah Khalilullah[1], M. U. Khan[1]

[1] *Department of Pharmaceutical Chemistry & Pharmacognosy, Unaizah College of Pharmacy, Qassim University, Saudi Arabia*

[2] *School of Biosciences, Cardiff University, King Edward VII Avenue, Cardiff CF103NB, U.K.*

[3] *Department of Pharmaceutical Chemistry, Faculty of Pharmacy, Misurata University, Misurata, Libya*

[4] *Department of Pharmaceutical Chemistry, College of Pharmacy, King Saud University, PO Box No. 2457, Riyadh, Saudi Arabia*

[5] *Medicinal Chemistry and Molecular Modelling Lab, Department of Pharmaceutical Chemistry, School of Pharmaceutical Education and Research, Jamia Hamdard, New Delhi-110062, India*

[6] *Buraidah College of Dentistry and Pharmacy, Buraidah, Al-Qassim, Saudi Arabia*

[7] *Department of Pharmacology & Toxicology, Unaizah College of Pharmacy, Qassim University, Saudi Arabia*

[*] Corresponding author Tel +966-50-2728652; E-mail: faizulazam@gmail.com; f.azam@qu.edu.sa

Table S1. Non-bond interactions of ivermectin with 15 potential COVID-19 targets and importin α.

S.No.	Target	Hydrogen bond interactions		Hydrophobic interactions		
		Residues	Distance	Type	Residues	Distance
1.	Main Protease	Gln189	1.67	Alkyl	Pro168	4.88
				Alkyl	Met165	3.76
				Alkyl	Pro168	4.07
				Alkyl	Met49	4.11
				Alkyl	Met49	5.34
				Alkyl	Leu50	4.49
				π-Alkyl	His41	3.96
2.	Papain-like protease	Tyr264	1.88	Alkyl	Pro248	5.47
		Tyr268	2.17	Alkyl	Pro248	4.87
				Alkyl	Met208	4.90
				Alkyl	Pro247	4.52
				Alkyl	Pro247	5.10
				Alkyl	Pro248	4.47
				π-Alkyl	Tyr268	5.21
				π-Alkyl	Tyr268	4.71
3.	RdRp (RTP site)	Ser549	1.87	Alkyl	Pro620	4.90
		Lys551	2.53	Alkyl	Lys798	4.69
		Lys621	2.18	π-Alkyl	U20	5.31
4.	RdRp (RNA site)	Lys545	2.71	Alkyl	Ala688	4.10
		Gln573	1.87	Alkyl	Ala688	3.70

		Ala685	1.85	Alkyl	Ala688	4.56
				Alkyl	Ala688	4.73
				Alkyl	Val557	4.03
				Alkyl	Leu576	4.79
				Alkyl	Lys577	4.30
5.	Helicase (Nsp13; ADP site)	Gln537	1.98	Alkyl	Ala312	4.40
		Ser539	2.81	Alkyl	Ala313	4.38
		Glu540	1.77	Alkyl	Ala316	4.30
		Glu540	2.01	Alkyl	Lys320	5.29
				Alkyl	Lys320	4.12
6.	Helicase (Nsp13; NCB site)	Arg212	2.81	Alkyl	Arg178	4.97
		Arg339	2.58	Alkyl	Arg178	4.64
		Arg339	2.61	Alkyl	Ala312	4.96
				Alkyl	Arg178	4.79
				Alkyl	Cys309	4.50
				Alkyl	Met378	4.07
				π-Alkyl	Hie311	5.31
7.	Nsp14 (ExoN)	Gln145	2.52	Alkyl	Ala187	4.99
				Alkyl	Ala187	4.24
				Alkyl	Ala187	4.26
				Alkyl	Pro141	4.79
				Alkyl	Pro142	5.25
				Alkyl	Pro141	4.17
				π-Alkyl	His95	4.96
				π-Alkyl	Phe146	4.89
				π-Alkyl	Phe146	4.35

				π-Alkyl	Phe146	5.31
				π-Alkyl	Trp186	4.74
				π-Alkyl	Phe190	5.22
8.	Nsp14 (N7-MTase)	-	-	Alkyl	Ala307	4.66
				Alkyl	Ala307	3.85
				Alkyl	Arg310	4.71
				Alkyl	Arg310	4.43
				Alkyl	Cys340	4.80
				Alkyl	Arg310	4.40
				Alkyl	Pro342	3.95
				Alkyl	Pro335	4.10
				Alkyl	Pro335	4.25
				Alkyl	Lys336	4.74
				π-Alkyl	Trp292	5.10
				π-Alkyl	His314	4.81
				π-Alkyl	His314	4.64
9.	Spike RBD	Gln493	2.04	Alkyl	Leu455	4.87
		Ser494	2.10	Alkyl	Leu455	5.31
		Glu484	2.10	π-Alkyl	Tyr449	4.88
				π-Alkyl	Tyr449	5.09
				π-Alkyl	Phe456	5.02
				π-Alkyl	Tyr505	5.40
10.	Spike monomer	-	-	Alkyl	Arg403	4.63
				Alkyl	Val350	4.64
				Alkyl	Pro507	4.17
11.	Spike trimer	Asn334	2.49	Alkyl	Pro337	4.21

		Arg357	3.08	Alkyl	Val171	3.95
		Arg357	3.05	π-Alkyl	Phe168	5.05
12.	S2 (post fusion state)	Leu1166	2.72	Alkyl	Ala972	5.42
		Ala972	3.02			
13.	N protein (C domain)	Arg73	2.30	Alkyl	Ala90	3.72
		Gln35	2.47	Alkyl	Ala90	5.19
		Gln35	2.34	Alkyl	Ala90	4.27
		Gln35	2.58	π-Alkyl	Trp84	4.70
		Thr36	2.50	π-Alkyl	Trp84	3.94
				π-Alkyl	Trp84	5.28
				π-Alkyl	Trp84	5.07
14.	N protein (N domain)	-	-	Alkyl	Ala50	3.77
				Alkyl	Arg52	4.28
				π-Alkyl	Tyr69	5.31
15.	Nsp9	Val7	2.40	Alkyl	Pro6	4.53
		Val7	1.91	Alkyl	Ala8	4.46
		Gln11	2.19	Alkyl	Ala8	4.70
		Gln11	2.70	Alkyl	Ala8	3.85
				Alkyl	Pro6	4.49
				Alkyl	Met101	4.28
16	Importin α	Trp231	2.73	Alkyl	Arg227	5.24
		Arg238	2.95	π-Alkyl	Trp184	4.21
		Asn228	2.46	π-Alkyl	Trp184	5.11
		Ser149	1.75	π-Alkyl	Trp184	5.44
				π-Alkyl	Trp184	5.18
				π-Alkyl	Trp231	4.81

	π-Alkyl	Trp231	4.50
	π-Alkyl	Trp231	4.90
	π-Alkyl	Trp231	5.37
	π-Alkyl	Trp231	4.87

Table S2. Results of docking and MM/GBSA computations of ivermectin in complex with 15 potential COVID-19 targets and importin α.

S.N	Targets	Docking models (Top 10)	ΔG_{Bind} (Auto Dock Vina)	MM/GBSA						
				ΔG_{Bind}	ΔG_{Coul}	ΔG_{HBond}	ΔG_{Lipo}	SolvGB	ΔG_{vdw}	Lig SE
1	Main Protease	1M1	-7.2	-68.81	-14.75	-0.70	-38.62	28.05	-48.83	22.05
		1M2	-6.8	-79.35	-10.16	-0.44	-53.80	28.52	-59.49	34.37
		1M3	-6.5	-64.22	-7.89	-0.54	-46.78	29.52	-55.04	42.12
		1M4	-6.3	-53.20	-16.79	-0.85	-38.61	34.87	-50.42	28.50
		1M5	-6.3	-57.39	-11.19	-1.09	-22.75	23.57	-42.10	25.07
		1M6	-6.3	-63.57	-14.31	-0.37	-37.64	27.09	-46.96	16.29
		1M7	-6.2	-67.38	-7.85	-0.72	-41.92	25.09	-54.29	13.88
		1M8	-6.1	-52.35	-3.32	-0.41	-36.94	29.35	-47.20	12.88
		1M9	-6.1	-52.57	-0.02	-0.57	-40.05	23.80	-41.10	12.58
		1M10	-6.1	-43.31	-6.39	-0.36	-27.48	27.41	-43.44	34.20
2	Papain-like protease	2M1	-7.1	-18.31	18.30	-1.15	-40.19	14.80	-36.38	41.06
		2M2	-6.8	-52.49	-1.60	-0.71	-47.57	14.55	-31.27	33.92
		2M3	-6.7	-60.61	-7.97	-0.44	-52.07	25.94	-42.95	28.76
		2M4	-6.7	-25.93	4.56	-0.08	-33.07	39.74	-42.11	7.11
		2M5	-6.6	-43.53	5.53	-1.08	-39.01	39.42	-42.59	15.51
		2M6	-6.6	-52.88	-1.49	0.00	-43.78	30.41	-38.90	1.18
		2M7	-6.5	-43.35	-3.25	-1.54	-43.52	29.35	-38.86	20.73
		2M8	-6.5	-50.95	7.44	-0.71	-49.28	17.29	-40.45	22.85
		2M9	-6.4	-36.14	5.60	-0.83	-34.69	33.57	-44.13	20.11
		2M10	-6.2	-31.73	-3.82	-0.77	-29.73	30.71	-36.88	9.42
3		3M1	-9.9	24.72	-14.81	-1.56	-30.08	87.47	-51.21	47.42

	RdRp (RTP site)	3M2	-9.6	-29.10	3.94	-1.23	-27.33	61.01	-68.92	19.48
		3M3	-9	21.18	-25.01	-1.05	-36.31	88.74	-29.70	35.68
		3M4	-9	22.81	21.83	-0.85	-27.23	52.54	-44.43	39.19
		3M5	-8.3	19.86	11.50	-0.91	-17.42	57.81	-50.43	54.91
		3M6	-8.3	-25.65	4.03	-1.39	-41.23	55.95	-68.32	35.62
		3M7	-8.2	9.32	-13.21	-1.08	-5.28	55.71	-38.28	35.13
		3M8	-8.1	16.16	-27.62	-0.84	-33.08	97.56	-45.68	45.01
		3M9	-8.1	-42.57	-28.13	-1.09	-23.93	79.00	-69.29	13.18
		3M10	-8.1	42.43	-0.30	-1.26	-23.05	95.62	-50.92	51.14
4	RdRp (RNA site)	4M1	-8.9	-38.28	-1.80	-0.48	-41.27	28.94	-43.52	32.69
		4M2	-8.3	-47.86	-6.81	-0.99	-32.66	36.19	-47.13	15.00
		4M3	-8.2	-53.11	2.46	-0.46	-35.35	23.54	-47.18	14.40
		4M4	-8.2	-50.75	-11.05	-0.45	-36.64	33.00	-54.49	16.44
		4M5	-8	-70.06	-22.56	-0.89	-37.87	30.74	-47.33	12.87
		4M6	-8	-66.03	-3.07	-0.15	-39.75	29.33	-55.54	5.91
		4M7	-7.9	-45.50	-1.77	-0.46	-41.99	32.17	-46.89	20.33
		4M8	-7.7	-62.35	-5.06	-0.19	-40.79	20.05	-40.85	6.88
		4M9	-7.7	-66.23	4.63	-0.53	-45.18	23.45	-52.66	9.60
		4M10	-7.7	-59.82	-1.43	-0.26	-46.53	33.43	-59.34	17.73
5	Helicase (Nsp13; ADP site)	5M1	-8.2	-51.45	3.58	-0.47	-37.04	25.60	-47.67	10.53
		5M2	-8.1	-58.36	-14.00	-1.08	-44.85	40.20	-47.14	20.30
		5M3	-7.4	-41.60	0.07	-1.05	-25.70	25.30	-46.38	15.40
		5M4	-7.4	-43.57	-4.76	-0.94	-20.96	26.38	-41.90	8.24
		5M5	-7.2	-42.84	-1.62	-0.62	-30.25	33.94	-43.98	15.09
		5M6	-7	-43.91	0.88	-0.79	-28.14	23.51	-42.16	4.90
		5M7	-6.9	-30.56	-8.96	-1.16	-21.45	34.31	-32.69	25.67

		5M8	-6.9	-32.24	0.44	-1.28	-27.50	29.49	-48.16	22.49
		5M9	-6.9	-34.07	-1.23	-1.33	-13.37	25.09	-40.68	9.57
		5M10	-6.9	-52.34	-9.45	-1.38	-33.29	29.46	-41.89	6.86
6	Helicase (Nsp13; NCB site)	6M1	-10.2	-71.63	-10.34	-0.27	-83.87	49.51	-52.32	34.01
		6M2	-10.2	-59.26	0.08	-0.80	-58.73	41.96	-47.35	48.88
		6M3	-9.5	-48.00	-8.02	-1.92	-63.46	48.25	-41.88	37.87
		6M4	-9.4	-64.90	-2.35	-0.80	-67.62	39.23	-54.21	33.49
		6M5	-9.1	-23.86	-10.36	-2.56	-76.80	52.78	-18.76	61.21
		6M6	-9	-44.09	2.39	-0.02	-48.93	38.78	-48.64	29.46
		6M7	-9	-41.99	-9.17	-0.43	-80.43	45.95	-32.95	46.37
		6M8	-8.8	-66.82	-9.00	-0.62	-48.24	38.02	-53.13	12.52
		6M9	-8.7	-59.52	7.21	-0.64	-49.76	28.87	-56.91	18.11
		6M10	-8.6	-56.95	4.99	-0.22	-78.26	39.82	-54.22	47.58
7	Nsp14 (ExoN)	7M1	-8.7	-58.71	-4.40	-0.37	-42.85	36.28	-53.26	21.70
		7M2	-8.5	-49.54	-0.71	-0.70	-40.54	34.61	-45.91	24.56
		7M3	-8.4	-53.50	2.90	-0.30	-44.91	34.07	-53.04	20.80
		7M4	-8.1	-53.02	-0.77	-0.71	-42.29	38.50	-50.67	14.45
		7M5	-8.1	-41.37	-19.01	-0.77	-35.30	46.23	-47.43	30.89
		7M6	-8	-34.12	2.70	-0.22	-36.32	19.28	-33.99	27.81
		7M7	-7.9	-63.96	-5.31	-0.14	-38.29	24.52	-44.44	8.19
		7M8	-7.9	-42.33	-16.42	-0.46	-31.59	53.72	-48.73	20.86
		7M9	-7.6	-34.19	-0.92	-0.35	-33.47	37.79	-42.88	17.71
		7M10	-7.5	-41.04	-10.47	-0.21	-32.30	33.63	-39.72	30.75
8	Nsp14 (N7-MTase)	8M1	-9.8	-78.91	-10.49	-0.27	-54.97	36.66	-61.37	22.25
		8M2	-9.1	-50.94	-6.57	-0.81	-47.29	41.10	-51.95	19.83
		8M3	-9	-69.23	-2.52	-1.10	-47.82	27.97	-56.40	16.16

		8M4	-8.9	-71.39	2.70	-1.12	-47.37	28.82	-54.57	8.47
		8M5	-8.4	-45.59	1.20	-1.02	-26.99	34.29	-49.87	27.33
		8M6	-8.1	-57.03	0.30	-1.24	-38.65	32.34	-51.46	31.54
		8M7	-7.8	-59.56	-9.60	-0.86	-36.52	42.51	-52.96	16.25
		8M8	-7.8	-19.38	0.32	-1.20	-31.75	37.59	-35.42	28.81
		8M9	-7.6	-20.57	7.59	-1.44	-17.55	31.10	-41.74	29.72
		8M10	-7.4	-51.03	-7.08	-1.19	-38.31	35.98	-51.59	30.67
9	Spike RBD	9M1	-7.6	-63.61	-14.25	-1.04	-42.92	27.98	-45.85	17.45
		9M2	-7.1	-40.83	-10.93	-1.22	-23.62	22.72	-34.57	11.25
		9M3	-6.9	-50.27	-5.46	-0.29	-37.67	17.08	-38.93	18.86
		9M4	-6.8	-44.81	-11.13	-0.39	-26.99	25.76	-35.30	30.79
		9M5	-6.7	-69.13	-11.49	-1.71	-39.45	24.60	-45.26	20.97
		9M6	-6.4	-41.75	-0.30	-0.16	-30.06	19.32	-37.66	9.96
		9M7	-6.3	-53.83	0.30	-0.05	-37.48	14.48	-34.24	5.48
		9M8	-6.2	-52.18	-8.56	-0.66	-29.49	19.94	-31.65	12.56
		9M9	-6.1	-50.37	-3.73	-0.01	-32.47	16.78	-32.88	4.76
		9M10	-5.8	-48.26	-3.58	-0.25	-32.57	20.11	-36.46	18.89
10	Spike monomer (close)	10M1	-5.5	-55.86	-4.40	-0.05	-39.85	17.87	-33.46	7.64
		10M2	-5.5	-19.44	-16.77	-1.24	-9.04	23.55	-13.51	4.09
		10M3	-5.5	-43.82	-12.18	-1.06	-27.70	19.88	-24.35	15.68
		10M4	-5.4	-55.19	-13.02	-0.25	-32.92	17.14	-30.20	6.00
		10M5	-5.4	-36.13	-0.30	-0.02	-24.63	12.22	-26.47	0.39
		10M6	-5.3	-54.61	-18.71	-0.72	-37.01	32.33	-38.71	28.25
		10M7	-5.3	-4.85	5.90	-0.58	-10.11	3.98	-10.48	13.18
		10M8	-5.3	-29.01	1.75	-0.18	-22.04	5.34	-16.68	4.99
		10M9	-5.2	-14.00	0.41	-0.47	-11.45	8.70	-12.75	1.00

		10M10	-5.2	-55.30	-16.69	-1.92	-32.54	24.58	-33.97	14.56
11	Spike trimer (open)	11M1	-8.2	-71.20	-1.84	-0.86	-54.53	27.07	-46.38	10.21
		11M2	-8	-52.79	-3.06	-1.08	-37.63	29.81	-44.18	30.66
		11M3	-7.6	-61.08	-2.92	-0.19	-36.32	22.75	-42.30	10.27
		11M4	-7.5	-61.96	-4.15	-0.03	-54.68	20.74	-37.72	20.06
		11M5	-7.5	-52.38	-3.91	-0.15	-39.60	24.30	-32.71	25.00
		11M6	-7.3	-51.41	-1.00	-1.15	-61.34	29.43	-39.51	44.07
		11M7	-7.3	-55.82	1.18	-0.01	-45.29	17.36	-34.74	14.74
		11M8	-7.2	-61.95	3.59	-0.61	-39.23	15.05	-51.12	27.10
		11M9	-7	-72.40	-0.33	-0.81	-38.38	14.86	-49.10	8.60
		11M10	-7	-53.00	-4.59	-0.77	-35.87	23.92	-44.85	14.87
12	S2 (post fusion state)	12M1	-6	-40.41	0.32	-0.78	-22.69	18.97	-34.76	23.43
		12M2	-5.9	-47.95	1.47	-1.15	-27.93	17.40	-39.96	8.94
		12M3	-5.7	-54.73	-2.52	0.00	-40.67	15.14	-33.61	10.54
		12M4	-5.6	-33.76	-0.20	-0.22	-29.17	27.02	-42.52	15.04
		12M5	-5.5	-31.64	-1.66	-0.01	-28.85	24.59	-36.78	17.89
		12M6	-5.5	-21.64	-4.21	-0.86	-13.30	30.25	-36.32	29.04
		12M7	-5.4	-55.04	-1.88	-0.01	-37.05	12.40	-32.39	21.49
		12M8	-5.4	-31.83	-2.66	-1.65	-21.34	24.54	-34.67	11.23
		12M9	-5.4	-47.32	-1.19	-0.02	-34.09	22.83	-40.47	10.86
		12M10	-5.3	-59.55	-8.91	-0.22	-30.96	27.39	-45.20	10.16
13	N protein (C domain)	13M1	-6.6	-43.08	1.94	-0.79	-38.34	26.86	-46.04	17.87
		13M2	-6.5	-54.67	-7.77	-0.50	-43.56	24.11	-39.13	31.60
		13M3	-6.2	-57.02	-8.28	-0.91	-37.67	26.51	-43.74	17.17
		13M4	-6.2	-59.89	-8.26	-0.71	-49.02	25.64	-43.42	21.36
		13M5	-6.1	-55.44	3.85	-0.40	-43.61	28.24	-50.93	12.95

		13M6	-6.1	-74.58	-15.43	-1.30	-46.28	31.11	-44.83	12.51
		13M7	-6	-75.33	-9.61	-0.78	-50.50	27.96	-50.23	10.83
		13M8	-6	-52.03	-8.25	-1.26	-39.87	28.52	-39.89	12.71
		13M9	-5.9	-74.91	-6.92	-0.49	-61.47	21.91	-40.37	14.79
		13M10	-5.8	-72.42	-9.56	-0.69	-54.56	26.33	-42.68	18.36
14	N protein (N domain)	14M1	-8.2	-54.80	-11.84	-2.62	-34.99	35.80	-50.86	33.29
		14M2	-8	-45.67	-4.55	-1.84	-45.75	21.72	-40.33	29.16
		14M3	-8	-62.48	-6.83	-1.03	-41.21	24.23	-39.69	14.56
		14M4	-7.7	-52.73	-7.13	-1.55	-37.75	27.31	-39.46	17.43
		14M5	-7.6	-57.18	-0.94	-1.74	-41.86	27.04	-47.73	5.46
		14M6	-7.6	-63.69	-17.38	-1.96	-37.56	34.32	-45.23	24.31
		14M7	-7.5	-53.06	-2.02	-1.33	-32.08	23.39	-39.56	25.34
		14M8	-7.4	-63.93	-25.04	-1.18	-35.35	29.84	-38.64	16.73
		14M9	-7.4	-67.44	-13.89	-0.53	-42.74	32.84	-50.30	9.53
		14M10	-7.3	-69.03	-3.60	-0.11	-54.29	31.69	-58.15	5.48
15	Nsp9	15M1	-5.9	-84.70	-9.29	-0.48	-59.65	14.77	-43.69	16.60
		15M2	-5.8	-63.43	-4.59	-0.50	-38.36	10.47	-34.39	8.58
		15M3	-5.6	-51.43	-17.64	-0.77	-32.96	18.49	-26.79	21.47
		15M4	-5.6	-70.78	-16.48	-0.95	-38.69	13.32	-32.88	8.31
		15M5	-5.6	-73.66	-4.28	-0.25	-44.05	13.21	-39.99	9.18
		15M6	-5.5	-52.73	0.55	-0.11	-29.08	9.00	-39.43	12.51
		15M7	-5.4	-76.54	-23.21	-0.94	-36.04	17.81	-32.67	-0.42
		15M8	-5.4	-42.16	4.33	-0.39	-23.34	11.39	-31.92	21.92
		15M9	-5.3	-84.85	-12.53	-0.79	-50.48	14.06	-42.88	20.54
		15M10	-5.3	-47.13	2.59	-0.14	-24.60	10.59	-38.12	17.36
16	Importin α	16M1	-7.4	-43.60	-1.41	-0.33	-42.20	30.91	-45.76	23.71

	16M2	-7.4	-54.34	-1.86	-1.53	-43.47	27.75	-44.34	22.27
	16M3	-7.2	-44.89	6.21	-0.31	-36.86	33.73	-53.25	14.02
	16M4	-7.2	-59.70	-9.28	-0.06	-38.76	31.45	-47.79	13.37
	16M5	-7	-51.09	-1.57	-0.14	-39.83	27.79	-50.23	20.42
	16M6	-7	-63.16	1.00	-1.04	-34.40	28.67	-52.88	22.07
	16M7	-6.9	-49.50	-9.38	-0.59	-33.08	27.13	-38.96	22.44
	16M8	-6.9	-43.67	1.96	-1.03	-39.78	42.26	-51.11	10.84
	16M9	-6.9	-66.04	-24.26	-1.45	-35.74	37.83	-45.41	6.34
	16M10	-6.9	-65.63	-22.43	-1.46	-34.64	27.99	-39.93	10.02

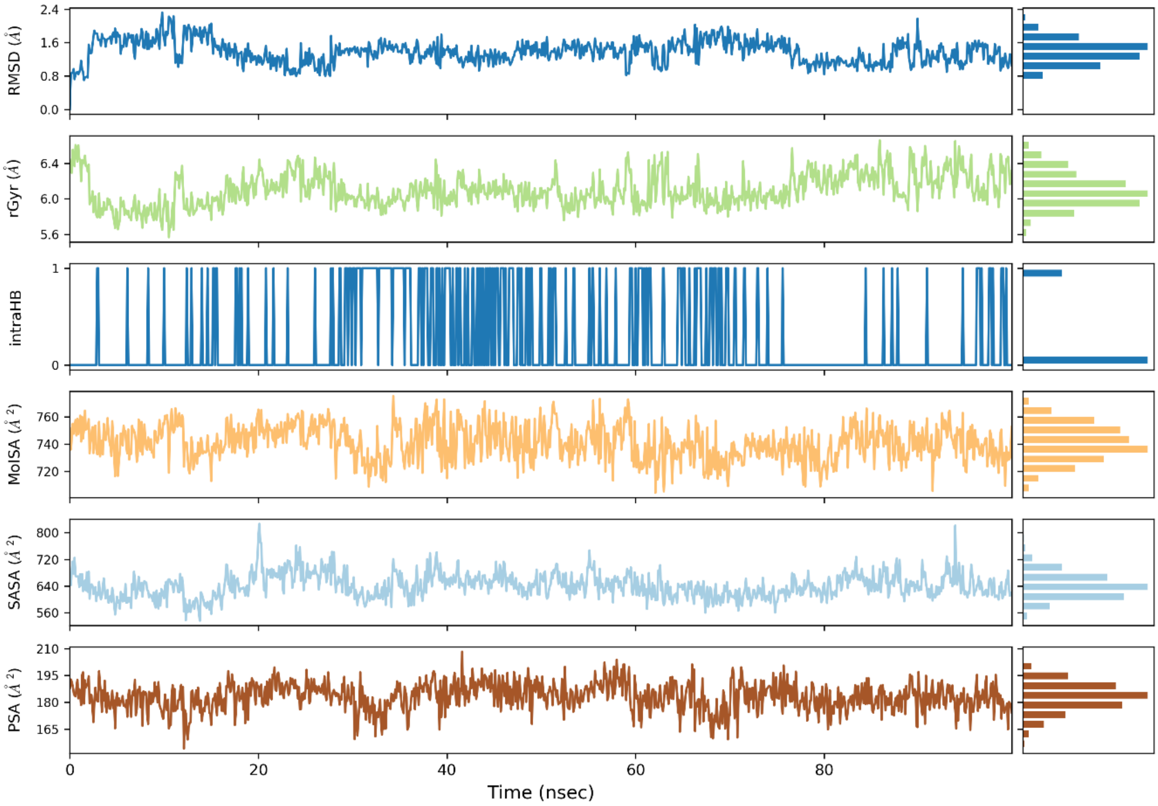

Fig. S1. Root mean square deviation (RMSD) of ivermectin with respect to the reference conformation in Nsp9 binding pocket; rGyr: Radius of Gyration which measures the 'extendedness' of a ligand; intraHB: Intramolecular Hydrogen Bonds; MolSA: Molecular Surface Area; SASA: Solvent Accessible Surface Area; PSA: Polar Surface Area

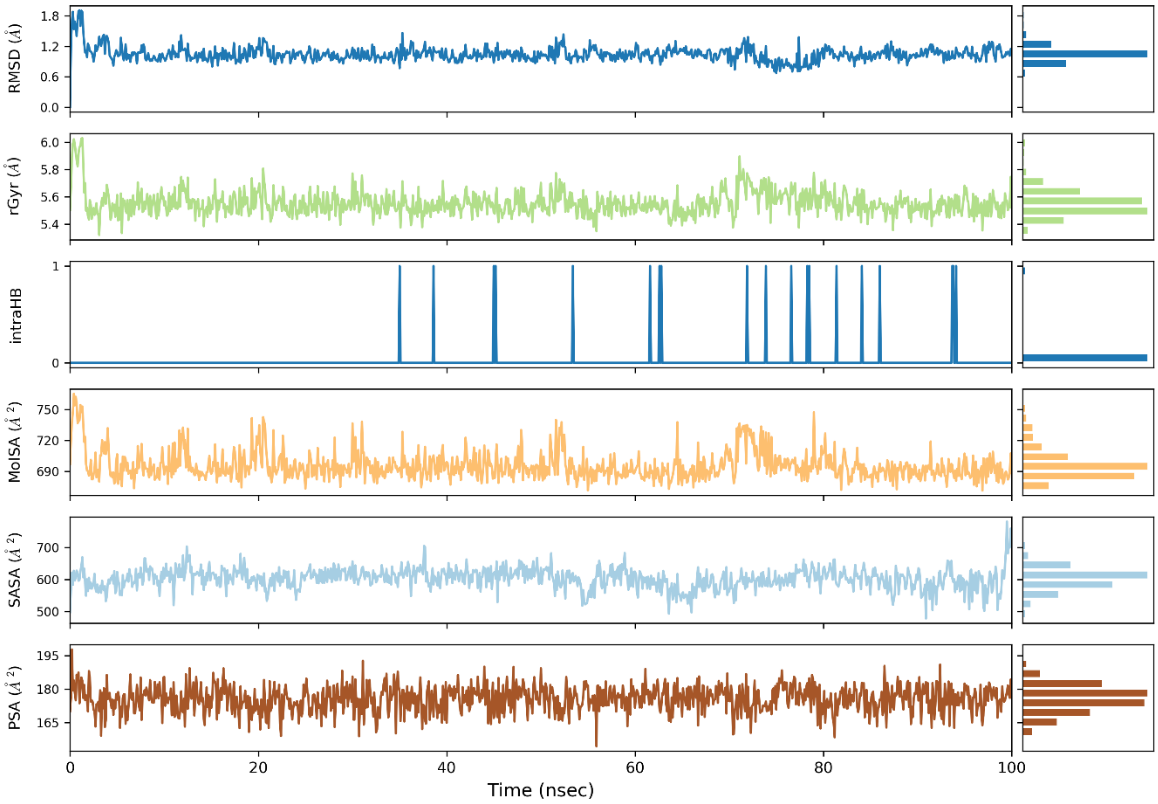

Fig. S2. Root mean square deviation (RMSD) of ivermectin with respect to the reference conformation in importin α binding pocket; rGyr: Radius of Gyration which measures the 'extendedness' of a ligand; intraHB: Intramolecular Hydrogen Bonds; MolSA: Molecular Surface Area; SASA: Solvent Accessible Surface Area; PSA: Polar Surface Area.

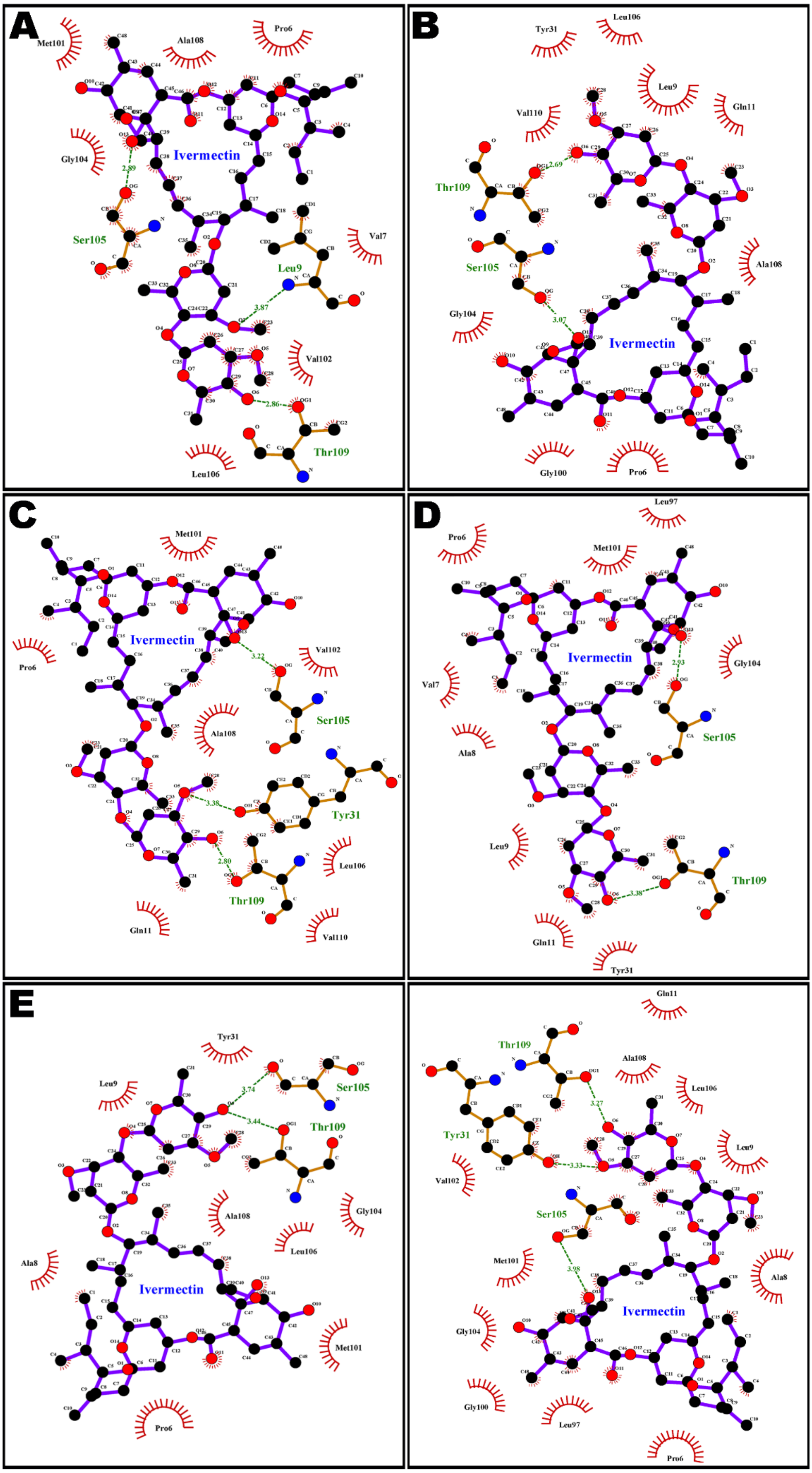

Fig. S3. Analysis of hydrogen bond lengths between ivermectin and residues of Nsp9 target during the MD simulation trajectory. Snapshots were taken at 50ns (A), 60ns (B), 70ns (C), 80ns (D), 90ns (E) and 100ns (F).

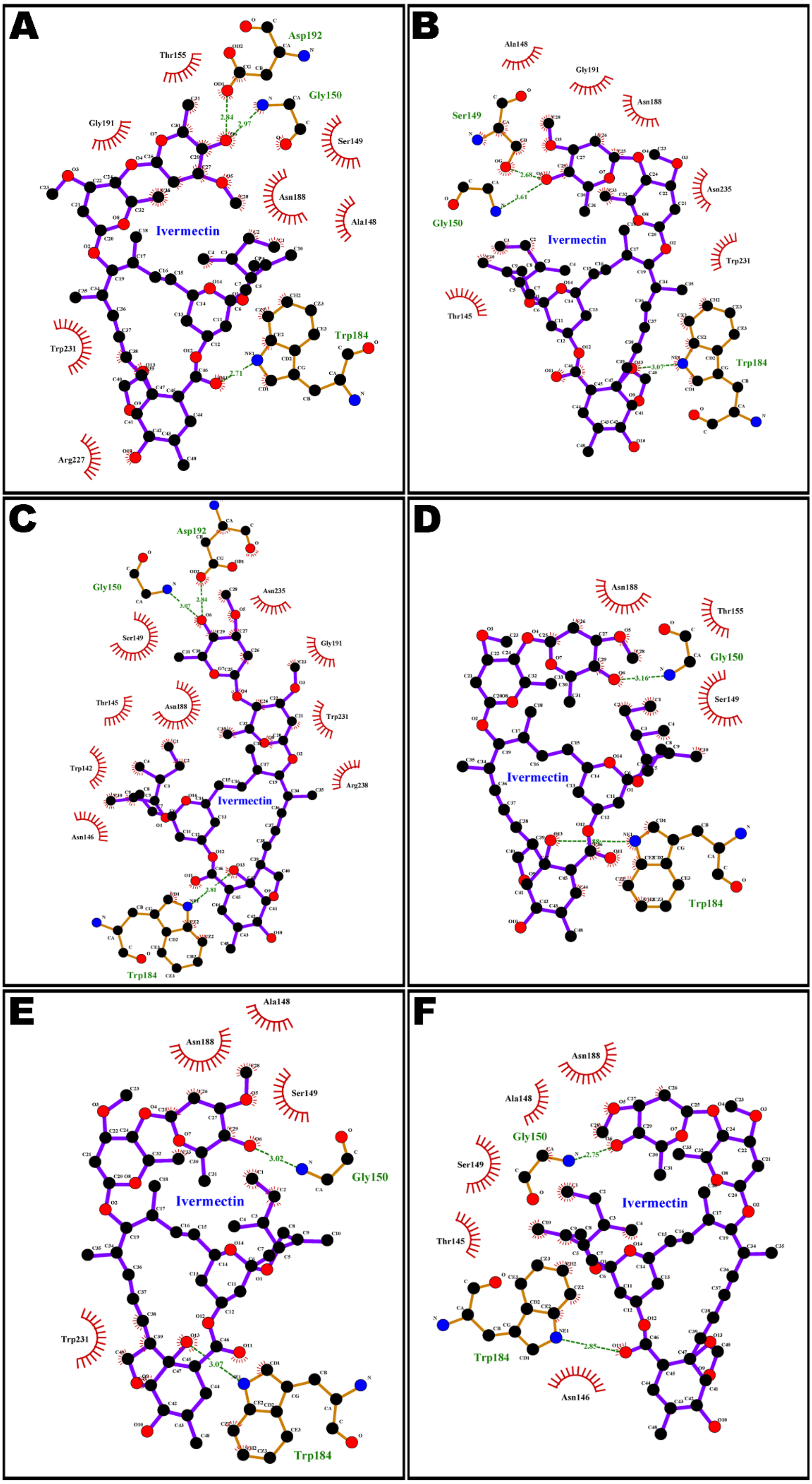

Fig. S4. Analysis of hydrogen bond lengths between ivermectin and residues of importin α target during the MD simulation period. Snapshots were taken at 50ns (A), 60ns (B), 70ns (C), 80ns (D), 90ns (E) and 100ns (F).

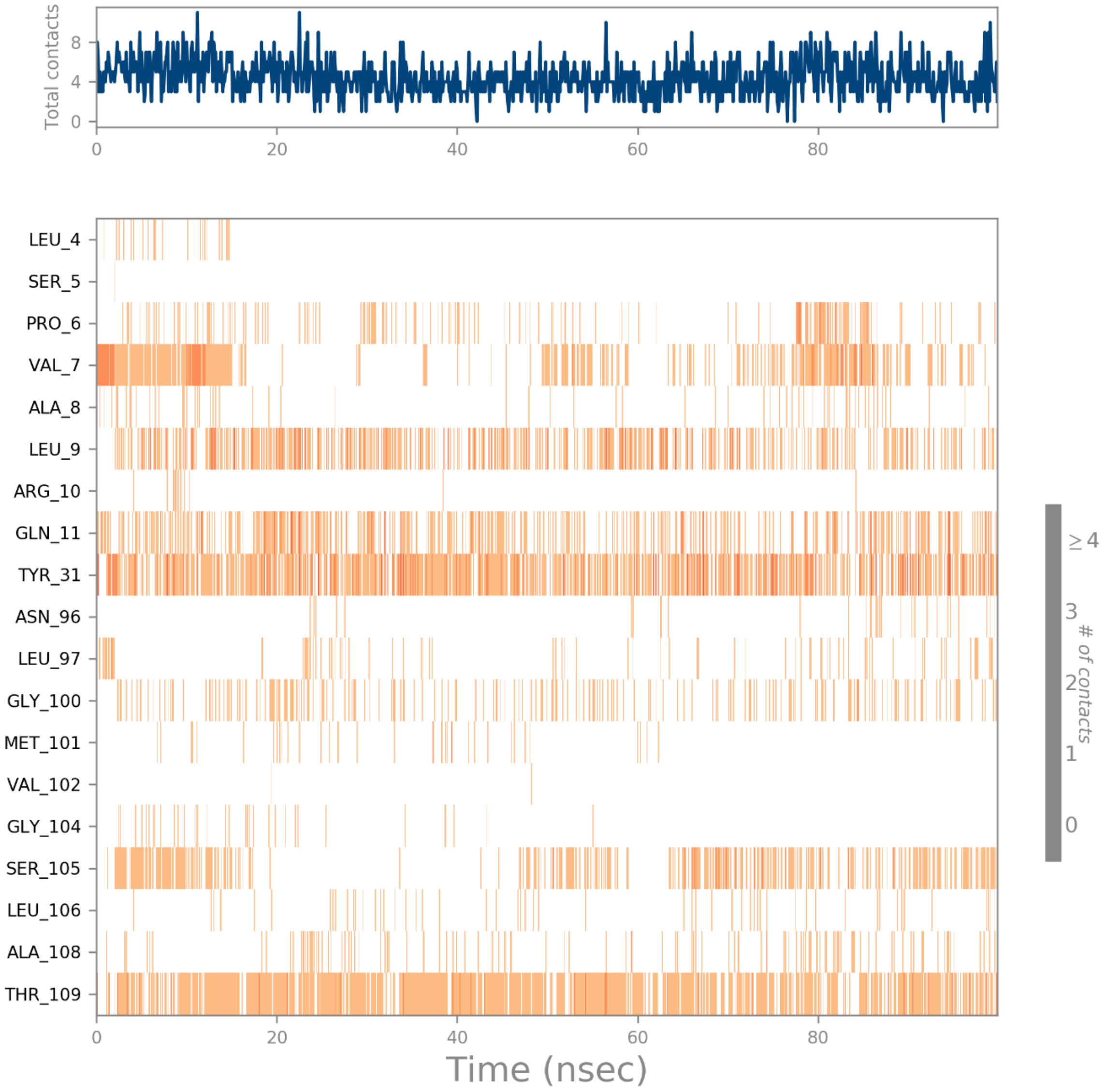

Fig. S5. A timeline representation of the interactions and contacts (H-bonds, Hydrophobic, Ionic, Water bridges) between residues of Nsp9 and ivermectin in each trajectory frame. Some residues make more than one specific contact with the ligand, which is represented by a darker shade of orange, according to the scale to the right of the plot.

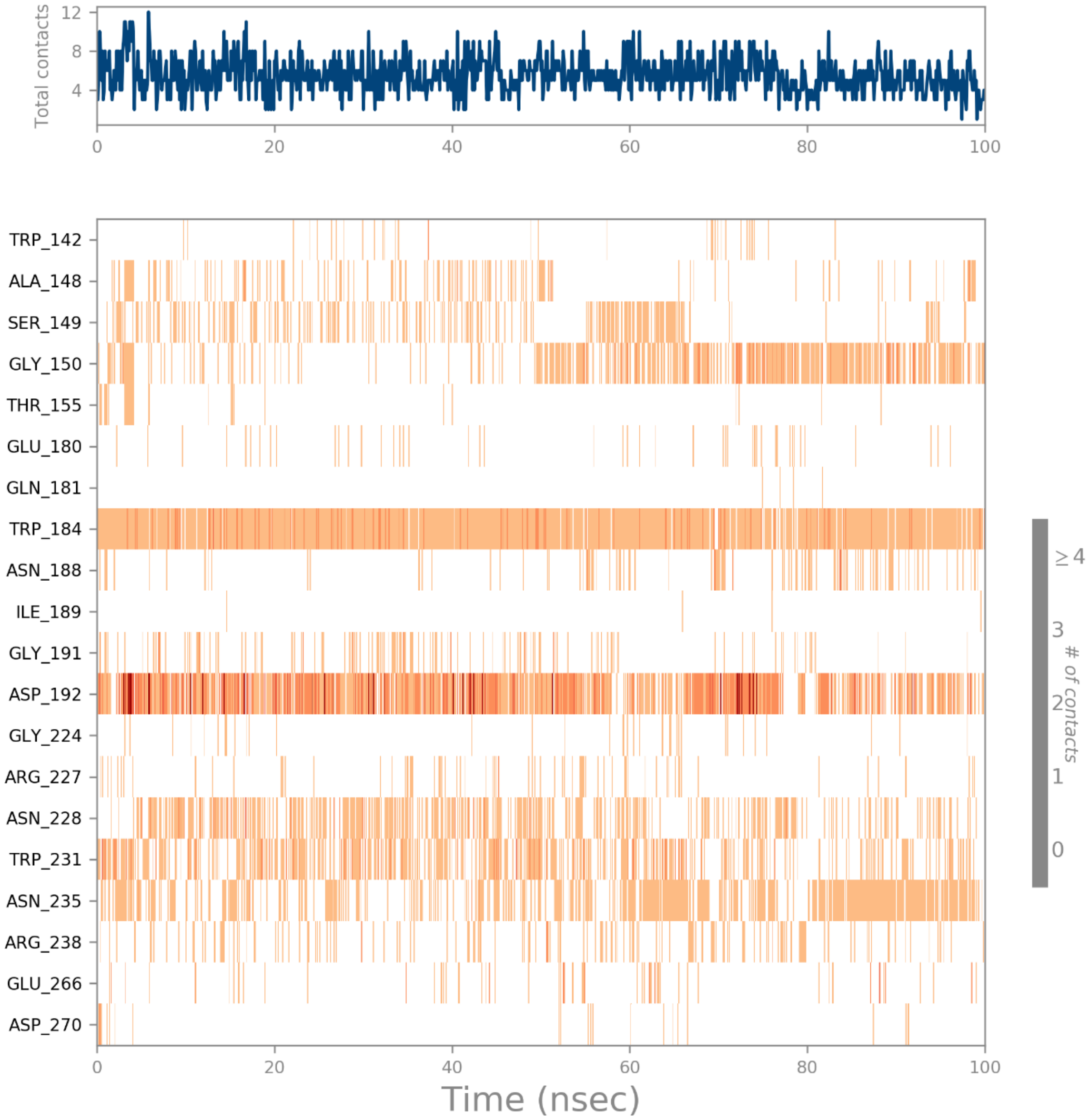

Fig. S6. A timeline representation of the interactions and contacts (H-bonds, Hydrophobic, Ionic, Water bridges) between residues of IMPα and ivermectin in each trajectory frame. Some residues make more than one specific contact with the ligand, which is represented by a darker shade of orange, according to the scale to the right of the plot.