Table S1: Viral-human homologs proteins metabolic pathways enrichment analysis.

S.No	Human Uniprot IDs	Homologous Virus IDs	Number of Pathways	Pathway Source	Pathway name	p-value
1	sp|P00374|DYR_HUMAN	gb:ABD28857	9	REACTOME	Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template	0.001016
				WikiPathways	ATM Signaling	0.001069
				REACTOME	Signaling by ERBB4	0.001123
				SMPDB	Cetuximab Action Pathway	0.001225
				SMPDB	Gefitinib Action Pathway	0.001225
				SMPDB	Panitumumab Action Pathway	0.001225
				SMPDB	Trastuzumab Action Pathway	0.001225
				Spike	DNA damage induced G1-S checkpoint	0.001474
2	sp|P04183|KITH_HUMAN	gb:AXN75107	9	KEGG	p53 signaling	0.001004
				WikiPathways	miRNA Regulation of DNA Damage Response	0.001004
				REACTOME	RNA Polymerase II Transcription	0.001055
				REACTOME	Post-translational protein phosphorylation	0.00108
				REACTOME	G2/M Transition	0.001198
		gb:AST09487		Panther_Pathway	p53	0.001222
				Spike	DAPk family	0.001222
				REACTOME	Generic Transcription Pathway	0.001227
				PID	Validated targets of C-MYC transcriptional activation	0.001634
3	sp|P04818|TYSY_HUMAN	gb:QCA43223	4	KEGG	Epithelial cell signaling in Helicobacter pylori infection	0.001163
				REACTOME	Immune System	0.001186
		gb:BBA90853		PID	Beta5 beta6 beta7 and beta8 integrin cell surface interactions	0.001209
				WikiPathways	Cells and Molecules involved in local acute inflammatory response	0.001209
4	sp|P09341|GROA_HUMAN	gb:AEV80662	5	PID	Signaling events mediated by Stem cell factor receptor (c-Kit)	0.001001
				KEGG	Endocytosis	0.001179
				REACTOME	Signal Transduction	0.001231
				REACTOME	Innate Immune System	0.00134
				KEGG	Epithelial cell signaling in Helicobacter pylori infection	0.001706
5	sp|P19875|CXCL2_HUMAN	gb:AEV80661	9	Panther_Pathway	p53_pathway_feedback_loops_2	0.001033
				WikiPathways	Neural Crest Cell Migration in Cancer	0.001033

				WikiPathways	TNF related weak inducer of apoptosis (TWEAK) Signaling	0.001033
				KEGG	Transcriptional misregulation in cancer	0.001072
				Panther_Pathway	PI_3-Kinase	0.001083
				PID	Syndecan-1-mediated signaling events	0.001083
				WikiPathways	Interleukin-11 Signaling	0.001083
				REACTOME	Signal Transduction	0.001191
				KEGG	Legionellosis	0.001766
6	sp|P23921|RIR1_HUMAN	gb:AXN75085 gb:AST09466 gb:AUL80484	14	REACTOME	p53-Dependent G1 DNA Damage Response	0.001002
				REACTOME	p53-Dependent G1/S DNA damage checkpoint	0.001002
				REACTOME	Cell Cycle, Mitotic	0.001022
				PID	mTOR signaling	0.001049
				REACTOME	G1/S DNA Damage Checkpoints	0.001097
				SMPDB	Morphine Metabolism Pathway	0.001123
				Spike	Response to DSB	0.001123
				KEGG	MicroRNAs in cancer	0.001159
				KEGG	Hepatitis C	0.001218
				WikiPathways	Integrated Breast Cancer	0.001218
				WikiPathways	Pyrimidine metabolism and related diseases	0.00127
				ACSN2	PENTOSE_PHOSPHATE	0.001426
				WikiPathways	Nucleotide Metabolism	0.001591
				HumanCyc	superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis	0.001764
7	sp|P31350|RIR2_HUMAN	gb:AZY90656 gb:AST09433	12	KEGG	p53 signaling	0.001006
				WikiPathways	miRNA Regulation of DNA Damage Response	0.001006
				WikiPathways	Pyrimidine metabolism and related diseases	0.001035
				ACSN2	DNA_DAMAGE_RESPONSE	0.001049
				KEGG	Melanoma	0.001049
				BioCarta	regulation of cell cycle progression by plk3	0.001162
				REACTOME	TP53 Regulates Transcription of Genes Involved in G2 Cell Cycle Arrest	0.001162
				WikiPathways	TGF-B Signaling in Thyroid Cells for Epithelial-Mesenchymal Transition	0.001162
				NetPath	Fibroblast growth factor-1	0.001183

				REACTOME	The role of GTSE1 in G2/M progression after G2 checkpoint	0.001183
				WikiPathways	Nucleotide Metabolism	0.001296
				HumanCyc	superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis	0.001438
8	sp|P35354|PGH2_HUMAN	gb:AEV80548	16	KEGG	Bacterial invasion of epithelial cells	0.001091
				KEGG	Pancreatic cancer	0.001091
				NetPath	Fibroblast growth factor-1	0.001091
				NetPath	IL6	0.001091
				REACTOME	The role of GTSE1 in G2/M progression after G2 checkpoint	0.001091
				BioCarta	er associated degradation (erad)	0.0011
				PID	Degradation of beta catenin	0.0011
				REACTOME	TP53 Regulates Transcription of Genes Involved in G2 Cell Cycle Arrest	0.0011
				REACTOME	Downstream signaling events of B Cell Receptor (BCR)	0.001179
				ACSN2	PI3K_AKT_MTOR	0.001208
				REACTOME	Protein ubiquitination	0.001224
				REACTOME	Regulation of TP53 Activity through Methylation	0.001227
				REACTOME	Immune System	0.001266
				KEGG	Kaposi sarcoma-associated herpesvirus infection	0.001488
				INOH	Prostaglandin Leukotriene metabolism	0.001649
				Panther_Pathway	Inflammation_mediated_by_chemokine_and_cytokine_signaling	0.001848
9	sp|P49916|DNLI3_HUMAN	gb:AAY97564 gb:AST09563	8	PID	Class I PI3K signaling events	0.001034
				REACTOME	Signaling by EGFR	0.001034
				BioCarta	pertussis toxin-insensitive ccr5 signaling in macrophage	0.00104
				KEGG	Nucleotide excision repair	0.001103
				ACSN2	MITOCHONDRIAL_GENES	0.001159
				REACTOME	Transcriptional regulation by small RNAs	0.001159
				IPAVS	Gq_activated_pathways_in_maladaptive_hypertrophy	0.001174
				KEGG	Th17 cell differentiation	0.001201

Table S2: Viral proteins homologous with human proteins sharing homologous epitopes.

S. No	Virus Homolog ID	Virus Protein name	Human Homologs IDs	Human Protein name
1	gb:AXN75085	ribonucleotide reductase large subunit [Akhmeta virus]	sp|P23921|RIR1_HUMAN	Ribonucleoside-diphosphate reductase large subunit
2	gb:AST09466	ribonucleotide reductase large subunit [NY_014 poxvirus]	sp|P23921|RIR1_HUMAN	Ribonucleoside-diphosphate reductase large subunit
3	gb:AEV80548	prostaglandin G/H synthase 2 [Cercopithecine betaherpesvirus 5]	sp|P35354|PGH2_HUMAN	Prostaglandin-G/H synthase 2
4	gb:AAY97564	DNA ligase [Monkeypox virus]	sp|P49916|DNLI3_HUMAN	DNA ligase 3
5	gb:AST09563	ATP-dependent DNA ligase [NY_014 poxvirus]	sp|P49916|DNLI3_HUMAN	DNA ligase 3
6	gb:AZY90656	CPXV051 protein [Cowpox virus]	sp|P31350|RIR2_HUMAN	Ribonucleoside-diphosphate reductase subunit M2
7	gb:AST09433	ribonucleotide reductase small subunit [NY_014 poxvirus]	sp|P31350|RIR2_HUMAN	Ribonucleoside-diphosphate reductase subunit M2
8	gb:QCA43223	ORF13 [Human alphaherpesvirus 3]	sp|P04818|TYSY_HUMAN	Thymidylate synthase
9	gb:BBA90853	ORF70 [Human gammaherpesvirus 8]	sp|P04818|TYSY_HUMAN	Thymidylate synthase
10	gb:AQY16903	MC152 [Molluscum contagiosum virus subtype 1]	sp|Q9H2F3|3BHS7_HUMAN	3 beta-hydroxysteroid dehydrogenase type 7
11	gb:ADZ29327	NMDA receptor-like protein [Cowpox virus]	sp|Q9HC24|LFG4_HUMAN	Protein lifeguard 4
12	gb:AZT86284	MC066L [Molluscum contagiosum virus]	sp|P07203|GPX1_HUMAN	Glutathione peroxidase 1
13	gb:AXN75107	thymidine kinase [Akhmeta virus]	sp|P04183|KITH_HUMAN	Thymidine kinase, cytosolic
14	gb:AST09487	thymidine kinase [NY_014 poxvirus]	sp|P04183|KITH_HUMAN	Thymidine kinase, cytosolic
15	gb:QCF48225	interleukin-10 [Human gammaherpesvirus 4]	sp|P22301|IL10_HUMAN	Interleukin-10
16	gb:ABD28857	ORF2 [Human gammaherpesvirus 8	sp|P00374|DYR_HUMAN	Dihydrofolate reductase
17	gb:AAY97032	dUTPase [Monkeypox virus]	tr|H0YNW5|H0YNW5_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase
18	gb:AUL80434	CPXV049 protein [Vaccinia virus]	tr|A0A0C4DGL3|A0A0C4DGL3_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase
19	gb:AUL80132	CPXV044 protein [Vaccinia virus]	sp|Q8IV08|PLD3_HUMAN	5'-3' exonuclease PLD3
20	gb:AAY97407	unknown [Monkeypox virus]	sp|Q9HC24|LFG4_HUMAN	Protein lifeguard 4

21	gb:AUL80484	hypothetical protein [Vaccinia virus]	sp|P23921|RIR1_HUMAN	Ribonucleoside-diphosphate reductase large subunit
22	gb:AUL80431	CPXV045 protein [Vaccinia virus]	tr|A0A3B3ITT3|A0A3B3IT T3_HUMAN	Monoglyceride lipase
23	gb:AEV80662	chemokine vCXCL7 [Cercopithecine betaherpesvirus 5]	sp|P09341|GROA_HUMA N	Growth-regulated alpha protein
24	gb:AEV80661	chemokine vCXCL7 [Cercopithecine betaherpesvirus 5]	sp|P19875|CXCL2_HUMA N	C-X-C motif chemokine 2

Table S3: The hydrogen bonding interaction between the top ranked virus-human molecular mimic epitope and HLA and TLR receptors residues. The interactions was identified by molecular docking of epitope within HLA and TLR4 receptors.

HLA Receptor (Chain A) interactions with Human-virus identical epitope (Chain B)
ASN(84):A<-->PHE(1):B
TYR(79):A<-->ASP(4):B
ASN(15):A<-->CYS(5):B
THR(83):A<-->LEU(13):B
THR(83):A<-->ASP(15):B
TLR Receptor (Chain A) interaction with Human-virus identical epitope (Chain B)
CYS(585):A<-->ASP(6):B
GLU(586):A<-->CYS(7):B
GLU(586):A<-->LEU(8):B
LYS(595):A<-->CYS(1):B
VAL(620):A<-->CYS(1):B
ASN(624):A<-->LEU(2):B

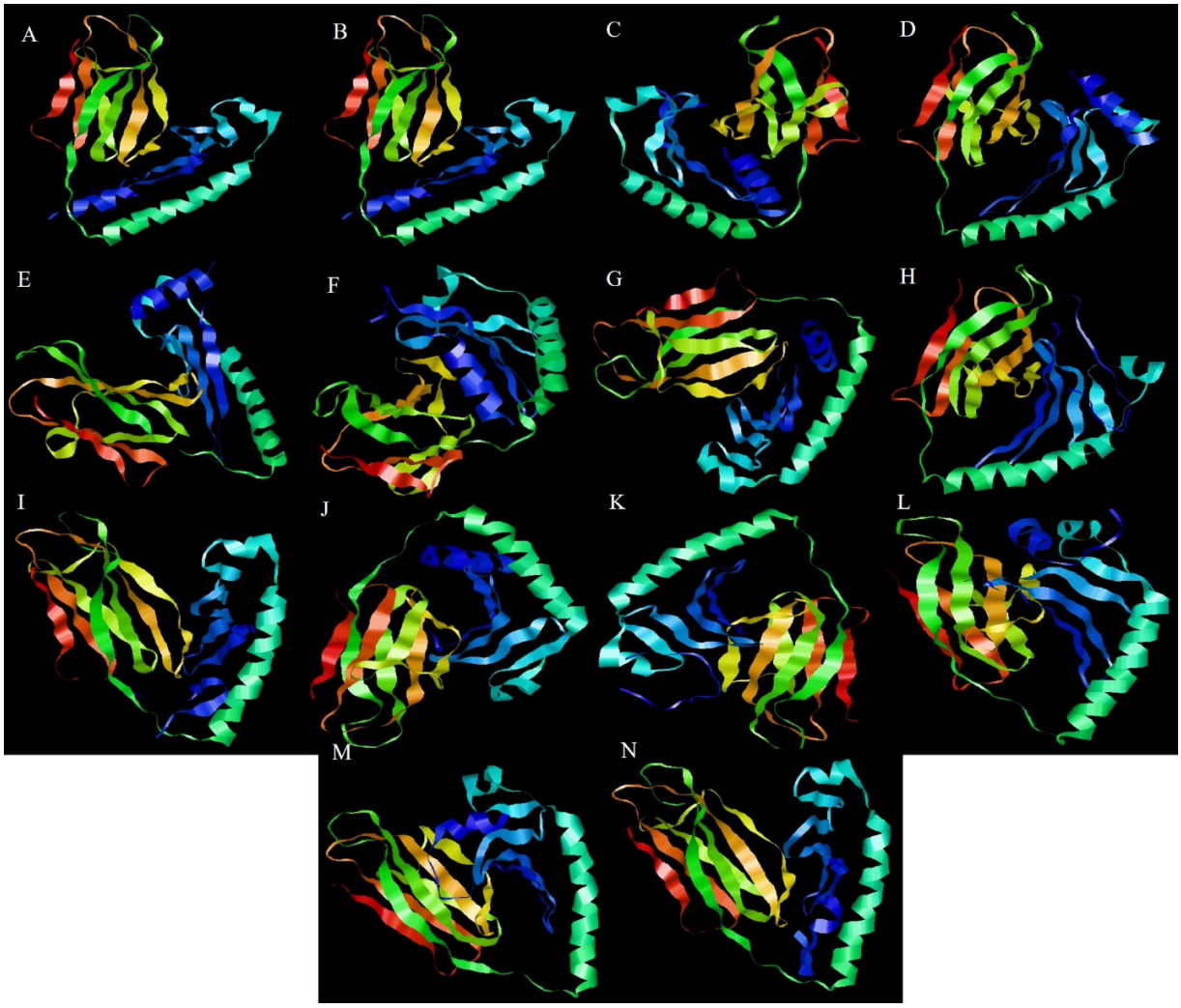

Figure S1: Molecular docking results of mimicking human peptides docked with HLA receptor.

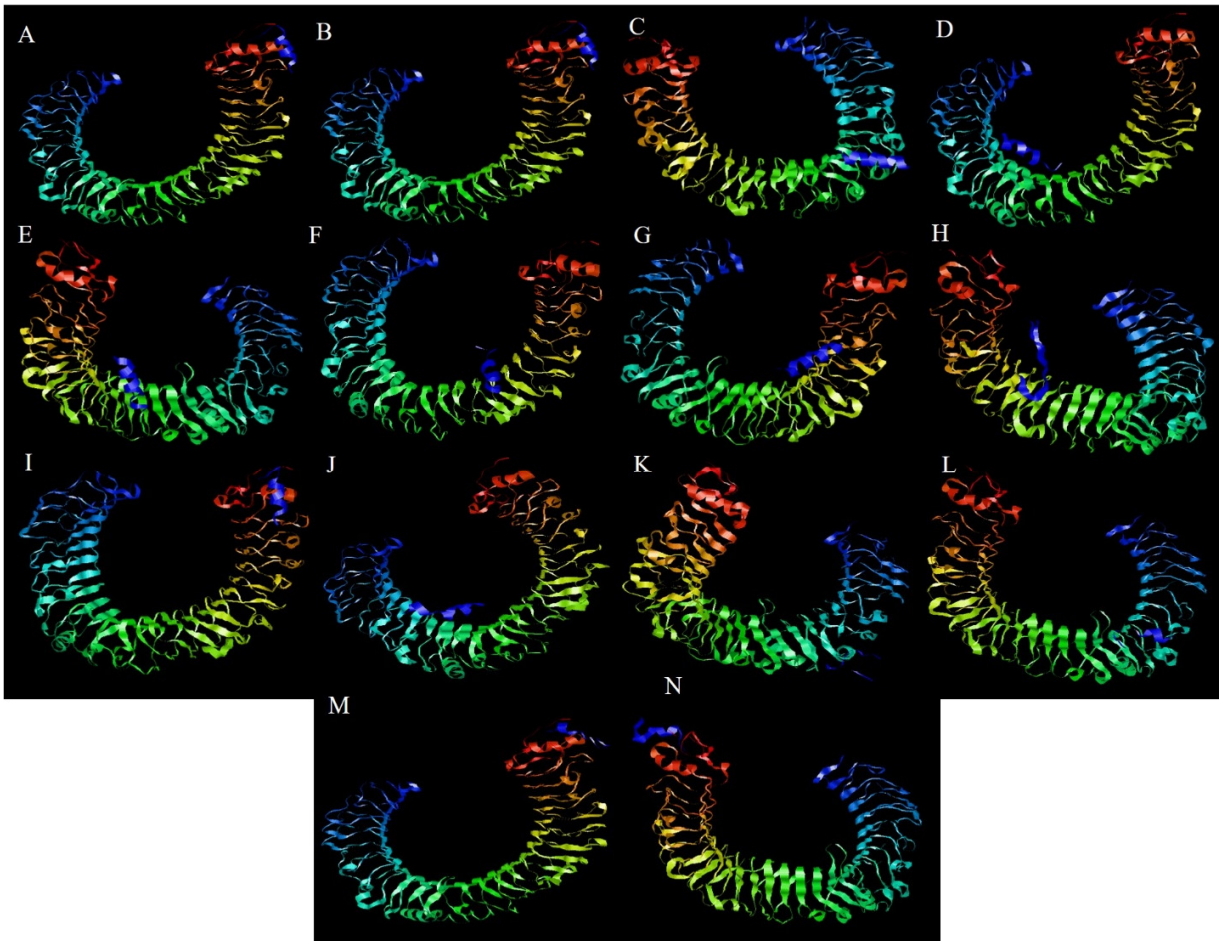

Figure S2: Molecular docking results of mimicking human peptides docked with TLR4 receptor.

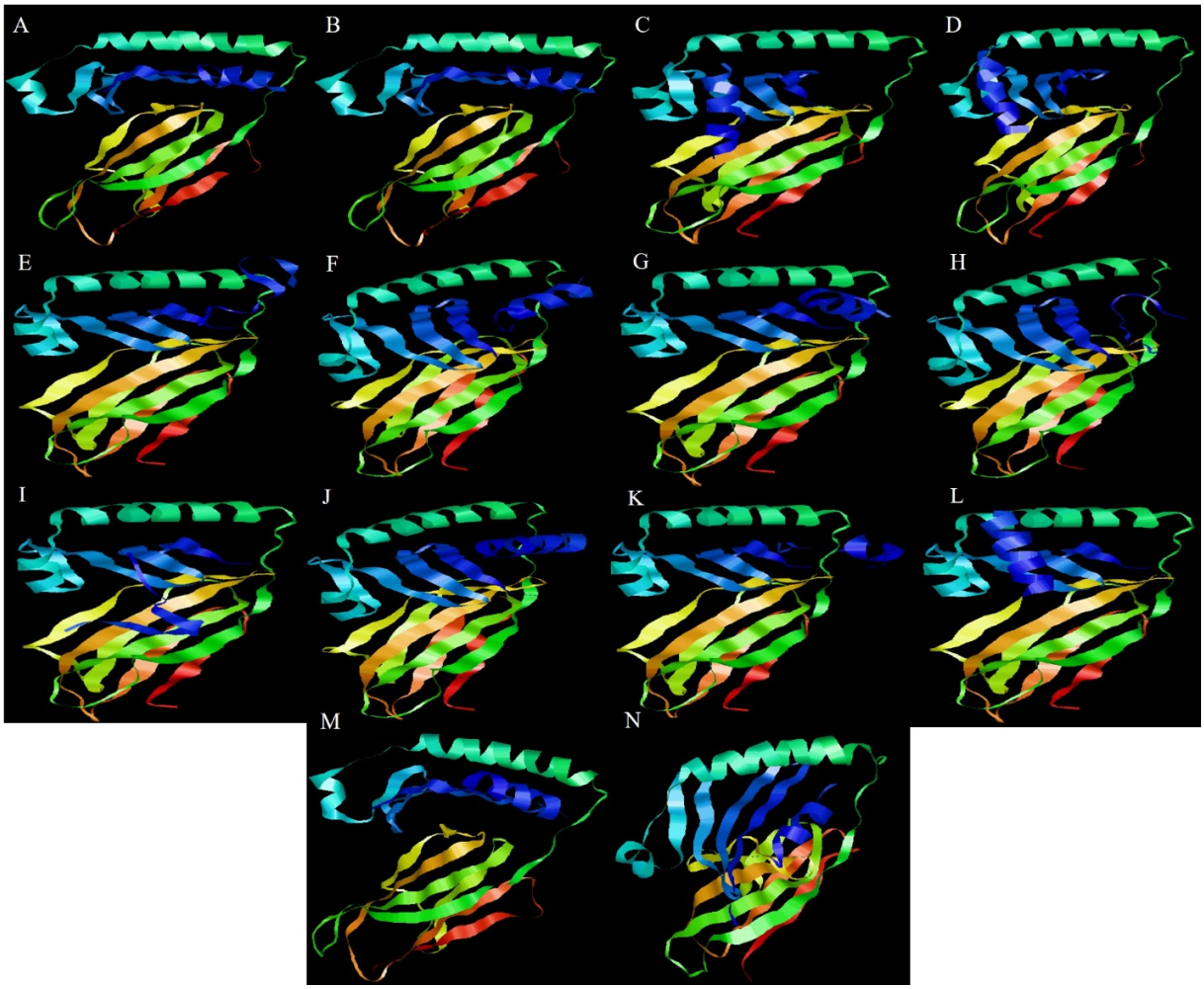

Figure S3: Molecular docking results of mimicking viral peptides docked with HLA receptor.

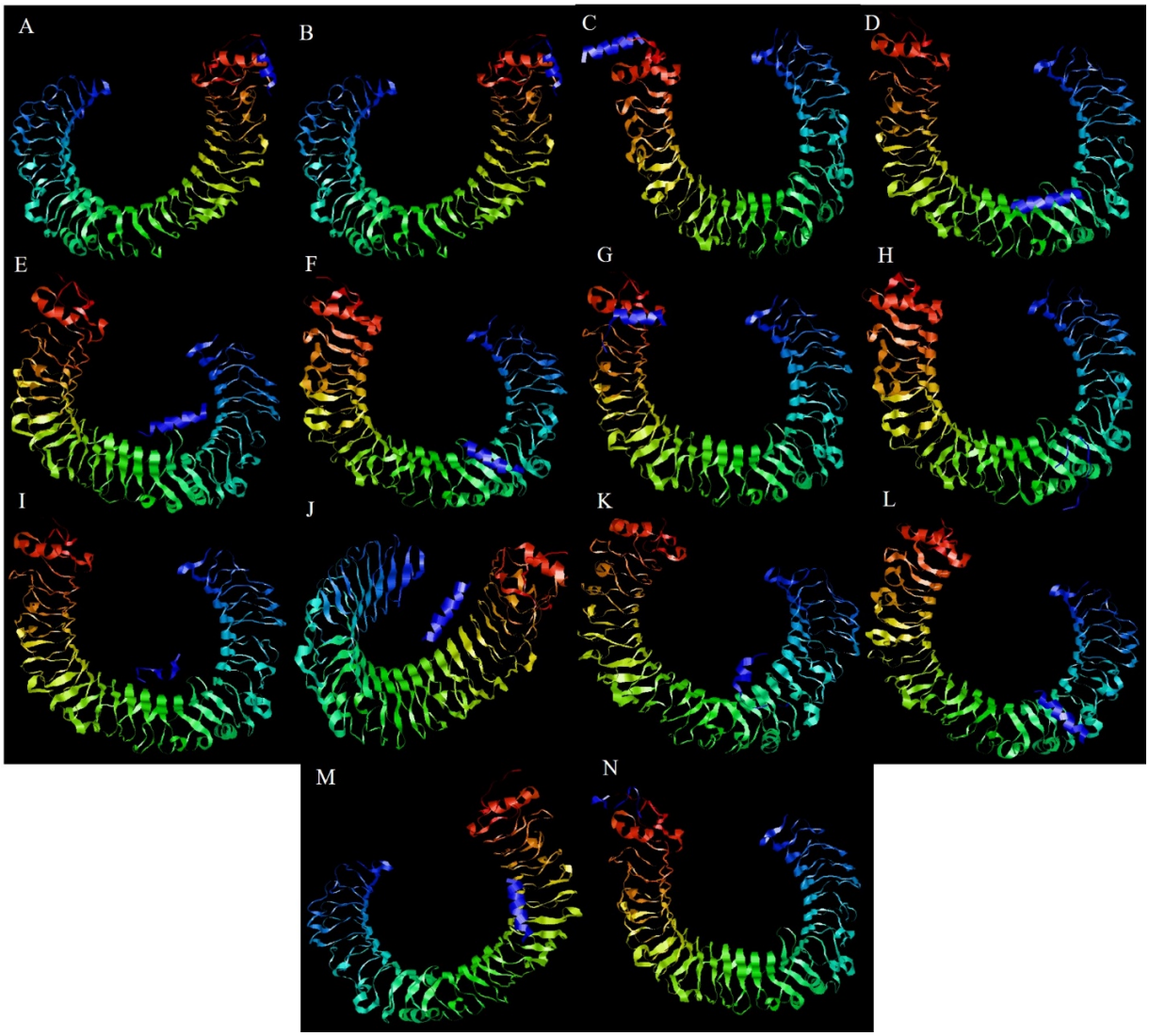

Figure S4: Molecular docking results of mimicking viral peptides docked with TLR4 receptor.