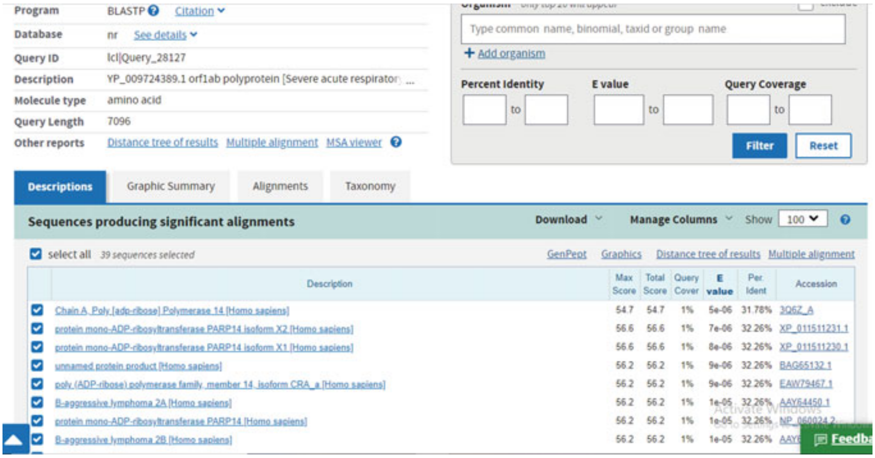

Program	BLASTP Citation
Database	nr See details
Query ID	lcl|Query_28127
Description	YP_009724389.1 orf1ab polyprotein [Severe acute respirator ...
Molecule type	amino acid
Query Length	7096
Other reports	Distance tree of results Multiple alignment MSA viewer

Sequences producing significant alignments

☑ select all 39 sequences selected

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☑	Chain A, Poly [adp-ribose] Polymerase 14 [Homo sapiens]	54.7	54.7	1%	5e-06	31.78%	3Q6Z_A
☑	protein mono-ADP-ribosyltransferase PARP14 isoform X2 [Homo sapiens]	56.6	56.6	1%	7e-06	32.26%	XP_011511231.1
☑	protein mono-ADP-ribosyltransferase PARP14 isoform X1 [Homo sapiens]	56.6	56.6	1%	8e-06	32.26%	XP_011511230.1
☑	unnamed protein product [Homo sapiens]	56.2	56.2	1%	9e-06	32.26%	BAG65132.1
☑	poly (ADP-ribose) polymerase family, member 14, isoform CRA_a [Homo sapiens]	56.2	56.2	1%	9e-06	32.26%	EAW79467.1
☑	B-aggressive lymphoma 2A [Homo sapiens]	56.2	56.2	1%	1e-05	32.26%	AAY64450.1
☑	protein mono-ADP-ribosyltransferase PARP14 [Homo sapiens]	56.2	56.2	1%	1e-05	32.26%	NP_060024.2
☑	B-aggressive lymphoma 2B [Homo sapiens]	56.2	56.2	1%	1e-05	32.26%	AAY

Fig. 9.1 BLAST output showing the foreignness of ORF1ab to human proteome

9.1 Determining the Foreignness of ORF1ab Poly Protein of Novel Corona Virus to Human Proteome Using BLAST

BLAST [8] is a basic local alignment search tool from NCBI. BLAST performs alignment for the comparison of any two sequences and identifies their degree of similarity. This tool is used to identify the degree of foreignness [9] between the human proteome and the targeted protein ORF1ab poly protein of Novel Corona Virus. In case the viral protein does not share any similarity, it would be recognized as FOREIGN to humans thus can be an immunogenic protein (Fig. 9.1).

Inference: The above BLAST result shows that the sequence of ORF1ab (Novel Corona Virus) shares 31% sequence similarity to Homo sapiens with a query coverage 1% only. This indicates that the sequence is not close to the human proteome and possesses foreignness; thus it can be antigenic and pathogenic and hence can be used for further analysis.

9.2 Identification of Antigenic Regions Using PVS

PVS [10] codes for Protein variability server that harbors many tools for the annotation of proteins. Antigenic Peptide prediction is a tool in PVS that would predict the antigenic regions within the protein having potential to trigger the production of antibodies in the host. Along with the antigenic peptides antigenic propensity of amino acids is also displayed in the tool output. The use of Peptide vaccines is always preferable than the whole organism Vaccine due to several parameters like less cost, high efficiency and lower risk of side effects (Fig. 9.2).