

viHumans

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UniProt Id ▾ P04618

Keyword ▾ X

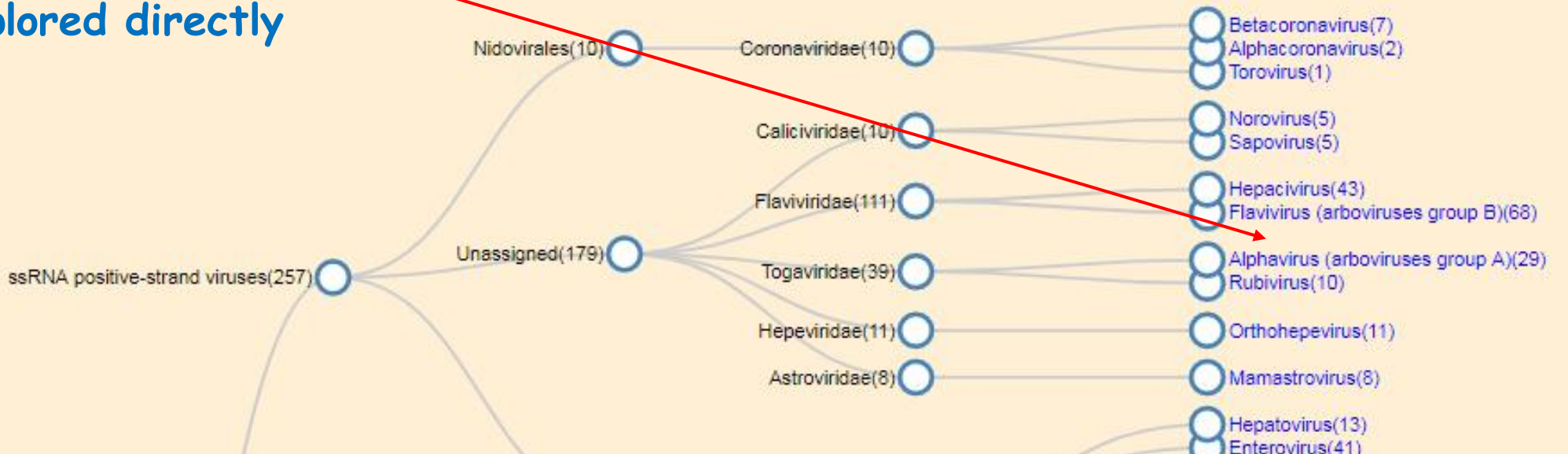
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User can type different keywords as options for searching the database
A sample "name/entry" for each keyword is also provided for reference
User can add multiple fields

Different viral species can be explored directly

Search by Taxonomy





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Information on a particular viral species can be explored such as their lineage, genome information, length and protein count

Total Hits: 8

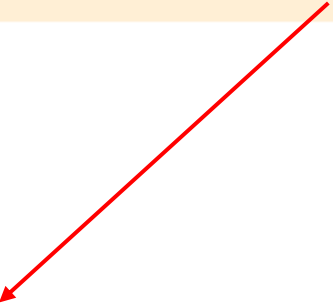
Organism	Taxonomy	Taxo(ID)	NCBI Refseq	Genome length	Protein Count
Human astrovirus-1 (HAstV-1)	Viruses> SsRNA Viruses> SsRNA Positive-strand Viruses> No DNA Stage> Astroviridae> Mamastrovirus> Mamastrovirus 1> Human Astrovirus-1 (HAstV-1)	12456	NC_001897.1 ; AJ005695.1	6813 bp	703
Human astrovirus-2 (HAstV-2)	Viruses> SsRNA Viruses> SsRNA Positive-strand Viruses> No DNA Stage> Astroviridae> Mamastrovirus> Mamastrovirus 1> Human Astrovirus-2 (HAstV-2)	12701			98
Human astrovirus-3 (HAstV-3)	Viruses> SsRNA Viruses> SsRNA Positive-strand Viruses> No DNA Stage> Astroviridae> Mamastrovirus> Mamastrovirus 1> Human Astrovirus-3 (HAstV-3)	35740			57
Human astrovirus-4 (HAstV-4)	Viruses> SsRNA Viruses> SsRNA Positive-strand Viruses> No DNA Stage> Astroviridae> Mamastrovirus> Mamastrovirus 1> Human Astrovirus-4 (HAstV-4)	35300			90
Human astrovirus-5 (HAstV-5)	Viruses> SsRNA Viruses> SsRNA Positive-strand Viruses> No DNA Stage> Astroviridae> Mamastrovirus> Mamastrovirus 1> Human Astrovirus-5 (HAstV-5)	35741			54
Human astrovirus-6 (HAstV-6)	Viruses> SsRNA Viruses> SsRNA Positive-strand Viruses> No DNA Stage> Astroviridae> Mamastrovirus> Mamastrovirus 1> Human Astrovirus-6 (HAstV-6)	37130			22
Human astrovirus-7 (HAstV-7)	Viruses> SsRNA Viruses> SsRNA Positive-strand Viruses> No DNA Stage> Astroviridae> Mamastrovirus> Mamastrovirus 1> Human Astrovirus-7 (HAstV-7)	38950			8
Human astrovirus-8 (HAstV-8)	Viruses> SsRNA Viruses> SsRNA Positive-strand Viruses> No DNA Stage> Astroviridae> Mamastrovirus> Mamastrovirus 1> Human Astrovirus-8 (HAstV-8)	43358			100

Information on a viral protein can be explored on clicking the ID



Total Hits: [703](#)
 Reviewed: [3](#)
 Unreviewed: [700](#)

Uniprot ID	Status	Protein Name	Organism	Role(s)	Experimentally known Structure(s)	Experimentally known Ligand(s)	PubMed ID
O12792	Reviewed	♦Capsid polyprotein VP90 [Cleaved into: Capsid polyprotein VP70	Human astrovirus-1 (HAstV-1)	The capsid polyprotein VP90 self-assembles and undergoes a proteolytic cleavage by host caspases to yield the VP70 virions. This immature virion is composed of 180 VP70 subunits with 90 dimeric spikes and displays a T=3 icosahedral symmetry. The mature virion is obtained by further cleavages	Not Available	Not Available	8293952 8021608 22743104
POC6K4	Reviewed	♦Non-structural polyprotein 1A [Cleaved into: VPg ♦ Protein p19	Human astrovirus-1 (HAstV-1)	♦Non-structural polyprotein 1A: contains the viral protease participating in the cleavage of the polyprotein into functional products. ♦ VPg: protein covalently attached to the 5' extremity of the genomic and subgenomic RNAs.	Not Available	Not Available	8021608 8254779 11799197
Q67726	Reviewed	♦Non-structural polyprotein 1AB [Cleaved into: VPg ♦ Protein p19	Human astrovirus-1 (HAstV-1)	♦Non-structural polyprotein 1AB: contains the viral protease participating in the cleavage of the polyprotein into functional products. It contains also the activities necessary for replication of genomic RNA-- as well as transcription of subgenomic mRNA. ♦ VPg: protein covalently attached to the 5' extremity	Not Available	Not Available	8021608 8254779 11799197
A0A0A7EAL4	Unreviewed	♦Capsid polyprotein VP90 [Cleaved into: Capsid	Human astrovirus-1 (HAstV-1)	The capsid polyprotein VP90 self-assembles and undergoes a proteolytic cleavage by host caspases to yield the VP70 virions. This immature virion is composed of 180 VP70 subunits with 90 dimeric	Not Available	Not Available	Not Available

Name and Taxonomic details for the viral protein



Name & Taxonomy

UniProt ID	P04618
Status	Reviewed
Host	Homo Sapiens (Human) [TaxID: 9606]
Gene Name	Rev[Gene ID: 155908]
Protein Name	Protein Rev (ART/TRS) (Anti-repression transactivator) (Regulator of expression of viral proteins) 
Organism Name	Human Immunodeficiency Virus Type 1 Group M Subtype B (isolate HXB2) (HIV-1)
Taxonomic Lineage	Viruses> Retro-transcribing Viruses> Retroviridae> Orthoretrovirinae> Lentivirus> Primate Lentivirus Group> Human Immunodeficiency Virus 1> HIV-1 Group M> HIV-1 M:B> Human Immunodeficiency Virus Type 1 Group M Subtype B (isolate HXB2) (HIV-1)
RefSeq	NC_001802.1 ; AF033819.3 
PubMed ID	3040055 ; 8806671 ; 10984616 ; 11827166 ; 15567440 ; 10328811
Pathways Involved	Various pathway(s) in which protein is involved
KEGG	vg:155908
Reactome	R-HSA-162585 ; R-HSA-162588 ; R-HSA-162592 ; R-HSA-162594 ; R-HSA-164516 ; R-HSA-164525 ; R-HSA-164843 ; R-HSA-165054 ; R-HSA-173107 ; R-HSA-175474 ; R-HSA-175567 ; R-HSA-177539 ; R-HSA-180689 ; R-HSA-180746 ; R-HSA-180910 ;

Sequence Information

Sequence level details for the viral protein

Sequence	MAGRSGDSDEELIRTVRLIKLLYQSNPPPNEGTRQARRNRRRRWRERQRQIHSISERILGTYLGRSAEPVPLQLPPLERLTLDCEDCGTSQGVGSP QILVESPTVLESGTKE
Length	116
Alternate Sequence	Not Available
Non-standard residue	Not Available
Date of last Sequence modification	13-08-1987
Protein Existence	Evidence at protein level

Amino Acid composition

Amino Acid	Count	% Frequency	Amino Acid	Count	% Frequency
Alanine (A)	3	2.58	Leucine (L)	13	11.20
Arginine (R)	16	13.79	Lysine (K)	2	1.72
Asparagine (N)	4	3.44	Methionine (M)	1	.86
Aspartic Acid (D)	4	3.44	Phenylalanine (F)	0	0
Cysteine (C)	2	1.72	Proline (P)	10	8.62

Sum of Absolute Deviation from Amino Acid Occurrence Frequencies 51.68

Aliphatic Index 78.91

Instability Index 86.73

Secondary Structure features

% Number of Residues in Helices	% Number of Residues in Strands	% Number of Residues in Coils
36.20	0	63.79

Structural Difficulty(SD) index 12.31

Function

Information via experimental data and computational annotations is provided for each section

Role(s)	Not Available
EC	Not Available
Experimentally known GO terms	GO:0003700 ; GO:0003723 ; GO:0006278 ; GO:0016032 ; GO:0019058 ; GO:0019061 ; GO:0019064 ; GO:0019068 ; GO:0030260 ; GO:0030430 ; GO:0042802 ; GO:0044196 ; GO:0051028 ; GO:0051169 ; GO:0075713
Subcellular Location	Host nucleus, host nucleolus . Host cytoplasm . Note=The presence of both nuclear import and nuclear export signals leads to continuous shuttling between the nucleus and cytoplasm. .
Domain(s)	Not Available
Motif(s)	MOTIF 34 50 Nuclear localization signal and RNA-binding (RRE). ; MOTIF 73 84 Nuclear export signal and binding to XPO1.

Function
Structures
Binding Pockets/
Active Sites
Ligands Availability

Structure Availability

Methods of 3D structure generation	Predicted/Modelled
Experimentally known structure	Not Available
Active Site(s)	Not Available
Predicted 3D Structures	Generation of 3D structure using the below softwares
<ul style="list-style-type: none">• I-Tasser• Raptor-X	P04618.pdb P04618.pdb
	ProtSAV Score 0.7 0.5
Binding pocket(s)	
<ul style="list-style-type: none">• I-Tasser• Raptor-X	Binding Pocket 1 Binding Pocket 2 Binding Pocket 3 Binding Pocket 4 Binding Pocket 5 Pockets.zip Not Available

Ligand Availability

Experimentally known Ligand(s)	CHEMBL1293282
Virtually Screened Ligands	Not Applicable