VBRC

Viral Bioinformatics Resource Center

www.biovirus.org

VBRC Collaborators

- University of Alabama at Birmingham (UAB)
  - Elliot Lefkowitz
  - Puri Bangalore
  - Barrett Bryant
- University of Victoria (UVic)
  - Chris Upton

Family	Genus	Species	Disease	Category
Arenaviridae	Arenavirus: LCMV-complex	Lymphocytic Chorimeningitis Virus	Lymphocytic choriomeningitis	A
		Lassa Virus	Lassa Fever	A
	Arenavirus: Tacaribe complex	Junin Virus	Argentine hemorrhagic fever	A
		Machupo Virus	Bolivian hemorrhagic fever	A
		Guanarito Virus	Venezuelan hemorrhagic fever	A
		Sabia Virus	Sabia-associated hemorrhagic fever	A
Bunyaviridae	Hantavirus	Hanta Virus	Hantavirus Pulmonary Syndrome	A
		Hantaan virus	Korean hemorrhagic fever	C
		Puumala virus	Hemorrhagic Fever with Renal Syndrome	C
	Nairovirus	Crimean-Congo Hemorrhagic Fever Virus	Crimean-Congo Hemorrhagic Fever	C
	Orthobunyavirus	California encephalitis group (La Crosse)	Encephalitis	B
	Phlebovirus	Rift Valley Fever Virus	Rift Valley Fever	A
Filoviridae	Ebola-Like Virus	Ebola Virus	Ebola Hemorrhagic Fever	A
	Marburg-Like Virus	Marburg Virus	Marburg Hemorrhagic Fever	A
Flaviviridae	Flavivirus	Dengue Virus	Dengue hemorrhagic fever	A
		Kyasanar Forest Disease Virus	Kyasanur Forest disease	B
		Omsk Hemorrhagic Fever Virus	Omsk hemorrhagic fever	B
		Japanese encephalitis virus group	West Nile encephalitis	B
		Yellow Fever Virus	Yellow fever	C
		Tick-borne Encephalitis virus	Tick-borne encephalitis	C
Paramyxoviridae	Unclassified	Nipah virus		C
	Morbillivirus	Equine morbillivirus		C
Poxviridae	Orthopoxvirus	Variola major	Smallpox	A
Togaviridae	Alphaviruses	Venezuelan equine encephalitis virus	Venezuelan encephalitis	B
		Eastern equine encephalitis virus	Eastern equine encephalitis	B
		Western equine encephalitis virus	Western equine encephalitis	B

Viral Bioinformatics Resource Center for BioDefense - Mozilla Firefox

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data | analysis | announcements | links

Welcome

The Viral Bioinformatics Resource Center (VBRC) at the University of Alabama at Birmingham and the University of Victoria is funded by the National Institutes of Health through the National Institute of Allergy and Infectious Diseases. It was established to provide comprehensive genomics resources to the scientific community for basic and applied research on viruses selected from the NIAID lists of Category A, B, and C priority pathogens that are considered to be possible bioterrorist threats or emerging or re-emerging infectious diseases.

The VBRC provides researchers with:

1. a repository of virus species and strains under study
2. a relational database that stores the genomic sequences of these viruses
3. annotation and analysis of virus genes and genomes
4. web-based data mining and sequence analysis tools
5. software for analysis of complete genomes
6. help and training in the use of all VBRC resources

We hope you will find this site both easy to use and helpful, and we want to know what additional features you would find useful. Please give us your input by sending us a message via the "feedback" link below.

VBRC

Last Modified:
Sun, 10 Oct 2004 17:42:42 GMT

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Viral Biodefense Bioinformatics Resource

- UAB
  - Elliot Lefkowitz
- USAMRIID
  - Kevin Anderson (DHS)
  - George Korch (DTRA)
  - Charles Millard
- Funding
  - USAMRMC

PBR

The Poxvirus Bioinformatics Resource

www.poxvirus.org

PBR Collaborators

- UAB
  - Elliot Lefkowitz
- St. Louis University
  - Mark Buller
- University of Victoria
  - Chris Upton
- ATCC
  - Charles Buck
- Medical College of Wisconsin
  - Paula Traktman

Design Philosophy

- Useful and Used
- Data access and basic analytical tools
  - Supports all investigators
  - Web-based application requirements
    - Web Browser, Java plugin
- Comprehensive analytical tools
  - Designed for viral genomes
  - Java application
    - Java Web-start

Architecture

- Database
  - Microsoft SQL Server 2000
- Web Server
  - Windows 2003
  - Microsoft IIS 6.0
- Visualization
  - Java applets
- Search Services (BLAST)
  - Sun Solaris
  - Linux Cluster (MPI)

Poxvirus Bioinformatics Resource Center - Mozilla

Poxvirus Bioinformatics Resource Center

data | analysis | reagents | literature | discussion | announcements | links

Welcome

Welcome to the Poxvirus Bioinformatics Resource Center. This Center has been established to provide resources to the scientific community for basic research and to facilitate the development of novel antiviral therapies and vaccines against human orthopoxvirus infections as well as approaches for environmental detection of virions and the rapid diagnosis of disease.

The Center provides a relational database that supports data storage of poxvirus genomic sequences, and annotation and analysis of poxvirus genes; web-based data mining and sequence analysis tools; software for analysis of complete genomes; a poxvirus literature resource; a repository of poxvirus species and strains (at ATCC); and a discussion forum.

The Poxvirus Bioinformatics Resource Center was created by a consortium of laboratories. An Advisory Committee has been established to help guide the development of this Center. Funding for this project is being provided by the National Institute for Allergy and Infectious Diseases, and the Defense Advanced Research Projects Agency. Suggestions for improvement of the Center are welcomed (see Feedback).

Click for information on changes to the PBR virus designations.

PBR

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Wed, 02 Apr 2003 21:57:16 GMT

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Google™ Search

Search poxvirus.org

Search WWW

PBR Genomes - Mozilla

Virus (Click for Gene Map)	Complete Genome?	Genome Size (bases)	Accession Number (Click for NCBI Record)	ATCC Number
Amsacta moorei entomopoxvirus, complete genome.	Y	232,392	AF250284	
Camelpox virus CMS, complete genome	Y	202,205	AY009089	
Camelpox virus isolate M-96 from Kazakhstan, complete genome	Y	205,719	AF438165	
Cowpox virus strain Brighton Red, complete genome	Y	224,499	AF482758	VR-302
Cowpox virus strain GRI-90, complete genome	Y	223,666	X94355	
Ectromelia virus Moscow strain Unpublished	Y	209,771	AF012825	VR-1374
Ectromelia virus strain Naval complete genome (unpublished) Unpublished	Y	207,620	None	
Fowlpox virus, complete genome.	Y	288,539	AF198100	
Goatpox virus strain G20-LKV, complete genome.	Y	149,723	AY077836	
Goatpox virus strain Pellor, complete genome.	Y	149,599	AY077835	
Lumpy skin disease virus isolate Neethling vaccine LW 1959, complete genome	Y	150,509	AF409138	
Lumpy skin disease virus strain Neethling isolate 2490, complete genome.	Y	150,773	AF325528	
Lumpy skin disease virus isolate Neethling Warmbaths LW, complete genome	Y	150,793	AF409137	
Molluscum contagiosum virus subtype 1, complete genome	Y	190,289	U60315	
Monkeypox virus strain Zaire-96-I-16, complete genome.	Y	196,858	AF380138	
Melanoplus sanguinipes entomopoxvirus, complete genome.	Y	236,120	AF063866	
Myxoma virus strain Lausanne, complete genome	Y	161,773	AF170726	VR-115
Rabbitpox virus Strain Utrecht, complete genome Unpublished	Y	197,731	None	
Rabbit fibroma virus, complete genome.	Y	159,857	AF170722	VR-364
Sheeppox virus strain A, complete genome.	Y	150,057	AY077833	
Sheeppox virus strain NISKHI, complete genome.	Y	149,662	AY077834	
Sheeppox virus strain TU-V02127, complete genome.	Y	149,955	NC_004002	
Swinepox virus isolate 17077-99, complete genome.	Y	146,454	AF410153	
Vaccinia virus, complete genome; strain Copenhagen with "C" inserted at position 114378. See Senkevich et. al., Virology V. 300, p 296.	Y	191,738	M35027	
Vaccinia virus strain Ankara, complete genomic sequence	Y	177,923	U94848	VR-1508
Vaccinia virus (strain Tian Tan) complete genome	Y	189,274	AF095689	
Vaccinia virus (strain Tian Tan) complete genome updated sequence	Y	189,279	None	
Vaccinia virus (strain WR Western Reserve) complete genome	Y	194,711	AY243312	
Variola major virus (strain Bangladesh-1975) complete genome	Y	186,103	L22579	
Variola virus Congo-1965 left near-terminal region.	N	29,309	U18337	
Variola minor virus complete genome; strain Garcia-1966	Y	186,986	Y16780	
Variola major virus DNA complete genome; strain India-1967	Y	185,578	X69198	
Variola virus Somalia-1977 left variable region.	N	29,539	U18340	
Variola virus Somalia-1977 right near-terminal region.	N	30,869	U18341	
Yaba-like disease virus (YLDV), complete genome.	Y	144,575	AJ293568	VR-587

Virus Coding Strategies – RNA Genomes

- Segmented genomes
- Ambisense genomes
- Overlapping genes
- RNA editing
- Polyprotein processing
- RNA structural motifs
- Alternative regulatory motifs

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Data

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Complete Genomes Available in the Viral Bioinformatics Resource Center for Biodefense

Virus (Click for Gene Map)	Complete Genome?	Genome Size (bases)	Accession Number (Click for NCBI Record)
Australian bat lyssavirus, complete genome	Y	11,822	NC_003243
Alkhurma virus, complete genome	Y	10,685	NC_004355
Andes virus segment L, complete sequence	Y	6,562	NC_003468
Andes virus segment M, complete sequence	Y	3,671	NC_003467
Andes virus segment S, complete sequence	Y	1,871	NC_003466
Apoi virus, genome	Y	10,116	NC_003676
Aura virus, complete genome	Y	11,824	NC_003900
Bovine coronavirus, complete genome	Y	31,028	NC_003045
Barmah Forest virus, complete genome	Y	11,488	NC_001786
Crimean-Congo hemorrhagic fever virus strain 30908 segment L, complete sequence	Y	12,112	AY675240
Crimean-Congo hemorrhagic fever virus strain Hodzha segment M, complete sequence	Y	5,356	AY223476
Crimean-Congo hemorrhagic fever virus strain Hodzha segment S, complete sequence	Y	1,673	AY223475
Crimean-Congo hemorrhagic fever virus segment L, complete sequence	Y	12,164	NC_005301
Crimean-Congo hemorrhagic fever virus segment M, complete sequence	Y	5,055	NC_005300
Crimean-Congo hemorrhagic fever virus segment S, complete sequence	Y	1,672	NC_005302
Crimean-Congo hemorrhagic fever virus strain Matin L protein gene, complete cds	Y	12,168	AY422208

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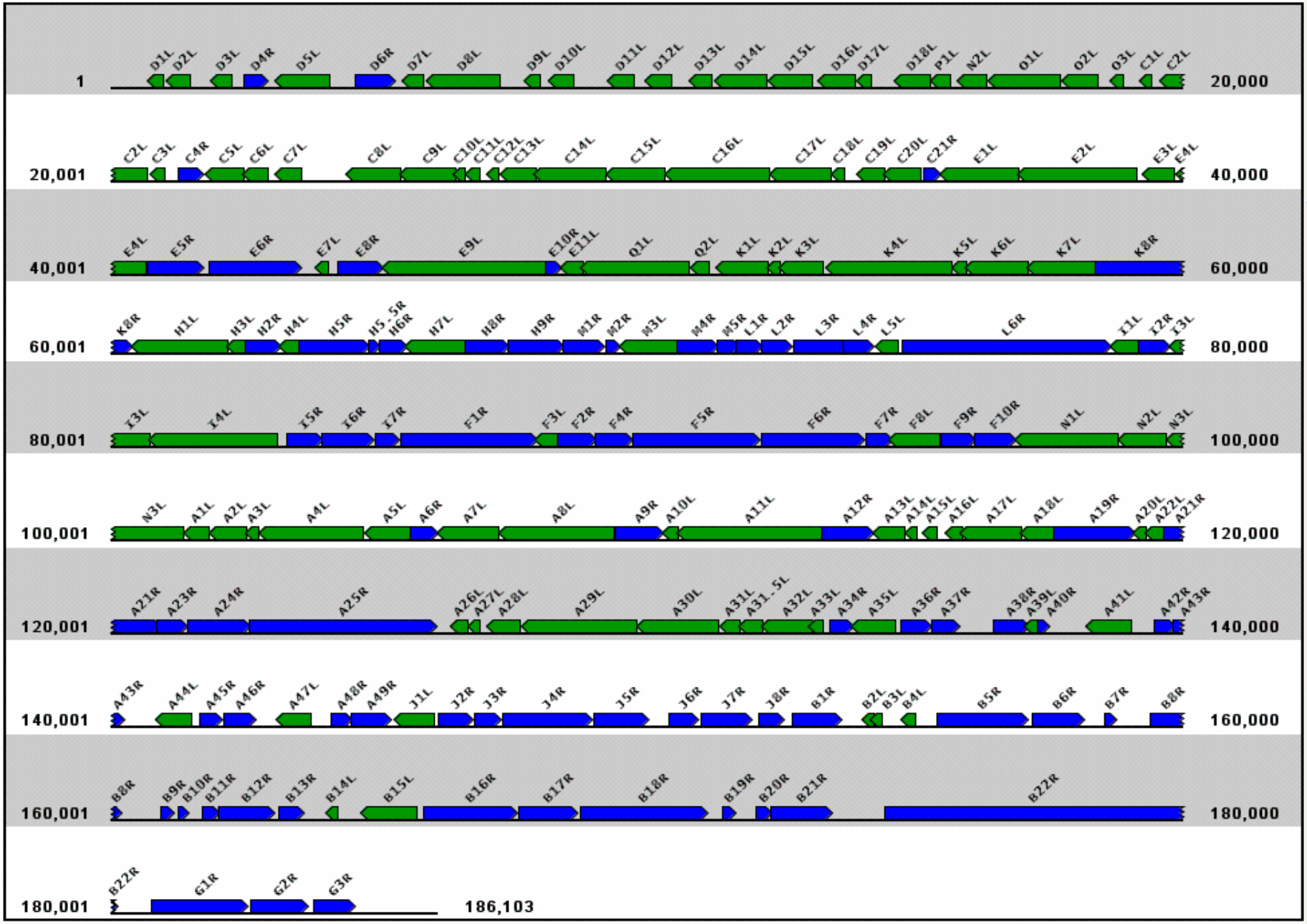
Venezuelan equine encephalitis virus strain 66637, complete genome	Y	11,420	AF004458
Venezuelan equine encephalitis virus strain 83U434, complete genome	Y	11,441	U55362
Western equine encephalomyelitis virus, complete genome	Y	11,484	NC_003908
West Nile virus isolate Ast99-901, complete genome	Y	10,998	AY278441
West Nile virus strain Chin-01, complete genome	Y	11,028	AY490240
West Nile virus strain Eg101, complete genome	Y	11,029	AF260968
West Nile virus, complete genome	Y	10,962	NC_001563
West Nile virus strain IS-98 STD, complete genome	Y	11,029	AF481864
West Nile virus isolate LEIV-Krnd88-190, complete genome	Y	10,741	AY277251
West Nile virus isolate LEIV-Vlg99-27889, complete genome	Y	10,845	AY277252
West Nile virus isolate LEIV-Vlg00-27924, complete genome	Y	10,842	AY278442
West Nile virus strain NY99-flamingo382-99, complete genome	Y	11,029	AF196835
West Nile virus strain NY99-eqhs, complete genome	Y	11,029	AF260967
West Nile virus strain RO97-50, complete genome	Y	11,029	AF260969
West Nile virus strain TVP 8533 complete genome	Y	11,029	AY289214
West Nile virus isolate WN MD 2000-crow265, complete genome	Y	11,029	AF404753
West Nile virus isolate WN NY 2000-crow3356, complete genome	Y	11,029	AF404756
West Nile virus isolate WN NY 2000-grouse3282, complete genome	Y	11,029	AF404755
West Nile virus isolate WN Italy 1998-equine, complete genome	Y	11,029	AF404757
West Nile virus isolate WN NJ 2000 MQ5488, complete genome	Y	11,029	AF404754
Yellow fever virus vaccine strain 17D-213, complete genome	Y	10,862	U17067
Yellow fever virus vaccine strain 17DD, complete genome	Y	10,862	U17066
Yellow fever virus strain 85-82H Ivory Coast, complete genome	Y	10,862	U54798
Yellow fever virus strain ASIBI, complete genome	Y	10,862	AY640589
Yellow fever virus, complete genome	Y	10,862	NC_002031
Yellow fever virus French viscerotropic strain, complete genome	Y	10,862	U21056
Yellow fever virus strain Gambia 2001, complete genome	Y	10,862	AY572535
Yellow fever virus strain Ivory Coast 1999, complete genome	Y	10,862	AY603338
Yellow fever virus strain Trinidad 79A isolate 788379, complete genome	Y	10,760	AF094612
Yellow fever virus complete genome, 17D vaccine strain	Y	10,862	X03700
Yokose virus, complete genome	Y	10,857	NC_005039
Zaire Ebola virus, complete genome	Y	18,959	NC_002549
Zaire ebolavirus strain Zaire 1995, complete genome	Y	18,961	AY354458

Variola major virus strain Bangladesh



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Data

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Poxvirus Gene Search

Enter appropriate parameters and click **Submit** to get a list of matching genes.

Search Field	Search Parameters	
Virus:	All virus genomes Amsacta moorei entomopoxvirus (232,392 bp) Camelpox virus M-96 (205,719 bp) Camelpox virus strain CMS (202,205 bp) Cowpox virus strain Brighton Red (224,499 bp) (Hold down the Ctrl Key to make multiple selections)	
Gene name:		
PBR name: (pre or post 3/1/2003 name)		
Genome position:	Start:	End:
Description:		
Notes:		
Molecular Weight:	Greater Than or Equal To:	Less Than or Equal To:
pI:	Greater Than or Equal To:	Less Than or Equal To:
Prosite motif:	Not selected 2-oxo acid dehydrogenases acyltransferase component lip Aldehyde dehydrogenases active sites ATP synthase c subunit signature ATP-dependent DNA ligase signatures and profile (Hold down the Ctrl Key to make multiple selections)	
Contains one or more putative transmembrane domains?	☐	
Contains coiled-coil segments?	☐	
Contains secretory signal peptides?	☐	
Sort Order		
First:	Virus name	ascending
Second:	genome position	ascending
Third:		

Submit Reset

Wildcard characters are automatically added at the beginning and end of the Gene name, PBR name, Description, and Notes fields. You can add additional wildcard characters using the percent sign (%) to match zero or more of any character or the underscore (_) to match any single character.

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Poxvirus Gene Search

Search Constraints	
Molecular weight greater than or equal to:	40000
Molecular weight less than or equal to:	60000
pI greater than or equal to:	5
pI less than or equal to:	6
Contains one or more putative transmembrane domains?	Yes
Sorted by	Virus name (ascending)
Sorted by	Genome position (ascending)

Sort Order		
First:	Virus name	ascending
Second:	genome position	ascending
Third:		

Change Sort Order

Number of genes matching search criteria: **6**

(Page 1 of 1)

Download in fastA format: Peptide Sequence | Save as file | Download

Select to Download?	Virus	Gene Name (Click for gene record)	PBR Name	Strand	Start	Finish	Protein Length	Molecular Weight	pI	tm#	sps	coil	Descr
☐	AMEV-EPB	AMV118	AMEV-EPB_131	-	100672	99512	386	44,338.00	5.33	1	N	N	PROT
☑	AMEV-EPB	AMV141	AMEV-EPB_154	+	127730	129088	452	52,579.20	5.54	1	N	N	AMV
☑	FWPV-FCV	FPV181	FWPV-FCV_181	-	213769	212660	369	42,081.40	5.55	1	N	N	PROT
☑	MSEV-TUC	MSV184	MSEV-TUC_184	+	164558	165805	415	48,315.60	5.86	2	N	N	ORF I
☐	MSEV-TUC	MSV214	MSEV-TUC_214	-	186301	185141	386	44,949.40	5.25	1	N	Y	ORF I
☐	MSEV-TUC	MSV216	MSEV-TUC_216	-	188543	187431	370	43,325.60	5.00	1	N	N	ORF I

PBR Database Sequence Record - Mozilla

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Data

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Poxvirus Gene Record for: ECTV-MOS:EVM161

Last updated by dbo On 5/30/2002 3:20:14 PM

Virus: Ectromelia virus Moscow strain
Genbank Locus Name: EVM161
Gene Name: EVM161
PBR Gene Number: ECTV-MOS_162
Molecule: Protein
Strand: Forward
Protein Length: 344
Nucleotide Length: 1035
Start: 182164
Finish: 183198
Molecular Weight: 38574.41
pI: 4.49
Description: (AF012825) serpin C7R [Ectromelia virus] >gi|6634111|emb|CAB64267.1| (AJ244012) Spi-2 protein [Ectromelia virus]

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Protein Analysis	
Amino Acids:	Composition
Number of putative Transmembrane Domains:	0 (Click for the Complete TransMem Record)
Prosite Motifs:	1. Serpins signature
Coiled-coil Segments:	None
Secretory Signal Peptides:	None

BLAST Results	
Database	BLAST Results
Genbank Protein	View Summary
Poxvirus Proteins (ortholog search)	View Summary

Notes

Protein Sequence

```
MDIFREIASS MKGENVFISS ASISSVLTIL YYGANGSTAE QLSKYVEKEE NNDTVNAQCI SFKSMNKVYG RYSAMFKDSF
LRKIGDNFQT VDFTDCRTID AINKCVDIFT EGKINPLLTE QLSPDTRLLA ISAVYFKAKW LMPFEKEFTS DYPFYVSPTE
MVDVSMMSMY GEPFNHASVK ESFGNFSIIE LPYVGDTSMM VILPDKIDGL ESIEQNLTDT NFKKWCNSLE ATFIDVHIPK
FKVTGSYNLV DTLVKLGLTD VFCSTGDYSN MCNSDVSVDA MIHKTYIDVN EEYTEAAAAT CALVSDCAST VTNEFCADHP
FIYVIRHVDG KILFVGRYCS PTTN
```

Nucleotide Sequence

```
ATGGATATCT TCAGGGAGAT CGCATCTTCT ATGAAAGGAG AGAACGTATT CATTTCTTCA GCGTCAATCT CGTCAGTATT
GACAATATTG TATTATGGAG CTAACGGATC CACTGCTGAA CAGCTATCAA AATATGTAGA AAAGGAGGAG AACAATGATA
CGGTTAATGC TCAGTGTATC TCATTCAAAT CCATGAATAA AGTATATGGG AGATATTCTG CCATGTTTAA AGATTCCTTT
TTGAGAAAAA TTGGCGATAA TTTCCAAACT GTTGACTTCA CTGATTGTCG CACTATAGAT GCTATCAATA AGTGTGTTGA
TATTTTTACT GAGGGGAAAA TCAATCCACT ATTGACTGAA CAATTGTCTC CAGATACCCG TCTCCTAGCA ATTAGTGCCG
TATACTTTAA AGCAAAATGG TTGATGCCAT TCGAAAAGGA ATTCACCAGT GATTATCCAT TTTACGTATC ACCAACGGAA
ATGGTAGACG TAAGTATGAT GTCTATGTAC GGCGAGCCAT TTAATCACGC ATCTGTAAAA GAATCATTCG GCAACTTTTC
AATCATAGAA CTACCATATG TTGGAGATAC TAGTATGATG GTAATTCTTC CAGACAAGAT TGATGGATTA GAATCCATAG
AACAAAATCT AACAGATACA AATTTTAAGA AATGGTGTAA CTCTCTGGAA GCTACGTTTA TCGATGTACA CATTCCCAAG
TTTAAGGTAA CAGGCTCGTA TAATCTGGTG GATACTCTAG TAAAGTTGGG ACTGACAGAT GTATTCTGTT CAACTGGAGA
TTATAGCAAT ATGTGTAATT CAGATGTGAG TGTCGACGCT ATGATCCACA AAACGTATAT AGATGTCAAT GAAGAGTATA
CAGAAGCAGC TGCAGCAACT TGTGCACTGG TGTCAGACTG TGCATCAACA GTTACAAATG AGTTCTGTGC AGATCATCCG
TTCATCTATG TGATTAGGCA TGTTGATGGC AAAATTCTTT TCGTTGGTAG ATATTGCTCT CCAACAACTA ATTAA
```

PBR BLAST Results - Mozilla Firefox

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Select to Download?	Hit	Query	Alignment	Expect Value	Query Length	Query Begin	Query End	Hit Length	Hit Begin	Hit End	% Ident	% Similarity	Description
☐	gi|4090821|gb|AAC99566.1|	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	100	100	serpin C7R [Ectromelia viru
☐	gi|6857178|gb|AAF30285.1|AF219903_1	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	100	100	serine protease inhibitor [Ec
☐	gi|3334643|emb|CAA07772.1|	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	99	99	serpin [Ectromelia virus]
☐	gi|19718169|gb|AAG37694.1|	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	95	97	CMP188R [Camelpox virus
☐	gi|18483101|gb|AAL73898.1|AF438165_188	ECTV-MOS_162	Retrieve	0	344	1	344	386	43	386	95	97	putative serpin I-2 protein;
☐	gi|3097033|emb|CAA75288.1|	ECTV-MOS_162	Retrieve	0	344	1	344	345	1	344	96	97	B12R [Cowpox virus]
☐	gi|335821|gb|AAA48346.1|	ECTV-MOS_162	Retrieve	0	344	1	344	345	1	344	94	96	SPI-2 >gi|134826|sp|P15059
☐	gi|1174422|sp|P42926|SPI2_RABPU	ECTV-MOS_162	Retrieve	0	344	1	344	345	1	344	94	96	Serine proteinase inhibitor 2
☐	gi|17529953|gb|AAL40631.1|AF380138_173	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	94	96	B12R [Monkeypox virus] >
☐	gi|885841|gb|AAA69453.1|	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	93	97	B12R [Variola virus] >gi|439
☐	gi|885779|gb|AAA69393.1|	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	92	96	D2R [Variola virus] >gi|583
☐	gi|123123|sp|P07385|SPI2_COWPX	ECTV-MOS_162	Retrieve	0	344	1	344	341	1	341	92	95	Serine proteinase inhibitor 2
☐	gi|10120524|pdb|1F0C|A	ECTV-MOS_162	Retrieve	4.27022e-158	344	1	308	305	1	305	91	94	Chain A, Structure Of The V
☐	gi|10120504|pdb|1C8O|A	ECTV-MOS_162	Retrieve	9.53514e-150	344	1	303	300	1	300	90	92	Chain A, 2.9 A Structure Of
☐	gi|68752|pir||WMVZB4	ECTV-MOS_162	Retrieve	4.32002e-118	344	128	344	222	5	221	95	97	antithrombin-III homolog 3 -
☐	gi|6969871|gb|AAF34083.1|	ECTV-MOS_162	Retrieve	2.37048e-116	344	128	344	222	5	221	94	96	TB14R [Vaccinia virus (stra
☐	gi|6634109|emb|CAB64266.1|	ECTV-MOS_162	Retrieve	2.39257e-084	344	1	341	357	1	356	46	64	Spi-1 protein [Ectromelia vi
☐	gi|4090828|gb|AAC99573.1|	ECTV-MOS_162	Retrieve	2.39257e-084	344	1	341	370	14	369	46	64	serpin C14R [Ectromelia vir
☐	gi|18483115|gb|AAL73912.1|AF438165_202	ECTV-MOS_162	Retrieve	1.71463e-082	344	1	341	372	16	371	46	63	putative serpin I-1 protein;
☐	gi|134824|sp|P15058|SPI1_VACCV	ECTV-MOS_162	Retrieve	2.23938e-082	344	1	341	353	1	352	46	63	Serine proteinase inhibitor 1
☐	gi|20153194|gb|AAM13655.1|AF482758_206	ECTV-MOS_162	Retrieve	2.92472e-082	344	1	341	372	18	371	46	64	V207 [Cowpox virus] >gi|47
☐	gi|1174419|sp|P42927|SPI1_COWPX	ECTV-MOS_162	Retrieve	2.92472e-082	344	1	341	355	1	354	46	64	Serine proteinase inhibitor 1
☐	gi|5830756|emb|CAB54795.1|	ECTV-MOS_162	Retrieve	3.8198e-082	344	1	341	372	16	371	47	63	D14R protein [Variola mino
☐	gi|6969642|gb|AAF33854.1|	ECTV-MOS_162	Retrieve	3.8198e-082	344	1	341	353	1	352	46	63	TC19L [Vaccinia virus (strai

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Select to Download?	Hit	Query	Alignment	Expect Value	Query Length	Query Begin	Query End	Hit Length	Hit Begin	Hit End	% Ident	% Similarity	Description
☐	ECTV-MOS_162	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	100	100	ECTV-MOS_162 EVI
☐	ECTV-NAV_169	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	100	100	ECTV-NAV_169 EV-
☐	CMLV-CMS_240	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	95	97	CMLV-CMS_240 188
☐	CMLV-M96_191	ECTV-MOS_162	Retrieve	0	344	1	344	386	43	386	95	97	CMLV-M96_191 CM
☐	CPXV-GRI_02_018	ECTV-MOS_162	Retrieve	0	344	1	344	345	1	344	96	97	CPXV-GRI_02_018 E
☐	CPXV-GRI_193	ECTV-MOS_162	Retrieve	0	344	1	344	345	1	344	96	97	CPXV-GRI_193 B12F
☐	VACV-WR_195	ECTV-MOS_162	Retrieve	0	344	1	344	345	1	344	94	96	VACV-WR_195 VAC
☐	RPXV-UTR_175	ECTV-MOS_162	Retrieve	0	344	1	344	345	1	344	94	96	RPXV-UTR_175 RPX
☐	MPXV-ZRE_173	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	94	96	MPXV-ZRE_173 B12
☐	VARV-BSH_176	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	93	97	VARV-BSH_176 B12F
☐	VARV-SML_02_008	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	93	97	VARV-SML_02_008
☐	VARV-IND_181	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	93	97	VARV-IND_181 B13I
☐	VARV-GAR_189	ECTV-MOS_162	Retrieve	0	344	1	344	344	1	344	92	96	VARV-GAR_189 D2F
☐	CPXV-BR_211	ECTV-MOS_162	Retrieve	0	344	1	344	341	1	341	92	95	CPXV-BR_211 V207
☐	VACV-COP_242	ECTV-MOS_162	Retrieve	2.43865e-120	344	128	344	222	5	221	95	97	VACV-COP_242 VV-
☐	VACV-TAN_231	ECTV-MOS_162	Retrieve	1.33813e-118	344	128	344	222	5	221	94	96	VACV-TAN_231 TB1
☐	VACV-TTup_242	ECTV-MOS_162	Retrieve	1.33813e-118	344	128	344	222	5	221	94	96	VACV-TTup_242 an-
☐	ECTV-NAV_176	ECTV-MOS_162	Retrieve	1.3506e-086	344	1	341	370	14	369	46	64	ECTV-NAV_176 EV-
☐	ECTV-MOS_169	ECTV-MOS_162	Retrieve	1.3506e-086	344	1	341	370	14	369	46	64	ECTV-MOS_169 EVI
☐	CMLV-CMS_257	ECTV-MOS_162	Retrieve	9.67906e-085	344	1	341	372	16	371	46	63	CMLV-CMS_257 200
☐	CMLV-M96_205	ECTV-MOS_162	Retrieve	9.67906e-085	344	1	341	372	16	371	46	63	CMLV-M96_205 CM
☐	VACV-WR_205	ECTV-MOS_162	Retrieve	1.26412e-084	344	1	341	353	1	352	46	63	VACV-WR_205 VAC
☐	CPXV-BR_221	ECTV-MOS_162	Retrieve	1.651e-084	344	1	341	372	18	371	46	64	CPXV-BR_221 V217
☐	VACV-TAN_004	ECTV-MOS_162	Retrieve	2.15627e-084	344	1	341	353	1	352	46	63	VACV-TAN_004 TC1

BLAST Viewer

Exit About

PROGRAM: blastp
DATABASE: poxpep
QUERY SEQUENCE: ECTV-MOS_162 EVM161

Sort By
- Bit Score
- Query From

Sort

e-Value Filter

= 0 | e-100 to 0 | e-10 to e-100 | .01 to e-10 | > .01 | Select All

Hit Selection

Hide Checked Hits

Show All Hits

Horizontal Zoom

Level 1 | Level 2 | Level 3 | Level 4

Number of Amino Acids

1 — 50 — 100 — 150 — 200 — 250 — 300 — 344

VARV-SML_02_008	VARV-SML_02_008 B12R
VARV-BSH_176	VARV-BSH_176 B12R
VARV-GAR_189	VARV-GAR_189 D2R
CPXV-BR_211	CPXV-BR_211 V207
VACV-COP_242	VACV-COP_242 VV-Cop-B14R
VACV-TAN_231	VACV-TAN_231 TB14R
VACV-TTup_242	VACV-TTup_242 an-TB14R
ECTV-MOS_169	ECTV-MOS_169 EVM168
ECTV-NAV_176	ECTV-NAV_176 EV-N-197

```
          Query: ECTV-MOS_162
Query Definition: EVM161
    Query Length: 344
             Hit: VACV-COP_242
  Hit Definition: VACV-COP_242 VV-Cop-B14R
     Hit Length: 222

   Hit E value: 2.43865E-120;  Score (bits): 425
    % Identity: 95;  % Similar: 97
Alignment Gaps:
    Query from: 128 to 344;  Hit from: 5 to 221

Query:  128  LLAISAVYFKAKWLMPFEKEFTSDYPFYVSPTEMVDVSMMSMYGEPFNHASVKESFGNFS 187
             LLAISAVYFKAKWL PFEKEFTSDYPFYVSPTEMVDVSMMSMYGE FNHASVKESFGNFS
  Hit:    5  LLAISAVYFKAKWLTPFEKEFTSDYPFYVSPTEMVDVSMMSMYGELFNHASVKESFGNFS  64

Query:  188  IIELPYVGDTSMMVILPDKIDGLESIEQNLTDTNFKKWCNSLEATFIDVHIPKFKVTGSY 247
```

Java Applet Window

PBR XS BLAST Search - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

http://poxvirus.org/blast_xml.asp

Similarity Searching

Similarity Search | Ortholog Comparison | Genome Analysis

Retrieve Previous *Poxvirus* Blast Searches

Poxvirus
XS-BLAST Search (XML-SQL)

Submit Reset

Choose BLAST Parameters		
Query Sequence Type	BLAST Program	Search Database
Protein	blastp	Genomic Protein

Expectation value: .01

Search Name: Human Serpin

Your Email Address: elliotl@uab.edu

Input your query sequence in FASTA format:

```
>gi|51493263|ref|XP_372532.2| PREDICTED: serine (or cysteine)
proteinase inhibitor, clade A (alpha-1 antiproteinase,
antitrypsin), member 2 [Homo sapiens]
MTPGSTKHLHVPLLIPHSPPPRVAHPARAGCAHPKAALLGAPELPDRAVAQFCGICSNTRE
LMAQEGHCKDSSAMGEEAHHPLTPATPPFPPLSPDWGHMQPDFFVPVAVPAVFRGPPQLQC
PCAQKSSSGLVVEPGLSRTLLEMVKLTSMRGLCCLVPSSLVEDPQEDAAQKTDTSHHDQGD
```

PBR BLAST Results - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

http://poxvirus.org/blastResults.asp

Select to Download?	Hit	Query	Alignment	Expect Value	Query Length	Query Begin	Query End	Hit Length	Hit Begin	Hit End	% Ident	% Similarity	Description
☐	LSDV-1959_152	gi|51493263|ref|XP_372532.2|	Retrieve	2.33382e-014	466	220	456	337	2	214	24	47	22595844 serpin-like protein [lump
☐	SPPV-A_122	gi|51493263|ref|XP_372532.2|	Retrieve	3.9809e-014	466	220	456	337	2	214	25	46	122 SPPV-A_122 122
☐	SPPV-TU_143	gi|51493263|ref|XP_372532.2|	Retrieve	3.9809e-014	466	220	456	337	2	214	25	46	21492599 Serpin [Sheeppox virus]
☐	LSDV-NEE_215	gi|51493263|ref|XP_372532.2|	Retrieve	3.9809e-014	466	220	456	337	2	214	24	46	LSDV149 LSDV149 serpin-like pr
☐	LSDV-WARM_151	gi|51493263|ref|XP_372532.2|	Retrieve	3.9809e-014	466	220	456	337	2	214	24	46	22595684 serpin-like protein [lump
☐	SPPV-NISKHI_123	gi|51493263|ref|XP_372532.2|	Retrieve	3.9809e-014	466	220	456	337	2	214	25	46	123 SPPV-NISKHI_123 123
☐	GTPV-Pellor_121	gi|51493263|ref|XP_372532.2|	Retrieve	2.8529e-012	466	220	456	337	2	214	24	45	121 GTPV-Pellor_121 121
☐	GTPV-G20LKV_123	gi|51493263|ref|XP_372532.2|	Retrieve	2.8529e-012	466	220	456	337	2	214	24	45	123 GTPV-G20LKV_123 123
☐	ECTV-NAV_176	gi|51493263|ref|XP_372532.2|	Retrieve	3.726e-012	466	220	452	370	15	244	23	47	EV-N-197 serpin C14R [Ectromeli
☐	ECTV-MOS_169	gi|51493263|ref|XP_372532.2|	Retrieve	3.726e-012	466	220	452	370	15	244	23	47	EVM168 (AF012825) serpin C14R
☐	YMTV-YLD_010	gi|51493263|ref|XP_372532.2|	Retrieve	6.3556e-012	466	215	412	383	26	208	24	46	10L putative serine protease inhibit
☐	CPXV-GRI_201	gi|51493263|ref|XP_372532.2|	Retrieve	2.41513e-011	466	218	452	375	17	249	22	46	B20R B20R protein [Cowpox virus
☐	CMLV-CMS_257	gi|51493263|ref|XP_372532.2|	Retrieve	3.15425e-011	466	220	452	372	17	246	22	46	200R serpin
☐	CMLV-M96_205	gi|51493263|ref|XP_372532.2|	Retrieve	3.15425e-011	466	220	452	372	17	246	22	46	CMLV205 (NC_003391) putative
☐	MPXV-ZRE_180	gi|51493263|ref|XP_372532.2|	Retrieve	5.38034e-011	466	220	452	357	2	231	21	46	B19R SERINE PROTEINASE INH
☐	RPXV-UTR_005	gi|51493263|ref|XP_372532.2|	Retrieve	5.38034e-011	466	220	452	357	2	231	22	46	RPXV-UTR_005 Serine proteinase
☐	VACV-COP_015	gi|51493263|ref|XP_372532.2|	Retrieve	7.02694e-011	466	220	452	353	2	227	22	45	VV-Cop-C12L serine protease [Va
☐	VACV-TAN_004	gi|51493263|ref|XP_372532.2|	Retrieve	7.02694e-011	466	220	452	353	2	227	22	45	an-TC19L Serpin (SPI)
☐	VACV-WR_205	gi|51493263|ref|XP_372532.2|	Retrieve	9.17747e-011	466	220	452	353	2	227	22	45	VACWR205 serine protease inhibit
☐	VARV-IND_193	gi|51493263|ref|XP_372532.2|	Retrieve	2.04453e-010	466	220	452	372	17	246	22	46	B25R SERINE PROTEINASE INH
☐	VARV-GAR_201	gi|51493263|ref|XP_372532.2|	Retrieve	2.04453e-010	466	220	452	372	17	246	22	46	D14R SERINE PROTEINASE INH
☐	VARV-BSH_185	gi|51493263|ref|XP_372532.2|	Retrieve	2.04453e-010	466	220	452	372	17	246	22	46	B21R SERINE PROTEINASE INH
☐	CPXV-BR_221	gi|51493263|ref|XP_372532.2|	Retrieve	5.94866e-010	466	220	452	372	19	246	22	45	V217 CPXV-BR_221 V217

BLAST Viewer

Exit About

```
        PROGRAM:  blastp
       DATABASE:  poxpep
 QUERY SEQUENCE:  gi|51493263|ref|XP_372532.2| PREDICTED: serine (or cysteine) proteinase inhibito
```

Sort By

- (•) Bit Score
- ( ) Query From

Sort

e-Value Filter

[x] = 0 | [x] e-100 to 0 | [x] e-10 to e-100 | [x] .01 to e-10 | [x] > .01 | Select All

Hit Selection

Hide Checked Hits

Show All Hits

Horizontal Zoom

(•) Level 1 ( ) Level 2 ( ) Level 3 ( ) Level 4

Number of Amino Acids

1 — 50 100 150 200 250 300 350 400 450 — 466

[ ]	VACV-COP_015	VV-Cop-C12L serine protease [Vaccinia virus] -gi|1
[ ]	VACV-WR_205	VACWR205 serine protease inhibitor-like SPI-1; hos
[ ]	VARV-GAR_201	D14R SERINE PROTEINASE INHIBITOR 1 ; D14R protein
[ ]	VARV-BSH_185	B21R SERINE PROTEINASE INHIBITOR 1 ; B25R [Variol

```
   Hit E value: 9.17747E-11;  Score (bits): 62
    % Identity: 22;  % Similar: 45
Alignment Gaps: 33
    Query from: 220 to 452;  Hit from: 2 to 227

Query:  220  DLYKELADLSQTSNVLVTPTSVAMAFAML---SLGTKADTRTEILEGLNVNLTE---TPE 273
             D++KEL       NVL++P S+    ++L   + G+ A+  ++ +E +N N  +     +
  Hit:    2  DIFKELILKHTDENVLISPVSILSTLSILNHGAAGSTAEQLSKYIENMNENTPDDNNDMD  61

Query:  274  AKIHECFQQVLQALSRPDTRLQLTTGSSLFVNKSMKLVDTFLEDTKKLYHSEASSINFRD 333
               I  C                L T + ++ + S++   +FL+  K     +  ++NF +
  Hit:   62  VDIPYC--------------ATLATANKIYGSDSIEFHASFLQKIK----DDFQTVNFNN 103
```

Java Applet Window

BLAST Viewer

Exit About

PROGRAM: blastx
DATABASE: nr
QUERY SEQUENCE: sars

Sort By

- Bit Score
- Query From

Sort

e-Value Filter

= 0 | e-100 to 0 | e-10 to e-100 | .01 to e-10 | > .01 | Select All

Hit Selection

Hide Checked Hits

Show All Hits

Horizontal Zoom

Level 1 | Level 2 | Level 3 | Level 4

Number of Nucleotides

1 — 4000 — 8000 — 12000 — 16000 — 20000 — 24000 — 28000 — 29715

gi|26007546|ref	ORF1ab polyprotein [Murine hepatitis virus]
gi|26008095|ref	transmembrane domain 2 [Bovine coronavirus]
gi|22219303|pdb	Chain A, Structure Of Coronavirus Main Proteinase
gi|25121564|ref	coronavirus nsp3 (HD2) [Murine hepatitis virus]
gi|26008087|ref	coronavirus nsp5 [Bovine coronavirus]
gi|25121551|ref	coronavirus nsp6 [Avian infectious bronchitis viru
gi|25121568|ref	coronavirus nsp7 (GFL); growth-factor-like protein
gi|25121569|ref	coronavirus nsp9 (RdRp); RNA-dependent RNA polyme
gi|6625761|gb|A	RNA-directed RNA polymerase [murine hepatitis viru
gi|26008091|ref	coronavirus nsp10 (MB, NTPase/HEL); metal-binding
gi|25121571|ref	coronavirus nsp11 [Murine hepatitis virus]
gi|26008094|ref	coronavirus nsp13 [Bovine coronavirus]
gi|5565844|gb|A	spike glycoprotein [murine hepatitis virus]
gi|6706916|gb|A	spike glycoprotein [bovine coronavirus]
gi|6179905|gb|A	membrane protein [murine hepatitis virus]
gi|11640712|gb|	nucleocapsid protein [Equine coronavirus]

BLAST Viewer Usage:
CLICK on HIT NAME to view sequence record.
CLICK on HIT GRAPHIC to view alignment(s).

Java Applet Window

PBR Orthologs - Mozilla

PBR

data | analysis | reagents | literature | discussion | announcements | links | home

Orthologs

Similarity Search | Ortholog Comparison | Genome Analysis

- Poxvirus Ortholog Clusters (POCs): Analysis and alignments of poxvirus gene families
- Pairwise Ortholog Comparisons: View lists of genes shared or missing between two genomes
- Multi-genome Ortholog Comparisons: View lists of genes shared between two or more genomes
- Graphical Ortholog Synteny Comparisons: Graphical gene comparison

teams & people | address book | acknowledgements | feedback

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PBR Shared Orthologs Syntenic Plot - Mozilla

PBR

data | analysis | reagents | literature | discussion | announcements | links | home

Orthologs

Similarity Search | Ortholog Comparison | Genome Analysis

graphically display shared gene orthologs

Select the appropriate parameters and press the **Submit** button
to get a scatter plot of orthologs shared between any pair of virus genomes

Submit Reset

Parameters	Options
Query (X-Axis)	Vaccinia virus strain WR
Hit (Y-Axis)	Variola major virus strain Bangladesh
Comparison	Sensitive

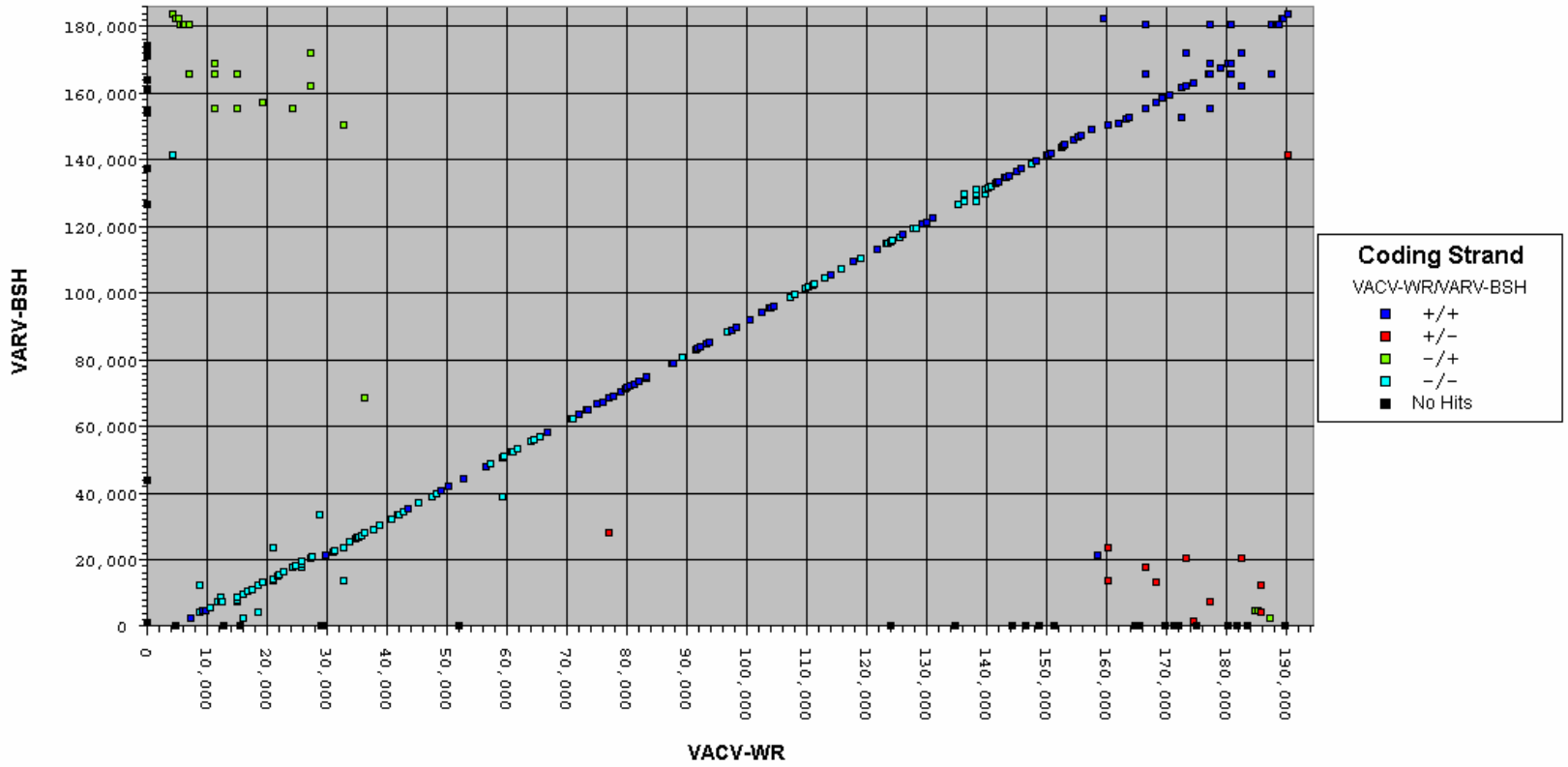
PBR Gene Synteny - Mozilla

Zoom In

Save Figure

- Right-click to save GIF.
- Click to save PostScript.

Gene Synteny of
Vaccinia virus strain WR
vs.
Variola major virus strain Bangladesh

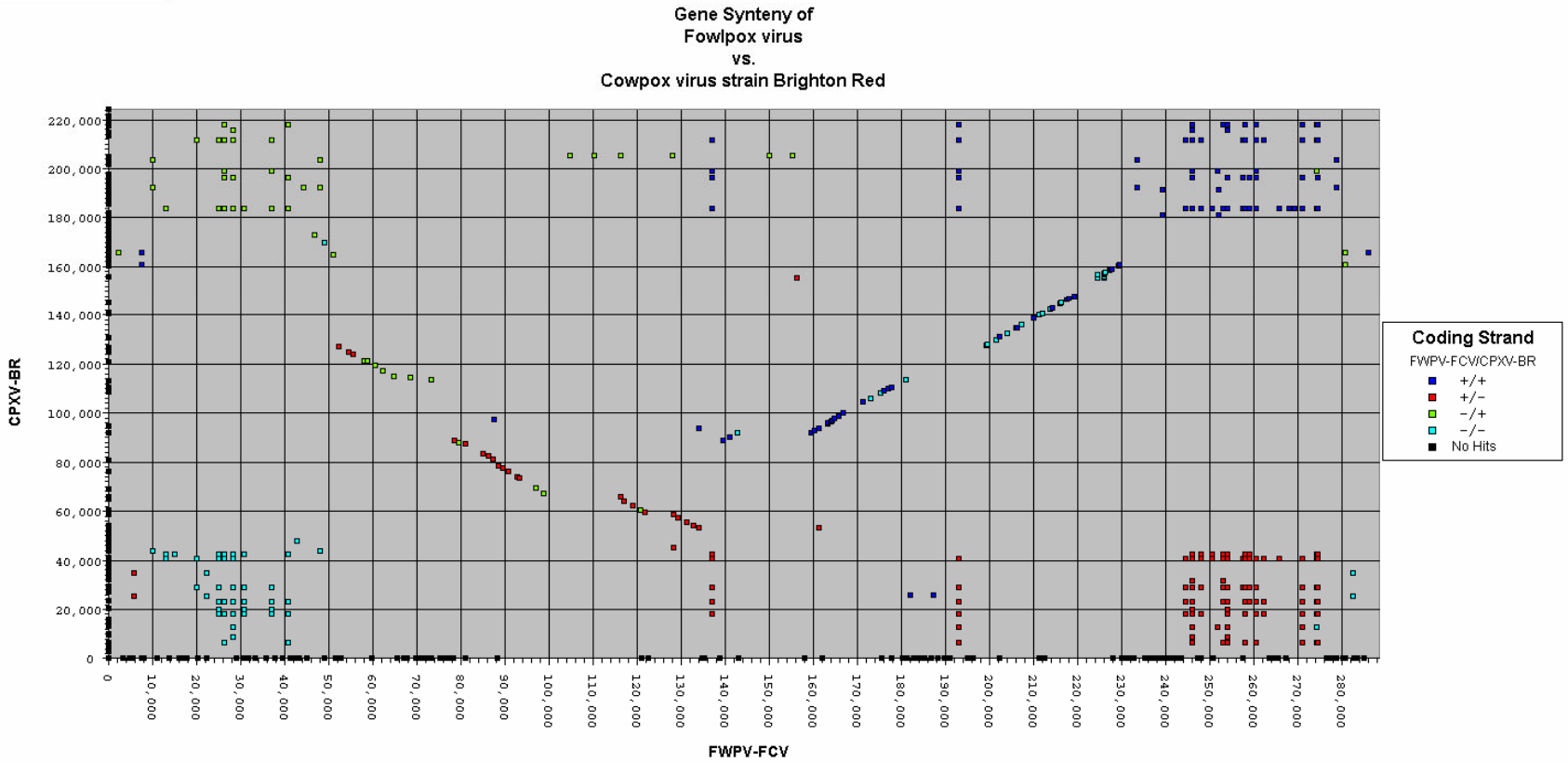


Mouse over a point to view the genes it represents.
Click on a point to view the BLAST comparison results.

PBR Gene Synteny - Mozilla

Save Figure

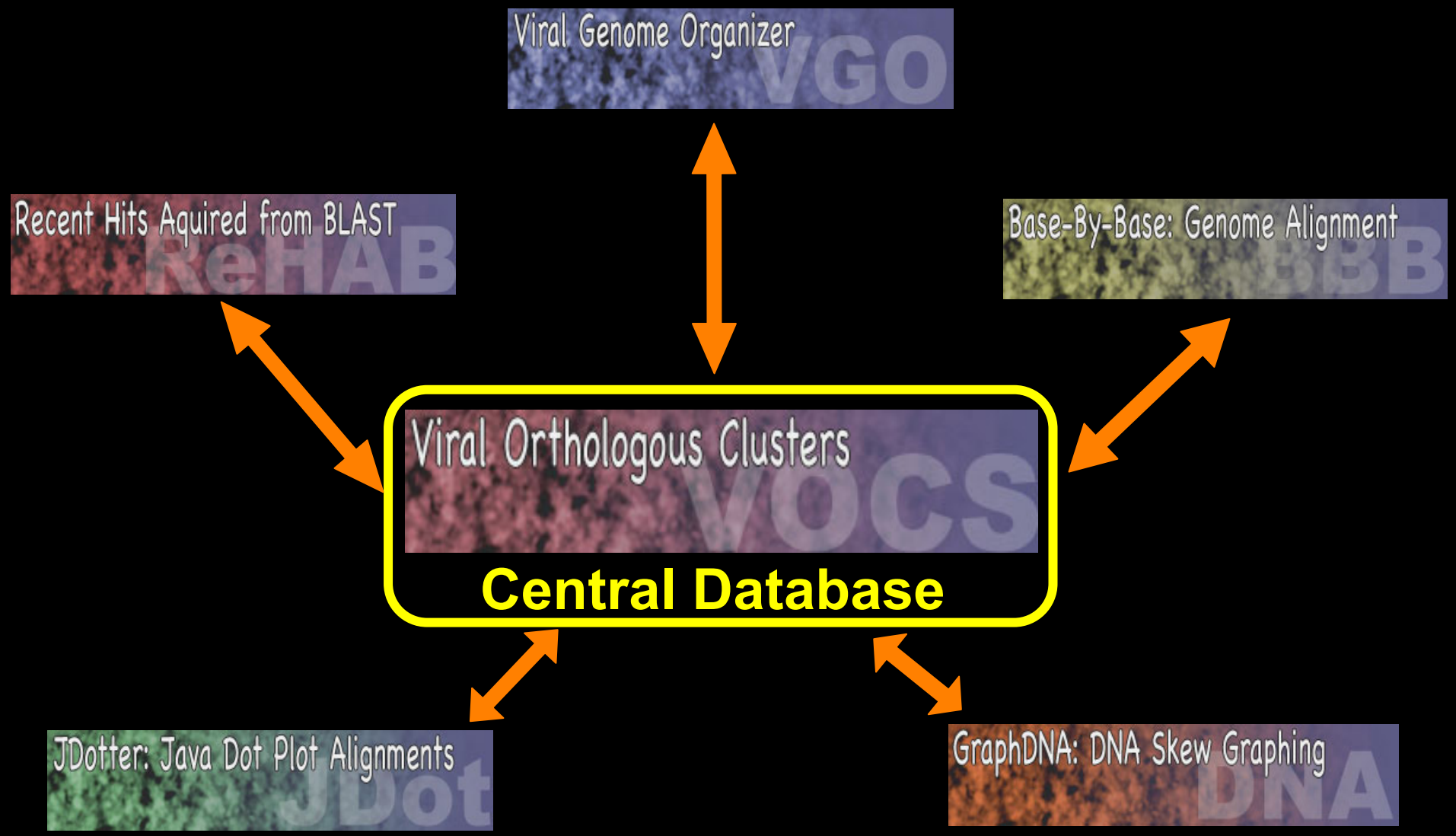
- Right-click to save GIF.
- Click to save PostScript.



New Tools for Virus Bioinformatics

Tool Development Goals

- Able to work with:
  - Genes/proteins
  - Families of orthologs
  - Promoter sequences
  - Complete genomes
- Corrected annotations/sequences
- EASY TO USE!!


Viral Genome Organizer
VGO
Recent Hits Aquired from BLAST
ReHAB
Base-By-Base: Genome Alignment
BBB
Viral Orthologous Clusters
VOCS
Central Database
JDotter: Java Dot Plot Alignments
JDot
GraphDNA: DNA Skew Graphing
DNA

Pox Virus Orthologous Clusters File Select Column Clipboard Sequence

Pox Virus Orthologous Clusters - POCs [Pocsdb@athena.bioc.uvic.ca:4445]

Sequence Query | Gene Family Analyzer

Query Specification

Protein/DNA Selector

☑ Gene Name / ORF	matches	B[23]R
☑ Gene DNA Sequence	matches	AAGCTT
☑ Upstream DNA Sequence	matches	TA[TA]ATG
☑ Protein Sequence	ends with	[RK]DEL

Molecular weight / Isoelectric point / AA Count

☑ MW	is between	30000	and	35000
☑ pI	is between	7.0	and	8.0
☑ AA Count	is between	400	and	450

Virus Selector

☑ Select these viruses

Amsacta moorei entomopoxvirus
Camelpox virus (M-96)
Fowlpox virus (virulent FPV; Fowlpox Challenge Virus)
Lumpy skin disease virus (Neethling 2490)

☑ Do NOT select these viruses

Amsacta moorei entomopoxvirus
Camelpox virus (M-96)
Fowlpox virus (virulent FPV; Fowlpox Challenge Virus)
Lumpy skin disease virus (Neethling 2490)

Gene view | Gene count | 5 | Family view | Family count

Viral Orthologous Clusters V2.0 (VOCS) [16x11] DB:lgy_msl

File Select Column Clipboard Edit Sequence Blast Alignment Analysis JDotter LAJ

Genes in family "Complement binding (secreted)"

Gene name	Fragment	No. of amino acids	pI	ORF start	ORF stop	ORF strandedness	Molec. weight
VARV-Bsh-D15L	no	263	8.56	12297	13088	bottom	28816
VARV-Gar-B18L	no	263	8.56	12452	13243	bottom	28842
VARV-Ind-D12L	no	263	8.47	11600	12391	bottom	28789
VACV-Cop-C3L	no	263	7.77	21760	22551	bottom	28629
VACV-Tan-TC3L	no	263	7.77	18219	19010	bottom	28629
MPXV-Zre-D14L	no	216	6.78	19060	19710	bottom	23423
CMLV-M96-023	no	265	7.78	21474	22271	bottom	28922
ECTV-Mos-017	no	262	8.22	26776	27564	bottom	28640
RPXV-Utr-017	no	263	7.34	23317	24108	bottom	28614
CPXV-BR-034	no	263	7.78	35125	35916	bottom	28555
CMLV-CMS-23L	no	265	7.78	19786	20583	bottom	28922
ECTV-Nav-28	no	262	8.03	24659	25447	bottom	28689
VACV-WR-025	no	263	7.77	18677	19468	bottom	28629
CPXV-GRI-C17L	no	259	7.78	34788	35567	bottom	28193
VACV-DUK-031	no	263	7.32	23912	24703	bottom	28680
VACV-DUK-LGY-038	no	263	7.32	23912	24703	bottom	28680

Display Annotations Sequences Coding Regions

Differences in gene content

Viral Orthologous Clusters V2.0 (VOCS) (lgy_msl@athena.bioc.uvic.ca:4450)

File Admin Select View Draw Tools Help DB Info

Sequence Query | Gene Family Analyzer

Family Query

☑ Select Gene Families that...

Criteria List

Contain MPXV-Zre AND
Contain VARV-Bsh AND
Contain VARV-Gar AND
Contain VARV-Ind AND
Do NOT Contain MPXV-SL

○ Contain
◉ Do NOT Contain

VACV-Acambis
MPXV-WRAIR-LGY
VACV-DUK
VACV-DUK-LGY
MPXV-SL

○ OR
◉ AND

Add Criteria | Add operator | Delete Criteria

Virus Selector

☐ Select these viruses

14-16
16-18
18-1
Amsacta moorei entomopoxvirus (Moyer)
Bovine papular stomatitis virus (BV-AR02)
Camelpox virus (Kazakhstan M-96)

☐ Do NOT select these viruses

14-16
16-18
18-1
Amsacta moorei entomopoxvirus (Moyer)
Bovine papular stomatitis virus (BV-AR02)
Camelpox virus (Kazakhstan M-96)

Gene view | Gene count | 7 | Family view | Family count

Viral Orthologous Clusters V2.0 (VOCS) [215x12] DB:lgy_msl

File Select Column Clipboard Edit Sequence Blast Alignment Analysis JDotter LAJ

Gene Results Table

Gene name [a]	Family name	Fragment	No. of amino acids	pI	ORF start	ORF stop	ORF strandedness
MPXV-WRAIR-LGY-29.5-F	INF resistance (PKR inhibitor)	yes	43	4.29	27566	27697	bottom
MPXV-Zre-A26L	CPV-ATI protein (Bang-A27L)	yes	75	6.60	135473	135700	bottom
MPXV-Zre-A27L	CPV-ATI protein (Bang-A27L)	yes	696	4.99	135815	137905	bottom
MPXV-Zre-B15L	Unknown (Cop-B17L)	yes	78	6.81	173429	173665	bottom
MPXV-Zre-B18R-f	kelch-like (EV-M-167)	yes	70	7.88	177857	178069	top
MPXV-Zre-B1R-f	Kelch-like (Cop-A55R)	yes	70	6.03	158318	158530	top
MPXV-Zre-C3L	INF resistance (PKR inhibitor)	yes	43	4.29	27672	27803	bottom
MPXV-Zre-D14L	Complement binding (secreted)	no	216	6.78	19060	19710	bottom
MPXV-Zre-D15L-f	Kelch-like (Cop-C2L)	yes	105	5.52	19834	20151	bottom
MPXV-Zre-D16L-f	Kelch-like (Cop-C2L)	yes	77	8.82	20205	20438	bottom
MPXV-Zre-D17L-f	Kelch-like (Cop-C2L)	yes	98	9.33	20440	20736	bottom
MPXV-Zre-D18L-f	Kelch-like (Cop-C2L)	yes	107	6.82	20819	21142	bottom
MYXV-Lau-m140R	Kelch-like (Cop-A55R)	no	553	7.76	135375	137036	top

Display | Family | Annotations | Sequences | Coding Regions

Viral Genome Organizer

File Tools View Help

Working List (select one or more organisms for display):

Ectromelia virus (Moscow) Start: 90940 End: 91161 Length: 222 Note: Mouse Selection

Cowpox virus (Brighton Red) Start: 98907 End: 99098 Length: 192 Note: Mouse Selection

Sequence Map Display

File Tools Analysis View Help

Cowpox virus (Brighton Red) Go To: CPV-B-001 Viewing Options...

Top Strand Genes

CPV-B-100 CPV-B-102 CPV-B-103 CPV-B-104 CPV-B-105 CPV-B-106 CPV-B-107 CPV-B-109

4500 95000 95500 96000 96500 97000 97500 98000 98500 99000 99500 100000 100500

Bottom Strand Genes

CPV-B-101 CPV-B-108

Ectromelia virus (Moscow) Go To: EV-M-001 Viewing Options...

Top Strand Genes

EV-M-073 EV-M-075 EV-M-076 EV-M-077 EV-M-078 EV-M-079 EV-M-080 EV-M-082

86500 87000 87500 88000 88500 89000 89500 90000 90500 91000 91500 92000 92500

Bottom Strand Genes

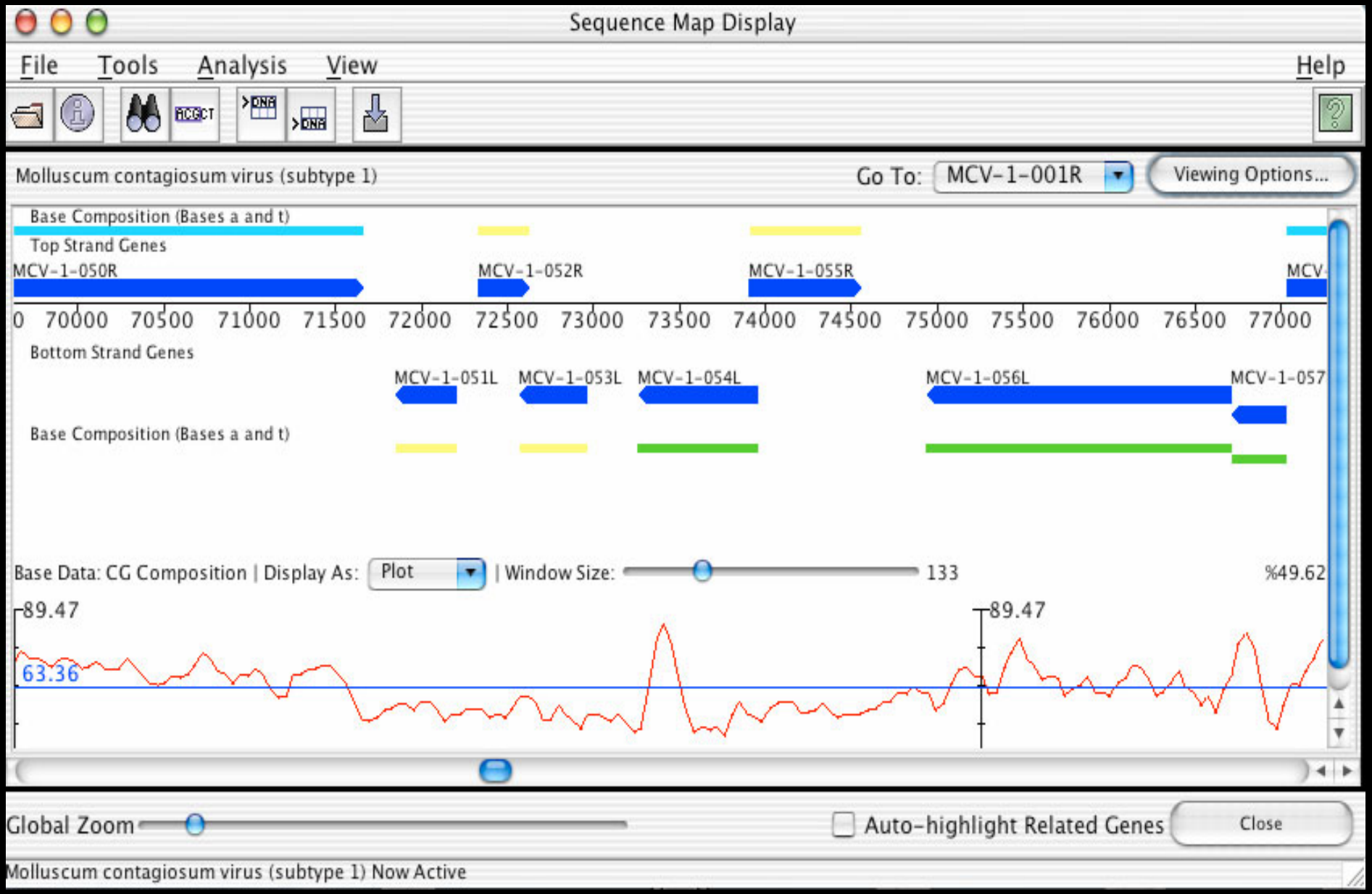
EV-M-074 EV-M-081

Global Zoom

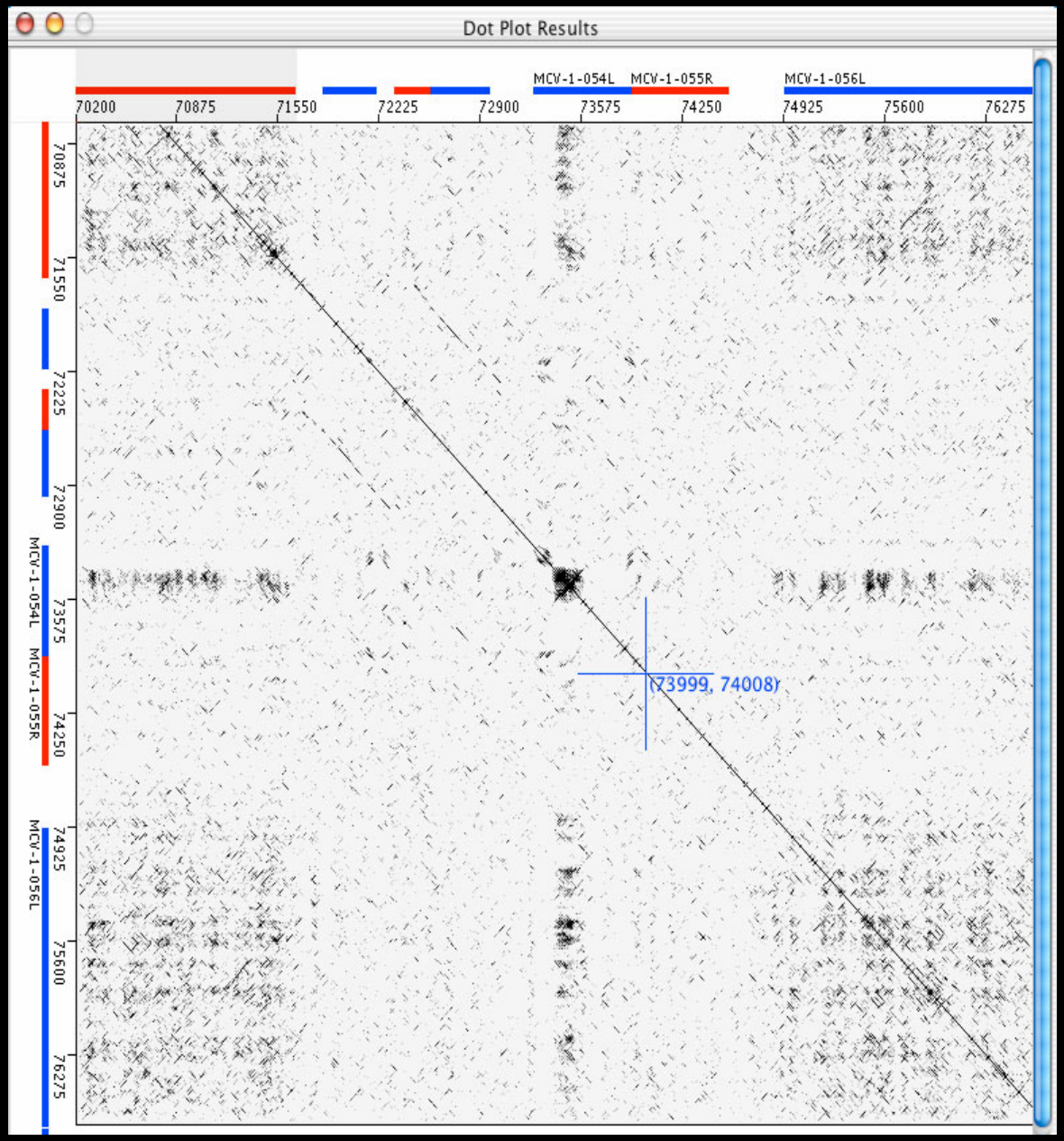
Auto-highlight Related Genes

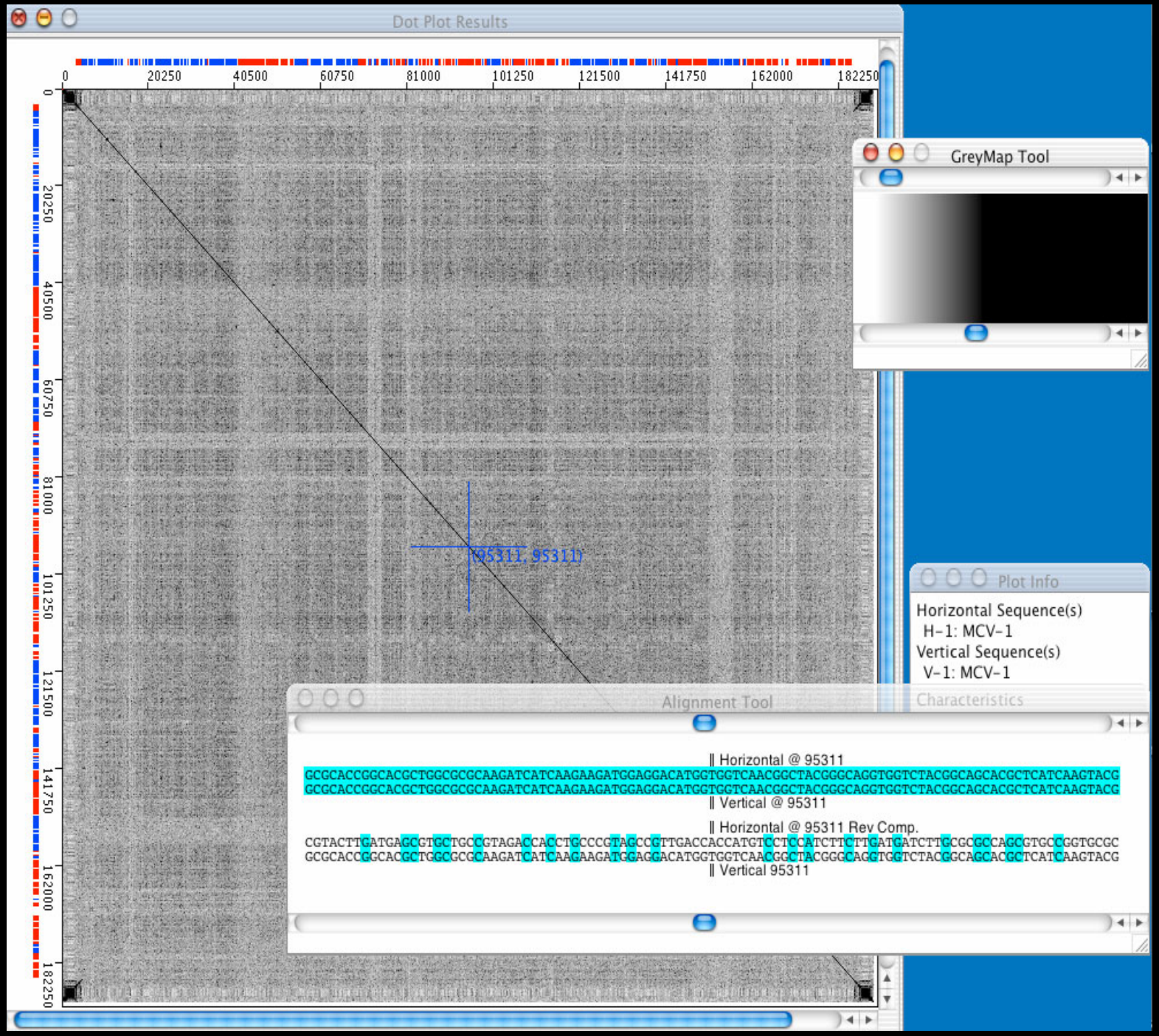
Close

Ectromelia virus (Moscow) Now Active


Sequence Map Display
File
Tools
Analysis
View
Help
Molluscum contagiosum virus (subtype 1)
Go To:
MCV-1-001R
Viewing Options...
Base Composition (Bases a and t)
Top Strand Genes
MCV-1-050R
MCV-1-052R
MCV-1-055R
MCV-
0
70000
70500
71000
71500
72000
72500
73000
73500
74000
74500
75000
75500
76000
76500
77000
Bottom Strand Genes
MCV-1-051L
MCV-1-053L
MCV-1-054L
MCV-1-056L
MCV-1-057
Base Composition (Bases a and t)
Base Data: CG Composition | Display As:
Plot
| Window Size:
133
%49.62
89.47
63.36
89.47
Global Zoom
Auto-highlight Related Genes
Close
Molluscum contagiosum virus (subtype 1) Now Active

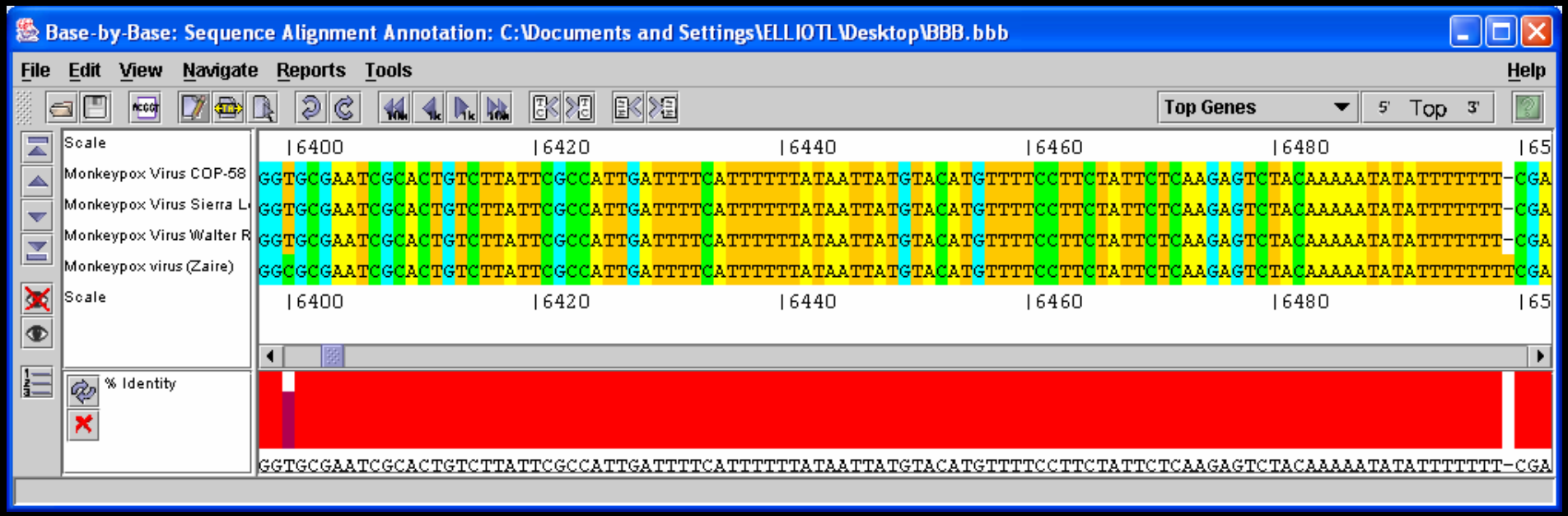
JDotter


Dot Plot Results
MCV-1-054L
MCV-1-055R
MCV-1-056L
70200
70875
71550
72225
72900
73575
74250
74925
75600
76275
(73999, 74008)


Dot Plot Results
0
20250
40500
60750
81000
101250
121500
141750
162000
182250
(95311, 95311)
GreyMap Tool
Plot Info
Horizontal Sequence(s)
H-1: MCV-1
Vertical Sequence(s)
V-1: MCV-1
Characteristics
Alignment Tool
|| Horizontal @ 95311
GCGCACCGGCACGCTGGCGCGCAAGATCATCAAGAAGATGGAGGACATGGTGGTCAACGGCTACGGGCAGGTGGTCTACGGCAGCACGCTCATCAAGTACG
GCGCACCGGCACGCTGGCGCGCAAGATCATCAAGAAGATGGAGGACATGGTGGTCAACGGCTACGGGCAGGTGGTCTACGGCAGCACGCTCATCAAGTACG
|| Vertical @ 95311
|| Horizontal @ 95311 Rev Comp.
CGTACTTGATGAGCGTGCTGCCGTAGACCACCTGCCCGTAGCCGTTGACCACCATGTCCTCCATCTTCTTGATGATCTTGCGCGCCAGCGTGCCGGTGCGC
GCGCACCGGCACGCTGGCGCGCAAGATCATCAAGAAGATGGAGGACATGGTGGTCAACGGCTACGGGCAGGTGGTCTACGGCAGCACGCTCATCAAGTACG
|| Vertical 95311

Base-By Base

Genomic Sequence Alignment and Editing



Base-by-Base: Sequence Alignment Annotation: C:\Documents and Settings\ELLIOTL\Desktop\BBB.bbb

File Edit View Navigate Reports Tools Help

Top Genes 5' Top 3'

Scale
Frame 1
Frame 2
Frame 3
Monkeypox Virus COP-58
Monkeypox Virus Sierra L
Frame 1
Frame 2
Frame 3
Monkeypox Virus Walter R
Frame 1
Frame 2
Frame 3
Monkeypox virus (Zaire)
Frame 1
Frame 2
Frame 3
Scale

|6400 |6420 |6440 |6460 |6480 |65

C E S H C L I R H * F S F F I I M Y M F S F Y S Q E S T K I Y F F - R
G A N R T V L F A I D F H F L * L C T C F P S I L K S L Q K Y I F F D
V R I A L S Y S P L I F I F Y N Y V H V F L L F S R V Y K N I F F S I

GGTGCGAATCGCACTGTCTTATTCGCCATTGATTTTCATTTTTTATAATTATGTACATGTTTTCCTTCTATTCTCAAGAGTCTACAAAAATATATTTTTTT-CGA
GGTGCGAATCGCACTGTCTTATTCGCCATTGATTTTCATTTTTTATAATTATGTACATGTTTTCCTTCTATTCTCAAGAGTCTACAAAAATATATTTTTTT-CGA

V R I A L S Y S P L I F I F Y N Y V H V F L L F S R V Y K N I F F S I
C E S H C L I R H * F S F F I I M Y M F S F Y S Q E S T K I Y F F - R
G A N R T V L F A I D F H F L * L C T C F P S I L K S L Q K Y I F F D

GGTGCGAATCGCACTGTCTTATTCGCCATTGATTTTCATTTTTTATAATTATGTACATGTTTTCCTTCTATTCTCAAGAGTCTACAAAAATATATTTTTTT-CGA

C E S H C L I R H * F S F F I I M Y M F S F Y S Q E S T K I Y F F - R
G A N R T V L F A I D F H F L * L C T C F P S I L K S L Q K Y I F F D
V R I A L S Y S P L I F I F Y N Y V H V F L L F S R V Y K N I F F S I

GGCGCGAATCGCACTGTCTTATTCGCCATTGATTTTCATTTTTTATAATTATGTACATGTTTTCCTTCTATTCTCAAGAGTCTACAAAAATATATTTTTTTTCGA

A R I A L S Y S P L I F I F Y N Y V H V F L L F S R V Y K N I F F F D
R E S H C L I R H * F S F F I I M Y M F S F Y S Q E S T K I Y F F S I
G A N R T V L F A I D F H F L * L C T C F P S I L K S L Q K Y I F F R

|6400 |6420 |6440 |6460 |6480 |65

Visual Overview

File View

Monkeypox Virus COP-58
Monkeypox Virus Sierra Leone
Monkeypox Virus Walter Reed 267
Monkeypox virus (Zaire)

0 20000 40000 60000 80000 100000 120000 140000 160000

Legend: Insertion Substitution Deletion

Differences

Base-by-Base: Sequence Alignment Annotation: /Users/cup/Desktop/MPXV-Science/MPXVs-final.bbb

Top Genes | 5' Top 3'

Scale
Frame 1
Frame 2
Frame 3
Monkeypox virus (Zaire)
Differences
Monkeypox Virus Sierra Leone
User Events
Frame 1
Frame 2
Frame 3
Scale

152940 152960 152980 153000 153020 153040

CHECK THIS OUT

Sequence Selection Mode

Gene: MPXV-Zre-A43R

Select a sequence below to see a comparison of this gene in relation to the same region on that partcular sequence.

Monkeypox Virus Sierra Leone

Gene Information/Comparison

Gene Name	MPXV-Zre-A43R
Strand	Top
ORF Start	149281
ORF Stop	149874
Length	594
Aligned Length	594
Differences	8
Difference %	1.35%
Subs	5, 1 (5)
Inserts	3, 3 (1)
Deletes	0
200b Upstream Diffs	0
AA Changes	4
Silent Changes	2

CDS Alignment Statistics

Monkeypox Virus Sierra Leone vs. Monkeypox Virus Walter Reed 267

Gene Name	Length	Aligned Length	Differences	Difference %	Subs	Inserts	Deletes	200b Upstream Diffs	AA Changes	Silent Changes	Counterpart	Length	Length Difference
MPXV-SL-169	1194	1466	272	18.55%	2, 1 (2)	0	270	0	2	1	MPXV-WRAIR-169	1464	-270
MPXV-SL-163	297	325	24	7.38%	0	0	24	0	0	0	MPXV-WRAIR-163	321	-24
MPXV-SL-114	339	339	19	5.60%	1, 1 (1)	18, 18 (1)	0	0	1	0	MPXV-WRAIR-114	321	18
MPXV-SL-014	480	480	9	1.88%	0	9, 9 (1)	0	0	0	0	MPXV-WRAIR-014	471	9
MPXV-SL-131	1521	1563	21	1.34%	0	21, 3 (1), 18 (1)	0	0	0	0	MPXV-WRAIR-131	1500	21
MPXV-SL-029	1479	1489	10	0.67%	0	0	10	0	3	0	MPXV-WRAIR-029	1473	6
MPXV-SL-026	450	450	3	0.67%	3, 1 (3)	0	0	0	1	2	MPXV-WRAIR-026	450	0
MPXV-SL-007	429	429	2	0.47%	2, 1 (2)	0	0	0	1	1	MPXV-WRAIR-007	429	0
MPXV-SL-023	1125	1128	4	0.35%	1, 1 (1)	0	3	0	0	1	MPXV-WRAIR-023	1128	-3
MPXV-SL-095	657	657	2	0.30%	2, 1 (2)	0	0	0	0	2	MPXV-WRAIR-095	657	0
MPXV-SL-081	1002	1002	3	0.30%	3, 1 (3)	0	0	0	1	2	MPXV-WRAIR-081	1002	0
MPXV-SL-127	348	348	1	0.29%	1, 1 (1)	0	0	0	1	0	MPXV-WRAIR-127	348	0
MPXV-SL-067	375	375	1	0.27%	1, 1 (1)	0	0	0	0	1	MPXV-WRAIR-067	375	0
MPXV-SL-083	402	402	1	0.25%	1, 1 (1)	0	0	0	1	0	MPXV-WRAIR-083	402	0
									1	2	MPXV-WRAIR-004	1314	0
									1	2	MPXV-WRAIR-174	1314	0
									0	1	MPXV-WRAIR-093	441	0
									0	1	MPXV-WRAIR-028	456	0
									1	0	MPXV-WRAIR-166	450	0
									1	0	MPXV-WRAIR-070	498	0
									1	0	MPXV-WRAIR-019	534	0
									1	2	MPXV-WRAIR-175	1773	0
									1	2	MPXV-WRAIR-003	1773	0
									0	1	MPXV-WRAIR-123	615	0
									1	0	MPXV-WRAIR-017	645	0
									0	1	MPXV-WRAIR-089	633	0
									0	1	MPXV-WRAIR-094	702	0
									0	1	MPXV-WRAIR-144	834	0
									0	2	MPXV-WRAIR-153	1680	0
									0	2	MPXV-WRAIR-158	1695	0
									1	0	MPXV-WRAIR-090	945	0
MPXV-SL-016	951	951	1	0.11%	1, 1 (1)	0	0	0	1	0	MPXV-WRAIR-016	951	0

Alignment Info

File

Sequences

Monkeypox Virus COP-5
(9469 bases/residues)
Monkeypox Virus Sierra
(8756 bases/residues)
Monkeypox Virus Walter
(9195 bases/residues)
Monkeypox virus (Zaire)
(6858 bases/residues)

Percent Identity Scores

Sequences

	1	2	3	4
1	100%	99.96%	100%	99.56%
2	99.96%	100%	99.96%	99.55%
3	100%	99.96%	100%	99.56%
4	99.56%	99.55%	99.56%	100%

Close

Viral Orthologous Clusters
VOCS

Viral Genome Organizer
VGO

Base-By-Base: Genome Alignment
BBB

JDotter: Java Dot Plot Alignments
JDot

GFS Java User Interface
GFSJ

Nucleotide Amino Acid Alignment
NAP

Hydrophobicity Grapher
HYDRO

GraphDNA: DNA Skew Graphing
DNA

Recent Hits Aquired from BLAST
ReHAB

Random Sequence Statistics
RSS

Codon Statistics
CS

VBRC Curation

Knowledge DataBase
KDB

VBRC Knowledge Database

- Mini review of available structure-function information
  - Human-curated database based on the literature
- Bibliographic information
- Available scientific resources
    - clones, mutants, and antibodies
- Empirically-derived properties
  - MW, pI . . .
  - Post-translational modifications
  - Expression
- Functional Assignments
  - Gene Ontology controlled vocabulary
    - Molecular function
    - Biological Process
    - Cellular component
  - Virulence Ontology

Three-Tiered Curation Process

1) UAB/UVic full-time curators
   - B.S., M.S., Ph.D.-level personnel
2) Editorial Board
   - P.I.'s working within the virus family
   - Review records generated from tier 1
3) Scientific Community
   - Feedback

KDB Curation Application

- Jason Pokorny, MCW
  - Initial development
- Systematic compilation of gene-specific information
- Collaborative application (Future development)
  - Multiple users
  - Editorial comments
  - Feedback

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Knowledge Database Curation

Select What to Annotate

Create New Annotatable Object | Quit Annotating

ID:	Annotatable Objects:	
17	**SPECIES: Name:** Vaccinia Virus **taxID:** 10245 **ICTV:** VACV **PBR:** VACV **STRAIN: Name:** WR (Western Reserve) **taxID:** 10254 **PBR:** VACV-WR **SEQUENCE: GI:**61395 **Gene:** 0 **Product:** <NONE> **Definition:** F8 polypeptide thymidine kinase [2] [Vaccinia virus]	S
18	**SPECIES: Name:** Vaccinia Virus **taxID:** 10245 **ICTV:** VACV **PBR:** VACV **STRAIN: Name:** WR (Western Reserve) **taxID:** 10254 **PBR:** VACV-WR **LOCUS: Name:**A14 **Description:** <NONE>	S
14	**SPECIES: Name:** Vaccinia Virus **taxID:** 10245 **ICTV:** VACV **PBR:** VACV **STRAIN: Name:** WR (Western Reserve) **taxID:** 10254 **PBR:** VACV-WR **LOCUS: Name:**F18 **Description:** <NONE>	S
22	**LOCUS: Name:**Generic A10L - Copenhagen ORF Name **Description:** VACV-COP_160	S
23	**LOCUS: Name:**Generic A11R - Copenhagen ORF Name **Description:** VACV-COP_164	S
24	**LOCUS: Name:**Generic A12L - Copenhagen ORF Name **Description:** VACV-COP_165	S

Page 1 of 33 Next >>

Sort By: Species - name Go

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Knowledge Database Curation

Currently Annotating: **SPECIES:** **Name:** Vaccinia Virus **taxID:** 10245 **ICTV:** VACV **PBR:** VACV
STRAIN: **Name:** WR (Western Reserve) **taxID:** 10254 **PBR:** VACV-WR
Change **LOCUS:** **Name:** A14 **Description:** <NONE>

Summary Identification Homology Properties 1 Properties 2 Function Reagents Interactions

Manual Save

Mini-Review:

Short Description (max 150): Repression of 90 aa A1

Long Functional Name (max 80):

Short Functional Name (max 30): A14L membrane protein

PBR (poxvirus.org) ID for gene/virus:

Miscellaneous notes:

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Add Reference | Delete Selected References

PMID:	Date:	Authors:	Title:	Journal:	Edit	Del
7269243	Aug 1981	Ichihashi Y	Unit Complex of vaccinia polypeptides linked by disulfide bridges.	Virology	E	☐
Notes: A14 is primarily disulfide-linked dimer						
8030247	Aug 1 1994	Takahashi T;Oie M;Ichihashi Y;	N-terminal amino acid sequences of vaccinia virus structural proteins	Virology	E	☐
Notes: A14 monomer and dimer detected in virions (IHD)						
9032312	Mar 1997	RodrC-guez JR, Risco C, Carrascosa...	Characterization of early stages in vaccinia virus membrane biogenes...	J Virol	E	☐
Notes: A14 identified as A17-interacting protein						
9311819	Oct 1997	Salmons T, Kuhn A, Wylie F, Schlei...	Vaccinia virus membrane proteins p8 and p16 are cotranslationally in...	J Virol	E	☐
Notes: A14 detected as co-translationally associated with ER and associated with ERGIC						
0009445029	Feb 1998	Rodriguez JR;Risco C;Carrascosa JL...	Vaccinia virus 15-kilodalton (A14L) protein is essential for assembl...	J Virol	E	☐
Notes: Essential role for A14 in morphogenesis elucidated with IPTG-inducible recombinant						
10196242	May 1999	Betakova T, Wolffe EJ, Moss B	Regulation of vaccinia virus morphogenesis: phosphorylation of the A...	J Virol	E	☐
Notes: A14 phosphorylation is dependent upon F10 expression; A14 phosphorylated on serine residues						
10729144	Apr 2000	Traktman P, Liu K, DeMasi J, Rolli...	Elucidating the essential role of the A14 phosphoprotein in vaccinia...	J Virol	E	☐
Notes: Essential role for A14 in assembly of virion membrane elucidated through TET-dependent recombinant; repression of A14 leads to the accumulation of 25-nm vesicles and a few crescents near large virosomes						
12885904	Aug 2003	Mercer J, Traktman P	Investigation of structural and functional motifs within the vaccini...	J Virol	E	☐

start | C:\Documents and Se... | Microsoft PowerPoint ... | annotate1 - Mozilla F

annotate6 - Mozilla Firefox

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Knowledge Database Curation

Currently **SPECIES:** **Name:** Vaccinia Virus **taxID:** 10245 **ICTV:** VACV **PBR:** VACV
Annotating: **STRAIN:** **Name:** WR (Western Reserve) **taxID:** 10254 **PBR:** VACV-WR
Change **LOCUS:** **Name:** A14 **Description:** <NONE>

Summary | Identification | Homology | Properties 1 | Properties 2 | **Function** | Reagents | Interactions

Function | GO Term Assignment

Function:

Add Function | Delete Selected Functions

Function:	Type:	Description:	Notes:	Edit:	Del:
essential for IMV morphogenesis	Morphogenesis			E	☐

Gene Ontology Term Assignment: (Molecular Function, Biological Process, and Cellular Component)

Assign Ontology Term | Delete Selected Terms

Term:	Notes:	Edit:	Del:
GO:0019068		E	☐

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File Edit View Go Bookmarks Tools Help

Knowledge Database Curation

Currently SPECIES: **Name:** Vaccinia Virus **taxID:** 10245 **ICTV:** VACV **PBR:** VACV
Annotating: STRAIN: **Name:** WR (Western Reserve) **taxID:** 10254 **PBR:** VACV-WR
Change LOCUS: **Name:** A14 **Description:** <NONE>

Summary | Identification | Homology | Properties 1 | Properties 2 | Function | **Reagents** | Interactions

Antibodies | Mutants

Primary Antibodies to A14:

Add Antibody | Delete Selected Antibodies

Antibody:	Type:	Application:	Create Method:	Ref Type:	Edit:	Del:

Mutants:

Add Mutant | Delete Selected Mutants

Mutant:	Type:	Notes:	Edit:	Del:

A45R (VACV-COP_207)

Synonyms: superoxide dismutase, TA56R, SalF8R

Gene Ontology

Molecular Function

Molecular Function | 0003674
- enzyme | 0003824
  - oxidoreductase | 0016491
    - oxidoreductase, acting on superoxide radicals as acceptor | 0016721
      - **superoxide dismutase | 0004784 | NOT IDA**
        - copper, zinc superoxide dismutase | 0004785
        - iron superoxide dismutase | 0008382
        - manganese superoxide dismutase | 0008383
        - nickel superoxide dismutase | 0016954

GO Function	Definition	GO Evidence	Reference
NOT superoxide dismutase	Catalysis of the reaction: 2 peroxide radical + 2 H+ = O2 + hydrogen peroxide.	IDA - Inferred from direct assay	PMID: 11435582

Component

Component | 0005575
- extracellular | 0005576

identification | classification

A45R (VACV-COP_207)

Synonyms: superoxide dismutase, TA56R, S

Property	Value	Evidence
Encapsidated	YES	IDA - Direct Ass
Essential	NO	IMP - Mutant Phen
Secreted	UNKNOWN	

Temporality	Evidence
☐ Early ☐ Intermediate ☑ Late	ISS - Sequence Similarity
☐ Early ☐ Intermediate ☑ Late	IEP - Expression Pattern

Localization

identification | classification | ontology | reagents | summary

A45R (VACV-COP_207)

Synonyms: superoxide dismutase, TA56R, SalF8R

Reagents

Antibody:	Applications:	Reference:	
MAb 2.B.11 Mouse Anti A45R IgG2a	WB	PMID: 11435582	Details/Requisition
Smith, Geoffrey L | The Wright-Fleming Institute, Imperial College School of Medicine | St. Mary's Campus, Norfolk Place, London W2 1PG, United Kingdom			
Mutant:	**Type:**	**Reference:**	
v-delta-A45R deletion mutant	Null (Deletion) Mutant	PMID: 11435582	Details/Requisition
Smith, Geoffrey L | The Wright-Fleming Institute, Imperial College School of Medicine | St. Mary's Campus, Norfolk Place, London W2 1PG, United Kingdom			
vRA45R revertant	Revertant Mutant	PMID: 11435582	Details/Requisition
Smith, Geoffrey L | The Wright-Fleming Institute, Imperial College School of Medicine | St. Mary's Campus, Norfolk Place, London W2 1PG, United Kingdom			
Recombinant:	**Type:**	**Target:**	**Reference:**
none available			