SUPPORTING INFORMATION

Improved virus isoelectric point estimation by prediction and exclusion of genome-binding regions

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S1. Polynucleotide-binding region predictions

Polynucleotide-binding regions (PBRs) were predicted based on conserved structures (arginine-rich regions, beta sheets, beta turns and disordered termini), as well as via two previously existing XNA-binding prediction tools, Pprint and DRNApred. The predictions were trained and validated using separate sets of proteins containing known PBRs, as detailed in Sections S4.1 and S4.2. The Matthews Correlation Coefficients (MCCs) were calculated for each protein as a means of evaluating the prediction. The distributions of MCCs for all prediction are summarized in Table S1. Based on these results, the combination of ARG rich regions and Beta turns was selected as the best overall PBR prediction method.

Table S1: Predictive power of structure-based and existing (Pprint and DRNApred) methods for predicting polynucleotide-binding regions (PBRs) in training (n = 36 PBRs, 25 proteins) and validation (n = 57 PBRs, 40 proteins) sets of virus capsid proteins. An ‘x’ indicates that the structure was included in the overall prediction, which may combine predictions from multiple structures. The row in yellow indicates best overall prediction.

Predicted Structures				Matthews Correlation Coefficient (MCC)	
ARG rich	Beta sheets	Beta turns	Disordered termini	Training	Validation
x				0.32 ± 0.29	0.27 ± 0.32
	x			0.05 ± 0.23	0.06 ± 0.13
		x		0.07 ± 0.20	-0.01 ± 0.11
			x	0.16 ± 0.31	0.11 ± 0.39
x	x			0.30 ± 0.29	0.25 ± 0.31
x		x		0.34 ± 0.28	0.26 ± 0.29
x			x	0.28 ± 0.25	0.24 ± 0.39
	x	x		0.07 ± 0.21	0.03 ± 0.15
	x		x	0.19 ± 0.30	0.14 ± 0.33
		x	x	0.20 ± 0.25	0.10 ± 0.33
x	x	x		0.29 ± 0.26	0.24 ± 0.28
x	x		x	0.27 ± 0.26	0.22 ± 0.38
x		x	x	0.28 ± 0.23	0.24 ± 0.36
	x	x	x	0.20 ± 0.24	0.13 ± 0.30
x	x	x	x	0.27 ± 0.24	0.22 ± 0.38
Pprint				0.22 ± 0.27	0.19 ± 0.28
DRNApred				0.17 ± 0.23	0.11 ± 0.19

S2. Empirical isoelectric point data by method of measurement

The empirical isoelectric point (pI) values for the 32 viruses in this study are shown in Figure S1, colored by method of pI determination. Electrophoretic mobility tends to be associated with lower pI measurements. However, there are few comparisons between electrophoretic mobility and alternative methods (such as isoelectric focusing and aggregation). In addition, some of the lowest isoelectric point measurements (HHAV and AAV4) were determined via isoelectric focusing. Confirmation of both the low and high range of isoelectric points by multiple methods would be invaluable in determining potential bias in these methods.

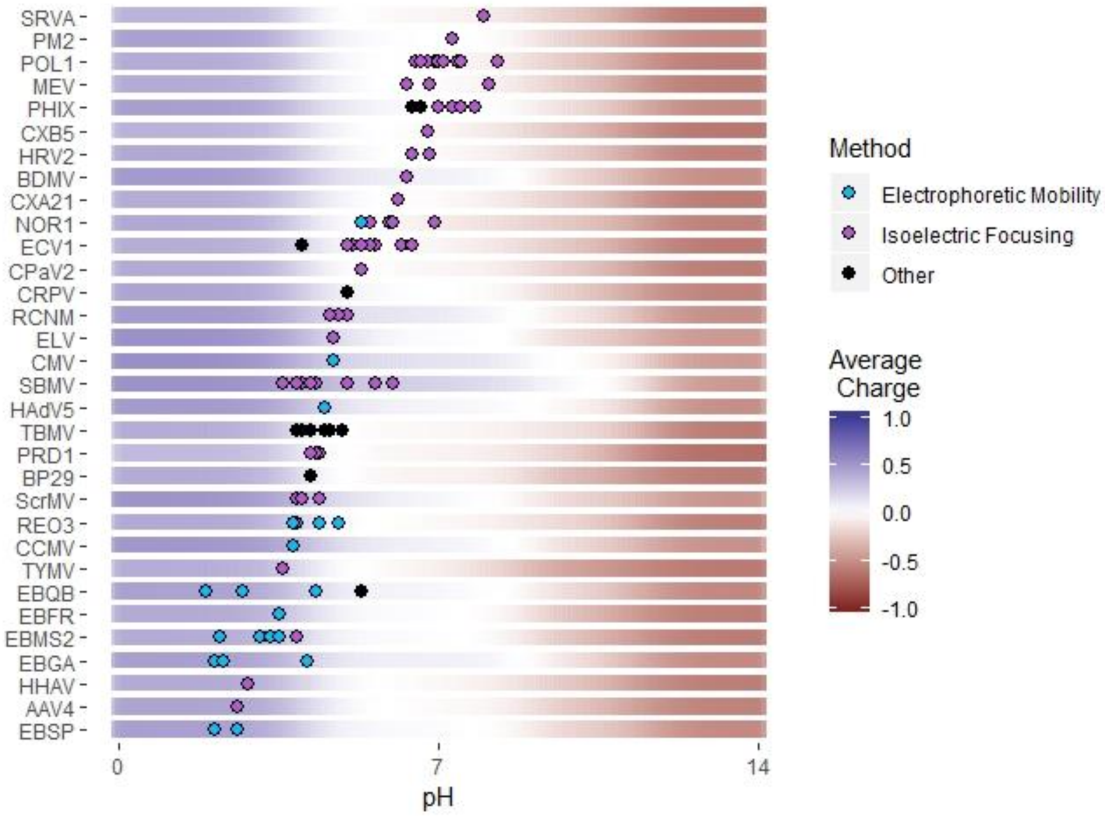

Figure S1: Distribution of empirical isoelectric points (filled circles) based on method of measurement. The theoretical charge of the (unmodified) virus capsid proteomes from pH 0 to 14 is displayed as color bars in the background. Based on unmodified theoretical charge, empirical pIs would be expected to fall within the white region of each bar.

S3. Empirical isoelectric point data

The empirical isoelectric points (pIs) used in this study are supplied in Table S2. While many empirical pIs were summarized from Michen and Graule’s review (1), citations to the original papers are supplied here for reference.

Table S2. Empirical isoelectric point (pI) values from the literature used in this study

Abbreviation	Virus	pI	Reference
AAV4	Adeno-associated virus – 4	2.6	(2)
BDMV	Belladonna mottle virus	6.3	(3)
BP29	Bacillus phage phi29	4.2	(4)
CCMV	Cowpea chlorotic mottle virus	3.8	(5)
CMV	Cucumber mosaic virus 4	4.7	(6)
CPaV2	Canine parvovirus 2 (Dog)	5.3	(7)
CRPV	Cottontail rabbit papillomavirus	5	(8)
CXA21	Human coxsackievirus A 21	6.1	(9)
CXB5	Human coxsackievirus B 5	6.75	(10)
EBFR	Enterobacteria phage fr	3.5	(11)
EBGA	Enterobacteria phage GA	4.1	(11)
EBGA	Enterobacteria phage GA	2.1	(12)
EBGA	Enterobacteria phage GA	2.3	(12)
EBMS2	Enterobacteria phage MS2	3.9	(11)
EBMS2	Enterobacteria phage MS2	3.5	(13)
EBMS2	Enterobacteria phage MS2	3.1	(12)
EBMS2	Enterobacteria phage MS2	3.9	(12)
EBMS2	Enterobacteria phage MS2	3.9	(14)
EBMS2	Enterobacteria phage MS2	3.5	(15)
EBMS2	Enterobacteria phage MS2	2.2	(16)
EBMS2	Enterobacteria phage MS2	3.3	(16)
EBMS2	Enterobacteria phage MS2	3.5	(16)
EBMS2	Enterobacteria phage MS2	3.9	(17)
EBQB	Enterobacteria phage Qb	4.3	(11)
EBQB	Enterobacteria phage Qb	1.9	(12)
EBQB	Enterobacteria phage Qb	2.7	(12)
EBQB	Enterobacteria phage Qb	5.3	(14)
EBSP	Enterobacteria phage SP	2.1	(12)
EBSP	Enterobacteria phage SP	2.6	(12)
ECV1	Human echovirus 1	4	(10)
ECV1	Human echovirus 1	5.1	(9)
ECV1	Human echovirus 1	5.6	(9)
ECV1	Human echovirus 1 (4CH-1)	5.5	(17)
ECV1	Human echovirus 1 (R115)	6.2	(17)
ECV1	Human echovirus 1 (V212)	6.4	(17)

ECV1	Human echovirus 1 (V239)	5.3	(17)
ECV1	Human echovirus 1 (V248)	5	(17)
ELV	Erysimum latent virus	4.7	(3)
HAdV5	Human adenovirus 5	4.5	(18)
HHAV	Hepatitis A virus	2.8	(19)
HRV2	Human rhinovirus 2	6.4	(20)
HRV2	Human rhinovirus 2	6.8	(21)
MEV	Mengo encephalomyocarditis virus L	8.1	(22)
MEV	Mengo encephalomyocarditis virus M	6.3	(22)
MEV	Mengo encephalomyocarditis virus S	6.8	(22)
NOR1	Norovirus VLP	5.3	(15)
NOR1	Norovirus VLP (Funabashi, Norwalk)	5.9	(23)
NOR1	Norovirus VLP (Kashiwa)	5.5	(23)
NOR1	Norovirus VLP (Narita)	6.9	(23)
NOR1	Norovirus VLP (Seto, Hawaii)	6	(23)
PHIX	Enterobacteria phage ΦX174	6.6	(24)
PHIX	Enterobacteria phage ΦX174	7	(25)
PHIX	Enterobacteria phage ΦX174	7.3	(25)
PHIX	Enterobacteria phage ΦX174	7.5	(25)
PHIX	Enterobacteria phage ΦX174	7.8	(25)
PHIX	Enterobacteria phage ΦX174	6.6	(26)
PHIX	Enterobacteria phage ΦX174	6.4	(27)
PM2	Pseudoalteromonas phage PM2	7.3	(28)
POL1	Poliovirus 1	6.9	(29)
POL1	Poliovirus 1	7.4	(19)
POL1	Poliovirus 1 (Brunender)	7.4	(30)
POL1	Poliovirus 1 (Brunhilde)	7	(31)
POL1	Poliovirus 1 (Brunhilde)	7.1	(17)
POL1	Poliovirus 1 (Chat)	7.5	(32)
POL1	Poliovirus 1 (LSc2ab)	6.75	(10)
POL1	Poliovirus 1 (LSc2ab)	6.75	(10)
POL1	Poliovirus 1 (LSc2ab)	6.6	(9)
POL1	Poliovirus 1 (LSc2ab)	6.6	(17)
POL1	Poliovirus 1 (Mahoney)	8.3	(33)
POL1	Poliovirus 2 (Sabin T2)	6.5	(9)
PRD1	Enterobacteria phage PRD1 (PR722)	4.2	(25)
PRD1	Enterobacteria phage PRD1 (PR722)	4.3	(25)
PRD1	Enterobacteria phage PRD1 (PR722)	4.3	(25)
PRD1	Enterobacteria phage PRD1 (PR722)	4.4	(25)
RCNM	Red clover necrotic mosaic virus (A)	5	(34)
RCNM	Red clover necrotic mosaic virus (B)	4.8	(34)
RCNM	Red clover necrotic mosaic virus (C)	4.6	(34)
REO3	Mammalian orthoreovirus 3 (Dearing)	3.9	(33)
REO3	Mammalian orthoreovirus 3 (Dearing)	3.8	(35)
REO3	Mammalian orthoreovirus 3 (Dearing)	3.8	(36)
REO3	Mammalian orthoreovirus 3 (Dearing)	3.8	(36)
REO3	Mammalian orthoreovirus 3 (Dearing)	4.4	(36)

REO3	Mammalian orthoreovirus 3 (Dearing)	4.8	(36)
SBMV	Southern bean mosaic virus (Var 1)	3.9	(37)
SBMV	Southern bean mosaic virus (Var 1)	6	(37)
SBMV	Southern bean mosaic virus (Var 2)	4.3	(37)
SBMV	Southern bean mosaic virus (Var 2)	5.6	(37)
SBMV	Southern bean mosaic virus (Var 3)	4.2	(37)
SBMV	Southern bean mosaic virus (Var 3)	5	(37)
SBMV	Southern bean mosaic virus (Var 4)	3.6	(37)
SBMV	Southern bean mosaic virus (Var 4)	4	(37)
ScrMV	Scrophularia mottle virus	4	(3)
ScrMV	Scrophularia mottle virus (Anagyris)	4.4	(38)
ScrMV	Scrophularia mottle virus (Czech isolate)	3.9	(38)
SRVA	Simian rotavirus A (SA11)	8	(10)
TBMV	Tobacco mosaic virus (Cucumber)	4	(39)
TBMV	Tobacco mosaic virus (Cucumber)	4.9	(39)
TBMV	Tobacco mosaic virus (Green aucuba)	4.5	(39)
TBMV	Tobacco mosaic virus (Holmes’ masked)	3.9	(39)
TBMV	Tobacco mosaic virus (Holmes’ rip-gras)	4.5	(39)
TBMV	Tobacco mosaic virus (J14D1)	4.2	(39)
TBMV	Tobacco mosaic virus (Ordinary)	3.9	(39)
TBMV	Tobacco mosaic virus (Yellow aucuba)	4.6	(39)
TYMV	Turnip yellow mosaic virus	3.6	(3)

S4. Virus capsid proteins

S4.1. Experimental set

Table S3 provides a summary of capsid proteins for viruses with empirical pI data used in this study for all pI predictions and PBR prediction training. Protein sequences, DNA- or RNA-binding regions (PBRs), and information about the number of copies of each protein in the virus capsid were obtained from the UniProt database (www.uniprot.org) (40) and additional references as noted in Table S3. Where information was not available for the copy number of minor proteins within the capsid (“Unknown”), those proteins were not included in the pI calculation. The “Binding Regions” listed in Table S3 were used as a training set for predicting PBRs throughout the entire experimental set of proteins.

Table S3. Viral capsid proteins referenced for pI and PBR prediction in this study

Abbreviation	Virus	UniProt Entry	Protein name	Copy Number	Binding regions	References
AAV4	Adeno-associated virus 4	O41855	Major capsid (VP1)	60	119-125, 139-145, 165-171, 298-305	(41, 42)
BDMV	Belladonna mottle virus	P15158	Capsid (CP)	180		(43)
BP29	*Bacillus* phage Φ29	B3VMP4	Capsid fiber protein (P8.5)	165		(44)
BP29	*Bacillus* phage Φ29	P03681	Primer terminal protein (TP) (TP)	1		(45, 46)
BP29	*Bacillus* phage Φ29	P04331	Tail knob protein gp9 (Distal tube protein) (P9)	6		(44, 47)
BP29	*Bacillus* phage Φ29	P04332	Portal protein (P10)	12	1-14	(44, 47, 48)
BP29	*Bacillus* phage Φ29	P13849	Major capsid protein (P8)	235		(44, 49)
BP29	*Bacillus* phage Φ29	P15132	Morphogenesis protein 1 (P13)	2		(44, 50, 51)
BP29	*Bacillus* phage Φ29	P20345 [1 – 691]	Pre-neck appendage protein (gP12)	12		(44)
BP29	*Bacillus* phage Φ29	P68930	Proximal tail-tube connector (P11)	12		(44, 46)
CCMV	Cowpea chlorotic mottle virus	P03601	Capsid (CP)	180	11-23	(5, 52–54)
CMV	Cucumber virus (FNY)	P69466	Capsid (CP)	180	10-22	(5, 52, 55)
CPAV2	Canine parvovirus 2 (Dog)	P17455	Major capsid, 143 AA N-terminus (VP1)	6		(56–58)
CPAV2	Canine parvovirus 2 (Dog)	P17455 [144-727]	Major capsid, smaller variant (VP2)	54		(57, 58)
CRPV	Cottontail rabbit papillomavirus (Kansas)	P03102	Major capsid (L1)	360	497-504	(59, 60)
CRPV	Cottontail rabbit papillomavirus (Kansas)	P03108	Minor capsid (L2)	72	1-9	(60, 61)
CXA21	Coxsackievirus A21	P22055 [1541 – 1562]	Viral protein genome linked (VPg)	1		(62)
CXA21	Coxsackievirus A21	P22055 [2 – 69]	Inner capsid (VP4)	60		(62)
CXA21	Coxsackievirus A21	P22055 [342 – 581]	Capsid (VP3)	60		(62)
CXA21	Coxsackievirus A21	P22055 [582 – 879]	Capsid (VP1)	60		(62)
CXA21	Coxsackievirus A21	P22055 [70 – 341]	Capsid (VP2)	60		(62)
CXB5	Human coxsackievirus B5 (Peterborough)	Q03053 [1519 – 1540]	Viral protein genome linked (VPg)	1		(63)
CXB5	Human coxsackievirus B5 (Peterborough)	Q03053 [2 – 69]	Inner capsid (VP4)	60		(63)
CXB5	Human coxsackievirus B5 (Peterborough)	Q03053 [331 – 566]	Capsid (VP3)	60		(63)
CXB5	Human coxsackievirus B5 (Peterborough)	Q03053 [566 – 851]	Capsid (VP1)	60		(63)
CXB5	Human coxsackievirus B5 (Peterborough)	Q03053 [70 – 330]	Capsid (VP2)	60		(63)
EBFR	Enterobacteria phage fr	P03614	Capsid (CP)	178	32-105	(64–67)

EBFR	Enterobacteria phage fr	P15966	Maturation (A)	1	26-233	(64, 65)
EBGA	Enterobacteria phage GA	P07234	Capsid (CP)	178	18-93	(68)
EBGA	Enterobacteria phage GA	P07394	Maturation (A)	1		(68)
EBMS2	Escherichia phage MS2	P03610	Maturation (A2)	1	26-233	(69–72)
EBMS2	Escherichia phage MS2	P03612	Capsid (CP)	178	32-105	(69, 73, 74)
EBSP	Enterobacteria phage SP	P09673	Major capsid (CP)	178		(75)
EBSP	Enterobacteria phage SP	P09677	Minor capsid (A1)	6		(75)
EBSP	Enterobacteria phage SP	P09676	Maturation (A2)	1	156-174, 255-265, 321-325	(75)
EBQB	Escherischia phage Qb	P03615	Capsid (CP)	178	32-95	(76–81)
EBQB	Escherischia phage Qb	Q8LTE2	Maturation (A2)	1		(76, 81–83)
EBQB	Escherischia phage Qb	Q8LTE1	Minor capsid protein (A1)	6		(80, 81, 83)
ECV1	Echovirus 1 (strain Human/Egypt/Farouk/1951) (E-1)	O91734 [567 – 850]	Capsid (VP1)	60		(84, 85)
ECV1	Echovirus 1 (strain Human/Egypt/Farouk/1951) (E-1)	O91734 [70 – 330]	Capsid (VP2)	60		(84, 85)
ECV1	Echovirus 1 (strain Human/Egypt/Farouk/1951) (E-1)	O91734 [331 – 567]	Capsid (VP3)	60		(84, 85)
ECV1	Echovirus 1 (strain Human/Egypt/Farouk/1951) (E-1)	O91734 [2 – 69]	Inner capsid (VP4)	60		(84, 85)
ECV1	Echovirus 1 (strain Human/Egypt/Farouk/1951) (E-1)	O91734 [1518 – 1539]	Viral protein genome linked (VPg)	1		(84, 85)
ELV	Erysimum latent virus	P35927	Capsid (CP)	180		(86, 87)
HAdV5	Human adenovirus C5	P03253	Protease (Protease)	10		(88, 89)
HAdV5	Human adenovirus C5	P03271	Packaging protein (IVa2)	7	440-449	(89–91)
HAdV5	Human adenovirus C5	P03281	hexon-interlacing protein (IX)	240		(88, 89, 92)
HAdV5	Human adenovirus C5	P04133	Hexon protein (L3)	720		(88, 89, 92)
HAdV5	Human adenovirus C5	P11818	Fiber protein (L5)	36		(88, 89, 93)
HAdV5	Human adenovirus C5	P12537 [1 – 570]	Hexon-linking protein (IIIa)	60		(88, 89, 94)
HAdV5	Human adenovirus C5	P12538	Penton protein (L2)	60		(88, 89, 94)
HAdV5	Human adenovirus C5	P24936 [1 – 111]	Hexon-linking protein N (inner capsid) (VIIIN)	120		(88, 89)
HAdV5	Human adenovirus C5	P24936 [158 – 227]	Hexon-linking protein C (inner capsid) (VIIIC)	120		(88, 89)
HAdV5	Human adenovirus C5	P24937 [34 – 239]	Endosome lysis protein (VI)	360		(89, 91)
HAdV5	Human adenovirus C5	P24938	core-capsid bridging protein (CoreCapsid)	157		(88, 89, 91)
HAdV5	Human adenovirus C5	P68951 [25 – 198]	Histone-like nucleoprotein (HistoneLike)	1070	1-173	(88, 89, 91, 94)
HAdV5	Human adenovirus C5	Q2KS10 [33 – 51]	Core protein X (X)	143	1-19	(88, 89)
HHAV	Hepatitis A virus	P08617 [1497 – 1519]	Viral protein genome linked (VPg)	1		(95–97)
HHAV	Hepatitis A virus	P08617 [1 – 23]	Inner capsid (VP4)	Unknown		(95–97)

HHAV	Hepatitis A virus	P08617 [24 – 245]	Capsid (VP2)	60		(95–97)
HHAV	Hepatitis A virus	P08617 [246 – 491]	Capsid (VP3)	60		(95–97)
HHAV	Hepatitis A virus	P08617 [492 – 765]	Capsid (VP1)	60		(95–97)
HRV2	Human rhinovirus 2	P04936 [1487 – 1507]	Viral protein genome linked (VPg)	1		(98)
HRV2	Human rhinovirus 2	P04936 [2 – 69]	Inner capsid (VP4)	60		(98)
HRV2	Human rhinovirus 2	P04936 [331 – 565]	Capsid (VP3)	60		(98)
HRV2	Human rhinovirus 2	P04936 [565 – 85]	Capsid (VP1)	60		(98)
HRV2	Human rhinovirus 2	P04936 [70 – 330]	Capsid (VP2)	60		(98)
MEV	Mengo encephalomyocarditis virus	P12296 [138 – 393]	Capsid (VP2)	60		(98)
MEV	Mengo encephalomyocarditis virus	P12296 [1609 – 1628]	Viral protein genome linked (VPg)	1		(99)
MEV	Mengo encephalomyocarditis virus	P12296 [394 – 624]	Capsid (VP3)	60		(99, 100)
MEV	Mengo encephalomyocarditis virus	P12296 [625 – 901]	Capsid (VP1)	60		(99)
MEV	Mengo encephalomyocarditis virus	P12296 [68 – 137]	Inner capsid (VP4)	60		(99)
NOR1	Norwalk Virus (Funabashi)	Q83883 [963 – 1100]	Viral protein genome linked (VPg)	1		(101, 102)
NOR1	Norwalk Virus (Funabashi)	Q83884	Capsid (VP1)	180		(102)
NOR1	Norwalk Virus (Funabashi)	Q83885	Structural/packaging (VP2)	1		(102)
PHIX	Enterobacteriaphage ΦX174 (Sanger)	P03641	Capsid (F)	60		(103–106)
PHIX	Enterobacteriaphage ΦX174 (Sanger)	P03643	Major spike (G)	60		(103, 104, 107, 108)
PHIX	Enterobacteriaphage ΦX174 (Sanger)	P03646	Minor spike (H)	12		(103, 104)
PHIX	Enterobacteriaphage ΦX174 (Sanger)	P69592	DNA-binding (J)	60	1-38	(103, 109, 110)
PM2	Pseudoalteromonas phage PM2	P15794	Major capsid protein (P2)	1200		(111–113)
PM2	Pseudoalteromonas phage PM2	Q37958	Protein P4 (P4)	300		(112–115)
PM2	Pseudoalteromonas phage PM2	Q9XJR1	Protein P6 (P6)	60		(112, 113, 116)
PM2	Pseudoalteromonas phage PM2	Q9XJR2	Protein P5 (P5)	Unknown		(112, 113)
PM2	Pseudoalteromonas phage PM2	Q9XJR3	Spike Protein (P1)	60		(112, 113)
PM2	Pseudoalteromonas phage PM2	Q9XJR5	Protein P8 (P8)	Unknown		(112, 113)
PM2	Pseudoalteromonas phage PM2	Q9XJR6	Protein P3 (P3)	240		(112, 113, 116)
PM2	Pseudoalteromonas phage PM2	Q9XJR8	Peptidoglycan hydrolase P7 (P7)	Unknown		(112, 113)
PM2	Pseudoalteromonas phage PM2	Q9XJR9	Protein P9 (P9)	Unknown		(112, 113)
POL1	Poliovirus 1 (Mahoney)	P03300 [1544 – 1565]	Viral protein genome linked (VPg)	1		(117–119)
POL1	Poliovirus 1 (Mahoney)	P03300 [2 – 69]	Inner capsid (VP4)	60	34	(117, 118, 120)

POL1	Poliovirus 1 (Mahoney)	P03300 [342 – 579]	Capsid (VP3)	60	223	(117, 118, 120)
POL1	Poliovirus 1 (Mahoney)	P03300 [580 – 881]	Capsid (VP1)	60	129	(117, 118, 120)
POL1	Poliovirus 1 (Mahoney)	P03300 [70 – 341]	Capsid (VP2)	60		(117, 118)
PRD1	Enterobacteria phage PR772	P09009	DNA terminal protein (Protein P8) (P8)	1		(121–124)
PRD1	Enterobacteria phage PR772	P13559	Endolysin (Protein P15) (P15)	Unknown		(122, 124, 125)
PRD1	Enterobacteria phage PR772	P22535	Major capsid protein P3 (Protein P3) (P3)	705		(121, 126, 127)
PRD1	Enterobacteria phage PR772	P22536	Spike protein P5 (Protein P5) (P5)	33		(121, 127, 128)
PRD1	Enterobacteria phage PR772	P27378	Adsorption protein P2 (Protein P2) (P2)	11		(121, 124, 128)
PRD1	Enterobacteria phage PR772	P27379	Packaging efficiency factor P6 (P6)	12		(121, 124, 126)
PRD1	Enterobacteria phage PR772	P27380	Transglycosylase (EC 4.2.2.n1) (Protein P7) (P7)	20		(121, 124)
PRD1	Enterobacteria phage PR772	P27381	DNA packaging ATPase P9 (Protein P9) (P9)	12		(121, 124, 126)
PRD1	Enterobacteria phage PR772	P27382	Infectivity protein P11 (P11)	Unknown		(121, 124)
PRD1	Enterobacteria phage PR772	P27384	Penton protein P31 (GpC) (Protein C) (P31)	11		(121, 124, 128)
PRD1	Enterobacteria phage PR772	P27387	Packaging protein P20 (P20)	6		(121, 124, 126)
PRD1	Enterobacteria phage PR772	P27388	Packaging protein P22 (GpK) (Protein K) (P22)	6		(121, 124)
PRD1	Enterobacteria phage PR772	P27389	Protein P18 (GpM) (Protein M) (P18)	Unknown		(121, 124)
PRD1	Enterobacteria phage PR772	P27390	Protein P34 (Protein O) (GpO) (P34)	Unknown		(121, 124)
PRD1	Enterobacteria phage PR772	P27391	Minor capsid protein P30 (Protein P) (GpP) (P30)	55		(121, 124, 126)
PRD1	Enterobacteria phage PR772	P27392	Protein P16 (GpS) (Protein S) (P16)	11		(121, 124, 126)
PRD1	Enterobacteria phage PR772	Q3T4M7	Protein P32 (P32)	Unknown		(121, 124)
RCNM	Red clover necrotic mosaic virus	P22955	Capsid (CP)	180	1-46	(129–131)
REO3	Reovirus 3 (Dearing)	P03525	Inner capsid protein sigma-2 (S2)	150		(132–137)
REO3	Reovirus 3 (Dearing)	P03527	Outer capsid protein sigma-3 (S3)	39		(134, 138, 139)
REO3	Reovirus 3 (Dearing)	P03528	Outer capsid protein sigma-1 (S1)	36		(134, 140–143)
REO3	Reovirus 3 (Dearing)	P0CK31	Inner polymerase lambda-3 (L3)	12		(134, 144)
REO3	Reovirus 3 (Dearing)	P11078	Outer capsid protein mu-1 (M1)	39		(134, 145, 146)
REO3	Reovirus 3 (Dearing)	P11079	Outer capsid protein lambda-2 (L2)	60	893-900	(134, 147, 148)

REO3	Reovirus 3 (Dearing)	P12418	Inner microtubule-associated protein mu-2 (M2)	12		(134, 149–151)
REO3	Reovirus 3 (Dearing)	P15024	Inner capsid protein lambda-1 (L1)	120		(134, 152, 153)
SBMV	Southern bean mosaic virus	O72158	Capsid (CP)	180	26-35	(154)
ScrMV	Scrophularia mottle virus	Q3BD98	Capsid (CP)	180		(155)
SRVA	Simian rotavirus A (SA11)	A2T3P5	Outer capsid glycoprotein VP7 (VP7)	780		(156)
SRVA	Simian rotavirus A (SA11)	A2T3R5	Inner capsid protein VP2 (VP2)	120		(156, 157)
SRVA	Simian rotavirus A (SA11)	A2T3S0	RNA-directed RNA polymerase (RdRp)	12		(156)
SRVA	Simian rotavirus A (SA11)	A2T3S5	Protein VP3 (VP3)	12		(156)
SRVA	Simian rotavirus A (SA11)	A2T3T0	Intermediate capsid protein VP6 (VP6)	690		(156)
SRVA	Simian rotavirus A (SA11)	A2T3S5	Outer capsid protein VP4 (VP4)	180		(156)
TBMV	Tobacco mosaic virus (Vulgare)	P69687	Capsid (CP)	2130		(158–163)
TYMV	Turnip yellow mosaic virus	P03608	Capsid (CP)	180	67-68, 180	(164–171)

S4.2. Validation set

A validation set for confirming the effectiveness of PBR prediction methods was acquired by searching the UniProt database for reviewed entries of proteins occurring within the virion with annotated regions for RNA- or DNA-binding, as shown in Table S4. In order to include a diversity of viruses and avoid over-representing features typical of a subset of viruses, enveloped virus proteins were included in the validation set. Preference was given to proteins with PBRs referenced by publication wherever possible. Genome polyproteins were excluded from the search because the XNA-binding regions in these sequences frequently occurred outside a capsid protein sequence.

Table S4: Capsid proteins used to validate polynucleotide-binding region predictions

Virus	UniProt Entry	Protein Name	Binding Regions	References
Arctic squirrel hepatitis virus (ASHV)	Q64897	Capsid protein (Core antigen) (Core protein) (HBcAg) (p21.5)	160-179, 181-187	(172)
Avian infectious bronchitis virus (Arkansas 99) (IBV)	Q64960	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	29-16	(173)
Bacillus phage B103 (Bacteriophage B103)	Q37883	DNA terminal protein (Gene product 3) (gp3) (Protein p3)	1-73	(174)
Bacillus phage Nf (Bacteriophage Nf)	P06812	DNA terminal protein (Gene product 3) (gp3) (Protein p3)	1-73	(175, 176)
Bat coronavirus (BtCoV/133/2005)	Q0Q4E6	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	33-175	(177)
Beak and feather disease virus (BFDV)	Q9YUC8	Capsid protein	1-4, 15-54	(178)
Bovine coronavirus (98TXSF-110-ENT) (BCV)	Q91A22	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	52-194	(179)
Canary circovirus (CaCV)	Q8QME6	Probable capsid protein	1-39	(180)
Canine coronavirus (BGF10) (CCoV)	Q7T6S8	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	33-159	(181)
Chicken anemia virus (Germany Cuxhaven-1) (CAV)	Q99153	Capsid protein (CA1) (Coat protein)	1-43	(182, 183)
Chimpanzee hepatitis B virus (United Kingdom/LSH/1988)	P12901	Capsid protein (Core antigen) (Core protein) (HBcAg) (p21.5)	155-183	(184)
Enterobacteria phage f2 (Bacteriophage f2)	P03611	Capsid protein (CP) (Coat protein)	31-104	(185, 186)
Enterobacteria phage JP34 (Bacteriophage JP34)	P34700	Capsid protein (CP) (Coat protein)	31-104	(187)
Enterobacteria phage MX1 (Bacteriophage MX1)	O64306	Maturation protein A2 (MP) (A2) (Assembly protein) (A protein)	159-177, 227-237, 295-299	(188, 189)
Enterobacteria phage R17 (Bacteriophage R17)	P69170	Capsid protein (CP) (Coat protein)	31-104	(190)
Enterobacteria phage ZR (Bacteriophage ZR)	P69171	Capsid protein (CP) (Coat protein)	32-105	(191, 192)
Equine coronavirus (NC99) (ECoV)	Q9DQX6	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	52-193	(193)

Hepatitis delta virus genotype I (American) (HDV)	P0C6L5	Large delta antigen (L-HDAg) (p27)	97-107	(194)
Human adenovirus B serotype 7 (HAdV-7)	P03273	Packaging protein 1 (Packaging protein IVa2)	440-448	(195)
Human adenovirus C serotype 2 (HAdV-2)	P03272	Packaging protein 1 (Packaging protein IVa2)	440-449	(196)
Human coronavirus 229E (HCoV-229E)	P15130	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	22-148	(197–199)
Human herpesvirus 1 (17) (HHV-1)	P10231	Tegument protein UL47 (82/81 kDa tegument protein) (VMW82/81) (VP13/14)	9-12, 50-75	(200, 201)
Human herpesvirus 2 (HG52) (HHV-2)	P89467	Tegument protein UL47 (82/81 kDa tegument protein) (VMW82/81) (VP13/14)	9-12, 57-84, 70-73, 527-530	(202)
Human immunodeficiency virus type 1 group M subtype A (MAL) (HIV-1)	P04599	Virion infectivity factor (Vif) (SOR protein) [Cleaved into: p17; p7]	75-114	(203)
Human SARS coronavirus (SARS-CoV)	P59595	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	42-187	(204–209)
Maize stripe virus (MStV)	P27207	Nucleoprotein (Coat protein) (CP) (Nucleocapsid protein) (Protein N) (Protein pc3)	201-316	(210)
Middle East respiratory syndrome-related coronavirus (United Kingdom/H123990006/2012)	K9N4V7	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	33-175	(211)
Porcine circovirus 2 (PCV2)	O56129	Capsid protein	1-47	(212, 213)
Porcine epidemic diarrhea virus (CV777) (PEDV)	Q07499	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	16-146	(214–216)
Porcine hemagglutinating encephalomyelitis virus (67N)	Q8BB23	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	52-194	(217)
Porcine transmissible gastroenteritis coronavirus (FS772/70)	P05991	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	33-159	(218)
Reston ebolavirus (Philippines-96) (REBOV)	Q91DD6	Minor nucleoprotein VP30 (Transcription activator VP30)	26-4	(219)
Rice dwarf virus (Akita) (RDV)	Q85448	Protein P7 (55 kDa core protein)	128-249, 325-355	(220)
Rice gall dwarf virus (RGDV)	A4PBP8	Protein P7	129-251, 321-351	(221)
Rice stripe virus (M) (RSV)	P68560	Nucleoprotein (Coat protein) (CP) (Nucleocapsid protein) (Protein N) (Protein pc3)	201-322	(222, 223)
Satellite tobacco necrosis virus 1	P03606	Capsid protein (Coat protein)	1-19	(224)
Simian virus 40 (SV40)	P03093	Minor capsid protein VP2 (Minor structural protein VP2)	313-352	(225, 226)
Turkey coronavirus (Indiana) (TCV)	Q9PZ51	Nucleoprotein (Nucleocapsid protein) (NC) (Protein N)	29-16	(227, 228)
Wheat yellow head virus (WYHV)	P84254	Nucleoprotein (Coat protein) (CP) (Nucleocapsid protein) (Protein N) (Protein pc3)	198-314	(229)
Wound tumor virus (NJ) (WTV)	P31610	Protein P7 (60 kDa core protein)	129-253, 331-361	(230)

S5. R functions

The R code used to predict PBR regions in capsid proteins is provided below. Since most functions rely on secondary structure prediction via NetSurfP 2.0 (231, 232), the input to all functions is assumed to be the spreadsheet (.csv) output of NetSurfP 2.0 (here assigned to the object ‘netSurf’), with columns identifying the virus (‘Abbreviation’) and protein (‘ID’) for a given sequence. Results of this code as applied to the proteomes in Table S3 are provided in the Supporting Information following the References.

```
ARGrichFinder <- function(RKratioMin = 0.24, netSurfDF = netSurf, gapMax = 10,  RKmin = 5,
                          AAaccepted = c("R", "K"), turnClause = F, turnMin = 2){
  # Function to find Arginine- and Lysine-rich windows of indeterminate length in proteome sequences
  # gapMax: maximum allowed distance between consecutive R/K’s in ARG-rich zones
  # RKmin= 5 excludes chance occurrence of 1 to 4 R/K's within AA sequence
  # RKratioMin: the optimizable variable
  # turnClause allows the same code to be adapted to find turns, as in the function ‘betaTurnFinder’
  netSurfDF$isRK = netSurfDF$seq %in% AAaccepted
  netSurfRK = netSurfDF %>% filter(isRK == T)
  netSurfRK$regionID = cumsum(c(1, abs(diff(netSurfRK$n)) > gapMax))

  RKsumm = netSurfRK %>% group_by(regionID, Abbreviation, ID) %>% summarize(RKcount = n(), start = min(n),
                                                             end = max(n), RKratio = n()/(max(n)-min(n)+1),
                                                             turn = sum((q8 %in% c("T", "S"))))



  if(turnClause == TRUE){RKsumm = RKsumm %>% filter((RKcount >= RKmin & RKratio >= RKratioMin)|
                                               (turn > 0 & RKcount >= turnMin))
  } else{RKsumm = RKsumm %>% filter(RKcount >= RKmin & RKratio >= RKratioMin)}

  netSurfPred = left_join(netSurfDF, ungroup(RKsumm))
    netSurfPred$Prediction = 0
    netSurfPred$Prediction[netSurfPred$n >= netSurfPred$start & netSurfPred$n <= netSurfPred$end] = 1
    netSurfPred = netSurfPred %>% group_by(Abbreviation, ID, n, seq) %>%
      summarize(Prediction = sum(Prediction))
    return(ungroup(netSurfPred))
}
```

```
betaTurnFinder <- function(){
  # A function to predict beta turn PBRs based on netSurfP output.
  ## A special instance of the ARGrichFinder that ignores minimum RK ratio. Minimum number of
  ## basic residues is determined by 'turnMin' rather than 'RKmin', and histidines are added to
  ## accepted basic residues.
  ## Both RKratioMin and RKmin are set to unattainably high values to preclude the identification of
  ## other ARG-rich regions.
  ## turnClause = T: only ARG-rich regions on beta turns considered
  ## turnMin = 2: at least 2 basic residues must occur on a given region
  ## gapMax: maximum distance between consecutive basic residues
  ## AAaccepted: arginine, lysine and histidine are all counted as basic residues
  output = ARGrichFinder(1.2, gapMax = 4, RKmin = 999, turnMin = 2,
                         turnClause = T, AAaccepted = c("R", "K", "H"))
  return(output)
}
```

```
# Supporting function for betaSheetFinder
netBasic <- function(AAvec, posVec = c('R', 'H', 'K'), negVec = c('C', 'D', 'E', 'Y')){
  ### Identifies the number of net positive (basic) or negative (acidic) ionizable amino acids
  # within a polypeptide sequence (vector input ‘AAvec’)
  AAs <- table(AAvec)
  netPos = sum(AAs[names(AAs) %in% posVec])-sum(AAs[names(AAs) %in% negVec])
  return(netPos)
}
```

```
betaSheetFinder <- function(chargeMin = 0, netSurfDF = netSurf, maxDistance = 1, minLength = 12,
                       posVec = c('R', 'K','H'), negVec = c('C', 'D', 'E'), q8allowed = c("E")){
  ## function that identifies and returns beta sheet PBRs. chargeMin is the minimum
  # (positive) net charge to consider the region basic. maxDistance is the distance allowed
  # between AAs to consider part of the same sheet (maxDistance = 1 implies no gaps). minLength
  # is the minimum length of betasheets to be considered.
  require(dplyr)
```

```
  betas = netSurfDF[netSurfDF$q8 %in% q8allowed, ]
  betas$regionID = cumsum(c(1, abs(diff(betas$n)) > maxDistance))

  betaCharges = as.data.frame(betas %>% group_by(regionID) %>% summarize(netC = netBasic(seq, posVec, negVec), len = n()))
  betaCharges = ungroup(betaCharges)
  basicCharges = filter(betaCharges, netC >= chargeMin & len >= minLength)

  basicBetas = filter(betas, regionID %in% basicCharges$regionID)
  netSurfPred = left_join(netSurfDF, basicBetas)
  netSurfPred$Prediction = !(is.na(netSurfPred$regionID))
  return(netSurfPred)
}


disTermFinder <- function(disorderMin = 0.66, netSurfDF= netSurf){
  # Function to identify disordered C- and N-termini PBRs based on netSurfP output
  require(dplyr)
  randos = netSurfDF[netSurfDF$disorder > disorderMin, ]
  netSurfSumm = netSurfDF %>% group_by(Abbreviation, ID) %>% summarize(len = n())
  randos$regionID = cumsum(c(1, abs(diff(randos$n)) > 1))

  randos = as.data.frame(left_join(randos, netSurfSumm, by = c("Abbreviation", "ID")))

  #N-termini include residue 1
  Nterms = as.data.frame(randos %>% group_by(regionID) %>% filter(1 %in% n))
  #C-termini include the final residue
  Cterms = as.data.frame(randos %>% group_by(regionID) %>% filter(0 %in% (n - len)))
  randTerms = distinct(rbind(ungroup(Nterms), ungroup(Cterms)))
  netSurfPred = left_join(netSurfDF, randTerms)
  netSurfPred$Prediction = !(is.na(netSurfPred$regionID))
  return(netSurfPred)
}
```

```
predJoin <- function(fOutput1, fOutput2){
  # Function to merge 2 predictions (just define Prediction as A OR B)
  predJ = left_join(fOutput1, fOutput2, by = c("Abbreviation", "ID", "n", "seq"))
  predJ$Prediction = predJ$Prediction.x | predJ$Prediction.y
  predJ$Prediction.x = NULL
  predJ$Prediction.y = NULL
  return(predJ)
}
```

References

1. Michen B, Graule T. 2010. Isoelectric points of viruses. J Appl Microbiol 109:388–397.
2. Salo RJ, Mayor HD. 1978. Isoelectric Focusing of Parvoviruses. Intervirology 10:87–93.
3. Petrzik K. 1993. Physicochemical properties of four tymoviruses. Acta Virol 37:271–275.
4. Rubio V, Salas M, Viñuela E. 1974. Biophysical properties of bacteriophage phi29. Virology 57:112–121.
5. Suci PA, Klem MT, Douglas T, Young M. 2005. Influence of electrostatic interactions on the surface adsorption of a viral protein cage. Langmuir 21:8686–8693.
6. van Regenmortel MHV. 1967. Biochemical and biophysical properties of cucumber mosaic virus. Virology 31:391–396.
7. Weichert WS, Parker JSL, Wahid ATM, Chang SF, Meier E, Parrish CR. 1998. Assaying for structural variation in the parvovirus capsid and its role in infection. Virology 250:106–117.
8. Beard JW, Wykoff RWG. 1938. The pH stability of papilloma virus protein. J Biol Chem 123:461–470.
9. Murray JP, Parks GA. 1980. Poliovirus adsorption on oxide surfaces, p. 97–133. *In* Kavanaugh, MC, Leckie, JO (eds.), Particulates in Water. American Chemical Society.
10. Butler M, Medlen AR, Taylor GR. 1985. Electrofocusing of viruses and sensitivity to disinfection. Water Sci Technol 17:201–210.
11. Armanious A, Aeppli M, Jacak R, Refardt D, Sigstam T, Kohn T, Sander M. 2015. Viruses at Solid-Water Interfaces: A Systematic Assessment of Interactions Driving Adsorption. Environ Sci Technol 50:732–743.

12. Langlet J, Gaboriaud F, Duval JFL, Gantzer C. 2008. Aggregation and surface properties of F-specific RNA phages: Implication for membrane filtration processes. Water Res 42:2769–2777.

13. Dika C, Duval JFL, Ly-Chatain HM, Merlin C, Gantzer C. 2011. Impact of internal RNA on aggregation and electrokinetics of viruses: Comparison between MS2 phage and corresponding virus-like particles. Appl Environ Microbiol 77:4939–4948.

14. Overby LR, Barlow GH, Doi RH, Jacob M, Spiegelman S. 1966. Comparison of two serologically distinct ribonucleic acid bacteriophages. II. Properties of the nucleic acids and coat proteins. J Bacteriol 92:739–745.

15. Redman JA, Grant SB, Olson TM, Hardy ME, Estes MK. 1997. Filtration of recombinant norwalk virus particles and bacteriophage MS2 in quartz sand: Importance of electrostatic interactions. Environ Sci Technol 31:3378–3383.

16. Yuan B, Pham M, Nguyen TH. 2008. Deposition kinetics of bacteriophage MS2 on a silica surface coated with natural organic matter in a radial stagnation point flow cell. Environ Sci Technol 42:7628–7633.

17. Zerda KS, Gerba CP. 1984. Agraose isoelectrofocusing of intact virions. J Virol Methods 9:1–6.

18. Trilisky EI, Lenhoff AM. 2007. Sorption processes in ion-exchange chromatography of viruses. J Chromatogr A 1142:2–12.

19. Nasser AM, Battagelli D, Sobsey MD. 1992. Isoelectric focusing of hepatitis A virus in sucrose gradients. Isr J Med Sci 28:73.

20. Korant BD, Lonberg-Holm K, Yin FH, Noble-Harvey J. 1975. Fractionation of biologically active and inactive populations of human rhinovirus type 2. Virology 63:384–394.

21. Schnabel U, Groiss F, Blaas D, Kenndler E. 1996. Determination of the pI of Human Rhinovirus Serotype 2 by Capillary Isoelectric Focusing. Anal Chem 68:4300–4303.

22. Chlumecka V, D'Obrenan P, Colter JS. 1973. Electrophoretic studies of three variants of Mengo Encephalomyelitis Virus. Can J Biochem 51:1521–1526.

23. Goodridge L, Goodridge C, Wu J, Griffiths M, Pawliszyn J. 2004. Isoelectric Point Determination of Norovirus Virus-like Particles by Capillary Isoelectric Focusing with Whole Column Imaging Detection. Anal Chem 76:48–52.

24. Aach VHG. 1963. Elektrophoretische Untersuchungen an Mutanten des Phagen PhiX174 290–293.

25. Brorson K, Shen H, Lute S, Pérez JS, Frey DD. 2008. Characterization and purification of bacteriophages using chromatofocusing. J Chromatogr A 1207:110–121.

26. Horká M, Kubíček O, Růžička F, Holá V, Malinovská I, Šlais K. 2007. Capillary isoelectric focusing of native and inactivated microorganisms. J Chromatogr A 1155:164–171.

27. Sinsheimer RL. 1959. Purification and properties of bacteriophage φX174. J Mol Biol 1:37–42.

28. Schäfer R, Hinnen R, Franklin RM. 1974. Structure and Synthesis of a Lipid-Containing Bacteriophage: Properties of the Structural Proteins and Distribution of the Phospholipid. Eur J Biochem 50:15–27.

29. Brioen P, Thomas AAM, Boeye A. 1985. Lack of quantitative correlation between the neutralization of poliovirus and the antibody-mediated pI shift of the virions. J Gen Virol 66:609–613.

30. La Colla P, Marcialis MA, Merreu GP, Loddo B. 1972. Behaviour of a guanidine-dependent strain of poliovirus 1 in sucrose density and pH gradients. Experientia 28:1115–1117.

31. Mandel B. 1971. Characterization of type 1 poliovirus by electrophoretic analysis. Virology 44:554–568.

32. Ward RL. 1978. Mechanism of poliovirus inactivation by ammonia. J Virol 26:299–305.

33. Floyd R, Sharp DG. 1979. Viral aggregation: Buffer effects in the aggregation of poliovirus and reovirus at low and high pH. Appl Environ Microbiol 38:395–401.

34. Gallo J, Musil M. 1984. Isoelectric points of red clover necrotic mosaic virus serotypes. Acta Virol 28:82—83.

35. Taylor DH, Bosmann HB. 1981. Measurement of the electrokinetic properties of vaccinia and reovirus by laser-illuminated whole-particle microelectrophoresis. J Virol Methods 2:251–260.

36. Taylor DH, Bosmann HB. 1981. The electrokinetic properties of reovirus type 3: electrophoretic mobility and zeta potential in dilute electrolytes. J Colloid Interface Sci 83:153–162.

37. Magdoff-Fairchild BS. 1967. Electrophoretic and bouyant density variants of southern bean mosaic virus. Virology 31:142–153.

38. Honetslegrová J, Petrzik K, Spak J, Pelikánová J. 1994. Comparison of the Czech Scrophularia isolate with the Italian Anagyris strain of scrophularia mottle virus. Acta Virol 38:21—24.

39. Oster G. 1951. The isoelectric points of some strains of tobacco mosaic virus. J Biol Chem 190:55–59.

40. The UniProt Consortium. 2019. UniProt: a worldwide hub of protein knowledge. Nucleic Acids Res 47:D506-515.

41. Grieger JC, Snowdy S, Samulski RJ. 2006. Separate Basic Region Motifs within the Adeno-Associated Virus Capsid Proteins Are Essential for Infectivity and Assembly. J Virol 80:5199–5210.

42. Chiorini JA, Yang L, Liu Y, Safer B, Kotin RM. 1997. Cloning of adeno-associated virus type 4 (AAV4) and generation of recombinant AAV4 particles. J Virol 71:6823–6833.

43. Suryanarayana S, Rao NA, Murthy MRN, Savithrin HS. 1989. Primary Structure of Belladonna Mottle Virus Coat Protein. J Biol Chem 264:6273–6279.

44. Vlček Č, Pačes V. 1986. Nucleotide sequence of the late region of Bacillus phage φ29 completes the 19285-bp sequence of φ29 genome. Comparison with the homologous sequence of phage PZA. Gene 46:215–225.

45. Hirofumi Y, Ito J. 1982. Nucleotide sequence of the major early region of bacteriophage φ29. Gene 17:323–335.

46. Escarnís C, Salas M. 1982. Nucleotide sequence of the early genes 3 and 4 of bacteriophage ø29. Nucleic Acids Res 10:5785–5798.

47. García JA, Méndez E, Salas M. 1984. Cloning, nucleotide sequence and high level expression of the gene coding for the connector protein of Bacillus subtilis phage φ 29. Gene 30:87–98.

48. Xiao F, Moll WD, Guo S, Guo P. 2005. Binding of pRNA to the N-terminal 14 amino acids of connector protein of bacteriophage phi29. Nucleic Acids Res 33:2640–2649.

49. Innis CA, Garvey KJ, Ito J. 1986. Nucleotide sequence of phage ø29 gene 7: structure of intergenic spacer between the major early and late genes. Nucleic Acids Res 14:7129.

50. Xiang Y, Morais MC, Cohen DN, Bowman VD, Anderson DL, Rossmann MG. 2008. Crystal and cryoEM structural studies of a cell wall degrading enzyme in the bacteriophage φ29 tail. Proc Natl Acad Sci U S A 105:9552–9557.

51. Garvey KJ, Saedi MS, Ito J. 1986. Nucleotide sequence of Bacillus phage Ø29 genes 14 and 15: homology of gene 15 with other phage lysozymes. Nucleic Acids Res 14:10001–10008.

52. Annamalai P, Apte S, Wilkens S, Rao ALN. 2005. Deletion of Highly Conserved Arginine-Rich RNA Binding Motif in Cowpea Chlorotic Mottle Virus Capsid Protein Results in Virion Structural Alterations and RNA Packaging Constraints. J Virol 79:3277–3288.

53. Dasgupta R, Kaesberg P. 1982. Complete nucleotide sequences of the coat protein messenger RNAs of brome mosaic virus and cowpea chlorotic mottle virus. Nucleic Acids Res 10:703–713.

54. Allison RF, Janda M, Ahlquist P. 1989. Sequence of cowpea chlorotic mottle virus RNAs 2 and 3 and evidence of a recombination event during bromovirus evolution. Virology 172:321–330.

55. Owen J, Shintaku M, Aeschleman P, Ben Tahar S, Palukaitis P. 1990. Nucleotide sequence and evolutionary relationships of cucumber mosaic virus (CMV) strains: CMV RNA 3. J Gen Virol 71:2243–2249.

56. Simpson AA, Chandrasekar V, Hébert B, Sullivan GM, Rossmann MG, Parrish CR. 2000. Host range and variability of calcium binding by surface loops in the capsids of canine and feline parvoviruses. J Mol Biol 300:597–610.

57. Parrish CR, Aquadro CF, Carmichael LE. 1988. Canine host range and a specific epitope map along with variant sequences in the capsid protein gene of canine parvovirus and related feline, mink, and raccoon parvoviruses. Virology 166:293–307.

58. Horiuchi M, Goto H, Ishiguro N, Shinagawa M. 1994. Mapping of determinants of the host range for canine cells in the genome of canine parvovirus using canine parvovirus/mink enteritis virus chimeric viruses. J Gen Virol 75:1319–1328.

59. Schäfer F, Florin L, Sapp M. 2002. DNA binding of L1 is required for human papillomavirus morphogenesis in vivo. Virology 295:172–181.

60. Giri I, Danos O, Yaniv M. 1985. Genomic structure of the cottontail rabbit (Shope) papillomavirus. Proc Natl Acad Sci U S A 82:1580–1584.

61. Wang JW, Roden RBS. 2013. L2, the minor capsid protein of papillomavirus. Virology 445:175–186.

62. Hughest PJ, North C, Minor PD, Stanway G. 1989. The complete nucleotide sequence of coxsackievirus A21. J Gen Virol 70:2943–2952.

63. Zhang G, Wilsden LG, Knowles LNJ, McCauley JW. 1993. Complete nucleotide sequence of a coxsackie B5 virus and its relationship to swine vesicular disease virus. J Gen Virol 74:845–853.

64. Adhin MR, Avots A, Berzin V, Overbeek GP, van Duin J. 1990. Complete nucleotide sequence of the group I RNA bacteriophage fr. Biochim Biophys Acta - Gene Struct Expr 1050:104–109.

65. Berzin V, Avots A, Jansone I, Gintnere L, Tsimanis A. 1987. Sequence of the genes coding for the A-protein and coat protein of bacteriophage fr. Nucleic Acids Res 15:6741.

66. Berzin VM, Avots AI, Iansone I V, Tsimanis AI. 1986. Primary structure of a fragment of cDNA from phage fr. Bioorg Khim 12:149–152.

67. Wittmann-Liebold B, Wittmann HG. 1967. Coat proteins of strains of two RNA viruses: Comparison of their amino acid sequences. Mol

Gen Genet MGG 100:358–363.

68. INOKUCHI Y, TAKAHASHI R, HIROSE T, INAYAMA S, JACOBSON AB, HIRASHIMA A. 1986. The Complete Nucleotide Sequence of the Group II RNA Coliphage GA1. J Biochem 99:1169–1180.

69. Rolfsson Ó, Middleton S, Manfield IW, White SJ, Fan B, Vaughan R, Ranson NA, Dykeman E, Twarock R, Ford J, Cheng Kao C, Stockley PG. 2016. Direct Evidence for Packaging Signal-Mediated Assembly of Bacteriophage MS2. J Mol Biol 428:431–448.

70. Shiba T, Suzuki Y. 1981. Localization of A protein in the RNA-A protein complex of RNA phage MS2. Biochim Biophys Acta - Nucleic Acids Protein Synth 654:249–255.

71. Vandekerckhove JS, Fiers W, Jou M, Volckaert A, Jou M. 1977. Sequence of the A-Protein of Coliphage sequence of the corresponding. J Biol Chem 252:7773–7782.

72. Fiers W, Contreras R, Duerinck F, Haegmean G, Merregaert J, Jou WM, Raeymakers A, Volckaert G, Ysebaert M, Van de Kerckhove J, Nolf F, Van Montagu M. 1975. A-Protein gene of bacteriophage MS2. Nature 256:273–278.

73. Spingola M, Peabody DS. 1997. MS2 coat protein mutants which bind Qβ RNA. Nucleic Acids Res 25:2808–2815.

74. Jou WMIN, Haegeman G, Ysebaert M, Fiers W. 1972. Nucleotide Sequence of the Gene Coding for the Bacteriophage MS2 Coat Protein. Nature 237:82–88.

75. Inokuchi Y, Jacobson AB, Hirose T, Inayama S, Hirashima A. 1988. Analysis of the complete nucleotide sequence of the group IV RNA coliphage SP. Nucleic Acids Res 16:6205–6221.

76. Rumnieks J, Tars K. 2014. Crystal structure of the bacteriophage qβ coat protein in complex with the rna operator of the replicase gene. J Mol Biol 426:1039–1049.

77. Lim F, Spingola M, Peabody DS. 1996. The RNA-binding site of bacteriophage Qβ coat protein. J Biol Chem 271:31839–31845.

78. Maita T, Konigsberg W. 1971. The amino acid sequence of the Qbeta coat protein. J Biol Chem 246:5003–5024.

79. Horn WT, Tars K, Grahn E, Helgstrand C, Baron AJ, Lago H, Adams CJ, Peabody DS, Phillips SE V, Stonehouse NJ, Liljas L, Stockley PG. 2006. Structural Basis of RNA Binding Discrimination between Bacteriophages Qbeta and MS2. Structure 14:487–495.

80. Kozlovska TM, Cielēns I, Dreilinņa D, Dišlers A, Baumanis V, Ose V, Pumpēns P. 1993. Recombinant rna phage qβ capsid particles synthesized and self-assembled in escherichia coli. Gene 137:133–137.

81. Bacher JM, Bull JJ, Ellington AD. 2003. Evolution of phage with chemically ambiguous proteomes. BMC Evol Biol 12:1–12.

82. Friedman SD, Genthner FJ, Gentry J, Sobsey MD, Vinje J, Irol J V. 2009. Gene Mapping and Phylogenetic Analysis of the Complete Genome from 30 Single-Stranded RNA Male-Specific Coliphages (Family Leviviridae) □. J Virol 83:11233–11243.

83. Domingo-Calap P, Cuevas M, Sanjua R. 2009. The Fitness Effects of Random Mutations in Single-Stranded DNA and RNA Bacteriophages. PLoS Genet 5:e1000742.

84. Huttunen P, Santti J, Pulli T, Hyypia T. 1996. The major echovirus group is genetically coherent and related to coxsackie B viruses. J Gen Virol 77:715–725.

85. Oberste MS, Maher K, Kilpatrick DR, Pallansch MA. 1999. Molecular evolution of the human enteroviruses: correlation of serotype with VP1 sequence and application to picornavirus classification. J Virol 73:1941–1948.

86. Srifah P, Keese P, Weiller G, Gibbs A. 1992. Comparisons of the genomic sequences of erysimum latent virus and other tymoviruses : a search for the molecular basis of their host specificities. J Gen Virol 73:1437–1447.

87. Srifah P, Keese P, Shukla D, Gibbs A. 1990. The primary structure of the virion protein gene and encoded protein of erysimum latent tymovirus. J Gen Virol 71:3085–3088.

88. Evans VC, Barker G, Heesom KJ, Fan J, Bessant C, Matthews DA. 2012. De novo derivation of proteomes from transcriptomes for transcript and protein identification. Nat Methods 9:1207–1211.

89. Chroboczek J, Bieber F, Jacrot B. 1992. The sequence of the genome of adenovirus type 5 and its comparison with the genome of adenovirus type 2. Virology 186:280–285.

90. van Beveren CP, Maat J, Dekker BMM, van Ormondt H. 1981. The nucleotide sequence of the gene for protein IVa2 and of the 5' leader segment of the major late mRNAs of adenovirus type 5. Gene 16:179–189.

91. Russell WC, Precious B. 1982. Nucleic Acid-binding Properties of Adenovirus Structural Polypeptides. J Gen Virol 63:69–79.

92. Kinloch R, Mackay N, Mautner V. 1984. Adenovirus hexon. Sequence comparison of subgroup C serotypes 2 and 5. J Biol Chem 259:6431–6436.

93. Chroboczek J, Jacrot B. 1987. The sequence of adenovirus fiber: Similarities and differences between serotypes 2 and 5. Virology 161:549–554.

94. Neumann R, Chroboczek J, Jacrot B. 1988. Determination of the nucleotide sequence for the penton-base gene of human adenovirus type 5. Gene 69:153–157.

95. Cohen JI, Rosenblum B, Ticehurst JR, Daemer RJ, Feinstone SM, Purcell RH. 1987. Complete nucleotide sequence of an attenuated hepatitis A virus: comparison with wild-type virus. Proc Natl Acad Sci 84:2497 LP – 2501.

96. Cohen JI, Ticehurst JR, Purcell RH, Buckler-White A, Baroudy BM. 1987. Complete nucleotide sequence of wild-type hepatitis A virus: comparison with different strains of hepatitis A virus and other picornaviruses. J Virol 61:50–59.

97. Lemon SM, Murphy PC, Shields PA, Ping LH, Feinstone SM, Cromeans T, Jansen RW. 1991. Antigenic and genetic variation in cytopathic hepatitis A virus variants arising during persistent infection: evidence for genetic recombination. J Virol 65:2056–2065.

98. Skern T, Sommergruber W, Blaas D, Gruendler P, Fraundorfer F, Pieler C, Fogy I, Kuechler E. 1985. Human rhinovirus 2: complete nucleotide sequence and proteolytic processing signals in the capsid protein region. Nucleic Acids Res 13:2111–2126.

99. Fata-Hartley CL, Palmenberg AC. 2005. Dipyridamole Reversibly Inhibits Mengovirus RNA Replication. J Virol 79:11062 LP – 11070.

100. Krishnaswamy S, Rossmann MG. 1990. Structural refinement and analysis of Mengo virus. J Mol Biol 211:803–844.

101. Hardy ME, Estes MK. 1996. Completion of the Norwalk virus genome sequence. Virus Genes 12:287–290.

102. Jiang X, Wang M, Wang K, Estes MK. 1993. Sequence and Genomic Organization of Norwalk Virus. Virology 195:51–61.

103. Sanger F, Air GM, Barrell BG, Brown NL, Coulson AR, Fiddes JC, Hutchison CA, Slocombe PM, Smith M. 1977. Nucleotide sequence of bacteriophage φX174 DNA. Nature 265:687–695.

104. Sanger F, Coulson AR, Friedmann T, Air GM, Barrell BG, Brown NL, Fiddes JC, Hutchison CA, Slocombe PM, Smith M. 1978. The nucleotide sequence of bacteriophage φX174. J Mol Biol 125:225–246.

105. Air GM, Coulson AR, Fiddes JC, Friedmann T, Hutchison CA, Sanger F, Slocombe PM, Smith AJH. 1978. Nucleotide sequence of the F protein coding region of bacteriophage φX174 and the amino acid sequence of its product. J Mol Biol 125:247–254.

106. Air GM. 1976. Amino acid sequences from the gene F(Capsid) protein of bacteriophage φX174. J Mol Biol 107:433–443.

107. Air GM, Sanger F, Coulson AR. 1976. Nucleotide and amino acid sequences of gene G of φX174. J Mol Biol 108:519–533.

108. Air GM, Blackburn EH, Sanger F, Coulson AR. 1975. The nucleotide and amino acid sequences of the N (5′) terminal region of gene G of

bacteriophage φX174. J Mol Biol 96:703–719.

109. Bernal RA, Hafenstein S, Esmeralda R, Fane BA, Rossmann MG. 2004. The φX174 protein J mediates DNA packaging and viral attachment to host cells. J Mol Biol 337:1109–1122.

110. Freymeyer DK, Shank PR, Edgell MH, Hutchison CA, Vanaman TC. 1977. Amino acid sequence of the small core protein from bacteriophage φX174. Biochemistry 16:4550–4556.

111. HINNEN R, CHASSIN R, SCHAFER R, FRANKLIN RM, HITZ H, SCHAFER D. 1976. Structure and Synthesis of a Lipid-Containing Bacteriophage. Eur J Biochem 68:139–152.

112. Kivelä HM, Männistö RH, Kalkkinen N, Bamford DH. 1999. Purification and protein composition of PM2, the first lipid-containing bacterial virus to be isolated. Virology 262:364–374.

113. Männistö RH, Kivelä HM, Paulin L, Bamford DH, Bamford JKH. 1999. The Complete Genome Sequence of PM2, the First Lipid-Containing Bacterial Virus To Be Isolated. Virology 262:355–363.

114. Marcoli R, Pirrotta V, Franklin RM. 1979. Interaction Between Bacteriophage PM2 Protein IV and DNA. J Mol Biol 131:107–131.

115. Miller FD, Winkfein RJ, Rattner JB, Van de Sande JH. 1984. Sequence analysis of a PM2-DNA anti-Z-IgG-binding region. Biosci Rep 4:885–895.

116. Abrescia NGA, Grimes JM, Kivelä HM, Assenberg R, Sutton GC, Butcher SJ, Bamford JKH, Bamford DH, Stuart DI. 2008. Insights into virus evolution and membrane biogenesis from the structure of the marine lipid-containing bacteriophage PM2. Mol Cell 31:749–761.

117. Racaniello VR, Baltimore D. 1981. Molecular cloning of poliovirus cDNA and determination of the complete nucleotide sequence of the viral genome. Proc Natl Acad Sci 78:4887 LP – 4891.

118. Kitamura N, Semler BL, Rothberg PG, Larsen GR, Adler CJ, Dorner AJ, Emini EA, Hanecak R, Lee JJ, van der Werf S, Anderson CW, Wimmer E. 1981. Primary structure, gene organization and polypeptide expression of poliovirus RNA. Nature 291:547–553.

119. Kitamura N, Adler CJ, Rothberg PG, Martinko J, Nathenson SG, Wimmer E. 1980. The genome-linked protein of picornaviruses. VII. Genetic mapping of poliovirus VPg by protein and RNA sequence studies. Cell 21:295–302.

120. Ansardi DC, Luo M, Morrow CD. 1994. Mutations in the poliovirus P1 capsid precursor at arginine residues VP4-ARG34, VP3-ARG223, and VP1-ARG129 affect virus assembly and encapsidation of genomic RNA. Virology 199:20–34.

121. Saren A-M, Ravantti JJ, Benson SD, Burnett RM, Paulin L, Bamford DH, Bamford JKH. 2005. A Snapshot of Viral Evolution from Genome Analysis of the Tectiviridae Family. J Mol Biol 350:427–440.

122. Savilahti H, Bamford DH. 1987. The complete nucleotide sequence of the left very early region of Escherichia coli bacteriophage PRD1 coding for the terminal protein and the DNA polymerase. Gene 57:121–130.

123. Hsieh J-C, Jung G, Leavitt MC, Ito J. 1987. Primary structure of the DNA terminal protein of bacteriophage PRD1. Nucleic Acids Res 15:8999–9009.

124. Bamford JKH, Hänninen A-L, Pakula TM, Ojala PM, Kalkkinen N, Frilander M, Bamford DH. 1991. Genome organization of membrane-containing bacteriophage PRD1. Virology 183:658–676.

125. Pakula TM, Savilahti H, Bamford DH. 1989. Comparison of the amino acid sequence of the lytic enzyme from broad-host-range bacteriophage PRDl with sequences of other cell-wall-peptidoglycan lytic enzymes. Eur J Biochem 180:149–152.

126. Hong C, Oksanen HM, Liu X, Jakana J, Bamford DH, Chiu W. 2014. A Structural Model of the Genome Packaging Process in a Membrane-Containing Double Stranded DNA Virus. PLoS Biol 12.

127. Bamford JKH, Bamford DH. 1990. Capsomer proteins of bacteriophage PRD1, a bacterial virus with a membrane. Virology 177:445–451.

128. Caldentey J, Tuma R, Bamford DH. 2000. Assembly of bacteriophage PRD1 spike complex: Role of the multidomain protein P5. Biochemistry 39:10566–10573.

129. Park S-H, Sit TL, Kim K-H, Lommel SA. 2013. The red clover necrotic mosaic virus capsid protein N-terminal amino acids possess specific RNA binding activity and are required for stable virion assembly. Virus Res 176:107–118.

130. Park SH, Sit TL, Kim KH, Lommel SA. 2012. The Red clover necrotic mosaic virus capsid protein N-terminal lysine-rich motif is a determinant of symptomatology and virion accumulation. Mol Plant Pathol 13:744–754.

131. Xiong Z, Lommel SA. 1989. The complete nucleotide sequence and genome organization of red clover necrotic mosaic virus RNA-1. Virology 171:543–554.

132. Reinisch KM, Nibert ML, Harrison SC. 2000. Structure of the reovirus core at 3.6 Å resolution. Nature 404:960–967.

133. Liemann S, Chandran K, Baker TS, Nibert ML, Harrison SC. 2002. Structure of the reovirus membrane-penetration protein, μ1, in a complex with its protector protein, σ3. Cell 108:283–295.

134. Kobayashi T, Antar AAR, Boehme KW, Danthi P, Eby EA, Guglielmi KM, Holm GH, Johnson EM, Maginnis MS, Naik S, Skelton WB, Wetzel JD, Wilson GJ, Chappell JD, Dermody TS. 2007. A Plasmid-Based Reverse Genetics System for Animal Double-Stranded RNA Viruses. Cell Host Microbe 1:147–157.

135. Dermody TS, Schiff LA, Nibert ML, Coombs KM, Fields BN. 1991. The S2 gene nucleotide sequences of prototype strains of the three reovirus serotypes: characterization of reovirus core protein sigma 2. J Virol 65:5721–5731.

136. Cashdollar LW, Esparza J, Hudson GR, Chmelo R, Lee PW, Joklik WK. 1982. Cloning the double-stranded RNA genes of reovirus: sequence of the cloned S2 gene. Proc Natl Acad Sci 79:7644 LP – 7648.

137. Wiener JR, McLaughlin T, Joklik WK. 1989. The sequences of the S2 genome segments of reovirus serotype 3 and of the dsRNA-negative mutant ts447. Virology 170:340–341.

138. Ebert DH, Wetzel JD, Brumbaugh DE, Chance SR, Stobie LE, Baer GS, Dermody TS. 2001. Adaptation of Reovirus to Growth in the Presence of Protease Inhibitor E64 Segregates with a Mutation in the Carboxy Terminus of Viral Outer-Capsid Protein ς3. J Virol 75:3197 LP – 3206.

139. Giantini M, Seliger LS, Furuichi Y, Shatkin AJ. 1984. Reovirus type 3 genome segment S4: nucleotide sequence of the gene encoding a major virion surface protein. J Virol 52:984–987.

140. Duncan R, Horne D, William Cashdollar L, Joklik WK, Lee PWK. 1990. Identification of conserved domains in the cell attachment proteins of the three serotypes of reovirus. Virology 174:399–409.

141. Bassel-Duby R, Jayasuriya A, Chatterjee D, Sonenberg N, Maizel J V, Fields BN. 1985. Sequence of reovirus haemagglutinin predicts a coiled-coil structure. Nature 315:421–423.

142. Nagata L, Masri SA, Mah DCW, Lee PWK. 1984. Molecular cloning and sequencing of the reovirus (serotype 3) S1 gene which encodes the viral ceil attachment protein σ1. Nucleic Acids Res 12:8699–8710.

143. Cashdollar LW, Chmelo RA, Wiener JR, Joklik WK. 1985. Sequences of the S1 genes of the three serotypes of reovirus. Proc Natl Acad Sci 82:24 LP – 28.

144. Wiener JR, Joklik WK. 1989. The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis of the mode of divergence of the reovirus serotypes. Virology 169:194–203.

145. Jayasuriya AK, Nibert ML, Fields BN. 1988. Complete nucleotide sequence of the M2 gene segment of reovirus type 3 dearing and analysis of its protein product μ1. Virology 163:591–602.

146. Tarlow O, McCorquodale JG, McCrae MA. 1988. Molecular cloning and sequencing of the gene (M2) encoding the major virion structural protein (μ1-μ1C) of serotypes 1 and 3 of mammalian reovirus. Virology 164:141–146.

147. Luongo CL, Reinisch KM, Harrison SC, Nibert ML. 2000. Identification of the guanylyltransferase region and active site in reovirus mRNA capping protein lambda2. J Biol Chem 275:2804–2810.

148. Seliger LS, Zheng K, Shatkin AJ. 1987. Complete nucleotide sequence of reovirus L2 gene and deduced amino acid sequence of viral mRNA guanylyltransferase. J Biol Chem 262:16289–16293.

149. Wiener JR, Bartlett JA, Joklik WK. 1989. The sequences of reovirus serotype 3 genome segments M1 and M3 encoding the minor protein μ2 and the major nonstructural protein μNS, respectively. Virology 169:293–304.

150. Parker JSL, Broering TJ, Kim J, Higgins DE, Nibert ML. 2002. Reovirus Core Protein μ2 Determines the Filamentous Morphology of Viral Inclusion Bodies by Interacting with and Stabilizing Microtubules. J Virol 76:4483 LP – 4496.

151. Yin P, Keirstead ND, Broering TJ, Arnold MM, Parker JSL, Nibert ML, Coombs KM. 2004. Comparisons of the M1 genome segments and encoded mu2 proteins of different reovirus isolates. Virol J 1:6.

152. Bartlett JA, Joklik WK. 1988. The sequence of the reovirus serotype 3 L3 genome segment which encodes the major core protein lambda 1. Virology 167:31–37.

153. Harrison SJ, Farsetta DL, Kim J, Noble S, Broering TJ, Nibert ML. 1999. Mammalian reovirus L3 gene sequences and evidence for a distinct amino-terminal region of the lambda1 protein. Virology 258:54–64.

154. Lee L, Anderson EJ. 1998. Nucleotide sequence of a resistance breaking mutant of southern bean mosaic virus. Arch Virol 143:2189–2201.

155. Koenig R, Pleij CWA, Lesemann D-E, Loss S, Vetten HJ. 2005. Molecular characterization of isolates of anagyris vein yellowing virus, plantago mottle virus and scrophularia mottle virus -- comparison of various approaches for tymovirus classification. Arch Virol 150:2325–2338.

156. Small C, Barro M, Brown TL, Patton JT. 2007. Genome heterogeneity of SA11 rotavirus due to reassortment with “O” agent. Virology 359:415–424.

157. Patton JT, Jones MT, Kalbach AN, He YW, Xiaobo J. 1997. Rotavirus RNA polymerase requires the core shell protein to synthesize the double-stranded RNA genome. J Virol 71:9618–9626.

158. Nozu Y, Ono T, Okada Y. 1970. Amino acid sequences of some common Japanese strains of tobacco mosaic virus. J Biochem 68:39–52.

159. Guilley H, Jonard G, Kukla B, Richards KE. 1979. Sequence of 1000 nucleotides at the 3′ end of tobacco mosaic virus RNA. Nucleic Acids Res 6:1287–1308.

160. FUNATSU G, TSUGITA A, FRAENKEL-CONRAT H. 1964. STUDIES ON THE AMINO ACID SEQUENCE OF TOBACCO MOSAIC VIRUS PROTEIN. V. AMINO ACID SEQUENCES OF TWO PEPTIDES FROM TRYPTIC DIGESTS AND LOCATION OF AMIDE GROUP. Arch Biochem Biophys 105:25–41.

161. Anderer FA, Wittmann-Liebold B, Wittmann HG. 1965. [Further studies on amino acid sequence of proteins in tobacco mosaic virus]. Zeitschrift fur Naturforschung Tl B, Chemie, Biochem Biophys Biol und verwandte Gebiete 20:1203–1213.

162. Tsugita A, Gish DT, Young J, Fraenkel-Conrat H, Knight CA, Stanley WM. 1960. THE COMPLETE AMINO ACID SEQUENCE OF THE PROTEIN OF TOBACCO MOSAIC VIRUS. Proc Natl Acad Sci U S A 46:1463–1469.

163. Goelet P, Lomonossoff GP, Butler PJ, Akam ME, Gait MJ, Karn J. 1982. Nucleotide sequence of tobacco mosaic virus RNA. Proc Natl Acad Sci 79:5818 LP – 5822.

164. Bink HHJ, Roepan SK, Pleij CWA. 2004. Two histidines of the coat protein of turnip yellow mosaic virus at the capsid interior are crucial for viability. Proteins Struct Funct Bioinforma 55:236–244.

165. Ehresmann B, Briand J -P, Reinbolt J, Witz J. 1980. Identification of Binding Sites of Turnip Yellow Mosaic Virus Protein and RNA by Crosslinks Induced in situ. Eur J Biochem 108:123–129.

166. Guilley H, Briand JP. 1978. Nucleotide sequence of turnip yellow mosaic virus coat protein mRNA. Cell 15:113–122.

167. Briand JP, Jonard G, Guilley H, Richards K, Hirth L. 1977. Nucleotide sequence (n=159) of the amino-acid-accepting 3’-OH extremity of turnip-yellow-mosaic-virus RNA and the last portion of its coat-protein cistron. Eur J Biochem 72:453–463.

168. Silberklang M, Prochiantz A, Haenni AL, Rajbhandary UL. 1977. Studies on the sequence of the 3’-terminal region of turnip-yellow-mosaic-virus RNA. Eur J Biochem 72:465–478.

169. Dreher TW, Bransom KL. 1992. Genomic RNA sequence of turnip yellow mosaic virus isolate TYMC, a cDNA-based clone with verified

infectivity. Plant Mol Biol 18:403–406.

170. Morch M-D, Drugeon G, Benicourt C. 1982. Analysis of the in vitro coding properties of the 3′ region of turnip yellow mosaic virus genomic RNA. Virology 119:193–198.

171. Stehelin D, Peter R, Duranton H. 1973. Studies on the primary structure of turnip yellow mosaic virus protein. III. Primary structure of the chymotryptic peptides of aminoethylated protein. Complete sequence. Biochim Biophys Acta 317:253–265.

172. Testut P, Renard CA, Terradillos O, Vitvitski-Trepo L, Tekaia F, Degott C, Blake J, Boyer B, Buendia MA. 1996. A new hepadnavirus endemic in arctic ground squirrels in Alaska. J Virol 70:4210–4219.

173. Williams AK, Wang L, Sneed LS, Collisson EW. 1996. Nucleocapsid gene sequence analysis of several strains of infectious bronchitis virus describing the evolutionary relationship of IBV within the coronaviridae family. EMBL/GenBank/DDBJ Nucleotide Sequence.

174. Pecenková T, Benes V, Paces J, Vlcek C, Paces V. 1997. Bacteriophage B103: complete DNA sequence of its genome and relationship to other Bacillus phages. Gene 199:157–163.

175. Leavitt MC, Ito J. 1987. Nucleotide sequence of Bacillus phage Nf terminal protein gene. Nucleic Acids Res 15:5251–5259.

176. Mizukami Y, Sekiya T, Hirokawa H. 1986. Nucleotide sequence of gene F of Bacillus phage Nf. Gene 42:231–235.

177. Tang XC, Zhang JX, Zhang SY, Wang P, Fan XH, Li LF, Li G, Dong BQ, Liu W, Cheung CL, Xu KM, Song WJ, Vijaykrishna D, Poon LLM, Peiris JSM, Smith GJD, Chen H, Guan Y. 2006. Prevalence and genetic diversity of coronaviruses in bats from China. J Virol 80:7481–7490.

178. Bassami MR, Berryman D, Wilcox GE, Raidal SR. 1998. Psittacine beak and feather disease virus nucleotide sequence analysis and its relationship to porcine circovirus, plant circoviruses, and chicken anaemia virus. Virology 249:453–459.

179. Chouljenko VN, Lin XQ, Storz J, Kousoulas KG, Gorbalenya AE. 2001. Comparison of genomic and predicted amino acid sequences of respiratory and enteric bovine coronaviruses isolated from the same animal with fatal shipping pneumonia. J Gen Virol 82:2927–2933.

180. Todd D, Weston J, Ball NW, Borghmans BJ, Smyth JA, Gelmini L, Lavazza A. 2001. Nucleotide sequence-based identification of a novel circovirus of canaries. Avian Pathol 30:321–325.

181. Sanchez-Morgado JM, Poynter S, Morris TH. 2004. Molecular characterization of a virulent canine coronavirus BGF strain. Virus Res 104:27–31.

182. Noteborn MH, de Boer GF, van Roozelaar DJ, Karreman C, Kranenburg O, Vos JG, Jeurissen SH, Hoeben RC, Zantema A, Koch G. 1991. Characterization of cloned chicken anemia virus DNA that contains all elements for the infectious replication cycle. J Virol 65:3131–3139.

183. Meehan BM, Todd D, Creelan JL, Earle JA, Hoey EM, McNulty MS. 1992. Characterization of viral DNAs from cells infected with chicken anaemia agent: sequence analysis of the cloned replicative form and transfection capabilities of cloned genome fragments. Arch Virol 124:301–319.

184. Vaudin M, Wolstenholme AJ, Tsiquaye KN, Zuckerman AJ, Harrison TJ. 1988. The complete nucleotide sequence of the genome of a hepatitis B virus isolated from a naturally infected chimpanzee. J Gen Virol 69 (Pt 6):1383–1389.

185. Weber K, Konigsberg W. 1967. Amino acid sequence of the f2 coat protein. J Biol Chem 242:3563–3578.

186. Nichols JL, Robertson HD. 1971. Sequences of RNA fragments from the bacteriophage f2 coat protein cistron which differ from their R17 counterparts. Biochim Biophys Acta 228:676–681.

187. Adhin MR, Hirashima A, van Duin J. 1989. Nucleotide sequence from the ssRNA bacteriophage JP34 resolves the discrepancy between serological and biophysical classification. Virology 170:238–242.

188. Beekwilder J, Nieuwenhuizen R, Poot R, van Duin J. 1996. Secondary structure model for the first three domains of Q beta RNA. Control of A-protein synthesis. J Mol Biol 256:8–19.

189. Beekwilder MJ, Nieuwenhuizen R, van Duin J. 1995. Secondary structure model for the last two domains of single-stranded RNA phage Q beta. J Mol Biol 247:903–917.

190. Weber K. 1967. Amino acid sequence studies on the tryptic peptides of the coat protein of the bacteriophage R17. Biochemistry 6:3144–3154.

191. Nishihara T, Fujisaki S, Nishimura Y, Minami Y, Yubisui T. 2006. Analysis of six new genes encoding lysis proteins and coat proteins in Escherichia coli group A RNA phages. Microbiol Immunol 50:61–66.

192. Nishihara T, Nozu Y, Okada Y. 1970. Amino acid sequence of the coat protein of the RNA phage ZR. J Biochem 67:403–413.

193. Guy JS, Breslin JJ, Breuhaus B, Vivrette S, Smith LG. 2000. Characterization of a coronavirus isolated from a diarrheic foal. J Clin Microbiol 38:4523–4526.

194. Makino S, Chang MF, Shieh CK, Kamahora T, Vannier DM, Govindarajan S, Lai MM. 1987. Molecular cloning and sequencing of a

human hepatitis delta (delta) virus RNA. Nature 329:343–346.

195. Engler JA, van Bree MP. 1982. The nucleotide sequence of the gene encoding protein IVa2 in human adenovirus type 7. Gene 19:71–80.

196. Gingeras TR, Sciaky D, Gelinas RE, Bing-Dong J, Yen CE, Kelly MM, Bullock PA, Parsons BL, O'Neill KE, Roberts RJ. 1982. Nucleotide sequences from the adenovirus-2 genome. J Biol Chem 257:13475–13491.

197. Thiel V, Herold J, Schelle B, Siddell SG. 2001. Infectious RNA transcribed in vitro from a cDNA copy of the human coronavirus genome cloned in vaccinia virus. J Gen Virol 82:1273–1281.

198. Myint S, Harmsen D, Raabe T, Siddell SG. 1990. Characterization of a nucleic acid probe for the diagnosis of human coronavirus 229E infections. J Med Virol 31:165–172.

199. Schreiber SS, Kamahora T, Lai MM. 1989. Sequence analysis of the nucleocapsid protein gene of human coronavirus 229E. Virology 169:142–151.

200. Ushijima Y, Luo C, Goshima F, Yamauchi Y, Kimura H, Nishiyama Y. 2007. Determination and analysis of the DNA sequence of highly attenuated herpes simplex virus type 1 mutant HF10, a potential oncolytic virus. Microbes Infect 9:142–149.

201. McGeoch DJ, Dalrymple MA, Davison AJ, Dolan A, Frame MC, McNab D, Perry LJ, Scott JE, Taylor P. 1988. The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1. J Gen Virol 69 (Pt 7):1531–1574.

202. Dolan A, Jamieson FE, Cunningham C, Barnett BC, McGeoch DJ. 1998. The genome sequence of herpes simplex virus type 2. J Virol 72:2010–2021.

203. Alizon M, Wain-Hobson S, Montagnier L, Sonigo P. 1986. Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients. Cell 46:63–74.

204. Guan Y, Zheng BJ, He YQ, Liu XL, Zhuang ZX, Cheung CL, Luo SW, Li PH, Zhang LJ, Guan YJ, Butt KM, Wong KL, Chan KW, Lim W, Shortridge KF, Yuen KY, Peiris JSM, Poon LLM. 2003. Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China. Science 302:276–278.

205. Tsui SKW, Chim SSC, Lo YMD. 2003. Coronavirus genomic-sequence variations and the epidemiology of the severe acute respiratory syndrome. N Engl J Med. United States.

206. Marra MA, Jones SJM, Astell CR, Holt RA, Brooks-Wilson A, Butterfield YSN, Khattra J, Asano JK, Barber SA, Chan SY, Cloutier A,

Coughlin SM, Freeman D, Girn N, Griffith OL, Leach SR, Mayo M, McDonald H, Montgomery SB, Pandoh PK, Petrescu AS, Robertson AG, Schein JE, Siddiqui A, Smailus DE, Stott JM, Yang GS, Plummer F, Andonov A, Artsob H, Bastien N, Bernard K, Booth TF, Bowness D, Czub M, Drebot M, Fernando L, Flick R, Garbutt M, Gray M, Grolla A, Jones S, Feldmann H, Meyers A, Kabani A, Li Y, Normand S, Stroher U, Tipples GA, Tyler S, Vogrig R, Ward D, Watson B, Brunham RC, Krajden M, Petric M, Skowronski DM, Upton C, Roper RL. 2003. The Genome sequence of the SARS-associated coronavirus. Science 300:1399–1404.

207. Zeng FY, Chan CWM, Chan MN, Chen JD, Chow KYC, Hon CC, Hui KH, Li J, Li VYY, Wang CY, Wang PY, Guan Y, Zheng B, Poon LLM, Chan KH, Yuen KY, Peiris JSM, Leung FC. 2003. The complete genome sequence of severe acute respiratory syndrome coronavirus strain HKU-39849 (HK-39). Exp Biol Med (Maywood) 228:866–873.

208. Rota PA, Oberste MS, Monroe SS, Nix WA, Campagnoli R, Icenogle JP, Peñaranda S, Bankamp B, Maher K, Chen M-H, Tong S, Tamin A, Lowe L, Frace M, DeRisi JL, Chen Q, Wang D, Erdman DD, Peret TCT, Burns C, Ksiazek TG, Rollin PE, Sanchez A, Liffick S, Holloway B, Limor J, McCaustland K, Olsen-Rasmussen M, Fouchier R, Günther S, Osterhaus ADME, Drosten C, Pallansch MA, Anderson LJ, Bellini WJ. 2003. Characterization of a novel coronavirus associated with severe acute respiratory syndrome. Science 300:1394–1399.

209. Ruan YJ, Wei CL, Ee AL, Vega VB, Thoreau H, Su STY, Chia J-M, Ng P, Chiu KP, Lim L, Zhang T, Peng CK, Lin EOL, Lee NM, Yee SL, Ng LFP, Chee RE, Stanton LW, Long PM, Liu ET. 2003. Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection. Lancet (London, England) 361:1779–1785.

210. Huiet L, Klaassen V, Tsai JH, Falk BW. 1991. Nucleotide sequence and RNA hybridization analyses reveal an ambisense coding strategy for maize stripe virus RNA3. Virology 182:47–53.

211. Bermingham A, Chand MA, Brown CS, Aarons E, Tong C, Langrish C, Hoschler K, Brown K, Galiano M, Myers R, Pebody RG, Green HK, Boddington NL, Gopal R, Price N, Newsholme W, Drosten C, Fouchier RA, Zambon M. 2012. Severe respiratory illness caused by a novel coronavirus, in a patient transferred to the United Kingdom from the Middle East, September 2012. Euro Surveill Bull Eur sur les Mal Transm = Eur Commun Dis Bull 17:20290.

212. Cheung AK. 2003. Transcriptional analysis of porcine circovirus type 2. Virology 305:168–180.

213. Hamel AL, Lin LL, Nayar GP. 1998. Nucleotide sequence of porcine circovirus associated with postweaning multisystemic wasting syndrome in pigs. J Virol 72:5262–5267.

214. Bridgen A, Duarte M, Tobler K, Laude H, Ackermann M. 1993. Sequence determination of the nucleocapsid protein gene of the porcine epidemic diarrhoea virus confirms that this virus is a coronavirus related to human coronavirus 229E and porcine transmissible gastroenteritis virus. J Gen Virol 74 (Pt 9):1795–1804.

215. Duarte M, Tobler K, Bridgen A, Rasschaert D, Ackermann M, Laude H. 1994. Sequence analysis of the porcine epidemic diarrhea virus genome between the nucleocapsid and spike protein genes reveals a polymorphic ORF. Virology 198:466–476.

216. Kocherhans R, Bridgen A, Ackermann M, Tobler K. 2001. Completion of the porcine epidemic diarrhoea coronavirus (PEDV) genome sequence. Virus Genes 23:137–144.

217. Sasseville AM-J, Boutin M, Gélinas A-M, Dea S. 2002. Sequence of the 3'-terminal end (8.1 kb) of the genome of porcine haemagglutinating encephalomyelitis virus: comparison with other haemagglutinating coronaviruses. J Gen Virol 83:2411–2416.

218. Britton P, Cármenes RS, Page KW, Garwes DJ, Parra F. 1988. Sequence of the nucleoprotein gene from a virulent British field isolate of transmissible gastroenteritis virus and its expression in Saccharomyces cerevisiae. Mol Microbiol 2:89–99.

219. Ikegami T, Calaor AB, Miranda ME, Niikura M, Saijo M, Kurane I, Yoshikawa Y, Morikawa S. 2001. Genome structure of Ebola virus subtype Reston: differences among Ebola subtypes. Brief report. Arch Virol 146:2021–2027.

220. Suzuki N. 1993. In vitro translation of rice dwarf phytoreovirus genome segments S4 to S10. Arch Virol 130:201–208.

221. Moriyasu Y, Maruyama-Funatsuki W, Kikuchi A, Ichimi K, Zhong B, Yan J, Zhu Y, Suga H, Watanabe Y, Ichiki-Uehara T, Shimizu T, Hagiwara K, Kamiunten H, Akutsu K, Omura T. 2007. Molecular analysis of the genome segments S1, S4, S6, S7 and S12 of a Rice gall dwarf virus isolate from Thailand; completion of the genomic sequence. Arch Virol 152:1315–1322.

222. Kakutani T, Hayano Y, Hayashi T, Minobe Y. 1991. Ambisense segment 3 of rice stripe virus: the first instance of a virus containing two ambisense segments. J Gen Virol 72 (Pt 2):465–468.

223. Hayano Y, Kakutani T, Hayashi T, Minobe Y. 1990. Coding strategy of rice stripe virus: major nonstructural protein is encoded in viral RNA segment 4 and coat protein in RNA complementary to segment 3. Virology 177:372–374.

224. Ysebaert M, van Emmelo J, Fiers W. 1980. Total nucleotide sequence of a nearly full-size DNA copy of satellite tobacco necrosis virus RNA. J Mol Biol 143:273–287.

225. Fiers W, Contreras R, Haegemann G, Rogiers R, Van de Voorde A, Van Heuverswyn H, Van Herreweghe J, Volckaert G, Ysebaert M.

1978. Complete nucleotide sequence of SV40 DNA. Nature 273:113–120.

226. Reddy VB, Thimmappaya B, Dhar R, Subramanian KN, Zain BS, Pan J, Ghosh PK, Celma ML, Weissman SM. 1978. The genome of simian virus 40. Science 200:494–502.

227. Breslin JJ, Smith LG, Fuller FJ, Guy JS. 1999. Sequence analysis of the turkey coronavirus nucleocapsid protein gene and 3’ untranslated region identifies the virus as a close relative of infectious bronchitis virus. Virus Res 65:187–193.

228. Breslin JJ, Smith LG, Fuller FJ, Guy JS. 1999. Sequence analysis of the matrix/nucleocapsid gene region of turkey coronavirus. Intervirology 42:22–29.

229. Seifers DL, Harvey TL, Martin TJ, Haber S, She YM, Ens W, Standing KG, Solomon R, Gera A. 2005. Association of a virus with wheat displaying yellow head disease symptoms in the great plains. Plant Dis 89:888—895.

230. Hillman BI, Anzola J V, Halpern BT, Cavileer TD, Nuss DL. 1991. First field isolation of wound tumor virus from a plant host: minimal sequence divergence from the type strain isolated from an insect vector. Virology 185:896–900.

231. Klausen MS, Jespersen MC, Nielsen H, Jensen KK, Jurtz VI, Sønderby CK, Sommer MOA, Winther O, Nielsen M, Petersen B, Marcatili P. 2019. NetSurfP-2.0: Improved prediction of protein structural features by integrated deep learning. Proteins Struct Funct Bioinforma 87:520–527.

232. DTU Health Tech. 2019. NetSurfP. 2.0. www.cbs.dtu.dk/services/NetSurfP.

Proteome sequences and associated polynucleotide-binding region (PBR) predictions. Notation above the sequence indicates positive PBR predition for the corresponding (below) residue, based on conserved structures: Beta sheets ('S'), Beta turns ('U'), Disordered termini ('D'), and arginine (ARG) rich ('R').

```
Adeno-associated virus 4
         Major capsid, 1 variant of 3 (VP1)  |  O41855
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich
                            1   MTDGYLPDWLEDNLSEGVREWWALQPGAPKPKANQQHQDNARGLVLPGYKYLGPGNGLDK 60
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich
                           61   GEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQQRLQGDTSFGGNLGRAVFQA 120
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich                                                      RRRRRRRRRR
                          121   KKRVLEPLGLVEQAGETAPGKKRPLIESPQQPDSSTGIGKKGKQPAKKKLVFEDETGAGD 180
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich
                          181   GPPEGSTSGAMSDDSEMRAAAGGAAVEGGQGADGVGNASGDWHCDSTWSEGHVTTTSTRT 240
         Beta sheet                                                                    SSSSS
         Beta turn
         Disordered termini
         ARG rich
                          241   WVLPTYNNHLYKRLGESLQSNTYNGFSTPWGYFDFNRFHCHFSPRDWQRLINNNWGMRPK 300
         Beta sheet             SSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          301   AMRVKIFNIQVKEVTTSNGETTVANNLTSTVQIFADSSYELPYVMDAGQEGSLPPFPNDV 360
         Beta sheet
         Beta turn                                                                UUUUU
         Disordered termini
         ARG rich
                          361   FMVPQYGYCGLVTGNTSQQQTDRNAFYCLEYFPSQMLRTGNNFEITYSFEKVPFHSMYAH 420
         Beta sheet
         Beta turn                                                              UU
         Disordered termini
         ARG rich
                          421   SQSLDRLMNPLIDQYLWGLQSTTTGTTLNAGTATTNFTKLRPTNFSNFKKNWLPGPSIKQ 480
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          481   QGFSKTANQNYKIPATGSDSLIKYETHSTLDGRWSALTPGPPMATAGPADSKFSNSQLIF 540
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          541   AGPKQNGNTATVPGTLIFTSEEELAATNATDTDMWGNLPGGDQSNSNLPTVDRLTALGAV 600
         Beta sheet
         Beta turn                                                    UU
         Disordered termini
         ARG rich
                          601   PGMVWQNRDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKHPPPQIFIKNTPVPANPATTF 660
         Beta sheet
         Beta turn                                        UUUUUU
         Disordered termini
         ARG rich
                          661   SSTPVNSFITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNYGQQNSLLWAPDAAGKYT 720
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          721   EPRAIGTRYLTHHL 734
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Belladonna mottle virus
         Capsid (CP)  |  P03601
         Beta sheet
         Beta turn
         Disordered termini     DDD
         ARG rich
                            1   MDSSEVVKVKQASIPAPGSILSQPNTEQSPAIVLPFQFEATTFGTAETAAQVSLQTADPI 60
         Beta sheet                     SSSSSSSSSSSSS
         Beta turn                     UU                                        UUU
         Disordered termini
         ARG rich
                           61   TKLTAPYRHAQIVECKAILTPTDLAVSNPLTVYLAWVPANSPATPTQILKLRVYGGQSFV 120
         Beta sheet                                                               SSSSSSSSSS
         Beta turn                                                                        UU
         Disordered termini
         ARG rich
                          121   LGGAISAAKTIEVPLNLDSVNRMLKDSVTYTDTPKLLAYSRAPTNPSKIPTASIQISGRI 180
         Beta sheet             SSS
         Beta turn              UUUU
         Disordered termini
         ARG rich
                          181   RLSKPMLIAN 190




Bacillus phage phi29
         Portal protein  (P10)  |  P04332
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDD
         ARG rich                 RRRRRRRRRRRRRRRRRRRR
                            1   MARKRSNTYRSINEIQRQKRNRWFIHYLNYLQSLAYQLFEWENLPPTINPSFLEKSIHQF 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   GYVGFYKDPVISYIACNGALSGQRDVYNQATVFRAASPVYQKEFKLYNYRDMKEEDMGVV 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   IYNNDMAFPTTTPTLELFAAELAELKEIISVNQNAQKTPVLIRANDNNQLSLKQVYNQYEG 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          181   NAPVIFAHEALDSDSIEVFKTDAPYVVDKLNAQKNAVWNEMMTFLGIKNANLEKKERMVT 240
         Beta sheet
         Beta turn
         Disordered termini                                                  DDDDDDDDDDDDDDD
         ARG rich
                          241   DEVSSNDEQIESSGTVFLKSREEACEKINELYGLNVKVKFRYDIVEQMRRELQQIENVSR 300
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDD
         ARG rich
                          301   GTSDGETNE 309


         Proximal tail-tube connector (P11)  |  P68930
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich
                            1   MSSYTMQLRTYIEMWSQGETGLSTAEKIEKGRPKLFDFNYPIFDESYRTIFETHFIRNFY 60
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Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   MREIGFETEGLFKFHLETWLMINMPYFNKLFESELIKYDPLENTRVGVKSNTKNDTDRND 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   NRDVKQDLTSNGTSSTDAKQNDTSKTTGNEKSSGSGSITDDNFKRDLNADTADDRLQLTT 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   KDGEGVLEYASQIEEHNENKKRDTKTSNTTDTTSNTTGTSTLDSDSKTSNKANTTSNDKL 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241   NSQINSVEDYIEDRVGKIGTQSYARLVMDYREALLRIEQRIFNEMQELFMLVY 293


Pre-neck appendage protein (gP12)  |  P20345 [1 – 691]
Beta sheet
Beta turn
Disordered termini     D
ARG rich
                   1   MSTKPELKRFEQFGEMMVQLYERYLPTAFDESLTLLEKMNKIIHYLNEIGKVTNELIEEW 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   NKVMEWILNDGLEDLVKETLERWYEEGKFADLVIQVIDELKQFGVSVKTYGAKGDGVTDD 120
Beta sheet
Beta turn                                      UUUU           UU
Disordered termini
ARG rich
                 121   IRAFEKAIESGFPVYVPYGTFMVSRGIKLPSNTVLTGAGKRNAVIKFMDSVGRGESLMYN 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   QNVTTGNENIFLSSFTLDGNNKRLGQGISGIGGSRESNLSIRACHNVYIRDIEAVDCTLH 240
Beta sheet
Beta turn                                                         UU           UUU
Disordered termini
ARG rich
                 241   GIDITCGGLDYPYLGDGTTAPNPSENIWIENCEATGFGDDGITTHHSQYINILNCYSHDP 300
Beta sheet
Beta turn              U
Disordered termini
ARG rich
                 301   RLTANCNGFEIDDGSRHVVLSNNRSKGCYGGIEIKAHGDAPAAYNISINGHMSVEDVRSY 360
Beta sheet                                                               SSSSSSSSSS
Beta turn                                           UUUUUU
Disordered termini
ARG rich
                 361   NFRHIGHHAATDPQSVSAKNIVASNLVSIRPNNKRGFQDNATPRVLAVSAYYGVVINGLT 420
Beta sheet             SS
Beta turn                                UUU
Disordered termini
ARG rich
                 421   GYTDDPNLLTETVVSVQFRARNCSLNGVGLTGFSNSDNGIYVIGGSRGGDAVNISNVTLN 480
Beta sheet
Beta turn
Disordered termini
ARG rich
                 481   NSGRYGVSIGSGIENVSITNISGIGDGINSPVALVSTINSNPEISGLSSIGYPTAARVAG 540
Beta sheet
Beta turn
Disordered termini
ARG rich
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                 541   TDYNDGLTLFNGAFRASTTSSGKIHSEGFIMGSTSGCEASVSKSGVLTSSSSKTSSERSL 600
Beta sheet                                                  SSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 601   IAGSSTSEAKGTYNTILGSLGAVADEQFAALISASQSRASGNHNLILSSYGINTTGSYKV 660
Beta sheet
Beta turn
Disordered termini
ARG rich
                 661   NGGFEKINWELDSLNGRIKARDTVTGGNTWS 691


Morphogenesis protein 1 (P13)  |  P15132
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MVYVSNKYLTMSEMKVNAQYILNYLSSNGWTKQAICGMLGNMQSESTINPGLWQNLDEGN 60
Beta sheet
Beta turn                                                                     UUUUU
Disordered termini
ARG rich                                                                 RRRRRRRRRR
                  61   TSLGFGLVQWTPASNYINWANSQGLPYKDMDSELKRIIWEVNNNAQWINLRDMTFKEYIK 120
Beta sheet
Beta turn              UUUUUU
Disordered termini
ARG rich               RRRRRR
                 121   STKTPRELAMIFLASYERPANPNQPERGDQAEYWYKNLSGGGGGGLQLAQFPMDIINISQ 180
Beta sheet
Beta turn                     UU         UUUU
Disordered termini
ARG rich
                 181   GENGSFSHKGTLCIDFVGKTEKYPYYAPCDCTCVWRGDASAYLAWTSDKEVMCADGSVRY 240
Beta sheet
Beta turn                             UUUUU                                UU
Disordered termini
ARG rich
                 241   ITWVNVHESPLPFDVGKKLKKGDLMGHTGIGGNVTGDHWHFNVIDGKEYQGWTKKPDSCL 300
Beta sheet
Beta turn
Disordered termini
ARG rich
                 301   AGTELHIYDVFAVNNVEIINGNGYDWKTSDWQDGDGGDGDDDNDNNKTKDLITLLLSDAL 360
Beta sheet
Beta turn              UUUU
Disordered termini
ARG rich
                 361   HGWKA 365


Major capsid protein  (P8)  |  P13849
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MRITFNDVKTSLGITESYDIVNAIRNSQGDNFKSYVPLATANNVAEVGAGILINQTVQND 60
Beta sheet
Beta turn                                     UUUUU                UUU
Disordered termini
ARG rich                      RRRRRRRRRRRRRRRRRRRRRRRRRRRR
                  61   FITSLVDRIGLVVIRQVSLNNPLKKFKKGQIPLGRTIEEIYTDITKEKQYDAEEAEQKVF 120
Beta sheet
Beta turn                     UUUUUUUUU
Disordered termini
ARG rich
                 121   EREMPNVKTLFHERNRQGFYHQTIQDDSLKTAFVSWGNFESFVSSIINAIYNSAEVDEYE 180
Beta sheet
Beta turn
Disordered termini
ARG rich                                                 RRRRRRRRRRRRRRRRRRRRRRRRRR
                 181   YMKLLVDNYYSKGLFTTVKIDEPTSSTGALTEFVKKMRATARKLTLPQGSRDWNSMAVRT 240
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Beta sheet
Beta turn
Disordered termini
ARG rich               R
                 241   RSYMEDLHLIIDADLEAELDVDVLAKAFNMNRTDFLGNVTVIDGFASTGLEAVLVDKDWF 300
Beta sheet                                     SSSSSSSSSSSSSSSSSS
Beta turn                          UUUU
Disordered termini
ARG rich
                 301   MVYDNLHKMETVRNPRGLYWNYYYHVWQTLSVSRFANAVAFVSGDVPAVTQVIVSPNIAA 360
Beta sheet
Beta turn
Disordered termini
ARG rich
                 361   VKQGGQQQFTAYVRATNAKDHKVVWSVEGGSTGTAITGDGLLSVSGNEDNQLTVKATVDI 420
Beta sheet
Beta turn
Disordered termini                           DDDDDD
ARG rich
                 421   GTEDKPKLVVGEAVVSIRPNNASGGAQA 448


Capsid fiber protein  (P8.5)  |  B3VMP4
Beta sheet
Beta turn                                                          UUUUU
Disordered termini
ARG rich
                   1   MMVSFTARAKSNVMAYRLLAYSQGDDIIEISHAAENTIPDYVAVKDVDKGDLTQVNMYPL 60
Beta sheet
Beta turn                                                                   UUU
Disordered termini
ARG rich
                  61   AAWQVIAGSDIKVGDNLTTGKDGTAVPTDDPSTVFGYAVEEAQEGQLVTLVISRSKEISI 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   EVDDIKDAGDTGKRLLKINTPSGARNIIIENEDAKALINGETTNTNKKNLQDLLFSDGNV 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   KAFLQATTTDENKTALQQLLVSNADVLGLLSGNPTSDNKINLRTMIGAGVPYSLPAATTT 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241   TLGGVKKGAAVTASTATDVATAVKDLNSLITVLKNAGIIS 280


Tail knob protein gp9 (Distal tube protein) (P9)  |  P04331
Beta sheet
Beta turn                                     UUUU             UUUU
Disordered termini
ARG rich                                                       RRRRRRRRRRRRRRRRRRRR
                   1   MAYVPLSGTNVRILADVPFSNDYKNTRWFTSSSNQYNWFNRKSRVYEMSKVTFMGFRENK 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   PYVSVSLPIDKLYSASYIMFQNADYGNKWFYAFVTELEFKNSAVTYVHFEIDVLQTWMFD 120
Beta sheet                 SSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 121   MKFQESFIVREHVKLWNDDGTPTINTIDEGLSYGSEYDIVSVENHKPYDDMMFLVIISKS 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   IMHGTPGEEESRLNDINASLNGMPQPLCYYIHPFYKDGKVPKTYIGDNNANLSPIVNMLT 240
Beta sheet
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         Beta turn                                     UUUUUUUUUUUUUUU           UU
         Disordered termini
         ARG rich                                      RRRRRRRRRRRRRRR
                          241   NIFSQKSAVNDIVNMYVTDYIGLKLDYKNGDKELKLDKDMFEQAGIADDKHGNVDTIFVK 300
         Beta sheet
         Beta turn                                                        UUUUUUUU
         Disordered termini
         ARG rich
                          301   KIPDYEALEIDTGDKWGGFTKDQESKLMMYPYCVTEITDFKGNHMNLKTEYINNSKLKIQ 360
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          361   VRGSLGVSNKVAYSVQDYNADSALSGGNRLTASLDSSLINNNPNDIAILNDYLSAYLQGN 420
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          421   KNSLENQKSSILFNGIMGMIGGGISAGASAAGGSALGMASSVTGMTSTAGNAVLQMQAMQ 480
         Beta sheet
         Beta turn                                                                  UUUUUUUUUU
         Disordered termini
         ARG rich                                           RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                          481   AKQADIANIPPQLTKMGGNTAFDYGNGYRGVYVIKKQLKAEYRRSLSSFFHKYGYKINRV 540
         Beta sheet                     SSSSSSSSSSSSSS
         Beta turn              UUUUUUUUU
         Disordered termini
         ARG rich               RRRRRRRRRRRRRRRRR
                          541   KKPNLRTRKAFNYVQTKDCFISGDINNNDLQEIRTIFDNGITLWHTDNIGNYSVENELR 599


         Primer terminal protein (TP) (TP)  |  P03681
         Beta sheet
         Beta turn
         Disordered termini     DD
         ARG rich                 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                            1   MARSPRIRIKDNDKAEYARLVKNTKAKIARTKKKYGVDLTAEIDIPDLDSFETRAQFNKW 60
         Beta sheet
         Beta turn                       UUUUU
         Disordered termini
         ARG rich
                           61   KEQASSFTNRANMRYQFEKNAYGVVASKAKIAEIERNTKEVQRLVDEKIKAMKDKEYYAG 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   GKPQGTIEQRIAMTSPAHVTGINRPHDFDFSKVRSYSRLRTLEESMEMRTDPQYYEKKMI 180
         Beta sheet
         Beta turn                                         UU
         Disordered termini
         ARG rich
                          181   QLQLNFIKSVEGSFNSFDAADELIEELKKIPPDDFYELFLRISEISFEEFDSEGNTVENV 240
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          241   EGNVYKILSYLEQYRRGDFDLSLKGF 266




Cowpea chlorotic mottle virus
         Capsid (CP)  |  P03601
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich                      RRRRRRRRRRRRRRRRRRRR
                            1   MSTVGTGKLTRAQRRAAARKNKRNTRVVQPVIVEPIASGQGKAIKAWTGYSVSKWTASCA 60
         Beta sheet
         Beta turn                                   UUUUUUUUU
         Disordered termini
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         ARG rich
                           61   AAEAKVTSAITISLPNELSSERNKQLKVGRVLLWLGLLPSVSGTVKSCVTETQTTAAASF 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   QVALAVADNSKDVVAAMYPEAFKGITLEQLTADLTIYLYSSAALTEGDVIVHLEVEHVRP 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          181   TFDDSFTPVY 190




Cucumber virus strain FNY
         Capsid (CP)  |  P03601
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich                 RRRRRRRRRRRRRRRRRRRR
                            1   MDKSESTSAGRNRRRRPRRGSRSAPSSADANFRVLSQQLSRLNKTLAAGRPTINHPTFVG 60
         Beta sheet
         Beta turn                             UUUUUUU
         Disordered termini
         ARG rich                              RRRRRRRRRRRRRR           RRRRRRRRRRRRRRRRRRRR
                           61   SERCRPGYTFTSITLKPPKIDRGSYYGKRLLLPDSVTEYDKKLVSRIQIRVNPLPKFDST 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich               RRRRRRR
                          121   VWVTVRKVPASSDLSVAAISAMFADGASPVLVYQYAASGVQANNKLLYDLSAMRADIGDM 180
         Beta sheet
         Beta turn                                        UUU
         Disordered termini
         ARG rich
                          181   RKYAVLVYSKDDALETDELVLHVDIEHQRIPTSGVLPV 218




Canine parvovirus 2 (Dog)
         Major capsid, 1 variant of 3 (VP1)  |  O41855
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich                    RRRRRRRRRRRRR
                            1   MAPPAKRARRGLVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYAAYLRSGKNPYLYF 60
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich                    RRRRRRRRRRRRRRRRRRRRRRRRR                RRRRRRRRRR
                           61   SPADQRFIDQTKDAKDWGGKIGHYFFRAKKAIAPVLTDTPDHPSTSRPTKPTKRSKPPPH 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                     RRRRRRRRRRRR
                          121   IFINLAKKKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERATGSGNGSGGGGGGGSGG 180
         Beta sheet                                  SSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          181   VGISTGTFNNQTEFKFLENGWVEITANSSRLVHLNMPESENYRRVVVNNMDKTAVNGNMA 240
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          241   LDDIHAQIVTPWSLVDANAWGVWFNPGDWQLIVNTMSELHLVSFEQEIFNVVLKTVSESA 300
         Beta sheet                                                               SSSSSSSSSS
```

```
Beta turn
Disordered termini
ARG rich
                 301   TQPPTKVYNNDLTASLMVALDSNNTMPFTPAAMRSETLGFYPWKPTIPTPWRYYFQWDRT 360
Beta sheet             SS
Beta turn
Disordered termini
ARG rich
                 361   LIPSHTGTSGTPTNIYHGTDPDDVQFYTIENSVPVHLLRTGDEFATGTFFFDCKPCRLTH 420
Beta sheet
Beta turn
Disordered termini
ARG rich
                 421   TWQTNRALGLPPFLNSLPQSEGATNFGDIGVQQDKRRGVTQMGNTNYITEATIMRPAEVG 480
Beta sheet
Beta turn
Disordered termini
ARG rich
                 481   YSAPYYSFEASTQGPFKTPIAAGRGGAQTDENQAADGNPRYAFGRQHGQKTTTTGETPER 540
Beta sheet
Beta turn
Disordered termini
ARG rich
                 541   FTYIAHQDTGRYPEGDWIQNINFNLPVTNDNVLLPTDPIGGKTGINYTNIFNTYGPLTAL 600
Beta sheet
Beta turn
Disordered termini
ARG rich
                 601   NNVPPVYPNGQIWDKEFDTDLKPRLHVNAPFVCQNNCPGQLFVKVAPNLTNEYDPDASAN 660
Beta sheet               SSSSSSSSSSSSSSSSSSSS
Beta turn                          UUUUUUUUUUUUUU
Disordered termini
ARG rich                 RRRRRRRRRRRRRRRRRRRRR
                 661   MSRIVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSINVDNQFNYVPSNIGGMKIVYEKSQ 720
Beta sheet
Beta turn
Disordered termini
ARG rich
                 721   LAPRKLY 727


Capsid (VP2)  |  P22055 [70 - 341]
Beta sheet                                                               SS
Beta turn
Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
ARG rich
                   1   MSDGAVQPDGGQPAVRNERATGSGNGSGGGGGGGSGGVGISTGTFNNQTEFKFLENGWVE 60
Beta sheet             SSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                  61   ITANSSRLVHLNMPESENYRRVVVNNMDKTAVNGNMALDDIHAQIVTPWSLVDANAWGVW 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   FNPGDWQLIVNTMSELHLVSFEQEIFNVVLKTVSESATQPPTKVYNNDLTASLMVALDSN 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   NTMPFTPAAMRSETLGFYPWKPTIPTPWRYYFQWDRTLIPSHTGTSGTPTNIYHGTDPDD 240
Beta sheet                                             SSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 241   VQFYTIENSVPVHLLRTGDEFATGTFFFDCKPCRLTHTWQTNRALGLPPFLNSLPQSEGA 300
Beta sheet
Beta turn
Disordered termini
ARG rich
                 301   TNFGDIGVQQDKRRGVTQMGNTNYITEATIMRPAEVGYSAPYYSFEASTQGPFKTPIAAG 360
```

```
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          361   RGGAQTDENQAADGNPRYAFGRQHGQKTTTTGETPERFTYIAHQDTGRYPEGDWIQNINF 420
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          421   NLPVTNDNVLLPTDPIGGKTGINYTNIFNTYGPLTALNNVPPVYPNGQIWDKEFDTDLKP 480
         Beta sheet                                                    SSSSSSSSSSSSSSSSSSSS
         Beta turn                                                               UUUUUUUUUUU
         Disordered termini
         ARG rich                                                      RRRRRRRRRRRRRRRRRRRRR
                          481   RLHVNAPFVCQNNCPGQLFVKVAPNLTNEYDPDASANMSRIVTYSDFWWKGKLVFKAKLR 540
         Beta sheet
         Beta turn              UUU
         Disordered termini
         ARG rich
                          541   ASHTWNPIQQMSINVDNQFNYVPSNIGGMKIVYEKSQLAPRKLY 584




Cottontail rabbit papillomavirus (Kansas)
         Major capsid (L1)  |  P03102
         Beta sheet
         Beta turn                                                                  UUU
         Disordered termini     D
         ARG rich
                            1   MAVWLSTQNKFYLPPQPVTKIPSTDEYVTRTNVFYYASSDRLLTVGHPYYEIRDKGTMLV 60
         Beta sheet                                                SSSSSSSSSSSS
         Beta turn                                               UUU
         Disordered termini
         ARG rich
                           61   PKVSPNQYRVFRIKLPDPNKFAFGDKQLYDPEKERLVWCLRGIEVNRGQPLGVSVTGNPI 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   FNKFDDVENPTKYYNNHADQQDYRKSMAFDPKQVQLLMLGCVPATGEHWAQAKQCAEDPP 180
         Beta sheet
         Beta turn                                                                     UUUU
         Disordered termini
         ARG rich
                          181   QQTDCPPIELVNTVIEDGDMCEIGFGAMDHKTLQASLSEVPLELAQSISKYPDYLKMQKD 240
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                         RRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                          241   QFGDSMFFYARREQMYARHFFSRAGGDKENVKSRAYIKRTQMQGEANANIATDNYCITPS 300
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          301   GSLVSSDSQVFNRAYWLQKAQGMNNGVCWDNQIFVTVVDNTRGTILSLVTKSKEQIKKTH 360
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          361   GKTVHFSSYLRHVEEYELQFVLQLCKVKLTPENLSYLHSMHPTIIDNWQLSVSAQPSGTL 420
         Beta sheet
         Beta turn                                         UUUU
         Disordered termini
         ARG rich                                                                  RRRRRRRRR
                          421   EDQYRYLQSIATKCPPPEPPKENTDPYKNYKFWEVDLSEKLSDQLDQYPLGRKFLNQSGL 480
         Beta sheet
         Beta turn
         Disordered termini       DDDDDDDDDDDDDDDDDDDDDDD
         ARG rich               RRRRRRRRRRRRRRRRRRRRRRRR
                          481   QRIGTKRPAPAPVSIVKSSKRKRRT 505
```

```
         Minor capsid (L2)  |  P03108
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDD
         ARG rich                  RRRRRR
                            1   MVARSRKRRAAPQDIYPTCKIAGNCPADIQNKFENKTIADKILQYGSLGVFFGGLGISSA 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   GGSGGRLGYTPLSGGGGRVIAAAPVRPPITTESVGPLDIVPEVADPGGPTLVSLHELPAE 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   TPYVSSTNVTGDGAAEPLPAGHGGSQISDVTSGTSGTVSRTHINNPVFEAPMTGDQDVSD 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          181   VHVFAHSESSITINQTENTGGELIEMVPLRHPPRSEGDFRETSFSTSTPIPDRSALRSIN 240
         Beta sheet
         Beta turn                                UUU
         Disordered termini
         ARG rich
                          241   VASRRYQQVQVENPAFLNRPRELVQFENTFDNPAFVDDEQLSLLFEQDLDTVVATPDPAF 300
         Beta sheet                               SSSSSSSSSSSSSS
         Beta turn                            UUUUUUUUUUUU      UUUU
         Disordered termini
         ARG rich                   RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                          301   QDVVRLSRPSFTQSRAGRVRVSRLGRTLTMQTRSGKAFGPAKHFYYELSSIAEGPEPDIL 360
         Beta sheet
         Beta turn                                                             UUU
         Disordered termini
         ARG rich
                          361   IPESEQETSFTDATSKDTQQEAEVYADGSTLETDTSADENLTLVFSDRGRGQGSHVPIPG 420
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                                                  RRRRRR
                          421   KSTIGGPVNIGDSKYYTLNPGETTSFEADVISPVFIFEGNADGTYYLEEPLRKKRRKSIF 480
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          481   LLADGSVAVYAE 492




Coxsackievirus A21
         Major capsid, 1 variant of 3 (VP1)  |  O41855
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   GIEDLIDTAIKNALRVSQPLRPSQLKQPNGVNSQEVPALTAVETGASGQAIPSDVVETRH 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   VINYKTRSESCLESFFGRAACVTILSLTNSSKSGEEKKHFNIWNITYTDTVQLRRKLEFF 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   TYSRFDLEMTFVFTENYPSTASGEVRNQCDQIMYIPPGAPRPSSWDDYTWQSSSNPSIFY 180
         Beta sheet
         Beta turn                                                                       UUU
```

```
Disordered termini
ARG rich
                 181   MYGNAPPRMSIPYVGIANAYSHFYDGFARVPLEGENTDAGDTFYGLVSINDFGVLAVRAV 240
Beta sheet                   SSSSSSSSSSSSSSSSSSSS
Beta turn              UUUUUUUUUUUUUUUUUUUUUU    UUUU
Disordered termini
ARG rich                           RRRRRRRRRRRRRRRRRRRRRRR
                 241   NRSNPHTIHTSVRVYMKPKHIRCWCPRPPRAVLYRGEGVDMISSAIQPLTKVDSITTF 298


Capsid (VP2)  |  P22055 [70 - 341]
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   SPNVEACGYSDRVRQITLGNSTITTQEAANAIVAYGEWPTYINDSEANPVDAPTEPDVSS 60
Beta sheet
Beta turn                         UUUUU                                       UUU
Disordered termini
ARG rich
                  61   NRFYTLESVSWKTTSRGWWWKLPDCLKDMGMFGQNMYYHYLGRSGYTIHVQCNASKFHQG 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   ALGVFLIPEFVMACNTESKTSYVSYINANPGERGGEFTNTYNPSNTDVSEGRQFAALDYL 180
Beta sheet                                                   SSSSSSSSSSSS
Beta turn                                                UU
Disordered termini
ARG rich
                 181   LGSGVLAGNAFVYPHQIINLRTNNSATIVVPYVNSLVIDCMAKHNNWGIVILPLAPLAFA 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241   ATSSPQVPITVTIAPMCTEFNGLRNITIPVHQ 272


Capsid (VP3)  |  P22055 [342 - 581]
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   GLPTMNTPGSNQFLTSDDFQSPCALPNFDVTPPIHIPGEVKNMMELAEIDTLIPMNAVDG 60
Beta sheet                                                    SSSSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                  61   KVNTMEMYQIPLNDNLSKAPIFCLSLSPASDKRLSHTMLGEILNYYTHWTGSIRFTFLFC 120
Beta sheet             S
Beta turn                                                                     UUUUU
Disordered termini
ARG rich
                 121   GSMMATGKLLLSYSPPGAKPPTNRKDAMLGTHIIWDLGLQSSCSMVAPWISNTVYRRCAR 180
Beta sheet                   SSSSSSSSSSSS
Beta turn
Disordered termini                                                                    D
ARG rich
                 181   DDFTEGGFITCFYQTRIVVPASTPTSMFMLGFVSACPDFSVRLLRDTSHISQSKLIARTQ 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241    240


Inner capsid (VP4)  |  P22055 [2 - 69]
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   GAQVSTQKTGAHENQNVAANGSTINYTTINYYKDSASNSATRQDLSQDPSKFTEPVKDLM 60
```

```
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   LKTAPALN 68


         Viral protein genome linked (VPg)  |  P22055 [1541 – 1562]
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich
                            1   GAYTGLPNKKPNVPTIRIAKVQ 22




Human coxsackievirus B5 (Peterborough)
         Major capsid, 1 variant of 3 (VP1)  |  O41855
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   FYQGPPGEAVERAIARVADTISSGPVNSESIPALTAAETGHTSQVVPADTMQTRHVKNYH 60
         Beta sheet
         Beta turn                                    UUU
         Disordered termini
         ARG rich                                                      RRRRRRRRRRRRRRRRR
                           61   SRSESTVENFLCRSACVYYTTYKNHGTDGDNFAYWVINTRQVAQLRRKLEMFTYARFDLE 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   LTFVITSTQEQSTIQGQDSPVLTHQIMYVPPGGPVPTKINSYSWQTSTNPSVFWTEGSAP 180
         Beta sheet                                                                  SSSSSSS
         Beta turn                                    UUUU
         Disordered termini
         ARG rich                                                                         RR
                          181   PRISIPFISIGNAYSMFYDGWAKFDKQGTYGINTLNNMGTLYMRHVNDGSPGPIVSTVRI 240
         Beta sheet             SSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich               RRRRRRRRRRRRRRRRRRRRRR
                          241   YFKPKHVKTWVPRPPRLCQYQKAGNVNFEPTGVTESRTEITAMQTT 286


         Capsid (VP2)  |  P22055 [70 – 341]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   SPSAEECGYSDRVRSITLGNSTITTQECANVVVGYGTWPTYLKDEEATAEDQPTQPDVAT 60
         Beta sheet
         Beta turn                                                    UUUUU
         Disordered termini
         ARG rich
                           61   CRFYTLESVMWQQSSPGWWWKFPDALSNMGLFGQNMQYHYLGRAGYTVHVQCNASKFHQG 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   CLLVVCVPEAEMGCATLANKPDQKSLSNGETANTFDSQNTTGQTAVQANVINAGMGVGVG 180
         Beta sheet                                                   SSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          181   NLTIFPHQWINLRTNNSATIVMPYINSVPMDNMFRHNNFTLMIIPFAPLSYSTGATTYVP 240
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
```

```
                          241   ITVTVAPMCAEYNGLRLAGKQ 261


         Capsid (VP3)  |  P22055 [342 - 581]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   GLPTMLTPGSNQFLTSDDFQSPSAMPQFDVTPEMAIPGQVNNLMEIAEVDSVVPVNNTEG 60
         Beta sheet                                                           SSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                           61   KVSSIEAYQIPVQSNSTNGSQVFGFPLIPGASSVLNRTLLGEILNYYTHWSGSIKLTFMF 120
         Beta sheet             SS
         Beta turn
         Disordered termini
         ARG rich
                          121   CGSAMATGKFLLAYSPPGAGAPTTRKEAMLGTHVIWDVGLQSSCVLCIPWISQTHYRYVV 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          181   VDEYTAGGYITCWYQTNIVVPADTQSDCKILCFVSACNDFSVRMLKDTPFIKQDSF 236


         Inner capsid (VP4)  |  P22055 [2 - 69]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   GAQVSTQKTGAHETGLRASGNSIIHYTNINYYKDAASNSANRQEFAQDPGKFTEPVKDIM 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   IKSMPALN 68


         Viral protein genome linked (VPg)  |  P22055 [1541 - 1562]
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich
                            1   GAYTGMPNQKPKVPTLRQAKVQ 22




Enterobacteria phage fr
         Maturation (A)  |  P15966
         Beta sheet
         Beta turn                      UUUUUU                                   UUUUUU
         Disordered termini     D
         ARG rich                RRRRRRRRRRRRRRRRRR
                            1   MRKFIPTERMSKSHVVSVREYADGELEDNSLPLIYRSNWSPGQYTSTGPRTKEWHYPSSY 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   SRGAIGIKALDQGKYARLGTSWGREFEERAGYGMSIDARSCYSLFPVSQNLTWIDVPTNV 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                                        RRRRRRRRRRRRRRRRRRR
                          121   ANRATTEVLGKVTQGNFNLGVALAEARSTASQLSTQTIALIKAYTAARRGNWRQALRYLA 180
         Beta sheet
         Beta turn                  UUUUUU                            UUUUU
         Disordered termini
         ARG rich               RRRRRRRRRRRRRRR
                          181   LNENRKFNSKSVASRWLELQFGWMPLLSDIQGAYEMLTKVHLKAFMPMRAVRQVGQNVSL 240
```

```
         Beta sheet                      SSSSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          241   SGRLTSPAASYKSTCNISRRIVIWFYINDARLAWLSSLGILNPLGIVWEKVPFSFLVDWL 300
         Beta sheet                                                       SSSSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          301   LPVGNMLEGLTAPIGCSYQSGTVTDVISGESTITADDIYGWDTVRPATAKVQISAVHRGV 360
         Beta sheet             S
         Beta turn
         Disordered termini
         ARG rich
                          361   QSVWPTTGVYVKSPFSMVHTLDALALFRQRLWK 393


         Capsid (CP)  |  P03601
         Beta sheet                                                                     SSSS
         Beta turn
         Disordered termini     DD
         ARG rich                                                     RRRRRRRRRRRRRRRRRRRRRR
                            1   MASNFEEFVLVDNGGTGDVKVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSANNRKYT 60
         Beta sheet             SSSSSSSSSSSSS        SSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich               RRRRRRR
                           61   VKVEVPKVATQVQGGVELPVAAWRSYMNMELTIPVFATNDDCALIVKALQGTFKTGNPIA 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   TAIAANSGIY 130




Enterobacteria phage GA
         Maturation (A)  |  P15966
         Beta sheet
         Beta turn                      UUUUUU     UUUU                           UUUUUU
         Disordered termini
         ARG rich                  RRRRRRRRRRRRRRRRRRRR                 RRRRRRRRRRRRRRRRRRRR
                            1   MFPKSNIDRNYKVKLISYDKKGKLVSDDSFEQVENYLFQNRSTTYKPGYIRRDFRRPTNF 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich               RRRRR
                           61   WNGYRCFNQPVGTFTRKLSDGGRQVADYGIVNPNKFTANSQHLGDNMVIYPGPFSINIDQ 120
         Beta sheet
         Beta turn                                                           UUUUUU
         Disordered termini
         ARG rich
                          121   RASVEVLNKLSQSNLNIGVAIAEAKMTASLLAKQSIALIRAYTAAKRGNWREVLSQLLIS 180
         Beta sheet
         Beta turn               UUUUUUUU
         Disordered termini
         ARG rich
                          181   EHRFRAPAKDLGGRWLELQYGWLPLMSDLKAAYDLLTQTKLPAFMPLRVTRTVGGTHNYK 240
         Beta sheet                      SSSSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          241   VRNVESAGDTWSYRHRLSVNYRIWYFISDPRLAWASSLGLLNPLEIYWEKTPWSFVVDWF 300
         Beta sheet                             SSSSSSSSSSSSSSSSSS      SSSSSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          301   LPVGNLIEAMSNPLGLDIISGTKTWQLESKLNATLPASGWSGTAKLTAYAKAYDRSTFYS 360
         Beta sheet
         Beta turn
```

```
         Disordered termini
         ARG rich
                          361   FPTPLPYVKSPLSGLHLANALALINQRLKR 390


         Capsid (CP)  |  P03601
         Beta sheet                                                                    SSSSS
         Beta turn
         Disordered termini     D
         ARG rich                                                    RRRRRRRRRRRRRRRRRRRRRRR
                            1   MATLRSFVLVDNGGTGNVTVVPVSNANGVAEWLSNNSRSQAYRVTASYRASGADKRKYAI 60
         Beta sheet             SSSSSSSSSSSS        SSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich               RRRRRR
                           61   KLEVPKIVTQVVNGVELPGSAWKAYASIDLTIPIFAATDDVTVISKSLAGLFKVGNPIAE 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   AISSQSGFYA 130




Escherichia phage MS2
         Maturation (A)  |  P15966
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   MRAFSTLDRENETFVPSVRVYADGETEDNSFSLKYRSNWTPGRFNSTGAKTKQWHYPSPY 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   SRGALSVTSIDQGAYKRSGSSWGRPYEEKAGFGFSLDARSCYSLFPVSQNLTYIEVPQNV 120
         Beta sheet
         Beta turn                                                                UUUUUUUUUU
         Disordered termini
         ARG rich                                                        RRRRRRRRRRRRRRRRRRR
                          121   ANRASTEVLQKVTQGNFNLGVALAEARSTASQLATQTIALVKAYTAARRGNWRQALRYLA 180
         Beta sheet                                                               SSSSSSSSSSSSS
         Beta turn                  UUUUUUUUUUU                       UUU
         Disordered termini
         ARG rich               RRRRRRRRRRRRRRR
                          181   LNEDRKFRSKHVAGRWLELQFGWLPLMSDIQGAYEMLTKVHLQEFLPMRAVRQVGTNIKL 240
         Beta sheet             S        SSSSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          241   DGRLSYPAANFQTTCNISRRIVIWFYINDARLAWLSSLGILNPLGIVWEKVPFSFVVDWL 300
         Beta sheet                                                               SSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          301   LPVGNMLEGLTAPVGCSYMSGTVTDVITGESIISVDAPYGWTVERQGTAKAQISAMHRGV 360
         Beta sheet             S
         Beta turn
         Disordered termini
         ARG rich
                          361   QSVWPTTGAYVKSPFSMVHTLDALALIRQRLSR 393


         Capsid (CP)  |  P03601
         Beta sheet                                                   SSSSSSSSSSSSS     SSSS
         Beta turn
         Disordered termini     DD
         ARG rich                                                     RRRRRRRRRRRRRRRRRRRRRR
                            1   MASNFTQFVLVDNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSAQNRKYT 60
         Beta sheet             SSSSSSSSSSSSS         SSSSSSSSSSSS
```

```
         Beta turn
         Disordered termini
         ARG rich               RRRRRRR
                           61   IKVEVPKVATQTVGGVELPVAAWRSYLNMELTIPIFATNSDCELIVKAMQGLLKDGNPIP 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   SAIAANSGIY 130




Escherischia phage Qb
         Minor capsid protein (A1)  |  Q8LTE1
         Beta sheet
         Beta turn                           UUUU                                        UUU
         Disordered termini     D
         ARG rich                                                             RRRRRRRRRRRRRR
                            1   MAKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNR 60
         Beta sheet              SSSSSSSSSSSSSSSS      SSSSSSSSSSSSSS
         Beta turn              UUUUUUUU
         Disordered termini
         ARG rich               RRRRRRRR
                           61   KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFVRTELAALLASP 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   LLIDAIDQLNPAYWTLLIAGGGSGSKPDPVIPDPPIDPPPGTGKYTCPFAIWSLEEVYEP 180
         Beta sheet
         Beta turn                UUU
         Disordered termini
         ARG rich
                          181   PTKNRPWPIYNAVELQPREFDVALKDLLGNTKWRDWDSRLSYTTVRGCRGNGYIDLDATY 240
         Beta sheet
         Beta turn                     UUUUUUUUUUUU
         Disordered termini
         ARG rich                      RRRRRRRRRRRRRRRRRRRRRRRRRR
                          241   LATDQAMRDQKYDIREGKKPGAFGNIERFIYLKSINAYCSLSDIAAYHADGVIVGFWRDP 300
         Beta sheet
         Beta turn                         UUUUUU
         Disordered termini
         ARG rich
                          301   SSGGAIPFDFTKFDKTKCPIQAVIVVPRA 329


         Maturation (A2)  |  P03610
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich                                                        RRRRRRRRRRRRRRRRRRR
                            1   MPKLPRGLRFGADNEILNDFQELWFPDLFIESSDTHPWYTLKGRVLNAHLDDRLPNVGGR 60
         Beta sheet                                          SSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich               RRRRRRRR
                           61   QVRRTPHRVTVPIASSGLRPVTTVQYDPAALSFLLNARVDWDFGNGDSANLVINDFLFRT 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                                     RRRRRRRRRRRRRRRRRRRRRR
                          121   FAPKEFDFSNSLVPRYTQAFSAFNAKYGTMIGEGLETIKYLGLLLRRLREGYRAVKRGDL 180
         Beta sheet
         Beta turn                                                               UUUUUUUUUU
         Disordered termini
         ARG rich               RRRRRRRRRRRRRRRR                      RRRRRRRRRRRRRRRRRRR
                          181   RALRRVIQSYHNGKWKPATAGNLWLEFRYGLMPLFYDIRDVMLDWQNRHDKIQRLLRFSV 240
         Beta sheet                               SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
```

```
         ARG rich                                   RRRRRRRRRRRRRRRRRRRRR
                          241   GHGEDYVVEFDNLYPAVAYFKLKGEITLERRHRHGISYANREGYAVFDNGSLRPVSDWKE 300
         Beta sheet                                                      SSSSSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich                                                                RRRRRRRRRRR
                          301   LATAFINPHEVAWELTPYSFVVDWFLNVGDILAQQGQLYHNIDIVDGFDRRDIRLKSFTI 360
         Beta sheet             SSSS  SSSSSSSSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich               RRRRRRR
                          361   KGERNGRPVNVSASLSAVDLFYSRLHTSNLPFATLDLDTTFSSFKHVLDSIFLLTQRVKR 420
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          421    420


         Capsid (CP)  |  P03601
         Beta sheet
         Beta turn                           UUUU                                        UUU
         Disordered termini     D
         ARG rich                                                             RRRRRRRRRRRRRR
                            1   MAKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNR 60
         Beta sheet              SSSSSSSSSSSSSS
         Beta turn              UUUUUUUU
         Disordered termini
         ARG rich               RRRRRRRR
                           61   KNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFVRTELAALLASP 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   LLIDAIDQLNPAY 133




Enterobacteria phage SP
         Minor capsid protein (A1)  |  Q8LTE1
         Beta sheet                                                      SSSSSSSSSSSSSS
         Beta turn                        UUUU                                           UUU
         Disordered termini     D
         ARG rich
                            1   MAKLNQVTLSKIGKNGDQTLTLTPRGVNPTNGVASLSEAGAVPALEKRVTVSVAQPSRNR 60
         Beta sheet              SSSSSSSSSSSSSSS      SSSSSSSSSSSSSS
         Beta turn              UUUUUUUU
         Disordered termini
         ARG rich
                           61   KNFKVQIKLQNPTACTRDACDPSVTRSAFADVTLSFTSYSTDEERALIRTELAALLADPL 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   IVDAIDNLNPAYWAALLVASSGGGDNPSDPDVPVVPDVKPPDGTGRYKCPFACYRLGSIY 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                 RRRRRRRRRRRRRRRRRRR
                          181   EVGKEGSPDIYERGDEVSVTFDYALEDFLGNTNWRNWDQRLSDYDIANRRRCRGNGYIDL 240
         Beta sheet                                                             SSSSSSSSSSSS
         Beta turn                            UUUUUUUU
         Disordered termini
         ARG rich                             RRRRRRRRRRRRRRRRR
                          241   DATAMQSDDFVLSGRYGVRKVKFPGAFGSIKYLLNIQGDAWLDLSEVTAYRSYGMVIGFW 300
         Beta sheet             S
         Beta turn
         Disordered termini
         ARG rich
                          301   TDSKSPQLPTDFTQFNSANCPVQTVIIIPSL 331
```

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         Maturation (A2)  |  P03610
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich
                            1   MPTLPRGLRFGSNGEVLNDFEALWFPERHTVDLSNGTCKLTGYITNLPGYSDIFPNKGVT 60
         Beta sheet                                          SSSSSSSSSSSS
         Beta turn                           UUUUU
         Disordered termini
         ARG rich
                           61   AARTPYRSTVPVNHLGYRPVTTVEYIPDGTYVRLDGHVKFEGDLVNGSVDLTNFVISLAA 120
         Beta sheet
         Beta turn                                                         UUUUUUUUUUUUUUUUU
         Disordered termini
         ARG rich                           RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                          121   QGGFDYQSVIGPRFSARFSAFSTKYGVLLGEGRETLKYLLLVVRRMREGYRAVRRGDLKR 180
         Beta sheet
         Beta turn              UU
         Disordered termini
         ARG rich               RR           RRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                          181   LRNVISTFEPSTIKGKRARAEFSQTYRDKLTGNKVEVRPSEGKWNSSSASDLWLEFRYGL 240
         Beta sheet                                                           SSSSSSSSSSSSSS
         Beta turn                                            UUU
         Disordered termini
         ARG rich                              RRRRRRRRRRRRRRRRRRRRRRRRR
                          241   MPLFYDIQSVMEDFMRVHKKIAKIQRFSAGHGKLETVSSRFYPDVHFSLEVTAVLQRRHR 300
         Beta sheet             SSSSSS
         Beta turn                                    UUUU
         Disordered termini
         ARG rich
                          301   WGVIYQDTGSFATFNNGRLVPVKDWKTAAFALLNPAEVAWEVTPYSFVVDWFVNVGDMLE 360
         Beta sheet                      SSSSSSSSSSSSSSSSSSSSS
         Beta turn                    UU
         Disordered termini
         ARG rich                     RRRRRRRRRRRRRRRRRRRRRR
                          361   QMGQLYRHVDVVDGFDRKDIKLKSVSVRVLTNDVAHVASFQLRQAKLLHSYYSRVHTVAF 420
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          421   PQISPQLDTEIRSVKHVIDSIALLTQRVKR 450


         Capsid (CP)  |  P03601
         Beta sheet                                             SSSSSSSSSSSSSSSSSSSSSSS
         Beta turn                                                                       UUU
         Disordered termini     D
         ARG rich
                            1   MAKLNQVTLSKIGKNGDQTLTLTPRGVNPTNGVASLSEAGAVPALEKRVTVSVAQPSRNR 60
         Beta sheet              SSSSSSSSSSSSSS
         Beta turn              UUUUUUUU
         Disordered termini
         ARG rich
                           61   KNFKVQIKLQNPTACTRDACDPSVTRSAFADVTLSFTSYSTDEERALIRTELAALLADPL 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   IVDAIDNLNPAY 132




Echovirus 1 (strain Human/Egypt/Farouk/1951) (E-1)
         Major capsid, 1 variant of 3 (VP1)  |  O41855
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
```

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                   1   FYQGDVQNAVEGAMVRVADTVQTSATNSERVPNLTAVETGHTSQAVPGDTMQTRHVINNH 60
Beta sheet
Beta turn
Disordered termini
ARG rich                                                       RRRRRRRRRRRRRRRRR
                  61   VRSESTIENFLARSACVFYLEYKTGTKEDSNSFNNWVITTRRVAQLRRKLEMFTYLRFDM 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   EITVVITSSQDQSTSQNQNAPVLTHQIMYVPPGGPIPVSVDDYSWQTSTNPSIFWTEGNA 180
Beta sheet                                                                    SSSSS
Beta turn
Disordered termini
ARG rich                                                                          R
                 181   PARMSIPFISIGNAYSNFYDGWSHFSQAGVYGFTTLNNMGQLFFRHVNKPNPAAITSVAR 240
Beta sheet             SSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich               RRRRRRRRRRRRRRRRR
                 241   IYFKPKHVRAWVPRPPRLCPYINSTNVNFEPKPVTEVRTNIITT 284


Capsid (VP2)  |  P22055 [70 – 341]
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   SPTVEECGYSDRVRSITLGNSTITTQECANVVVGYGEWPEYLSDNEATAEDQPTQPDVAT 60
Beta sheet                                                 SSSSSSSSSSSSSSSSS
Beta turn                                                                     UUU
Disordered termini
ARG rich
                  61   CRFYTLDSVQWENGSPGWWWKFPDALRDMGLFGQNMYYHYLGRAGYTIHVQCNASKFHQG 120
Beta sheet
Beta turn                                      UUUU
Disordered termini
ARG rich
                 121   CILVVCVPEAEMGSAQTSGVVNYEHISKGEIASRFTTTTTAEDHGVQAAVWNAGMGVGVG 180
Beta sheet
Beta turn                                                UUU
Disordered termini
ARG rich
                 181   NLTIFPHQWINLRTNNSATIVMPYVNSVPMDNMYRHHNFTLMIIPFVPLDFSAGASTYVP 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241   ITVTVAPMCAEYNGLRLAGHQ 261


Capsid (VP3)  |  P22055 [342 – 581]
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   GLPTMNTPGSNQFLTSDDFQSPSAMPQFDVTPEMHIPGEVRNLMEIAEVDSVMPINNDSA 60
Beta sheet                                                            SSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                  61   AKVSSMEAYRVELSTNTNAGTQVFGFQLNPGAESVMNRTLMGEILNYYAHWSGSIKITFV 120
Beta sheet             SSS
Beta turn                                     UUUU                            UUUUU
Disordered termini
ARG rich
                 121   FCGSAMTTGKFLLSYAPPGAGAPKTRKDAMLGTHVVWDVGLQSSCVLCIPWISQTHYRFV 180
Beta sheet
Beta turn              UU
Disordered termini
ARG rich
                 181   EKDPYTNAGFVTCWYQTSVVSPASNQPKCYMMCMVSACNDFSVRMLRDTKFIEQTSF 237
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         Inner capsid (VP4)  |  P22055 [2 – 69]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   GAQVSTQKTGAHETSLSATGNSIIHYTNINYYKDAASNSANRQDFTQDPGKFTEPMKDVM 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   IKTLPALN 68


         Viral protein genome linked (VPg)  |  P22055 [1541 – 1562]
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich
                            1   GAYTGMPNQKPKVPTLRQAKVQ 22




Erysimum latent virus
         Capsid (CP)  |  P03601
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDD
         ARG rich
                            1   MTSSRSTELIETQEDVVRKLSQKTPVSNFSALPLPNGPQAPTQLQPFQFEFPLPAGQEGS 60
         Beta sheet                                SSSSSSSSSSSSS
         Beta turn                              UUUU
         Disordered termini
         ARG rich
                           61   VTLPLATFPKMATFLSRHRRAQLTQLHAVVSPSAVSIGHPLTVQLIWVPASSTTTSSQIL 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   GTYGGQQISVGGQVTNSSPAKVSANLLMMNPHIKDSTSYTDTPKLLVYSTPAVPDDKLTT 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          181   SSASIIVFGEVLLSSPQLNPSA 202




Human adenovirus C5
         core-capsid bridging protein (CoreCapsid)  |  P24938
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich                                     RRRRRRRRRRRRRRRRRRRR
                            1   MSKRKIKEEMLQVIAPEIYGPPKKEEQDYKPRLKRVKKKKKDDDDELDDEVELLHATAP 60
         Beta sheet
         Beta turn              UUUUUUUUUUUUUUUU           UUUUUUUU
         Disordered termini
         ARG rich               RRRRRRRRRRRRRRRR
                           61   RRRVQWKGRRVKRVLRPGTTVVFTPGERSTRTYKRVYDEVYGDEDLLEQANERLGEFAYG 120
         Beta sheet
         Beta turn              UUUU                                                     UUU
         Disordered termini
         ARG rich
                          121   KRHKDMLALPLDEGNPTPSLKPVTLQQVLPALAPSEEKRGLKRESGDLAPTVQLMVPKRQ 180
         Beta sheet
         Beta turn              U
```

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Disordered termini
ARG rich
                 181   RLEDVLEKMTVEPGLEPEVRVRPIKQVAPGLGVQTVDVQIPTTSSTSIATATEGMETQTS 240
Beta sheet
Beta turn
Disordered termini
ARG rich                                               RRRRRRRRRRRRR
                 241   PVASAVADAAVQAVAAAASKTSTEVQTDPWMFRVSAPRRPRGSRKYGAASALLPEYALHP 300
Beta sheet
Beta turn
Disordered termini
ARG rich                       RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                 301   SIAPTPGYRGYTYRPRRRATTRRRTTTGTRRRRRRRQPVLAPISVRRVAREGGRTLVLPT 360
Beta sheet
Beta turn
Disordered termini
ARG rich               RR
                 361   ARYHPSIV 368


Histone-like nucleoprotein (HistoneLike)  |  P68951 [25 - 198]
Beta sheet
Beta turn
Disordered termini
ARG rich                RRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                   1   AKKRSDQHPVRVRGHYRAPWGAHKRGRTGRTTVDDAIDAVVEEARNYTPTPPPVSTVDAA 60
Beta sheet
Beta turn
Disordered termini
ARG rich                    RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                  61   IQTVVRGARRYAKMKRRRRRVARRHRRRPGTAAQRAAAALLNRARRTGRRAAMRAARRLA 120
Beta sheet
Beta turn
Disordered termini                                                          D
ARG rich                                   RRRRRRRRRRRRRRRRRRRRRRRRR
                 121   AGIVTVPPRSRRRAAAAAAAAISAMTQGRRGNVYWVRDSVSGLRVPVRTRPPRN 174


Hexon-linking protein (IIIa)  |  P12537 [1 - 570]
Beta sheet
Beta turn
Disordered termini     DDDDD
ARG rich
                   1   MMQDATDPAVRAALQSQPSGLNSTDDWRQVMDRIMSLTARNPDAFRQQPQANRLSAILEA 60
Beta sheet
Beta turn                                     UUUU
Disordered termini
ARG rich
                  61   VVPARANPTHEKVLAIVNALAENRAIRPDEAGLVYDALLQRVARYNSGNVQTNLDRLVGD 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   VREAVAQRERAQQQGNLGSMVALNAFLSTQPANVPRGQEDYTNFVSALRLMVTETPQSEV 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   YQSGPDYFFQTSRQGLQTVNLSQAFKNLQGLWGVRAPTGDRATVSSLLTPNSRLLLLLIA 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241   PFTDSGSVSRDTYLGHLLTLYREAIGQAHVDEHTFQEITSVSRALGQEDTGSLEATLNYL 300
Beta sheet
Beta turn
Disordered termini
ARG rich
                 301   LTNRRQKIPSLHSLNSEEERILRYVQQSVSLNLMRDGVTPSVALDMTARNMEPGMYASNR 360
Beta sheet
Beta turn
Disordered termini
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ARG rich
                 361   PFINRLMDYLHRAAAVNPEYFTNAILNPHWLPPPGFYTGGFEVPEGNDGFLWDDIDDSVF 420
Beta sheet
Beta turn
Disordered termini
ARG rich                           RRRRRRRRRRRRRRR
                 421   SPQPQTLLELQQREQAEAALRKESFRRPSSLSDLGAAAPRSDASSPFPSLIGSLTSTRTT 480
Beta sheet
Beta turn
Disordered termini                                                 DDDDDDDDDDDDDDDDD
ARG rich                                                     RRRRRRRRRRRRRRRRRRRRRR
                 481   RPRLLGEEEYLNNSLLQPQREKNLPPAFPNNGIESLVDKMSRWKTYAQEHRDVPGPRPPT 540
Beta sheet
Beta turn
Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
ARG rich               RRRRRRRRR
                 541   RRQRHDRQRGLVWEDDDSADDSSVLDLGGS 570


Packaging protein (IVa2)  |  P03271
Beta sheet
Beta turn
Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
ARG rich
                   1   METRGRRPAALQHQQDQPQAHPGQRAARSAPLHRDPDYADEDPAPVERHDPGPSGRAPTT 60
Beta sheet
Beta turn
Disordered termini     DDDDDDDDDDDDD
ARG rich
                  61   AVQRKPPQPAKRGDMLDRDAVEQVTELWDRLELLGQTLKSMPTADGLKPLKNFASLQELL 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   SLGGERLLADLVRENMRVRDMLNEVAPLLRDDGSCSSLNYQLHPVIGVIYGPTGCGKSQL 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   LRNLLSSQLISPTPETVFFIAPQVDMIPPSELKAWEMQICEGNYAPGPDGTIIPQSGTLR 240
Beta sheet
Beta turn
Disordered termini
ARG rich                                                                RRRRRRRRRRR
                 241   PRFVKMAYDDLILEHNYDVSDPRNIFAQAAARGPIAIIMDECMENLGGHKGVSKFFHAFP 300
Beta sheet
Beta turn               UUUUUUUU                                     UUU
Disordered termini
ARG rich               RRRRRRRRR
                 301   SKLHDKFPKCTGYTVLVVLHNMNPRRDMAGNIANLKIQSKMHLISPRMHPSQLNRFVNTY 360
Beta sheet
Beta turn                          UUUUUUUUUU                      UUU
Disordered termini
ARG rich
                 361   TKGLPLAISLLLKDIFRHHAQRSCYDWIIYNTTPQHEALQWCYLHPRDGLMPMYLNIQSH 420
Beta sheet
Beta turn
Disordered termini                              DDDD
ARG rich                     RRRRRRRRRRRRRRRRRRRRRRR
                 421   LYHVLEKIHRTLNDRDRWSRAYRARKTPK 449


hexon-interlacing protein (IX)  |  P03281
Beta sheet
Beta turn
Disordered termini     DDDD
ARG rich
                   1   MSTNSFDGSIVSSYLTTRMPPWAGVRQNVMGSSIDGRPVLPANSTTLTYETVSGTPLETA 60
Beta sheet
Beta turn
Disordered termini
ARG rich
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                  61   ASAAASAAAATARGIVTDFAFLSPLASSAASRSSARDDKLTALLAQLDSLTRELNVVSQQ 120
Beta sheet
Beta turn
Disordered termini                  DDDDDDD
ARG rich
                 121   LLDLRQQVSALKASSPPNAV 140


Penton protein (L2)  |  P12538
Beta sheet
Beta turn
Disordered termini     D
ARG rich
                   1   MRRAAMYEEGPPPSYESVVSAAPVAAALGSPFDAPLDPPFVPPRYLRPTGGRNSIRYSEL 60
Beta sheet
Beta turn                                                                     UUU
Disordered termini
ARG rich
                  61   APLFDTTRVYLVDNKSTDVASLNYQNDHSNFLTTVIQNNDYSPGEASTQTINLDDRSHWG 120
Beta sheet
Beta turn
Disordered termini
ARG rich                                    RRRRRRRRRRRRRRRRRRRRR
                 121   GDLKTILHTNMPNVNEFMFTNKFKARVMVSRLPTKDNQVELKYEWVEFTLPEGNYSETMT 180
Beta sheet
Beta turn                                         UUUUUUUU
Disordered termini
ARG rich
                 181   IDLMNNAIVEHYLKVGRQNGVLESDIGVKFDTRNFRLGFDPVTGLVMPGVYTNEAFHPDI 240
Beta sheet
Beta turn                          UUU
Disordered termini
ARG rich                            RRRRRRRRRRRRRRRRRRR
                 241   ILLPGCGVDFTHSRLSNLLGIRKRQPFQEGFRITYDDLEGGNIPALLDVDAYQASLKDDT 300
Beta sheet
Beta turn
Disordered termini
ARG rich
                 301   EQGGGGAGGSNSSGSGAEENSNAAAAAMQPVEDMNDHAIRGDTFATRAEEKRAEAEAAAE 360
Beta sheet                                                   SSSSSSSSSSSSS
Beta turn                                        UUU
Disordered termini
ARG rich                          RRRRRRRRRRRRRRRRRR
                 361   AAAPAAQPEVEKPQKKPVIKPLTEDSKKRSYNLISNDSTFTQYRSWYLAYNYGDPQTGIR 420
Beta sheet
Beta turn
Disordered termini
ARG rich
                 421   SWTLLCTPDVTCGSEQVYWSLPDMMQDPVTFRSTRQISNFPVVGAELLPVHSKSFYNDQA 480
Beta sheet
Beta turn                           UUUUU
Disordered termini
ARG rich
                 481   VYSQLIRQFTSLTHVFNRFPENQILARPPAPTITTVSENVPALTDHGTLPLRNSIGGVQR 540
Beta sheet                        SSSSSSSSSSSSSS
Beta turn                    UUU
Disordered termini
ARG rich
                 541   VTITDARRRTCPYVYKALGIVSPRVLSSRTF 571


Hexon protein (L3)  |  P04133
Beta sheet
Beta turn
Disordered termini     DD
ARG rich
                   1   MATPSMMPQWSYMHISGQDASEYLSPGLVQFARATETYFSLNNKFRNPTVAPTHDVTTDR 60
Beta sheet              SSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                  61   SQRLTLRFIPVDREDTAYSYKARFTLAVGDNRVLDMASTYFDIRGVLDRGPTFKPYSGTA 120
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Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   YNALAPKGAPNPCEWDEAATALEINLEEEDDDNEDEVDEQAEQQKTHVFGQAPYSGINIT 180
Beta sheet
Beta turn                           UUUUU                   UUUUUUUUU
Disordered termini
ARG rich                                                        RRRRRRRRRRRRRRRRRR
                 181   KEGIQIGVEGQTPKYADKTFQPEPQIGESQWYETEINHAAGRVLKKTTPMKPCYGSYAKP 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241   TNENGGQGILVKQQNGKLESQVEMQFFSTTEATAGNGDNLTPKVVLYSEDVDIETPDTHI 300
Beta sheet
Beta turn
Disordered termini
ARG rich
                 301   SYMPTIKEGNSRELMGQQSMPNRPNYIAFRDNFIGLMYYNSTGNMGVLAGQASQLNAVVD 360
Beta sheet
Beta turn                                 UUU
Disordered termini
ARG rich
                 361   LQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDPDVRIIENHGTEDELPNYCFPLGGV 420
Beta sheet
Beta turn
Disordered termini
ARG rich
                 421   INTETLTKVKPKTGQENGWEKDATEFSDKNEIRVGNNFAMEINLNANLWRNFLYSNIALY 480
Beta sheet
Beta turn                                       UU
Disordered termini
ARG rich
                 481   LPDKLKYSPSNVKISDNPNTYDYMNKRVVAPGLVDCYINLGARWSLDYMDNVNPFNHHRN 540
Beta sheet
Beta turn                                                           UU
Disordered termini
ARG rich
                 541   AGLRYRSMLLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMVLQSSLGND 600
Beta sheet
Beta turn
Disordered termini
ARG rich
                 601   LRVDGASIKFDSICLYATFFPMAHNTASTLEAMLRNDTNDQSFNDYLSAANMLYPIPANA 660
Beta sheet                                                            SSSSSSSSSSS
Beta turn
Disordered termini
ARG rich                        RRRRRRRRRRRRRRRRR
                 661   TNVPISIPSRNWAAFRGWAFTRLKTKETPSLGSGYDPYYTYSGSIPYLDGTFYLNHTFKK 720
Beta sheet             SSSSS
Beta turn
Disordered termini
ARG rich
                 721   VAITFDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTKDWFLVQMLANYNIGYQG 780
Beta sheet
Beta turn                                           UUU
Disordered termini
ARG rich                      RRRRRRRRRRRRRRRRRRRRRRRRR
                 781   FYIPESYKDRMYSFFRNFQPMSRQVVDDTKYKDYQQVGILHQHNNSGFVGYLAPTMREGQ 840
Beta sheet
Beta turn                                         UUUUU
Disordered termini
ARG rich                           RRRRRRRRRRRRRRRRRRRR
                 841   AYPANFPYPLIGKTAVDSITQKKFLCDRTLWRIPFSSNFMSMGALTDLGQNLLYANSAHA 900
Beta sheet                          SSSSSSSSSSSSSSSSS
Beta turn                                        UUUUUUU
Disordered termini
ARG rich
                 901   LDMTFEVDPMDEPTLLYVLFEVFDVVRVHRPHRGVIETVYLRTPFSAGNATT 952
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Fiber protein (L5)  |  P11818
Beta sheet
Beta turn
Disordered termini     DDDDDD
ARG rich
                   1   MKRARPSEDTFNPVYPYDTETGPPTVPFLTPPFVSPNGFQESPPGVLSLRLSEPLVTSNG 60
Beta sheet
Beta turn                                                    UUUU
Disordered termini
ARG rich
                  61   MLALKMGNGLSLDEAGNLTSQNVTTVSPPLKKTKSNINLEISAPLTVTSEALTVAAAAPL 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   MVAGNTLTMQSQAPLTVHDSKLSIATQGPLTVSEGKLALQTSGPLTTTDSSTLTITASPP 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   LTTATGSLGIDLKEPIYTQNGKLGLKYGAPLHVTDDLNTLTVATGPGVTINNTSLQTKVT 240
Beta sheet
Beta turn                                               UU
Disordered termini
ARG rich
                 241   GALGFDSQGNMQLNVAGGLRIDSQNRRLILDVSYPFDAQNQLNLRLGQGPLFINSAHNLD 300
Beta sheet
Beta turn                                                                               UUU
Disordered termini
ARG rich
                 301   INYNKGLYLFTASNNSKKLEVNLSTAKGLMFDATAIAINAGDGLEFGSPNAPNTNPLKTK 360
Beta sheet
Beta turn              UUU                              UUUUU                  UUUU
Disordered termini
ARG rich
                 361   IGHGLEFDSNKAMVPKLGTGLSFDSTGAITVGNKNNDKLTLWTTPAPSPNCRLNAEKDAK 420
Beta sheet                       SSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 421   LTLVLTKCGSQILATVSVLAVKGSLAPISGTVQSAHLIIRFDENGVLLNNSFLDPEYWNF 480
Beta sheet
Beta turn                                               UUUUUUUU            UUU
Disordered termini
ARG rich
                 481   RNGDLTEGTAYTNAVGFMPNLSAYPKSHGKTAKSNIVSQVYLNGDKTKPVTLTITLNGTQ 540
Beta sheet
Beta turn
Disordered termini
ARG rich
                 541   ETGDTTPSAYSMSFSWDWSGHNYINEIFATSSYTFSYIAQE 581


Protease (Protease)  |  P03253
Beta sheet
Beta turn                                                UU       UU
Disordered termini
ARG rich
                   1   MGSSEQELKAIVKDLGCGPYFLGTYDKRFPGFVSPHKLACAIVNTAGRETGGVHWMAFAW 60
Beta sheet
Beta turn                UUU
Disordered termini
ARG rich
                  61   NPHSKTCYLFEPFGFSDQRLKQVYQFEYESLLRRSAIASSPDRCITLEKSTQSVQGPNSA 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   ACGLFCCMFLHAFANWPQTPMDHNPTMNLITGVPNSMLNSPQVQPTLRRNQEQLYSFLER 180
Beta sheet
Beta turn                   UUU
Disordered termini
```

```
         ARG rich
                          181   HSPYFRSHSAQIRSATSFCHLKNM 204


         Endosome lysis protein (VI)  |  P24937 [34 - 239]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   AFSWGSLWSGIKNFGSTVKNYGSKAWNSSTGQMLRDKLKEQNFQQKVVDGLASGISGVVD 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                                 RRRRRRRRRR
                           61   LANQAVQNKINSKLDPRPPVEEPPPAVETVSPEGRGEKRPRPDREETLVTQIDEPPSYEE 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                                                  RRRRRRRRR
                          121   ALKQGLPTTRPIAPMATGVLGQHTPVTLDLPPPADTQQKPVLPGPTAVVVTRPSRASLRR 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich               RRRRRRRRR
                          181   AASGPRSLRPVASGNWQSTLNSIVGL 206


         Hexon-linking protein C  (inner capsid) (VIIIC)  |  P24936 [158 - 227]
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich
                            1   GRPSFTPRQAILTLQTSSSEPRSGGIGTLQFIEEFVPSVYFNPFSGPPGHYPDQFIPNFD 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   AVKDSADGYD 70


         Hexon-linking protein N (inner capsid) (VIIIN)  |  P24936 [1 - 111]
         Beta sheet
         Beta turn
         Disordered termini     DD
         ARG rich
                            1   MSKEIPTPYMWSYQPQMGLAAGAAQDYSTRINYMSAGPHMISRVNGIRAHRNRILLEQAA 60
         Beta sheet
         Beta turn
         Disordered termini                                                DDDDDDDD
         ARG rich
                           61   ITTTPRNNLNPRSWPAALVYQESPAPTTVVLPRDAQAEVQMTNSGAQLAGG 111


         Core protein X (X)  |  Q2KS10 [33 - 51]
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDD
         ARG rich                RRRRRRRRRRRRRRRR
                            1   MRRAHHRRRRASHRRMRGG 19




Hepatitis A virus
         Major capsid, 1 variant of 3 (VP1)  |  O41855
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                           RRRRRRRRRRR
                            1   VGDDSGGFSTTVSTEQNVPDPQVGITTMKDLKGKANRGKMDVSGVQAPVGAITTIEDPVL 60
         Beta sheet
```

```
Beta turn
Disordered termini
ARG rich
                  61   AKKVPETFPELKPGESRHTSDHMSIYKFMGRSHFLCTFTFNSNNKEYTFPITLSSTSNPP 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   HGLPSTLRWFFNLFQLYRGPLDLTIIITGATDVDGMAWFTPVGLAVDTPWVEKESALSID 180
Beta sheet
Beta turn                      UUUUUU
Disordered termini
ARG rich
                 181   YKTALGAVRFNTRRTGNIQIRLPWYSYLYAVSGALDGLGDKTDSTFGLVSIQIANYNHSD 240
Beta sheet
Beta turn
Disordered termini                                      D
ARG rich
                 241   EYLSFSCYLSVTEQSEFYFPRAPLNSNAMLSTES 274


Capsid (VP2)  |  P22055 [70 - 341]
Beta sheet
Beta turn
Disordered termini
ARG rich                                                          RRRRRRRRRRRRRRRR
                   1   DIEEEQMIQSVDRTAVTGASYFTSVDQSSVHTAEVGSHQVEPLRTSVDKPGSKKTQGEKF 60
Beta sheet                                                     SSSSSSSSSSSSSS
Beta turn                         UUUUUUUUU
Disordered termini
ARG rich
                  61   FLIHSADWLTTHALFHEVAKLDVVKLLYNEQFAVQGLLRYHTYARFGIEIQVQINPTPFQ 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   QGGLICAMVPGDQSYGSIASLTVYPHGLLNCNINNVVRIKVPFIYTRGAYHFKDPQYPVW 180
Beta sheet                               SSSSSSSSSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 181   ELTIRVWSELNIGTGTSAYTSLNVLARFTDLELHGLTPLSTQ 222


Capsid (VP3)  |  P22055 [342 - 581]
Beta sheet
Beta turn
Disordered termini     D
ARG rich
                   1   MMRNEFRVSTTENVVNLSNYEDARAKMSFALDQEDWKSDPSQGGGIKITHFTTWTSIPTL 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   AAQFPFNASDSVGQQIKVIPVDPYFFQMTNTNPDQKCITALASICQMFCFWRGDLVFDFQ 120
Beta sheet
Beta turn                  UUUUUU
Disordered termini
ARG rich
                 121   VFPTKYHSGRLLFCFVPGNELIDVSGITLKQATTAPCAVMDITGVQSTLRFRVPWISDTP 180
Beta sheet                            SSSSSSSSSSSSSSSS       SSSSSSSSSSSSSSSSSS
Beta turn               UUUUUUUUUUUU
Disordered termini
ARG rich
                 181   YRVNRYTKSAHQKGEYTAIGKLIVYCYNRLTSPSNVASHVRVNVYLSAINLECFAPLYHA 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241   MDVTTQ 246
```

```
         Inner capsid (VP4)  |  P22055 [2 – 69]
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich
                            1   MNMSRQGIFQTVGSGLDHILSLA 23


         Viral protein genome linked (VPg)  |  P22055 [1541 – 1562]
         Beta sheet
         Beta turn
         Disordered termini                          DD
         ARG rich
                            1   GVYHGVTKPKQVIKLDADPVESQ 23




Human rhinovirus 2
         Major capsid, 1 variant of 3 (VP1)  |  O41855
         Beta sheet
         Beta turn
         Disordered termini     DD
         ARG rich
                            1   IAQNPVENYIDEVLNEVLVVPNINSSNPTTSNSAPALDAAETGHTSSVQPEDVIETRYVQ 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   TSQTRDEMSLESFLGRSGCIHESKLEVTLANYNKENFTVWAINLQEMAQIRRKFELFTYT 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   RFDSEITLVPCISALSQDIGHITMQYMYVPPGAPVPNSRDDYAWQSGTNASVFWQHGQAY 180
         Beta sheet                                                               SSSSSSSSSS
         Beta turn                                                            UUUUUUUUUUUUUU
         Disordered termini
         ARG rich
                          181   PRFSLPFLSVASAYYMFYDGYDEQDQNYGTANTNNMGSLCSRIVTEKHIHKVHIMTRIYH 240
         Beta sheet             SSSSSSSSSS
         Beta turn              UUUUUU
         Disordered termini
         ARG rich
                          241   KAKHVKAWCPRPPRALEYTRAHRTNFKIEDRSIQTAIVTRPIITTA 286


         Capsid (VP2)  |  P22055 [70 – 341]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   SPTVEACGYSDRIIQITRGDSTITSQDVANAIVAYGVWPHYLSSKDASAIDKPSQPDTSS 60
         Beta sheet                                                   SSSSSSSSSSSSSSS
         Beta turn                                                                  UUU
         Disordered termini
         ARG rich
                           61   NRFYTLRSVTWSSSSKGWWWKLPDALKDMGIFGENMFYHYLGRSGYTIHVQCNASKFHQG 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   TLIVALIPEHQIASALHGNVNVGYNYTHPGETGREVKAETRLNPDLQPTEEYWLNFDGTL 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          181   LGNITIFPHQFINLRSNNSATIIAPYVNAVPMDSMRSHNNWSLVIIPICPLETSSAINTI 240
         Beta sheet
         Beta turn
         Disordered termini
```

```
         ARG rich
                          241   PITISISPMCAEFSGARAKRQ 261


         Capsid (VP3)  |  P22055 [342 – 581]
         Beta sheet
         Beta turn                                          UUUU
         Disordered termini
         ARG rich
                            1   GLPVFITPGSGQFLTTDDFQSPCALPWYHPTKEISIPGEVKNLVEICQVDSLVPINNTDT 60
         Beta sheet                                                          SSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                           61   YINSENMYSVVLQSSINAPDKIFSIRTDVASQPLATTLIGEISSYFTHWTGSLRFSFMFC 120
         Beta sheet             S
         Beta turn
         Disordered termini
         ARG rich
                          121   GTANTTVKLLLAYTPPGIAEPTTRKDAMLGTHVIWDVGLQSTISMVVPWISASHYRNTSP 180
         Beta sheet                  SSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          181   GRSTSGYITCWYQTRLVIPPQTPPTARLLCFVSGCKDFCLRMARDTNLHLQSGAI 235


         Inner capsid (VP4)  |  P22055 [2 – 69]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   GAQVSRQNVGTHSTQNSVSNGSSLNYFNINYFKDAASNGASKLEFTQDPSKFTDPVKDVL 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   EKGIPTLQ 68


         Viral protein genome linked (VPg)  |  P22055 [1541 – 1562]
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich                      RRRRRRRRRR
                            1   GPYSGEPKPKTKIPERRVVTQ 21




Mengo encephalomyocarditis virus
         Major capsid, 1 variant of 3 (VP1)  |  O41855
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   GVENAEKGVTENTDATADFVAQPVYLPENQTKVAFFYDRSSPIGAFAVKSGSLESGFAPF 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   SNKACPNSVILTPGPQFDPAYDQLRPQRLTEIWGNGNEETSEVFPLKTKQDYSFCLFSPF 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   VYYKCDLEVTLSPHTSGAHGLLVRWCPTGTPTKPTTQVLHEVSSLSEGRTPQVYSAGPGT 180
         Beta sheet                                                                  SSSSSSS
         Beta turn                                                                UUUUU
         Disordered termini
         ARG rich                                                                 RRRRRRRRRR
```

```
                 181   SNQISFVVPYNSPLSVLPAVWYNGHKRFDNTGDLGIAPNSDFGTLFFAGTKPDIKFTVYL 240
Beta sheet             SSSSSSSSSS
Beta turn
Disordered termini
ARG rich               RRRRRRRRRRR
                 241   RYKNMRVFCPRPTVFFPWPTSGDKIDMTPRAGVLMLE 277


Capsid (VP2)  |  P22055 [70 - 341]
Beta sheet
Beta turn                                                     UUUUU
Disordered termini
ARG rich
                   1   DQNTEEMENLSDRVSQDTAGNTVTNTQSTVGRLVGYGTVHDGEHPASCADTASEKILAVE 60
Beta sheet                                                   SSSSSSSSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                  61   RYYTFKVNDWTSTQKPFEYIRIPLPHVLSGEDGGVFGATLRRHYLVKTGWRVQVQCNASQ 120
Beta sheet
Beta turn
Disordered termini
ARG rich                                       RRRRRRRRRRRRRRRRRR
                 121   FHAGSLLVFMAPEYPTLDVFAMDNRWSKDNLPNGTRTQTNRKGPFAMDHQNFWQWTLYPH 180
Beta sheet                                            SSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 181   QFLNLRTNTTVDLEVPYVNIAPTSSWTQHASWTLVIAVVAPLTYSTGASTSLDITASIQP 240
Beta sheet
Beta turn
Disordered termini                    D
ARG rich
                 241   VRPVFNGLRHEVLSRQ 256


Capsid (VP3)  |  P22055 [342 - 581]
Beta sheet
Beta turn                     UUU
Disordered termini
ARG rich
                   1   SPIPVTIREHAGTWYSTLPDSTVPIYGKTPVAPANYMVGEYKDFLEIAQIPTFIGNKVPN 60
Beta sheet                                                     SSSSSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                  61   AVPYIEASNTAVKTQPLAVYQVTLSCSCLANTFLAALSRNFAQYRGSLVYTFVFTGTAMM 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   KGKFLIAYTPPGAGKPTSRDQAMQATYAIWDLGLNSSYSFTVPFISPTHFRMVGTDQANI 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   TNVDGWVTVWQLTPLTYPPGCPTSAKILTMVSAGKDFSLKMPISPAPWSPQ 231


Inner capsid (VP4)  |  P22055 [2 - 69]
Beta sheet
Beta turn
Disordered termini     DDDDDDDDDDDDDD
ARG rich
                   1   GNSTSSDKNNSSSEGNEGVIINNFYSNQYQNSIDLSANATGSDPPKTYGQFSNLLSGAVN 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   AFSNMLPLLA 70
```

```
         Viral protein genome linked (VPg)  |  P22055 [1541 - 1562]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   GPYNETTRIKPKTLQLLDVQ 20




Norwalk Virus (Funabashi)
         Major capsid, 1 variant of 3 (VP1)  |  O41855
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDD
         ARG rich
                            1   MMMASKDATSSVDGASGAGQLVPEVNASDPLAMDPVAGSSTAVATAGQVNPIDPWIINNF 60
         Beta sheet                                                      SSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                           61   VQAPQGEFTISPNNTPGDVLFDLSLGPHLNPFLLHLSQMYNGWVGNMRVRIMLAGNAFTA 120
         Beta sheet                                                                        S
         Beta turn                                                                UUUUU
         Disordered termini
         ARG rich
                          121   GKIIVSCIPPGFGSHNLTIAQATLFPHVIADVRTLDPIEVPLEDVRNVLFHNNDRNQQTM 180
         Beta sheet             SSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          181   RLVCMLYTPLRTGGGTGDSFVVAGRVMTCPSPDFNFLFLVPPTVEQKTRPFTLPNLPLSS 240
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          241   LSNSRAPLPISSMGISPDNVQSVQFQNGRCTLDGRLVGTTPVSLSHVAKIRGTSNGTVIN 300
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          301   LTELDGTPFHPFEGPAPIGFPDLGGCDWHINMTQFGHSSQTQYDVDTTPDTFVPHLGSIQ 360
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          361   ANGIGSGNYVGVLSWISPPSHPSGSQVDLWKIPNYGSSITEATHLAPSVYPPGFGEVLVF 420
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          421   FMSKMPGPGAYNLPCLLPQEYISHLASEQAPTVGEAALLHYVDPDTGRNLGEFKAYPDGF 480
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                           RRRRRRRRRRRRRRRRRRRRRR
                          481   LTCVPNGASSGPQQLPINGVFVFVSWVSRFYQLKPVGTASSARGRLGLRR 530


         Capsid (VP2)  |  P22055 [70 - 341]
         Beta sheet
         Beta turn
         Disordered termini     DD
         ARG rich
                            1   MAQAIIGAIAASTAGSALGAGIQVGGEAALQSQRYQQNLQLQENSFKHDREMIGYQVEAS 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   NQLLAKNLATRYSLLRAGGLTSADAARSVAGAPVTRIVDWNGVRVSAPESSATTLRSGGF 120
         Beta sheet
```

```
         Beta turn
         Disordered termini
         ARG rich
                          121   MSVPIPFASKQKQVQSSGISNPNYSPSSISRTTSWVESQNSSRFGNLSPYHAEALNTVWL 180
         Beta sheet
         Beta turn
         Disordered termini                                  DDD
         ARG rich
                          181   TPPGSTASSTLSSVPRGYFNTDRLPLFANNRR 212


         Viral protein genome linked (VPg)  |  P22055 [1541 – 1562]
         Beta sheet
         Beta turn                                    UU
         Disordered termini     DDDDDDDDDDDD
         ARG rich                RRRRRRRRRRRRRRRRRRRRRR
                            1   GKNKGKTKKGRGRKNNYNAFSRRGLSDEEYEEYKKIREEKNGNYSIQEYLEDRQRYEEEL 60
         Beta sheet
         Beta turn                                 UUUUUUUUUUUUU                UUUU
         Disordered termini
         ARG rich                                  RRRRRRRRRRRRRRRRRRR          RRRRRRRRRRRRR
                           61   AEVQAGGDGGIGETEMEIRHRVFYKSKSKKHQQEQRRQLGLVTGSDIRKRKPIDWTPPKN 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich               RRRRRRRRRRRRRR
                          121   EWADDDREVDYNEKINFE 138




Enterobacteriaphage phiX174 (Sanger)
         Capsid (F)  |  P03641
         Beta sheet
         Beta turn                                                                     UU
         Disordered termini     DD
         ARG rich
                            1   MSNIQTGAERMPHDLSHLGFLAGQIGRLITISTTPVIAGDSFEMDAVGALRLSPLRRGLA 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   IDSTVDIFTFYVPHRHVYGEQWIKFMKDGVNATPLPTVNTTGYIDHAAFLGTINPDTNKI 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   PKHLFQGYLNIYNNYFKAPWMPDRTEANPNELNQDDARYGFRCCHLKNIWTAPLPPETEL 180
         Beta sheet                                                                    SSSSS
         Beta turn
         Disordered termini
         ARG rich
                          181   SRQMTTSTTSIDIMGLQAAYANLHTDQERDYFMQRYHDVISSFGGKTSYDADNRPLLVMR 240
         Beta sheet             SSSSSSSS                               SSSSSSSSSSSS
         Beta turn                                           UUUUUU
         Disordered termini
         ARG rich
                          241   SNLWASGYDVDGTDQTSLGQFSGRVQQTYKHSVPRFFVPEHGTMFTLALVRFPPTATKEI 300
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                         RRRRRRRRRRRRRRRRRRRRRRRRRRR
                          301   QYLNAKGALTYTDIAGDPVLYGNLPPREISMKDVFRSGDSSKKFKIAEGQWYRYAPSYVS 360
         Beta sheet                                                      SSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          361   PAYHLLEGFPFIQEPPSGDLQERVLIRHHDYDQCFQSVQLLQWNSQVKFNVTVYRNLPTT 420
         Beta sheet
         Beta turn
         Disordered termini
```

```
         ARG rich
                 421   RDSIMTS 427


         Major spike (G)  |  P03643
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                   1   MFQTFISRHNSNFFSDKLVLTSVTPASSAPVLQTPKATSSTLYFDSLTVNAGNGGFLHCI 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                  61   QMDTSVNAANQVVSVGADIAFDADPKFFACLVRFESSSVPTTLPTAYDVYPLNGRHDGGY 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                 121   YTVKDCVTIDVLPRTPGNNVYVGFMVWSNFTATKCRGLVSLNQVIKEIICLQPLK 175


         Minor spike (H)  |  P03646
         Beta sheet
         Beta turn
         Disordered termini    DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich
                   1   MFGAIAGGIASALAGGAMSKLFGGGQKAASGGIQGDVLATDNNTVGMGDAGIKSAIQGSN 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                  61   VPNPDEAAPSFVSGAMAKAGKGLLEGTLQAGTSAVSDKLLDLVGLGGKSAADKGKDTRDY 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                 121   LAAAFPELNAWERAGADASSAGMVDAGFENQKELTKMQLDNQKEIAEMQNETQKEIAGIQ 180
         Beta sheet
         Beta turn                 UUUUU
         Disordered termini
         ARG rich
                 181   SATSRQNTKDQVYAQNEMLAYQQKESTARVASIMENTNLSKQQQVSEIMRQMLTQAQTAG 240
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                 241   QYFTNDQIKEMTRKVSAEVDLVHQQTQNQRYGSSHIGATAKDISNVVTDAASGVVDIFHG 300
         Beta sheet
         Beta turn
         Disordered termini                               D
         ARG rich
                 301   IDKAVADTWNNFWKDGKADGIGSNLSRK 328


         DNA-binding (J)  |  P69592
         Beta sheet
         Beta turn
         Disordered termini    DDDDDDDDDDD
         ARG rich                RRRRRRRRRRRRRRRRRRRRRRRRRRR
                   1   MSKGKKRSGARPGRPQPLRGTKGKRKGARLWYVGGQQF 38




Pseudoalteromonas phage PM2
         Spike Protein (P1)  |  Q9XJR3
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
```

```
                   1   MIVKKKLAAGEFAETFKNGNNITIIKAVGELVLRAYGADGGEGLRTIVRQGVSIKGMNYT 60
Beta sheet
Beta turn                                                                       UUUUUUU
Disordered termini
ARG rich
                  61   SVMLHTEYAQEIEYWVGDLDYSFQEQTTKSRDVNSFQIPLRDGVRELLPEDASRNRASIK 120
Beta sheet                                                         SSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich                                                           RRRRRRRRRRRR
                 121   SPVDIWIGGENMTALNGIVDGGRKFEAGQEFQINTFGSVNYWVSDEEIRVFKEYSARAKY 180
Beta sheet             S                                                 SSSSSSSSSS
Beta turn
Disordered termini
ARG rich               RRRRRR                          RRRRRRRRR
                 181   AQNEGRTALEANNVPFFDIDVPPELDGVPFSLKARVRHKSKGVDGLGDYTSISVKPAFYI 240
Beta sheet             SS
Beta turn
Disordered termini
ARG rich
                 241   TEGDETTDTLIKYTSYGSTGSHSGYDFDDNTLDVMVTLSAGVHRVFPVETELDYDAVQEV 300
Beta sheet                                 SSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 301   QHDWYDESFTTFIEVYSDDPLLTVKGYAQILMERT 335


Major capsid protein (P2)  |  P15794
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MRSFLNLNSIPNVAAGNSCSIKLPIGQTYEVIDLRYSGVTPSQIKNVRVELDGRLLSTYK 60
Beta sheet
Beta turn                        UUUUUUU      UUUUUUUU
Disordered termini
ARG rich                         RRRRRRRRRRRRRRRRRRRRR
                  61   TLNDLILENTRHKRKIKAGVVSFHFVRPEMKGVNVTDLVQQRMFALGTVGLTTCEIKFDI 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   DEAAAGPKLSAIAQKSVGTAPSWLTMRRNFFKQLNNGTTEIADLPRPVGYRIAAIHIKAA 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   GVDAVEFQIDGTKWRDLLKKADNDYILEQYGKAVLDNTYTIDFMLEGDVYQSVLLDQMIQ 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241   DLRLKIDSTMDEQAEIIVEYMGVWSRNGF 269


Protein P3 (P3)  |  Q9XJR6
Beta sheet
Beta turn
Disordered termini     DDDDDDDDDD
ARG rich
                   1   MNTSVPTSVPTNQSVWGNVSTGLDALISGWARVEQIKAAKASTGQGRVEQAMTPELDNGA 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   AVVVEAPKKAAQPSETLVFGVPQKTLLLGFGGLLVLGLVMRGNK 104


Protein P4 (P4)  |  Q37958
Beta sheet
Beta turn
```

```
Disordered termini     DDD                                 DDDD
ARG rich                                             RRRRRRRRRR
                   1   MQKPSGKGLKYFAYGVAISAAGAILAEYVRDWMRKPKAKS 40


Protein P5 (P5)  |  Q9XJR2
Beta sheet
Beta turn
Disordered termini     DDDDDDDDDDDDDDDDDDDDDD
ARG rich
                   1   MKKAHMFLATAAALGVAMFPTQINEAARGLRNNNPLNIKEGSDGGAQWEGEHELDLDPTF 60
Beta sheet
Beta turn                 UUUUUUUUUUUUUUU                                        UU
Disordered termini
ARG rich                  RRRRRRRRRRRRRRRRRRRR
                  61   EEFKTPVHGIRAGARILRTYAVKYGLESIEGIIARWAPEEENDTENYINFVANKTGIPRN 120
Beta sheet
Beta turn              UU
Disordered termini
ARG rich
                 121   QKLNDETYPAVISAMIDMENGSNPYTYDEIKKGFEWGFYG 160


Protein P6 (P6)  |  Q9XJR1
Beta sheet
Beta turn
Disordered termini     D
ARG rich
                   1   MANFLTKNFVWILAAGVGVWFYQKADNAAKTATKPIADFLAELQFLVNGSNYVKFPNAGF 60
Beta sheet
Beta turn                                                   UUUUUUUUUUU
Disordered termini
ARG rich                                                      RRRRRRRRR
                  61   VLTRDALQDDFIAYDDRIKAWLGTHDRHKDFLAEILDHERRVKPVYRKLIGNIIDASTIR 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   AASGVEL 127


Peptidoglycan hydrolase P7 (P7)  |  Q9XJR8
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MINKTTIKTVLITLGVLAAVNKVSALRSVKRLIS 34


Major capsid protein  (P8)  |  P13849
Beta sheet
Beta turn
Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
ARG rich
                   1   MLGALMGVAGGAPMGGASPMGGMPSIASSSSAETGQQTQSGNFTGGGINFGSNNNNQLLI 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   VGAVVIGLFLVIKRK 75


Tail knob protein gp9 (Distal tube protein) (P9)  |  P04331
Beta sheet
Beta turn                                                   UUUU
Disordered termini     DDDDD
ARG rich                                                                  RRRRR
                   1   MRTTTKKQIERTDPTLPNVHHLVVGATGSGKSAFIRDQVDFKGARVLAWDVDEDYRLPRV 60
Beta sheet
Beta turn
Disordered termini
ARG rich               RRRRRRRRRRRRRRRRRRR                                        R
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```
                          61   RSIKQFEKLVKKSGFGAIRCALTVEPTEENFERFCQLVFAISHAGAPMVVIVEELADVAR 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich               RRRRRRRRRRRRRRRRR
                         121   IGKASPHWGQLSRKGRKYGVQLYVATQSPQEIDKTIVRQCNFKFCGALNSASAWRSMADN 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                    RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                         181   LDLSTREIKQLENIPKKQVQYWLKDGTRPTEKKTLTFK 218




Poliovirus 1 (Mahoney)
         Major capsid, 1 variant of 3 (VP1)  |  O41855
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           1   GLGQMLESMIDNTVRETVGAATSRDALPNTEASGPTHSKEIPALTAVETGATNPLVPSDT 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                                       RRRRRRRRRRRRRRRRRRRR
                          61   VQTRHVVQHRSRSESSIESFFARGACVTIMTVDNPASTTNKDKLFAVWKITYKDTVQLRR 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich               RRRRRRRRR
                         121   KLEFFTYSRFDMELTFVVTANFTETNNGHALNQVYQIMYVPPGAPVPEKWDDYTWQTSSN 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                         181   PSIFYTYGTAPARISVPYVGISNAYSHFYDGFSKVPLKDQSAALGDSLYGAASLNDFGIL 240
         Beta sheet                        SSSSSSSSSSSSSSSSSSSS
         Beta turn                     UUUUUUUUUUUUUUUUUUUU    UUUU
         Disordered termini
         ARG rich                 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                         241   AVRVVNDHNPTKVTSKIRVYLKPKHIRVWCPRPPRAVAYYGPGVDYKDGTLTPLSTKDLT 300
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                         301   TY 302


         Capsid (VP2)  |  P22055 [70 – 341]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           1   SPNIEACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEYLRDSEANPVDQPTEPDVAA 60
         Beta sheet
         Beta turn                          UUUU                                       UUU
         Disordered termini
         ARG rich
                          61   CRFYTLDTVSWTKESRGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQG 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                         121   ALGVFAVPEMCLAGDSNTTTMHTSYQNANPGEKGGTFTGTFTPDNNQTSPARRFCPVDYL 180
         Beta sheet                                                                SSSSSSSSSSSS
         Beta turn                                                              UU
         Disordered termini
         ARG rich
                         181   LGNGTLLGNAFVFPHQIINLRTNNCATLVLPYVNSLSIDSMVKHNNWGIAILPLAPLNFA 240
         Beta sheet
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         Beta turn
         Disordered termini
         ARG rich
                          241   SESSPEIPITLTIAPMCCEFNGLRNITLPRLQ 272


         Capsid (VP3)  |  P22055 [342 - 581]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   GLPVMNTPGSNQYLTADNFQSPCALPEFDVTPPIDIPGEVKNMMELAEIDTMIPFDLSAT 60
         Beta sheet                                                           SSSSSSSSSSSSSS
         Beta turn                      UUUUUUUUU
         Disordered termini
         ARG rich               RRRRRRRRRRRRRRR
                           61   KKNTMEMYRVRLSDKPHTDDPILCLSLSPASDPRLSHTMLGEILNYYTHWAGSLKFTFLF 120
         Beta sheet             SS
         Beta turn                                    UUUU
         Disordered termini
         ARG rich
                          121   CGFMMATGKLLVSYAPPGADPPKKRKEAMLGTHVIWDIGLQSSCTMVVPWISNTTYRQTI 180
         Beta sheet                    SSSSSSSSSSSS
         Beta turn
         Disordered termini                                                         DDDDDD
         ARG rich
                          181   DDSFTEGGYISVFYQTRIVVPLSTPREMDILGFVSACNDFSVRLLRDTTHIEQKALAQ 238


         Inner capsid (VP4)  |  P22055 [2 - 69]
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   GAQVSSQKVGAHENSNRAYGGSTINYTTINYYRDSASNAASKQDFSQDPSKFTEPIKDVL 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   IKTAPMLN 68


         Viral protein genome linked (VPg)  |  P22055 [1541 - 1562]
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich
                            1   GAYTGLPNKKPNVPTIRTAKVQ 22




Enterobacteria phage PR772
         Proximal tail-tube connector (P11)  |  P68930
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   MEKVKAWLIKYKWWIVAAIGGLAAFLLLKNRGGGSGGGGEYMVGSGPVYQQAGSGAVDNT 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   MALAALQANTQLSAQNAQLQAQMDASRLQLETQLNIETLAADNAHYSTQSQLQLGMAQVD 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                                            RRRRRRRRRRR
                          121   LSKYLGDLQSTTSTALAGMQSDTAKYQSNIQLQAENIRANTSLAEIDAQKYIVGKQADIA 180
         Beta sheet
         Beta turn              UUUUUUUUU
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         Disordered termini
         ARG rich               RRRRRRRRR
                          181   KYQAKTERRGQDYGFALGLLNFGGKFF 207


         Endolysin (EC 3.2.1.17) (Beta-1,4-N-acetylmuramidase) (Lysozyme) (Lytic enzyme)
(Muramidase) (Protein P15) (P15)  |  P09009
         Beta sheet
         Beta turn                                          UUUUU
         Disordered termini
         ARG rich                         RRRRRRRRRRRRRRRRRRRRRRRR
                            1   MQYTLWDIISRVESNGNLKALRFEPEYYQRRMERGDWDNSIIQNIRAANKCSLGTARMIY 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                                     RRRRRRRRRRRRRRRRRRRRRR
                           61   CSSWGAVQIMGFNLYLNGAFNLSVAHFMENEAYQVNEFRRFLLKNGLTEYTPERLASDKA 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich               RRRRRRR
                          121   ARVKFAKVYNGAESYADLILQACQFYGVK 149


         Protein P16 (GpS) (Protein S) (P16)  |  P27392
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDD
         ARG rich
                            1   MDKKKLLYWVGGGLVLILIWLWFRNRPAAQVASNWEGPPYMTYNQPQAGSVTLPVAGYTS 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   PSPTLPNRNRSCGCNPAVSAAMAQGADLASKLTDSITSQLNDYASSLNDYLASQAGV 117


         Protein P18 (GpM) (Protein M) (P18)  |  P27389
         Beta sheet
         Beta turn                                                                   UUUU
         Disordered termini
         ARG rich
                            1   MPFGLIVIGIILAIAAYRDTLGELFSIIKDVSKDAKGFGYWVLAAVILGFAASIKPIKEP 60
         Beta sheet
         Beta turn
         Disordered termini                                  D
         ARG rich
                           61   VNAFMILLMIVLLIRKRGAIDQISNQLRGS 90


         Major capsid protein (P2)  |  P15794
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   MANFNVPKLGVFPVAAVFDIDNVPEDSSATGSRWLPSIYQGGNYWGGGPQALHAQVSNFD 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   SSNRLPYNPRTENNPAGNCAFAFNPFGQYISNISSAQSVHRRIYGIDLNDEPLFSPNAAS 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   ITNGGNPTMSQDTGYHNIGPINTAYKAEIFRPVNPLPMSDTAPDPETLEPGQTEPLIKSD 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          181   GVYSNSGIASFIFDRPVTEPNPNWPPLPPPVIPIIYPTPALGIGAAAAYGFGYQVTVYRW 240
         Beta sheet
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Beta turn
Disordered termini
ARG rich
                 241   EEIPVEFIADPETCPAQPTTDKVIIRTTDLNPEGSPCAYEAGIILVRQTSNPMNAVAGRL 300
Beta sheet                                                          SSSSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 301   VPYVEDIAVDIFLTGKFFTLNPPLRITNNYFADDEVKENTVTIGNYTTTLSSAYYAVYKT 360
Beta sheet
Beta turn
Disordered termini
ARG rich
                 361   DGYGGATCFIASGGAGISALVQLQDNSVLDVLYYSLPLSLGGSKAAIDEWVANNCGLFPM 420
Beta sheet
Beta turn
Disordered termini
ARG rich
                 421   SGGLDKTTLLEIPRRQLEAINPQDGPGQYDLFILDDSGAYASFSSFIGYPEAAYYVAGAA 480
Beta sheet
Beta turn
Disordered termini
ARG rich
                 481   TFMDVENPDEIIFILRNGAGWYACEIGDALKIADDEFDSVDYFAYRGGVMFIGSARYTEG 540
Beta sheet
Beta turn                              UUUUUU
Disordered termini
ARG rich                     RRRRRRRRRRRRRRRR
                 541   GDPLPIKYRAIIPGLPRGRLPRVVLEYQAVGMSFIPCQTHCLGKGGIISKV 591


Packaging protein P20 (P20)  |  P27387
Beta sheet
Beta turn
Disordered termini                                            DDD
ARG rich
                   1   MVNWELLKNPINWLIVILMLTIAGMAATLVCNHFGKNAVTSE 42


Packaging protein P22 (GpK) (Protein K) (P22)  |  P27388
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MQLITDMAEWSSKPFRPDMSLTGWLAFVGLIIVAIILWQQIIRFIIE 47


Protein P3 (P3)  |  Q9XJR6
Beta sheet
Beta turn
Disordered termini     DDDDDD
ARG rich
                   1   MAQVQQLTPAQQAALRNQQAMAANLQARQIVLQQSYPVIQQVETQTFDPANRSVFDVTPA 60
Beta sheet              SSSSSSSSSSSSSSSSS                             SSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                  61   NVGIVKGFLVKVTAAITNNHATEAVALTDFGPANLVQRVIYYDPDNQRHTETSGWHLHFV 120
Beta sheet             S
Beta turn
Disordered termini
ARG rich
                 121   NTAKQGAPFLSSMVTDSPIKYGDVMNVIDAPATIAAGATGELTMYYWVPLAYSETDLTGA 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   VLANVPQSKQRLKLEFANNNTAFAAVGANPLEAIYQGAGAADCEFEEISYTVYQSYLDQL 240
Beta sheet
Beta turn
Disordered termini
ARG rich
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                 241   PVGQNGYILPLIDLSTLYNLENSAQAGLTPNVDFVVQYANLYRYLSTIAVFDNGGSFNAG 300
Beta sheet
Beta turn                                                            UUU
Disordered termini
ARG rich                       RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                 301   TDINYLSQRTANFSDTRKLDPKTWAAQTRRRIATDFPKGVYYCDNRDKPIYTLQYGNVGF 360
Beta sheet
Beta turn
Disordered termini
ARG rich
                 361   VVNPKTVNQNARLLMGYEYFTSRTELVNAGTISTT 395


Minor capsid protein P30 (Protein P) (GpP) (P30)  |  P27391
Beta sheet
Beta turn
Disordered termini     DD
ARG rich
                   1   MALINPQFPYAGPVPIPGPAPTETMPLLNYRVEGRIAGIQQARQFMPFLQGPHRAVAEQT 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   YHAIGTGIQMGQTFNQPLINTQEG 84


Penton protein P31 (GpC) (Protein C) (P31)  |  P27384
Beta sheet
Beta turn
Disordered termini     DD
ARG rich
                   1   MNVNNPNQMTVTPVYNGCDSGEGPQSVRGYFDAVAGENVKYDLTYLADTQGFTGVQCIYI 60
Beta sheet                                                              SSSSSSSSSSS
Beta turn
Disordered termini
ARG rich                                                   RRRRRRRRRRRRRR
                  61   DNAENDGAFEIDVEETGQRIKCPAGKQGYFPLLVPGRAKFVARHLGSGKKSVPLFFLNFT 120
Beta sheet             SS
Beta turn
Disordered termini
ARG rich
                 121   IAQGVW 126


Protein P32 (P32)  |  Q3T4M7
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MGEFGKTLITIVTAIIGVAIIAVIVSQRSNTAGVIQSATSGFSNILKSALAPII 54


Protein P34 (Protein O) (GpO) (P34)  |  P27390
Beta sheet
Beta turn
Disordered termini                                                           DDDDDD
ARG rich
                   1   MNDFVGPIVTVLTAIIGVAILAVLVSRNSNTAGVIKAGSGGFSSMLGTALSPVTGGTGFA 60
Beta sheet
Beta turn
Disordered termini     DDDDDDDD
ARG rich
                  61   MTNNYSGF 68


Protein P5 (P5)  |  Q9XJR2
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MANQQIGGSTVTYNGAIPMGGPVAINSVIEIAGTEVLVDLKLDYATGKISGVQTLYIDLR 60
Beta sheet                                                  SSSSSSSSSSSSSSS
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Beta turn
Disordered termini
ARG rich
                  61   DFLGDVTVTMPDTGQRITARAGTQGYYPVLSTNLMKFIVSATIDGKFPMNFINFPIALGV 120
Beta sheet
Beta turn                   UUUU
Disordered termini
ARG rich
                 121   WPSGIKGDKGDPGAPGPAGGTVVVEDSGASFGESLLDTTSEPGKILVKRISGGSGITVTD 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   YGDQVEIEASGGGGGGGGVTDALSLMYSTSTGGPASIAANALTDFDLSGALTVNSVGTGL 240
Beta sheet                                       SSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 241   TKSAAGIQLAAGKSGLYQITMTVKNNTVTTGNYLLRVKYGSSDFVVACPASSLTAGGTIS 300
Beta sheet
Beta turn
Disordered termini
ARG rich
                 301   LLIYCNVLGVPSLDVLKFSLCNDGAALSNYIINITAAKIN 340


Protein P6 (P6)  |  Q9XJR1
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MDTEEIKEEMQEAAEAAIENAVETAELETAAIKAEGAAAAAEQSAEQAAVMAATLAASVE 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   ANAAQQIAEHSEQVQTQEEKISWLENQVMAMASNLQMMQEAVTALTVSQSLTPEPSPVPA 120
Beta sheet
Beta turn
Disordered termini                DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
ARG rich
                 121   VEVEAMPEAVTVEILPESAGDQQEAEPVPSVGDQQETAPRKRFRAI 166


Peptidoglycan hydrolase P7 (P7)  |  Q9XJR8
Beta sheet
Beta turn
Disordered termini     DD
ARG rich
                   1   MSGALQWWETIGAASAQYNLDPRLVAGVVQTESSGNPRTTSGVGAMGLMQLMPATAKSLG 60
Beta sheet
Beta turn                                                            UUU
Disordered termini
ARG rich
                  61   VTNAYDPTQNIYGGAALLRENLDRYGDVNTALLAYHGGTNQANWGAKTKSYPGKVMKNIN 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   LLFGNSGPVVTPAAGIAPVSGAQEMTAVNISDYTAPDLTGLTMGAGSPDFTGGASGSWGE 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   ENIPWYRVDKHVANAAGSAYDAVTDAVSAPVEAAGNYALRGVVIIAAVAIVVVGLYFLFQ 240
Beta sheet
Beta turn
Disordered termini                  DDDDDDDDDDDD
ARG rich
                 241   DEINSAAMKMIPAGKAAGAAAKALA 265
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         Major capsid protein  (P8)  |  P13849
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDD
         ARG rich                 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                           1   MAKKKPVEKNGLVYKEFQKQVSNLKKAGLIPKTLDVRKVKPTKHYKGLVSKYKDVATGGA 60
         Beta sheet
         Beta turn                                                              UUUUU
         Disordered termini
         ARG rich               R               RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                          61   KLAAIPNPAVIETLEARGESIIKKGGKAYLKARQQINQRGQIVNPFTVRVTKRGEVVRRY 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich               RRRRRRRRRRRRRRRRRRRR
                         121   RKTTPEGKPVYITQRELPIKFENMEQWLTELKAAGFQLQPGEQIYFTFNGNYSRRTYTSF 180
         Beta sheet
         Beta turn                                 UUU                     UUUUUUU
         Disordered termini
         ARG rich
                         181   DEAFNKFMTYDIIIDAVAGKLKVEDEADLVKSVGFQRISGPEAKAYNRNRIVLPEMQFSQ 240
         Beta sheet
         Beta turn
         Disordered termini              DDDDDDDDDD
         ARG rich                 RRRRRRRRRRRRRRR
                         241   AAKKKYKRRQKRGYGSKGV 259


         Tail knob protein gp9 (Distal tube protein) (P9)  |  P04331
         Beta sheet
         Beta turn                                          UUUUUUUUUU      UU
         Disordered termini     DD
         ARG rich                  RRRRRRRRRRRRRRRRRRR          RRRRRRRRRRRRRR
                           1   MTIRMPNDRQRILVLGKTGTGKTCAAVWHLSQKDFKRKAWIVLNHKGDDLIDSIEGANHV 60
         Beta sheet
         Beta turn                  UUUU
         Disordered termini
         ARG rich
                          61   DLNFRPKKPGLYIYHPIPDVDDAEVTQLLWDIHAMGDIGVYVDEGYMIPNRDPAFQALLT 120
         Beta sheet
         Beta turn                UUUU
         Disordered termini
         ARG rich                 RRRRRRRRRRRRRRRRRRR
                         121   QGRSKKIPMIILSQRPVWLTRFAISESDFFQIFQLGDQRDRQTVQGFVPVDLEKLMQAPV 180
         Beta sheet
         Beta turn                    UUUU
         Disordered termini                                                    DDDD
         ARG rich                                                      RRRRRRRRR
                         181   NTVPALKKFHSIYYDVGANNCVIMTPVPTADAVLARFDLGKKRKQTL 227




Red clover necrotic mosaic virus
         Capsid (CP)  |  P03601
         Beta sheet                                                            SSSSSSSSSSSSS
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich                  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                           1   MSSKAPKKSKQRSQPRNRTPNTSVKTVAIPFAKTQIIKTVNPPPKPARGILHTQLVMSVV 60
         Beta sheet             SSSSSS                              SSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          61   GSVQMRTNNGKSNQRFRLNPSNPALFPTLAYEAANYDMYRLKKLTLRYVPLVTVQNSGRV 120
         Beta sheet
         Beta turn                                                                    UU
         Disordered termini
         ARG rich
                         121   AMIWDPDSQDSAPQSRQEISAYSRSVSTAVYEKCSLTIPADNQWRFVADNTTVDRKLVDF 180
         Beta sheet
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```
         Beta turn
         Disordered termini
         ARG rich
                          181   GQLLFVTHSGSDGIETGDIFLDCEVEFKGPQPTASIVQKTVIDLGGTLTSFEGPSYLMPP 240
         Beta sheet                                                                  SSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          241   DAFITSSSFGLFVDVAGTYLLTLVVTCSTTGSVTVGGNSTLVGDGRAAYGSSNYIASIVF 300
         Beta sheet             SSSSS
         Beta turn
         Disordered termini
         ARG rich
                          301   TSSGVLSTTPSVQFSGSSGVSRVQMNICRCKQGNTFILG 339




Reovirus 3 (Dearing)
         Inner capsid protein lambda-1 (L1)  |  P15024
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich                RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                            1   MKRIPRKTKGKSSGKGNDSTERADDGSSQLRDKQNNKAGPATTEPGTSNREQYKARPGIA 60
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich                                                     RRRRRRRRRRRRRRRRRRR
                           61   SVQRATESAEMPMKNNDEGTPDKKGNTKGDLVNEHSEAKDEADEATKKQAKDTDKSKAQV 120
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDD
         ARG rich
                          121   TYSDTGINNANELSRSGNVDNEGGSNQKPMSTRIAEATSAIVSKHPARVGLPPTASSGHG 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          181   YQCHVCSAVLFSPLDLDAHVASHGLHGNMTLTSSDIQRHITEFISSWQNHPIVQVSADVE 240
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          241   NKKTAQLLHADTPRLVTWDAGLCTSFKIVPIVPAQVPQDVLAYTFFTSSYAIQSPFPEAA 300
         Beta sheet
         Beta turn                UUUUUUU
         Disordered termini
         ARG rich
                          301   VSRIVVHTRWASNVDFDRDSSVIMAPPTENNIHLFKQLLNTETLSVRGANPLMFRANVLH 360
         Beta sheet
         Beta turn                           UU
         Disordered termini
         ARG rich
                          361   MLLEFVLDNLYLNRHTGFSQDHTPFTEGANLRSLPGPDAEKWYSIMYPTRMGTPNVSKIC 420
         Beta sheet
         Beta turn                     UUUUUUUUU
         Disordered termini
         ARG rich
                          421   NFVASCVRNRVGRFDRAQMMNGAMSEWVDVFETSDALTVSIRGRWMARLARMNINPTEIE 480
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          481   WALTECAQGYVTVTSPYAPIVNRLMPYRISNAERQISQIIRIMNIGNNATVIQPVLQDIS 540
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          541   VLLQRISPLQIDPTIISNTMSTVSESTTQTLSPASSILGKLRPSNSDFSSFRVALAGWLY 600
         Beta sheet
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Beta turn
Disordered termini
ARG rich
                 601   NGVVTTVIDDSSYPKDGGSVTSLENLWDFFILALALPLTTDPCAPVKAFMTLANMMVGFE 660
Beta sheet
Beta turn                          UU       UUUUU
Disordered termini
ARG rich
                 661   TIPMDNQIYTQSRRASAFSTPHTWPRCFMNIQLISPIDAPILRQWAEIIHRYWPNPSQIR 720
Beta sheet
Beta turn
Disordered termini
ARG rich
                 721   YGAPNVFGSANLFTPPEVLLLPIDHQPANVTTPTLDFTNELTNWRARVCELMKNLVDNQR 780
Beta sheet
Beta turn
Disordered termini
ARG rich                                                                       RRRR
                 781   YQPGWTQSLVSSMRGTLDKLKLIKSMTPMYLQQLAPVELAVIAPMLPFPPFQVPYVRLDR 840
Beta sheet
Beta turn
Disordered termini
ARG rich               RRRRRRRRRRRRRR
                 841   DRVPTMVGVTRQSRDTITQPALSLSTTNTTVGVPLALDARAITVALLSGKYPPDLVTNVW 900
Beta sheet
Beta turn
Disordered termini
ARG rich
                 901   YADAIYPMYADTEVFSNLQRDMITCEAVQTLVTLVAQISETQYPVDRYLDWIPSLRASAA 960
Beta sheet
Beta turn
Disordered termini
ARG rich
                 961   TAATFAEWVNTSMKTAFDLSDMLLEPLLSGDPRMTQLAIQYQQYNGRTFNIIPEMPGSVI 1020
Beta sheet
Beta turn                                                                    UUUUUU
Disordered termini
ARG rich
                 1021   ADCVQLTAEVFNHEYNLFGIARGDIIIGRVQSTHLWSPLAPPPDLVFDRDTPGVHIFGRD 1080
Beta sheet
Beta turn              UU
Disordered termini
ARG rich
                 1081   CRISFGMNGAAPMIRDETGLMVPFEGNWIFPLALWQMNTRYFNQQFDAWIKTGELRIRIE 1140
Beta sheet
Beta turn
Disordered termini
ARG rich
                 1141   MGAYPYMLHYYDPRQYANAWNLTSAWLEEITPTSIPSVPFMVPISSDHDISSAPAVQYII 1200
Beta sheet
Beta turn
Disordered termini
ARG rich
                 1201   STEYNDRSLFCTNSSSPQTIAGPDKHIPVERYNILTNPDAPPTQIQLPEVVDLYNVVTRY 1260
Beta sheet
Beta turn
Disordered termini
ARG rich
                 1261   AYETPPITAVVMGVP 1275


Penton protein (L2)  |  P12538
Beta sheet
Beta turn                                                     UUUUUUUUUUU
Disordered termini
ARG rich
                   1   MANVWGVRLADSLSSPTIETRTRQYTLHDLCSDLDANPGREPWKPLRNQRTNNIVAVQLF 60
Beta sheet
Beta turn
Disordered termini
ARG rich                                      RRRRRRRRRRRRRRRR
                  61   RPLQGLVLDTQLYGFPGAFDDWERFMREKLRVLKYEVLRIYPISNYSNEHVNVFVANALV 120
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Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   GAFLSNQAFYDLLPLLIINDTMIGDLLGTGASLSQFFQSHGDVLEVAAGRKYLQMENYSN 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   DDDDPPLFAKDLSDYAKAFYSDTYEVLDRFFWTHDSSAGVLVHYDKPTNGHHYLLGTLTQ 240
Beta sheet
Beta turn                                          UUU
Disordered termini
ARG rich
                 241   MVSAPPYIINATDAMLLESCLEQFSANVRARPAQPVTRLDQCYHLRWGAQYVGEDSLTYR 300
Beta sheet
Beta turn                             UUUUU
Disordered termini
ARG rich
                 301   LGVLSLLATNGYQLARPIPRQLTNRWLSSFVSQIMSDGVNETPLWPQERYVQIAYDSPSV 360
Beta sheet
Beta turn
Disordered termini
ARG rich
                 361   VDGATQYGYVRKNQLRLGMRISALQSLSDTPSPVQWLPQYTIDQAAMDEGDLMVSRLTQL 420
Beta sheet
Beta turn                                    UUUU
Disordered termini
ARG rich                                                               RRRRRRRRRRRR
                 421   PLRPDYGNIWVGDALSYYVDYNRSHRVVLSSELPQLPDTYFDGDEQYGRSLFSLARKIGD 480
Beta sheet
Beta turn                                    UUUUUUU
Disordered termini
ARG rich               RRRRRRRRRRR
                 481   RSLVKDTAVLKHAYQAIDPNTGKEYLRSRQSVAYFGASAGHSGADQPLVIEPWIQGKISG 540
Beta sheet
Beta turn
Disordered termini
ARG rich
                 541   VPPPSSVRQFGYDVARGAIVDLARPFPSGDYQFVYSDVDQVVDGHDDLSISSGLVESLLS 600
Beta sheet                  SSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 601   SCMHATAPGGSFVVKINFPTRPVWHYIEQKILPNITSYMLIKPFVTNNVELFFVAFGVHQ 660
Beta sheet
Beta turn
Disordered termini
ARG rich
                 661   HSSLTWTSGVYFFLVDHFYRYETLSTISRQLPSFGYVDDGSSVTGIETISIENPGFSNMT 720
Beta sheet
Beta turn                                        UUUU             UUUUUUU
Disordered termini
ARG rich                                            RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                 721   QAARIGISGLCANVGNARKSIAIYESHGARVLTITSRRSPASARRKSRLRYLPLIDPRSL 780
Beta sheet
Beta turn
Disordered termini
ARG rich               RRRRR
                 781   EVQARTILPADPVLFENVSGASPHVCLTMMYNFEVSSAVYDGDVVLDLGTGPEAKILELI 840
Beta sheet
Beta turn
Disordered termini
ARG rich
                 841   PATSPVTCVDIRPTAQPSGCWNVRTTFLELDYLSDGWITGVRGDIVTCMLSLGAAAAGKS 900
Beta sheet
Beta turn                                               UUUU         UUUUUUUUUU
Disordered termini
ARG rich                                                RRRRRRRRRRRRRRRRRRRRRRR
                 901   MTFDAAFQQLIKVLSKSTANVVLVQVNCPTDVVRSIKGYLEIDSTNKRYRFPKFGRDEPY 960
Beta sheet
Beta turn                                                                        U
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Disordered termini
ARG rich
                 961   SDMDALEKICRTAWPNCSITWVPLSYDLRWTRLALLESTTLSSASIRIAELMYKYMPIMR 1020
Beta sheet
Beta turn              UUUU
Disordered termini
ARG rich
                 1021   IDIHGLPMEKRGNFIVGQNCSLVIPGFNAQDVFNCYFNSALAFSTEDVNAAMIPQVSAQF 1080
Beta sheet
Beta turn
Disordered termini
ARG rich
                 1081   DATKGEWTLDMVFSDAGIYTMQALVGSNANPVSLGSFVVDSPDVDITDAWPAQLDFTIAG 1140
Beta sheet
Beta turn
Disordered termini
ARG rich
                 1141   TDVDITVNPYYRLMTFVRIDGQWQIANPDKFQFFSSASGTLVMNVKLDIADKYLLYYIRD 1200
Beta sheet
Beta turn
Disordered termini
ARG rich
                 1201   VQSRDVGFYIQHPLQLLNTITLPTNEDLFLSAPDMREWAVKESGNTICILNSQGFVLPQD 1260
Beta sheet
Beta turn
Disordered termini
ARG rich
                 1261   WDVLTDTISWSPSIPTYIVPPGDYTLTPL 1289


Hexon protein (L3)  |  P04133
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MSSMILTQFGPFIESISGITDQSNDVFEDAAKAFSMFTRSDVYKALDEIPFSDDAMLPIP 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   PTIYTKPSHDSYYYIDALNRVRRKTYQGPDDVYVPNCSIVELLEPHETLTSYGRLSEAIE 120
Beta sheet
Beta turn                                      UUUU
Disordered termini
ARG rich
                 121   NRAKDGDSQARIATTYGRIAESQARQIKAPLEKFVLALLVAEAGGSLYDPVLQKYDEIPD 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   LSHNCPLWCFREICRHISGPLPDRAPYLYLSAGVFWLMSPRMTSAIPPLLSDLVNLAILQ 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241   QTAGLDPSLVKLGVQICLHAAASSSYSWFILKTKSIFPQNTLHSMYESLEGGYCPNLEWL 300
Beta sheet
Beta turn                                UUUU
Disordered termini
ARG rich                                 RRRRRRRRRRRRRRRRRRR          RRRRRRRRRRRRR
                 301   EPRSDYKFMYMGVMPLSAKYARSAPSNDKKARELGEKYGLSSVVGELRKRTKTYVKHDFA 360
Beta sheet
Beta turn
Disordered termini
ARG rich               RRRRRR
                 361   SVRYIRDAMACTSGIFLVRTPTETVLQEYTQSPEIKVPIPQKDWTGPIGEIRILKDTTSS 420
Beta sheet
Beta turn
Disordered termini
ARG rich
                 421   IARYLYRTWYLAAARMAAQPRTWDPLFQAIMRSQYVTARGGSGAALRESLYAINVSLPDF 480
Beta sheet
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```
Beta turn
Disordered termini
ARG rich
                 481   KGLPVKAATKIFQAAQLANLPFSHTSVAILADTSMGLRNQVQRRPRSIMPLNVPQQQVSA 540
Beta sheet
Beta turn
Disordered termini
ARG rich
                 541   PHTLTADYINYHMNLSPTSGSAVIEKVIPLGVYASSPPNQSINIDISACDASITWDFFLS 600
Beta sheet
Beta turn                                                               UUUUUUUU
Disordered termini
ARG rich
                 601   VIMAAIHEGVASSSIGKPFMGVPASIVNDESVVGVRAARPISGMQNMIQHLSKLYKRGFS 660
Beta sheet
Beta turn
Disordered termini
ARG rich
                 661   YRVNDSFSPGNDFTHMTTTFPSGSTATSTEHTANNSTMMETFLTVWGPEHTDDPDVLRLM 720
Beta sheet
Beta turn
Disordered termini
ARG rich
                 721   KSLTIQRNYVCQGDDGLMIIDGTTAGKVNSETIQNDLELISKYGEEFGWKYDIAYDGTAE 780
Beta sheet
Beta turn
Disordered termini
ARG rich
                 781   YLKLYFIFGCRIPNLSRHPIVGKERANSSAEEPWPAILDQIMGVFFNGVHDGLQWQRWIR 840
Beta sheet
Beta turn
Disordered termini
ARG rich
                 841   YSWALCCAFSRQRTMIGESVGYLQYPMWSFVYWGLPLVKAFGSDPWIFSWYMPTGDLGMY 900
Beta sheet
Beta turn
Disordered termini
ARG rich                                                                   RRRRRRRR
                 901   SWISLIRPLMTRWMVANGYVTDRCSTVFGNADYRRCFNELKLYQGYYMAQLPRNPKKSGR 960
Beta sheet
Beta turn
Disordered termini
ARG rich               RRRRRRR                 RRRRRRRRRRRRR
                 961   AASREVREQFTQALSDYLMQNPELKSRVLRGRSEWEKYGAGIIHNPPSLFDVPHKWYQGA 1020
Beta sheet
Beta turn                                 UUUUU
Disordered termini
ARG rich
                 1021   QEAAIATREELAEMDETLMRARRHSYSSFSKLLEAYLLVKWRMCEAREPSVDLRLPLCAG 1080
Beta sheet
Beta turn
Disordered termini
ARG rich
                 1081   IDPLNSDPFLKMVSVGPMLQSTRKYFAQTLFMAKTVSGLDVNAIDSALLRLRTLGADKKA 1140
Beta sheet
Beta turn                                                                   UUUUUUU
Disordered termini
ARG rich
                 1141   LTAQLLMVGLQESEADALAGKIMLQDVNTVQLARVVNLAVPDTWMSLDFDSMFKHHVKLL 1200
Beta sheet
Beta turn              UUUUUU
Disordered termini           D
ARG rich
                 1201   PKDGRHLNTDIPPRMGWLRAILRFLGAGMVMTATGVAVDIYLEDIHGGGRSLGQRFMTWM 1260
Beta sheet
Beta turn
Disordered termini           D
ARG rich
                 1261   RQEGRSA 1267


Outer capsid protein mu-1 (M1)  |  P11078
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Beta sheet
Beta turn
Disordered termini     DDDD
ARG rich
                   1   MGNASSIVQTINVTGDGNVFKPSAETSSTAVPSLSLSPGMLNPGGVPWIAVGDETSVTSP 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   GALRRMTSKDIPETAIINTDNSSGAVPSESALVPYIDEPLVVVTEHAITNFTKAEMALEF 120
Beta sheet
Beta turn                    UUU
Disordered termini
ARG rich
                 121   NREFLDKMRVLSVSPKYSDLLTYVDCYVGVSARQALNNFQKQVPVITPTRQTMYVDSIQA 180
Beta sheet
Beta turn
Disordered termini
ARG rich                                                                RRRRRRRRRRR
                 181   ALKALEKWEIDLRVAQTLLPTNVPIGEVSCPMQSVVKLLDDQLPDDSLIRRYPKEAAVAL 240
Beta sheet
Beta turn
Disordered termini
ARG rich               RRR
                 241   AKRNGGIQWMDVSEGTVMNEAVNAVAASALAPSASAPPLEEKSKLTEQAMDLVTAAEPEI 300
Beta sheet
Beta turn
Disordered termini
ARG rich
                 301   IASLAPVPAPVFAIPPKPADYNVRTLRIDEATWLRMIPKSMNTPFQIQVTDNTGTNWHLN 360
Beta sheet
Beta turn
Disordered termini
ARG rich
                 361   LRGGTRVVNLDQIAPMRFVLDLGGKSYKETSWDPNGKKVGFIVFQSKIPFELWTAASQIG 420
Beta sheet
Beta turn
Disordered termini
ARG rich
                 421   QATVVNYVQLYAEDSSFTAQSIIATTSLAYNYEPEQLNKTDPEMNYYLLATFIDSAAITP 480
Beta sheet
Beta turn
Disordered termini
ARG rich
                 481   TNMTQPDVWDALLTMSPLSAGEVTVKGAVVSEVVPADLIGSYTPESLNASLPNDAARCMI 540
Beta sheet
Beta turn
Disordered termini
ARG rich
                 541   DRASKIAEAIKIDDDAGPDEYSPNSVPIQGQLAISQLETGYGVRIFNPKGILSKIASRAM 600
Beta sheet
Beta turn                                             UUUUUUU
Disordered termini
ARG rich                                              RRRRRRRRRRRRRRRRRRR
                 601   QAFIGDPSTIITQAAPVLSDKNNWIALAQGVKTSLRTKSLSAGVKTAVSKLSSSESIQNW 660
Beta sheet
Beta turn
Disordered termini                         DDDDDDDDDDDDDDDDDDDDDDDDDDDD
ARG rich                                             RRRRRRRRRRRRRRRRRR
                 661   TQGFLDKVSAHFPAPKPDCPTSGDSGESSNRRVKRDSYAGVVKRGYTR 708


Inner microtubule-associated protein mu-2 (M2)  |  P12418
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MAYIAVPAVVDSRSSEAIGLLESFGVDAGADANDVSYQDHDYVLDQLQYMLDGYEAGDVI 60
Beta sheet
Beta turn                  UUUUUUU
Disordered termini
ARG rich                                                      RRRRRRRRRRRRRRRRRRRRR
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                  61   DALVHKNWLHHSVYCLLPPKSQLLEYWKSNPSAIPDNVDRRLRKRLMLKKDLRKDDEYNQ 120
Beta sheet
Beta turn
Disordered termini
ARG rich               RRRRRR
                 121   LARAFKISDVYAPLISSTTSPMTMIQNLNRGEIVYTTTDRVIGARILLYAPRKYYASTLS 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   FTMTKCIIPFGKEVGRVPHSRFNVGTFPSIATPKCFVMSGVDIESIPNEFIKLFYQRVKS 240
Beta sheet
Beta turn                                 UUUUUUU           UUUUUUUUUUUU
Disordered termini
ARG rich                                  RRRRRRRRRRRRR
                 241   VHANILNDISPQIVSDMINRKRLRVHTPSDRRAAQLMHLPYHVKRGASHVDVYKVDVVDM 300
Beta sheet
Beta turn
Disordered termini
ARG rich
                 301   LFEVVDVADGLRNVSRKLTMHTVPVCILEMLGIEIADYCIRQEDGMLTDWFLLLTMLSDG 360
Beta sheet                                 SSSSSSSSSSSSSSSSSS
Beta turn                 UUUU                                               UUUUU
Disordered termini
ARG rich
                 361   LTDRRTHCQYLMNPSSVPPDVILNISITGFINRHTIDVMPDIYDFVKPIGAVLPKGSFKS 420
Beta sheet
Beta turn
Disordered termini
ARG rich
                 421   TIMRVLDSISILGIQIMPRAHVVDSDEVGEQMEPTFEQAVMEIYKGIAGVDSLDDLIKWV 480
Beta sheet
Beta turn
Disordered termini
ARG rich
                 481   LNSDLIPHDDRLGQLFQAFLPLAKDLLAPMARKFYDNSMSEGRLLTFAHADSELLNANYF 540
Beta sheet
Beta turn                                UUUU
Disordered termini
ARG rich
                 541   GHLLRLKIPYITEVNLMIRKNREGGELFQLVLSYLYKMYATSAQPKWFGSLLRLLICPWL 600
Beta sheet
Beta turn
Disordered termini
ARG rich
                 601   HMEKLIGEADPASTSAEIGWHIPREQLMQDGWCGCEDGFIPYVSIRAPRLVIEELMEKNW 660
Beta sheet
Beta turn                                UUUUUUUUUUUUUUUUUUUUU
Disordered termini
ARG rich
                 661   GQYHAQVIVTDQLVVGEPRRVSAKAVIKGNHLPVKLVSRFACFTLTAKYEMRLSCGHSTG 720
Beta sheet
Beta turn
Disordered termini
ARG rich
                 721   RGAAYSARLAFRSDLA 736


Outer capsid protein sigma-1 (S1 )  |  P03528
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MDPRLREEVVRLIIALTSDNGASLSKGLESRVSALEKTSQIHSDTILRITQGLDDANKRI 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   IALEQSRDDLVASVSDAQLAISRLESSIGALQTVVNGLDSSVTQLGARVGQLETGLAELR 120
Beta sheet
Beta turn
Disordered termini
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ARG rich
                 121   VDHDNLVARVDTAERNIGSLTTELSTLTLRVTSIQADFESRISTLERTAVTSAGAPLSIR 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   NNRMTMGLNDGLTLSGNNLAIRLPGNTGLNIQNGGLQFRFNTDQFQIVNNNLTLKTTVFD 240
Beta sheet
Beta turn
Disordered termini
ARG rich
                 241   SINSRIGATEQSYVASAVTPLRLNSSTKVLDMLIDSSTLEINSSGQLTVRSTSPNLRYPI 300
Beta sheet                           SSSSSSSSSSSSSS  SSSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 301   ADVSGGIGMSPNYRFRQSMWIGIVSYSGSGLNWRVQVNSDIFIVDDYIHICLPAFDGFSI 360
Beta sheet                                                             SSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 361   ADGGDLSLNFVTGLLPPLLTGDTEPAFHNDVVTYGAQTVAIGLSSGGAPQYMSKNLWVEQ 420
Beta sheet             SS
Beta turn
Disordered termini
ARG rich
                 421   WQDGVLRLRVEGGGSITHSNSKWPAMTVSYPRSFT 455


Inner capsid protein sigma-2 (S2)  |  P03525
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MARAAFLFKTVGFGGLQNVPINDELSSHLLRAGNSPWQLTQFLDWISLGRGLATSALVPT 60
Beta sheet
Beta turn                                 UUUUU    UUUU
Disordered termini
ARG rich
                  61   AGSRYYQMSCLLSGTLQIPFRPNHRWGDIRFLRLVWSAPTLDGLVVAPPQVLAQPALQAQ 120
Beta sheet
Beta turn
Disordered termini
ARG rich
                 121   ADRVYDCDDYPFLARDPRFKHRVYQQLSAVTLLNLTGFGPISYVRVDEDMWSGDVNQLLM 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   NYFGHTFAEIAYTLCQASANRPWEYDGTYARMTQIVLSLFWLSYVGVIHQQNTYRTFYFQ 240
Beta sheet
Beta turn                UU
Disordered termini
ARG rich
                 241   CNRRGDAAEVWILSCSLNHSAQIRPGNRSLFVMPTSPDWNMDVNLILSSTLTGCLCSGSQ 300
Beta sheet
Beta turn                           UUUU
Disordered termini
ARG rich                                               RRRRRRRRRRRRR
                 301   LPLIDNNSVPAVSRNIHGWTGRAGNQLHGFQVRRMVTEFCDRLRRDGVMTQAQQNQVEAL 360
Beta sheet
Beta turn
Disordered termini
ARG rich
                 361   ADQTQQFKRDKLETWAREDDQYNQAHPNSTMFRTKPFTNAQWGRGNTGATSAAIAALI 418


Outer capsid protein sigma-3 (S3)  |  P03527
Beta sheet
Beta turn
Disordered termini
ARG rich
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                            1   MEVCLPNGHQVVDLINNAFEGRVSIYSAQEGWDKTISAQPDMMVCGGAVVCMHCLGVVGS 60
         Beta sheet
         Beta turn                UUUUUUUUUU
         Disordered termini
         ARG rich                 RRRRRRRRRRRRRRRR
                           61   LQRKLKHLPHHRCNQQIRHQDYVDVQFADRVTAHWKRGMLSFVAQMHEMMNDVSPDDLDR 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   VRTEGGSLVELNWLQVDPNSMFRSIHSSWTDPLQVVDDLDTKLDQYWTALNLMIDSSDLI 180
         Beta sheet
         Beta turn                   UUUUU
         Disordered termini
         ARG rich                                                                    RRRRRRR
                          181   PNFMMRDPSHAFNGVKLGGDARQTQFSRTFDSRSSLEWGVMVYDYSELEHDPSKGRAYRK 240
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich               RRRRRRR                                 RRRRRRRRRRRRRRRRR
                          241   ELVTPARDFGHFGLSHYSRATTPILGKMPAVFSGMLTGNCKMYPFIKGTAKLKTVRKLVE 300
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          301   AVNHAWGVEKIRYALGPGGMTGWYNRTMQQAPIVLTPAALTMFPDTIKFGDLNYPVMIGD 360
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          361   PMILG 365




Southern bean mosaic virus
         Capsid (CP)  |  P03601
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
         ARG rich                                        RRRRRRRRRRRRRR
                            1   MAKRLTKQQLTKAIANTLEAPATQSRRPRNRRRRRSAARQPQSTQAGVSMAPIAQGTMVR 60
         Beta sheet                                                                  SSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                           61   LREPSLRTAGGVTVLTHSELSTELSVTNAIVITSELVMPYTMGTWLRGVAANWSKYSLLS 120
         Beta sheet             SSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          121   VRYTYLPSCPSTTSGSIHMGFQYDMADTLPVSVNQLSNLRGYVSGQVWSGSSGLCYINGT 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          181   RCLDTANAITTTLDVGQLGKKWYPFKTSTDFTTAVGVNVNIATPLVPARLIIAMLDGSSS 240
         Beta sheet                SSSSSSSSSSSSSSS
         Beta turn
         Disordered termini                                 D
         ARG rich
                          241   TAVSTGRLYVSYTIQLIEPTALALNN 266




Scrophularia mottle virus
         Capsid (CP)  |  P03601
         Beta sheet
         Beta turn
```

```
         Disordered termini     DDD
         ARG rich
                            1   MEEVKPIKVQQPSIPAPGTKLVPNDGQQSPAMVMPFQLTVTDFGVKETSVQITLSSDPGI 60
         Beta sheet
         Beta turn                     UU
         Disordered termini
         ARG rich
                           61   AAITASYRHASIVECQAVLFPNRTSSSNPTHCDLVWVPANSTASPTTILKTFGGSRFTLG 120
         Beta sheet                                                             SSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          121   GPITANQIITIPLPLDSVNCRIKDSVLYTDSPRLLAHSPAPSTTQTVPSGSLIIRGKIRL 180
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          181   SSPLLQPSSSS 191
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Simian rotavirus A (SA11)
         RNA-directed RNA polymerase (RdRp)  |  A2T3S0
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                            1   MGKYNLILSEYLSFIYNSQSAVQIPIYYSSNSELENRCIEFHSKCLENSKNGLSLRKLFV 60
         Beta sheet
         Beta turn                                        UUUUUUUUUU
         Disordered termini
         ARG rich                                   RRRRRRRRRRRRRRRR
                           61   EYNDVIENATLLSILSYSYDKYNAVERKLVKYAKGKPLEADLTVNELDYENNKITSELFP 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                             RRRRRRRRRRRRRRRR            RR
                          121   TAEEYTDSLMDPAILTSLSSNLNAVMFWLEKHENDVAEKLKVYKRRLDLFTIVASTINKY 180
         Beta sheet
         Beta turn                 UUUUUUU      UUU
         Disordered termini
         ARG rich               RRRRRRRRRRRRRRRRRRR
                          181   GVPRHNAKYRYEYDVMKDKPYYLVTWANSSIEMLMSVFSHDDYLIAKELIVLSYSNRSTL 240
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          241   AKLVSSPMSILVALVDINGTFITNEELELEFSNKYVRAIVPDQTFDELNQMLDNMRKAGL 300
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          301   VDIPKMIQDWLVDRSIEKFPLMAKIYSWSFHVGFRKQKMLDAALDQLKTEYTENVDDEMY 360
         Beta sheet
         Beta turn                                                           UUUUUUUU
         Disordered termini
         ARG rich                                                            RRRRRRRRRRRRRRR
                          361   REYTMLIRDEVVKMLEEPVKHDDHLLRDSELAGLLSMSSASNGESRQLKFGRKTIFSTKK 420
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich                                       RRRRRRRRRRRRRRRR
                          421   NMHVMDDMANERYTPGIIPPVNVDKPIPLGRRDVPGRRTRIIFILPYEYFIAQHAVVEKM 480
         Beta sheet
         Beta turn                  UUUU
         Disordered termini
         ARG rich
                          481   LIYAKHTREYAEFYSQSNQLLSYGDVTRFLSNNTMVLYTDVSQWDSSQHNTQPFRKGIIM 540
         Beta sheet
         Beta turn
```

```
Disordered termini
ARG rich
                 541   GLDILANMTNDAKVLQTLNLYKQTQINLMDSYVQIPDGNVIKKIQYGAVASGEKQTKAAN 600
Beta sheet
Beta turn                           UUUUUU
Disordered termini
ARG rich                       RRRRRRRRRRRRRRRRRRR
                 601   SIANLALIKTVLSRISNKHSFATKIIRVDGDDNYAVLQFNTEVTKQMIQDVSNDVRETYA 660
Beta sheet
Beta turn                                                     UU
Disordered termini
ARG rich                                 RRRRRRRRRRRRRRRRRRRRRRR
                 661   RMNAKVKALVSTVGIEIAKRYIAGGKIFFRAGINLLNNEKRGQSTQWDQAAILYSNYIVN 720
Beta sheet                                 SSSSSSSSSSSS
Beta turn              UUU
Disordered termini
ARG rich
                 721   RLRGFETDREFILTKIMQMTSVAITGSLRLFPSERVLTTNSTFKVFDSEDFIIEYGTTDD 780
Beta sheet
Beta turn
Disordered termini
ARG rich
                 781   EVYIQRAFMSLSSQKSGIADEIAASSTFKNYVTRLSEQLLFSKNNIVSRGIALTEKAKLN 840
Beta sheet
Beta turn                                         UUUU
Disordered termini
ARG rich                                     RRRRRRRRRRRRRRRRRRRR
                 841   SYAPISLEKRRAQISALLTMLQKPVTFKSSKITINDILRDIKPFFTVSDAHLPIQYQKFM 900
Beta sheet
Beta turn
Disordered termini
ARG rich
                 901   PTLPDNVQYIIQCIGSRTYQIEDDGSKSAISRLISKYSVYKPSIEELYKVISLHENEIQL 960
Beta sheet
Beta turn                                                                     UUUUU
Disordered termini
ARG rich
                 961   YLISLGIPKIDADTYVGSKIYSQDKYRILESYVYNLLSINYGCYQLFDFNSPDLEKLIRI 1020
Beta sheet
Beta turn              UUUUU
Disordered termini
ARG rich                                                      RRRRRRRRRRRRRRRRRR
                 1021   PFKGKIPAVTFILHLYAKLEVINYAIKNGSWISLFCNYPKSEMIKLWKKMWNITSLRSPY 1080
Beta sheet
Beta turn
Disordered termini            D
ARG rich
                 1081   TNANFFQD 1088


Capsid (VP2)  |  P22055 [70 – 341]
Beta sheet
Beta turn
Disordered termini     DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
ARG rich                  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR           RRR
                   1   MAYRKRGARRETNLKQDERMQEKEDSKNINNDSPKSQLSEKVLSKKEEIITDNQEEVKIS 60
Beta sheet
Beta turn                                                                        UU
Disordered termini
ARG rich               RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                  61   DEVKKSNKEESKQLLEVLKTKEEHQKEVQYEILQKTIPTFEPKESILKKLEDIKPEQAKK 120
Beta sheet               SSSSSSSSSSSSSS
Beta turn              UUUUUU
Disordered termini
ARG rich               RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                 121   QTKLFRIFEPKQLPIYRANGERELRNRWYWKLKRDTLPDGDYDVREYFLNLYDQVLMEMP 180
Beta sheet
Beta turn                          UUUUUUUU
Disordered termini
ARG rich                                                          RRRRRRRRRRRRRRR
                 181   DYLLLKDMAVENKNSRDAGKVVDSETAAICDAIFQDEETEGAVRRFIAEMRQRVQADRNV 240
Beta sheet
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Beta turn
Disordered termini
ARG rich
                 241   VNYPSILHPIDHAFNEYFLQHQLVEPLNNDIIFNYIPERIRNDVNYILNMDRNLPSTARY 300
Beta sheet
Beta turn
Disordered termini
ARG rich
                 301   IRPNLLQDRLNLHDNFESLWDTITTSNYILARSVVPDLKELVSTEAQIQKMSQDLQLEAL 360
Beta sheet
Beta turn
Disordered termini
ARG rich
                 361   TIQSETQFLTGINSQAANDCFKTLIAAMLSQRTMSLDFVTTNYMSLISGMWLLTVIPNDM 420
Beta sheet
Beta turn
Disordered termini
ARG rich
                 421   FIRESLVACQLAIINTIVYPAFGMQRMHYRNGDPQTPFQIAEQQIQNFQVANWLHFVNYN 480
Beta sheet
Beta turn
Disordered termini
ARG rich
                 481   QFRQVVIDGVLNQVLNDNIRNGHVVNQLMEALMQLSRQQFPTMPVDYKRSIQRGILLLSN 540
Beta sheet
Beta turn
Disordered termini
ARG rich
                 541   RLGQLVDLTRLLSYNYETLMACITMNMQHVQTLTTEKLQLTSVTSLCMLIGNATVIPSPQ 600
Beta sheet
Beta turn
Disordered termini
ARG rich                                              RRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                 601   TLFHYYNVNVNFHSNYNERINDAVAIITAANRLNLYQKKMKSIVEDFLKRLQIFDVARVP 660
Beta sheet
Beta turn
Disordered termini
ARG rich               RRRRRRRRRRRRRRRRRRRR
                 661   DDQMYRLRDRLRLLPVEIRRLDIFNLIAMNMEQIERASDKIAQGVIIAYRDMQLERDEMY 720
Beta sheet
Beta turn
Disordered termini
ARG rich
                 721   GYVNIARNLDGFQQINLEELMRSGDYAQITNMLLNNQPVALVGALPFITDSSVISLIAKL 780
Beta sheet
Beta turn                       UUUU
Disordered termini
ARG rich                        RRRRRRRRRRRRRR
                 781   DATVFAQIVKLRKVDTLKPILYKINSDSNDFYLVANYDWIPTSTTKVYKQVPQQFDFRAS 840
Beta sheet
Beta turn
Disordered termini
ARG rich
                 841   MHMLTSNLTFTVYSDLLAFVSADTVEPINAVAFDNMRIMNEL 882


Capsid (VP3)  |  P22055 [342 - 581]
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MKVLALRHSVAQVYADTQVYVHDDTKDSYENAFLISNLTTHNILYLNYSIKTLEILNKSG 60
Beta sheet
Beta turn                                                        UUUUUUUUU
Disordered termini
ARG rich
                  61   IAAIALQSLEELFTLIRCNFTYDYELDIIYLHDYSYYTNNEIRTDQHWITKTNIEEYLLP 120
Beta sheet                         SSSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich                                                                 RRRRRRRRRR
                 121   GWKLTYVGYNGSETRGHYNFSFKCQNAATDDDLIIEYIYSEALDFQNFMLKKIKERMTTS 180
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Beta sheet
Beta turn                                  UUUU
Disordered termini
ARG rich               RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                181   LPIARLSNRVFRDKLFPSLLKEHKNVVNVGPRNESMFTFLNYPTIKQFSNGAYLVKDTIK 240
Beta sheet
Beta turn                                                   UUU
Disordered termini
ARG rich
                241   LKQERWLGKRISQFDIGQYKNMLNVLTAIYYYYNLYKSKPIIYMIGSAPSYWIYDVRHYS 300
Beta sheet
Beta turn
Disordered termini
ARG rich                                  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
                301   DFFFETWDPLDTPYSSIHHKELFFINDVKKLKDNSILYIDIRTDRGNADWKKWRKTVEEQ 360
Beta sheet
Beta turn
Disordered termini
ARG rich
                361   TINNLDIAYEYLRTGKAKVCCVKMTAMDLELPISAKLLHHPTTEIRSEFYLLLDTWDLTN 420
Beta sheet
Beta turn
Disordered termini
ARG rich
                421   IRRFIPKGVLYSFINNIITENVFIQQPFKVKVLNDSYIVALYALSNDFNNRSEVIKLINN 480
Beta sheet
Beta turn
Disordered termini
ARG rich
                481   QKQSLITVRINNTFKDEPKVGFKNIYDWTFLPTDFDTKEAIITSYDGCLGLFGLSISLAS 540
Beta sheet
Beta turn
Disordered termini
ARG rich
                541   KPTGNNHLFILSGTDKYYKLDQFANHTSISRRSHQIRFSESATSYSGYIFRDLSNNNFNL 600
Beta sheet
Beta turn
Disordered termini
ARG rich
                601   IGTNIENSVSGHVYNALIYYRYNYSFDLKRWIYLHSIDKVDIEGGKYYELAPIELIYACR 660
Beta sheet
Beta turn                                                                UUUUUUUU
Disordered termini
ARG rich
                661   SAKEFATLQDDLTVLRYSNEIENYINTVYSITYADDPNYFIGIQFRNIPYKYDVKIPHLT 720
Beta sheet
Beta turn
Disordered termini
ARG rich
                721   FGVLHISDNMVPDVIDILKIMKNELFKMDITTSYTYMLSDGIYVANVSGVLSTYFKIYNV 780
Beta sheet                                       SSSSSSSSSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich                                        RRRRRRRRRRRRRRRRRRRRR
                781   FYKNQITFGQSRMFIPHITLSFNNMRTVRIETTKLQIKSIYLRKIKGDTVFDMVE 835


Inner capsid (VP4)  |  P22055 [2 - 69]
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MASLIYRQLLTNSYTVDLSDEIQEIGSTKSQNVTINPGPFAQTGYAPVNWGPGEINDSTT 60
Beta sheet
Beta turn
Disordered termini
ARG rich
                  61   VEPLLDGPYQPTTFNPPVDYWMLLAPTTPGVIVEGTNNTDRWLATILIEPNVQSENRTYT 120
Beta sheet
Beta turn
Disordered termini
ARG rich
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                 121   IFGIQEQLTVSNTSQDQWKFIDVVKTTANGSIGQYGPLLSSPKLYAVMKHNEKLYTYEGQ 180
Beta sheet
Beta turn
Disordered termini
ARG rich
                 181   TPNARTAHYSTTNYDSVNMTAFCDFYIIPRSEESKCTEYINNGLPPIQNTRNVVPLSLTA 240
Beta sheet                                          SSSSSSSSSSSSSSSS    SSSSSSSSSSS
Beta turn
Disordered termini
ARG rich
                 241   RDVIHYRAQANEDIVISKTSLWKEMQYNRDITIRFKFANTIIKSGGLGYKWSEISFKPAN 300
Beta sheet             SSSSSSS
Beta turn
Disordered termini
ARG rich
                 301   YQYTYTRDGEEVTAHTTCSVNGVNDFSFNGGYLPTDFVVSKFEVIKENSYVYIDYWDDSQ 360
Beta sheet                 SSSSSSSSSSSSSSSSSSSSSSSSSS                          SSS
Beta turn
Disordered termini
ARG rich
                 361   AFRNVVYVRSLAANLNSVMCTGGSYNFSLPVGQWPVLTGGAVSLHSAGVTLSTQFTDFVS 420
Beta sheet             SSSSSSSSSSSS    SSSSSSSSSSSSSSSSS
Beta turn
Disordered termini
ARG rich                   RRRRRRRRRRRRRRRRRRRRRR
                 421   LNSLRFRFRLAVEEPHFKLTRTRLDRLYGLPAADPNNGKEYYEIAGRFSLISLVPSNDDY 480
Beta sheet
Beta turn
Disordered termini
ARG rich                                                                     RRRRRR
                 481   QTPIANSVTVRQDLERQLGELREEFNALSQEIAMSQLIDLALLPLDMFSMFSGIKSTIDA 540
Beta sheet
Beta turn
Disordered termini
ARG rich               RRRRRRRRRRRRRR
                 541   AKSMATNVMKKFKKSGLANSVSTLTDSLSDAASSISRGSSIRSIGSSASAWTDVSTQITD 600
Beta sheet
Beta turn
Disordered termini
ARG rich
                 601   ISSSVSSVSTQTSTISRRLRLKEMATQTEGMNFDDISAAVLKTKIDKSTQISPNTIPDIV 660
Beta sheet
Beta turn
Disordered termini
ARG rich
                 661   TEASEKFIPNRAYRVINNDDVFEAGIDGKFFAYKVDTFEEIPFDVQKFADLVTDSPVISA 720
Beta sheet
Beta turn
Disordered termini
ARG rich
                 721   IIDFKTLKNLNDNYGITKQQAFNLLRSDPRVLREFINQDNPIIRNRIEQLIMQCRL 776


Intermediate capsid protein VP6 (VP6)  |  A2T3S5
Beta sheet
Beta turn
Disordered termini
ARG rich
                   1   MDVLYSLSKTLKDARDKIVEGTLYSNVSDLIQQFNQMIITMNGNEFQTGGIGNLPIRNWN 60
Beta sheet
Beta turn
Disordered termini
ARG rich                                                                       RRRR
                  61   FNFGLLGTTLLNLDANYVETARNTIDYFVDFVDNVCMDEMVRESQRNGIAPQSDSLRKLS 120
Beta sheet
Beta turn
Disordered termini
ARG rich               RRRRRR
                 121   AIKFKRINFDNSSEYIENWNLQNRRQRTGFTFHKPNIFPYSASFTLNRSQPAHDNLMGTM 180
Beta sheet
Beta turn                                                UU
Disordered termini
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         ARG rich
                          181   WLNAGSEIQVAGFDYSCAINAPANIQQFEHIVPLRRVLTTATITLLPDAERFSFPRVINS 240
         Beta sheet                                        SSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          241   ADGATTWFFNPVILRPNNVEVEFLLNGQIINTYQARFGTIVARNFDTIRLSFQLMRPPNM 300
         Beta sheet                            SSSSSSSSSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          301   TPAVAVLFPNAQPFEHHATVGLTLRIESAVCESVLADASETLLANVTSVRQEYAIPVGPV 360
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          361   FPPGMNWTDLITNYSPSREDNLQRVFTVASIRSMLIK 397


         Outer capsid glycoprotein VP7 (VP7)  |  A2T3P5
         Beta sheet
         Beta turn
         Disordered termini     DD
         ARG rich
                            1   MYGIEYTTVLTFLISIILLNYILKSLTRIMDFIIYRFLFIIVILSPFLRAQNYGINLPIT 60
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                           61   GSMDTAYANSTQEETFLTSTLCLYYPTEAATEINDNSWKDTLSQLFLTKGWPTGSVYFKE 120
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          121   YTNIASFSVDPQLYCDYNVVLMKYDATLQLDMSELADLILNEWLCNPMDITLYYYQQTDE 180
         Beta sheet                                                                 SSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          181   ANKWISMGSSCTIKVCPLNTQTLGIGCLTTDATTFEEVATAEKLVITDVVDGVNHKLDVT 240
         Beta sheet             SSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          241   TATCTIRNCKKLGPRENVAVIQVGGSDILDITADPTTAPQTERMMRINWKKWWQVFYTVV 300
         Beta sheet
         Beta turn
         Disordered termini
         ARG rich
                          301   DYVDQIIQVMSKRSRSLNSAAFYYRV 326




Tobacco mosaic virus (Vulgare)
         Capsid (CP)  |  P03601
         Beta sheet
         Beta turn
         Disordered termini     D
         ARG rich
                            1   MSYSITTPSQFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSEVWKPSPQVT 60
         Beta sheet
         Beta turn                                            UUU
         Disordered termini
         ARG rich
                           61   VRFPDSDFKVYRYNAVLDPLVTALLGAFDTRNRIIEVENQANPTTAETLDATRRVDDATV 120
         Beta sheet
         Beta turn
         Disordered termini                                           D
         ARG rich
                          121   AIRSAINNLIVELIRGTGSYNRSSFESSSGLVWTSGPAT 159
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Turnip yellow mosaic virus
         Capsid (CP)  |  P03601
         Beta sheet
         Beta turn
         Disordered termini     DDDDDDD
         ARG rich
                            1   MEIDKELAPQDRTVTVATVLPAVPGPSPLTIKQPFQSEVLFAGTKDAEASLTIANIDSVS 60
         Beta sheet                    SSSSSSSSSSSSS
         Beta turn                    UU
         Disordered termini
         ARG rich
                           61   TLTTFYRHASLESLWVTIHPTLQAPTFPTTVGVCWVPANSPVTPAQITKTYGGQIFCIGG 120
         Beta sheet                                                            SSSSSSSSSSSSS
         Beta turn
         Disordered termini
         ARG rich
                          121   AINTLSPLIVKCPLEMMNPRVKDSIQYLDSPKLLISITAQPTAPPASTCIITVSGTLSMH 180
         Beta sheet             S
         Beta turn
         Disordered termini             D
         ARG rich
                          181   SPLITDTST 189
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