

下痢症ウイルスレファレンス 活動報告

2013年7月11日（名古屋）

Proposal for a Unified Norovirus Genotyping and Strain Nomenclature

Annelies Kroneman, Harry Vennema, Jan Vinjé, , Peter A. White, Grant Hansman, Kim Green, Vito Martella, Kazuhiko Katayama, Marion Koopmans

- **An ORF1-ORF2 recombination, chimeric virus was increased.**
- **Need to know ORF1 character that related to pathogenicity of NoV.**
- **New system was developed to understand NoV evolution mechanism.**

A cryptogram previously proposed for caliciviruses would further facilitate communication by inclusion of the genogroup and genotype assignment as follows:

Host / Hu (human) Bo (bovine), Mu (murine), Po (porcine), Ca (canine). A list of the host name abbreviations is published on the norovirus typing tool website.

NoroNet: <http://www.rivm.nl/mpf/norovirus/typingtool>

Country code (ISO) / FR, DE, US, JP, etc

year of sampling / .

genogroup and genotype /

(ORF1 and ORF2)

GII.P4_GII.4, or if only the

ORF2 sequence is known:

GII.4 variant name city, if necessary followed by a serial number.

For example:

norovirus GII/Hu/FR/2004/GII.P12-GII.3/Paris23

norovirus GII/Hu/GB/2010/GII.P4_GII.4_New-Orleans2009/London48,

or if only the capsid sequence is known:

norovirus GII/Hu/FR/2004/GII.12/Paris25.

Norovirus Typing Tool - (Closed/ Open access)

You may can either:

- A. paste one or more sequences in FASTA format in the input field.
- B. upload a FASTA file.
- C. revisit results of a previous run

A) Paste nucleotide sequence(s) in FASTA format:

```
>AB287451
GGCGTCGATGACGCCNCCCCATCTGATGGGTCCACAGCCAACCTCGTCCCAGAGGTCAACAATGAGGTTATGGCTTTGGA
GCCC GTT GTT GGT GCC GCG ATT GCG GC ACCT GTAG CGG GCC AAC AAA ATG TA ATT G ACC CCT GG ATT AG AA TA AT TTTG
TACAAGCCA
```

B) Or, upload a FASTA with nucleotide sequences:

C) Or, revisit results from a previous run:

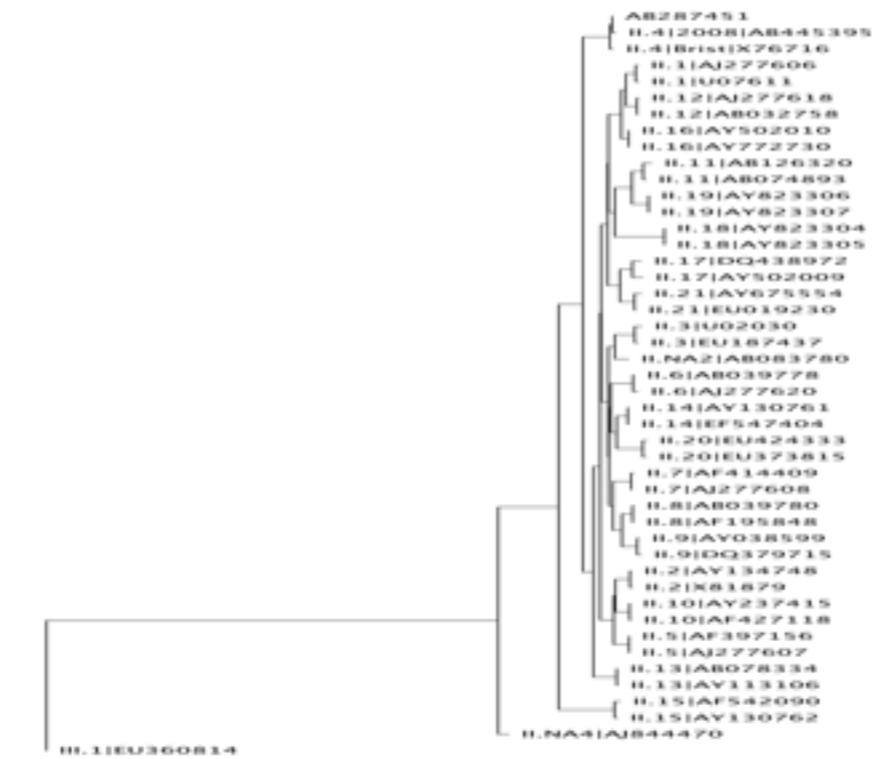
Job-id:

Norovirus Typing Tool

You may bookmark this page to revisit results of this job (1582787771) later.

Name	Length	Report	ORF 1	ORF 2	Genome
AB287451	169	Report	NA	NoV II.4 2004	
AB112331	938	Report	NoV II.d	NoV II.5	
AB287450	167	Report	NA	NoV II.6	

Download results: [XML File](#), [Table \(CSV format\)](#), [Table \(Excel format\)](#)



Fields Virology 6th edition に収載予定のGI ORF2 標準配列

Reference Virus	Genogroup	Genotype	Accession Number
Hu/NoV/GI.1/Norwalk/1968/US	I	1	M87661
Hu/NoV/GI.2/Southampton/1991/UK	I	2	L07418
Hu/NoV/GI.3/Desert Shield 395/1990/SA	I	3	U04469
Hu/NoV/GI.4/Chiba 407/1987/JP	I	4	AB022679
Hu/NoV/GI.5/Musgrove/1989/UK	I	5	AJ277614
Hu/NoV/GI.6/BS5(Hesse3)/1997/DE	I	6	AF093797
Hu/NoV/GI.7/Winchester/1994/UK	I	7	AJ277609
Hu/NoV/GI.8/Boxer/2001/US	I	8	AF538679
Hu/NoV/GI.9/Vancouver730/2004/CA	I	9	HQ637267

NoV GI のORF2領域を用いたジェノタイプは9種類

NoV GII standard strains

Reference Virus	Genogroup	Genotype	Accession
Hu/NoV/GII.1/Hawaii/1971/US	II	1	U07611
Hu/NoV/GII.2/Melksham/1994/UK	II	2	X81879
Hu/NoV/GII.3/Toronto 24/1991/CA	II	3	U02030
Hu/NoV/GII.4/Bristol/1993/UK	II	4	X76716
Hu/NoV/GII.5/Hillingdon/1990/UK	II	5	AJ277607
Hu/NoV/GII.6/Seacroft/1990/UK	II	6	AJ277620
Hu/NoV/GII.7/Leeds/1990/UK	II	7	AJ277608
Hu/NoV/GII.8/Amsterdam/1998/NL	II	8	AF195848
Hu/NoV/GII.9/VA97207/1996/US	II	9	AY038599
Hu/NoV/GII.10/Erfurt546/2000/DE	II	10	AF427118
Po/NoV/GII.11/Sw918/1997/JP	II	11	AB074893
Hu/NoV/GII.12/Wortley/1990/UK	II	12	AJ277618
Hu/NoV/GII.13/Fayetteville/1998/US	II	13	AY113106
Hu/NoV/GII.14/M7/1999/US	II	14	AY130761
Hu/NoV/GII.15/J23/1999/US	II	15	AY130762
Hu/NoV/GII.16/Tiffin/1999/US	II	16	AY502010
Hu/NoV/GII.17/CS-E1/2002/US	II	17	AY502009
Po/NoV/GII.18/OH-QW101/2003/US	II	18	AY823304
Po/NoV/GII.19/OH-QW170/2003/US	II	19	AY823306
Hu/NoV/GII.20/Luckenwalde591/2002/DE	II	20	EU373815
Hu/NoV/GII.21/IF1998/2003/IR	II	21	AY675554
Hu/NoV/GII.22/YURI/JP	II	22	AB083780

NoV GII のORF2領域を用いたジェノタイプは22種類



Genotype番号比較表

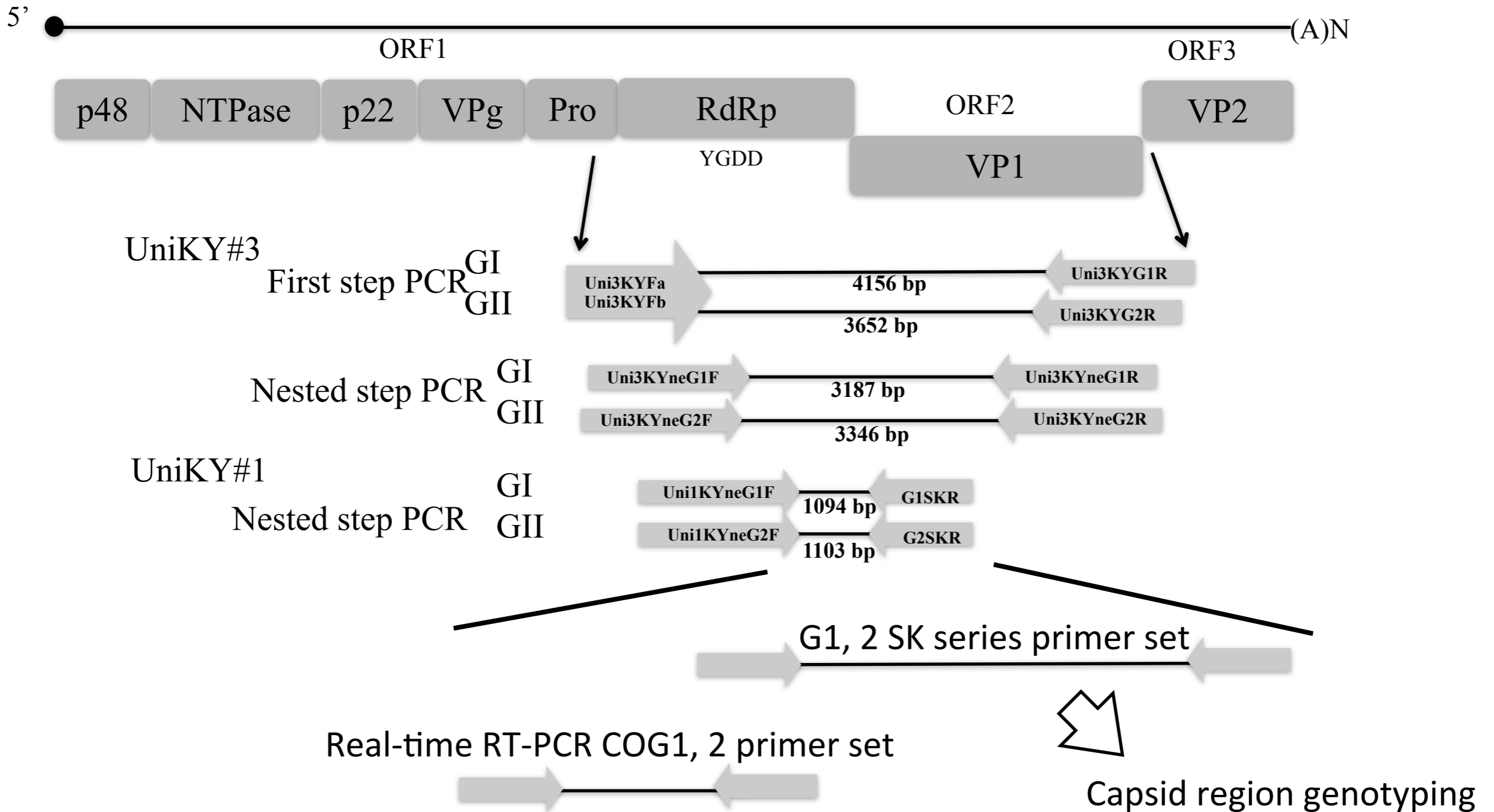
Capsid N/S regionに基づく genotype		VP1全長アミノ酸配列に基づく genotype				
	Genotype number	Accession number	Strain name	Genotype number	Accession number	Strain name
Genogroup I	GI/1	M87661	Norwalk/68/US*	GI.1	M87661	Norwalk/68/US*
	GI/2	L07418	Southampton/91/UK*	GI.2	L07418	Southampton/91/UK*
	GI/3	U04469	DesertShield/90/US	GI.3	U04469	DesertShield/90/US
	GI/4	AB042808	Chiba407/87/JP*	GI.4	AB042808	Chiba407/87/JP*
	GI/5	AJ277614	Musgrove/89/UK	GI.5	AJ277614	Musgrove/89/UK
	GI/6	AF093797	Hesse (BS5) /98/GE*	GI.6	AF093797	Hesse (BS5) /98/GE*
	GI/7	AJ277609	Winchester/94/UK	GI.7	AJ277609	Winchester/94/UK
	GI/8	AB081723	WUG1/00/JP*	GI.8	AF538679	Boxer/01/US**
	GI/9	AB039774	SaitamaSzUG1/99/JP*	GI.9	HQ637267	Vancouver730/2004/CA
	GI/10	AF538679	Boxer/01/US**			
	GI/11	AB058547	SaitamaKU8GI/99/JP			
	GI/12	AB058525	SaitamaKU19aGI/00/JP			
	GI/13	AB112132	SaitamaT35aGI/01/JP			
	GI/14	AB112100	SaitamaT25GI/01/JP			
Genogroup II	GII/1	U07611	Hawaii*	GII.1	U07611	Hawaii*
	GII/2	X81879	Melksham	GII.2	X81879	Melksham
	GII/3	AB067542	SaitamaU201*	GII.3	U02030	Tronto
	GII/4	X86557	Lordsdale/93/UK*	GII.4	X76716	Bristol
	GII/5	AJ277607	Hillingdon/90/UK	GII.5	AJ277607	Hillingdon/90/UK
	GII/6	AB039776	SaitamaU3*	GII.6	AJ277620	Seacroft/90/UK
	GII/7	AJ277608	Leeds/90/UK	GII.7	AJ277608	Leeds/90/UK
	GII/8	AB067543	SaitamaU25*	GII.8	AF195848	Amsterdam
	GII/9	AY054299	IdahoFalls	GII.9	AY038599	VA97207/97
	GII/10	AY237415	Mc37*	GII.10	AF427118	Erfurt/546/00/DE
	GII/11	AB112221	SaitamaT29GII	GII.11	AB074893	SwNoV/Sw918/97/JP
	GII/12	AB039775	SaitamaU1*	GII.12	AJ277618	Wortley/90/UK
	GII/13	AY130761	M7/99/US	GII.13	AY113106	Fayettevil/98/US**
	GII/14	AB078334	Kashiwa47	GII.14	AY130761	M7/99/US**
	GII/15	AB058582	SaitamaKU80aGII	GII.15	AY130762	J23/1999/US**
	GII/16	AB112260	SaitamaT53GII	GII.16	AY502010	Triffin/1999/US
	GII/17	AF195847	Alphatron	GII.17	AY502009	CSE1/2002/US
	GII/18	AB083780	Akita-Yuri	GII.18	AY823304	SwNoV/OHQW101/2003/US
	GII/19	EF630529	Hokkaido299	GII.19	AY823306	SwNoV/OHQW170/2003/US
			GII.20	EU373815	Luckenwalde591/2002/DE	
			GII.21	AY675554	IF1998/2003/IR	
			GII.22	AB083780	YURI/JP	

*Full-length genome sequence

**Unpublished

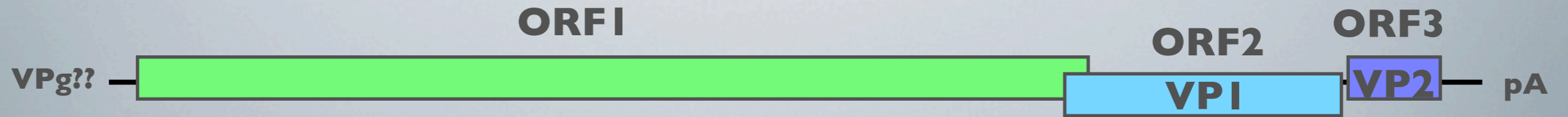
Map of UniKY RT-PCR region and a related conventional RT-PCR region

Norwalk virus genome (M87661)



UniKY RT-PCR system will be able to provide RdRp region genotyping and also confirm capsid region genotyping. It also will identify chimeric viruses.

New Standard NoV-Plasmids v2



Protease region - VP2 region

GI/1 NV68 prototype	3000-7500	3.5 Kb
GII/4 2006b Saga I strain	3000-7400	3.4 Kb

Proteaseの上流に存在する高度保存領域から、VP2下流までを含む。Long RT-PCRに対応。

ノロウイルスレファレンスセンター

宮城県保健環境センター

埼玉県衛生研究所

千葉市環境保健研究所 医科学課

愛知県衛生研究所

名古屋市衛生研究所

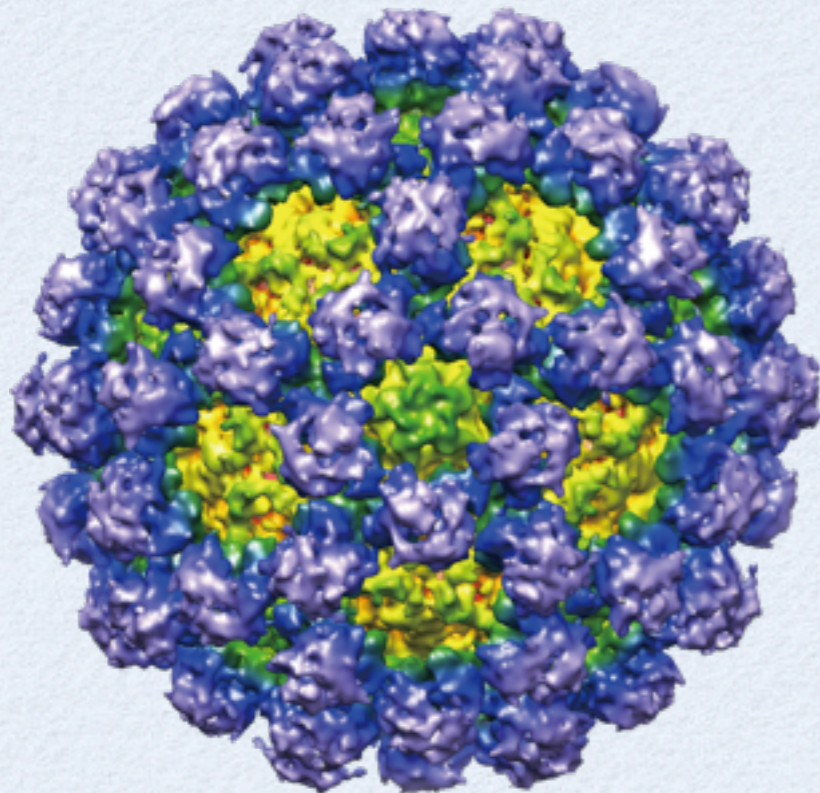
大阪市立環境科学研究所

堺市衛生研究所

広島県衛生研究所

長崎市保健環境試験所

佐賀県衛生薬業センター



担当委員の変更がある場合、お知らせください

katayama@nih.go.jp