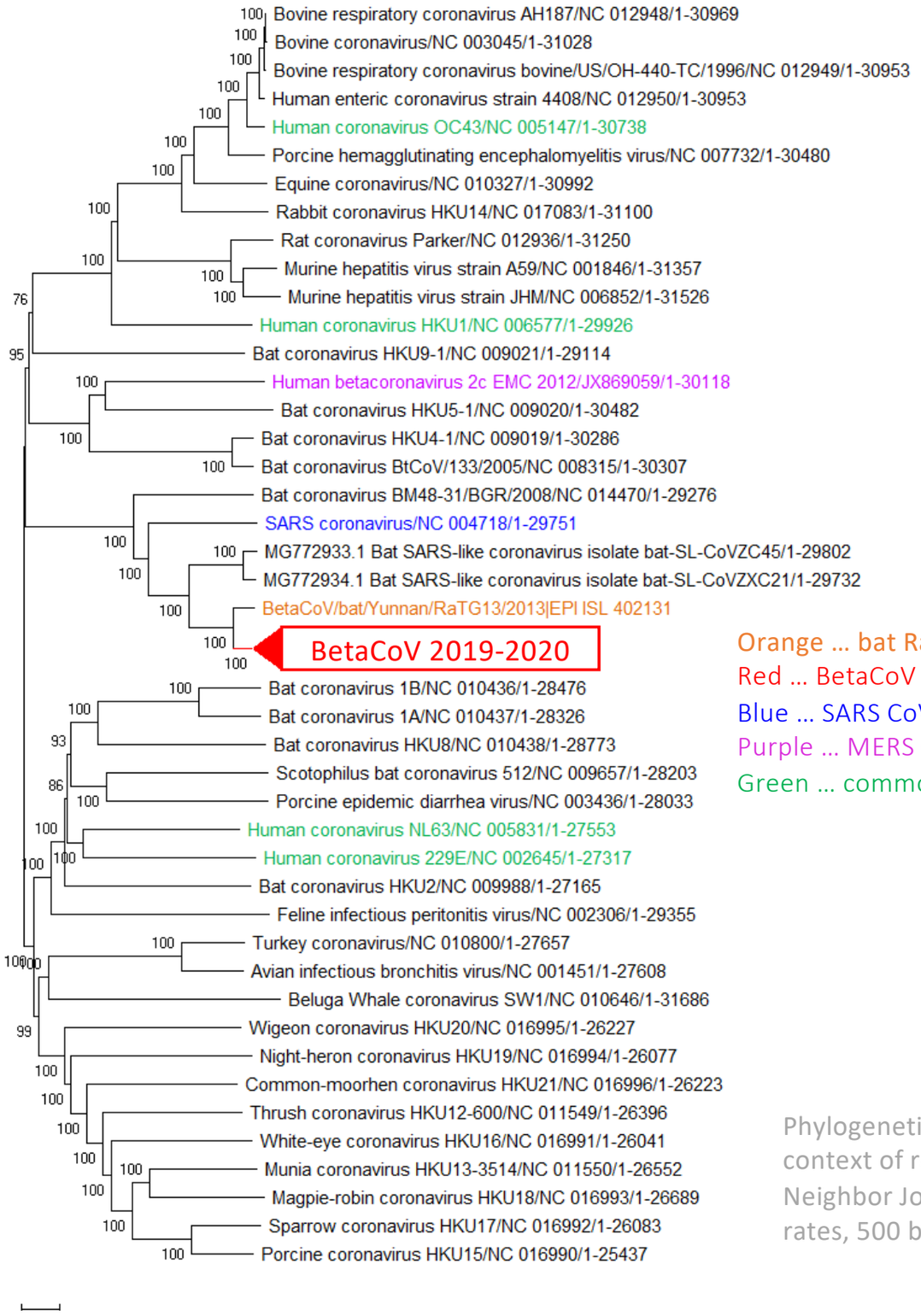
Full genome tree all CoV families



Orange … bat RaTG13
Red … BetaCoV 2019-2020
Blue … SARS CoV
Purple … MERS CoV
Green … common cold CoV

Phylogenetic tree of Wuhan CoV full genome sequences in context of representatives of all CoV families (whole genome Neighbor Joining, Maximum Composite Likelihood, uniform rates, 500 bootstrap, MegaX)

by BII, A*STAR Singapore

- New nearest bat precursor shared by Zhengli Shi's lab included (RaTG13/EPI_ISL_402131)

Genome identity to BetaCoV:

- 96% RaTG13 (nearest bat precursor)
- 88% ZC45/ZXC21 bat precursor
- 80% SARS

We gratefully acknowledge the Originating and Submitting laboratories of sequence data in alphabetic order:

P.R. China: Guangdong Provincial Center for Diseases Control and Prevention, Guangdong Provincial Public Health
Hubei Provincial CDC
Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College
National Institute for Viral Disease Control and Prevention, at the Chinese Center for Disease Control and Prevention
Wuhan Institute of Virology, Chinese Academy of Sciences
Wuhan Jinyintan Hospital
Zhejiang Provincial Center for Disease Control and Prevention

Japan: Department of Virology III, National Institute of Infectious Diseases;

Thailand: Bamrasnaradura Hospital, Nonthaburi
Department of Disease Control, Ministry of Public Health
Department of Medical Sciences, Ministry of Public Health
Thai Red Cross Emerging Infectious Diseases - Health Science Centre.

USA: Division of Viral Diseases, Centers for Disease Control and Prevention
Illinois Department of Public Health, Chicago Laboratory
Providence Regional Medical Center

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SHORT COMMUNICATION

A common RNA motif in the 3′ end of the genomes of astroviruses, avian infectious bronchitis virus and an equine rhinovirus

Christine Monceyron Jonassen, Tom Ø. Jonassen and Bjørn Grinde

Department of Virology, National Institute of Public Health, PO Box 4404 Torshov, N-0403 Oslo, Norway

In the 3′ non-coding region of the genomes of infectious bronchitis virus, an avian coronavirus and the picornavirus equine rhinovirus serotype 2, there is a motif with remarkable similarity, both in sequence and folding, to the second RNA stem–loop from the 3′ end of the genomes of human astroviruses. This motif was also found in astroviruses of sheep, pig and turkey, suggesting that it is a common feature of all astroviruses. The conserved nature of the motif indicates that there has been strong selection for its preservation. There is significant homology between the regions flanking this motif in infectious bronchitis virus and a continuous RNA sequence at the same distance from the 3′ poly(A) tail in some related mammalian coronaviruses. These observations suggest that the presence of the motif in these three viral families is the result of at least two separate RNA recombination events.

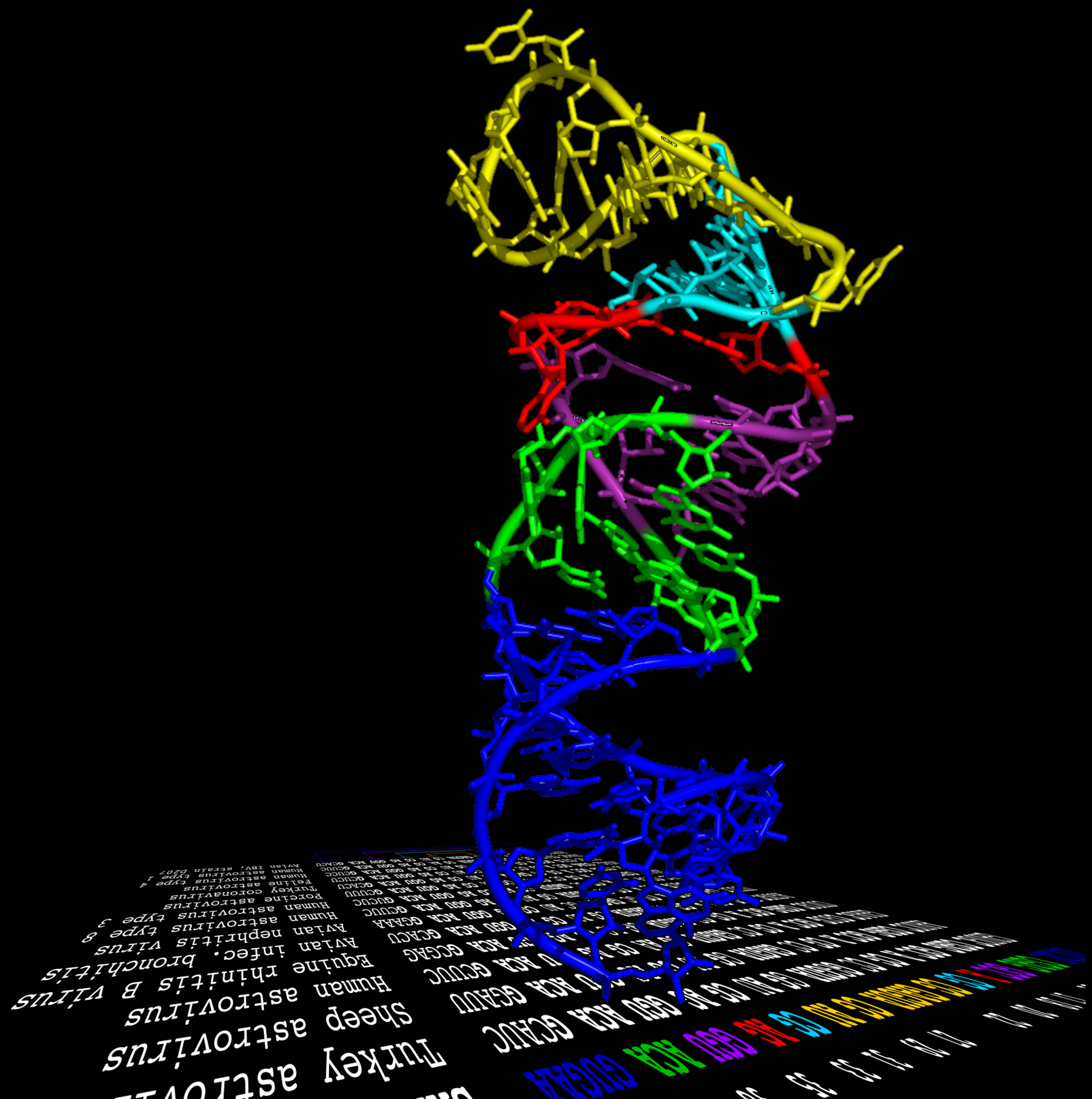
Astroviruses are non-enveloped particles with a plus-strand

stem of 6 base pairs and a 31 nt loop region with more uncertain interaction between the nucleotides. The biological importance of the basal stem is substantiated by nucleotide covariations among HAstV serotypes, i.e. sequence differences are compensated by other differences to maintain base pairing (Monceyron *et al.*, 1997).

IBV is a coronavirus with a 27·6 kb plus-strand RNA genome containing a 0·3–0·5 kb 3′ NCR and a poly(A) tail (Williams *et al.*, 1993). Different strains have different tissue tropisms, infecting respiratory, reproductive and gastrointestinal organs as well as the kidneys of chicken (Siddell *et al.*, 1983). In IBV this stem–loop II-like motif (s2m) can be folded exactly like the HAstV stem–loop II, and we have suggested its presence in these very different viruses to be the result of a natural RNA recombination between an astrovirus and IBV (Monceyron *et al.*, 1997).

Recombination among distantly related groups of viruses is probably important in the evolution of RNA viruses. In contrast to recombination within certain viral species, however, transfer of RNA from one virus family to another seems very rare. Because of the high rates of nucleotide substitution in RNA viruses, traces of such recombinations are not easily detected. Examples of recombination among distant groups of

2019 Novel Coronavirus (2019-nCoV)
s2m RNA



s2m RNA sequence alignments relative to SARS

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UUCAU CGAG GCC A CG CG GAGUA CG AU CG AG GGU ACA GUGAA   SARS
UUCAC CGAG GCC A CG CG GAGUA CG AU CG AG UGU ACA GUGAA   2019-nCoV 25/26
UUCAC CGAG GCC A CG CG G GUA CG AU CG AG UGU ACA GUGAA   2019-nCoV 1/26
AUGAU CAUG GCA A CC CU GUGUA CU UC CU UC GGU ACA GUGGA   MERS (ref.)
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5     10    14    17 18   20   22      27  29   31  33   35   38   41    45
UUCAU CGAG GCC A CG CG GAGUA CG AU CG AG GGU ACA GUGAA   SARS  coronavirus
GAUGC CGAG GCC A CG CC GGGUA GG AU CG AG GGU ACA GCAUC   Turkey astrovirus
AAUCC CGAG GCC A CG CC GAGUA GG AU CG AG GGU ACA GGAUU   Sheep astrovirus
GAAGC CGCG GCC A CG CC GAGUA GG AA CG AG GGU ACA GCUUC   Human astrovirus
CUCGC CGAG GCC A CG CC GAGUA GG AC CG AG GGU ACA GCGAG   Equine rhinitis B virus
AGUGC CGGG GCC A CG CG GAGUA CG AU CG AG GGU ACA GCACU   Avian infec. bronchitis
UUUCC CGAG GCC A CG GC GAGUA GC AU CG AG GGU ACA GGAAA   Avian nephritis virus
GAAGC CGCG GCC A CG CC GAGUA GG AU CG AG GGU ACA GCUUC   Human astrovirus type 8
GAGAC CGCG GCC A CG CC GAGUA GG AU CG AG GGU ACA GUCUC   Human astrovirus type 3
AAAGC CGAG GCC A CG CC GAGUA GG AA CG AG GGU ACA GCUUU   Porcine astrovirus
AGUGC CGAG GCC A CG CG GAGUA CG AU CG AG GGU ACA GCACU   Turkey coronavirus
AGAGC CGAG GCC A CG CC GAGUA GG AU CG AG GGU ACA GCUCU   Feline astrovirus
GGAGC CGCG GCC A CG CC GAGUA GG AU CG AG GGU ACA GCUCC   Human astrovirus type 4
GAAGC CGCG GCC A CG CC GAGUA GG AA CG AG GGU ACA GCUUC   Human astrovirus type 1
AGUGC CAGG GCC A CG CG GAGUA CG AU CG AG GGU ACA GCACU   Avian IBV, strain D207
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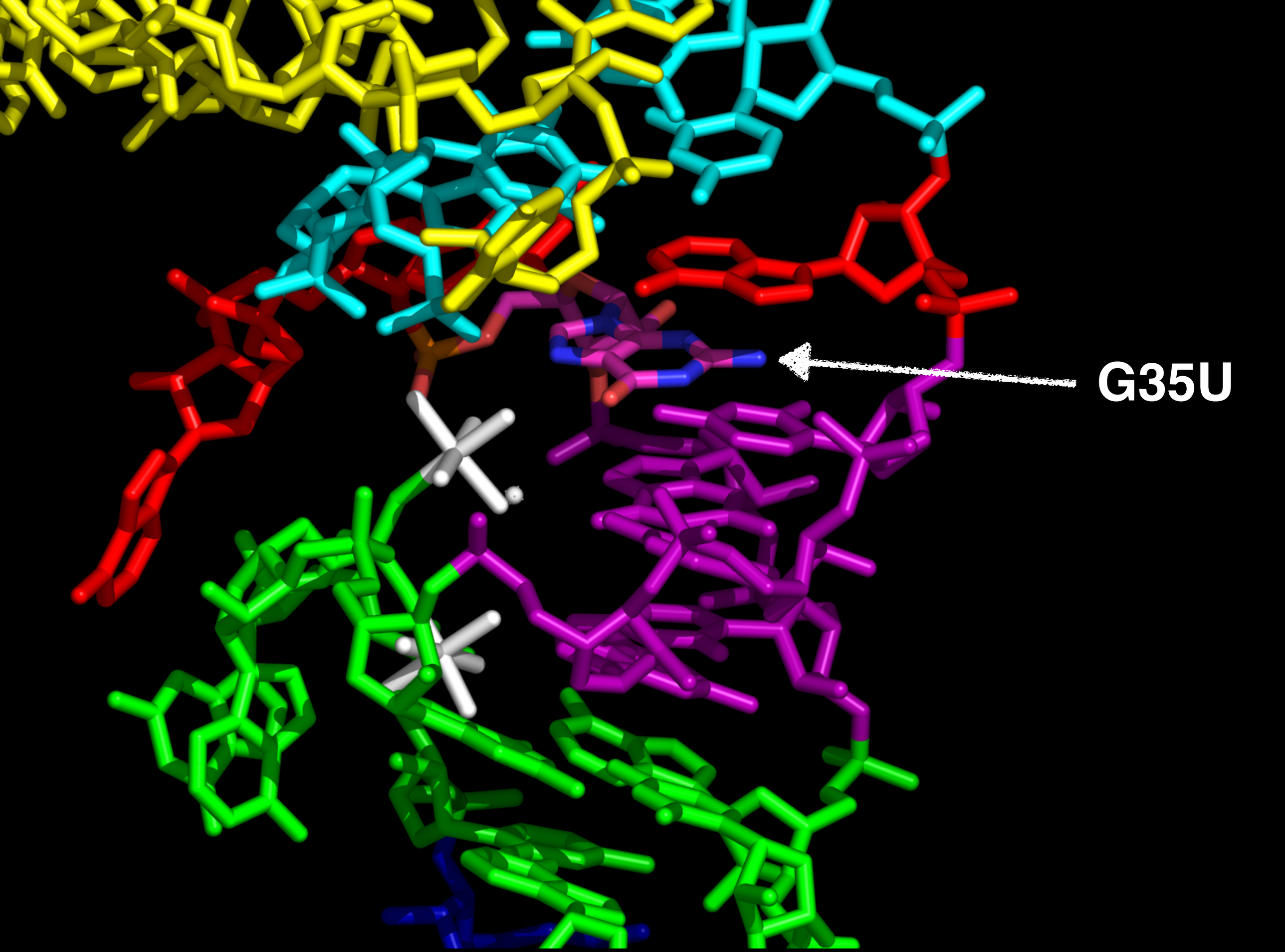
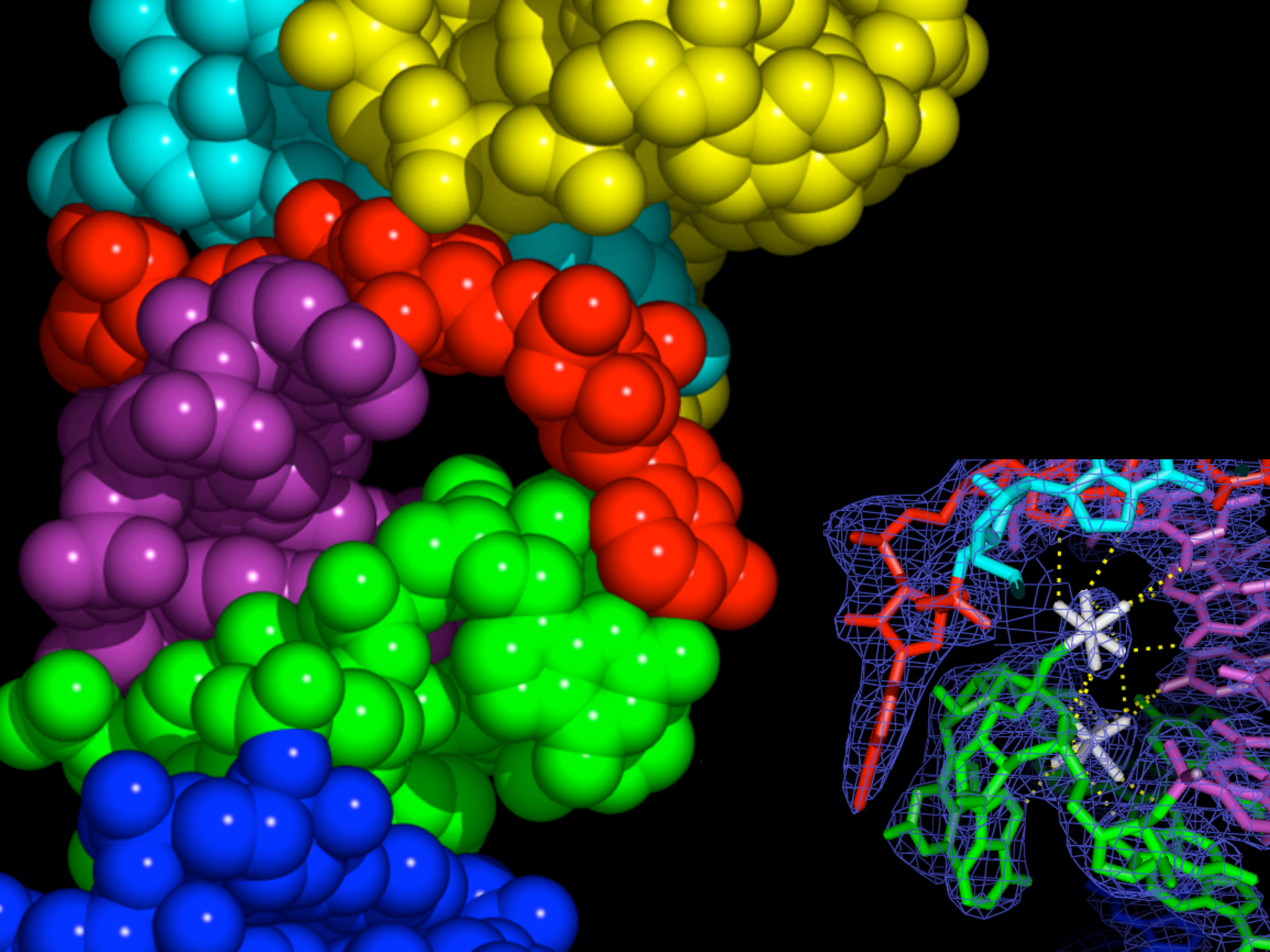
U9C changes a wobble into a Watson-Crick CG pair: pobably inconsequential

G35U (if real) may change the interior where Mg binds (see figure on next page), with consequences for drug design

(A23 deletion in one of 26 2019-nCoV isolates is probably an error.)


G35U