

Electronic Supplementary Material

A DNA Aptamer Based Method for Detection of SARS-CoV-2 Nucleocapsid Protein

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CLUSTAL 2.1 multiple sequence alignment

Sars-N	MSDNGPQSNQRSPRITFGGPTSTDNNQNNGRNGARPQKRRPQGLPNNTASWFTALTQH
Sars2-N	MSDNGPQ-NQRNAPRITFGGPDSTGSNNGERSGARSKQRRPQGLPNNTASWFTALTQH ***** ***, *****:***., *** * , ***, *****
Sars-N	GKEELRFPRGQQGVPIINTSGPDDQIGYYRRATRRVRGGDGKMKELSPRWFYLYLGTGPEA
Sars2-N	GKEDLKFPKRQGVPIINTNSSPDDQIGYYRRATRRIRGGDGKMKDLSPRWFYLYLGTGPEA ***;*:*****:*****:*****;*****:*****:*****
Sars-N	SLPYGANKEIVVVATEGALNTPKDHHGTRNPNNNAATVLQLPQGTTLPKGFYAEGRGG
Sars2-N	GLPYGANKDGIIWVATEGALNTPKDHHGTRNPANNAAVLQLPQGTTLPKGFYAEGRGG .*****:***:*****:***** **** *****:*****
Sars-N	SQASSRSSRSRGNSRNSTPGSSRGNSPARMASGGETALALLLDRLNQLESKVSGKGQ
Sars2-N	SQASSRSSRSRNNSRNSTPGSSRGTSARMAGNGDAALALLLDRLNQLESKMSGKGQ *****:..*****:*****.*****..***:*****:*****:*****
Sars-N	QQQQQTVTKSAEASKKPRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDLIRQGTDYK
Sars2-N	QQQQQTVTKSAEASKKPRQKRTATKAYNVTQAFGRRGPEQTQGNFGDQELIRQGTDYK *****:*****:*****:*****:*****:*****:*****:*****:*****
Sars-N	HWPQIAQFAPSASAFFGMSRIGMEVTPSGTWTLYHGAIKLDDKDPQFKDNVILLNKHIDA
Sars2-N	HWPQIAQFAPSASAFFGMSRIGMEVTPSGTWTYTGAIKLDDKDPNFKDQVILLNKHIDA *****:*****:*****:*****:*****:*****:*****:*****:*****
Sars-N	YKTFPPTEPKDKKKKTDEAQPLPQRQQKQPTVTLPAADMDDFSRQLQNSMSGASADST
Sars2-N	YKTFPPTEPKDKKKKADETQALPQRQQKQPTVTLPAADLDDFSKQLQQSMS--SADST *****:***:*.*****:*****:*****:*****:*****:*****
Sars-N	QA
Sars2-N	QA **

Fig. S1: The amino acid sequence alignment of N proteins of SARS-CoV and SARS-CoV-2. The GeneBank accession numbers for N protein of SARS-CoV and SARS-CoV-2 are NP_828858.1 and YP_009724397.2, respectively. The alignment was performed by ClustalW software at <https://www.genome.jp/tools-bin/clustalw>.

Table S1. Sequences of DNA aptamers used in this study.

Aptamers	Sequences (5'-3')
N Aptamer 1 (88 nt)	bio-GCAATGGTACGGTACTTCCGGATGCGGAAACTGGCTATTGGT GAGGCTGGGCGGTCGTGCAGCAAAAGTGCACGCTACTTGCTAA
N Aptamer 2 (78 nt)	bio-GCAATGGTACGGTACTTCCGGATGCGGAAACTGGCTATTGGT GAGGCTGGGCGGTCGTGCAGCAAAAGTGCACGCT
N Aptamer 3 (57 nt)	bio-GCAATGGTACGGTACTTCCGGATGCGGAAACTGGCTATTGGT GAGGCTGGGCGGT
Aptamer n.c. (33 nt)	bio- GCAATGGTACGGTACTTCCGGATGCGGAAACTG