

Supplementary Table 1. Similarity of GT103 epitope sequence in complement factor H to viral protein sequences

Description	Max Score	Total Score	Query Coverage	E value	Percent Identity	Accession Length	Accession Number
TPA: single-stranded-DNA-specific exonuclease RecJ [Caudoviricetes sp.]	26.1	26.1	87%	137	100	550	DAR72922.1
TPA: single-stranded-DNA-specific exonuclease RecJ [Caudoviricetes sp.]	26.1	26.1	87%	137	100	550	DAU83478.1
hypothetical protein [Vibrio phage vB_VaS_L1]	26.1	26.1	87%	141	100	151	UYE90950.1
tailfiber like protein [uncultured Mediterranean phage uvMED]	25.7	45	87%	194	100	3378	BAR35338.1
TPA: portal protein [Caudoviricetes sp.]	25.7	25.7	87%	195	100	488	DAE94357.1
TPA: hypothetical protein [Herelleviridae sp.]	25.7	25.7	87%	197	100	244	DAM34908.1
truncated glycoprotein G [Human metapneumovirus]	25.7	25.7	100%	199	87.5	181	AQW35136.1
truncated glycoprotein G [Human metapneumovirus]	25.7	25.7	100%	199	87.5	181	AQW35125.1
TPA: hypothetical protein [Caudoviricetes sp.]	24.4	24.4	100%	556	80	873	DAN04143.1
TPA: portal protein [Caudoviricetes sp.]	24.4	24.4	100%	558	80	501	DAT09665.1
envelope glycoprotein [Human immunodeficiency virus 1]	24	24	100%	790	75	784	ADF84092.1
Tail Collar Domain [Bacteriophage sp.]	24	24	100%	792	87.5	525	UWI25721.1
TPA: hypothetical protein [Caudoviricetes sp.]	24	24	100%	795	87.5	393	DAH31300.1
glycoprotein [Human metapneumovirus]	24	24	100%	801	87.5	233	WAB07545.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	801	87.5	228	AHV79585.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	801	87.5	228	AHV79531.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	801	87.5	228	AHV79907.1

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attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	220	AHV79610.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	802	87.5	219	QDJ04475.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79736.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	802	87.5	217	BAV89105.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79862.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	802	87.5	217	QDQ17751.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	802	87.5	217	QDQ17753.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79504.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79468.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79673.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79700.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79880.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79477.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79522.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79979.1
attachment glycoprotein G [Human metapneumovirus]	24	24	100%	802	87.5	217	AHV79682.1

Description	Max Score	Total Score	Query Coverage	E value	Percent Identity	Accession Length	Accession Number
attachment glycoprotein [Human metapneumovirus]	24	24	100%	803	87.5	207	QOJ53020.1
G protein [Human metapneumovirus]	24	24	100%	803	87.5	200	UZH75054.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	803	87.5	196	QBH22185.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	195	QOJ53021.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	194	QOJ53033.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	194	QOJ53030.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	193	QOJ53028.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	193	QBH22163.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	193	QOJ53034.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	193	QOJ53024.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	192	QOJ53023.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	192	QBH22169.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	192	QBH22189.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	192	QBH22198.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	191	QDQ17749.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	190	QQO58271.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	190	QOJ52975.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	190	QOJ52974.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	188	QOJ53027.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	804	87.5	187	QOJ53025.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	805	87.5	183	QOJ53022.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	805	87.5	182	QOJ52979.1
truncated glycoprotein G [Human metapneumovirus]	24	24	100%	805	87.5	181	AQW35090.1
attachment protein [Human metapneumovirus]	24	24	100%	805	87.5	181	WBQ86670.1
truncated glycoprotein G [Human metapneumovirus]	24	24	100%	805	87.5	181	AQW35089.1

Description	Max Score	Total Score	Query Coverage	E value	Percent Identity	Accession Length	Accession Number
truncated glycoprotein G [Human metapneumovirus]	24	24	100%	805	87.5	181	AQW35096.1
attachment protein [Human metapneumovirus]	24	24	100%	805	87.5	181	QLL99762.1
attachment protein [Human metapneumovirus]	24	24	100%	805	87.5	181	WBQ86428.1
truncated glycoprotein G [Human metapneumovirus]	24	24	100%	805	87.5	181	AQW35120.1
type II integral membrane glycoprotein [Human metapneumovirus]	24	24	100%	805	87.5	180	AGL42251.1
type II integral membrane glycoprotein [Human metapneumovirus]	24	24	100%	805	87.5	180	AGL42249.1
type II integral membrane glycoprotein [Human metapneumovirus]	24	24	100%	805	87.5	180	AGL42252.1
type II integral membrane glycoprotein [Human metapneumovirus]	24	24	100%	805	87.5	180	AGL42257.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	805	87.5	178	QOJ53032.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	805	87.5	177	QOJ53026.1
glycoprotein G [Human metapneumovirus]	24	24	100%	805	87.5	177	UFI08032.1
glycoprotein G [Human metapneumovirus]	24	24	100%	805	87.5	177	UFI08045.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	806	87.5	175	QOJ53029.1
glycoprotein G protein [Human metapneumovirus]	24	24	100%	806	87.5	168	AGO64581.1
glycoprotein G [Human metapneumovirus]	24	24	100%	807	87.5	166	UFI08064.1
glycoprotein G [Human metapneumovirus]	24	24	100%	807	87.5	166	UFI08037.1
glycoprotein G [Human metapneumovirus]	24	24	100%	807	87.5	166	UFI08053.1
glycoprotein G [Human metapneumovirus]	24	24	100%	807	87.5	166	UFI08035.1
glycoprotein G [Human metapneumovirus]	24	24	100%	807	87.5	166	UFI08058.1
glycoprotein G [Human metapneumovirus]	24	24	100%	807	87.5	166	UFI08050.1
glycoprotein G [Human metapneumovirus]	24	24	100%	807	87.5	166	UFI08049.1
glycoprotein G [Human metapneumovirus]	24	24	100%	807	87.5	166	UFI08055.1

Description	Max Score	Total Score	Query Coverage	E value	Percent Identity	Accession Length	Accession Number
glycoprotein G [Human metapneumovirus]	24	24	100%	807	87.5	166	UFI08056.1
glycoprotein G [Human metapneumovirus]	24	24	100%	807	87.5	166	UFI08052.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	808	87.5	159	QOJ52978.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	808	87.5	159	QOJ53035.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	808	87.5	155	AEX20357.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	808	87.5	155	AEX20361.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	808	87.5	155	AEX20354.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	808	87.5	155	AEX20358.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	808	87.5	155	AEX20360.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	808	87.5	155	AEX20359.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	808	87.5	155	AEX20356.1
attachment glycoprotein [Human metapneumovirus]	24	24	100%	811	87.5	138	QOJ53031.1
envelope glycoprotein [Human immunodeficiency virus 1]	23.5	23.5	87%	1122	85.71	858	ABD34929.1
envelope glycoprotein [Human immunodeficiency virus]	23.5	23.5	87%	1122	85.71	855	QGI16690.1
TPA: tail spike [Caudoviricetes sp.]	23.5	23.5	87%	1123	85.71	734	DAI82863.1
TPA: putative Fe-S oxidoreductase [Caudoviricetes sp.]	23.5	23.5	87%	1124	85.71	656	DAW28679.1
TPA: single-stranded-DNA-specific exonuclease RecJ [Caudoviricetes sp.]	23.5	23.5	87%	1125	85.71	550	DAN68301.1
envelope glycoprotein [Human immunodeficiency virus 1]	23.5	23.5	100%	1126	87.5	521	ATU76965.1
envelope glycoprotein [Human immunodeficiency virus 1]	23.5	23.5	100%	1126	87.5	521	ATU76953.1
envelope glycoprotein [Human immunodeficiency virus 1]	23.5	23.5	100%	1126	87.5	520	ATU76971.1

A BLASTp search was run using the query sequence PIDNGDIT to search the National Center for Biotechnology Information non-redundant protein sequence database, specifying taxonomy ID: 10239 (all viruses).

Bacteriophage Protein Alignments to PIDNGDIT Epitope

>MAG TPA: single-stranded-DNA-specific exonuclease RecJ [Caudoviricetes sp.]

Sequence ID: DAR72922.1 Length: 550

Range 1: 430 to 436

Score:26.1 bits(54), Expect:137,

Identities:7/7(100%), Positives:7/7(100%), Gaps:0/7(0%)

Query 1 PIDNGDI 7

PIDNGDI

Sbjct 430 PIDNGDI 436

>MAG TPA: portal protein [Caudoviricetes sp.]

Sequence ID: DAE94357.1 Length: 488

Range 1: 162 to 168

Score:25.7 bits(53), Expect:195,

Identities:7/7(100%), Positives:7/7(100%), Gaps:0/7(0%)

Query 2 IDNGDIT 8

IDNGDIT

Sbjct 162 IDNGDIT 168

>MAG TPA: tail spike [Caudoviricetes sp.]

Sequence ID: DAI82863.1 Length: 734

Range 1: 502 to 508

Score:23.5 bits(48), Expect:1123,

Identities:6/7(86%), Positives:7/7(100%), Gaps:0/7(0%)

Query 1 PIDNGDI 7

P+DNGDI

Sbjct 502 PVDNGDI 508

>MAG TPA: putative Fe-S oxidoreductase [Caudoviricetes sp.]

Sequence ID: DAW28679.1 Length: 656

Range 1: 257 to 263

Score:23.5 bits(48), Expect:1124,

Identities:6/7(86%), Positives:7/7(100%), Gaps:0/7(0%)

Query 1 PIDNGDI 7

P+DNGDI

Sbjct 257 PVDNGDI 263

>MAG TPA: hypothetical protein [Caudoviricetes sp.]

Sequence ID: DAN04143.1 Length: 873

Range 1: 91 to 100

Score:24.4 bits(50), Expect:556,

Identities:8/10(80%), Positives:8/10(80%), Gaps:2/10(20%)

Query 1 PI--DNGDIT 8

PI DNGDIT

Sbjct 91 PIYDDNGDIT 100

>MAG TPA: portal protein [Caudoviricetes sp.]

Sequence ID: DAT09665.1 Length: 501

Range 1: 151 to 160

Score:24.4 bits(50), Expect:558,

Identities:8/10(80%), Positives:8/10(80%), Gaps:2/10(20%)

Query 1 PI--DNGDIT 8

PI DNGDIT

Sbjct 151 PISWDNGDIT 160

>MAG TPA: hypothetical protein [Herelleviridae sp.]

Sequence ID: DAM34908.1 Length: 244

Range 1: 45 to 51

Score:25.7 bits(53), Expect:197,

Identities:7/7(100%), Positives:7/7(100%), Gaps:0/7(0%)

Query 2 IDNGDIT 8

IDNGDIT

Sbjct 45 IDNGDIT 51

>hypothetical protein [Vibrio phage vB_VaS_L1]

Sequence ID: UYE90950.1 Length: 151

Range 1: 24 to 30

Score:26.1 bits(54), Expect:141,

Identities:7/7(100%), Positives:7/7(100%), Gaps:0/7(0%)

Query 1 PIDNGDI 7

PIDNGDI

Sbjct 24 PIDNGDI 30

>tailfiber like protein [uncultured Mediterranean phage uvMED]

Sequence ID: BAR35338.1 Length: 3378

Range 1: 633 to 639

Score:25.7 bits(53), Expect:194,

Identities:7/7(100%), Positives:7/7(100%), Gaps:0/7(0%)

Query 2 IDNGDIT 8

IDNGDIT

Sbjct 633 IDNGDIT 639

Eukaryotic Virus Protein Alignments to PIDNGDIT Epitope

>truncated glycoprotein G, partial [Human metapneumovirus]

Sequence ID: AQW35136.1 Length: 181

>attachment protein, partial [Human metapneumovirus]

Sequence ID: QLL99667.1 Length: 181

Range 1: 45 to 52

Score:25.7 bits(53), Expect:199,

Identities:7/8(88%), Positives:7/8(87%), Gaps:0/8(0%)

Query 1 PIDNGDIT 8

PIDN DIT

Sbjct 45 PIDNSDIT 52

>glycoprotein [Human metapneumovirus]

Sequence ID: WAB07860.1 Length: 233

Range 1: 86 to 93

Score:24.0 bits(49), Expect:801,

Identities:7/8(88%), Positives:7/8(87%), Gaps:0/8(0%)

Query 1 PIDNGDIT 8

PIDN DIT

Sbjct 86 PIDNPDIT 93

>envelope glycoprotein, partial [Human immunodeficiency virus 1]

Sequence ID: ADF84092.1 Length: 784

Range 1: 187 to 194

Score:24.0 bits(49), Expect:790,

Identities:6/8(75%), Positives:8/8(100%), Gaps:0/8(0%)

Query 1 PIDNGDIT 8

PIDNG++T

Sbjct 187 PIDNGNVT 194

>envelope glycoprotein [Human immunodeficiency virus 1]

Sequence ID: ABD34929.1 Length: 858

Range 1: 189 to 195

Score:23.5 bits(48), Expect:1122,

Identities:6/7(86%), Positives:7/7(100%), Gaps:0/7(0%)

Query 1 PIDNGDI 7

PIDNG+I

Sbjct 189 PIDNGNI 195

>envelope glycoprotein, partial [Human immunodeficiency virus 1]

Sequence ID: ATU76965.1 Length: 521

Range 1: 184 to 191

Score:23.5 bits(48), Expect:1126,

Identities:7/8(88%), Positives:7/8(87%), Gaps:0/8(0%)

Query 1 PIDNGDIT 8

PIDNGD T

Sbjct 184 PIDNGDNT 191

Supplementary Fig. 1 BLAST alignment of the GT103 epitope in complement factor H, PIDNGDIT, to viral sequences in the National Center for Biotechnology Information database. The figure has been edited to remove duplicate findings. The majority of the numerous human metapneumovirus glycoprotein hits listed in **Supplementary Table 1** contains the sequence PIDNPDIT; only one entry contained the similar sequence PIDNSDIT.