**Suppl File S3 - Multiple sequence alignment of enterovirus 2A proteases that have a Cterminal DDx3EQ motif**

>EnterovirusD\_Proteinase|NP\_740416.1/1-143 proteinase 2A [Enterovirus D] | Length: 143 | #Patterns: 1

GGAFVGSYKIINYHLATDEEKERSVYVDWQSDVLVTTVAAHGKHQIARCRCNTGVYY-CKHKNRSYPVCFEG

PGIQWINESDYYPARYQTNTLLAMGPCQPGDCGGLLVCSHGVIGLVTAG-GEGIVAFTDIRNLLWLEDDAME

Q

>AXP08076.2/126-268 polyprotein, partial [Enterovirus D]

GGAFVGSYKIINYHLATDQEKQDAVYVDWQSDILVTTIAAHGKHQIARCKCNTGVYY-CRHKDRSYPVYFEG

PGIQWIEENEYYPARYQTNTLLASGPVEAGDCGGLLVCPHGVIGLVTAG-GNGVVAFTDIRNLLWLEDEAME

Q

>QBA83439.1/867-1009 polyprotein [enterovirus D68]QBA83463.1 polyprotein [enterovirus D68]QBA83469.1 polyprotein [enterovirus D68]

GGAFVGSFKIINYHLATTEERQSAIYVDWQSDVLVTPIAAHGRHQIARCKCNTGVYY-CRHRDKSYPVCFEG

PGIQWIEQNEYYPARYQTNVLLAAGPAEAGDCGGLLVCPHGVIGLLTAG-GGGIVAFTDIRNLLWLDTDAME

Q

>QTZ20033.1/878-1020 polyprotein, partial [Raccoon dog enterovirus]

GGAHVGPYKIINYHLATDEEKRDACWVDWSRDLLVCLTKSHGTQQIARCSCRCGVYF-CNSANKSYPVCFEG

PGIQYFEKNDYYPERYQSHVLLACGVAEPGDCGGVLACPHGVIGLVTGG-APGVVAFADVRDLLWVEDDAME

Q

>NP\_653149.1/876-1018 genome polyprotein [Enterovirus H]AAF85765.1 A2 polyprotein [A-2 plaque virus]

GGVVVGQYKIINYHLATTEDREKEIWSDPRRDLLVCASSVHGNNWIARCACRTGVYW-SRTYGKCFPVCFQG

PGIEKFQASEYYPERYQTHVLLAMGPAQPGDCGGLLCCPHGVIGLLTGG-DEGRVAFADIRDLLWVEDDVME

Q

>YP\_009246449.1/870-1011 polyprotein [Enterovirus SEV-gx]AMW87255.1 polyprotein [Enterovirus SEV-gx]

GGAHIGQYKVVNHHLLDPED--DPIWDSPQRDLAVILAPSHGKDVVARCKCRCGIYW-CRSKRKYYPVCFDE

PSFRYFDDNEYYPARFQSHVLLASGFAEPGDCGGILQCPHGVIGLVTGGDGQGTVAFADIRDLLWLEDDAME

Q

>AAS88605.2/126-268 polyprotein, partial [Echovirus E13]

GAVYVGNYRVVNRHLATHNDWQNCVWEDYNRDLLVSTTTAHGCDTIARCLCTAGVYY-CASRNKHYPVTFEG

PGLVEVQESEYYPKRYQSHVLLAAGFSEPGDCGGILRCEHGVIGIVTMG-GEGVVGFADVRDLLWLEDDAME

Q

>AAA42933.1/859-1002 polyprotein, partial [Coxsackievirus B3]

RGSVCGDYRLVNRHSATSADWQNCVWESYNRDLLVSTTTTHGCDIIARCQCTTGVYFLCVQKSKHIPISFEG

PGLVEVQDSEYYPRRYQSHVLLAAGFSEPGDCGGILRCEHGVIGIVTMG-GEGVVGFADIRDLLWLEDDAME

Q

>WBR19480.1/268-410 polyprotein, partial [Coxsackievirus A4]WBR19482.1 polyprotein, partial [Coxsackievirus A4]

GAVYVGNYRVVNRHLATHNDWANLVWEDSSRDLLVSSTTAQGCDTIARCNCQTGVYY-CNSRRKHYPVSFSK

PSLIFVEASEYYPARYQSHLMLAAGYSEPGDCGGILRCQHGVVGIVSTG-GNGLVGFADVRDLLWLDEEAME

Q

>ALU66466.1/872-1014 polyprotein [Enterovirus A89]

GAVYVGNYRIVNRHLAIPQDWTNLVWEDVNRDLLISSTTAHGCDTIARCQCTTGVYF-CKSRSKHYPVSFSK

PGLVFVNESMYYPARYQSHVLLAPGHAEPGDCGGILRCQHGVVGIVSTG-GDGLVGFADLRDILWLDDEVME

Q

>ABV25903.1/865-1007 polyprotein [enterovirus A124]

GAIYVGNYRVVNRHLATQQDWDNLVWEDYNRDLLVSQTTAHGCDTIARCDCTTGVYF-CKSMMKHYPVSFQG

PGLVHVKKNEYYPERYQSHVLLATGHSEPGDCGGILRCQHGVIGIVTMG-GDNLVGFADIRDLFWLDDEVME

Q

>QWT72253.1/862-1004 polyprotein [enterovirus A122]

GAVYVCNYRVINRHLATEEDWKNLVWEDYQRDLLVSNTKAHGCDTIARCKCQTGVYF-CKSQNKHYPISFQG

PGLVHVQANEYYPERYQSHVLLANGISKAGDCGGILRCQHGVIGLVTMG-GDGLVGFADIRDLLWLEDDVME

Q

>QOI17237.1/862-1004 polyprotein [enterovirus A122]

GAVYVCNYRIVNRHLATQSDWDNLEWEDYQRDILVSRTTAHGCDKIARCNCTTGVYF-CRSTSKHYPVSFQG

PGLVHVQANEYYPERYQSHVLLANGIAVPGDCGGILRCPHGVIGLVTMG-GDGLVGFADVRDLLWLEDEVME

Q

>AFR77805.1/870-1012 polyprotein [Enterovirus A90]

GAVYVGNYKIVNRHLATKEDWSNLVWEDYNRDLLVTSVCAQGCDIIARCSCKAGVYF-CKSMNKHYPISFQG

PGIVEVQANEFYPHRYQTHVLLGHGTSIPGDCGGILRCQHGVIGLVTMG-GDGLVGFADLRDLFWLDDEAME

Q

>ANN47502.1/871-1013 polyprotein [Enterovirus A121]

GAVYVGNYRIVNRHLATQKDWDNLVWESYERDLLVSTTTAQGCDTIARCKCRHGVYY-CNSMRKHYPVSFGE

PAFIYVDENEFYPARYQSHVISSAGIAVPGDCGGILRCEHGVIGLVTMG-GPNIVGFADIRDLLWLDDEVME

Q

>WBR19531.1/260-402 polyprotein, partial [Enterovirus A]

GAIYVGNYRIVNRHLATKKDWENLVWESYERDLLVSTITAHGCDKIARCKCRAGVYF-CKSMNRHYPVTFGE

PAFFHVDANEYYPERYQSHVISSAGIALPGDCGGILRCEHGVIGIVSIG-GPNLVGFADIRDLLWLDDEVME

Q

>APC23144.1/91-233 polyprotein, partial [enterovirus J103]

GAVYVGNYRIVNRHLANEFDAQSTVWDSYERDLLVSTTTAHGCDTIARCRCNTGVYF-CRSKGKHYPVCFQG

PGLTWIEANEYYPARYQSHVLLASGPAEPGDCGGILRCQHGVIGMVTAG-GNGLVAFADLRDLLWLEDDAME

Q

>AHY21610.1/863-1005 polyprotein [Enterovirus sp.]

GAVYVGNYRIVNRHLANEFDAANTVWESYERDLLVSTTTAHGCDTIARCSCTTGVYF-CRSKGKHYPVSFQG

PGLVEVQANEYYPHRYQSHVLLAHGFSEPGDCGGILRCQHGVIGLVTMG-GDGLVGFADLRDLLWLEDDAME

Q

>YP\_003359170.1/8-150 2A [Enterovirus J]

GAVFVGNYKITNLHLASTFDRESEVWSSYERDLIVSSTTAHGCDKLARCTCNTGVYF-CKSANKHFPVCFQG

PGLTFIEANEYYPARYQSHVLLAVGHAQPGDCGGILRCEHGVVGILTAG-GNGLVAFADLRDLLWIEDDAME

Q

>AAL69622.2/853-995 polyprotein [enterovirus A125]

GSVYVGSYKITNLHLATEFDLGSEIWRSYERDLIVSTTTASGCDNIARCNCNSGVYF-CKSKSKHYPVVFQG

PGLVQVGANDYYPDRYQSHVLLGVGPAEAGDCGGILRCQHGVIGILTAG-GDGLVAFADIRDLLWIEDDAME

Q

>QKE11198.1/843-985 polyprotein [Enterovirus J]

GAAYVAGYKVMNRHLATPEDWNNLVWDDYNRDLLVCTSGAQGADYIARCKCNTGVYY-CKSKGKHYPVSFQG

PGLAWIEANEYYPARYQSHVLLANGHAEPGDCGGIIRCIHGVIGLVTAG-GDGVVAFADIRDLLWIEDDCME

Q

>WPN04299.1/8-150 polyprotein, partial [Goat enterovirus]

GAVYVGNYKIMNRHLATQAEWDNLEWEDYNRDLIVSRVNAHGADKLARCNCSAGIYY-CKSRGKHYPVTFEG

PGIQWVDANNYYPGRYQSHMLLGIGFCEPGDCGGILRCQHGVIGIITAG-GPSLVAFADLRDLFWVEHEAME

Q

>ULF99594.1/847-989 MAG: polyprotein [Enterovirus sp.]

GAVYVGNYKIVNRHLATQKDWENLEWEEYNRDVLVSRVNAHGADKLARCRCNAGVYY-CKSRNKYYPVTFEG

PGIQLIDANQYYPEHYRTHVLLGIGPCKPGDCGGILRCQHGVIGFITAG-GPNLVAFADLRDLFWVEHEAME

Q

>WEM32007.1/847-989 polyprotein [Enterovirus F]

GAVYVGNYKIMNRHLAERSDWDNLVWESYERDLLVARVDAHGCDLIARCQCTAGVYY-CKSRMKHYPVIVTP

PSLVQIGASDYYPERYQSHVDLGIGFAEPGDCGGILRCQHGVIGILTAG-GNNMVAFADIRDLLWIEDDVME

Q

>WEM32010.1/840-982 polyprotein [Bovine enterovirus type 2]

GAVCVGSYRILNRHLATQADWENVVWESYERDLLVMRHDAAGSDVIARCNCTTGVYY-CKSRNKHYPVVVTP

PSLVHVDANDYYPERYQSHVLLGIGFAEPGDCGGILRCQHGCMGILTAG-GNNLVAFADLRDLLWIEDDAME

Q

>AKA64452.1/842-984 polyprotein [Dromedary camel enterovirus 19CC]

GAAYVGSYKIMNRHLASHDDWHRLVWESYGRDLLVSRVDAQGCDVIARCDCTTGVYY-CKSRNKHYPVVVTP

PSLAFIDESEYYPARYQSHVTLGVGFAEPGDCGGLLRCQHGVMGILTAG-GESLVAFADIRDLLWIEDDAME

Q

>QSX72499.1/855-997 polyprotein [Bovine enterovirus GX20-1]

GAIYVGNYKIVNRHLATYADWENEVWQSYHRDLLVTRVDAHGCDTIARCSCRTGIYY-CKSRDKHYPIVVTP

PSIFKIEANEYYPERMQTHILLGIGPGEPGDCGGILRCEHGVMGILTVG-GGDLVGFADIRDLLWIEDDAME

Q

>UUB82806.1/840-982 polyprotein [Enterovirus F]

GAIYVGNYKIVNRHLAHEVDWQKHVWDSYNRDLLVTRVDAHGCDKIARCNCRAGVYY-CRSSDKHFPVVVSE

PAVYLVEANEYYPEHYQTHVLLGIGIARPGDCGGILRCQHGVMGILTVG-GNNLVAFADVRDLLWVEDDVME

Q

>APC23145.1/16-158 polyprotein, partial [enterovirus A122]

GAVYVCNYKIVNRHLATREDRENLVWEDHRRDLLVSSTKAHGCDVIARCKCQSGVYF-CRSENKYYPVSFQN

PGLVHVRANKCHPERYQSHVLVANGISKASDCGGVLRCQHGVIGIVATS-SDNSVGFADLRDLLWLEDDVVE

Q

>AAL69623.2/857-999 polyprotein [Simian agent 5]

GAVYTCSYKILNRHLASPDDWKNVVWEDWNRDLLVTTVQAHGCHQVARCSCTTGVYY-SKYYNRFYPVSFQG

PGIVQMAANEYYPERAQTHVLLANGPAQPGDCGGLLCCTHGVVGILTAG-GDGLVAFADIRDLLWLDDEPME

Q

>WBR19554.1/270-412 polyprotein, partial [Coxsackievirus A11]

KAVYVAGYKICNYHLATPEDLQNAVSVMWDRDLLVTESRAQGVDTIARCACRTGIYY-CESRRKYYPVSFVG

PTFQYMEANDYYPARYQSHMLIGHGFASPGDCGGILRCQHGVIGIITAG-GEGIVAFSDIRDLHAYEEEAME

Q

>UEU84371.1/893-1035 polyprotein, partial [Coxsackievirus A24]

KAVYVAGYKICNYHLATPEDHDNAVSVLWNRDLLVVESRAQGTDTIARCNCKAGVYY-CESKRKYYPVTITE

PTFQYMEANDYYPARYQTHMLLGHGFAEPGDCGGILRCNHGVIGIITAG-GNGIVAFADIRDLWVYEEEAME

Q

>WPN77717.1/886-1028 polyprotein [Coxsackievirus A21]

KAVYVAGYKICNYHLATPSDHLNAISVLWDRDLMVVESRAQGTDTIARCSCRCGVYY-CESRRKYYPVTFTG

PTFRFMEANDYYPARYQSHMLIGCGFAEPGDCGGILRCTHGVIGIITAG-GEGVVAFADIRDLWVYEEEAME

Q

>AWU65871.1/896-1038 MAG: polyprotein, partial [Enterovirus C96]

KAVYVAGYKICNYHLATQEDMNNAVNIMWNRDLLVTQSRAQGTDTIARCHCKCGVYY-CESQRKYYPITVTG

PTFQFMEANEYFPARYQTHMLLGHGFANPGDCGGILRCNHGVMGIITAG-GNGIVAFADIRDLYMYEEEAME

Q

>AIX97183.1/883-1025 polyprotein [Enterovirus C105]

KAIYVAGYKICNYHLATQEDMEHAVAVMWDRDLMVVESRAQGIDTIARCSCKCGVYY-CESMRKYYPVTVEG

PTFRYMDANEYYPARYQSHMLIGAGFAMPGDCGGILRCTHGVMGLITAG-GEGVVAFADVRDLFAYEEEAME

Q

>QER78690.1/897-1038 polyprotein, partial [Enterovirus C96]

QAVYVAGYKIINYHLATSEDYRRCVRSMWERDLMVVESRAQGTDQIARCTCTTGVYY-CSSRNKHYPITITR

PTFQWMEANDYYPARYQSHMTMGHGFAEPGDCGGILRCQHGVMGLITAG-GNGIVAFADIRDLYV-EEEAME

Q

>ABM54518.1/890-1031 polyprotein [Enterovirus C99]

KGIFVAGYKIINYHLATAEDFRNCVRSMWERDLMVVESKAQGVDQIARCSCKTGVYY-CASRQKYYPITVTN

PTFQWMEKNEYYPGRYQSHMILGHGFAEPGDCGGILRCQHGVMGLITAG-GNGIVAFADVRDLYA-EDEAME

Q

>UBM82730.1/271-412 polyprotein, partial [Coxsackievirus A13]

KAVYVAGYKIVNYHLASPEDYRNCVRSTWERDLMVVESKAQGTDLIARCSCKTGVYY-CESRNKFYPITITP

PTFQWMEKNDFYPARYQSHMTIGSGFAAPGDCGGILRCQHGVIGLITAG-GNGLVAFADIRDLYV-EEEAME

Q

>ABM21509.1/893-1034 polyprotein [Coxsackievirus A13]

KGVYVAGYKIINYHLATPEDYRHCVKSMWERDLMVVESRAQGIDTIARCCCKTGVYY-CESRNKHYPITITS

PTFQWMERNDFYPARYQTHLTIGSGFAAPGDCGGIIRCQHGVMGLVTAG-GEGVVAFADIRDLYL-EDEAME

Q

>BAE20393.1/894-1035 polyprotein [Coxsackievirus A18]

KAVYVAGYKIVNYHLATASDFRNCVRSLWQRDLMVVESKAQGIDQIARCSCRCGVYY-CESRNKHYPITISS

PTFQWMEKNDYYPARYQTHITIGSGFAAPGDCGGVLRCQHGVMGLITAG-GEGVVAFADIRDLYV-EDEAME

Q

>WAB71077.1/223-364 polyprotein, partial [Coxsackievirus A13]

KAVYVAGYKIINYHLATAIDYQQCVRSMWERDIMIVESRAQGKDRIARCECRSGVYY-CESRGRHYPIIITR

PTFQWMEKNDFYPARYQSHMTIGHGFAAPGDCGGILRCQHGVMGLITAG-GNGLVAFADIRDLYV-EDEAME

Q