Reference sequence (1): PuDHAD
Identities normalised by aligned length.
Colored by: identity

```
                    cov     pid   1 [        .         .         .         .         :         .         .         .  80
 1 PuDHAD         100.0% 100.0%   ------------------------------------------------------MS--DKEKPVRRSQAWFGRLDR---DGFIYRSWMKN
 2 FtDHAD          95.0%  33.6%   ------------------------------------------------------MSEPLNRRSRLITQGIERSP-----NRAMLRA
 3 SsDHAD          95.0%  33.5%   --------------------------------------------------MPAKLNSPSRYHGIYNAP-----HRAFLRS
 4 SaDHAD          95.5%  33.5%   --------------------------------------------------MPESKLNSPLRYHGIYNAP-----HRAFLRS
 5 CnN1DHAD        94.6%  34.1%   ---------------------------------------------------MAFNKRSQNITQGVARSP-----NRSMYYA
 6 TvDHAD          95.1%  32.5%   ---------------------------------------------------MAENWRSRIITEGVQRTP-----NRAMLRA
 7 5j84-RlArDHT   100.0%  63.6%   ----------------------------------------------MKKKAEWPRKLRSQENYGGTSR--DVIYHRGWLKN
 8 6ovt-MtDHAD     95.1%  34.4%   ------------------------------------------MPQTTDEAASVSTVADIKPRSRDVTDGLEKAA----ARGMLRA
 9 5ze4-AtDHAD     95.7%  30.2%   MQATIFSPRATLFPCKPLLPSHNVNSRRPSIISCSAQSVTADPSPPITDTNKLNKYSSRITEPKSQGG-----SQAILHG
10 5oyn-CcXyDHT    99.7%  37.9%   -------------------------------------------MRSALSNRTPRRFRSRDWFDNPDHIDMTALYLERFMNY
   consensus/100%                 ...............................................S..hht...p.......pthh..
   consensus/90%                  ...............................................phpS..hhtsh.p.......cuhhps
   consensus/80%                  ...............................................phpSp.hhpshtp.s.....tRuhh+s
   consensus/70%                  ...............................................shphRspthhpGlp+ss.....pRuhL+u
```

```
                    cov     pid  81        .         1         .         .         .         .         :         .  160
 1 PuDHAD         100.0% 100.0%   RGIPHDQFDGRPVIGICNTFSELTPCNSHFRTLAEQVKIGVWESGGFPLEFPVMSLGETMLRPTAML-----FRNLASMD
 2 FtDHAD          95.0%  33.6%   VGFTDAD-FDKPIVGVANGHSTMNPCNAGIQPLADRAVAALREAGAMPQTFGVPTVTDGISMGTEGMKYSLVSREVIADS
 3 SsDHAD          95.0%  33.5%   VGLTDEE-IGKPLVAIATAWSEAGPCNFHTLALARVAKEGTKEAGLSPLAFPTMVVNDNIGMGSEGMRYSLVSRDLIADM
 4 SaDHAD          95.5%  33.5%   VGLTDGE-INKPLVAVATAWSEAGPCNFHTLSLAHVAKEGAKEGGLTPLAFPTIVVNDNIGMGTEGMRYSLVSRDLIADM
 5 CnN1DHAD        94.6%  34.1%   LGYQKED-FDKPMVGIANGHSTITPCNAGLQRLADAAIDAIKASGANPQVFGTPTISDGMSMGTEGMKYSLISREVIADC
 6 TvDHAD          95.1%  32.5%   VGFGDED-FNKPIVGVASAHSTITPCNMGIAALASRAEAGIRAAGGMPQLFGTITVSDGISMGTEGMKYSLVSRDVIADS
 7 5j84-RlArDHT   100.0%  63.6%   QGYPHDLFDGRPVIGILNTWSDMTPCNGHLRELAEKVKAGVWEAGGFPLEVPVFSASENTFRPTAMM-----YRNLAALA
 8 6ovt-MtDHAD     95.1%  34.4%   VGMDDED-FAKPQIGVASSWNEITPCNLSLDRLANAVKEGVFSAGGYPLEFGTISVSDGISMGHEGMHFSLVSREVIADS
 9 5ze4-AtDHAD     95.7%  30.2%   VGLSDDD-LLKPQIGISSVWYEGNTCNMHLLKLSEAVKEGVENAGMVGFRFNTIGVSDAISMGTRGMCFSLQSRDLIADS
10 5oyn-CcXyDHT    99.7%  37.9%   GITPEELRSGKPIIGIAQTGSDISPCNRIHLDLVQRVRDGIRDAGGIPMEFPVHPIFENCRRPTAAL-----DRNLSYLG
   consensus/100%                 .hh.ct...+P.lul.psh.phssCN..h..Lsp.s..uh.tuGh.s..hss.sh.-sh.hspthh.......Rpl....
   consensus/90%                  hGhsct...s+P.lulsssasphsPCNhth.tLuphshtuhhtuGh.P..Fss.sls-sh.hsothh......Rplhu..
   consensus/80%                  hGhsc-p..sKPhlGlussaSphsPCNnth.tLAptsctGlhpuGhhP.tFsshshls-shthsTtuM.....sRplhA.s
   consensus/70%                  lGhs---.hsKPllGlAssaS-hsPCNhthhpLActs+tGlcpAGuhPhtFsshslsDshuMGTcGMpaSL.SR-lIADs
```

```
                    cov     pid 161        .         .         .         :         .         2         .         .  240
 1 PuDHAD         100.0% 100.0%   VEESIRGNPLDGVVLLMGCDKTTPSLMMGAASCDLPTIGVSGGPMLSGKFR-----GRELGSGTDVWKMSEEVRAGQMSQ
 2 FtDHAD          95.0%  33.6%   IETAVSSQCMDGVLAIGGCDKNMPGAMIAMLRMNVPAIFCYAGTIKPGCWK-----GQALTI-VSSFEAVGAFQAGKMSK
 3 SsDHAD          95.0%  33.5%   VEAQFNAHAFDGLVGIGGCDKTTPGILMAMARLNVPSIYIYGGSAEPGYFM-----GKRLTI-EDVHEAIGAYLAKRITE
 4 SaDHAD          95.5%  33.5%   VEAQFNAHAFDALIGIGGCDKTTPGILMAMARLNVPSIYIYGGSAEPGFYL-----GRRLTI-EDVHEAIGAFIAGKIDE
 5 CnN1DHAD        94.6%  34.1%   IETAAQGQWMDGVVVIGGCDKNMPGGMIALARTNVPGIYVYGGTIKPGNWK-----GKDLTI-VSSFEAVGEFTAGRMSQ
 6 TvDHAD          95.1%  32.5%   IETVCNAQSMDGVLAIGGCDKNMPGAMIAMARMNIPAIFVYGGTIKPGHWQ-----GQDLTV-VSAFEAVGQFSAGKMDE
 7 5j84-RlArDHT   100.0%  63.6%   VEEAIRGQPMDGCVLLVGCDKTTPSLLMGAASCDLPSIVVTGGPMLNGYFR-----GERVGSGTHLWKFSEMVKAGEMTQ
 8 6ovt-MtDHAD     95.1%  34.4%   VEVVMQAERLDGSVLLAGCDKSLPGMLMAAARLDLAAVFLYAGSILPGRAKLSDGSERDVTI-IDAFEAVGACSRGLMSR
 9 5ze4-AtDHAD     95.7%  30.2%   IETVMSAQWYDGNISIPGCDKNMPGTIMAMGRLNRPGIMVYGGTIKPGHFQ-----DKTYDI-VSAFQSYGEFVSGSISD
10 5oyn-CcXyDHT    99.7%  37.9%   LVETLHGYPIDAVVLTTGCDKTTPAGIMAATTVNIPAIVLSGGPMLDGWHN-----NELVGSGTVINRSRRKLAAGEITE
   consensus/100%                 l...hpu..hDu.l.h.GCDKshPuhhhuhhphshssl hh.uGsh.sG.h.......tp.hs.....ap..t.h.tt.hsp
   consensus/90%                  lEt.hpup.hDu.lhlsGCDKshPuhhhuhsphsl PuIhl.uGsh.sGha.......sptls...s.ac..tth.uGphsp
   consensus/80%                  lEtshpup.hDGslhlsGCDKshPuhhhAuphsl PuIhlhGGshhsGhap.....scpls..hssacuhtth.AGphop
   consensus/70%                  lEsshpupshDGllhlsGCDKshPGhhMAhARhNl PuIhlYGGohhPGhap.....Gcclsl.sssacuhGthtAGchoc
```

```
                    cov     pid 241        :         .         .         .         :         .         3         .  320
 1 PuDHAD         100.0% 100.0%   EEFFEAESCMHRSHGICMTMGTASTMASMVEALGMSLPGNAAIPAVDARRNLLARASRRIVQMVKDDLVMSKILTRQAF
 2 FtDHAD          95.0%  33.6%   EDFEGIEKNACPTTGACGGMYTANTMSSSFEALGMSLLGSSQMACPDPEKADSVAESARVLVEAIRRDLKPRDIVTRKAI
 3 SsDHAD          95.0%  33.5%   NELYEIEKRAHPTLGTCSGLFTANTMGSMSEALGMALPGSASPTATSSRRVMYVKETGKALGSLIENGIKSREILTFEAF
 4 SaDHAD          95.5%  33.5%   HELYEIEKRAHPTVGTCSGMFTANTMGSMSEALGMALPGSASPTATSSRRIMYVRETGKAVSRLLENGVKSRDILTFEAF
 5 CnN1DHAD        94.6%  34.1%   EDFEGVEKNACPSTGSCGGMYTANTMSSSFEALGMSLLYSSTMANPDQEKVDSAAESARVLVEAVKQDIKPRDIITRKSI
 6 TvDHAD          95.1%  32.5%   ATLHAIEHHACPAGSCGGMFTANTMSSAFEAMGMSLMYSSTMTAEDAEKADSTELAGKVLVEAIRKNIRPRDIITRKSI
 7 5j84-RlArDHT   100.0%  63.6%   AEFLEAEASMSRSSGTCNTMGTASTMAKMAEALGMALSGNAAIPGVDSRRKVMAQLTGRRIVQMVKDDLKPSEIMTKQAF
 8 6ovt-MtDHAD     95.1%  34.4%   ADVDAIERAICPGEGACGGMYTANTMASAAEALGMSLPGSAAPPATDRRRDGFARRSGQAVVELLRRGITARDILTKEAF
 9 5ze4-AtDHAD     95.7%  30.2%   EQRKTVLHHSCPGAGACGGMYTANTMASAIEAMGMSLPYSSSIPAEDPLKLDECRLAGKYLLELLKVDLKPRDIITPKSL
10 5oyn-CcXyDHT    99.7%  37.9%   EEFIDRAASSPSAGICNTMGTASTMNAVAEALGLSLTGCAAIPAYPRERGQMAYKTGQRIVDLAYDDVKPLDILTKQAF
   consensus/100%                 tph.th.tt.t.s.GtC.shhTASTMsu..EAhGMuL.hsut.ss+...s..suphl.phh..slh..cIhT.puh
   consensus/90%                  tph.thttp.p.s.GtCssMhTASTMuS..EAhGMuL.hsus.ss.s.c+..st.suphlsphlcpslpsp-IlThpuh
   consensus/80%                  t-h.thEpphpPstGsCssMhTASTMuShhEALGMuL.hsus.susstc+h..st.oG+hllphlcpsl+sp-IlThpuh
   consensus/70%                  p-hhtlE+pusPosGsCuGMaTANTMuShhEALGMSLsGSuuhsAsDsc+s..sptoG+hlVchl+pslKsRDIlT+cAh
```

```
                    cov     pid 321        .         .         .         :         .         .         .        4 400
 1 PuDHAD         100.0% 100.0%   ENAIRVNAAIGGSTNAVIHLLAIAGRTLDLTLADWDALGHKLPCLVDLQPSGTHLMEDFYYAGGVPAVIRELGD--VIA
 2 FtDHAD          95.0%  33.6%   ENAIALIMATGGSTNAVLHYLAIAHAAQVPFAIDDIEAIRRRVPVLCDLKPSGKYVATDFHRAGGVPQVLKMLLKAGLIH
 3 SsDHAD          95.0%  33.5%   ENAITTLMAMGGSTNAVLHLLAIAYEAGVLTLDDFNRISKRTPYIASMKPGGDYVMADLDEVGGVPLVMKKLLDAGLLH
 4 SaDHAD          95.5%  33.5%   ENAIAVLMAMGGSTNAVLHLLAIAYEAGVLTLDDFNRISKRTPYIGSLKPGGDYVMADLDEVGGVPLVMKKLLDAGLLN
 5 CnN1DHAD        94.6%  34.1%   ENAVALIMATGGSTNAVLHYLAIAHAAEVEWTIDDFERIRRKVPVICNLKPSGQYVATDLHKAGGIPQVMKILLKAGMLH
 6 TvDHAD          95.1%  32.5%   ENAISVIMAVGGSTNAVLHFLAIAHSAEVPLTIDDFETIRQRVPVLCDLKPSGKYVTADLHRAGGIPQVMKMLNAGLLH
 7 5j84-RlArDHT   100.0%  63.6%   ENAIRTNAAIGGSTNAVLHLLAIAGRVGIDLSLDDWDRCGRDVPTIVNLMPSGKYLMEEFYAGGLPVVLKRLGEAGLLH
 8 6ovt-MtDHAD     95.1%  34.4%   ENAIAVVMAFGGSTNAVLHLLAIAHEANVALSLQDFSRIGSGVPHLADVKPFGRIVMSDVDHIGGVPVVMKALLDAGLLH
 9 5ze4-AtDHAD     95.7%  30.2%   RNAMVSVMALGGSTNAVLHLIAIARSVGLELTLDDFQKVSDAVPFLADLKPSGKYVMEDIHKIGGTPAVLRYLLELGLMD
10 5oyn-CcXyDHT    99.7%  37.9%   ENAIALVAAAGGSTNAQPFIVAMARHAGVEITADDYRA-AYDIPLIVNMQPAGKYLGERFHRAGGAPAVLWELLQQGRLH
   consensus/100%                 cNAh...hAhGgSTNA..HhlAiAhthtl.hshtDhpt.t.thPlssh.P.Gpalhtch..hGGhP.Vhh.Lhp..hht
   consensus/90%                  ENAIth.hAhGgSTNAVlHhlAIAhtstl.holsDapthtpthPhlsshpPuGpalht-h..hGGhP.Vh+.Lhp.Ghlp
   consensus/80%                  ENAIshlhAhGgSTNAVlHhLAIAtpstVtlolDDaptltpclPhlsslpPuGcYlhtDhccsGGlP.Vh+hLLctGllc
```

```
                                       consensus/70%   ENAIsllMAhGGSTNAVLHlLAIAtpAsVcLTlDDapplucclPhlssLKPuGcYVhpDhacsGGlPhVhKhLLcAGLLH

                      cov      pid  401                                                                            480
                                       .           .         .         :         .         .         .
 1  PuDHAD      100.0% 100.0%         RDALTVNGQTLWDNCKDAPN---WNREVIHAFNEPFKTEAGIAVLRGNLCPDGAVIKPSAAT-----------PALLKHK
 2  FtDHAD       95.0%  33.6%         GDALTITGQTLAEEALANVPDTPRADQDVIRPFDRPLYSQGHLAILKGNLAPEGAVAKITGLK-------------NPAIT
 3  SsDHAD       95.0%  33.5%         GDVLTVTGKTMKQNLEQYKYPNVPHSHIVRDVKNPIKPRGGIVILKGSLAPEGAVIKVAATN-------------VVKFE
 4  SaDHAD       95.5%  33.5%         GDVLTVTGKTMKQNLQEYRIPNVPHNHIVKDVKNPIKPRGGIVILKGSLAPEGAVIKVAATN-------------VTKFE
 5  CnN1DHAD     94.6%  34.1%         GDCLTITGRTLAEELENVPDTPRADQDVILPIEKALYKEGHLAILKGNLAEEGAVAKITGLK-------------NPVIT
 6  TvDHAD       95.1%  32.5%         GDCLTITGETIAERLRHVPDTPDPNQDVIRPFDQPLYATGHLAILKGNLASEGAVAKISGVK-------------NPQIT
 7  5j84-RlArDHT 100.0% 63.6%         KDALTVSGEIVWDEVKDVVN---WNEDVILPAEKALTSSGIVVLRGNLAPKGAVLKPSAAS-----------PHLLVHK
 8  6ovt-MtDHAD  95.1%  34.4%         GDCLTVTGHTMAENLAAI-TPPDPDGKVLRALANPIHPSGGITILHGSLAPEGAVVKTAGFD-------------SDVFE
 9  5ze4-AtDHAD  95.7%  30.2%         GDCMTVTGQTLAQNLENVPSLT-EGQEIIRPLSNPIKETGHIQILRGDLAPDGSVAKITGKE------------GLYFS
10  5oyn-CcXyDHT 99.7%  37.9%         GDLTVTGKTMSENLQGRET---SDREVIFPYHEPLAEKAGFLVLKGNLFDFAIM-KSSVIGEEFRKRYLSQPGQEGVFE
                                   consensus/100%  tDshulsGpuh.pththh......ttcllhshtpshh.puth.lL+GsLh..u.h.K.ssht...............hp
                                    consensus/90%  tDsLTloGpuhhpplttth......ppcllhshppslh.putlhlL+GsLsscGuVhK.suhp...............hhp
                                    consensus/80%  GDsLTlTGpuhtpplLpph.s...spcllhshppPlh.pGtlslL+GsLAs-GAVhK.suhp...............hhp
                                    consensus/70%  GDsLIVTGcuht-sLpsh.s.s.ssp-VI+shcpPltspGtlsIL+GsLAP-GAVhKhouhp...............sshap

                      cov      pid  481                     5                                                     560
                                       .           .         .         .         .         .         :         .
 1  PuDHAD      100.0% 100.0%         GRAVVFENSEHHMERYDDENLDVDENCVLVLKNCGPRGYPGMAEAGNMPLPPKILRKGITI-DMVRVSDARMSGTAYGTVV
 2  FtDHAD       95.0%  33.6%         GPARVFNSEDECMAAIMADKIK--PGDVLVIRYEGPKGGPGMREMLA--PTSAIIGKGLGESVGLITDGRFSGGTWGMVV
 3  SsDHAD       95.0%  33.5%         GKAKVYNSEDDAFKGVQSGEVS--EGEVVIIRYEGPKGAPGMPEMLR--VTAAIMGAGLN-NVALVTDGRFSGATRGPMV
 4  SaDHAD       95.5%  33.5%         GKAKVYNSEEQAFKGIQSNEVK--DGEVVVIRYEGPKGGPGMPEMLR--VTAAIVGAGLS-NVAMVTDGRFSGATRGPMV
 5  CnN1DHAD     94.6%  34.1%         GPARVFEDEQSAMEAILADKIN--AGDILVLRYLGPKGGPGMPEMLA--PTSAIIGKGLGESVGFITDGRFSGGTWGMVV
 6  TvDHAD       95.1%  32.5%         GPARVFDSEEACLDAILAGKIN--PGDVIVIRYEGPVGGPGMREMLA--PTSAIIGAGLGDSVGLITDGRFSGGTYGMVV
 7  5j84-RlArDHT 100.0% 63.6%         GRAVVFEDIDDYKAKINDDNLDIDENCVLVKNCGPKGYPGMAEVGNMGLPPKVLKKGIL-DMVRVSDARMSGTAYGTVV
 8  6ovt-MtDHAD  95.1%  34.4%         GTARVFDGERAALDALEDGTIT--VGDAVVIRYEGPKGGPGMREMLA--ITGAIKGAGLGKDVLLLTDGRFSGGTTGLCV
 9  5ze4-AtDHAD  95.7%  30.2%         GPALVFEGEESMLAAISADPMSF-KGTVVVIRGEGPKGGPGMPEMLT--PTSAIMGAGLGKECALLTDGRFSGGSHGFVV
10  5oyn-CcXyDHT 99.7%  37.9%         ARAIVFDGSDDYHKRINDPALEIDERCILVIRGAGPIGWPGSAEVVNMQPPDHLLKKGIM-SLPTLGDGRQSGTADSPSI
                                   consensus/100%  u.AhVaps.pthhtth.s...hp...tphhlh+..GPhGhPG..hht....sstlhtttGl..ph.hlsDuR.SGss.u..l
                                    consensus/90%  G.AhVapspcthhttl.sstlp...spllV1+.tGPhGhPGM.Ehht....sstlhtttGl..shshloDuRhSGsshG.hV
                                    consensus/80%  G.AhVFpsp-phhttl.sslp...sslVlRhpGP+GhPGM.Ehls....sstIhttGls.shshloDGRhSGsshG.sV
                                    consensus/70%  G.AhVF-uE-shhcuIpsspls..tGsllVIRhpGPKGuPGMsEML..s.sTuAIlGtGLs.slshlTDGRFSGuohGhsV

                      cov      pid  561                               6                                           640
                                       .           .         .         .         .         .         .         .
 1  PuDHAD      100.0% 100.0%         LHVAPEAAAGGPLALVQDGDIIELDVAARKLHLHVSDEELARRREAWQAPPAPMARGWVKLYVEHVQQANLGADLDFLRG
 2  FtDHAD       95.0%  33.6%         GHVAPEAFVGGPIALVEDGDSITIDAHRQLIQLNVDDAELARRRAAWKPPAPRYTRGVLAKFARLVSSASKGAVTD----
 3  SsDHAD       95.0%  33.5%         GHVAPEAMVGGPIAIVEDGDTIVIDVESERLDLKLSEEEIKNRLKRWSPPSPRYKSGLLAKYASLVSQASMGAVTRPA--
 4  SaDHAD       95.5%  33.5%         GHVAPEAMVGGPIAIVEDGDVIVIDVENERLDIKLSDAEIKRRLNNWSPPEPRYKSGLLAKYASLVAQSSMGAVTRPVIK
 5  CnN1DHAD     94.6%  34.1%         GHVAPEAYVGGTIALVQEGDSITIDAHKLLLQLNVPDEELARRRANWKQPAPRYTRGVLAKFSKLASTASKGAVTD----
 6  TvDHAD       95.1%  32.5%         GHVAPEAAVGGTIALVQEGDSITIDAHRRLLQLNVSEEELAARRAKWQPPAPRYTRGVLAKYAKLVSSSSLGAVTDRFV-
 7  5j84-RlArDHT 100.0% 63.6%         LHTSPEAAVGGPLAVVKNGDMIELDVPNRRLHLDISDEELARRLAEWQPNHDLPTSGYAFLHQQHVEGADTGADLDFLKG
 8  6ovt-MtDHAD  95.1%  34.4%         GHIAPEAVDGGPIALLRNGDRIRLDVAGRVLDVLADPAEFASRQQDFSPPPRYTTGVLSKYVKLVSSAAVGAVCG----
 9  5ze4-AtDHAD  95.7%  30.2%         GHICPEAQEGGPIGLIKNGDIITIDIGKKRIDTQVSPEEMNDRRKKWTAPAYKVNRGVLYKYIKNVQSASDGCVTDE---
10  5oyn-CcXyDHT 99.7%  37.9%         LNASPESAIGGGLSWLRTGDTIRIDLNTGRCDALVDEATIAARKQDGIPAVPATMTPWQEIYRAHASQLDTGGVLEFAVK
                                   consensus/100%  hphsPEu..GGsluhlppGD.I.lDh.t.hhph.hs.tphttR.tth..s......psh..ha.t.stt.s.Gssht....
                                    consensus/90%  hHhuPEAh.GGslull ppGD.I.lDhttthlph.ls.tEhttRhttapss.shhtpGhh.ha.phsppushGushc....
                                    consensus/80%  hHluPEAhsGGslAllpsGD.IplDstpphlplpls-tElpsRhtpWpsPssthppGhlthahphVppushGAVhc....
                                    consensus/70%  GHlAPEAhlGGPIAlVcsGDhIPlDltpchLclpls-tElApRptpWpPPsP+hspGlLtKYsphVupAuhGAVs-....

                      cov      pid  641         :    ] 653
 1  PuDHAD      100.0% 100.0%         KSGA--GIPKDNH
 2  FtDHAD       95.0%  33.6%         -------------
 3  SsDHAD       95.0%  33.5%         -------------
 4  SaDHAD       95.5%  33.5%         -------------
 5  CnN1DHAD     94.6%  34.1%         -------------
 6  TvDHAD       95.1%  32.5%         -------------
 7  5j84-RlArDHT 100.0% 63.6%         CRGN--AVGKDSH
 8  6ovt-MtDHAD  95.1%  34.4%         -------------
 9  5ze4-AtDHAD  95.7%  30.2%         -------------
10  5oyn-CcXyDHT 99.7%  37.9%         YQDLAAKLPRHNH
                                   consensus/100%  .............
                                    consensus/90%  .............
                                    consensus/80%  .............
                                    consensus/70%  .............
```

[MView](#) 1.63, Copyright © 1997-2018 [Nigel P. Brown](#)