```
              -> Gag P17 Matrix
CONSENSUS-A   MGArnSVLRGKKaDELEkiRLRPgGKKkYrLKHiVWaANeLdrFgLaEsLLESKEGCQkIltVLdPlVPT     70
ROD           -----------------R--------------------K--------------------------M---     70
NIHZ          ----------------------------K-------------------------------------     70
ISY           ---K-------------------------------------------T-------------IS--E-----     70
ST            ----------------------------------------------------------------------     70
UC2           ---------------------------------------------R---N---------------------     70
BEN           ------------------V-----------------------K------------------R--------     70
CAM2          ------------------V----------K---------------------------R--K--------     70
D194          ------------------V----N---R-----V---------------------------K--E-----     70
GH1           -----------------------S------------------K---------------------------     70
MDS           ----S-------------V-----------------------------------------------------     70
KR            ----S-------V---------------------------GK-----------------I---------     70
7924A                                                 x---------------------R-IS--------     34
60415K                                                x---------------------R-----------     34
FA                                                    x------------------------I---N-----     34
CONSENSUS-B   MGARgSVLSGKKTDELEKVRLRPGGKKrYmLKHivW?vNELdRFGLAE?lLeSKEGChKIltvLaPLvPT     68
D205          ---------------------------K-----V--A-----------S--------Q---K--------     70
UC1           ----S------------------------C----I-A-----------S---------------------     70
EHOA          -----------------------------------A----E------SR-G-----R--RK--G-----     70
60667K                                                x----E------N--G---------A--E-----     34
JA                                                    x-----------S---------------------     34
FT                                                    x-----------T---------------------     34
7810A                                                 xA----------T--G----------A-------     34
ON                                                    x-----------R---------------------     34
CONSENSUS-C                                           xANELDRFALAESLLETKEGCQKILTVLEPLVPT     34
2238                                                  ----------------------------------     34
CONSENSUS-D                                           xANELDRFGLAESLLENKEGCQKILSVLAPLVPT     34
FO784                                                 ----------------------------------     34
CONSENSUS-SD  MGaRNSVLSGKkADELEKiRLRPgGKKkYmLKHvVWAANELDRFGLAESLLeNKEGCQKILSVLAPLVPT     70
MM251         ----------------------------------------------------------------------     70
MM32H         ----------------------------------------------------------------------     70
MM1A11        ------------------------N---------------------------------------------     70
MM239         --V--------------------N-----------------------------------------------     70
MM142         ----------------------------------------------------------------------     70
MNE           ----------------------------------------------------------------------     70
SMMH4         -----------E------V----N--------------------------D--------------------     70
SMMH9         --V-----------------------------I-----------------------------------     70
SMMPBJ        ---------------------------R-Q---I-----------------------------------     70
6P12          ---------------------------R-K---I-----------------------------------     70
CONSENSUS-E                                           xARELDRFGLAESLLENKEGCHRILTVLEPLMPT     34
PA                                                    ----------------------------------     34
CONSENSUS-STM MGARSSVLSGKKADELEKVRLRPGGKKKYMLKHVVWAANELDRFGLAESLLESKEGCQKI?TVLEPLVPT     69
STM           ------------------------------------------------------------I---------     70
STM22579      -------------------------------------------------------------L---------     70
CONSENSUS-B   MGARgSVLSGKKTDELEKVRLRPGGKKrYmLKHivW?vNELdRFGLAE?lLeSKEGChKIltvLaPLvPT     68
BA_7312A                                              xA----------N--------Q---------M--     34
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HIV2/SIV GAG

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                                                                Gag P17 Matrix \/ P24 Capsid
CONSENSUS-A   GSENLkSLfNTvCViwC?HAEEKvKDTEeAk.kivqRHLvAETgTaeKMPntSRPtAPpSgkggNfPVQq    138
ROD           -----------------I----------G--.Q--R--------------S-------S-E----Y---H    139
NIHZ          -----------------I----------G--.Q-----------------------------..------    137
ISY           --------Y--T-----L-------------.R--G-------E-------I------------------    139
ST            -----------------I-----A-------.QK---------K-T----S----------N--------    139
UC2           -----------------L-------------.-L-------------------------------------    139
BEN           -----------------L-------------.-LA---------------------------R--Y----    139
CAM2          -----------------I-------------.R-AL---A----------D--------------Y---S    139
D194          -----------------L-------------.-LA----------------I------------------    139
GH1           -----------------L-------------.-L-----G----------S----------R-R------    139
MDS           ---------------F-I-------------.-FAR-------------------------R---Y---N    139
KR            -----------------L----------G--.Q-------------D---S----A-----R---Y----    139
7924A         --------------V--I-------------.---------------------------------Y---S    103
60415K        --------------A--I----------G--.Q-----------------S----------E-------H    103
FA            -----Q-----------L------------R.-L---------------------------S--------    103
CONSENSUS-B   GSENLKSLfNtVCViyCLHAeeKVKDTEEAK.KiAQsHLa?dt...EKmPatskptappSg..rnYPVQQ    131
D205          ----------I----F---------------.----R---A--...------N--------..G------    134
UC1           -------------------------------.----R---A--...-------R-------..G------    134
EHOA          --------Y------F---------------.----R---A--...-----M---SK-T-R..LA-----    134
60667K        --------------------G----------.----R--VGN-...-------R----S--..G------     98
JA            --------------V----------------.--------VN-...--T----R-------..-------     98
FT            ---------------F-----Q---------.-------VV-A...--V-----S------..-------     98
7810A         --------------V----------------.--------AN-...---------------..-------     98
ON            -------------------------------.-M-----VV-A...--T----R-------..-------     98
CONSENSUS-C   GSENLKSLYNTTCVIWCLHAEQKVKHTEERN.EVVERHLAAETKNAEKMPATSRPTAPSSGGRGNYPVQQ    103
2238          -------------------------------.-------------------------------------    103
CONSENSUS-D   GSENLKSLYNTVCVIWCLHAEEKVKDTEGAK.QIVQRHLVVETGTADKMPSTSRPTAPPSDRGRNYPVQQ    103
FO784         -------------------------------.-------------------------------------    103
CONSENSUS-SD  GSENLKSLYNTVcViWCIHAEEKVKHTEEAK.QIVQRHLVvETGTa?tMP?TSRPTAPpSGrGGNYPVQQ    137
MM251         -------------------------------.--------------E---K-------S-----------    139
MM32H         -------------------------------.--------------E---K-------S-----------    139
MM1A11        -------------------------------.--------------EI--K-------S-----------    139
MM239         -------------------------------.-------------TE---K-------S-----------    139
MM142         -------------------------------.--------M-----E---K-------F-----------    139
MNE           -------------------------------.--------------E---K-------S-----------    139
SMMH4         -------------------------------.--------------DR--A-------------------    139
SMMH9         ------------R-L----------------.--------------DK--A-------------------    139
SMMPBJ        --------------L----------------.--------------DK--A----------K--------    139
6P12          --------------L----------------.--------------DK--A----------K--------    139
CONSENSUS-E   GSENLKSLFNAVCVVYCLHAAVKVKDTEEAKKHVQQHHLVAGGKTTEKLPPQSRPTAPPSGGGGNYPVQQ    104
PA            ------------------------------------------------------------------------    104
CONSENSUS-STM GSENLKSLFNTVCVIWCIHAEEKVKHTEEAK.QVVKRHLVVETGTA?KMPATSRPTAPPSGRGGNYPVQQ    137
STM           -------------------------------.--------------N-----------------------    139
STM22579      -------------------------------.--------------D-----------------------    139
CONSENSUS-B   GSENLKSLfNtVCViyCLHAeeKVKDTEEAK.KiAQsHLa?dt...EKmPatskptappSg..rnYPVQQ    131
BA_7312A      ---------------W-----K---------.-L-----VV--...--T-TAD--A-TS--..-------     98
```

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CONSENSUS-A   ??gGNYtHvPLSPrTLNAWVKLvEeKKFGAEVVPGFQALSEGCTPYDINQmLNCVGDhQAAMQIIREIIN    206
ROD           .V------I-------------------------------------------------------------    208
NIHZ          .VA-----I----G--------------------------------------------------------    206
ISY           .I----V-L-------------------------------------------------------------    208
ST            .VA-------------------------------------------------------------------    208
UC2           .A----V-----------------------------------------------------Q-----------    208
BEN           .A----V-------------------------------------------------------------------    208
CAM2          .I-------------------------------------------------------------------    208
D194          .A----I-------------------------------------------------------------------    208
GH1           TG----I-----------------D-------------------------------------------    209
MDS           .I-------------------------------------------------------------------    208
KR            .IA---S-------------------------------------------------------------------    208
7924A         .I-------------------------------------------------------------------    172
60415K        .V------I-------------------------------------------------------------    172
FA            TG----V---------------I-D------------------------L-------------------    173
CONSENSUS-B   .vAGNYvHlPLSPRTLNAWVKLvEeKKFGaeVVPGFQALSEGCTPYDINQMLNCVGeHQAAmqiIREIIN    200
D205          .L-------------------------------------------------------------------    203
UC1           .I------M-------------------------------------------------D-------------    203
EHOA          .I----S-------------------------------------------------------------------    203
60667K        .I----S----------------------EN-------------------------D----IE-------    167
JA            .-------------------------------------------------------------------    167
FT            .-------V-------------I-----------------------------------------------    167
7810A         .-----------------------D-----------------------------------------------    167
ON            .-------V-------------I-----------------------------------------------    167
CONSENSUS-C   .VAGNYVHHPLSPRTLNAWVKLVEEKKFGAEVVPGFQALTEGCTPYDINQLLNCVGDHQAAMQIIREIIN    172
2238          .-------------------------------------------------------------------    172
CONSENSUS-D   .VGGNYVHLPLSPRTLNAWVKLVEDKKFGAEVVPGFQALSEGCTPYDINQMLNCVGEHQAAMQIIREIIN    172
FO784         .-------------------------------------------------------------------    172
CONSENSUS-SD  .iGGNYtHLPLSPRTLNAWVKLiEEKKFGAEVVpGFQALSEGCtPyDINQMLNCVGeHQAAMQIIReIIN    206
MM251         .-----V-------------------------------------------------D---------D---    208
MM32H         .-----V-------------------------------------------------D---------D---    208
MM1A11        .-----V-------------------------------------------------D---------D---    208
MM239         .-----V-------------------------------------------------D---------D---    208
MM142         .--------------------------------S---------L------------D---------D---    208
MNE           .V------------------------------------------------------------------    208
SMMH4         .V----V---------------V-----------------------------------------------    208
SMMH9         .V--------------------V----------------------x------------------------    208
SMMPBJ        .-------------------------------------------------------------------    208
6P12          .-------------------------------------------------------------------    208
CONSENSUS-E   .IGNNYVHSPLSPRTLNAWVKLVEEKKFGAEVVPGFQALSEGCTPYDINQMLNCVGEHQAAMQIIREIIN    173
PA            .-------------------------------------------------------------------    173
CONSENSUS-STM .VGGNYVHLPLSPRTLNAWVKLVEEKKFGAEVV?GFQALSEGCTPYDINQ?LNCVGEHQAAMQII?EIIN    203
STM           .--------------------------------P----------------L--------------K----    208
STM22579      .--------------------------------S----------------M--------------R----    208
CONSENSUS-B   .vAGNYvHlPLSPRTLNAWVKLvEeKKFGaeVVPGFQALSEGCTPYDINQMLNCVGeHQAAmqiIREIIN    200
BA_7312A      .-------V-----------------------------------------------------V------    167
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HIV2/SIV GAG

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CONSENSUS-A   eeAAdWDaqHPIP.GPLPAGQLR?PRGSDIAGTTSTVeEQIqWMfR?qNPvPVGnIYRRWiQIGLQKCVR    273
ROD           ----E--V-----.---------E----------------------P-----------------------    277
NIHZ          -------VA----.---------E----------------------P-----------------------    275
ISY           -------V-----.---------D-----------------E--Y-QE----------------------    277
ST            -------------.---------E----------------------P-------S---------------    277
UC2           -------------.---------D-------------D------Y-Q-----------------------    277
BEN           -------S-----.---------D-------------D------Y-P-----------------------    277
CAM2          --------N----.---------D----------------------A-----------------------    277
D194          -------------.---------D-------------D------Y-QP----------------------    277
GH1           D------------.---------D--------------------Y-P-----------------------    278
MDS           -------------.---------E-------------D--------A-----------------------    277
KR            -------V-----.---------E----------------------A---I-------------------    277
7924A         -V-----VA----.---------E----------------------A-----------------------    241
60415K        ----E--V-----.---------E-------------D--------P-----------------------    241
FA            -------------.---------D-------------D------Y-A---I---------V---------    242
CONSENSUS-B   EEAAdWDQQHP?P.GPlPAGQLRdPRGSDIAGTTSTVEEqIQWMyRaqnPvPVGNIYRRWIQlGLQKCVR    268
D205          -----------S-.--M-----------------------------------------------------    272
UC1           -----------I-.-----------------------------------------------I-------    272
EHOA          -----------S-.--M------E----------------------P-----------------------    272
60667K        ----E------S-.--M------E--------------------C-----------------I-------    236
JA            -----------V-.-------------------------E------------------------------    236
FT            -----------I-.--------------------------------QP--------------I-------    236
7810A         -----------S-.-------------------------------------I-------------------    236
ON            -----------I-.--------------------------------QP--------------I-------    236
CONSENSUS-C   EEAADWDEHHPVP.GPLPAGQLRDPRGSDIAGTTSTVEEQIQWMYRAQNPVPVGNIYRRWIQLGLQKCVR    241
2238          -------------.-------------------------------------------------------    241
CONSENSUS-D   DEAADWDQQHPQP.GPLPAGQLRDPRGSDIAGTTSTVEEQIQWMYRQQNPIPVGNIYRRWIQLGLQKCVR    241
FO784         -------------.-------------------------------------------------------    241
CONSENSUS-SD  EEAADWDLQHpQp.?Pq??GQLREPsGSDIAGTTStvdEQIQWMyRQQNPIPVGNIYrRWIQLGLQKCVR    272
MM251         -------------.A--Q.----------------S----------------------------------    276
MM32H         -------------.A--Q.----------------S----------------------------------    276
MM1A11        -------------.A--Q.----------------S----------------------------------    276
MM239         -------------.A--Q.----------------S----------------------------------    276
MM142         ------------Q.A--Q.------------------E---------------------------------    276
MNE           ------------Q.A--Q.-------------------------------------------------    276
SMMH4         -------------.G-LPA------R-----------------------------------------    277
SMMH9         ----------x--.G-IPA------x----------x-------x------------x------------    277
SMMPBJ        -------------.G-IPP------R-----------------------------------------    277
6P12          -------------.G-IPP------R-----------------------------------------    277
CONSENSUS-E   EEAADWDVQHPR..GQPPAQGLRDPSGSDIAGTTSTPAEQIEWMYRNPNPIPVGDIYRRWIQLGLQKCVR    241
PA            ------------..------------------------------------------------------    241
CONSENSUS-STM EEAADWD?QHPQP?GPLPAGQLREPSGSDIAGTTS??EEQIQWM?RQQNPIPVGNIYRRWIQLGLQKCVR    268
STM           -------M-----P--------------------SP-------Y-------------------------    278
STM22579      -------V-----.---------------------TV-------H-------------------------    277
CONSENSUS-B   EEAAdWDQQHP?P.GPlPAGQLRdPRGSDIAGTTSTVEEqIQWMyRaqnPvPVGNIYRRWIQlGLQKCVR    268
BA_7312A      -----------V-.--------------------------------G-S-I-------------------    236
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CONSENSUS-A   mYNPTNiLD?kQGPKEpFQSYVDRFYKSLRAEQtDpAVKNWMTQTLLvQnaNPDCKLVLKGLGmNPTLEE    342
ROD           ---------I-------------------------------------------------------------    347
NIHZ          ---------IN-----------------------------------I----------------------    345
ISY           ---------I------S------------------A-------------.S-------------------    346
ST            ---------I-------------------------------------------------------I------    347
UC2           ------V--V------S----------------A-----------------------------------    347
BEN           K--------I-----------------------------------I----------------------    347
CAM2          ---------I------S------------------------------------------------------    347
D194          ---------V------S-----------------------------I----------------------    347
GH1           ---------V-----------------------------------I----------------------    348
MDS           ---------V-------------------------A-----------I----------------------    347
KR            ---------V-------------------------------------------------------------    347
7924A         ---------V------S---                                                     261
60415K        ---------I----------                                                     261
FA            ------V--V------S---                                                     262
CONSENSUS-B   MYNpTNILDiKqGPKEPFQsYVDRFYKSLRAEQTDPAVKNWMTQTLLIQNANPDCKLVLKGLGMNPTLEE    338
D205          ------------------------------------------------------------------------    342
UC1           ------------------------------------------------------------------------    342
EHOA          ------------------------------------------------------------------------    342
60667K        -------------------N                                                     256
JA            -----------E--------                                                     256
FT            ---------V----------                                                     256
7810A         --------------------                                                     256
ON            ---S-----V----------                                                     256
CONSENSUS-C   MYNPTNILDVKQGPKEPFQS                                                     261
2238          --------------------                                                     261
CONSENSUS-D   MYNPTNILDIKQGPKETFQS                                                     261
FO784         --------------------                                                     261
CONSENSUS-SD  MYNPTnILDVKQGPKEpFQSYVDRFYKSlRAEQTDpAvKnWMTQTLLIQNANPDCKLVLKGLg?NPTLEE    341
MM251         -----------------------------------A---------------------------V------    346
MM32H         -----------------------------------A---------------------------V------    346
MM1A11        -----------------------------------A---------------------------V------    346
MM239         -----------------------------------A---------------------------V------    346
MM142         -------------------------------------------------------------T------    346
MNE           -----S-------------------------------------------------------M------    346
SMMH4         -------------------------------------------------------------M------    347
SMMH9         ----------------S--------------------x------------------------xI------    347
SMMPBJ        -------------------------------------------------------------I------    347
6P12          ----------------------------S----------S-----------------------I------    347
CONSENSUS-E   MYNPTNILDVKQGPKESFQS                                                     261
PA            --------------------                                                     261
CONSENSUS-STM MYNPVNILD?KQGPKE?FQSYVDRFYKSLRAEQADP?VKNWMT?T?LIQNANPDCKLVLKGLGMNPTLEE    333
STM           ---------V------T-------------------S------R-L------------------------    348
STM22579      ---------I------P-------------------A------Q-P------------------------    347
CONSENSUS-B   MYNpTNILDiKqGPKEPFQsYVDRFYKSLRAEQTDPAVKNWMTQTLLIQNANPDCKLVLKGLGMNPTLEE    338
BA_7312A      ---------V----------                                                     256
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HIV2/SIV GAG

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                                        X peptide \
                      P24 Capsid \/ X peptide      / P9 NC
CONSENSUS-A   MLTaCQGvGGPgQKARLMAEALKEam?PaPIPFAAAQQ....rrtikcWNCGKeGHSArQcrAPRRQGCW    407
ROD           ------------------------VIG-----------....-KAF------------------------    413
NIHZ          ---T--------------------V-A-----------....-K-F--------------WS--------    411
ISY           -------I------------------R-----------....K-A-------------------------    412
ST            --------------------------A-----------....-----------------------------    413
UC2           -------------------------LT-P---------....----R-----------K-----------    413
BEN           -------------------------G-S---------....-KA-RY----------------------    413
CAM2          -------------------------G-P---------....-----------------------------    413
D194          -----------S-------------LT-----------....--A-R-----------K-----------    413
GH1           -------------------------LT-P---------....-KV-R----------------------    414
MDS           --------------------------T----------....-----------------------------    413
KR            -------I-----------------LA-----------....-----------D----------------    413
CONSENSUS-B   MLTACQGIGGPGQKARLMAEALKEALTPapiPFAAaQqkAGKRgTVTCWNCGK?GHTArQCrAPRRQGCW    407
D205          -----------------------------------V-----------------Q----------------    412
UC1           ------------------------------------------------------V----K-----------    412
EHOA          ----------------------------STN------PR----.---------A-------K--------    411
CONSENSUS-SD  MLTACQGVgGPGQKaRLMAEALKeALapgplPFaA?QqkG?.rKpIkCwNCgKEGHSArQcRaPRRqGCW    408
MM251         ----------------------------V-I----A-KR-P.----------------------------    415
MM32H         ----------------------------V-I----A--R-P.----------------------------    415
MM1A11        ----------------------------V-I----A--R-P.----------------------------    415
MM239         ----------------------------V-I----A--R-P.----------------------------    415
MM142         ----------------------------A-I----A----P.----------------------------    415
MNE           -----------------------------------A----P.--------------------T-------    415
SMMH4         -------------------------R-DQ-----V----Q.--T-------------K-----------    416
SMMH9         --------x-----x--------D--TQ-----x-V----Q.x-I-x-x--x--------F-----x---    416
SMMPBJ        -----------------------D--TQ-------V----Q.--I-------------------------    416
6P12          -----------------------D--TQ-------V----Q.--I-------------------------    416
CONSENSUS-STM MLTACQGVGGPGQKARLMAEALKE?FQP?PLPFAAAQQQG..RRTVKCWNCGK?GHTAKQCK?PRRQGCW    397
STM           ------------------------V---D-----------..-----------A--------G-------    416
STM22579      -----------------------A---G----------..-----------E--------A-------    415
CONSENSUS-B   MLTACQGIGGPGQKARLMAEALKEALTPapiPFAAaQqkAGKRgTVTCWNCGK?GHTArQCrAPRRQGCW    407

                                        P9 NC \/ P6
CONSENSUS-A   KCGK?GHiManCPdRQAGFLG?GpwGKkpRNFPvaq?pqGL..................tPTAPP?DPav    455
ROD           ----P----T-----------L--------------V----..................------V----    465
NIHZ          ----S--V-------------I-H----A----A--V----..................------L----    463
ISY           ----S----------------L------------VPSS---..................------M----    464
ST            ----A-----K--E-------L--------------I----..................------I--VE    465
UC2           ----P----------------M-SR-----------A----..................I-----A---A    465
BEN           ----P--------E-------L--R---------T-A----..................I-----A---A    465
CAM2          ----P----T-----------I--------------V----..................------L----    465
D194          ----S--------E-------M--R--Q-----A--A----..................I-----I----    465
GH1           ----T--V--K--E-------M--------------A-P--..................I-----A----    466
MDS           ----T-----K----------I--------------V----..................------A----    465
KR            ----S--V-----E-------I------------TRV----..................------A---A    465
CONSENSUS-B   KCGkqGHIMSKCPERQAGFLGlGPWGKKPRNFPmtQvPQGvtPSAPPMnPAeGMTPrGAtPSAPPADPAv    477
D205          ----T-------------------------------------------------------------------    482
UC1           ------------------------------------------------D----------------------    482
EHOA          ---Q-----------------F-----------V.-A---IV---------F----Q--I---------E    480
CONSENSUS-SD  KCGkmgHVMAKCPeRQAGFLGlGPWGKKPRNFPMAQm?QGL..................tPTApPEdPAV    459
MM251         -----D-------D----------------------VH---..................-----------    467
MM32H         -----D-------D----------------------VH---..................-----------    467
MM1A11        -----D-------D----------------------VH---..................-----------    467
MM239         -----D-------D----------------------VH---..................M----------    467
MM142         -----D-------N----------------------VH---..................-------E---    467
MNE           ---Q---------D-------F---------------H---..................-----------    467
SMMH4         ----T--------------------------------P---..................I----------    468
SMMH9         ----A--------------------------------P---..................----x------    468
SMMPBJ        ----A--------------------------------P---..................-----------    468
6P12          ----A--------------------------------P---..................-----------    468
CONSENSUS-STM KCG??GHQMAKCPERQVGFLGFGPWGKKP?NFPMAQIPQGL??????...........??PTAPP?DPAA    444
STM           ---QQ------------------------H-----------..................T-----E----    468
STM22579      ---KP-----------------------R-----------TPTAPP...........EM-----V----    474
CONSENSUS-B   KCGkqGHIMSKCPERQAGFLGlGPWGKKPRNFPmtQvPQGvtPSAPPMnPAeGMTPrGAtPSAPPADPAv    477
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                                                                P6 \
CONSENSUS-A   dLLEkYmQQGrkQrE....QreRPYKEVTEDlLhlEqgetP?re??TEDLLHLNSLFGkDQ$   509
ROD           ----------KR---....----------------------Y--PP---------------   522
NIHZ          ----------KR---....--------------RF--A---C--.T---------------   519
ISY           ---------------....--Q-------------------H--.T------------N--   520
ST            ----------KR---....------------F-Q--KQ---C--.T---------------   521
UC2           ------L--------....----------------------R--.A----------------   521
BEN           E---R----------....------------------R---H--.E---------------   521
CAM2          ----------KR---....--Q-----------------A-C--.T---------------   521
D194          ---------------....----------------------H-G.A---------------   521
GH1           ----R------E---....-------------------KA-H--.A---------------   522
MDS           ---------------....------------------K--CK-.T------------T---   521
KR            ------L------K-....-KM------------------HK-.A----------------   521
CONSENSUS-B   EMLKsYMqmGrqQrE....sRERPYKEV.................TEDLLHLNSLFGEDQ$   516
D205          ---------------....---------.................---------------   521
UC1           -------K-------....---------.................---------------   521
EHOA          ----N---L-KK-K-....N--------.................----------------   519
CONSENSUS-SD  DLLKNYMklG?qQRE?????re?PYKEV.................TEDLLHLNSLFGeDQ$   495
MM251         -------Q--K----....S--K-----.................------------G--   506
MM32H         -------Q--K----KQRES--K-----.................------------G--   510
MM1A11        -------Q--K----KQRES--K----M.................------------G--   510
MM239         -------Q--K----KQRES--K-----.................------------G--   510
MM142         -------H--K----....S-GK-----.................------------G--   506
MNE           -------Q--K----....SKRK-----.................---------------   506
SMMH4         --------M-RK---....N--R-----.................---------------   507
SMMH9         --------V-RR---....N--R-----.................---------------   507
SMMPBJ        --------M-RR---....N--R-----.................---------------   507
6P12          --------M-RR---....N--R-----.................----------------   507
CONSENSUS-STM DLLRSYMQLGKKQRE....SRKTPYKEV.................TEDL?HLNSLFGEDQ    482
STM           ---------------....---------.................----L----------   507
STM22579      ---------------....---------.................----V-------      510
CONSENSUS-B   EMLKsYMqmGrqQrE....sRERPYKEV.................TEDLLHLNSLFGEDQ$   516
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