

Genome-wide identification, evolutionary relationship and expression analysis of AGO, DCL and RDR family genes in tea

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Supplementary Figure S1-a. Multiple Sequence alignment of CsAGO proteins: The names of the identified CsAGO genes are indicated to the left of the alignments. The length of the alignment is shown on the top, while the length of each protein is given on the right. Conserved consensus residues are shown at the bottom. Invariable residues conserved at 100% are highlighted in red, those conserved at >80% are shown in yellow and residues that are >60% conserved are highlighted in green. The sequences were aligned using ClustalX and viewed by GeneDoc.

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*      20      *      40      *      60      *
CsAGO2/3f : -----MNPHEHLETLVHLHCP-----LFIQDCPLLSLNSQTP-----TQSR : 36
CsAGO2/3d : ----- : -
CsAGO7 : -----MEETEEANTTKKCTP----- : 15
CsAGO10a : ----- : -
CsAGO2/3a : -----MERDGGRRYNRGRGGAAPRRSGGD----- : 24
CsAGO2/3b : -----MERDGGRRYNRGRGGAALPRSGDGGNR : 28
CsAGO6 : ----- : -
CsAGO4c : ----- : -
CsAGO4a : ----- : -
CsAGO4b : ----- : -
CsAGO2/3c : -----MERDG-RNYNRG-----APRGASCG----- : 19
CsAGO10b : ----- : -
CsAGO10c : ----- : -
CsAGO1 : MFGKDEKRRKRGRKLLVEADLAALAYLTDQGWYKSGFEIYILLASLYSFLSGSIASLGFSLLPSENGF : 72
CsAGO5c : -----MGRLRLWLGEREDDKNKGFRFRSPARERRGGWWSVVVGVATAVVIAREERD : 51
CsAGO5a : ----- : -
CsAGO5b : ----- : -
CsAGO2/3e : -----MGYDDYIEKKVEVVSNPCDEVGFTHPSQFVMLNNEEAGGPLPSSVGMQLQSE : 51

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80      *      100      *      120      *      140
CsAGO2/3f : FHGLNALESEEEPTADELLMVVVAVVTEEFLSFS-----LPRYQTHNHHHHYHGGQGGGGTYT : 98
CsAGO2/3d : -----MERSNYGRGGGGGGRRGG : 22
CsAGO7 : -----KTRSFGRNRP-----NHHHHHHYHQQQQQQLLQ----- : 47
CsAGO10a : -----MPMRQMKIIP-----EQHLVIKPQLQNSMNQHLVIFQLQNSMNQVHK----- : 43
CsAGO2/3a : --RGGNGGGGRGRGQGGGGRRGARAWPSEQSNQGGQ--GGGGGRGGGARAWFPQQGQNGGGGGGGG-- : 89
CsAGO2/3b : GGRGGNGGGGRGRGQGGGGRRGARAWPSELSQNGQCGGGGGGGRRGARAWAPPQQGQNGGGGGGGGG : 100
CsAGO6 : ----- : -
CsAGO4c : ----- : -
CsAGO4a : ----- : -
CsAGO4b : -----MMIMMATVTMAATAEGVAVKFPFMKAINPNLTLNRTS----- : 38
CsAGO2/3c : ---GGSGSGRGRGRG---RAWGSPSQGQNGGGGRGQ--- : 50
CsAGO10b : -----MPMRQMKIIP-----EQHLVIKPQLQ-----TMNQAK----- : 29
CsAGO10c : -----MPHWQKPEP-----QRHVISRRLQD-----SMHQSL----- : 29
CsAGO1 : PVRASGIIMVRRKRETELPGGSESSQEAASGGRRGGAQRPPAQQQQQQQGGGGHGGGRGWGQSQGGRR : 144
CsAGO5c : EKKYSRRRTEREREREREGRGHRG-----VQSSMSTRGRGR-----GDGGGRGRGRQPRRDQ-- : 105
CsAGO5a : -----MSGRGRGR-----GRG-----GRGQPRHDR----- : 20
CsAGO5b : -----MSGRNRGRSGSV-----GGDGGGRGRAQPRRTL----- : 29
CsAGO2/3e : DRVLGSRVSKVNPSETVFWCRDHKLGISTQVLLPLYNVAKQTFMAALERYKIHSNLSVKKDESGSDNMSSWY : 123

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*      160      *      180      *      200      *
CsAGO2/3f : AT-----LQPPQPPQGWGRPVQGRGPMRPPPR----- : 129
CsAGO2/3d : GG-----GGRGSVDR----- : 32
CsAGO7 : -----QSNRIGYCFNQNQYTPALLPLP----- : 71
CsAGO10a : -----PPKTAQNGKGFPTTHSQNTELHNQFPLPSKNRGR----- : 77
CsAGO2/3a : -----ARGWGPSQSGGQPVWDRVAVQGGPVGGGGGACRP : 123
CsAGO2/3b : GG-----ARAWGPSQSGQVWDRVAVQGGPVGGGGG-AYRP : 135
CsAGO6 : -----MEKEAVGSRRLPPP----- : 15
CsAGO4c : -----MDTFEKDNGTTESLPPP----- : 18
CsAGO4a : -----MEFPG-----ETDVLPPP----- : 14
CsAGO4b : -----ITILVLMYSFVSGSMALSFDLMDSFHDGNGATEALPPP----- : 77
CsAGO2/3c : -----VRAWGPSQSGGQWGP----- : 66
CsAGO10b : -----PPKTAQNGKGFPTTQEPQNTKIYNQTSPPSKNRGR----- : 63
CsAGO10c : -----SQESSEDAN-----KIEGSRGR----- : 47
CsAGO1 : GYGRGGGGGGGGPQRGGMAGQQYVGGPEYHQGRGGPRGGVSVQRGGSSSSVGGGLGVVPSA---GG : 213
CsAGO5c : -----PPPPSSGRGGGRGTAGGSAPYQAAPPQRP-- : 140
CsAGO5a : -----PSPASSSGRGGNHIIPPPASFQPALSSPTP----- : 55
CsAGO5b : -----PSP---AVQGRGRGGAG-PAPTQAPPPTVSQPP----- : 60
CsAGO2/3e : ASSLDVLESEVMKHSRALLLLSCDFGTWVNSRRLRSPSAVVAQAQQQSLSRKGGSSSSSSNSTVISGP : 195

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220      *      240      *      260      *      280
CsAGO2/3f : VRPTRQDSGEISDRGRGRIPGRRGSGRACQPAP----APRTQSLSSPEPPRFR---PDFQILEQPPASSL : 193
CsAGO2/3d : -----QYQGGGRRGGDPSIP-----DISSL : 52
CsAGO7 : PIMPLQLTVPPLPQNQTFRSKTHLQKHPWKQNNPLATSSDPEPQNSAVSPAPEGLGRQPGIPFRGKDGRR : 143
CsAGO10a : -----RRGKGGKPDNSDVMRPSLRPAS--VQPTGAFEADIPNGSRSRN-----SCVER : 126
CsAGO2/3a : PAPLQQVQGVGPTSGVWSGRPWSG---QSSSQ--PPIQVVPVQKLEQALPDIKELEISEKKPSPAII : 188
CsAGO2/3b : PAPLQQVQGVGPTSGVWSGRPWSGSPVAGQSSSQ--PPIQVVPVQKLEQALPDIRQLQISEKKPSSSI : 205
CsAGO6 : -----PIIPPTVKPEKLVTPERS----- : 33
CsAGO4c : -----PPVPADVPMRA-EADNAPEPVKN----- : 41
CsAGO4a : -----PEIPPDIDPIRVQEPEDVPEFTKTS----- : 40
CsAGO4b : -----PVPVNIIVLQA-EPDHAPPEVVK----- : 100
CsAGO2/3c : ---QQGQ-----GVWSGRPWIGQ--SSSSSQT--HQIQTVVPHRFPPEQLLPDVQSLSEIKKPKQLSI : 122
CsAGO10b : -----RRRGGGRKSDQGEVFMRPSRPTGVHKPARAGETDIPNGSVNGAN-----LCEVEM : 116
CsAGO10c : -----RRSAKGSK-----METAHNVKPEIFN-----VEP : 71
CsAGO1 : PSRPVPELHQATQASYQAGVTTQPVAYPKPAEMHGEASSSSPVPDPSLQVTSKVQGLSLQEGTSSQAIQ : 285
CsAGO5c : -----YASTSTPSSSQPPPTS-----SSLSQDVERKLIQSPPTTAAQPPSSSVQRPA-QPPLPAQDPAQ : 201
CsAGO5a : -----LASSASLSDMQLLKT--LQSPAPQALTLPEVQVTPPP-----PQSVKEAVQ : 101
CsAGO5b : -----VVSHSPSPSQAQSSSTTRTEVSSLSQDVESKLSMQTSPS-----PVQMTV : 106
CsAGO2/3e : TRIVYREALNESSEDLNLPFWQLEGTPTLPAFGCLGKYARGQSLLNKLETCPFNIPDFQILEQPPASSL : 267

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*      300      *      320      *      340      *      360
CsAGO2/3f : PR-TKENNIVLVRPDPKCGTHSIQSPKLVNHFVPMFNAKTTIHYIYDIDKEEVPKNSRPAK---IQKSHLRM : 262
CsAGO2/3d : KI-SSGNLLVVRPDPICGTLAIQSPKSVNHFVPRFNEKTTIHYDIDIKEDVSSKSRPAR---VSKSVLSM : 121
CsAGO7 : VMGTPQSLVVRPDPSCGVEGAVIS-FLNHFLLVQDFDPSHRTFHYDVTITPEVAS---SKVAFR : 203
CsAGO10a : GFPSSSKLSCAHPRGFC--QLGTCVVKANHFFAEL-PDKDLHQYDVTITPEVAS---RAVNAI : 186
CsAGO2/3a : LG-SSGKVVEMKRPDDCGTLAFRNTRFLANHFVVKFNQPSIMHYDVIDIKENMPPGSRRAKRPISKSDLRL : 259
CsAGO2/3b : PGGSSSKLIVPKPDDCGTLAFRNTRFLANHFVVKFNQPSIMHYDVIDIKENMPPGSRRAKRPISKSDLRL : 277
CsAGO6 : -----IISRRGFC--SAGRRIISLTHNHEKVVV-KSPNEIFYQYSSVSSSEDKRVEEN---KGIGRRI : 89
CsAGO4c : -----KAVRVPMAARRGVC--SKGRIPILTNHKEKVVN-TNVS-----VSYEDGRPVVDG---KGAGRRV : 93
CsAGO4a : -----EPKRVPMARRGVC--SKGRIPILTNHKEKVVN-TNVDGHHFHYSSVSYEDGRPVVDG---KGIGRRI : 101
CsAGO4b : -----KVMRVPMTARRGVC--SKGRIPILTNHKEKVVN-TNVDGHHFHYSSVSYEDGRPVVDG---KGVGRKV : 161
CsAGO2/3c : PE-SSDKRIVLIRPDRCGTLAVRSTRFLANHFVRFNPESTIMHYNDIKENMPPGSRRAKRPISKSDLRL : 193
CsAGO10b : GFPSSSKLSFAPRPGVC--QLGTCVVKANHFFAEL-PDKDLHQYDVTITPEVAS---RNVNAI : 176
CsAGO10c : --PPSNKSLVLRPFGVC--QLGTCVVKANHFFAEL-SEGDLTQYSVKILPEVNS-----TILNKAI : 129
CsAGO1 : PAPPSSKSMRFLRPGRC--SSGTCTVVKANHFFAEL-PDKDLHQYDVTITPEVAS---RGVNAI : 345
CsAGO5c : PP-LSTKSLRFPARPGVC--TVGRCTVVKANHFLLVDV-ADRDLLHYDVTITPEVAS---KVVCRRI : 260
CsAGO5a : PPPASKAVRFPARPGVC--TAGRCVVRANHFVMSV-----ITPEVTS-----KLLHREI : 149
CsAGO5b : LP-SSSKSLRFPARPGVC--TIGRCVVRANHFLLVDV-ANKDLLHYDVTITPEVAS---KVVCRRI : 165
CsAGO2/3e : PR-TKENNIVLVRPDPKCGTHSIQSPKLVNHFVPMFNAKTTIHYIYDIDKEEVPKNSRPAK---IQKSHLRM : 336

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Rp G 6 NHF v 6

CsAGO2/3f : **T**KDK**L**FSD**DP**SQ**F**PL**S**ST**A**Y**D**CG**D**KN**L**F**S**AV**E**LE**T**E-----**K**K**K**F**S**D**G**G**E**G**M**K----- : 311
CsAGO2/3d : **V**KDK**L**FSD**DP**QA**F**PL**S**RT**A**Y**D**CG**R**KN**L**F**S**AV**P**LE**T**G-----**T**K**V**D**F**S**G**E**D**DM**K**S----- : 170
CsAGO7 : **I**KQ**L**VE**D**NS**V**W**S**GA**L**P**V**Y**D**GR**K**NS**V**PM**E**FQ**S**DR**L**EFF**I**CL**P**IP**S**SK**L**I**S**PR**S**VD**S**Q----- : 264
CsAGO10a : **M**AE**L**V**K**LY**K**ES**D**IG**K**RL**P**A**Y**D**G**R**K**NS**L**Y**T**AG**E**LP**F**AW**K**-----**F**NI**K**L**V**DE**E**D**G**----- : 235
CsAGO2/3a : **I**TDK**L**FSD**DP**TR**F**PE**L**IST**Y**D**G**E**K**NI**F**SA**V**PL**T**G-----**T**F**V**EL**S**GG**E**D**T**AP----- : 308
CsAGO2/3b : **I**TDK**L**FSD**DP**TR**F**PE**L**IST**Y**D**G**E**K**NI**F**SA**V**PL**T**G-----**T**F**V**EL**S**GG**E**D**T**AP----- : 326
CsAGO6 : **I**DK**L**Y**Q**Y**I**-**S**SE**L**AG**K**K**F**A**Y**D**E**CK**S**L**T**Y**T**CG**L**P**L**Q**N**IS-----**E**FT**V**LE**S**FA**K**-----**R**GS**P**PH : 143
CsAGO4c : **E**RV**H**E**H**E**Y**-**D**TE**L**AG**K**D**F**A**Y**D**E**CK**S**L**T**IC**L**P**L**RN**K**L-----**E**FT**V**LE**D**V**S**-----**N**R**N**NG**R**SP**G** : 150
CsAGO4a : **I**DK**V**H**E**H**E**Y**-E**SE**L**AG**K**D**F**A**Y**D**E**CK**S**L**T**Y**T**CG**L**P**L**RN**K**M-----**E**FT**V**LE**D**V**S**PK**S**F**G**S**K**T**N**G**S**GS**P**GG : 163
CsAGO4b : **I**DR**V**H**E**H**E**Y**-D**TE**L**AG**K**D**F**A**Y**D**E**CK**S**L**T**Y**T**CG**L**P**L**RN**K**L-----**E**FT**V**LE**D**IS**S**-----**N**R**N**NG**R**SP**G** : 218
CsAGO2/3c : **T**RE**K**L**F**S**D**DP**TR**F**PE**Q**S**A**Y**D**G**E**K**NI**F**S**A**MP**L**PE**G**-----**N**S**V**V**L**S**G**G**E**D**V**AS----- : 242
CsAGO10b : **M**AE**L**V**K**LY**K**ES**D**IG**K**RL**P**A**Y**D**G**R**K**NS**L**Y**T**AG**E**LP**F**AW**K**-----**F**NI**K**L**V**DE**E**D**G**----- : 225
CsAGO10c : **M**AQ**L**V**K**L**H**R**D**T**D**L**G**R**M**L**P**V**Y**D**G**R**G**A**L**Y**T**AG**L**M**P**FT**L**K-----**K**F**T**I**L**AD**G**DE**S**----- : 178
CsAGO1 : **M**EQ**L**V**K**MY**R**ES**H**L**G**K**R**L**P**A**Y**D**G**R**K**NS**L**Y**T**AG**L**P**L**FT**S**K-----**E**F**K**T**I**L**D**E**D**D**G**----- : 394
CsAGO5c : **V**NAL**I**A**Y**Q**E**S**H**L**G**K**R**C**P**A**Y**D**G**R**K**NS**L**Y**T**AG**L**P**L**F**V**S**Q**-----**D**F**V**K**L**VER**E**T----- : 308
CsAGO5a : **I**N**K**L**V**E**L**Y**R**ES**H**L**G**K**R**L**A**Y**D**GR**K**NS**L**Y**T**AG**L**P**L**F**S**SK-----**D**E**V**I**K**L**V**D**Q**D**R**----- : 197
CsAGO5b : **I**SEL**I**A**Y**R**S**ES**H**L**G**K**R**L**A**Y**D**GR**K**NS**L**Y**T**AG**L**P**L**F**I**SK-----**D**E**V**I**K**L**V**D**K**Y**D**----- : 213
CsAGO2/3e : **T**KDK**L**FSD**DP**SQ**F**PL**S**ST**A**Y**D**CG**D**KN**L**F**S**AV**E**LE**T**E-----**K**K**K**F**S**D**G**E**G**M**K**----- : 385

6 aYDG 653 p 1

CsAGO2/3f : -----**V**S**I**V**I**T**I**E**V**K**K**L**R**F**G**K**D****V**Y**S**G-----**E**IM**S**I**F**RD**I**L**G****M**D**L**V**K**R**N**P**S**R**E**-**R**I : 361
CsAGO2/3d : -----**S**S**T**V**T**I**H**V**N**E**L**E**L**G**K**L**K**E**M**S**G**-----**K**V**L**S**T**PR**D**V**L****G**M**D**L**V**M**K**R**N**P**S**R**H**-**R**I : 220
CsAGO7 : -----**E**M**H**P**Q**L**K**L**R**I**N**I**K**L**R**I**G**F**F**Q**S**L**R**E**T**Q**Q**G**L**A**L**N**D**V**S**V**T**A**H**E**S**I**G**V**I**A**Y**L**Q**K**R**L**E**F**L**C**D**L**S**Q**R** : 323
CsAGO10a : -----**T**NG**P**K**R**V**R**E**K**V**V**I**F**A**R**A**N**L**H**L**G**Q**F**TA**G**-----**K**R**A**D**A**F**O**A**L****O**L**D**I**V**I**R**L**A**T**K**R**-**Y**C** : 292
CsAGO2/3a : -----**R**S**M**R**F**A**E**L**V**N**E**L**K**L**S**K**L**N**A**V**R**G-----**M**L**S**Y**V**R**D**V**F****G**M**D**L**V**M**K****N**P**S**R**H**-**M**L : 358
CsAGO2/3b : -----**R**S**M**R**F**A**E**L**V**N**E**L**K**L**S**K**L**N**D**V**R**G-----**M**L**S**Y**V**R**I**F**O****G**M**D**L**V**M**K****N**P**S**R**H**-**M**N : 376
CsAGO6 : **N**G**S**P**S**E**S**-**K**R**S**K**R**F**Q**S**K**S**E**V**N**A**K**I**P**L**K**S**L**A**L**Q**G**-----**S**E**V**E**N**I**D**A**L**R**V**L**D**I**L**R**O**H**A**A**K**Q**G**C**L** : 211
CsAGO4c : --**S**P**N**G**N**D**R**K**R**Q**R**R**P**Y**Q**S**K**T**S**V**E**I**S**F**A**A**K**I**P**Q**A**I**A**N**A**R**G**-----**H**E**S**E**N**S**O**A**L**R**V**L**D**I**L**R**O**H**A**A**K**Q**G**C**L** : 217
CsAGO4a : --**S**P**N**G**N**E**S**D**R**K**L**R**R**A**F**Q**S**K**T****S**V**E**I**S**F**A**A**K**I**P**Q**A**I**A**N**A**R**G**-----**Q**E**S**E**N**S**O**A**L**R**V**L**D**I**L**R**O**H**A**A**K**Q**G**C**L** : 232
CsAGO4b : --**S**P**N**E**N**D**R**K**R**Q**R**R**P**Y**Q**S**K**T**S**V**E**I**S**F**A**A**K**I**P**Q**A**I**A**N**A**R**G**-----**Q**E**S**E**N**S**O**A**L**R**V**L**D**I**L**R**O**H**A**A**K**Q**G**C**L** : 285
CsAGO2/3c : -----**R**S**M**R**F**A**E**L**V**N**E**L**K**L**S**K**L**N**D**V**R**G-----**M**L**S**Y**I**F**R**D**I**L**G****M**D**L**V**M**K**N**P**S**Q**H**-**R**I : 292
CsAGO10b : -----**I**NG**P**K**R**E**R**V**K**V**I**K**F**A**R**A**N**L**H**L**G**Q**F**TA**G**-----**K**R**A**D**A**F**O**A**L****O**L**D**I**V**I**R**L**A**T**K**R**-**Y**C** : 282
CsAGO10c : -----**I**G**M**A**K**-**E**R**E****V**E**T**I**K**F**G**A**H**A**S**M**H**Q**L**R**E**L**S**G-----**K**Q**V**D**T**E**L**A**L****O**L**D**I**V**I**R**L**A**Q**R**-**Y** : 234
CsAGO1 : -----**T**G**G**A**R**R**E**R**E**R**V**I**K**L**A**A**R**A**D**L**H**L**G**L**F**Q**G**-----**R**Q**A**D**A**F**O**A**L****O**L**D**I**V**I**R**L**A**T**K**R**-**Y**C** : 451
CsAGO5c : -----**T**S**R**R**E**R**E**R**V**A**I**K**F**A**A**K**A**D**L**H**L**Q**Q**F**H**G-----**R**Q**L**D**V**F**O**R**T**I**O**V**L**D**V**I**R**L**A**T**K**R**-**Y**C** : 363
CsAGO5a : -----**G**A**R**K**D**R**E**R**V**A**I**K**F**A**A**K**P**D**I**H**H**Q**E**F**R**G-----**R**Q**L**D**T**F**O**R**T**I**O**V**L**D**V**I**R**L**A**T**K**R**-**Y**C** : 252
CsAGO5b : -----**Q**T**R**R**E**L**E**K**A**I**K**A**A**K**D**I**H**L**H**Q**E**F**R**G-----**R**Q**D**A**F**O**A**L**O**L**D**I**V**I**R**L**A**T**K**R**-**Y**T** : 268
CsAGO2/3e : -----**V**S**I**V**I**T**I**E**V**K**K**L**R**F**G**K**D****V**Y**S**G-----**E**IM**S**I**F**RD**I**L**G****M**D**L**V**K**R**N**P**S**R**E**-**R**I : 435

5 I 6 6g p 6D66 4

CsAGO2/3f : **F**V**G**R**S**F**Y**P**T**T**S**N**K**D**D****L**D**G**C**V**T**A**S**K**G**F**Q**H**S**L**K**P**T**S**Q**G**L**A**L**C**L**D**Y**S**V**L**A**H**K**R**K**L**P**V**I**D**F**L**KE**H**V**G**F**K**Q**V**N**D**M : 433
CsAGO2/3d : **C**A**G**R**G**F**Y**S**A**T**S**--**A**D**D****I**G**V**C**I**T**A**S**K**G**F**Q**H**S**L**K**P**T**S**Q**G**L**A**L**C**L**D**Y**S**V**L**A**H**K**R**K**L**P**V**I**D**F**L**KE**H**V**R**G**F**R**G**V**N**D**V** : 290
CsAGO7 : **F**V**G**R**S**F**L**V**S**S**M**G**G**A**K****I**D**G**G**A**I**G**L**R**I**F**F**Q**S**L**R**E**T**Q**Q**G**L**A**L**N**D**V**S**V**T**A**H**E**S**I**G**V**I**A**Y**L**Q**K**R**L**E**F**L**C**D**L**S**Q**R : 395
CsAGO10a : **F**V**G**R**S**F**S**P**D**I**R**K**P**Q**R****F**D**G**L**E**S**W**C**G**F**Y**Q**S**I**R**E**T**Q**Q**M**G**L**S**L**N**I**D**M**S**A**A**A**I**E**A**L**P**V**I**D**F**V**A**Q**L**-----**L**G**K**D**V** : 359
CsAGO2/3a : **S**V**G**R**S**F**S**K**E**F**R**P**N**D**I**D**G**Y**I**A**A**F**R**G**S**Q**S**L**K**A**T**A**G**L**A**L**C**L**D**S**S**V**L**A**H**K**R**K**L**P**V**I**D**F**L**ME**-**Q**Q**F**G**-**L**N**D**V : 445
CsAGO2/3b : **S**V**G**R**S**F**S**K**E**F**R**P**N**D**I**D**G**Y**I**A**A**F**R**G**S**Q**S**L**K**A**T**A**G**L**A**L**C**L**D**S**S**V**L**A**H**K**R**K**L**P**V**I**D**F**L**ME**-**Q**Q**F**G**-**L**N**D**V : 445
CsAGO6 : **L**V**R**Q**S**F**H**D**S**R**N**F**A**D**V**G**G**V**L**G**C**R**G**H**S**F**R**T**Q**G**G**L**S**L**N**I**D**V**S**T**M**I**I****O**P**G**V**D**F**L**I**A**N-----**Q**N**V**K**D** : 284
CsAGO4c : **L**V**R**Q**S**F**H**D**S**R**N**F**A**D**V**G**G**V**L**G**C**R**G**H**S**F**R**T**Q**G**G**L**S**L**N**I**D**V**S**T**M**I**I****O**P**G**V**D**F**L**I**A**N-----**Q**N**V**K**D** : 282
CsAGO4a : **L**V**R**Q**S**F**H**D**S**R**N**F**A**D**V**G**G**V**L**G**C**R**G**H**S**F**R**T**Q**G**G**L**S**L**N**I**D**V**S**T**M**I**I****O**P**G**V**D**F**L**I**A**N-----**Q**N**V**K**D** : 352
CsAGO2/3c : **S**V**G**R**S**F**S**K**E**F**R**P**R**D**I**D**G**Y**I**A**A**Y**R**G**F**Q**H**S**L**K**P**T**S**Q**G**L**A**L**C**L**D**Y**S**V**L**A**H**K**R**K**L**P**V**I**D**F**L**V**E**N**V**E**G**F**R**-**V**N**D**M : 363
CsAGO10b : **F**V**G**R**S**F**S**P**D**I**R**K**P**Q**R****F**D**G**L**E**S**W**C**G**F**Y**Q**S**I**R**E**T**Q**Q**M**G**L**S**L**N**I**D**M**S**A**A**A**I**E**A**L**P**V**I**D**F**V**A**Q**L**-----**L**G**K**D**V** : 349
CsAGO10c : **S**V**G**R**F**F**S**P**N**L**R**P**Q****F****I****N**G**L**Q**S**W**R**G**F**Y**Q**S**I**K**P**T**Q**M**G**L**S**L**N**I**D**M**S**A**A**A**I**E**A**L**P**V**I**D**F**V**A**Q**L**-----**L**G**K**D**V** : 301
CsAGO1 : **F**V**G**R**S**F**S**P**D**I**R**K**P**Q**R****F**D**G**L**E**S**W**C**G**F**Y**Q**S**I**R**E**T**Q**Q**M**G**L**S**L**N**I**D**M**S**A**A**A**I**E**A**L**P**V**I**D**F**V**A**Q**L**-----**L**T**R**D**V** : 518
CsAGO5c : **V**V**G**R**S**F**S**P**Q**L**G**D**T**H**G**D**G****I**E**Y**W**K**G**Y**O**S**L**R**E**T**Q**Q**M**G**L**S**L**N**I**D**I**S**A**R**A**F**Y**F**V**L**V**S**D**F**V**A**T**Y**-----**C**N**I**R**D** : 430
CsAGO5a : **V**V**G**R**S**F**S**P**S**P**G**-**V**G**D****I**G**N**G**F**Q**Y**W**K**G**F**Y**Q**S**L**R**E**I**Q**M**G**L**S**L**N**I**D**M**S**A**R**A**F**Y**F**V**L**V**S**D**F**V**A**K**Y**-----**F**N**V**K**D** : 318
CsAGO5b : **V**V**G**R**S**F**S**P**I**L**G**E**V**G**D****I**D**G**L**Q**Y**W**K**G**F**Y**Q**S**L**R**E**T**Q**Q**M**G**L**S**L**N**I**D**M**S**A**R**A**F**Y**F**V**L**V**S**D**F**V**A**K**Y**-----**F**N**V**R**D** : 335
CsAGO2/3e : **F**V**G**R**S**F**Y**P**T**T**S**N**K**D**D****L**D**G**C**V**T**A**S**K**G**F**Q**H**S**L**K**P**T**S**Q**G**L**A**L**C**L**D**Y**S**V**L**A**H**K**R**K**L**P**V**I**D**F**L**KE**H**V**G**F**K**Q**V**N**D**M : 507

vgrsf5 6g G s t gl l D s a p6 d56

CsAGO2/3f : **R**R--**L**R**D**V**I**N-----**A**L**T**L**K**L**V**R**V**H**R**V**T**N**Q**Y**I**I**V**L**T**D**Q**N**T**R--**N**I**S**F**D**V**E**D**R**E**E**K**A**P**P**K**R****S**L**V**E**Y**R**G** : 497
CsAGO2/3d : **T**R--**L**R**D**V**I**N-----**A**L**E**L**K**L**V**V**N**H**R**I**T**K**Q**Y**I**T**A**G**L**T**D**R**S**T--**D**L**S**F**D**V**N**D**E**P**E**G**A**P**P**R**R****S**L**V**E**Y**R**G** : 354
CsAGO7 : **K**T**R**G**L**A**G**E**R**E**V**E**K**A**L**K**N**I**R**V**F**C**H**E**T**V**Q**R**Y**R**V**S**L**T**E**A**T**E--**N**L**W**F**D**H**S**G-----**R**T**L**R**V**N**Y**R**K**D : 459
CsAGO10a : **I**S**R**T**S**D**S****D**R**V**K**I**K**A**L**R**G**V**K**V**E**V**T**H**R**G**H**V**R**R**K**Y**R**Q**L**T**S**Q**P-----**T**R**E**L**V**F**P**V**D**D**S**T**M**K**S**V**Y**E**Y**Q**E** : 425
CsAGO2/3a : **R**T--**S**R**R**E**V**M**K**M**V**H**L**K**L**K**V**H**V**T**H**L**T**S**Q**Y**T**I**A**G**S**D**Q**N**T**R--**D**I**F**T**L**E**D**R**E**G**E**N**P**P**R**E**L****G**L**V**E**Y**R**G** : 495
CsAGO2/3b : **R**T--**S**R**R**E**V**M**E**M**V**H**L**K**L**K**V**H**V**T**H**L**T**S**Q**Y**T**I**A**G**S**D**Q**N**T**R--**D**I**F**T**L**E**D**R**E**G**E**N**P**P**R**E**L****G**L**V**E**Y**R**G** : 513
CsAGO6 : **P**F--**N**I**L**W**A**K**A**K**L**K**N**R**V**K**T**R**S**N**M**E**F****I**I**C**SE**K**P**C**Q**O**F**S**L**K**V**R**N**A**D**G**G**Y**G**A**E**L**I**D**V**I**D**V**Y**F**T**K** : 346
CsAGO4c : **P**F--**S**I**D**W**A**K-----**Q**K**G**D**D**D**E**G**V**Q**T**L**V**D**V**I**D**V**Y**F**V**N : 315
CsAGO4a : **P**F--**Q**V**D**W**A**K**A**K**L**K**N**L**R**I**K**V**I**P**S**N**M**E**Y**R**I**I**G**SE**S**P**C**K**E**Q**M**F**S**L**K**T**R**G**K**D--**E**N**E**S**V**D**V**I**D**V**Y**F**V**N : 348
CsAGO4b : **P**F--**S**I**D**W**A**K**A**K**L**K**N**L**R**V**K**T**N**P**S**T**E**Y**K**I**T**GSE**K**P**C**K**E**Q**M**F**S**L**K**Q**K**G**D**D**D**E**G**V**Q**T**L**V**D**V**Y**F**V**N : 420
CsAGO2/3c : **K**R--**S**R**R**D**V**M**R**-----**A**L**G**L**K**L**V**H**V**H**R**V**T**N**Q**Y**I**V**A**G**L**T**N**Q**A**R--**D**I**F**T**L**E**D**P**E**G**E**N**P**P**R**E**L****G**L**V**E**Y**R**G** : 427
CsAGO10b : **I**S**R**T**S**D**S****D**R**V**K**I**K**A**L**R**G**V**K**V**E**V**T**H**R**G**N**M**R**R**K**Y**R**Q**L**T**S**Q**P-----**T**R**E**L**V**F**P**V**D**D**S**T**M**K**S**V**Y**E**Y**Q**E** : 415
CsAGO10c : **Y**S**R**P**S**D**A****D**R**V**K**I**K**A**L**R**G**I**K**V**E**V**T**H**R**G**N**M**R**R**K**Y**R**Q**L**T**S**Q**P-----**T**R**E**L**I**F**P**V**D**E**E**K**N**M**K**S**V**Y**E**Y**Q**E : 367
CsAGO1 : **S**S**R**P**S**D**A****D**R**V**K**I**K**A**L**R**G**V**K**V**E**V**T**H**R**G**N**M**R**R**K**Y**R**Q**L**T**S**Q**P-----**T**R**E**L**T**F**P**V**D**E**R**G**T**M**K**S**V**Y**E**Y**Q**E : 584
CsAGO5c : **L**S**R**P**S**D**Q****D**R**V**K**I**K**A**L**R**M**V**K**V**L**H**S**E**D**V**K**R**--**K**I**S**G**V**S**V**R**P**-----**T**S**Q**L**T**F**P**D**S**G**D**T**Q**T**S**V**Y**E**Y**Q**E** : 494
CsAGO5a : **L**T**R**P**S**D**Q****D**R**V**K**R**A**L**R**I**K**V**E**L**A**H**K**K**H**Q**C**R**-**R**I**S**G**L**S**V**R**P**-----**T**N**Q**L**T**F**P**L**D**T**G**E**K**M**S**V**Y**E**Y**Q**E** : 383
CsAGO5b : **L**T**R**P**S**D**Q****D**R**I**K**V**R**A**L**R**I**R**V**E**L**H**R**E**D**G**K**R**Y**-**K**I**S**G**V**S**A**Q**P-----**T**S**Q**L**T**F**A**R**D**D**T**D**A**K**I**S**V**I**Q**Y**R**E : 400
CsAGO2/3e : **R**R--**L**R**D**V**I**N-----**A**L**T**L**K**L**V**R**V**H**R**V**T**N**Q**Y**I**I**V**L**T**D**Q**N**T**R--**N**I**S**F**D**V**E**D**R**E**E**K**A**P**P**K**R****S**L**V**E**Y**R**G** : 571

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CsAGO2/3f : **K**N**K**E**K**H**-**K**D**I**E****C**L**D**L**G**K**N**N**R**I**N**V**M**P**E**F**C**I**L**V**E**G**Q**R**F**P**R**E**H**L**S**R**D**G**T**I**L**K**N**M**S**L**V**P**K**R**M**N**T**I**C**E**M**Q : 568
CsAGO2/3d : **K**Y**G**K**E**L**M**-**K**D**I**E**S**L**D**L**G**K**N**R**I**N**V**M**P**E**F**C**I**L**V**E**G**Q**R**F**P**K**E**N**L**D**R**A**K**L**K**M**S**L**I**R**A**V**R**R**K**I**C**E**M**Q : 425
CsAGO7 : **H**Y**N**D**Y**Q**F**-**R**N**L**E**F**L**O**I**S**--**S**P**C**H**L**P**E**M**E**L**C**M**I**C**E**Q**K**F**L**G**-**K**L**S**D**D**K**A**K**L**K**M**S**R**F**R**A**K**I**C**E**M**Q** : 528
CsAGO10a : **M**G


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CsAG02/3f : CCLFNHANNAN-DRYFANLAKLNKALKLGSNVEIEPILP----RFEFEGHVMFVGDVNHHPGARNSTCPSI : 808
CsAG02/3d : CCLSNHAYEAK-DOYLANLAKLNKALKLGSNVEINQRILP----RFDGEGHVMFVGDVNHHPAARNSTCPSM : 660
CsAG07 : CCLYPNLGLKLS-SQFLANLAKLNKALKLGSTVAIYNLSLPSQIFRLFQADDVFIIMGADVTHHPHLPDDFPSV : 770
CsAG010a : CCLTKHVFRIS-KOYLANVSLKINVRMGRNNTVLDALISCKTIF--LVSDIPTIIFGADVTHHPENEDSSPSI : 731
CsAG02/3a : CCLVGIANKGK-DQDLANLAKLNKALKLGSNVEINQPLP----GFEGDEHVMFVGDVNHHPKAFNASCPSI : 807
CsAG02/3b : CCLVGIANKGK-DQDLANLAKLNKALKLGSNVEINQMLP----GFEGDEHVMFVGDVNHHPKAFNASCPSI : 825
CsAG06 : CISP---TRIN-DOYLVNVLKLNKALKLGSTNSLAIIEHSAVIE--LTKDPTIILGMDVSHGSPQRSDIPSI : 643
CsAG04c : CIAP---TRVN-DOYLVNVLKLNKALKLGSLNSMLAVEHAPSIF--LVSKVPTIILGMDVSHGSPQOSDIPSI : 594
CsAG04a : CIAP---TRVN-DOYLVNVLKLNKALKLGSLNSMLSIEFARNIF--VVSNNPTIILGMDVSHGSPQHSVDPSI : 649
CsAG04b : CIAP---TRVN-DOYLVNVLKLNKALKLGSLNSMLSVEHSPSIF--LVSKVPTIILGMDVSHGSPQOSDIPSI : 681
CsAG02/3c : CCLVGNANKGN-DOYLANLAKLNKALKLGSLNSMLQSPF-----SVPS : 714
CsAG010b : CCLTKHVFRIT-KOYLANVSLKINVRMGRNNTVLDALISCKTIF--LVSDIPTIIFGADVTHHPENEDSSPSI : 721
CsAG010c : CCLTKHVLRIS-KOYLANVSLKINVRMGRNNTVLDALISCKTIF--LVSDIPTIIFGADVTHHPESGEDCPSI : 673
CsAG01 : CCLTKHVFRMS-KOYLANVSLKINVRMGRNNTVLDALISCKTIF--LVSDIPTIIFGADVTHHPESGEDCPSI : 892
CsAG05c : CCLTKHVFRMS-KOYLANVSLKINVRMGRNNTVLDALISCKTIF--LVSDIPTIIFGADVTHHPESGEDCPSI : 796
CsAG05a : CCLTKHVFRMS-KOYLANVSLKINVRMGRNNTVLDALISCKTIF--LVSDIPTIIFGADVTHHPESGEDCPSI : 876
CsAG05b : CCLTKHVFRMS-KOYLANVSLKINVRMGRNNTVLDALISCKTIF--LVSDIPTIIFGADVTHHPESGEDCPSI : 705
CsAG02/3e : CCLFNHANNAN-DRYFANLAKLNKALKLGSNVEIEPILP----RFEFEGHVMFVGDVNHHPGARNSTCPSI : 882
Cc q 1 N6 6K6N K Gg n L g dv h Ps

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CsAG02/3f : AAVVATVNWPAANRYAARVCPQYHRSEKTLNFGTMCLELIQAYARIN----- : 855
CsAG02/3d : AAVVATLWPAANRYAARVCPQYHRKENTLNFGVMCELIIRIYAQIN----- : 707
CsAG07 : AAVVGSVNWPAANRYVSRMRSCTRHOETIEDLTAMVGEILDDFYEQE----- : 817
CsAG010a : AAVVASQDWPEVTKYAGLVCAEHRROELIQDLYKTWHDVVRGTFVSGG-----MIRDLVLRKATG----- : 792
CsAG02/3a : AAVVASVNWPAANRYVARICPEHRKEKIVNFGAICLDLVNTYAKLN----- : 854
CsAG02/3b : AAVVASVNWPAANRYVARICPEHRKEKIVNFGPMCLDLVNTYAKLN----- : 872
CsAG06 : AAVVGSRSWPLISRYRAAARTSSVHVESLFLKPLANGKDDGM-----RELLVDFEYQTS----- : 699
CsAG04c : AAVVSSRHWPILSRYRASVRTSPKVENIDSLYKRVSDTEDEGIFSKT---LSFNRELLLDLYVVS----- : 657
CsAG04a : AAVVSSRHWPILSRYRASVRTSPKVENIDSLYKRVSDTEDEGIFSKT---LSFNRELLLDLYVVS----- : 721
CsAG04b : AAVVSSRWQPLISRYRASVRTSPKVENIDSLYKRVSESEDEGIM-----RELLLEFYVT----- : 736
CsAG02/3c : SAITPAVSLNESYITCKESKCKDKAAIQ-----SDKTLK----- : 751
CsAG010b : AAVVASQDWPEVTKYAGLVCAEHRROELIQDLYKTWHDVVRGTFVSGG-----MIRDLVLRKATG----- : 782
CsAG010c : AAVVASQDWPEVTKYAGLVCAEHRROELIQDLYKTWHDVVRGTFVSGG-----MIRDLVLRKATG----- : 734
CsAG01 : AAVVASQDWPEVTKYAGLVCAEHRROELIQDLYKTWHDVVRGTFVSGG-----MIRDLVLRKATG----- : 953
CsAG05c : AAVVASMDWPEVTKYRGLVSAQPHREELINDLYKTIQDPQRTVHSG-----MIRRELLIAFRRTSTG----- : 857
CsAG05a : AAVVASMDWPEVTKYRGLVSAQPHREELINDLYKTIQDPQRTVHSG-----MIRRELLIAFRRTSTG----- : 937
CsAG05b : AAVVASMDWPEVTKYRGLVSAQPHREELINDLYKTIQDPQRTVHSG-----MIRRELLIAFRRTSTG----- : 766
CsAG02/3e : AAVVATVNWPAANRYAARVCPQYHRSEKTLNFGTMCLELIQAYARIN----- : 929
aA6v wp y Q e 6

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CsAG02/3f : -----KVKPQRIVVF--RDGVSEGFQFQVLLYELDAIR : 886
CsAG02/3d : -----KVKPARIVVF--RDGVSEGFQFQVLLYELDLK : 738
CsAG07 : -----TKLPKRIIFV--RDGVSEGFQFQVLLYELDAIR : 848
CsAG010a : -----KVKPQRIVVF--RDGVSEGFQFQVLLYELDAIR : 822
CsAG02/3a : -----KVKPQRIVVF--RDGVSEGFQFQVLLYELDLK : 885
CsAG02/3b : -----KVKPQRIVVF--RDGVSEGFQFQVLLYELDLK : 903
CsAG06 : -----NG-----RKPQAIIILF--RDGVSEGFQFQVLLYELDAIR : 731
CsAG04c : -----SG-----KRPQAIIILF--RDGVSEGFQFQVLLYELDAIR : 690
CsAG04a : VVVRDGGFIMALHPCCGQAALACSHIERCCAIEPVFRILRIETNPKNLHYGMDGVSEGFQFQVLLYELDAIR : 793
CsAG04b : -----SG-----KRPQAIIILF--RDGVSEGFQFQVLLYELDAIR : 769
CsAG02/3c : -----KVP-----KVP----- : 754
CsAG010b : -----KQPRIIFV--RDGVSEGFQFQVLLYELDAIR : 812
CsAG010c : -----KQPRIIFV--RDGVSEGFQFQVLLYELDAIR : 764
CsAG01 : -----KQPRIIFV--RDGVSEGFQFQVLLYELDAIR : 983
CsAG05c : -----KQPRIIFV--RDGVSEGFQFQVLLYELDAIR : 887
CsAG05a : -----KQPRIIFV--RDGVSEGFQFQVLLYELDAIR : 967
CsAG05b : -----KQPRIIFV--RDGVSEGFQFQVLLYELDAIR : 796
CsAG02/3e : -----KVKPQRIVVF--RDGVSEGFQFQVLLYELDLK : 960
kp rdgvse qf vl e

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CsAG02/3f : KAIYEE--HYRPTITLVAQKRHHQTRLEP-----EKMKDGGSTGNVPPGCTVVDKKTITHPFFDFDYLCSH : 948
CsAG02/3d : MAIYEE--HYRPTITLVAQKRHHQTRLEP-----ESMKDGGSPDNVPPGCTVVDKKTITHPFFDFDYLCSH : 800
CsAG07 : AACSRFP--SYKPPITFAVQKRHHQTRLEPNETQTHQSSSTRDQFLDENIPPGCTVVDKKTITHPFFDFDYLCSH : 919
CsAG010a : KACASLEPNYQFPVTFIVVQKRHHQTRLEFANN-----HRRSSTDKSGNIVPCTVVDKKTITHPFFDFDYLCSH : 889
CsAG02/3a : NAIYEG--NYRPTITLVAQKRHHQTRLEP-----ENERDGGASGNVPPGCTVVDKKTITHPFFDFDYLCSH : 947
CsAG02/3b : NAIYEG--NYRPTITLVAQKRHHQTRLEP-----ENERDGGASGNVPPGCTVVDKKTITHPFFDFDYLCSH : 965
CsAG06 : KAYQHIGEATIPKFTVIVAQKNHHTKFLPQSG----APENVPPGLFLCSI--CTVVDKRVVHPRNDFDFYMGCAQ : 797
CsAG04c : ESKFLDEKVSPEKFTVIVAQKNHHTKFLPQSG----SPNVNPP-----CTVIDNKVCHPNRDFDFYMGCAH : 749
CsAG04a : EACKFLDENWSPKFTVIVAQKNHHTKFLPQSG----SPNVNPP-----CTVIDNKVCHPNRDFDFYMGCAH : 852
CsAG04b : EACKFLDEKVSPEKFTVIVAQKNHHTKFLPQSG----SPNVNPP-----CTVIDNKVCHPNRDFDFYMGCAH : 828
CsAG02/3c : -----APKPSKPC-----AQNF----- : 766
CsAG010b : KACASLEPNYQFPVTFIVVQKRHHQTRLEFANN-----HRRSSTDKSGNIVPCTVVDKKTITHPFFDFDYLCSH : 879
CsAG010c : KACASLEPNYQFPVTFIVVQKRHHQTRLEFANN-----HNBKTSIDKSGNIVPCTVVDKKTITHPFFDFDYLCSH : 831
CsAG01 : KACASLEPNYQFPVTFIVVQKRHHQTRLEFANN-----HRBRNAVDRSGNIVPCTVVDKKTITHPFFDFDYLCSH : 1050
CsAG05c : KACVSLSENYLPPVTFVIVVQKRHHQTRLEFPAQ----HNBRSSTDRSGNIVPCTVVDKKTITHPFFDFDYLCSH : 954
CsAG05a : KACVSLSENYLPPVTFVIVVQKRHHQTRLEFPAQ----HSBRSSTDRSGNIVPCTVVDKKTITHPFFDFDYLCSH : 1034
CsAG05b : KACVSLSEADYLPVTFVIVVQKRHHQTRLEFPAE----HGBRSSTDRSGNIVPCTVVDKKTITHPFFDFDYLCSH : 863
CsAG02/3e : KAIYEE--HYRPTITLVAQKRHHQTRLEP-----EKMKDGGSTGNVPPGCTVVDKKTITHPFFDFDYLCSH : 1022
a p t qk h t lf pGt d hp dfy c h

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CsAG02/3f : YGSLGTSRPHYHYVLDWDEHNFTSDQLQKLIYDLGFT-----FARCTKPVSLVPPVYAY : 1002
CsAG02/3d : YGSMGTSRPHYHYVLDWDEHNFTSDQLQKLIYDMCF-----FARCTKPVSLVPPVYAY : 854
CsAG07 : WGVKTSRPHYHYVLDWDEHNFTSDQLQKLIYVNCY-----FVRCTKPVSLVPPVYAY : 973
CsAG010a : AGIQTTSRPAHYHYVLDWDEHNFTADGIQSLTNNLCYT-----YARCTRSVSLVPPVYAY : 943
CsAG02/3a : YGNLGTSPKTHYVLDWDEHNFTSDQLQKLIYHLCYT-----FARCTKPVSLVPPVYAY : 1001
CsAG02/3b : YGNLGTSPKTHYVLDWDEHNFTSDQLQKLIYHLCYT-----FARCTKPVSLVPPVYAY : 1011
CsAG06 : AGMIGTSRPAHYHYVLDWDEHNFTSDQLQKLIYHLCYT-----YORSTTAISVAVPVCYAH : 851
CsAG04c : AGMIGTTRPHTHYVLDWDEHNFTSDQLQKLIYHLCYT-----YORSTTAISVAVPVCYAH : 803
CsAG04a : AGMIGTTRPHTHYVLDWDEHNFTSDQLQKLIYHLCYT-----YORSTTAISVAVPVCYAH : 906
CsAG04b : AGMIGTTRPHTHYVLDWDEHNFTSDQLQKLIYHLCYT-----YORSTTAISVAVPVCYAH : 882
CsAG02/3c : ----- : -
CsAG010b : AGIQTTSRPAHYHYVLDWDEHNFTADGIQSLTNNLCYT-----YARCTRSVSLVPPVYAY : 933
CsAG010c : AGIQTTSRPAHYHYVLDWDEHNFTADGIQSLTNNLCYT-----YARCTRSVSLVPPVYAY : 885
CsAG01 : AGIQTTSRPAHYHYVLDWDEHNFTADGIQSLTNNLCYTYVVSFNPSQLFLNHLQIYARCTRSVSLVPPVYAY : 1122
CsAG05c : AGIQ-----VNSVPPVYAY : 969
CsAG05a : AGIQTTSRPHYHYVLDWDEHNFTADALQIT-----LTNMPVYAY : 1073
CsAG05b : AGIQTTSRPHYHYVLDWDEHNFTADALQIT-----YARCTRSVSLVPPVYAY : 917
CsAG02/3e : YGSLGTSRPHYHYVLDWDEHNFTSDQLQKLIYDLGFT-----FARCTKPVSLVPPVYAY : 1076
g gt p hy l de f t d q l r t p ya

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*          1460          *          1480          *          1500          *
CsAGO2/3f : LVA YRGRMPQEVVMEVSPVSVSSSSSS---ATSTSSLVSVS---SFDKDFYKLRHD----- : 1052
CsAGO2/3d : LVA YRGRMPQEVVVMKLPSPASSSSSSCS---SSSHAMVITQOSASFDEKFKLHP----- : 908
CsAGO7 : LAA YRGRGLYLERSDSSSISPFSSRNAAST---ISRAAF-----PKATPLPKLSEN----- : 1019
CsAGO10a : LAA FRARFYLEPDMQENGSSGGNA-----GKSTRANGESG---VRLPALKEN----- : 989
CsAGO2/3a : LVA YRGRQYQEVVMEFQPPPSVSSSSSS---SSSS-----AASLNERFYALHFD----- : 1047
CsAGO2/3b : LVA YRGRQYQEVVMEFQPPPSVSSSSSS---SSS-----AASLNERFYALHLD----- : 1064
CsAGO6 : LAAQQMGQFTIKFEEFSETSSGQK-----SLTSVGSAPVPELPLRLHDN----- : 893
CsAGO4c : LAA TQMGQFMKFEDMSETSSSHG-----GVT SAGAVPVQPLPLRLQENSCACSVYSHMASSFS : 860
CsAGO4a : LAA TQISLFMKFEDMSETSSSHG-----GLTSVGGPVPPELPLRLHSN----- : 948
CsAGO4b : LAA TQVQGFMKFEDQSETSSSHG-----GMTSAGARHVIDLARVTK----- : 923
CsAGO2/3c : ----- : -
CsAGO10b : LAA FRARFYMEPDMQENGSGGGQV-----GKSTRANGDTG---VRLPALKEN----- : 978
CsAGO10c : LAA FRARFYLEPHVHENAS-----MRA TRTVNGPC---IRLPLALKEK----- : 925
CsAGO1 : LAA FRARFYMEPETSDDSGSMSSAAVGRAGMMVPGARS TRVPGANAPVRLPALKDN----- : 1179
CsAGO5c : LAA FRARFYIEGETSESESTSGG-----RATRE---RNVEVRLPLLIKDN----- : 1011
CsAGO5a : LAA FRARFYIEGDTSENESTSGG-----RNTRE---RSIEVRLPLAIKAN----- : 1115
CsAGO5b : LAA FRARFYIEGETLEAGSSGGGRG-----AQAARE---RSLEVPQLPLIKDN----- : 964
CsAGO2/3e : LVA YRGRMPQEVVMEVSPVSVSSSSSS---ATSTSSLVSVS---SFDKDFYKLRHD----- : 1126
1 a

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1520          *          1540          *          1560          *          1580
CsAGO2/3f : -----LENIIMFFV----- : 1060
CsAGO2/3d : -----LENIIMFFI----- : 916
CsAGO7 : -----VKKLMFYC----- : 1027
CsAGO10a : -----VKRVMEYC----- : 997
CsAGO2/3a : -----VKDTMEFI----- : 1055
CsAGO2/3b : -----LKDTMFFI----- : 1072
CsAGO6 : -----VAGSMFYC----- : 901
CsAGO4c : IAMSTWPQRMCSGCGYGHCLVKVRSRSHKNPGRAYYVCPPAHGTRILLDHDSGSTDVMQAEAVEDGGNGDSSGGD : 932
CsAGO4a : -----VCSSMFFC----- : 956
CsAGO4b : -----VVQLAFCVLFVLVPSDAYPLLE----- : 945
CsAGO2/3c : ----- : -
CsAGO10b : -----VKRLQOGLQFRSMI IKEQE----- : 998
CsAGO10c : -----VKNVMFYC----- : 933
CsAGO1 : -----VKRCYLAAVAFWPVAVGSPLES----- : 1200
CsAGO5c : -----VKDVMFYC----- : 1019
CsAGO5a : -----VKDVMFYC----- : 1123
CsAGO5b : -----VKAVMFYC----- : 972
CsAGO2/3e : -----LENIIMFFV----- : 1134
f

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*          1600          *          1620          *          1640          *
CsAGO2/3f : ----- : -
CsAGO2/3d : ----- : -
CsAGO7 : ----- : -
CsAGO10a : ----- : -
CsAGO2/3a : ----- : -
CsAGO2/3b : ----- : -
CsAGO6 : ----- : -
CsAGO4c : IGDSEAGGDVVEGGEDESSEVVDRAPEFRPDLGFEAIEVGGAWESGEAVAPPWPKPRRGVWVDDYPSLLLPAL : 1004
CsAGO4a : ----- : -
CsAGO4b : ----- : -
CsAGO2/3c : ----- : -
CsAGO10b : ----- : -
CsAGO10c : ----- : -
CsAGO1 : ----- : -
CsAGO5c : ----- : -
CsAGO5a : ----- : -
CsAGO5b : ----- : -
CsAGO2/3e : ----- : -

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1660          *          1680          *          1700          *          1720
CsAGO2/3f : ----- : -
CsAGO2/3d : ----- : -
CsAGO7 : ----- : -
CsAGO10a : ----- : -
CsAGO2/3a : ----- : -
CsAGO2/3b : ----- : -
CsAGO6 : ----- : -
CsAGO4c : VRLVCSSEDEVHSSASNTFNPDLQPALGDRGKESKLDADRVLKLIPQWSESVEDWNSLIEPLIDKMFAPES : 1076
CsAGO4a : ----- : -
CsAGO4b : ----- : -
CsAGO2/3c : ----- : -
CsAGO10b : ----- : -
CsAGO10c : ----- : -
CsAGO1 : ----- : -
CsAGO5c : ----- : -
CsAGO5a : ----- : -
CsAGO5b : ----- : -
CsAGO2/3e : ----- : -

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*          1740          *          1760          *          1780          *          1800
CsAGO2/3f : ----- : -
CsAGO2/3d : ----- : -
CsAGO7 : ----- : -
CsAGO10a : ----- : -
CsAGO2/3a : ----- : -
CsAGO2/3b : ----- : -
CsAGO6 : ----- : -
CsAGO4c : NAIIVRWENQNYEVDNPLKLEHSLFDRLCPLLIIRLLPLRVFNLDNSSLTYGELCKQDTGYFDIHDAESVAG : 1148
CsAGO4a : ----- : -
CsAGO4b : ----- : -
CsAGO2/3c : ----- : -
CsAGO10b : ----- : -
CsAGO10c : ----- : -
CsAGO1 : ----- : -
CsAGO5c : ----- : -
CsAGO5a : ----- : -
CsAGO5b : ----- : -
CsAGO2/3e : ----- : -

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*      1820      *      1840      *      1860      *
CsAG02/3f : ----- : -
CsAG02/3d : ----- : -
CsAG07 : ----- : -
CsAG010a : ----- : -
CsAG02/3a : ----- : -
CsAG02/3b : ----- : -
CsAG06 : ----- : -
CsAG04c : ILLNRAFNFKFEFEDVRKLSAELCGRIHPQVLFPLIASQLEHAVDARDALKIKACLFSICTSLVARGRDSLLH : 1220
CsAG04a : ----- : -
CsAG04b : ----- : -
CsAG02/3c : ----- : -
CsAG010b : ----- : -
CsAG010c : ----- : -
CsAG01 : ----- : -
CsAG05c : ----- : -
CsAG05a : ----- : -
CsAG05b : ----- : -
CsAG02/3e : ----- : -

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      1880      *      1900      *      1920      *      1940
CsAG02/3f : ----- : -
CsAG02/3d : ----- : -
CsAG07 : ----- : -
CsAG010a : ----- : -
CsAG02/3a : ----- : -
CsAG02/3b : ----- : -
CsAG06 : ----- : -
CsAG04c : PIVLKIRNTIETILLWPSSNGDEVSKAQHGICDCLALMICTELQALESFRDLTSKNTSLVRMDSRDAAMRD : 1292
CsAG04a : ----- : -
CsAG04b : ----- : -
CsAG02/3c : ----- : -
CsAG010b : ----- : -
CsAG010c : ----- : -
CsAG01 : ----- : -
CsAG05c : ----- : -
CsAG05a : ----- : -
CsAG05b : ----- : -
CsAG02/3e : ----- : -

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*      1960      *      1980      *      2000      *
CsAG02/3f : ----- : -
CsAG02/3d : ----- : -
CsAG07 : ----- : -
CsAG010a : ----- : -
CsAG02/3a : ----- : -
CsAG02/3b : ----- : -
CsAG06 : ----- : -
CsAG04c : SVRSYVIHQLTRDKDCTYEASISMSFVLCMANVLI SACQKIPDSCCKRPFAREILPRLIQSVEVMMESEYRAA : 1364
CsAG04a : ----- : -
CsAG04b : ----- : -
CsAG02/3c : ----- : -
CsAG010b : ----- : -
CsAG010c : ----- : -
CsAG01 : ----- : -
CsAG05c : ----- : -
CsAG05a : ----- : -
CsAG05b : ----- : -
CsAG02/3e : ----- : -

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      2020      *      2040      *      2060      *      2080
CsAG02/3f : ----- : -
CsAG02/3d : ----- : -
CsAG07 : ----- : -
CsAG010a : ----- : -
CsAG02/3a : ----- : -
CsAG02/3b : ----- : -
CsAG06 : ----- : -
CsAG04c : CLQVFFSAVYHLKSTILPYTSDLLRVSLKSLREGSEKEKMAGAKLMSLMASEEAIVNSIAGGLEAITVLS : 1436
CsAG04a : ----- : -
CsAG04b : ----- : -
CsAG02/3c : ----- : -
CsAG010b : ----- : -
CsAG010c : ----- : -
CsAG01 : ----- : -
CsAG05c : ----- : -
CsAG05a : ----- : -
CsAG05b : ----- : -
CsAG02/3e : ----- : -

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*      2100      *
CsAG02/3f : ----- : -
CsAG02/3d : ----- : -
CsAG07 : ----- : -
CsAG010a : ----- : -
CsAG02/3a : ----- : -
CsAG02/3b : ----- : -
CsAG06 : ----- : -
CsAG04c : SLSSSDPSPDVRQVSEKLLACLTSL : 1461
CsAG04a : ----- : -
CsAG04b : ----- : -
CsAG02/3c : ----- : -
CsAG010b : ----- : -
CsAG010c : ----- : -
CsAG01 : ----- : -
CsAG05c : ----- : -
CsAG05a : ----- : -
CsAG05b : ----- : -
CsAG02/3e : ----- : -

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*          900          *          920          *          940          *          960
CsDCL1a : TDVNNPFLQARRDVYLGNEETLGGRRREYGFGLRHGVAFCGKSHPTFYCIRGAQAFDVIASGLVFNNAF : 827
CsDCL1b : TDANNPFLQARRDVYLGNEETLGGRRREYGFGLRHGVAFCGKSHPTFYCIRGAQAFDVIASGLVFNNAI : 222
CsDCL2 : ITVFRVLLDHNHLKLIK-----ELLAFHNSNDLAVLDYVLFPCSSNQPS----LINDGSSVFPFKILGHN : 842
CsDCL3 : EFFFGLGFCGLFVRLKSSRGGKFLFQGGSLWEPSSNYMLLPLISSLNVSDPEWRNMGNSCIVSVEFLKEN : 868
CsDCL4 : EMLYLVLDLDRSEFIFSEFV-----LGGKMGFGSGSPTFVLLPVLVLCYSKSTT-----DMLKLRCLSSPFIASRQ : 735
          1          1          6          6          6          6
          *          980          *          1000          *          1020
CsDCL1a : EICGNHLDLT-----KGRUMMADSFIVGVEDVGRVITAAHSGKRFVDSVRYDMIAENSF : 881
CsDCL1b : EICGNHLDLT-----KRRUMMADSFIVGVEDVGRVITAAHSGKRFVDSVRYDMIAENSF : 276
CsDCL2 : HMTNTPNSS-----CRQRTKNGLVCSMCENSDVYVTPHND-XVIVSIAGTLD----- : 888
CsDCL3 : AWLSAEQSSGDRGNSSVHGNTSIESECKATNVHLANKSITTKNREMVVLAITHG-RIVSVLRAVDNIGAES : 941
CsDCL4 : DARDSVIPHLN-----NHFLANLGHITINVDVYVYVAPCKDTEFTISDVVPE----- : 783
          6 a1          6          6V a h          5          d

          1040          *          1060          *          1080          *          1100
CsDCL1a : PRREGYLCELEYSYADYVQRKGVGLIYKQQLIRGRVSYCKNLLSPRFHSEAHGDE-----SEALDITY : 950
CsDCL1b : PRREGYLCELEYSYADYVQRKGVGLIYKQQLIRGRVSYCKNLLSPRFHSEAHGDE-----SEALDITY : 345
CsDCL2 : LHGNS-LLEKGCITVYKIVMSKIGIDLHGRSELNLRHIFTVCNLYHRCC-----KKRESRNA : 948
CsDCL3 : FDCNSDAIYSSYSSAFYSKKGIGITLHPGQFLLLKQSHNAHLVDFRNEGASFGKLEAVINKMAVEKPRN : 1015
CsDCL4 : --KNGYSFPNDSNIHIEHTITLNDGSGSRCHRHWYETSMAVMDVYHKEWLSG----- : 834
          y5 k5g l          1          1 l

          1120          *          1140          *          1160          *          1180
CsDCL1a : YVFLPPELCEVHFPLPASFVGAQR-----LPSTMRVRESMLLAQLKDLINYPVFA-SHLEAATAAS--CQEP : 1016
CsDCL1b : YVFLPPELCEVHFPLPASFVGAQR-----LPSTMRVRESMLLAQLKDLINYPVFA-SHLEAATAAS--CQET : 411
CsDCL2 : YVFLPPELCEVFMSPRIATVYSVSPVSTMRVRESMLLAQLKDLINYPVFA-SHLEAATAAS--CQET : 1006
CsDCL3 : HVHMPPELLVSDIVPINALSPYL-----LPSLMVRESMLLAQLKDLINYPVFA-SHLEAATAAS--CQET : 1086
CsDCL4 : -----NGPNSLPSLMVRESMLLAQLKDLINYPVFA-SHLEAATAAS--CQET : 890
          v ppe1          p          6PS6M R6Es 66A L4          6          6          c e

          *          1200          *          1220          *          1240          *          12
CsDCL1a : FCYERAEELGDAYLKVVSRRFLFLKYPKHEGQLTRLQQMVSNMVLYQVYLNGLQSYIQADRFAESMAAP : 1090
CsDCL1b : FCYERAEELGDAYLKVVSRRFLFLKYPKHEGQLTRMQQMVSNMVLYQVYLNGLQSYIQADRFAESMAAP : 485
CsDCL2 : -----TSKGFIRNPEPDEKMTIVP : 1026
CsDCL3 : FSMERLEELGDSVLKYSVCHLFLKYPKHEGQLSARRSWAVCNSTLHKLGTDNLQPIRDFGABERWIA : 1160
CsDCL4 : FSLERLEVLGDALFAVCRHFLFLDHTLDEGLTRKRSNIVNNSLKLATMSKLEQPIRDFGABERWIA : 964
          f er e lgd lk v lfl          eg l r v n l          lq 5I          F P 5 pG

          60          *          1280          *          1300          *          1320
CsDCL1a : VLPFDEDIETGSSFLDDEETALGVTPGEAQDAGYEDDEMEDGELESYSSYVIVSSKTLAVVVEALIGIY : 1164
CsDCL1b : VLPFDEDIETGSSFLDNERALGVTPGEAQDAGYEDDEMEDGELESYSSYVIVSSKTLAVVVEALIGIY : 559
CsDCL2 : DQ-----SGDYALDEESLSTRKVIYGRKRKSTVAVVVEALIGIY : 1070
CsDCL3 : QRSHPGPCSCG-----DTEVPLVLIKFTEDAKVYKCCDRHMMGSKTISVVEALIGIY : 1220
CsDCL4 : RPCPVICSYT-----EAIHSPQENSLTNDANVEVRCRGRHMMHKKTISVVEALIGIY : 1021
          d          e          r 6 sKt6 DVvEALIG 5

          1340          *          1360          *          1380          *          1400
CsDCL1a : VEGEKNAANHLKWKIGIDDFDEKLELCTTPNVPESITLRSINFDALGAININIKRGSVVEALITHSRPSS : 1238
CsDCL1b : VEGEKKAANNLKWIGIDDFDEKLELCTTPNVPESITLRSINFDALGAININIKRGSVVEALITHSRPSS : 633
CsDCL2 : STGEEASLSFMDLGHVWDEVNIPYRHFVQAER-----LVNKKYFSLRVAEALVVEALIGIY : 1139
CsDCL3 : VGGELTAAQLKRWLGVDALELSVDEAIVASVASTPAAKEETLRSKGLRGLLEALVVEALIGIY : 1294
CsDCL4 : VDSFKAAAFKRWLGVDALELSVDEAIVASVASTPAAKEETLRSKGLRGLLEALVVEALIGIY : 1095
          v gG aA          6kW6G6          df          1E L          F          gIlL62A tH S

          *          1420          *          1440          *          1460          *          1480
CsDCL1a : GVS-CYQRLEVFGDVAIDLITLKHLEFITYSLDPGRLLDRAAANNENFARVAVKHKLHMLDRHSGSALEKO : 1311
CsDCL1b : GVS-CYQRLEVFGDVAIDLITLKHLEFITYSLDPGRLLDRAAANNENFARVAVKHKLHMLDRHSGSALEKO : 706
CsDCL2 : ETPCYQRLEVLGDSVLDLITLKHLEFITYSLDPGRLLDRAAANNENFARVAVKHKLHMLDRHSGSALEKO : 1213
CsDCL3 : GVCYQRLEVFLGDSVLDLITLKHLEFITYSLDPGRLLDRAAANNENFARVAVKHKLHMLDRHSGSALEKO : 1368
CsDCL4 : WGG-CYQRLEVFLGDSVLDLITLKHLEFITYSLDPGRLLDRAAANNENFARVAVKHKLHMLDRHSGSALEKO : 1168
          CYQRLE56GD VLD LIT hL5          y 6 PG LdLR a VnN          5A          Avk          lh h6 h S          L          6

          *          1500          *          1520          *          1540          *
CsDCL1a : RDFVYRQDELKSKFGFNS-----FGLGDCAPKVLGDIIVSIIAGAILDSSGR- : 1358
CsDCL1b : RDFVYRQDELKSKFGFNS-----FGLGDCAPKVLGDIIVSIIAGAILDSSGR- : 753
CsDCL2 : VATIQNFQELQSDVTTG-----WESETTFKVLGDIIVSIIAGAILDSSGR- : 1259
CsDCL3 : TEYKFTISGSQRTQP-----LQGGGLTFLGDIIVSIIAGAILDSSGR- : 1412
CsDCL4 : NKYVNFIRTTALEKGVVEGSPCKPYGYGYLNGCTCTGYAKYVCEILGNDMGTFVGDIVSIIAGAILDSSGR : 1242
          V          f          k          6GD66ES aGAI          6D3g

          1560          *          1580          *          1600          *          1620
CsDCL1a : ---DTAVFQPLHPMVTPELTPHVEVRELQERQQQAEGLEYKARRNENAVTEVEFDG---VQVGIKQPQRK : 1426
CsDCL1b : ---DTAVFQPLHPMVTPELTPHVEVRELQERQQQAEGLEYKARRNENAVTEVEFDG---VQVGIKQPQRK : 821
CsDCL2 : KEVWLSIRPLHPMVTPELTPHVEVRELQERQQQAEGLEYKARRNENAVTEVEFDG---VQVGIKQPQRK : 1333
CsDCL3 : LDEWRIEPLHPMVTPELTPHVEVRELQERQQQAEGLEYKARRNENAVTEVEFDG---VQVGIKQPQRK : 1486
CsDCL4 : LNRNWKIVLSPVDFVMSFSKFLNPKQELKLDLDFHSSKPEFPIYKKNVFFVVEAKKAKNNWITACNTINK : 1316
          p16 P663p          6 P rEL e C          e          4          6          e          6          4k

          *          1640          *          1660          *          1680          *          1700
CsDCL1a : MAQKLAARCMPLCSEGGPAHAKR-----FTFAVRVNTTDELTEECIGEPMSVYKAKSAVLLLELLNK : 1493
CsDCL1b : MAQKLAARCMPLCSEGGPAHAKR-----FTFAVRVNTTDELTEECIGEPMSVYKAKSAVLLLELLNK : 880
CsDCL2 : TKKLAARCAVLSKSEGG-----MTGACEQQNACSSNFR----- : 1367
CsDCL3 : MAQKLAARCMPLCSEGGPAHAKR-----FTFAVRVNTTDELTEECIGEPMSVYKAKSAVLLLELLNK : 1560
CsDCL4 : AQRILAAQKLYGNISMAESSEQDLDSNFAGLRSSHNVDFQRQLRVFPNSRNFAGYLLSKSLEEVKSSLK : 1390
          A          aa          6          1          k          k          k

          *          1720          *          1740          *          1760
CsDCL1a : LYP----- : 1496
CsDCL1b : LYP----- : 883
CsDCL2 : ----- : -
CsDCL3 : NPYHSDDCSSKSCDIPGAFKRRNSLGNLVVSLLEEINYLKLDGNYSLICIGMPSAKSARLRRRILFLGDRSYEFE : 1634
CsDCL4 : NEARKLIGHDEASIDVTAPDAIPLDN-----LKLQESSRQCQLKVPVHSPQEPKTFPHRIRSIETEPQPSLEAQ : 1458

          1780          *          1800          *          1820          *          1840
CsDCL1a : ----- : -
CsDCL1b : ----- : -
CsDCL2 : ----- : -
CsDCL3 : KGLADATIGRRHVVDIVERGGQVRQAIELFGA-EIKWVADQMRKASKMNTVGVFLGRVSRGQSRVKRDGRALVME : 1707
CsDCL4 : GPQSTAGGDHNLVGGSCCKSAKSRHLHECAANCKWPPSFKCKEIGPSHLKBEFIFKVSVDIEEASDVIAAGPAP : 1532

          1860
CsDCL1a : ----- : -
CsDCL1b : ----- : -
CsDCL2 : ----- : -
CsDCL3 : HRDLVRSAAHDGYRDLGKMKTSQIS- : 1733
CsDCL4 : HSRKKDAABHAAGAELWLYKKNAGYLHD : 1559

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*           680           *           700           *           720           *           740
CsRDR1c : AAADIRKMGDFPHRIRNVAKYAARLGCSFSSRRELSVGRDEFEIIPDVEVVRGGIEYVFSDCGKISADFAAR : 587
CsRDR1a : AAADIRKMGDFPHRIRNVAKYAARLGCSFSSRRELSVSRHEIEIPDVEVVTGGNKYVFSDCGKISADFAAR : 543
CsRDR1b : AAADIRNMGDFRQIRRNAKYAARLGCSFSSTRELSVSRHEIEIPDVEVVTGRGKYVFSDCGKISSDFAAR : 541
CsRDR2 : KTEIDIRDMGCFNKRISYKGAARMGOLFSSTQCLEISAQEVETIPDVEITSDGVCYCFSDCGKISSNFAAR : 590
CsRDR5a : ANFVGEYIWTLERFLNHANGEKSLLRGSEAHRREFT-----IMQRLFYNG : 269
CsRDR5b : EVNEFASLLSILEVFLDHANGEKSLLRGSEAHRREFT-----IMQRLFYNG : 197
CsRDR6a : -----VGRFK-NRNIAKCAARMGCSFSSTVAVEVVEPNEVNAELLDIKRN---NVYVSDGKISADFAAR : 61
CsRDR6b : SVLNIKDMQKFT-DYNVAKCAARMGCSFSSTVAVEVPHKVEVNFKLDEDVRNR-----GVYVSDGKISADFAAR : 704
CsRDR6c : SVLNIKGMQKFT-DNRVAKCAARMGCSFSSTVAVEVPHKVEVNFKLDEDVRNR-----GVYVSDGKISADFAAR : 611
          g g f          a          aa4 g2 f S T e d          y fsdg6g 6

*           760           *           780           *           800
CsRDR1c : RVAVKCCKSSTPSAFCRYGGYKGVVID---TSIRKSLRRSFKYESENTKLDLAWSKYQPCFLNROLIS : 659
CsRDR1a : SVAKKCCELTSAPFCRYGGYKGVVAVD---SRSMKSLRMSSKYESDHKLDLRWCSMPSELNROFIT : 614
CsRDR1b : RVAKKCCKSSTPSAFCRYGGYKGVVAVD---NRSMKSLRMSSKYESDHKLDLAWSKYQPCFLNROLIT : 613
CsRDR2 : QVAKCCNHTSAPFCRYGGYKGVITVDR---NRFRMLGLSSLNFKESDKRMLNTSWSESMPCYLNRRAFR : 661
CsRDR5a : RAVKGTLVNRKPEKTQVR---SMIRVETDRSRVQFNSLETIGSNPKKNYLSRLIA : 331
CsRDR5b : RAVKGTLVNRKPEKTQVM---SMIRVEADSRSVQFNSLETIGSNPKKNYLSRLIA : 245
CsRDR6a : EVAEKLQTVNPCYQRYAGCKGVIACWPKNEKIRLSLRSKNFKESKHALLECSWTRFPQFPFLNROITIT : 135
CsRDR6b : EVAERLQCVNPCYQRYAGCKGVIACWPKNEKIRLSLRSKNFKESKHALLECSWTRFPQFPFLNROITIT : 778
CsRDR6c : EVAERLQCVNPCYQRYAGCKGVIACWPKNEKIRLSLRSKNFKESKHALLECSWTRFPQFPFLNROITIT : 685
          va r L          a q1ry g kvv          46slr s6 k 23          1 6 w          p lnr

*           820           *           840           *           860           *           880
CsRDR1c : LLSILGVDRIFFEKQKEVDQLDTLLDPLRAQEAELELMAPGENTNIKEMLCGYCPDAEPFLSMMLQTFRS : 733
CsRDR1a : LLSILGVEDDHFERQSEVEEELDNMLDSLRAWEAELELMCTGENTNIKEMLCGYCPDAEPFLSMMLQTFRA : 688
CsRDR1b : LLSILGVDRDHFERQSEVEEELNTLDPLMAQEAELELMSPGENTNIKEMLCGYCPDAEPFLSMMLRAFR : 687
CsRDR2 : LLSILGVEDDTFAEMQDLCLGKMLSKEAALDLVESMGRDAKGIVKMLQGEVENPMEYLSMLIRAHDD : 735
CsRDR5a : LLSYGVPKYFLDLTNALEDQACVSNKRTALKVAINHGEMDDNTTAQMLISGT-PLEPYIQYRILSVLAK : 404
CsRDR5b : ----- : -
CsRDR6a : LLSILKVADETFWKQSMIKCKLNMTVNTEVAFDVLTASCAEC-GNTAAIMLSAGEKQTELHIRGMITCIRA : 208
CsRDR6b : LLSALNVPDEFWQSMIKCKLNDADVAFDVLTASCAEC-GNVGAMLSAGENQEPHIRGMITCIRA : 851
CsRDR6c : LLSALNVPDEFWQSMIKCKLNDADVAFDVLTASCAEC-GNVGAMLSAGENQEPHIRGMITCIRA : 758
          lls l v d f          q          1          a          1          m          g          p          ep          1

*           900           *           920           *           940           *           960
CsRDR1c : AKLLELRTTRIFVPKGRSMMGCLDERTLEYGVFVQISGAGDR---MHGSSSSQRKFIVEBKVVVA : 799
CsRDR1a : AKLLELRTKARIFVPKGREMLGCLDERTLEYGVFVQISGVGHRAFYDDLMLMPSDSDSDQPNFIVQKVVVA : 762
CsRDR1b : AKLLELRTTRIFVPKGRSMMGCLDERTLEYGVFVQISGVGHRPFYDDLMLLGGSSDSDQHNRVEGKVVVA : 761
CsRDR2 : NQLSDLRTRCIFVPQGRILIGCLDEDTILNYGVYVIRMTKAELQAGE---QSSFQRIDTSVLIGKVVVT : 806
CsRDR5a : EVRKLGK-GKLPESFYLMGTADPEESNSDEWCVIL-----DNGSISQVLVI : 454
CsRDR5b : ----- : -
CsRDR6a : QLWGLREKARIFSSGRWLMGCLDELVLEQGCFVQVSSPTLENCFAN---HGSRFSGTKNLLVIKEFVVIT : 280
CsRDR6b : QLWGLREKSRIFVSGRWLMGCLDELAVLEQGCFIQVSTPLENCFAN---HGSRFSKPKKNVQVIKEFVVIT : 923
CsRDR6c : QLWGLREKSRIFVSGRWLMGCLDELAVLEQGCFIQVSNPLENCFAN---HGSRFSKPKKNVQVIKEFVVIT : 830
          1          f          gr          gldel          1          g          C          I          Q          V          N          P          L          E          N          C          F          A          N          g          v

*           980           *           1000           *           1020           *
CsRDR1c : KNPCLHFGDIRVLVAVVAPALH---MVDCVVPQKGLR----- : 835
CsRDR1a : KNPCLHFGDOVRLVAVVAPALH---MVDCVVPQKGLR----- : 798
CsRDR1b : KNPCLHFGDOVRLVAVVAPALH---MVDCVVPQKGLRLVDADKHMSFVSINLLMRLPVDKHRFGLKAT : 831
CsRDR2 : KNPCLHFGDIRVLVAVVAPALH---GWNCVFVPQKGLR----- : 844
CsRDR5a : RNECLHFGDIHVLKAVYYGLEDFVGNAKYALFESTKGRR----- : 494
CsRDR5b : ----- : -
CsRDR6a : KNPCLHFGDIRVLVAVVAPALH---SDCLVFPQKGLR----- : 316
CsRDR6b : KNPCLHFGDIRLLVAVVAPALH---LVDCVVPQKGLR----- : 959
CsRDR6c : KNPCLHFGDIRLLVAVVAPALH---LVDCVVPQKGLR----- : 866
          npclhpgd r l av          1          c          fpqkg r

1040           *           1060           *           1080           *           1100
CsRDR1c : -----PHNECSGSDLDGDLYFWSDSLIPE--RQIKPMDYTAQSMLDHDVIE----- : 885
CsRDR1a : -----PHNECSGSDLDGDLYFWCWDPDLIPE--QVKPMDYTAQSMLDHDVIESYALFLLLF : 857
CsRDR1b : AASCGTASTYIILPHNECSGSDLDGDLYFWCWDPDLIPE--QVKPMDYTAQSMLDHDVIESESKEWRSIQ : 903
CsRDR2 : -----PHNECSGSDLDGDLYFWNENLIPE--QVTPMDYTGRPRSDHDVLE----- : 894
CsRDR5a : -----SVGSELANGFDGDMYWSRNPELLRHFKPSYPMSRIYSTPNACNTKKSELSAELEHEL : 555
CsRDR5b : ----- : -
CsRDR6a : -----PHTNEASGSDLDGDLYFWTDNENLIPPKRSWVPMDYTAEVKSPRTVTOR----- : 368
CsRDR6b : -----PHTNEASGSDLDGDLYFWTDNENLIPPKRSYPMDYEVPKLPRVNQK----- : 1011
CsRDR6c : -----PHTNEASGSDLDGDLYFWTDNENLIPPKRSYPMDYEVPKLPRVNQK----- : 918
          ph ne sg dldg y w l pp          pmdy          v

1120           *           1140           *           1160           *           1180
CsRDR1c : -----EVEEYFNYLNDSLGIIANAHTWFADR---EPNKMSDFCIAELFSIAV : 934
CsRDR1a : VISCSS-----TFFLLVLRLIEEQEPANYVNNSLGIIANAHTWFADR---EPSKMSDFCIAELFSIAV : 925
CsRDR1b : SMPQHSLGWDPMSNRDLNDHREVEYFNYVNSLGIIANAHTWFADR---EPLKMSDFCIAELFSIAV : 975
CsRDR2 : -----EHKEFVDYINDTLGTISTAHLHADDR---EPSLKSSCKLADLHSMA : 943
CsRDR5a : FQLFKR-----TRFQQSYNMSVADSWLAFMDRLLLGLCSCSEKDSMKETTMHHIDIYCEAL : 613
CsRDR5b : -----NMSVADSWLAFMDRLLLGLCSSSVEKDRMKETTMHHIDIYCEAL : 291
CsRDR6a : -----DIDEFSKNVENLGAICNAHWHAAL---SEYGALDEKCITAEKAATAV : 417
CsRDR6b : -----DIDEFSRNVENLGAICNAHWHAAL---SEDGAQDEKCITAEKAATAV : 1060
CsRDR6c : -----DIDEFSRNVENLGAICNAHWHAAL---SEYGALDEKCITAEKAATAV : 967
          5          6          n          lg          i          ah          6          ad          a          c          la          A6

*           1200           *           1220           *           1240           *           12
CsRDR1c : DFPKTVPAEIPSDLRVKEYPDFMEPKDRTYESEVIGVLGFRAWKDIAPHNSIESFTREVARKS-YDPMEV : 1007
CsRDR1a : DFPKTVPAEIPDLRVVKEYPDFMEKSDKSTYESKRVLGKLFRAWKDISPQSSIKSFTKEAVANS-YDPMEV : 998
CsRDR1b : DFPKTVPAEIPTLRVVKEYPDFMEPKDRTYESEVIGKLFRAWKDISPQSSIKSFTKEAVANS-YDPMEV : 1048
CsRDR2 : DFPKTVCAPEMRFLKEYPDFMEQWKTPNYSKVLGLKLYRATVNSPHESAVLSWSEKIAQDA-YDPMEV : 1016
CsRDR5a : DFPKTVCKKKCDTDLLLPLTGILDPLDEVVPIQKAEFPHYPKPNKYHSTSVLGLIYEMVESFQSDLA : 687
CsRDR5b : DFPKTVCKKK-----THFNALP-----FWLSC : 311
CsRDR6a : DFPKTVQLVTMPSQLFKYYPDFMGEPFQSYSKKILGRLYRQELDAYDNVEAPSELTFPGDIPYDTLEY : 491
CsRDR6b : DFPKTVKIVTMPSQLFKYYPDFMGEAYRSYSKKILGRLYRQELDAYDNVEAYPEQTFPESIPYDGDLLEY : 1134
CsRDR6c : DFPKTVKIVTMPPPKLFKYYPDFMGEAFRSYSKKILGRLYRQELDAYDNVEAYPEQTFPESIPYDGDLLEY : 1041
          Dfpk3g          p          l          k          pdfm          y          s          g          l          r          y          p          d          yd          46

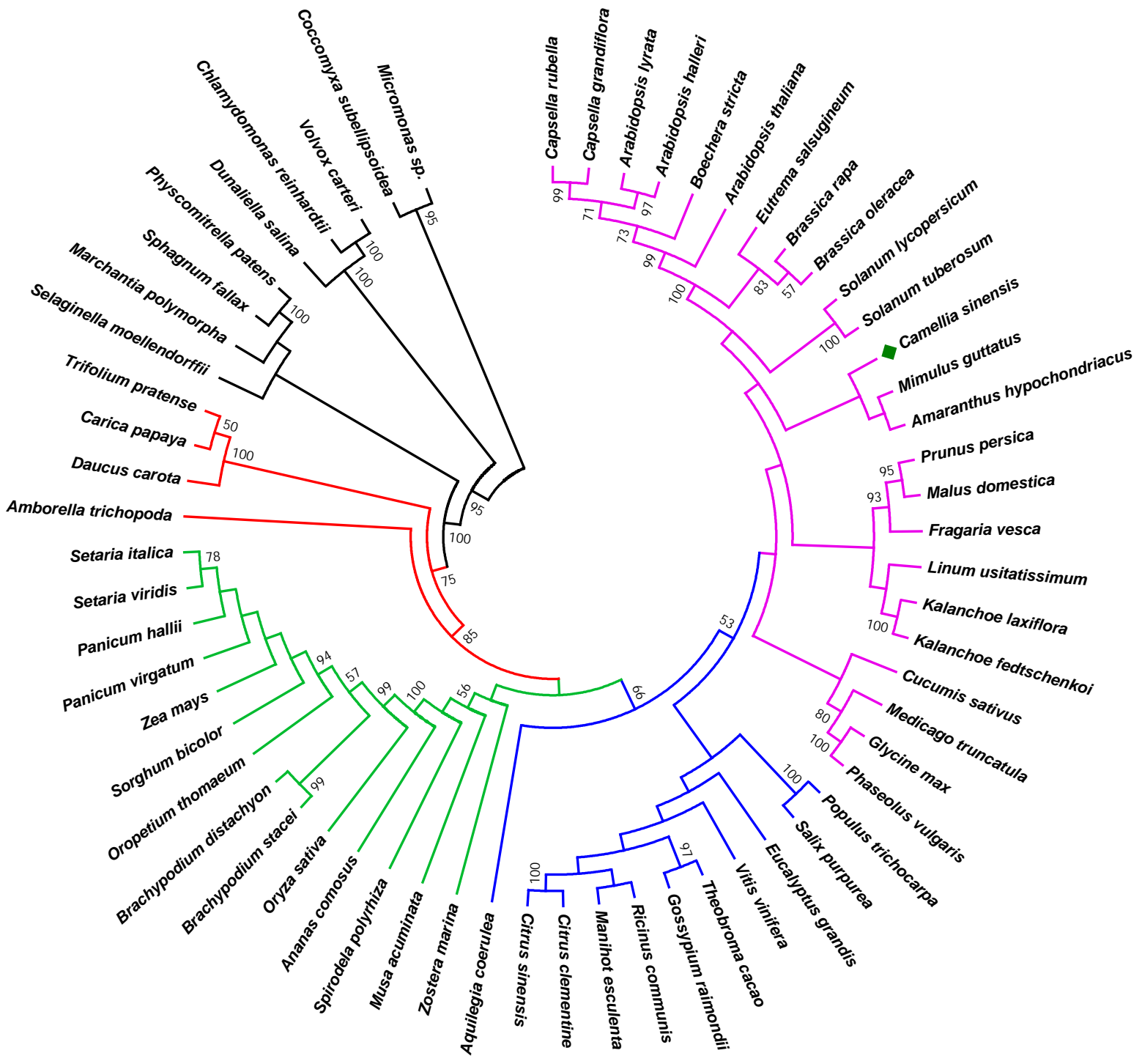
*           60           *           1280           *           1300           *           1320           *
CsRDR1c : DGFEDYDDDAYDKNEYDFKGNLDYGIKTEAEILGSIMKSTFDKRRD---SEAVGLAVRSLRKEAR : 1076
CsRDR1a : DGFEDYDDDAYDCNYDDKGNLDYGIKTEAEILGSIMKSTFDKRA---EKDVGLAVRSLRKEAR : 1067
CsRDR1b : DGFEDYDDDAYDKNEYDFKGNLDYGIKTEAEILGSIMKSTFDKRRD---SEAVGLAVRSLRKEAR : 1117
CsRDR2 : NGFEDYDEVAQSHKEMYLDKMSTLNFYEAESDEILGNLRTKSAMLLDNRYGMEMKDRLVKSYLKEAR : 1090
CsRDR5a : KDVEMKLPCDDVEIPTSCMK-----LWGERYSQRCEMTEAMLLDDESK-----NDAANVTRKYQL : 746
CsRDR5b : MWISTRKAFA-----MVPRNLYGPD-----NTSAALKS----- : 342
CsRDR6a : PGSMDFADAWEHKSYDQLNGLLGQYKVREEEIVTGHIWSPKNSRQRG-----ELOEKLKHAYSLRKEFP : 562
CsRDR6b : PGSMDFADAWEHKSYDQLNGLLGQYKVREEEIVTGHIWSPKNSRQRG-----DLOEKLKHAYSLRKEFP : 1205
CsRDR6c : PGSMDFADAWEHKSYDQLNGLLGQYKVREEEIVTGHIWSPKNSRQRG-----DLOEKLKHAYSLRKEFP : 1112
          g          d5i          a          k          y          1          y          ee          g          m          p          k          y          lrke

1340           *           1360           *           1380           *           1400
CsRDR1c : TFNRKEAASGVGDDVY---AKASAWYVYTHPRYWGCYNEGMN-----REHFLSFPWCYDRLIHIKRDK : 1140
CsRDR1a : SWFNTSGSESDAEDDVY-----AKASAWYVYTHPSWGRNEGTD-----REHFLSFPWCYDRLIHIKRKEK : 1131
CsRDR1b : TFNTSRATSDAEDDVY---AKASAWYVYTHPSWQYNGGMN-----DHDFLSFPWCYDRLIHIKRKEK : 1181
CsRDR2 : GWFESS-----CKADQQ-----KASAWYVYTHPSYCKES-----THCLGPPTLDGLLNIKSVO : 1143
CsRDR5a : LGAEFESPRNTDIYN-----ELAIYNITYDHAMGYENVKNCG-----FAWRWAGSALFKLHAIG : 805
CsRDR5b : ----- : -
CsRDR6a : QNEFKIS-DVSLDDEKNTLYEGASAWYVYTHPSWVKKSLEIQESNGTDQMLLSSWTAADYLARIKIRC : 635
CsRDR6b : QAFEKMGDFQDLSDAKNTMYERASAWYVYTHPSWVKKSLELHDSDGSGQMMVLSSWTAADYLARIKIRC : 1279
CsRDR6c : QAFEKMGDFQDLSDAKNTMYERASAWYVYTHPSWVKKSLELQESDGSGQMMVLSSWTAADYLARIKIRC : 1186
          f          dd          asawy          yhp          1          f          w          d          l          k

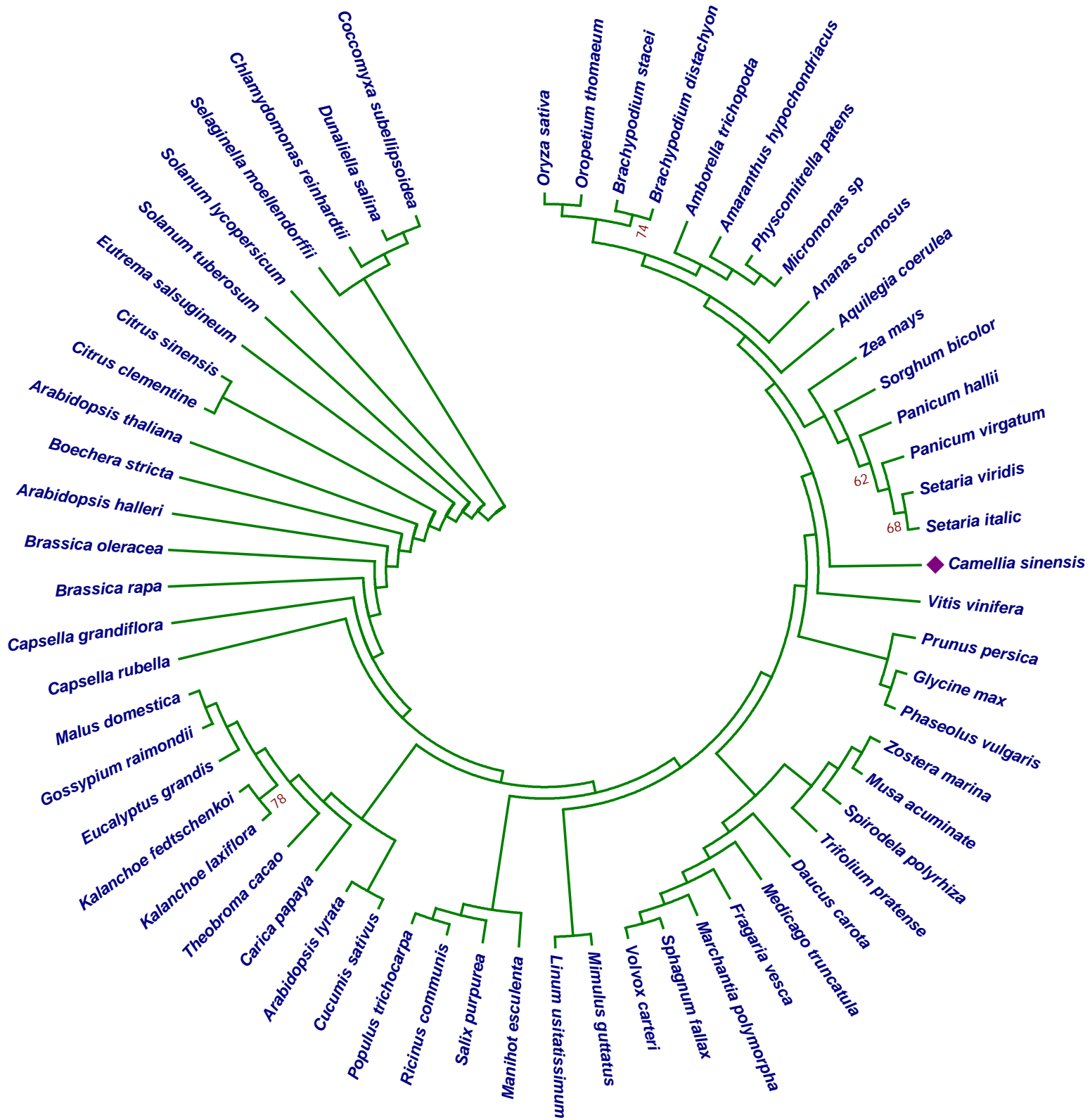
*           1420
CsRDR1c : SSI---RRALHSSLERQFSYGLS- : 1163
CsRDR1a : S-----RRLLHSSVEKO---SSGLSLG- : 1152
CsRDR1b : S-----RMALQLSSLORRQYGLSG- : 1202
CsRDR2 : S-----RKLSA----- : 1149
CsRDR5a : QSEKMEKPIVLPSVRELN--- : 826
CsRDR5b : ----- : -
CsRDR6a : RGIENFDSTKPINSLVYIADRI----- : 658
CsRDR6b : REIGNLDTTKPINSLAYADRDAIGN : 1306
CsRDR6c : REMGNLDTTKPINSLAYFADRDAIGY : 1213
          s

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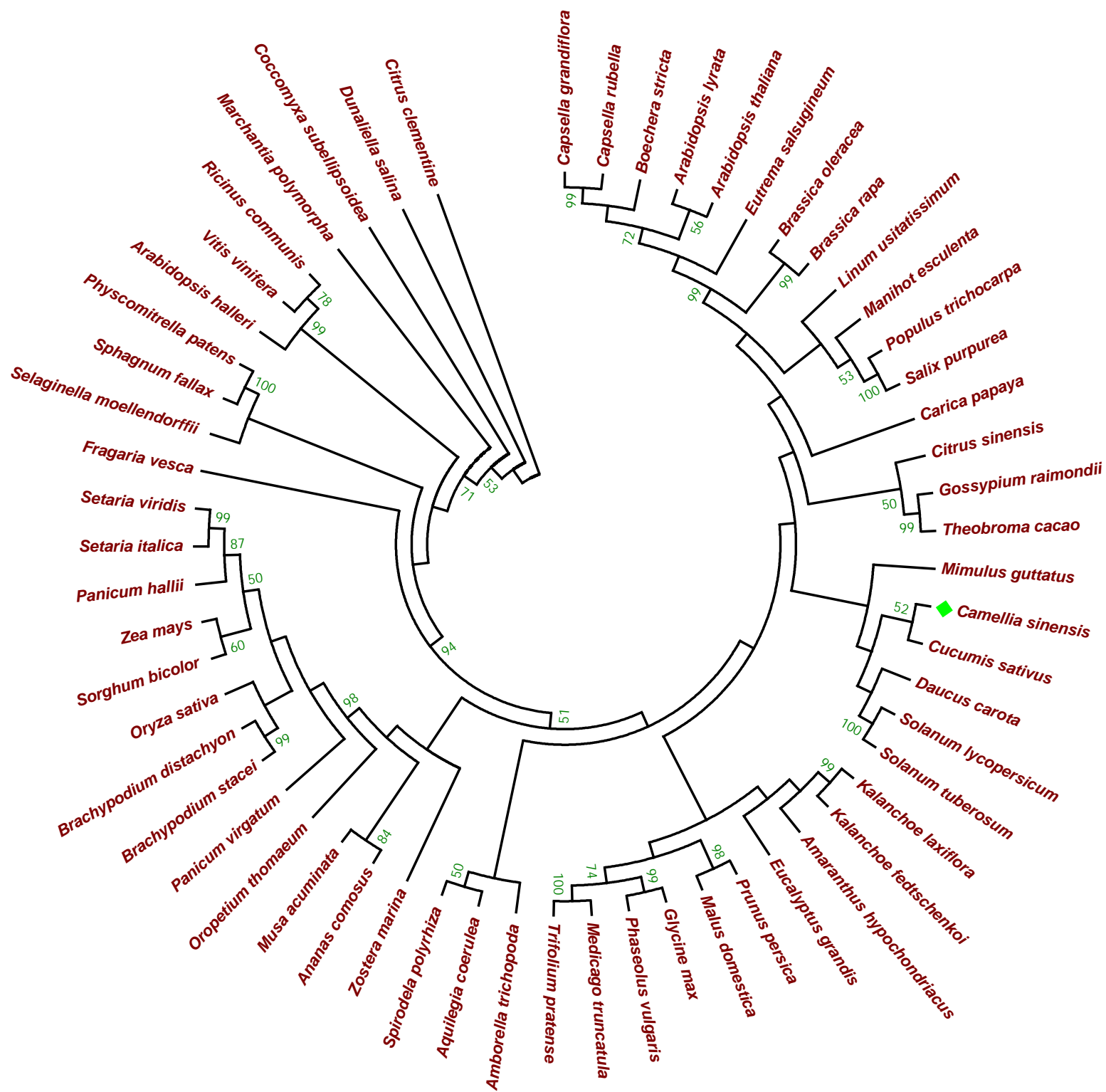
Supplementary Figure S2-a . The NJ phylogenetic tree of AGO family genes in 62 representative plant species.



Supplementary Figure S2-b. The NJ phylogenetic tree of DCL family genes in 62 representative plant species



Supplementary Figure S2-c: The NJ phylogenetic tree of RDR family genes in 59 representative plant species



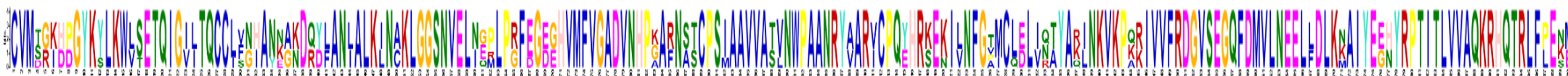
Supplementary Figure S3-a. Schematic diagram showing the logos of conserved motifs identified in CsAGO encoded proteins.



Motif 1



Motif 2



Motif 3



Motif 4



Motif 5



Motif 6



Motif 7



Motif 8



Motif 9

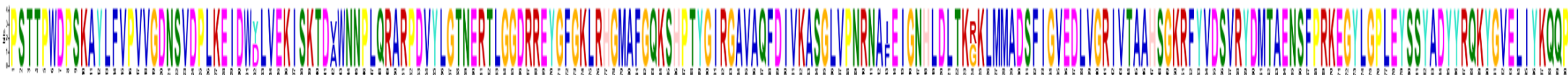


Motif 10

Supplementary Figure S3-b. Schematic diagram showing the logos of conserved motifs identified in CsDCL encoded proteins.



Motif 1



Motif 2



Motif 3



Motif 4



Motif 5



Motif 6



Motif 7



Motif 8



Motif 9



Motif 10

Supplementary Figure S3-c. Schematic diagram showing the logos of conserved motifs identified in CsRDR encoded proteins.



Motif 1



Motif 2



Motif 3



Motif 4



Motif 5



Motif 6



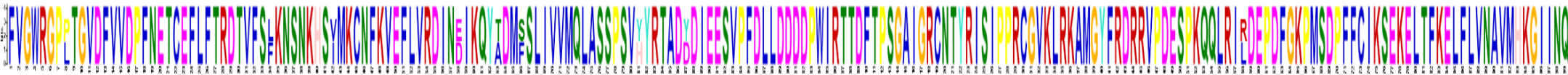
Motif 7



Motif 8



Motif 9



Motif 10

Supplementary Table S1-a. List of orthologous genes of AGOs from all plant lineages used to construct phylogenetic tree

Sl. No.	Plant Species Name	Protein ID	Score#	E value	Description *
1.	<i>Marchantia polymorpha</i>	Mapoly0001s0149.1	1496.9	0.0	Argonaute linker 1 domain
2.	<i>Physcomitrella patens</i>	Pp3c1_35770V3.6	1450.3	0.0	Argonaute linker 1 domain
3.	<i>Sphagnum fallax</i>	Sphfalx0001s0279.1	1458.4	0.0	Argonaute linker 1 domain
4.	<i>Selaginella moellendorffii</i>	110151	1459.9	0.0	Argonaute linker 1 domain
5.	<i>Ananas comosus</i>	Aco011930.1	1559.7	0.0	Argonaute linker 1 domain
6.	<i>Amborella trichopoda</i>	evm_27.model.AmTr_v1.0_scaffold00044.24	1547.7	0.0	Argonaute linker 1 domain
7.	<i>Musa acuminata</i>	GSMUA_AchrUn_randomT09260_001	1603.2	0.0	Argonaute linker 1 domain
8.	<i>Spirodela polyrhiza</i>	Spipo17G0036500	1588.2	0.0	Argonaute linker 1 domain
9.	<i>Zostera marina</i>	Zosma25g01490.1	1493.0	0.0	Argonaute linker 1 domain
10.	<i>Brachypodium distachyon</i>	Bradi5g18540.1	1557.0	0.0	Argonaute linker 1 domain
11.	<i>Brachypodium stacei</i>	Brast09G173700.1	1558.9	0.0	Argonaute linker 1 domain
12.	<i>Oryza sativa</i>	LOC_Os04g47870.2	1565.4	0.0	Argonaute linker 1 domain
13.	<i>Oropetium thomaeum</i>	Oropetium_20150105_01399A	1533.1	0.0	Argonaute linker 1 domain
14.	<i>Panicum hallii</i>	Pahal.G01956.1	1564.3	0.0	Argonaute linker 1 domain
15.	<i>Panicum virgatum</i>	Pavir.Ga01012.1	1557.0	0.0	Argonaute linker 1 domain
16.	<i>Setaria italica</i>	Seita.7G201100.1	1559.3	0.0	Argonaute linker 1 domain
17.	<i>Setaria viridis</i>	Sevir.7G213000.2	1562.4	0.0	Argonaute linker 1 domain
18.	<i>Sorghum bicolor</i>	Sobic.006G181000.1	1534.6	0.0	Argonaute linker 1 domain
19.	<i>Zea mays</i>	GRMZM2G039455_T01	1542.3	0.0	Argonaute linker 1 domain
20.	<i>Aquilegia coerulea</i>	Aqcoe3G009200.1	1623.6	0.0	Argonaute linker 1 domain
21.	<i>Amaranthus hypochondriacus</i>	AHYPO_012431-RA	1648.6	0.0	Argonaute linker 1 domain
22.	<i>Daucus carota</i>	DCAR_027248	1332.8	0.0	Argonaute linker 1 domain
23.	<i>Mimulus guttatus</i>	Migut.O00245.1	1672.5	0.0	Argonaute linker 1 domain
24.	<i>Solanum lycopersicum</i>	Solyc06g072300.2.1	1709.9	0.0	ARGONAUTE 1
25.	<i>Solanum tuberosum</i>	PGSC0003DMT400069313	1708.4	0.0	ARGONAUTE 1
26.	<i>Kalanchoe fedtschenkoi</i>	Kaladp0053s0463.1	1629.0	0.0	Argonaute linker 1 domain
27.	<i>Kalanchoe laxiflora</i>	Kalax.0373s0030.1	1632.1	0.0	Argonaute linker 1 domain
28.	<i>Eucalyptus grandis</i>	Eucgr.K02304.1	1674.1	0.0	Argonaute linker 1 domain
29.	<i>Vitis vinifera</i>	GSVIVT01029383001	1689.9	0.0	Argonaute linker 1 domain
30.	<i>Linum usitatissimum</i>	Lus10031331	1655.6	0.0	Argonaute linker 1 domain
31.	<i>Manihot esculenta</i>	Manes.02G219700.1	1681.8	0.0	Argonaute linker 1 domain
32.	<i>Populus trichocarpa</i>	Potri.012G037100.1	1681.0	0.0	Argonaute linker 1 domain
33.	<i>Ricinus communis</i>	29677.m000188	1707.6	0.0	Protein with all the AGO specific domains
34.	<i>Salix purpurea</i>	SapurV1A.0202s0350.1s	1676.0	0.0	Argonaute linker 1 domain

35.	<i>Citrus sinensis</i>	orange1.lg001466m	1679.8	0.0	Argonaute linker 1 domain
36.	<i>Citrus clementina</i>	Ciclev10018625m	1679.8	0.0	Argonaute linker 1 domain
37.	<i>Carica papaya</i>	evm.model.supercontig_44.130	1434.5	0.0	Argonaute linker 1 domain
38.	<i>Gossypium raimondii</i>	Gorai.008G294100.1	1663.7	0.0	Argonaute linker 1 domain
39.	<i>Theobroma cacao</i>	Thecc1EG013468t2	1677.1	0.0	Argonaute linker 1 domain
40.	<i>Arabidopsis halleri</i>	Araha.2117s0011.2	1574.7	0.0	Argonaute linker 1 domain
41.	<i>Arabidopsis lyrata</i>	AL1G55040.t1	1575.5	0.0	Argonaute linker 1 domain
42.	<i>Arabidopsis thaliana</i>	AT1G48410.2	1562.0	0.0	Argonaute linker 1 domain
43.	<i>Boechera stricta</i>	Bostr.25219s0559.1	1578.5	0.0	Argonaute linker 1 domain
44.	<i>Brassica oleracea capitata</i>	Bol043177	1545.8	0.0	Argonaute linker 1 domain
45.	<i>Brassica rapa</i>	Brara.H00354.1	1552.3	0.0	Argonaute linker 1 domain
46.	<i>Capsella grandiflora</i>	Cagra.1131s0020.1	1578.5	0.0	Argonaute linker 1 domain
47.	<i>Capsella rubella</i>	Carubv10008158m	1581.2	0.0	Argonaute linker 1 domain
48.	<i>Eutrema salsugineum</i>	Thhalv10011197m	1541.9	0.0	Argonaute linker 1 domain
49.	<i>Cucumis sativus</i>	Cucsa.112480.1	1638.2	0.0	Argonaute linker 1 domain
50.	<i>Fragaria vesca</i>	mrna09290.1-v1.0-hybrid	1578.5	0.0	Argonaute linker 1 domain
51.	<i>Glycine max</i>	Glyma.16G217300.1	1662.1	0.0	Argonaute linker 1 domain
52.	<i>Malus domestica</i>	MDP0000069525	1642.9	0.0	Argonaute linker 2 domain
53.	<i>Medicago trunculata</i>	Medtr6g477980.2	1628.6	0.0	Argonaute linker 1 domain
54.	<i>Phaseolus vulgaris</i>	Phvul.004G142900.1	1642.5	0.0	Argonaute linker 1 domain
55.	<i>Prunus persica</i>	Prupe.5G241600.2	1689.5	0.0	Argonaute linker 1 domain
56.	<i>Trifolium pratense</i>	Tp57577_TGAC_v2_mRNA26982	1261.5	0.0	Argonaute linker 1 domain
57.	<i>Chlamydomonas reinhardtii</i>	Cre16.g689647.t1.1	434.9	2.5E-131	Argonaute linker 1 domain
58.	<i>Dunaliella salina</i>	Dusal.0754s00004.1	449.9	3.6E-138	Argonaute linker 1 domain
59.	<i>Volvox carteri</i>	Vocar.0052s0031.1	412.9	2.8E-123	Argonaute linker 1 domain
60.	<i>Coccomyxa subellipsoidea</i>	56024	430.6	3.3E-130	Argonaute linker 1 domain
61.	<i>Micromonas sp. RCC299</i>	113410	334.3	4.3E-96	Argonaute linker 1 domain

#Smith-Watermann alignment score (based on BLOSUM45, with gap opening and extension penalties of -12 and -2 respectively)

*All protein sequences show presence of typical AGO specific domains viz. PAZ, PIWI, Argo-N, Argo-L1, Argo-Mid and Argo-L2. However, *Dunaliella salina* and *Volvox carteri* exhibited absence of miD domain, whereas PAZ domain was absent in *Micromonas sp.*

Supplementary Table S1-b. List of orthologous genes of DCLs from all plant lineages used to construct phylogenetic tree

Sl. No.	Plant Species Name	Protein ID	Score#	E value	Description *
1.	<i>Marchantia polymorpha</i>	Mapoly0003s0222.1	2016.1	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
2.	<i>Physcomitrella patens</i>	Pp3c2_15900V3.1	1979.5	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
3.	<i>Sphagnum fallax</i>	Sphfalx0020s0155.1	1958.3	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
4.	<i>Selaginella moellendorffii</i>	86110	1793.5	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
5.	<i>Ananas comosus</i>	Aco016650.1	2366.3	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
6.	<i>Amborella trichopoda</i>	evm_27.model.AmTr_v1.0_scaffold00018.3	2265.7	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
7.	<i>Musa acuminata</i>	GSMUA_Achr8T12350_001	1069.3	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
8.	<i>Spirodela polyrhiza</i>	Spipo1G0078500	2244.5	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
9.	<i>Zostera marina</i>	Zosma109g00390.1	2227.6	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
10.	<i>Brachypodium distachyon</i>	Bradi1g77087.1	2248.0	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
11.	<i>Brachypodium stacei</i>	Brast02G020300.1	2255.7	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
12.	<i>Oryza sativa</i>	LOC_Os0302970.1	2290.8	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
13.	<i>Oropetium thomaeum</i>	Oropetium_20150105_22551A	2213.0	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
14.	<i>Panicum hallii</i>	Pahal.I00170.1	2259.6	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
15.	<i>Panicum virgatum</i>	Pavir.Ib00062.1	2255.3	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
16.	<i>Setaria italica</i>	Seita.9G562200.1	2248.4	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
17.	<i>Setaria viridis</i>	Sevir.9G565900.1	2252.3	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
18.	<i>Sorghum bicolor</i>	Sobic.001527800.2	2271.1	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
19.	<i>Zea mays</i>	GRMZM2G040762_T01	1961.0	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
20.	<i>Aquilegia coerulea</i>	Aqcoe5G472300.2	2374.4	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
21.	<i>Amaranthus hypochondriacus</i>	AHYPO_01582-RA	2272.3	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
22.	<i>Daucus carota</i>	DCAR_022119	2273.4	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
23.	<i>Mimulus guttatus</i>	Migut.I00117.1	2330.4	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
24.	<i>Solanum lycopersicum</i>	Solyc10g005130.2.1	2238.8	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
25.	<i>Solanum tuberosum</i>	PGSC0003DMT400029301	2269.2	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
26.	<i>Kalanchoe fedtschenkoi</i>	Kaladp0072s0008.1	1321.2	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
27.	<i>Kalanchoe laxiflora</i>	Kalax.0054s0136.1	2265.7	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
28.	<i>Eucalyptus grandis</i>	Eucgr.D02653.1	2424.1	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
29.	<i>Vitis vinifera</i>	GSVIVT01027462001	1863.2	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1

30.	<i>Linum usitatissimum</i>	Lus10005142bt	1635.2	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
31.	<i>Manihot esculenta</i>	Manes.05G015200.1	2449.5	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
32.	<i>Populus trichocarpa</i>	Potri.002G181400.1	2422.1	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
33.	<i>Ricinus communis</i>	30076.m004468	2470.7	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
34.	<i>Salix purpurea</i>	SapurV1A.0003s0350.1	2400.6	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
35.	<i>Citrus sinensis</i>	orange1.1g000174m	2351.6	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
36.	<i>Citrus clementina</i>	Ciclev10018447m	2428.7	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
37.	<i>Carica papaya</i>	evm.model.supercontig_57.74	2153.6	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
38.	<i>Gossypium raimondii</i>	Gorai.001150400.1	2418.3	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
39.	<i>Theobroma cacao</i>	Thecc1EG005016t2	2441.8	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
40.	<i>Arabidopsis halleri</i>	Araha.2490s0029.1	2239.9	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
41.	<i>Arabidopsis lyrata</i>	AL1G11480.t1	2238.8	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
42.	<i>Arabidopsis thaliana</i>	AT1G01040.2	2216.4	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
43.	<i>Boechera stricta</i>	Bostr.5325s0024.1	2231.5	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
44.	<i>Brassica oleracea capitata</i>	Bol040724	2245.3	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
45.	<i>Brassica rapa</i>	Brara.J00078.1	2253.8	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
46.	<i>Capsella grandiflora</i>	Cagra.1968s0049.1	2273.8	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
47.	<i>Capsella rubella</i>	Carubv10008073m	2273.8	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
48.	<i>Eutrema salsugineum</i>	Thhalv10006531m	2224.1	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
49.	<i>Curcumis sativus</i>	Cucsa.260100.1	2430.6	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
50.	<i>Fragaria vesca</i>	mrna18596.1-v1.0-hybrid	2333.5	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
51.	<i>Glycine max</i>	Glyma.19G261200.2	2417.1	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
52.	<i>Malus domestica</i>	MDP0000619907	199.5	1.7E-52	DICER-LIKE PROTEIN 4
53.	<i>Medicago trunculata</i>	Medtr7g118350.1	2398.6	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
54.	<i>Phaseolus vulgaris</i>	Phvul.009G260000.1	2409.0	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
55.	<i>Prunus persica</i>	Prupe.2G200900.1	2419.0	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
56.	<i>Trifolium pratense</i>	Tp57577_TGAC_v2_mRNA4956	2400.9	0.0	ENDORIBONUCLEASE DICER HOMOLOG 1
57.	<i>Chlamydomonas reinhardtii</i>	Cre02.g141000.t1.1	97.1	3.5E-19	ENDORIBONUCLEASE DICER HOMOLOG 1
58.	<i>Dunaliella salina</i>	Dusal.0147s00002.1	74.7	2E-12	ENDORIBONUCLEASE DICER HOMOLOG 1
59.	<i>Volvox carteri</i>	Vocar.0003s0040.1	73.9	1E-13	ENDORIBONUCLEASE DICER HOMOLOG 1
60.	<i>Coccomyxa subellipsoidea</i>	33474	50.1	2E-6	Ribonuclease III
61.	<i>Micromonas sp. RCC299</i>	98380	52.4	1.4E-6	DEAD-BOX ATP-DEPENDENT RNA HELICASE 40

#Smith-Waterman alignment score (based on BLOSUM45, with gap opening and extension penalties of -12 and -2 respectively)

Supplementary Table S1-c. List of orthologous genes of RDRs from all plant lineages used to construct phylogenetic tree

Sl. No.	Plant Species Name	Protein ID	Score#	E value	Description *
1.	<i>Marchantia polymorpha</i>	Mapoly0151s0009.1	592.0	0.0	RNA-DEPENDENT RNA POLYMERASE
2.	<i>Physcomitrella patens</i>	Pp3c24_15800V3.6	844.3	0.0	RNA-DEPENDENT RNA POLYMERASE 1
3.	<i>Sphagnum fallax</i>	Sphfalx0166s0014.1	873.6	0.0	RNA-DEPENDENT RNA POLYMERASE 1
4.	<i>Selaginella moellendorffii</i>	150191	761.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
5.	<i>Ananas comosus</i>	Aco002958.1	1293.9	0.0	RNA-DEPENDENT RNA POLYMERASE 1
6.	<i>Amborella trichopoda</i>	evm_27.model.AmTr_v1.0_scaffold00176.15	1251.9	0.0	RNA-DEPENDENT RNA POLYMERASE 1
7.	<i>Musa acuminata</i>	GSMUA_Achr10T29960_001	1115.5	0.0	RNA-DEPENDENT RNA POLYMERASE 1
8.	<i>Spirodela polyrhiza</i>	Spipo15G0038000	1087.4	0.0	RNA-DEPENDENT RNA POLYMERASE 1
9.	<i>Zostera marina</i>	Zosma121g00800.1	1154.0	0.0	RNA-DEPENDENT RNA POLYMERASE 1
10.	<i>Brachypodium distachyon</i>	Bradi3g59910.1 (1122.8	0.0	RNA-DEPENDENT RNA POLYMERASE 1
11.	<i>Brachypodium stacei</i>	Brast04G010200.1	1189.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
12.	<i>Oryza sativa</i>	LOC_Os02g50330.1	922.5	0.0	RNA-DEPENDENT RNA POLYMERASE 1
13.	<i>Oropetium thomaeum</i>	Oropetium_20150105_04127A	1180.2	0.0	RNA-DEPENDENT RNA POLYMERASE 1
14.	<i>Panicum hallii</i>	Pahal.A03315.1	1196.4	0.0	RNA-DEPENDENT RNA POLYMERASE 1
15.	<i>Panicum virgatum</i>	Pavir.Aa00750.1	1132.5	0.0	RNA-DEPENDENT RNA POLYMERASE 1
16.	<i>Setaria italica</i>	Seita.1G312200.1	1209.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
17.	<i>Setaria viridis</i>	Sevir.1G318100.1	1205.7	0.0	RNA-DEPENDENT RNA POLYMERASE 1
18.	<i>Sorghum bicolor</i>	Sobic.004G246400.1	1182.9	0.0	RNA-DEPENDENT RNA POLYMERASE 1
19.	<i>Zea mays</i>	GRMZM2G481730_T01	1048.9	0.0	RNA-DEPENDENT RNA POLYMERASE 1
20.	<i>Aquilegia coerulea</i>	Aqcoe6G285700.1	1330.5	0.0	RNA-DEPENDENT RNA POLYMERASE 1
21.	<i>Amaranthus hypochondriacus</i>	AHYPO_003322-RA	1256.5	0.0	RNA-DEPENDENT RNA POLYMERASE 1
22.	<i>Daucus carota</i>	DCAR_030283	1358.2	0.0	RNA-DEPENDENT RNA POLYMERASE 1
23.	<i>Mimulus guttatus</i>	Migut.L01176.1	1432.2	0.0	RNA-DEPENDENT RNA POLYMERASE 1
24.	<i>Solanum lycopersicum</i>	Solyc05g007510.2.1	1397.5	0.0	RNA-DEPENDENT RNA POLYMERASE 1
25.	<i>Solanum tuberosum</i>	PGSC0003DMT400080319d	1384.4	0.0	RNA-DEPENDENT RNA POLYMERASE 1
26.	<i>Kalanchoe fedtschenkoi</i>	Kaladp0036s0212.1	1299.3	0.0	RNA-DEPENDENT RNA POLYMERASE 1
27.	<i>Kalanchoe laxiflora</i>	Kalax.0097s0091.1	1310.8	0.0	RNA-DEPENDENT RNA POLYMERASE 1
28.	<i>Eucalyptus grandis</i>	Eucgr.G02093.1	1325.8	0.0	RNA-DEPENDENT RNA POLYMERASE 1
29.	<i>Vitis vinifera</i>	GSVIVT01007792001	807.0	0.0	RNA-DEPENDENT RNA POLYMERASE 2

30.	<i>Linum usitatissimum</i>	Lus10019164	1356.7	0.0	RNA-DEPENDENT RNA POLYMERASE 1
31.	<i>Manihot esculenta</i>	Manes.15G135600.1	1445.3	0.0	RNA-DEPENDENT RNA POLYMERASE 1
32.	<i>Populus trichocarpa</i>	Potri.008G36100.1	1441.8	0.0	RNA-DEPENDENT RNA POLYMERASE 1
33.	<i>Ricinus communis</i>	30147.m013981	780.4	0.0	RNA-DEPENDENT RNA POLYMERASE 2
34.	<i>Salix purpurea</i>	Solanum SapurV1A.0015s0570.1	1387.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
35.	<i>Citrus sinensis</i>	orange1.1g002586m	1240.3	0.0	RNA-DEPENDENT RNA POLYMERASE 1
36.	<i>Citrus clementina</i>	Ciclev10007331m	95.9	6E-18	RNA-DEPENDENT RNA POLYMERASE
37.	<i>Carica papaya</i>	evm.model.supercontig_2.177	955.3	0.0	RNA-DEPENDENT RNA POLYMERASE 1
38.	<i>Gossypium raimondii</i>	Gorai.013G029000.1	1397.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
39.	<i>Theobroma cacao</i>	Thecc1EG011292t1	1387.9	0.0	RNA-DEPENDENT RNA POLYMERASE 1
40.	<i>Arabidopsis halleri</i>	Araha.9628s0001.1	645.2	0.0	RNA-DEPENDENT RNA POLYMERASE 2
41.	<i>Arabidopsis lyrata</i>	AL1G26820.t1	1332.8	0.0	RNA-DEPENDENT RNA POLYMERASE 1
42.	<i>Arabidopsis thaliana</i>	AT1G14790.1	1322.8	0.0	RNA-DEPENDENT RNA POLYMERASE 1
43.	<i>Boechera stricta</i>	Bostr.0124s0180.1	1250.7	0.0	RNA-DEPENDENT RNA POLYMERASE 1
44.	<i>Brassica oleracea capitata</i>	Bol038076	1315.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
45.	<i>Brassica rapa</i>	Brara.F01003.1	1314.7	0.0	RNA-DEPENDENT RNA POLYMERASE 1
46.	<i>Capsella grandiflora</i>	Cagra.3501s0013.1	1340.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
47.	<i>Capsella rubella</i>	Carubv10008144m	1337.0	0.0	RNA-DEPENDENT RNA POLYMERASE 1
48.	<i>Eutrema salsugineum</i>	Thhalv10006629m	1307.4	0.0	RNA-DEPENDENT RNA POLYMERASE 1
49.	<i>Cucumis sativus</i>	Cucsa.143700.1	1340.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
50.	<i>Fragaria vesca</i>	mrna06498.1-v1.0-hybrid	1152.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
51.	<i>Glycine max</i>	Glyma.02G086100.1	1341.3	0.0	RNA-DEPENDENT RNA POLYMERASE 1
52.	<i>Malus domestica</i>	MDP0000475729	1335.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
53.	<i>Medicago trunculata</i>	Medtr1g032630.1	1335.1	0.0	RNA-DEPENDENT RNA POLYMERASE 1
54.	<i>Phaseolus vulgaris</i>	Phvul.003G016600.2	1295.8	0.0	RNA-DEPENDENT RNA POLYMERASE 1
55.	<i>Prunus persica</i>	Prupe.1G334600.2	1357.8	0.0	RNA-DEPENDENT RNA POLYMERASE
56.	<i>Trifolium pratense</i>	Tp57577_TGAC_v2_mRNA38119	1272.3	0.0	RNA-DEPENDENT RNA POLYMERASE 1
57.	<i>Dunaliella salina</i>	Dusal.0696s00003.1	196.4	1E-51	RNA-DEPENDENT RNA POLYMERASE
58.	<i>Coccomyxa subellipsoidea</i>	20637	486.9	1.5E-155	RNA-DEPENDENT RNA POLYMERASE

#Smith-Watermann alignment score (based on BLOSUM45, with gap opening and extension penalties of -12 and -2 respectively)

Supplementary Table S2-a. Annotation of conserved MEME motifs identified in CsAGO proteins.

Motif No.	Width	Sequence	e-value	Pfam Annotation
1	51	TVVDTKICHPTEFDLYLCSHAGIQGTSRPTHYHVLWDENNFTA DDLQKLIY	2.2e-545	Piwi domain
2	200	FKISKQYLANVSLKINVKMGGRRNTVLLDAJSKRIPLVSDIPTIIFG ADVTHPZPGEDSSPSIAAVVASQDWPEVTKYAGLVCAQP HRZEJIQDLYKTWQDPQRGTVHGGMIRELLISFRKATGQKPLRII FYRDGVSEGGFYQVLLYELDAIRKACASLEPNYQPPVTFVVVQ KRHHTRLFAANHRDRNSTDRSGNILPG	1.2e-787	Piwi domain
3	200	CVMSGKHPGYKYLKWLSETQIGIJTQCCLFNHANKAKDQYLAN JALKINAKLGGSNVELNEPLPRFEGEGHVMFVGADVNHPGARN STCPSIAAVVATVNWPAANRYAARVCPQYHRKEKILNFGTMCL ELIQTYAKINKVKPKRIVVFRDGVSEGGQFDMVLNEELDLKKAI YEEHYRPTITLVVAQKRHQTRLPENM	4.1e-518	Piwi domain
4	48	LGGGVEAWRGFYQSLRPTQQGLSLNJDMSVTAFIGEPLPVIDFLA ZNLN	1.4e-356	Argo-L1 domain
5	29	YTYARCTKPVSLVPPAYYAHLAAYRARQY	1.8e-242	Unknown
6	48	SVVEYFREKYNKEJKYTDLPCLDLGKNNRPNYLPMEFCKJVEG QRYPK	2.4e-306	PAZ domain
7	60	FKVTIKFAAKLDLHKLKEYLRGKQSDIPQEALQVLDJVLRENPS KRYCPVGRSFFSPDFR	1.2e-342	Argo-N domain
8	29	QWNLLNKKVNVGGKVERWACINFSRSDQN	3.8e-225	Unknown
9	146	GPPQFLLCLLPERKNSDJYGPWKKKNLADFGIVTQCIAPTRVND QYLTNVLLKINAKLGGNSMLAIEHAPSIPLISKVPTMILGMDVS HGSPGQSDIPSIAAVVSSRHWPLISRYRASVRTQSPKVEMIDSLY KRVADSEDEGIM	1.2e-207	Piwi domain
10	41	NDDPVAKEFGIEVSKELTSVEGRVLPPLPKYGBTGGEVNV	1.2e-200	Argo-L2 domain

Supplementary Table S2-b. Annotation of conserved MEME motifs identified in CsDCL proteins.

Motif No.	Width	Sequence	e-value	Pfam Annotation
1	57	FCYZRLEFLGDAVLDYLITRHLFLKYPDLHPGQLTLRSAAVNN ENFAKVAVKKGLH	3.9e-157	RNaseIII domain
2	200	PSSTPWDPASKAYLFPVVGDNVDPKLEIDWDLVEKISKTDVW NNPLQRARPDVYLGNTERTLGGDRREYGFGLRHGMAFGQKS HPTYGIRGAVAQFDIVKASGLVPNRNAFEIGNHLDLTKGKLM ADSFIVGVEDLVGRIVTAAHSGKRFYVDSVRYDMTAENSFPRKE GYLGPLEYSSYADYYRQKYGVELIYKQQP	1.0e-089	PAZ domain
3	98	GHRWLSSKTJADVVEALIGAYYVEGGKKAANQLMKWIGIQIDF EPKELECTTRPSNVPEILRSINFDALEGALGYEFKDRGLLVEAIT HASRPSSGV	4.2e-062	Unknown
4	132	HLRHGSSALEKQIRDFVKEVKDELSKPGFNSFGLGDCKAPKVL GDIVESIAGAIFLDSGRDTAVFQPLLHPMVTPELPMHPVRELQE RCQQQAEGLEYKASRNGNLATVEVFIDGVQVGIAQNPQKKMA QK	2.7e-053	Unknown
5	61	FRKKGKVNLLVATSVAEGLDIQSCNLVIRFDLPKTVASYIQSRG RAMPDSDYILMVERGN	2.9e-051	Helicase C-terminal domain
6	80	WILSGRDACYNSKLFHLYMYDIECVDIGSLKDPFLTQVLEFAVV FGNELDAEVLMSMDLFIARTMITKASLVFRGSIDI	2.9e-031	Unknown
7	80	RGVSYCKNLLSPFEHSEANEGESEALDKTYVFLPPELFCVH PLPGSLVRGAQRLPSIMRRVESMLLAIQLKDIINYP	5.0e-027	PAZ domain
8	38	YKVESTGAVVSLNSSVGLIHFYCSKLPSEYFTPKPEF	5.2e-025	Unknown
9	29	QADRFAPAVVWVAPGDRPVTDDEDIGEPGPS	7.3e-020	Unknown
10	105	PHKNIIIVLVPNVVLVHQQFEVIKMHTDLZVEEYWGEKGVDEW DGKSWEZQDDHEVLVLTQPILLDALRKAFLRFEMICLLIFDEC HRARGRHPYVCIMKEFYH	1.8e-019	DEAD box helicase

Supplementary Table S2-c. Annotation of conserved MEME motifs identified in CsRDR proteins.

Motif No.	Width	Sequence	e-value	Pfam Annotation
1	94	EFFTNYIVNDSLGIICNAHVVHADREPYKALSEKCJTLAELASIA VDFPKTGVP AEMPSELKPKEYPDFMEKEDKTSYESKKVLGKLY RAIKDA	3.0e-258	RdRP domain
2	82	MSCGENGNILAEMLLAGYKPDAEPFLSMMLTCFRAAQLWGLR TKSRIFVPSGRWLMGCLDETRVLEYGQVVFQISGPGLENC	2.7e-226	RdRP domain
3	79	NSSIKLSLRMSMSKFESKHTKLDVLSWSRYQPGFLNRQIITLLST LGPVDEIFEKMQEEMIEKLDKMLTDPEVAFDVLE	7.1e-193	RdRP domain
4	70	EFTFEPASIPYDPDLEIPGFEDYIDDAWDHKCSYDGKLGGLLQ YGIKTEEEILTGHIWSMPKYFDRKRG	3.9e-145	Unknown
5	76	YSTDJSPRIASYNPRRTAIYRRILSILRDGIVIGNKKFDLAFSS QLRDNSAWMFASDEDITAADIRDWMGDFR	2.2e-130	RdRP domain
6	29	RPHPNECSGSDLDGDJYFVTWDEBLIPPQ	7.3e-110	RdRP domain
7	33	VIKGVVVAKNPCLHPGDIRVLEAVDVPALHHL	2.0e-109	RdRP domain
8	47	VHRVQITPCKVYFLGPEVEMSNRVJRHYKEYIDNFLRVSFVDEE WDK	2.3e-096	RdRP domain
9	47	YVFSDGIGKITPDLAREVAEKLQLKVNPPSAYQIRYAGCKGVIA CWP	9.3e-092	RdRP domain
10	200	FVGWRGPPTGVDFVDPFNETCEFLFTRDTVFSFKNSNKHSIMK CNFKVEFLVRDINEIKYADMFLIVVMQLASSPSVHYRTADD DIEESVPFDLLDDDDPWIRTTDFTPSGAIGRCNTYRISIPRCGVK LRKAMGYFRDRRVPDESPKQLRIRDEPDFGKMSDPFFCIKSE KELTFKELFLVNAVMMHKGIIHQH	1.9e-091	Unknown

Supplementary Table S4: List of primers used for qRT-PCR analysis

Sl No	Name	Primer sequence	Annealing temperature (°C)	Product size (bp)
1	CsAGO1-F	GGATTTGCACCAATATGATGTTTCAATTAC	60	219
	CsAGO1-R	CCTGTTCCATCATCTTCATCAATGAGAG		
2	CsAGO2/3a-F	GAAGCTAAATGCTTACTTACGAGGAATGCTC	61	161
	CsAGO2/3a-R	CATAGCCAAGGTCTTCGTTTGGTCTG		
3	CsAGO2/3d-F	GTTGTTGAAGGAAATGTCGCTGATTC	60	249
	CsAGO2/3d-R	CTCCTGACGAGATTCCAATGACATTTT		
4	CsAGO5a-F	GTGAATGAAGAATTTGGTATTCAAGTGAGG	60	254
	CsAGO5a-R	CTACGACACATAGAAATCAATTCACGGC		
5	CsAGO6-F	GAGGAATTTCACTAATGTTGGAGGAGGTG	61.3	245
	CsAGO6-R	CCATGTTGCTGTGCCTTGTCTTAACC		
6	CsAGO7-F	CAGAATAACCCTCTCTGGCTACCTCG	61.3	231
	CsAGO7-R	GAATTGGACTAGGAAATGATTGGCAAGG		
7	CsAGO10a-F	CAACATTAAACTTGTGGATGAAGAGGATGG	61.9	231
	CsAGO10a-R	GATCTTCCAACAGGGCAGTACCTCTTTG		
8	CsDCL1b-F	GGAAATCATTTGGATTTGACTAAACGC	59	210
	CsDCL1b-R	GTAATCAGCATAAGAGCTGTACTCCAATGG		
9	CsDCL1a-F	GCATGTACCAATGCCCTCAGAAATTG	60.5	221
	CsDCL1a-R	CACCATCACTTTCTGTTCTTTCAGAGACC		
10	CsDCL2-F	GAGGTAGACATCCCTATGTTTGCATTATG	58	225
	CsDCL2-R	GAATGTACTIONGGCTAACACAGATTTCGC		
11	CsDCL3-F	CAAATCTTCAAGTGAAGAATACTATGGAGC	60	200
	CsDCL3-R	GTTACCAAGTAGCACGATGGCATTTCATC		
12	CsDCL4-F	GAGCACCAAGAAGATGCTCTGGAGAC	60	253
	CsDCL4-R	CTCCACACAGGATAAATCAGCTTCAATTC		
13	CsRDR1a-F	GATTTCACTCCATTATTCTGCCTTGGTC	60	178
	CsRDR1a-R	CCACAATGGGTACTAGATCCAAATTGC		
14	CsRDR1b-F	GAGAACATCTGGCAGATTGAGCTTCG	61	211
	CsRDR1b-R	GCTCCAAACATAAAGAAGAAGATTGGCC		
15	CsRDR5a-F	GACGATAAAACTTCAAGTCGATCTTGC	57	166
	CsRDR5a-R	GGGAGCCTTCAATGCAATATCTACTG		
16	CsRDR5b-F	CTCTTGCTCCTTGCGATGAGATAGAATC	60	227
	CsRDR5b-R	CGACCCTCTCAATTCCAGTGATTTCTC		
17	CsRDR6a-F	GTGGCTTTTCGATGTTCTTACTGCTTC	58	250
	CsRDR6a-R	GGACTTGACACTTGAACAAAGCATTG		
18	CsRDR6b-F	GCAGATGTGGCGTTTGATGTTCTTAC	59	247
	CsRDR6b-R	CTTGATAAAGCATTGACCTTGTTTCG		
19	CsRDR6c-F	CATCATGTGCTGAGCAAGGAAATGTAG	59.6	232
	CsRDR6c-R	GAAGGATTGATACTTGGATAAAGCATTG		
20	18S rRNA-F*	TCTGCCCGTTGCTCTGATG	60	134
	18S rRNA-R	TCACCCGTCACCACCATAG		

F= Forward and R=Reverse; *AF207029.1 (Accession No.)