

>ara-1 Arabidopsis thaliana 1-cys

MPGITLGDTVPLEVETTHDKFKLHDYFANSWTVLFSHPGDFTPVCTTELGAMAKYAHEFDKRGVKLLGLSCD
DVQSHKDWIKDIEAFNHGSKVNYPIIADPNKEIIPQLNMIDPIENGPSRALHIVGPDSKIKLSFLYPSTTGRNMDV
LRALDSLLMASKHNNKIATPVNWKPDQPVVISPAVSDEEAKMFPQGFKTADLPSKKGYL RHTEVS

>ara-2 Arabidopsis thaliana 2-Cys peroxiredoxin A

MASVASSTLISSPSRVFPAKSSLSVSLRRTLSSPSASASLRSGFARRSSLSSTRRSFAVKAQADDLPLVGNK
APDFEAEAVFDQEFIKVKLSDYIGKKYVILFFYPLDFTFVCPTEITAFSDRHSEFEKLNTEVLGVSVDVSVFSLAWV
QTDRKSGGLDNLNYPLISDVTKSISKSGVLHIDQGIALRGLFIIDKEGVIQHSTINNLGIGRSVDETMRTLQALQYI
QENPDEVCPAGWKPGEKSMKDPKLSKEYFSAI

>ara-3 Arabidopsis thaliana 2-Cys peroxiredoxin B

MSMASIASSSTLLSSSRVLLPSKSSLLSPTVSPRIIPSSSASSSLCSGFSLSLTTNRSASRRNFAVKAQADDP
LVGNKAPDFEAEAVFDQEFIKVKLSEYIGKKYVILFFYPLDFTFVCPTEITAFSDRYEEFEKLNTEVLGVSVDVSVFSLH
AWVQTDRKSGGLDNLNYPLVSDITKSISKSGVLIPDQGIALRGLFIIDKEGVIQHSTINNLGIGRSVDETMRTLAL
QYVQENPDEVCPAGWKPGEKSMKDPKLSKEYFSAI

>ara-4 Arabidopsis thaliana peroxiredoxin Q

MAASSSFTLCNHTTLRTPLRKTLVTKQFSVPTKSSSENFFGSTLTHSSYISPVSSSLKGLIFAKVNGQAAPDF
TLKDQNGKPVSLKYYKGPVVLYFPADETPGCTKQACAFRDSYEKFKKAGAEVIGISGDDSASHKAFASKYKLP
YTLLSDEGNKVRKDWGVPDGLFGALPGRQTYVLDKNGVVQLIYNNQFQPEKHIDETLKFLLAA

>ara-6 Arabidopsis thaliana peroxiredoxin-2B

MAPIAVGDVVPDGTISFFDENDQLQTVSVHSLAAGKKVILFGVPGAFTPTCSMKHVPGFIEKAEELKSKGVDDII
CFSVNDPFLMKAWGKTYPENKHVKFVADGSGEYTHLLGLELDLKDGLGIRSRRFALLLDNLKVTVANLESGGG
FTVSSADDILEAL

>ara-7 Arabidopsis thaliana peroxiredoxin-2F

MAMSILKLRNLSALRSAANSARIGVSSRGFSKLAEGTDITSAAPGVSLQKARSWDEGVSSKFSTTPLSDIFKGGKV
VIFGLPGAYTGVCQQHVPSYKSHIDKFKAKGIDSVICVSVNDPFAINGWAEKLGAKDAIEFYGDFDGKFKHSLG
LDKDLAALLGPRSERWSAYVEDGKVKAVNVEEAPSDFKVTGAEVILGQI

>ara-8 Arabidopsis thaliana peroxiredoxin-2A

MAPIDVGDFVPDGSISFFDDDDQLQTVSVHSLAAGKKVILFGVPGAFTPTCSMNHVNGFIEKAEELKSNVDEI
ICLSGDDPFMITACSENKHVKFVEDGSGEYIQLLGLELEVKDKGLGVRSRGFALLLDNLKVVVNVGSGGDCSLF
QLMKMTTTTMSNLPTDLEEIISRVPRKYMRAVRLTCKRWNGMFKSQSFTKMHIGKEEAATRELQRTRMIVM
MDYN

>ara-9 Arabidopsis thaliana peroxiredoxin-2D

MAPITVGDVVPDGTISFFDENDQLQTVSVHSIAAGKKVILFGVPGAFTPTCSMSHVPFGFIGKAEELKSKGIDEIIC
FSVNDPVMKAWGKTYQENKHVKFVADGSGEYTHLLGLELDLKDGLGIRSRRFALLLDNLKVTVANVENGGGE
FTVSSAEDILKAL

>ara-10 Arabidopsis thaliana peroxiredoxin-2E

MATLSVSRFMSSSATVISVAKPLLSPTVSFTAPLSFTRSLAPNLSLKFRNRRTNSASATRSFATTPVTASISVGDK
LPDSTLSYLDPSTGDVKTVTVSSLTAGKKTILFAVPGAFTPTCSQKHVPGFVSKAGELRSKIDVIACISVNDAFVM
EAWRKDLGINDEVMLLSDGNGEFTGKLGVELDLRDKPVGLGVRSSRYAILADDGV
VKVLNLEEGGAFNTSSAEDMLKAL

>ara-11 Arabidopsis thaliana peroxiredoxin-2C

MAPITVGDVVPDGTISFFDENDQLQTVSVHSIAAGKKVILFGVPGAFTPTCSMSHVPFGFIGKAEELKSKGIDEIIC
FSVNDPVMKAWGKTYPENKHVKFVADGSGEYTHLLGLELDLKDGLGIRSRRFALLLDNLKVTVANVESGGEF
TVSSAEDILKAL

>ara-12 Homo sapiens PrxI (2-Cys)

MSSGNAKIGH PAPNFKATAVMPDGQFKDISLSDYKGYVVFYPLDFTFVCPT EIIAFSDRAEEFKKLN CQVIGA
SVDSHFCHLAWVNTPKKQGGGLPMNIPLVSDPKRTIAQDYGV LKADEGISFRGLFIIDDKGILRQITVNDPPCCR
SVDETLRLVQAFQFTDKHGEVCPAGWKPGSDTIKPDV PKTKEYFSKQK

>ara-13 Homo sapiens PrxII (2-Cys)

MASGNARIGKPAPDFKATAVVDGAFKEVKLSDYKGYV VLFYPLDFTFVCPT EIIAFSNRAEDFRKLGCEVLGVS
VDSQFNHLAWINTPRKEGGLPLNIPLLDGVDTRR LSEYGV LKTDEGIAYRGLFIIDGKGVLRQITVNDLPVGRSV
DEALRLVQAFQYTD EHGVEVCPAGWKPGSDTIKPNV DDSKEYFSKH N

>ara-14 Homo sapiens PrxIII (2-Cys)

MAAAVGRLLRASVARHVSAIPWGISATAALRPAACGR TSLTNLLCSGSSQAKLFSTSSSCHAPAVTQHAPYFKGT
AVVNGEFKDLSDDFKGYLVLFYPLDFTFVCPT EIVAFSDKANEFHDVNCEVVAVSVDSHFSLAWINTPRKN
GGLGHMNIALLSDLTKQJSRDYGV LLEGSLALRGLFIIDPNGVIKHL SVNDLPVGRSVEETLRLVKAFQYVETHG
EVC PANWTPDSPTIKPSPAASKEYFQKVNQ

>ara-15 Homo sapiens PrxIV (2-Cys)

MEALPLLAATTPDHGRHRRLLLLPLLLFLLPAGAVQGW ETERPRTREEECHFYAGGQVYPGEASRVSVADHSL
HLSKAKISK P APYWEGTAVIDG EFKELKLDYRGKYL VFFYPLDFTFVCPT EIIAFGDRLEEFRSINTEVVACSVDS
QFTHLAWINTPRRQGGLP IRIPLLSDLTHQISKDYGV YLEDSGHTLRGLFIIDDKGILRQITLNDLPVGRSVDETL
RLVQAFQYTDKHGEVCPAGWKPGSETIIPDAGK LKYFDKLN

>ara-16 Homo sapiens PrxV (atypical 2-Cys)

MGLAGVCALRRSAGYILVGGAGGQSAAAAARRCSEGEWASGGVRSFSRAAAAMAPIKVGDAIPAVEVFEGEP
GNKVNLAELFKGKGVLFVPGAFTPGCSKTHLPGFVEQAEAL KAKGVQVVA CLSVNDAFVTGEWGRAHKA E
GKVRLLADPTGAFGKETDLLLDDSLVSIFGNRR LKRFSMVVQDGIVKALNVEPDGTGLTCSLAPNIISQL

>ara-17 Homo sapiens PrxVI (1-Cys)

MPGGLLLGDVAPNFEANTTVGRIRFHD FLGDSW GILFSHP R DFTPVCTTELGRAAKLAPEFAKRNVKLI ALSIDS
VEDHLAWSKDINAYNCEEPTEKLPFPIIDDRNRELA ILLGMLDPAEKDEKGMPTARVVFVFGPKK LKLSILYPA
TTGRNFDEILRVVISLQLTAEKRVATPVDWKDGDSVMV LPTIPEEEAKKLPKGVFTKELPSGKKYLRYTPQ P

>11017-2940

MKPLRHHLTRICLVGLIVSLVMAAPAFAMGGDPP LDQPAPTF TLPSNTGDGEVLS D YRGQWV VLYFYPQ
DFTPGCTVEAQR FQQLPKYIERNTQVIGVSVDSV DSHA EFC DSEGLKFLLADEDGSVSKAYGSWMSYFSLRH
TYLIDPEGILREQYVKVRPVIHSEEVLARLDELQAAS

>11017-1161

MTLDIGDYAPEFTLPNADGESIDLKRFRGQWV VLYFYPRDNTPGCTKEACGFRDQYETYQTEQV VILGVSGDD
AKSHQKFINKQNL PFQLLSDLDFNVAKS YEAYGPKKFMGKEYEGIYRHSFLIDPDGKLAKIYRKVKAADHATDVL
QDLELLRK

>11017-5436

MALTAGTAAPAF TTKDTNGNTVSLADYAGKTVVLYFYPKDDTPGCTKEACSF RDNYTAYQGKDIVVFGVSGDDE
GSHQDFTSKFNLPFLLADVDHSLMKAYDVG GGYAQRVTVINGQQQIDKVYTSVNTDTHATDILADLGL

>11017-6007

MVHPLGLYNWDEISLIALGEEQKSHIQTKSMAIKVGN SVPDVTLQTPTGETVSLKNFLG EKIVVLYFYPKDDTPG
CTKEACGFRDSYTVFQEAGA EVIGVSN DTPNSHQQFANKYQLPFTLLSDGANQARKAFGVPSTLGLLPGRVTV
VIDTDGVVRHIFNSQLNFQGHIDESL KIVQSLTKDA

>11017-2698

MSQHEAHECLRVGQAAPDFTATAVYDQEFSEVKLSNYR GKYV VIFFYPLDFTFVCPT EITAFSDRYDAFKDLNTE
VLGISVDSEFSLAWTQTDRKSGGVGDLNYP LVS DIKKEISTAYNVLD PDAGVALRGLFIIDKEGVVQHATINLA

FGRNVDETLRTLQAIQHVQSHQDEVCWQPGDKTMNPDVKSQVYFESV

>11017-A0300

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VNSHKGWINDINETQNTVVNYPIADADQTVANLYGMIHPNANAKVTRTVFVIDPKKLRLLTYPPSTGRNN
EILRVLDSLQLTDNYSVATPVDWTDGDDVVVAPSISTADAKQKFKPGVNEIKPYLRMTPQPNR

>11017-4173

MSLATELQAVTENVRQQAPENVFTTMEAATAKLAATGITDQALQGTQMPDFELPDATGKSVSSELRAKGLL
ISFYRGNWCPCYCNLELQALQARLDDIAALGATLVAISPESPDQSLTTQEKFDLKFVLTDTGNQVARQFGLVFTLD
ESLRPIYNNFGIDITTHNGDQSFELVPATYLVAAAGTVLNHFVDVYRERLAPETALAWLQAAQ

>11017-5494

MSLRLGDTVNFQDSTAGTIDFFEWAGDSWVFLSHPADYTPVCTTELGSVSKLKPEFDKRHVKTIALSVDDA
QAHNGWIGDINETQNTTVDPILADADKKVSDLYDMIHPNANAKVTRTVFIIDNNKKLRASITYPPSTGRNFN
EILRVIDSLQLTDNYQVATPVDWQDGDVVVAPTIPTEEAKQKFKPGVTEIKPYLRMTPQPNK

>11017-2532

MTQSSGFFNQRYVNNFVPLPGKGEPAVGRAPDFELPRIGGDSVKLSDYRGQQPIFLAFTRIFTEKLCFPCYPHI
QDLKQRYSEIVDRGAELLMISSTDQVQSEQIVSDLDLPYPFLYNPKCESFRNYGAGQALGAPLPAQYIVDVGTI
RFRHMFVFDHNAAGMDEVLTILEGLIPQG

>11017-5336

MMTFAQSTSPKLLMGHTAPLLVQTLDHGLWRLADQTPHYTMVVFYRGLHCPVCEQYLTELDQKLSAFAQL
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NIGTHPFSRIDFDSLLAGLAYVIPNNYPLRGTA

>11017-4765

MVLTASTMLDLGTPAPNFQLPDVVSQQTISLETFAHRNVLLVMFICQHCPVFKHVQAEALQIGHDYSDQSLGIV
AISSNDIQSHPLDDPEHLTAMATSLGYNFPICFDEHQDVAKQYTAACPDDFFVDAHRKLVYRGQLDDSRPSNN
LMVTGEDLRGALDAALAEQPISANQKPSIGCNKWKPGNEPAYYG

>11017-3680

MAVFATERVPDVVFKTRVRDESVPGNPYRWQDKTTQDIFGGKRVVFLSLPGAFTPTCSSTHLPRYEELHEEIK
AQGVDEIICLSVNDAFVMFQWKGKHQGADKVFLLPDGNGEFTRKMGMLVDKSNLGFGMRSWRYSMVVNN
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>11017-3814

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VPLDNNYQTWKAYRNRYWPHLFLTNREGVITYHHIGEGAYQETEQTQALLG

>7120-2556

MISRRNFLHILLVSCFAVISWLNLPPTAYALGGKLPINQAPDFTLPTNTGDGKLSLGDRLGKVVLYFYPKDF
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PQGILRETFVKVNPVHSTEVLARLEKLQSTAS

>7120-2503

MSNIPQAGQPAPDFSTPDQNGNLVSLNDFQGGQWVVIYFYPKDDTPGCTTEAKDFTGLHQEFNQLGAKILGVS
PDSGKAHCKFIDKHNSINLLSDPEHQLIEAYGAWRLKKFMGKEYMGVARSTFLISTDGIAYAWPNVKTGHA
QAVLNKLQELINS

>7120-2375

MPLAVGTDAPAFTVKDTNGNTVSLSDFAGKTVVLYFYPKDDTPGCTKQACSFRAQSDYKNKDVVVLGVSAD
DEGSHQAFQKYNLNFPLADTNKTLISAYDVGDDGGYAKRVTVYIGPDGKIVHDASVNTTTHAGDVLAAALGL

>7120-3183

MPVKVGDSAPDFTLPAQNGSSVLSDFRGGKAVVLYFYPKDDTPGCTAESCAFRDRYEVFQTAGAEIIGVSGDS
NESHQKFASKYNLPFTLLSDKGDQVRKLYGATAAFGLFPGRVTTYVIDQQGVVQYVFDMSFNFQGHVEEALKTL
QQLASK

>7120-4641

MSITYGTQESLRVGGQAPDFTATAVVDQEFKTIKLSYRGKYVVLFFYPLDFTFVCPEITAFSDRYEEFKLNTEIL
GVSVDSEFSLAWIQTDKRSKGGVLDNYPLVSDIKKEVSDAYNVLDPAAGIALRGLFIIDKDGIIQHATINNLAFG
RSVDETLRTLQAIQYVQSHPDEVCPAGWQPGEKTMTPDPVSKVYFAAV

>7120-4404

MALRLGDTVNFQASTHGDIDFYAWAGDSWVVLFSHPADYTPVCTTELGTVAKLKPEFDKRNKAIALSVD
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DELLRVIDSLQLTDNYSVATPADWKDGDKVVIVPSLKDPEVLKEKFPKGYEVVKPYLRLTPQPNK

>7120-4642

MNADRHRYSKISVNSGVHLWFYHCIIYQLVDNFERFMLTSTDFSGLLNERFFRNFLPIPASNELRLDVGTPDFQLP
DITNGTLVKLSNYRGKQPILLAFTRIFTEKQYCPFCFPHIKALNENYEQFTNRGIEVLLVTSTDEKQSQIVVKDLGLK
MPLLSDPSCRAFRTYQVGQALGAPLPAQFVLDKDGRLRYKHLFSFFDHNASVEKLLGKFD

>7120-0513

MALTASTMVPIGTQAPDFHLPDVVSGKTISLSTFADKALLVMFICRHCPVFKHIQDELTRIGQDYSTSDLGIVAIS
ANDAKNYPDDAPESLKALAIELGWQFPFCYDETQETAKAYTAACTPDDFFVSDRQLAYRGQLDDSRPSNGKP
VTGADLRAAIDAVLAGKPVIGEQQPSIGCNKWKPTP

>7120-1206

MTILETSNTPVGGYAPDFELPGIDNQVHLSRYLDNFRAVGVVSLGNYCSYVNLVLDRLKGIQGEFGTDGFILIGI
NASDITEPSWSSLEKMKAFQAQNHENLFPYLWDSTQEVSRSGFATKTPIAFLIDSHGILRYRGQIDNHPQEPSSVG
EDYLRNAIAALFKGEEILVPETEPVGTSLIWRI

>29413-0485

MISRRNFLHILLVSCFAVISWLNFAPTAYALGGKLPAINQPAPDFTLPTNTGDGKLSLADFRGKWVLYFYPKDFT
SGCTIEARRFQQDLPTYVDKNVQIIGVSADDIDSHAFCDEGLKFPLLADTDGAVSKAYGSWIGFVSMRHSFII
DPQGILRETFVKVNPVHSTEVRLARLEKLQSAAS

>29413-0435

MSNFPQAGQPAPDFSTPDQNGNLVSLNDFHGQWVVIYFYPKDDTPGCTTEAKDFTGLHEEFHRLGAKILGVS
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AVLNKLQELTNS

>29413-0194

MPLAVGTDAPAFTVKDTNGNTVLSDFAGKTVVLYFYPKDDTPGCTKQACSFDAQSDYKNKDVVVLGVSAD
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>29413-3881

MPVKVGDSAPDFTLPAQNGSSVLSDFRGGKAVVLYFYPKDDTPGCTAESCAFRDRYEVFQTAGAEIIGVSGDS
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QLANK

>29413-2024

MSITYGTQESLRVGGQAPDFTATAVVDQEFKTIKLSYRGKYVVLFFYPLDFTFVCPEITAFSDRYEEFKLNTEIL
GVSVDSEFSLAWIQTDKRSKGGVLDNYPLVSDIKKEVSDAYNVLDPAAGIALRGLFIIDKDGIIQHATINNLAFG
RSVDETLRTLQAIQYVQSHPDEVCPAGWQPGEKTMTPDPVSKVYFAAV

>29413-1358

MALRLGDTVPNFTQASTHGDI DFYEWAGDSWVVLFSHPADYTPVCTTELGTVAKLKPEFDKRNVKAIALSVD
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DELLRVIDSLQ LTDNYSVATPADWKDGD KVVIVPSLKDPEVLKEKFPKGYEVVKPYLR LTPQPNK
>29413-2023

MLTSTDFSGLLNERFFRNFLPIPASNELRLDVGTPDFQLPDITNGTLVKLSNYRGKQPVLLAFTRIFTEKQYCPFCF
PHIKALNENYEQFTNRGIEVLLVTSTDEKQSQIVVKDLSLKMPLLSDPSCRTFRTYQVGGALGAPLPAQFVLDKD
GRLRYKHLFSFFDHNASIEKLEKFD
>29413-2915

MALTASIMVPIGTQAPDFHLPDVVSGKTISLSTFADKKALLVMFICRHCPVVKHIQDELTRIGQDYATRD LGIVAIS
ANDAENYPDDAPESLKALAIELGWQFPFCYDEQETAKAYTA ACTPDDFFVDDHRHLAYRGQLDDSRPSNGKP
VTGADLRAAIDAVLAGKPVIDEQKPSVGCNIKWKSTP
>29413-0627

MTILETSNTPVGGYAPDFELPGIDNHVHLSRYLDNFRVGVVSLGNHCPYVNL YLDR LKAIQGEFGAEGFILIGI
NASDITEPSWSSLEKMKAFANHKLNFYLDWSTQEVSRSFGATKTPIAFLIDSHGILRYRGQIDNHPQEPSSVG
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>39-L02380

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>39-E01510

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>39-O06760

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GEG
>39-A03490

MPVQVGD LAPDFTLTSQTGESVSLKDFRGNKAVVLYFYPKDDTPGCTAEACAFRDSYTFQETGAEVIGVSADSP
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MSAV
>39-M00250

MTSECIRVGLAAPDFAATAVIDQEFKTIKLE YRGKYVVLFFYPLDFTFVCPEITAFSDRAEEFSAINTQILGVSVD
EFSHLAWIQSDRQSGGVGDLNYPVLS DIKKEISAAYNVLDPEAGIALRGLFIIDKGGIIQHATINNLAFGRNVDET
RTLQAIQYVQANPDEVCPAGWQPGDKTMNPD PVKSKEFFAAI
>39-E02230

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PPSTRKTF AENHHLNYSLLSDFKGEVSTKYGAYICDGKNSNTIVYNRVAFLLDRNLRLIKIYPLHPLEEFTQKFLGEI
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>39-F00560

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LRVIDSLQ LTDNYSVATPADWQDGEDCVIVPSLKDPEELKQKFPKGYKEIKPYLRMTPQPNK
>39-J00990

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CYPHIKALNENYRAFVERGAEILMITSTDTAQSQTVVKDLGLKMPLLSDSSCGIFRLYHVGQALGAPLPAQFVLD
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>39-Q00510

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ANSIKTHPQDGPHELKNAETVGFSPYCYDETQEVAQAYTAACPDDFFLNSDRQLVYRGQLDDSRPGNNLP
VTGADLRAALDAILADQPINSQKPSIGCNIKWHPQ

>39-C03410

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YLKNAVSQLLASVAIAPETTPPIGSPIQWRR

>39-M02570

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DEIVCVSNDAFVMFQWGKQGGADKVLLPDGNGEFTRKMGMLVDKSNLFGMRSWRYSMVVNDGKIEK
IFVEPDFGDNCPDPEVSDADTMLAYLKG

>51142-1296

MLRRQILAILLAIIVIFSGTQTPALALGGPQPPLNESAPNFTLPTNTGDGEISLSDYRGQWVVLVYFYPQDFTPGCL
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REKFLGVRPAIHSQEVLAYLDEVNSNH

>51142-3358

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>51142-2409

MTIEGCLRVGQVAPDFTATVVIDQEFQTKLSSYRGKYVVLFFYPLDFTFVCPTEVIAFSDRYEEFAKINTEILAVSV
DSEFSLAWIQTPRTEGGVGDIAIYPLVSDLKEISTAYNILDPESGVALRGLFIIDKEGVIQHATINNLFSGRSVTEL
RTLKAIQHVQTNPEEVCADWQEGDKTMIPDPIKSIYFSAV

>51142-0135

MALQLGDTVDPDFTQETSEGTISFHEWAGDSWVVLFSHPADYTPVCTTELGTVASLKPEFDKRNKILALSVDV
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LRVIDSLQLTDYHQVATPANWKDGDCCVVVPSISTEEAKQKFPKGVTEVKPYLRMTPQPNK

>51142-4124

MMLTSTDFTGLINQRFFNNFLPIPATNQLLLGSIAPDFILPDITNNRMLRLGDYFHQQPVILAFTRIFTEKQYCPFC
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KTGTIQYKHLFSFMDHNASVDQLLKIS

>51142-3126

MGAIETVPSVVFKTRVRDESVPGNPYRWQDLTSEEIFKGKKVIVFSLPGAFTPTCSSNHLPRYEELYDEFKALGV
DEVICISVNDAFVTFQWGKQEAKNVLLPDGNGEFTRKMGMLVDKSNLFGMRSWRYSMLVNDCKIEKM
FVEPGYEDNCPDPEVSDADTMLAYLKGTESSGVSEPVKAFVG

>51142-3631

MLMVKTLSTMLPLGKAPNFSLEDVVSGKKISLDTFADKKALLVMFICVHCPFVKHLQDALAALGKEYVDKGLGI
VAISANDITTHPDDSPHEMKMAETLGLNFPFCYDESQEVAKAYTAACPDDFFLDRDNLVYRGQFDDSRPG
NDVPITGKDLKAAIEDVLRDRKVDVDTQQKPSIGCNIKWKAGNEPPYFGA

>7424-2927

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>7424-4280

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>7424-3638

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>7424-5046

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>7424-0090

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>7424-0397

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>7424-1402

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>7424-4031

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>7424-2508

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>7425-2289

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>7425-1511

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>7425-3716

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>7425-5136

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>7425-0928

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>7425-0215

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>7425-4300

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>7425-0955

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>7425-1596

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>8801-1115

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>8801-3492

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>8801-1631

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>8801-1491

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>8801-4218

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>8801-3616

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>8801-4240

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>7421-3389

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>7421-2376

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>7421-2375

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>7421-0506

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>7421-3158

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>7421-2155

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>7421-0029

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>7421-3964

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>7421-2108

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>843-15330

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>843-44920

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>843-60930

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>843-35830

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>843-36510

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>843-62780

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>843-59730

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>29133-F2425

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>29133-R6477

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>29133-F2872

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>29133-R0493

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>29133-F6082

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>29133-F6498

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>29133-F6083

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>29133-F6135

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>29133-F2528

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>29133-R4657

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>29133-R6111

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>med4-0903

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>med4-0079

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>med4-0345

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>med4-0856

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>med4-0283

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>9312-0897

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>9312-0082

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>9312-0353

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>9312-0944

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>9313-1012

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>9313-1622

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>9313-0387

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>9313-0754

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>9313-1186

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>120-0932

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>120-0093

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>120-0978

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>9601-09581

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>9601-00921

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>9601-03811

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>9601-10131

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>9211-08571

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>9211-15101

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>9211-00881

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>9211-09041

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>9215-09891

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>9215-00921

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>9215-03801

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>9215-10441

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>9215-03081

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>9301-09561

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>9301-00911

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>9301-03801

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>9301-10121

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>9303-10801

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>P9303-02611

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>9303-19011

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>9303-14621

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>9303-08311

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>9303-25151

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>9515-09851

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>9515-00891

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>9515-03821

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>9515-09331

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>1A-09761

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>1A-15651

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>1A-16391

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>1A-01441

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>1A-10331

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>1A-03631

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>2A-0304

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>2A-0727

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>2A-0787

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>2A-1443

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>2A-0352

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>2A-1649

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>6301-0883_d

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>6301-2152_c

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>6301-2287_c

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>6301-1915_d

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>6301-1793_d

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>6301-1657_c

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>6301-2361_c

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>7942-0642

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>7942-1942

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>7942-1806

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>7942-2180

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>7942-2309

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>7942-2449

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>7942-1730

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>9311-1400

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>9311-2508

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>9311-1556

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>9311-1322

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>9311-0254

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>9311-0689

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>9605-1406

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>9605-1141

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>9605-2307

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>9605-1324

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>9605-0215

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>9902-1080

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>9902-1316

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>9902-0386

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>9902-1150

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>9902-0242

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>JA23-2186

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>JA23-0523

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>JA23-1057

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>JA23-1376

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>JA23-2254

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>JA23-0113

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>JA23-0140

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>JA23-2461

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>JA33-0907

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>JA33-2145

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QLTGS

>JA33-0672

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>JA33-2305

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AVG

>JA33-0537

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>JA33-2849

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>JA33-1949

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>JA33-2781

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>7002-A0109

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>7002-A1108

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>7002-A0558

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>7002-A0320

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>7002-A1383

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>7002-A0793

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>307-1384

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>307-0392

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>307-1342

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>307-1238

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>307-0386

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>307-2285

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>7803-1236

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>7803-1042

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>7803-2172

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>7803-1118

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>8102-1280

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>8102-1015

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SLQG

>8102-2162

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>8102-1213

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>8102-0221

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>6803-0221

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>6803-0242

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>6803-0755

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>6803-1198

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>6803-1159

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>6803-1621

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>BP1-1194

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>BP1-1451

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LERLQG

>BP1-1198

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>BP1-1454

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>BP1-2261

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>BP1-1289

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>BP1-1788

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>101-2703

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>101-3959

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>101-3182

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>101-0235

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>101-5038

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>101-0234

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>101-3842

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>101-0162

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>101-2011

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