

A

1 112

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hsCHST11 (1) ---MKPALLEVMMNRICRMLATCGSFLVLFVFSQSMHPVMMRNPFGVICCRKGS-----RSPLEEVNPIQLELSNTAVLQ-----
dr_chst11 (1) ---MKQTILDLMRMSRIRCMVLAICGSSFLVLFVFSQSMFQPMRNRNPFPAAGGCCRKGSS-----RVALLEEVNPTQAEFSAAVLQ-----
hsCHST12 (1) -----TKAALFRFLVLDLGSVFMILLIIVYDSDAGAAPHYHTSPFRPHGPPPLP---TPGPDR---DRELTAADSDVDFDKFLSAGVQSDLLPRKE---TEQPP
dr_chst12a (1) -----GKSLFRFRIFVIVGAVFMILLIIVYDSDVGAANFYHTTSGPHPSRLSPQGRGPEKVKVEEDKSSFLTDIDAFVYQPLEGTADPTQVGRGPEPPGDDHNS
dr_chst12b (1) MGSITDRFVIMVYQLQFFLLGLFLFIIFIIIRDDVDKDTFYHAASSTPALPASVY---FSEF-----WTSDDLTKWKESSRSVKPLNTIIASAENNLTHMFM
hsCHST13 (1) -----MGRCCRRRVLAAACGAALLLCAAPRSRPAFNGRAIGSSWLGGK-----RSPLEEVLDLQDPRSTLAKVER-----
dr_chst13 (1) -----MIPKVGRFLATCGSSFLVLFVFSQMSKASQEIISGRDSFVVKSG-----RSPLEEVLDLQDPRSTLAKVER-----
hsCHST14 (1) -----MPFRFVPLAANGAEPLRARRAPGRARAGLGGPLLPISMFMFAIVASGG-----LLLMIEKGLLAEKPLFLHPGREGATWARGKAPK---
dr_chst14 (1) -----PPRKEYGIKRASGSLVHVRAPSSATTIRRSVAVPSVTFVAIVASGG-----LLLMIEKGLLAEKPLFLHPGREGATWARGKAPK---

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113 224

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hsCHST11 (80) -----MRRDQITDTCRANATSRR---KRRVITFD---LRHLVVDDEHELYCYVVKVACNWKRMVVLV---GRKYSN
dr_chst11 (80) -----ARRDQVATCCHAHASSR---KRRVITFD---LRHLVVDDEHELYCYVVKVACNWKRMVVLV---GRKYSN
hsCHST12 (93) APGSMEESVRGVDWSPRDARRSPDQGRQAERRSVYRGGCAN-SSLAFTPKRAFDDENSE---LSHLVDDRHGALICYVVKVACNWKRMVVLVSGLLH-RGAPYRD
dr_chst12a (104) SEKSDEKFPVPRREKHLSPIDPEKKQKQENRKLQVCGNKVDFDPGKNTFDDEPNKE---LDLHLVDDRHGALICYVVKVACNWKRMVVLVSESLV-DGVVYQD
dr_chst12b (99) QSS-----SK---NLKLRARRKRIKELCCQANSILIFPGKFRTFDQPSK---LDLHLVDDRHGALICYVVKVACNWKRMVVLVQKLLKAPGAPYLD
hsCHST13 (72) -----QRDLNLSASRRHAR---RQRLLQEF---LRHLVVDDEHELYCYVVKVACNWKRMVVLV---GQARGP
dr_chst13 (71) -----GRKLEEFCTHTRH---KRRVITFD---LRHLVVDDEHELYCYVVKVACNWKRMVVLV---GDRFRP
hsCHST14 (90) -PGG---L-----SLRAGDADLQVRDVRNRTIRAVCGQPGMP---RDPWDLVPGQRRTLRHLVVDDEHELYCYVVKVACNWKRMVVLVAG-----VLD
dr_chst14 (83) -----SDTAADVESQIVETIRNRTIRSVCGQRNMP---HSVWISLSLQKRTLQHLVVDDEHELYCYVVKVACNWKRMVVLVAG-----ALA

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225 336

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hsCHST11 (147) FMEIPANEHVSANIKTLN-----QYIPEINRRLKSYMKFLVREFFERLISAYRNKTKQYINISFKRYGKTLIKRORKN----TQEAELRKGDDVKEEESVALELD
dr_chst11 (147) FMEIPANEHVSANIKTLN-----QYIPEINRRLKSYMKFLVREFFERLISAYRNKTKQYINISFKRYGKTLIKRORKN----TQEAELRKGDDVKEEESVALELD
hsCHST12 (199) LRIRPREHVNNSAHLTFKWRRYGKIRHLKVKLKKYTKFLVREFFERLISAYRNKTKQYINISFKRYGKTLIKRORKN----TQEAELRKGDDVKEEESVALELD
dr_chst12a (211) PLDTPQELIHNLSLHFLFKWRRYGKIRHLKVKLKKYTKFLVREFFERLISAYRNKTKQYINISFKRYGKTLIKRORKN----TQEAELRKGDDVKEEESVALELD
dr_chst12b (189) PLDTPQELIHNLSLHFLFKWRRYGKIRHLKVKLKKYTKFLVREFFERLISAYRNKTKQYINISFKRYGKTLIKRORKN----TQEAELRKGDDVKEEESVALELD
hsCHST13 (135) FRASIQEHAHAGPRVPLA-----DFPAENRRLKAYLAFLVREFFERLISAYRNKTKQYINISFKRYGKTLIKRORKN----TQEAELRKGDDVKEEESVALELD
dr_chst13 (135) PLAIIPANEHHTAGNRSLS-----EYSTAEINRKLKAYLAFLVREFFERLISAYRNKTKQYINISFKRYGKTLIKRORKN----TQEAELRKGDDVKEEESVALELD
hsCHST14 (175) SVDLRKMDHREDLFLADL-----PEE---LRHLVVDDEHELYCYVVKVACNWKRMVVLVAG-----VLD
dr_chst14 (164) NVDIKVKMDHREDLFLADL-----PEE---LRHLVVDDEHELYCYVVKVACNWKRMVVLVAG-----VLD

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337 446

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hsCHST11 (247) FHTORPEEPEHMQTVYSLCHPCHTHYDLVCKYETLEESNMQALAVGSGYLRFYTKASTTIDEMTTEFQNLSEHQTVLEVYKDFKDLNYSVSYKYLE
dr_chst11 (247) FGTORPEEPEHMQTVYSLCHPCHTHYDLVCKYETLEESNMQALAVGSGYLRFYTKASTTIDEMTTEFQNLSEHQTVLEVYKDFKDLNYSVSYKYLE
hsCHST12 (310) FHTKLAPEPEHMQTVYSLCHPCHTHYDLVCKYETLEESNMQALAVGSGYLRFYTKASTTIDEMTTEFQNLSEHQTVLEVYKDFKDLNYSVSYKYLE
dr_chst12a (320) FSTEKMPPEPEHMQTVYSLCHPCHTHYDLVCKYETLEESNMQALAVGSGYLRFYTKASTTIDEMTTEFQNLSEHQTVLEVYKDFKDLNYSVSYKYLE
dr_chst12b (300) FHTKLAPEPEHMQTVYSLCHPCHTHYDLVCKYETLEESNMQALAVGSGYLRFYTKASTTIDEMTTEFQNLSEHQTVLEVYKDFKDLNYSVSYKYLE
hsCHST13 (235) FRIRREPEPEHMQTVYSLCHPCHTHYDLVCKYETLEESNMQALAVGSGYLRFYTKASTTIDEMTTEFQNLSEHQTVLEVYKDFKDLNYSVSYKYLE
dr_chst13 (235) FHTORPEEPEHMQTVYSLCHPCHTHYDLVCKYETLEESNMQALAVGSGYLRFYTKASTTIDEMTTEFQNLSEHQTVLEVYKDFKDLNYSVSYKYLE
hsCHST14 (270) EDPER---MNEHMPVYHLCQPCAHYDLYSYERLESASILERVAPQHFPERQRTWYKVPKELHYLCTTPQKFLLELPKILDESLEKGFENNTTTEYCRH
dr_chst14 (261) EDPER---MNEHMPVYHLCQPCAHYDLYSYERLESASILERVAPQHFPERQRTWYKVPKELHYLCTTPQKFLLELPKILDESLEKGFENNTTTEYCRH

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B

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hsCHST3 (1) ----MEKGLTLPQDCDFVHSLKNSYVAFLEFVIFIE----FENKISVYSRKLKQIPQALADANITDPALILAENASLLSLESDSAFSQLQSRNLNLSLQGVPEFMAAEEEBEEQRKEEPPRP
dr_chst3a (1) ----MKNVAVILCIVADYIE----FENKISVYSRKLKQIPQALADANITDPALILAENASLLSLESDSAFSQLQSRNLNLSLQGVPEFMAAEEEBEEQRKEEPPRP
dr_chst3b (1) ----MKNVAVILCIVADYIE----FENKISVYSRKLKQIPQALADANITDPALILAENASLLSLESDSAFSQLQSRNLNLSLQGVPEFMAAEEEBEEQRKEEPPRP
hsCHST7 (1) ----MKGRRRRRREYCKFALLHLVAVLLEPFLDGG---DQKGRKRCPCQRSVWVLEAAAG-----E----RE----QGAEARAAEFANQPRFFSNLGSVA
dr_chst7 (1) WSRAAQPNPSEAMKRLQKKYIILIGSVALLPVYDYRSKSPHKGQ---QKQPCDEESTALMSIRGAN-----STEDESNRSQ

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137 272

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hsCHST3 (127) AVAIP---RSLVLMNTRTSSSFVCFNQOCN---FYLDFEHWERTSFEPGAANASALVDRVLCQFLFLYVDEHFTI---LFEHMLQFPEFSGSSRCLCFVCPVFAVFLRCHNRK
dr_chst3a (68) SQAG---RSLVLMNTRTSSSFVCFNQOCN---FYLDFEHWERTSFEPGAANASALVDRVLCQFLFLYVDEHFTI---LFEHMLQFPEFSGSSRCLCFVCPVFAVFLRCHNRK
dr_chst3b (70) DSTG---QSLVLMNTRTSSSFVCFNQOCN---FYLDFEHWERTSFEPGAANASALVDRVLCQFLFLYVDEHFTI---LFEHMLQFPEFSGSSRCLCFVCPVFAVFLRCHNRK
hsCHST7 (94) EAVSREKQHYHHTWRTSSSFVCFNQOCN---FYLDFEHWERTSFEPGAANASALVDRVLCQFLFLYVDEHFTI---LFEHMLQFPEFSGSSRCLCFVCPVFAVFLRCHNRK
dr_chst7 (89) EAVSREKQHYHHTWRTSSSFVCFNQOCN---FYLDFEHWERTSFEPGAANASALVDRVLCQFLFLYVDEHFTI---LFEHMLQFPEFSGSSRCLCFVCPVFAVFLRCHNRK

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273 408

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hsCHST3 (252) CC---LNLTLMAEAKRREEMALAVRRCLEFQVLAEDPRDLRVLQVLRDPRAVLAASRVFAKRYTWKWKDDEG-----DQGLREEVQRIRGNISIRLSAEVCL
dr_chst3a (194) CC---LNLTLMAEAKRREEMALAVRRCLEFQVLAEDPRDLRVLQVLRDPRAVLAASRVFAKRYTWKWKDDEG-----DQGLREEVQRIRGNISIRLSAEVCL
dr_chst3b (196) CC---LNLTLMAEAKRREEMALAVRRCLEFQVLAEDPRDLRVLQVLRDPRAVLAASRVFAKRYTWKWKDDEG-----DQGLREEVQRIRGNISIRLSAEVCL
hsCHST7 (202) CERSCPVALRALEAEKSPVYVLDVLDLGVVLELRDPPGANNVQLVLRDPRAVLAASRVFAKRYTWKWKDDEG-----DQGLREEVQRIRGNISIRLSAEVCL
dr_chst7 (215) CS-KCQKDLRELEKESKSPVYVLDVLDLGVVLELRDPPGANNVQLVLRDPRAVLAASRVFAKRYTWKWKDDEG-----DQGLREEVQRIRGNISIRLSAEVCL

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409 534

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hsCHST3 (357) RCFAMLVGVYLVRYEVLVAGGKQKAREYVFAKLEFVPCQEDVQKNQCAHDG---GIVSICQNSSEQEKWFSVFPKLAQVQVACFAMKFLVYKLRDAAALTRSVSLEERTEFWT
dr_chst3a (298) SQKMLKRYVLYRYEVLVAGGKQKAREYVFAKLEFVPCQEDVQKNQCAHDG---GIVSICQNSSEQEKWFSVFPKLAQVQVACFAMKFLVYKLRDAAALTRSVSLEERTEFWT
dr_chst3b (250) -----
hsCHST7 (361) GAFAMLVGVYLVRYEVLVAGGKQKAREYVFAKLEFVPCQEDVQKNQCAHDG---GIVSICQNSSEQEKWFSVFPKLAQVQVACFAMKFLVYKLRDAAALTRSVSLEERTEFWT
dr_chst7 (323) NAFVYKMLKRYVLYRYEVLVAGGKQKAREYVFAKLEFVPCQEDVQKNQCAHDG---GIVSICQNSSEQEKWFSVFPKLAQVQVACFAMKFLVYKLRDAAALTRSVSLEERTEFWT

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C

1 141

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hsCHST15 (1) MRHCINCCIQLLPDGAHQVQCQGGPHHQCPTCGENKILFRVDSQMNLAVERVTEGENWGGELR---FVGGRCSLVGLIMTLMASYIIGAHQELLSPFYVGGFFNPSLMDSENPDTEKHHQSS
dr_chst15 (1) -----MDHKVLLSPEYELVCRNKQTRDWTGUTS---ENNRAGQVWGLTSLTYSVIRIIFSFVGLMIVLMASYIIRDQKGLFSPSPVFTVV---HQVQ

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142 282

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hsCHST15 (140) VNNVSYMKDYPSLTLNSTRITRITRQFDLEDLKQLHMFVTPNFKLSKSPCWYEESQNTDPTLNSVLYSKRFRITDARLRAFVHLAHACHRSLRCLFHYIIGQPKCGTDLDRLRHLEPK
dr_chst15 (101) VNNVSYMKDYPSLTLNSTRITRITRQFDLEDLKQLHMFVTPNFKLSKSPCWYEESQNTDPTLNSVLYSKRFRITDARLRAFVHLAHACHRSLRCLFHYIIGQPKCGTDLDRLRHLEPK

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283 423

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hsCHST15 (281) FFAKREPHWTRKRFGLVIRDLDRDRYFEDYLDLFLAAHQHGGQSSAEQSMNTIIGGEASASTMNDNNAVFPYDNDGEPFPLTDFPIHAFQPNALIVMLRDPVERLYSDYLYSSNKAADFREK
dr_chst15 (241) FFAKREPHWTRKRFGLVIRDLDRDRYFEDYLDLFLAAHQHGGQSSAEQSMNTIIGGEASASTMNDNNAVFPYDNDGEPFPLTDFPIHAFQPNALIVMLRDPVERLYSDYLYSSNKAADFREK

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424 563

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hsCHST15 (422) QCFENCLVYVAVVNTLNANVPRVQLGLVAVLLEWLSVDFQDFLIRLEDAHARVYVHVFQFLVGLPEKQGLLTKSPASNARFEDRNLGPHWITQKILRDFYVFNALQVLALEAFAKT
dr_chst15 (381) QCFENCLVYVAVVNTLNANVPRVQLGLVAVLLEWLSVDFQDFLIRLEDAHARVYVHVFQFLVGLPEKQGLLTKSPASNARFEDRNLGPHWITQKILRDFYVFNALQVLALEAFAKT

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D

1 138

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hsUST (1) MKKQHPGGGADPWFHAPMGAPPGLGMRARVPLLPFLFRSLRDYVFCMATLIVFCGLSLVQLSGPFFLILDRQYLGNSVYLDHGGFPPSVLFFPFSQVYVNRVKGCSRTVLLLRILEKHFNLVSDI
dr_ust (1) MNYSSSRLLNHSASHTRDN-----RQFVLSALGIFSLRDLVFCMATLIVFCGLSLVQLSGPFFLILDRQYLGNSVYLDHGGFPPSVLFFPFSQVYVNRVKGCSRTVLLLRILEKHFNLVSDI

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139 276

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hsUST (139) HNKRTLTHNEKMLKINISTAECPFLTRRVHFLNRRFGGQVPIYINIRDPNRLSNYFFRRFGDNRGQNHNRTRISNRKSERVLDINECINNYPECSNPRLFYIPYFCQHPREPGENALERAKLNNE
dr_ust (132) HNKRTLTHNEKMLKINISTAECPFLTRRVHFLNRRFGGQVPIYINIRDPNRLSNYFFRRFGDNRGQNHNRTRISNRKSERVLDINECINNYPECSNPRLFYIPYFCQHPREPGENALERAKLNNE

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277 414

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hsUST (277) NPLVGLIELEEDVLLILLERFLPYKGLIYVDKRRKGNVYKTKLTPAALVYQRMVEYVHVKVQPHLLVFLKRVHVSQPLRHHFITPTEPEEEDBEQKWLIDYKR-----
dr_ust (270) NPLVGLIELEEDVLLILLERFLPYKGLIYVDKRRKGNVYKTKLTPAALVYQRMVEYVHVKVQPHLLVFLKRVHVSQPLRHHFITPTEPEEEDBEQKWLIDYKR-----

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hsDSE (1) -----NRHTRGPFVFIYLCPVSYAYITDENPEVMIPTFNANY--SHMLYLSRAEVAEQLASREHAAARTEAVHTMLSELELFDWPKLTSAPWNEIGNNIGALAAVLYENIEARMAKIYERMAKQ
dr_dse (1) -----NRHTRGPFVFIYSLVLAAPGPAAVDPTGGVAPLGGNYGTHMLYGLTEVEEELQRAIGKKAQQQLREGEALERPEEELFPWSPALTSAPWNEIYGNNGLLSMTMLYPRRAGALVAKYMERMAKQ
hsDSEL (1) MALMPTGHLHLLFALIMFATFEESVYINSEWAVFTDDIDQFKTKVQDFRPNKLLKSMHLSLYDAGIQARQKRRASHLHFRALSAVTVMLNNTYLLPKKHADTSAPWNEIYGNNGPPALVYLLCHEDKVAFFVLYEDRMVYK
dr_dselb (1) -----MENQRSAFLLCVAVGLACGSSASDRYVSLNEHQRDNATLSHLHKLKYDHTVEVRLKPKASTARRRQVQLRANAVSILNAAVQQLNHEDLGRKRWNEIYGNNGPPALVYLLCHEDKVAFFVLYEDRMVYK
dr_dsela (1) -----NSLQQQRKPKKACAEQKLEAATSSSKKQLQNHHTTNTTAVLTAALVLAHQDTEKMGKVSINYMERWMLLSHWVDSGLSEGVAYSYTAKSITQVFLAQRHESDHTQMRVYK
157
hsDSE (138) SMLKDAFWDEVPFAHSLVFATADFLNLSKTCQQRVFNANASGYMYTETRYRNFVFMVYLNHHPQNCMLITGSLVNNQGYLQELAYITKQVFTMERSEVLLREITDGLSLYEGVAYSYTTSFQYMLVDRHFNINFGHPMAKQ
dr_dse (140) NMYKDAFWDEVPFAHSLVFATADFLNLSKTCQQRVFNANASGYMYTETRYRNFVFMVYLNHHPQNCMLITGSLVNNQGYLQELAYITKQVFTMERSEVLLREITDGLSLYEGVAYSYTTSFQYMLVDRHFNINFGHPMAKQ
hsDSEL (157) DMYENAPGDEVPFAHSLVFATADFLNLSKTCQQRVFNANASGYMYTETRYRNFVFMVYLNHHPQNCMLITGSLVNNQGYLQELAYITKQVFTMERSEVLLREITDGLSLYEGVAYSYTTSFQYMLVDRHFNINFGHPMAKQ
dr_dselb (143) DMYENAPGDEVPFAHSLVFATADFLNLSKTCQQRVFNANASGYMYTETRYRNFVFMVYLNHHPQNCMLITGSLVNNQGYLQELAYITKQVFTMERSEVLLREITDGLSLYEGVAYSYTTSFQYMLVDRHFNINFGHPMAKQ
dr_dsela (1) -----NSLQQQRKPKKACAEQKLEAATSSSKKQLQNHHTTNTTAVLTAALVLAHQDTEKMGKVSINYMERWMLLSHWVDSGLSEGVAYSYTAKSITQVFLAQRHESDHTQMRVYK
313
hsDSE (294) FHLRFLVLLFGFQRTVGLASNSYNMFGYSPESQLVFLIQLVYVNGSNNLALIRKRRHRRGHGQCFQRMFTLHTEVNNVNLALAEYGYSRPFTIESNGVNTYAGLIVGNTVSPFKSGKLGGRALVIVIAHAKVNSWDGMSFNFS
dr_dse (296) FHLRFLVLLFGFQRTVGLASNSYNMFGYSPESQLVFLIQLVYVNGSNNLALIRKRRHRRGHGQCFQRMFTLHTEVNNVNLALAEYGYSRPFTIESNGVNTYAGLIVGNTVSPFKSGKLGGRALVIVIAHAKVNSWDGMSFNFS
hsDSEL (312) FHLRFLVLLFGFQRTVGLASNSYNMFGYSPESQLVFLIQLVYVNGSNNLALIRKRRHRRGHGQCFQRMFTLHTEVNNVNLALAEYGYSRPFTIESNGVNTYAGLIVGNTVSPFKSGKLGGRALVIVIAHAKVNSWDGMSFNFS
dr_dselb (298) FHLRFLVLLFGFQRTVGLASNSYNMFGYSPESQLVFLIQLVYVNGSNNLALIRKRRHRRGHGQCFQRMFTLHTEVNNVNLALAEYGYSRPFTIESNGVNTYAGLIVGNTVSPFKSGKLGGRALVIVIAHAKVNSWDGMSFNFS
dr_dsela (129) FHLRFLVLLFGFQRTVGLASNSYNMFGYSPESQLVFLIQLVYVNGSNNLALIRKRRHRRGHGQCFQRMFTLHTEVNNVNLALAEYGYSRPFTIESNGVNTYAGLIVGNTVSPFKSGKLGGRALVIVIAHAKVNSWDGMSFNFS
469
hsDSE (450) HEHFDQNSFTFAPNQLVPEALYGFVYFFNVMVLSVAVKSKSFSVVGQTEDCSSKNSVXKHDLASCOQRVVAEKKLVVIRREAVGAYNPQANNNQNNLLHPQLLLVQHLGELVLEASFFRNLDIFVYVFNISV
dr_dse (452) HEHFDQNSFTFAPNQLVPEALYGFVYFFNVMVLSVAVKSKSFSVVGQTEDCSSKNSVXKHDLASCOQRVVAEKKLVVIRREAVGAYNPQANNNQNNLLHPQLLLVQHLGELVLEASFFRNLDIFVYVFNISV
hsDSEL (467) HEHFDQNSFTFAPNQLVPEALYGFVYFFNVMVLSVAVKSKSFSVVGQTEDCSSKNSVXKHDLASCOQRVVAEKKLVVIRREAVGAYNPQANNNQNNLLHPQLLLVQHLGELVLEASFFRNLDIFVYVFNISV
dr_dselb (453) HEHFDQNSFTFAPNQLVPEALYGFVYFFNVMVLSVAVKSKSFSVVGQTEDCSSKNSVXKHDLASCOQRVVAEKKLVVIRREAVGAYNPQANNNQNNLLHPQLLLVQHLGELVLEASFFRNLDIFVYVFNISV
dr_dsela (284) HEHFDQNSFTFAPNQLVPEALYGFVYFFNVMVLSVAVKSKSFSVVGQTEDCSSKNSVXKHDLASCOQRVVAEKKLVVIRREAVGAYNPQANNNQNNLLHPQLLLVQHLGELVLEASFFRNLDIFVYVFNISV
625
hsDSE (603) HSAFVQRKGLVYKMMWDDDTYSEKNTFASVTPRGVYNGVYVNVIMHRSFTLAVYVPIGSDSDVQFTVHGDS--QQLVETATEKRAYTYLWTGATV-----QSFAQIADRHKLLDNNIAIKSSI-----PEVKDYAAVVE
dr_dse (605) HSAFVQRKGLVYKMMWDDDTYSEKNTFASVTPRGVYNGVYVNVIMHRSFTLAVYVPIGSDSDVQFTVHGDS--EELVETATEKRAYTYLWTGATV-----KPMAMLVDOQKVVPEVPIGIKEQP-----PEVEYAAVVE
hsDSEL (621) KCAIMDVWDARVYKMFVPHHNSFMASVQEAQAAEFKRRWTFQVNVYVQMEPTITRVAIVYVYVYVNSCRVSDSNPLGISEANVNTVSVVIVDHNKTRFNLGFGFASADQGTFRPLDTGAVKVRVDRITLPPKFKFNIVY
dr_dselb (607) KCAIMDVWDARVYKMFVPHHNSFMASVQEAQAAEFKRRWTFQVNVYVQMEPTITRVAIVYVYVYVYVNSCRVSDSNPLGISEANVNTVSVVIVDHNKTRFNLGFGFASADQGTFRPLDTGAVKVRVDRITLPPKFKFNIVY
dr_dsela (438) KCAIMDVWDARVYKMFVPHHNSFMASVQEAQAAEFKRRWTFQVNVYVQMEPTITRVAIVYVYVYVYVNSCRVSDSNPLGISEANVNTVSVVIVDHNKTRFNLGFGFASADQGTFRPLDTGAVKVRVDRITLPPKFKFNIVY
781
hsDSE (744) QNQHFKFVQLLQVLSRVNNTASAKTERRRFRKQKTEEAETFAISQQQQQSKSKKNRAKRYKVFVAETLFAQIEVNE-----KLRQKQILQAKEVLEEDEMKDLVDFVYKHKNGLGRVQANVVTISRRA
dr_dse (745) QNQHFKFVQLLQVLSRVNNTASAKTERRRFRKQKTEEAETFAISQQQQQSKSKKNRAKRYKVFVAETLFAQIEVNE-----KLRQKQILQAKEVLEEDEMKDLVDFVYKHKNGLGRVQANVVTISRRA
hsDSEL (777) GLVLRVLLVLPQWVLSRKRKRLVLLVLAALPFLVDVSTVSEPKAWTR---TEAEGSLSSEGHHMDVATVTRKGRALVLEQVFNSSDPLVRYVAVVLELELDFVADCEKYSVLSRFLVGRVQLVQD
dr_dselb (762) LLTFLVLAFLKRRKLSLNSMLVHCTLLVYVAVVLLSNVYFGVLLVKNPKD-----SSLYHSDSNIPVAVYVITSNPSSSLELQHDVNSSDVPLVRYVAVVLELELDFVADCEKYSVLSRFLVGRVQLVQD
dr_dsela (587) GAVLRSVYVPLQVLRVNSVLAASLAVVLELLVSSSDVLLVRYKWHGA-GTDPELQVPTQQQLLAVVYVITSNPSSSLELQHDVNSSDVPLVRYVAVVLELELDFVADCEKYSVLSRFLVGRVQLVQD
937
hsDSE (894) PSLASVYTRVFLVNLN-----IATFVVMAMOLYVQRVOSLHGQ-----KLDVALLIDVLLVNVVSCSOSQC-----KLDVALLIDVLLVNVVSCSOSQC-----
dr_dse (885) VFSTTSYRFLVNLN-----IATFVVLAVLITRQRVOSLHGQ-----KLDVALLIDVLLVNVVSCSOSQC-----KLDVALLIDVLLVNVVSCSOSQC-----
hsDSEL (930) TKVHLQNLVHEPNRGLAQYFAMNKDKRRKFRRESLEFQRSQMKGAFDRVRAIARVRLVYVSAVFLVSSSSTWIKLHLEQVYVAAVAVLADPRAWIYKNSVSPSLYSLKNNPEHAKVLEGGKKNLNGYAFVLEPR
dr_dselb (909) VKVHLQNLVHEPNRGLAQYFAMNKDKRRKFRRESLEFQRSQMKGAFDRVRAIARVRLVYVSAVFLVSSSSTWIKLHLEQVYVAAVAVLADPRAWIYKNSVSPSLYSLKNNPEHAKVLEGGKKNLNGYAFVLEPR
dr_dsela (742) THFVLSVPLRAG-----GR--P-----VVEVREARVTVQVNNVAVVNLCSVWALKLFLVLAATPSVAVVADPRAWIYKNSVSPSLYSLKNNPEHAKVLEGGKKNLNGYAFVLEPR
1093
hsDSE (959) -----
dr_dse (950) -----
hsDSEL (1086) KEVSKSNVAQLLHMLVNTAAALINTDLPVTSOLVPEDEVHFTQKTERFAPLQSPSPASLNGVLLVNSTNLVYVYEGEPTNTNVVQNNPRDLEKLIENIQTWVDRVGYVFMDFMD----
dr_dselb (1060) MIVSQPDPNPQLLQVLMVHNSACVSSGLPTQTLVHPEDEVHFTQKTERFAPLQSPSPASLNGVLLVNSTNLVYVYEGEPTNTNVVQNNPRDLEKLIENIQTWVDRVGYVFMDFMD----
dr_dsela (863) QLVRSNSAVQLLHMLVNTAAALINTDLPVTSOLVPEDEVHFTQKTERFAPLQSPSPASLNGVLLVNSTNLVYVYEGEPTNTNVVQNNPRDLEKLIENIQTWVDRVGYVFMDFMD----
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