A

Predicted NLSs in query sequence

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ESYIEDEDSFRNCLLSCERLQDEEASMGASYSKSLIKLLLGIDILQPAII 150
KTLFEKLPEYFFENKNSDEINIPRLIVSQLKWLDRVVDGKDLTTKIMQLI 200
SIAPENLQHDIITSLPEILGDSQHADVGKELSDLLIENTSLTVPILDVLS 250
SLRLDPNFLLKVRQLVMDKLSSIRLEDLPVIIKFILHSVTAMDTLEVISE 300
LREKLDLQHCVLPSRLQASQVKLKSKGRASSSGNQESSGQSCIILLFDVI 350
KSAIRYEKTISEAWIKAIENTASVSEHKVFDLVMLFIIYSTNTQTKKYID 400
RVLRNKIRSGCIQEQLLQSTFSVHYLVLKDMCSSILSLAQSLLHSLDQSI 450
ISFGSLLYKYAFKFFDTYCQQEVVGALVTHICSGNEAEVDTALDVLLELV 500
VLNPSAMMMNAVFVKGILDYLDNISPQQIRKLFYVLSTLAFSKQNEASSH 550
IQDDMHLVIRKQLSSTVFKYKLIGIIGAVTMAGIMAADRSESPSLTQERA 600
NLSDEQCTQVTSLLQLVHSCSEQSPQASALYYDEFANLIQHEKLDPKALE 650
WVGHTICNDFQDAFVVDSCVVPEGDFPFPVKALYGLEEYDTQDGIAINLL 700
PLLFSQDFAKDGGPVTSQESGQKLVSPLCLAPYFRLLRLCVERQHNGNLE 750
EIDGLLDCPIFLTDLEPGEKLESMSAKERSFMCSLIFLTLNWFREIVNAF 800
CQETSPEMKGKVLTRLKHIVELQIILEKYLAVTPDYVPPLGNFDVETLDI 850
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GQLNKEFTGKEEKTSLLLHNSHAFFRELDIEVFSILHCGLVTKFILDTEM 950
HTEATEVVQLGPPELLFLLEDLSQKLESMLTPPIARRVPFLKNKGSRNIG 1000
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GEHSQPLEELLSQSVHYLQNFHQSIPSFQCALYLIRLLMVILEKSTASAQ 1150
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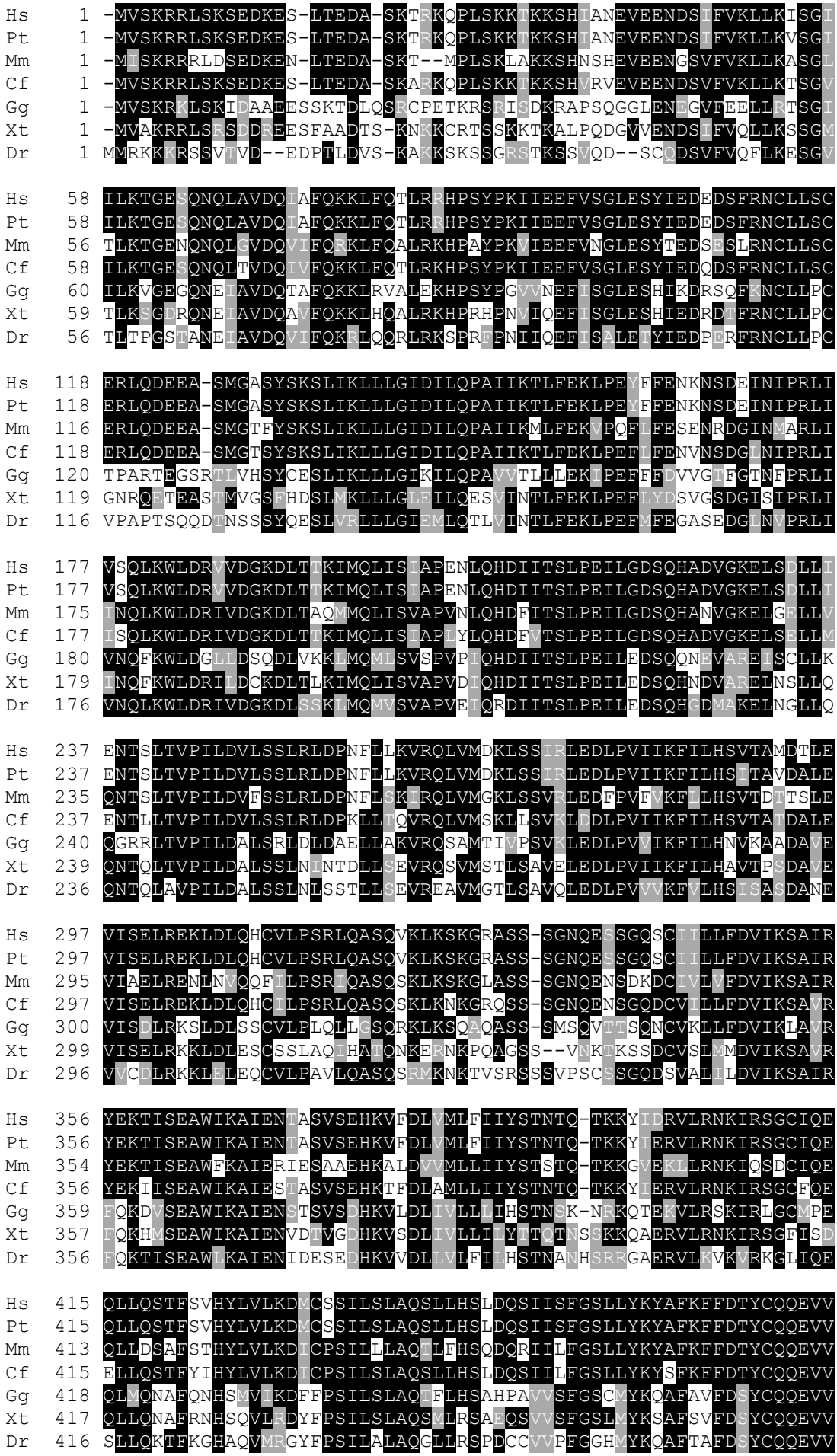
EEIAGVGVPELINSPKDASSSTFPTLTRHTFVVFFRVMMAELEKTVKKIE 1250
PGTAADSQQIHEEKLLYWNMAVRDFSILINLIKVFDSHPVLHVCLKYGRL 1300
FVEAFLKQCMPLLDFSFRKHREDVLSLLETFQLDTRLLHHLCGHSKIHQD 1350
TRLTQHVPLLKKTLELLVCRVKAMLTLNNCREAFWLGNLKNRDLQGEEIK 1400
SQNSQESTADESEDDMSSQASKSKATEDGEEDEVSAGEKEQDSDESYDDS 1450
D                                                    1451
```

B

Position	Sequence	Score
2-27	VSKRRLSKSEDKESLTEDASKTRKQP	10.1
24-55	RKQPLSKKTKKSHIANEVEENDSIFVKLLKIS	7.2
2-30	VSKRRLSKSEDKESLTEDASKTRKQPLSK	6.8
24-58	RKQPLSKKTKKSHIANEVEENDSIFVKLLKISGII	5.7
30-55	KKTKKSHIANEVEENDSIFVKLLKIS	5.6

Figures S1A and B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Mm 1 -MISKRRRLDSEDKEN-LTEDA-SKT--MPLSKLAKKSHNSHEVEENGSVFVKLLKASGL
Cf 1 -MVSKRRLSKSEDKES-LTEDA-SKARKQPLSKKIKKSHVRVEVEENDSVFVKLLKTSGV
Gg 1 -MVSKRKLSKIDAAEESSKTDLQSRCPETKRSRISDKRAPSQGGLENEGVFEELLRTSGI
Xt 1 -MVAKRRLSRSDDREESFAADTS-KNKKCRTSSKKTKALPQDGVVENDSIFVQLLKSSGM
Dr 1 MMRKKKRSSVTVD--EDPTLDVS-KAKKSKSSGRSTKSSVQD--SCQDSVFVQFLKESGV
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Cf 58 ILKTGESQNQLTVDQIVFQKKLFQTLRKHPSYPKIIEEFVSGLESYIEDQDSFRNCLLSC
Gg 60 ILKVGEGQNEIAVDQTAFQKKLRVALEKHPSYPGVVNEFISGLESHIKDRSQFKNCLLPC
Xt 59 TLKSGDRQNEIAVDQAVFQKKLHQALRKHPRHPNVIQEFISGLESHIEDRDTFRNCLLPC
Dr 56 TLTPGSTANEIAVDQVIFQKRLQQRLRKSPRFPNIIQEFISALETYIEDPERFRNCLLPC
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Pt 118 ERLQDEEA-SMGASYSKSLIKLLLGIDILQPAIIKTLFEKLPEYFFENKNSDEINIPRLI
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Gg 120 TPARTEGSRTLVHSYCESLIKLLLGIKILQPAVVTLLLEKIPEFFFDVVGTFGTNFPRLI
Xt 119 GNRQETEASTMVGSFHDSLMKLLLGLEILQESVINTLFEKLPEFLYDSVGSDGISIPRLI
Dr 116 VPAPTSQQDTNSSSYQESLVRLLLGIEMLQTLVINTLFEKLPEFMFEGASEDGLNVPRLI
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Cf 177 ISQLKWLDRIVDGKDLTTKIMQLISIAPLYLQHDFVTSLPEILGDSQHADVGKELSELLM
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Pt 237 ENTSLTVPILDVLSSLRLDPNFLLKVRQLVMDKLSSIRLEDLPVIIKFILHSITAVDALE
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Dr 236 QNTQLAVPILDALSSLNLSSTLLSEVREAVMGTLSAVQLEDLPVVVKFVLHSISASDANE
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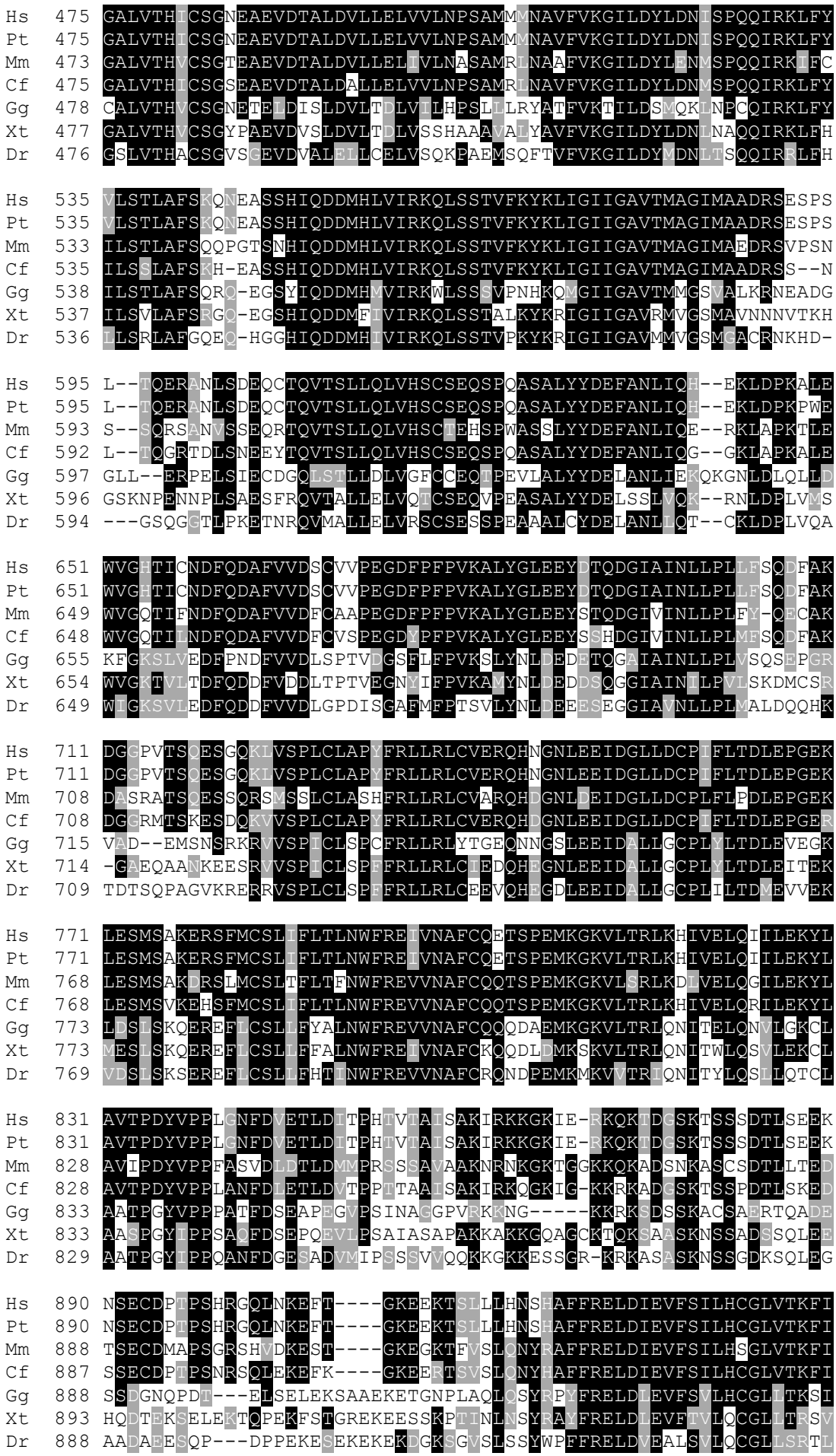
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Cf 475 GALVTHICSGSEAEVDTALDALLELVVLNPSAMRLNAVFVKGILDYLDNMSPQQIRKLFY
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Dr 594 ---GSQGGTLPKETNRQVMALLELVRSCSESSPEAAALCYDELANLIQT--CKLDPLVQA
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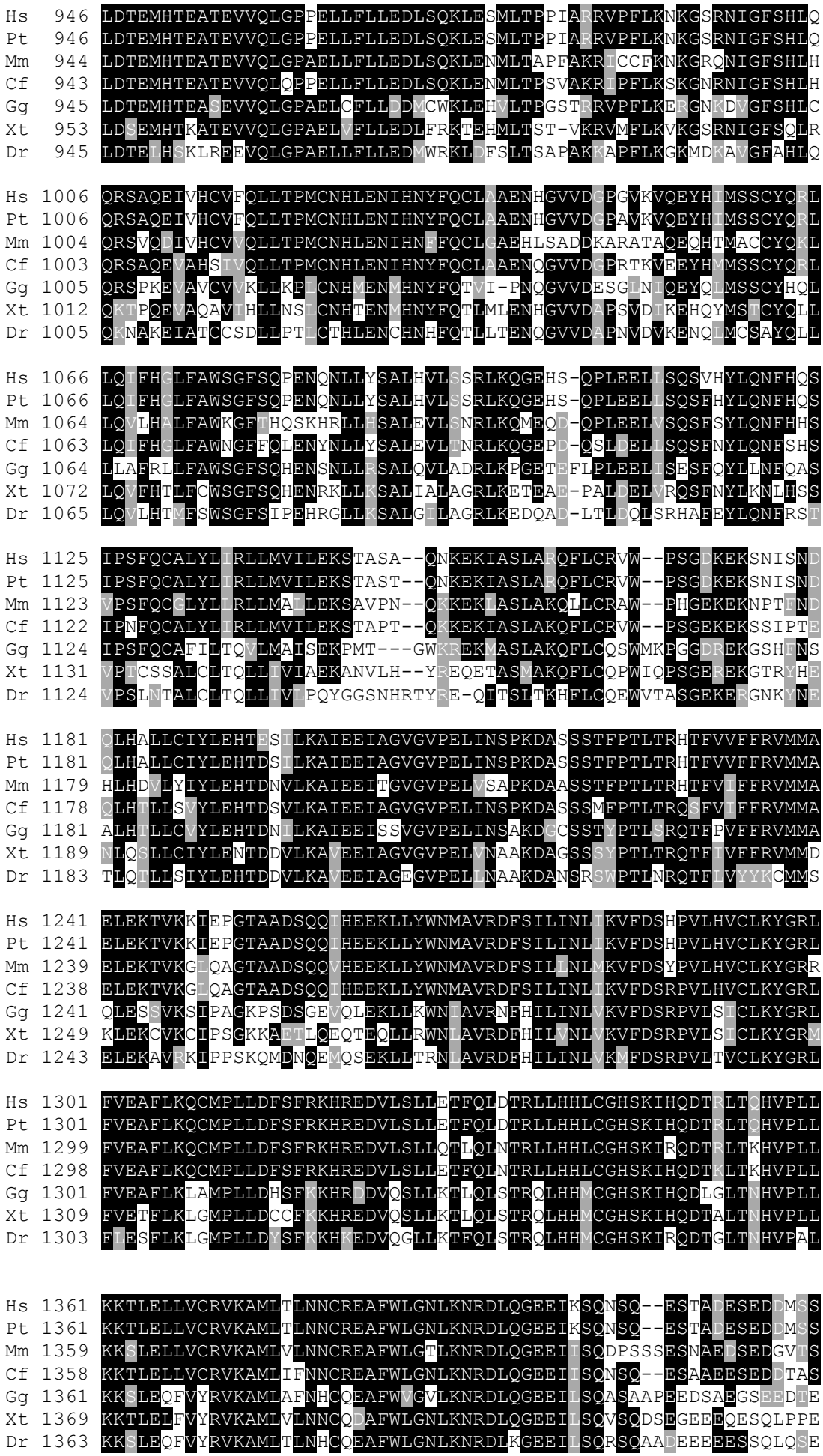
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Xt 1369 KKTLELFVYRVKAMLVLNNCQDAFWLGNLKNRDLQGEEILSQVSQDSEGEEEQESQLPPE
Dr 1363 KKSLEQFVYRVKAMLTLNHCQEAFWLGNLKNRDLKGEEILSQRSQAADEEEEESSQLQSE

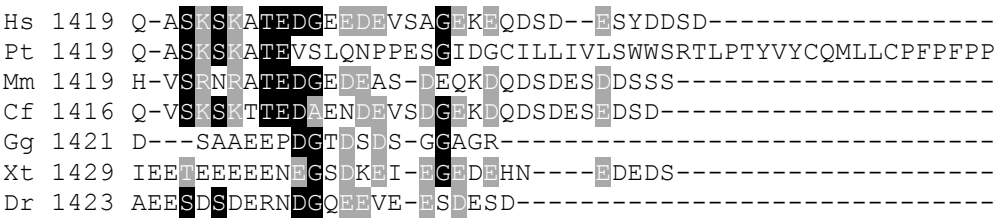

Hs 1419 Q-ASKSKATEDGEEDEVSAGEKEQDSD--ESYDDSD------------------
Pt 1419 Q-ASKSKATEVSLQNPPESGIDGCILLIVLSWWSRTLPTYVYCQMLLCPFPFPP
Mm 1419 H-VSRNRATEDGEDEAS-DEQKDQDSDESDDSSS--------------------
Cf 1416 Q-VSKSKTTEDAENDEVSDGEKDQDSDESEDSD---------------------
Gg 1421 D---SAAEEPDGTDSDS-GGAGR-------------------------------
Xt 1429 IEETEEEEENEGSDKEI-EGEDEHN----EDEDS--------------------
Dr 1423 AEESDSDERNDGQEEVE-ESDESD-------------------------------

Figure S1C

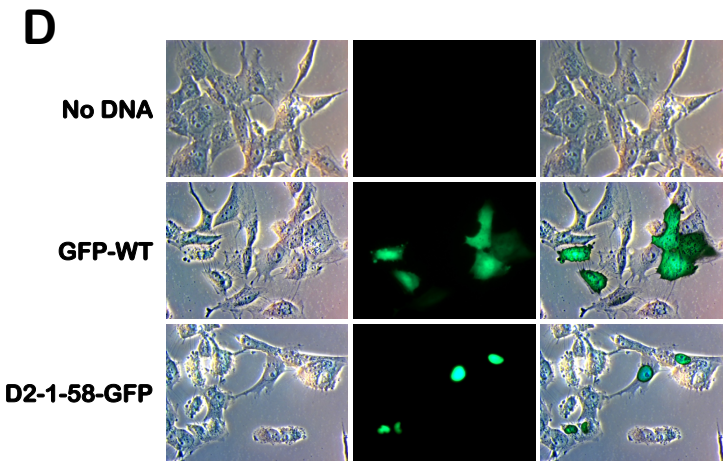
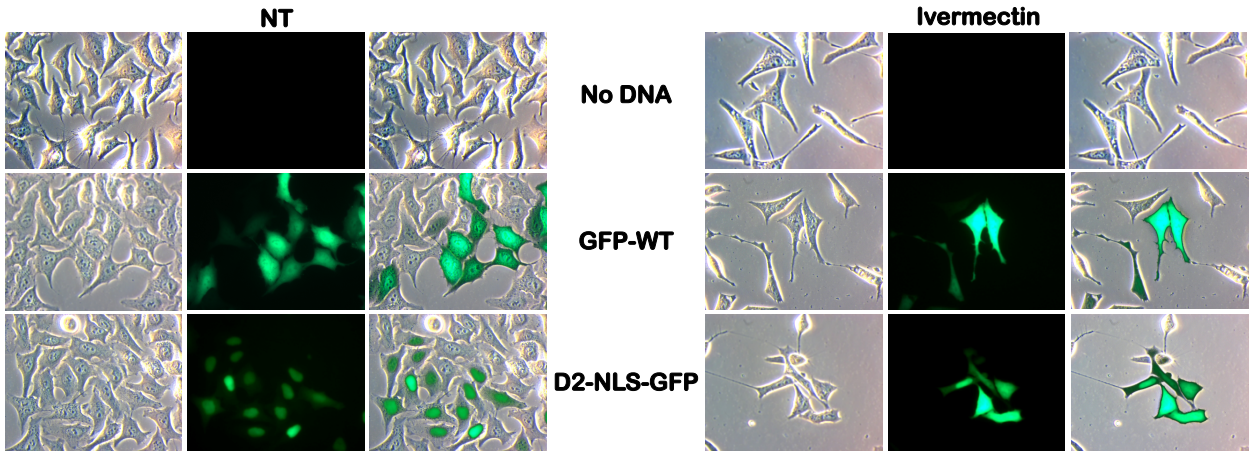
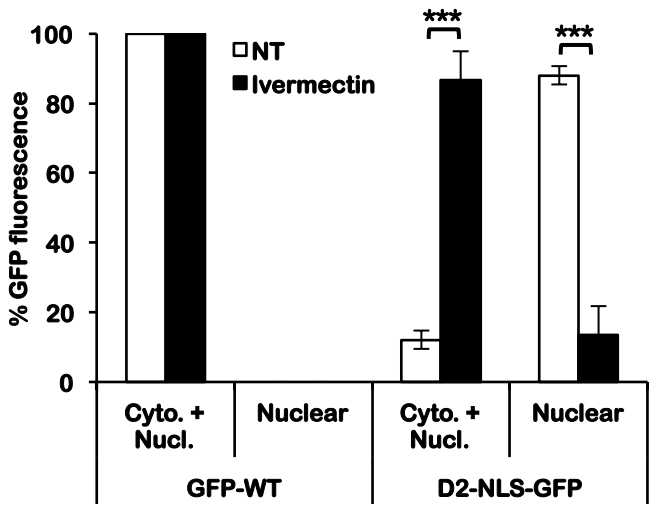


Figure S1D

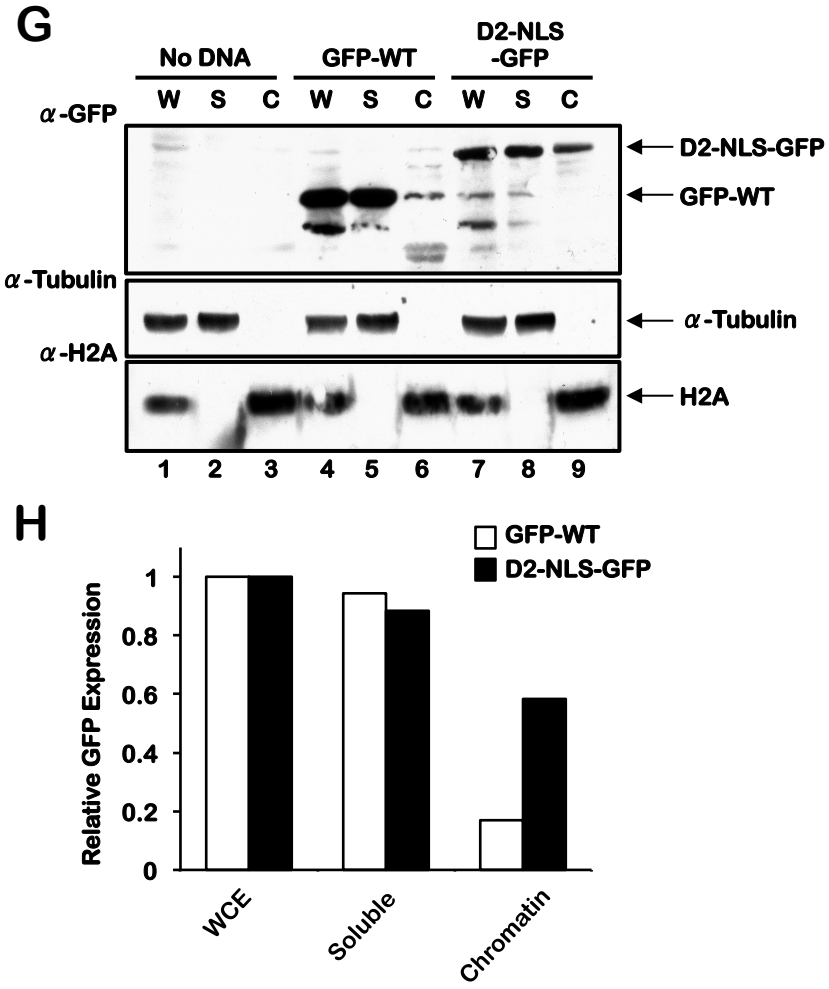
E



F



Figures S1E and F



Figures S1G and H