

CT and CRF DH receptor sequences

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>ClecCT/DHR1-CLEC000667

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LWYRLVIPNTDVIVKNRVWCQCLHVVLHYFLACSYAWMLAEGVYLHTLLVSAFTSEQKLVKILTACSWLVPFFFTALYTTLRL
ASGDTQQCWIDESDSKMLVFLVATSMLLNFLFCNIVRVVVKLRAGPNQSARPSTALLQALRATLLLLPLLGLNYLLTPFR
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EIV

>HhalCT/DHR1-XP_024216452.1

DSDFLQCAIYNESKSKNLEGSYCEATWDGWSCWQETPAGTTAYAHCPKFITGFDPNLLAHKICTENGTWFKHPDSGMV
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NGVWCQCLHVILHYFLLSCYAWMLAEGVYLHTLLVSAFTSEQKLVRLITVFSWTAPLFFIFLYSVLRLVFDLTDQCWINDSDY
SSVLVVLVVASMGLNLGFLCNIVRVVVGKLRAGPSQSSRPSQALLQALRATLLLLPLLGLNYLLTPFRPPNDHPLESYYEILSAF
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>ApisCT/DHR1-XP_016661057.1

IVGTAYKICNKNATWFKHPISGAVWSNYTTCINHEDYNWTQQINTIYQTGYLVSFIALLLSIALTYFKSLRCARNTLHMHMFT
SFAINLLWLLWYRLVVEHPSVVLHNGWWCQILHVILHYFLLTNYAWMLAEGFYLHTLLVFAFTSEDTLVRWSWTLAWST
PLVVISLYTLRTIYDHTSECWINESPFTEVLVVPVCMALNLVFLCNIVRVLWVKLQAGPSHLSNSTPSRLLQAFRATLLL
LPLLGLHYLLTPFRPPKQHPWEPFYEVVSATSSSQGLCVATLFCFLNGEVVAQIKRQWQFMFFRTRANSYTATTVSVRQFV
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>TcasCT/DHR1-TC002694

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HMNLFSSFAMNFLWLLWYSLVNDQDVLHENKLWCRVLHVLFVFLISNYSWMLCEGIYLHTVLVSAFISERRLLRCMLA
LGWGIPLLTTSIYAPVRSVLGENVDELGRCWTQDGRFNKILMVPVITVFLNVIFLNIVRVLLIKLRKGPANGGSGSGASRT
SLQALRATMLLVPLLGLNFLTFRPEANHPWEYVYEVVSALTASLQGIQPFMFFWYRDQNHWS

>DmelCT/DHR1-CG32843

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LAILGYFKSLKCARITLHMNLFASFAANNSLWLVWYLLVMPNSELLHQSPMRCVALHITLHYFLLSNYSWMLCEGFYLHTVL
VAFISEKRLVKWLIAGFWGSPAIVFVYSMARGLGGTPEDNRHCWMNQNTNYQNILMVPVCISMFLNLLFCNIVRVVLLK
LNAPASIQGSCGPSRTVLQAFRATLLLVPLLGLQYILTPFRPAPKHPWENTYIISAFTASFQGLCVAILFCFCNGEVIAQMKR
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>AmelCT/DHR-LOC412591

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RCIVANTDLLLNNGMTCRLLHIVLHYFLLTNYAWMLCEGFYLHTLLVSAFTSEQKLVKWLMLIGWPVPAIIVTIYACLRATSN
DLTDTEQCWINEGNYMNVLVYPVCVSTLLNVLFLFNIVRVLLMKLKLAGPSIGTQPSRSMRQAFRATLLLVPLLGLHYLVIPFR
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>AgamCT/DHR1-AGAP009770

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WLLALGWGSPAFFIVLYGFLRGYASPPNDTIECWMDSSFNKVFVGPVCISMLLNLVFLFNIMRVLLKLPAGPQGGAGP
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>AaegCT/DHR1-AAEL010043

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GEEKV

>Dmelhector-CG4395

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CLENGSWYRHPVSNQTSWNYTNCVDYEDLEFRQFINELYVKGYALSLLALLISIIIFLGFKSLRCTRIRIHVHLFASLACTVAV
ILWYRLVVERSETIAENPLWCIGLHLVHVYFMLVNYFWMFCEGLHLHLVLLVVFVKDTIVMRWFVIVSWFSPPIAIVYGLAR
HFSSPDNKHCWITDSLWYFVSPITLSLLASFILINLVRVIRKLPQSAQPAPLAIRKAVRATIILVPLFGLQHFLLPYRPDAG
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>ClecCT/DHR2-CLEC025204

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NYLWMFCEGLHLHLVVFVKDNSAMRWFCYIGWVFPGILTAIYASVRYWYTEETRQCWMNESHTQWILTAPVCFMS
LASLGLINVVRLTLKHCNSANPAPIGLRKAVRAALILVPLFGIHHILIPFRPEPNAPGERAYQIFSALLVSLQVIISYRYKNTG
KVLMMFKCLSISDRATIKPNFN

>HhaICT/DHR2-XP_024217979.1

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VIGNPIVVQENRFMCQALHVLLQYLMVANLWMFCEGLHLHLVVFVKDDNAMRWFFYFIGWFLPAILAGIYALVRSSY
PDETSQCWLSESHQWILTVPVLLSMLASLGLINVVRLTLKHCNSANPAPIGLRKAVRAALILVPLFGIHHILIPFRPEPNG
PGERVYQVFSALLVSLQGFVSLFCFANVDVHAFAKAMARRIRRRATDNGNLATQTRREV

>ApisCT/DHR2-XP_016661373.1

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>AaegCT/DHR2-AAEL006490

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QAVTVLRSISASNARHDQQTQLFCPRRFDGWTCWESQPAGTIAQNFPCNFVLGFDASRLAYRICHANGSWFTHPESGRE
WSNYTNCIDVDDMKFRRLVNDLYIGGYTISLVTLIVSLCVFFSRTLKCTRIRIHINLFTSLALSACAFWILWYKFVVEDPDVTNR
NGNWCIALHILLHYLMLVNYFWMFCEGLQLHLVLVVIFKIDAIAMRWFFTIGWILPVAFVSIYASVRNKYTLDEHCWMNE
SHAMWLLTIPVCFSLVASLVLINVVRLTLKLNSTSPNAPLGLKATRATLILIPFGLQHILLPFRPDKGCELERYYQVVSVA
LISLQGACVSLFCFANHDVIFAIKCQLSRFFPTLVHHPFRESYNGGQPATQSRDMVV

>TcasCT/DHR2-TC013321

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ALHLVVHYLMLANMWMFCEGLHLHLVVFVRDAETMKWFFALGWGAPFIIVLIYSVVRIFILKDNMCMWMAADSYYS
SWILTAPVCISLLVSLIFLINLVRVILTIMHPNSANPAPMGLRRAARAALILIPFGLQHILIPFRPDMYDPYEHLYQYVTVVVVT
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>AgamCT/DHR2-AGAP001175

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>ApisCT/DHR3-XP_016661370

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VNNCLWLWVYEAVDNLPVLMTNGLGCKLLHVLVQYFLVATYFWMFCEGLYLHTLLVVTFLTESKVMPLHTIGWGIPAL
LVSTYAAALRTATPGETLHCWIHESLWSILSGPVCLSMANLVLINIVRLLVVKLHARQITMSSPKHVAPRERAQSFLRSFK
RNNCSVDSYDKAPASSRTGKAVRATLILIPLLGLQYIVTPFRPEPGTSEVPYQVTSAVVASCOGLCVALLFCFCNGEVLSE
MKKRWKHCWINKNGSWNPCMRGTSVSSPQHHPRLVTEDEQQTQRTGSIQVLPKDSAECLQNVQL

>HhaICT/DHR3-XP_014287171

MIYTREEIDNITAIKKECFAVAENYTEGLFCPREFDGWTCINATPAGTVLHFPYFQLGFDPKRTAHRPCLENGTWFRHP
ETNKPWSNYTTCVDLEDLFCFEMRNQVNFYIKAGYMISSLAALLSLFIFFFYFRSLTCTRIQIHKNFFISLAINLLWLIWYEA
VLDNHTVIYENGVGCQILHVILQYFLVTTYFWGFCEGLYLYLLVVTFLTESKVMVCLYLIGWGPALIVSAYASLRISTNKD
TDYCW

IQESIYRWTLIIPVGLSMIANLIFLITIVRVVLTKLHAAQKTTSPNSFKDKNASIRSKRSTVLSDTAFSERTKKAVRATLILIPILIGLQ
YVVMIVRPEQKTTWEYTYELTEAIVASSQGLCVALLFCFCNGEVTA AVRKKWRQCRLSKRKPWNCSGVT SVSFRSSFVQ
EMAGVVPPPHIDGLATGNCQL

>ClecCT/DHR3-CLECO13307

MIITQFMFTDGFSGPCKEFDGWTCINATSPGAVIHVPCPYFIFGFDPKRLGHRTCLEDTWFRHPDSNKTWTNYTTCVDTD
DLKMRTQVNLIYKAGYTFSLAALLSIIFFYFKSLTCTRIQIHKNLFI SLAVNNLLWLWVYEAVVDNIPVLLSNGIGCQILHVLV
QYFMVATYLMWFCEGLYHLLVVTFTVESKVM PVLHLIGWGV PALLVTVYASLRVSTKDDTLHCWIHESLYSWSLSGPVC
LSMIANLVFLINIVRLLTKLRLPRRSTISSQGLPSGR TKKAVRATLILIPLLGLQYIVTPFRPEQGT SWEYPYQVTSALVASCQGL
CVALLFCFFNGEVFLNLFNLKEENS NFALVLGCSGHEEKVATVQAE

>ClecCRF/DHR1-CLECO25139

MCITKKNFQEIRCFKLMEEERDQKDV CERSWDGLLWPPSRPGAAYLPCFEELHGIKYDTSQNATR WCHPNGTWANYSN
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PCVLLVILLHYFHLTNFFWMFVEGFYLYMLVVKFTQENIKLRVYLAIGWGNFCLKMNI NVLYTMFQIVMDPFQKGCHWM
MPNMTDWIYQTPAIIVLVINLMFLVMIMLVLITKLSATNVETQQYRKA AKALLVLIPLLGITYILFIVGPSKGPYANLYEYVR
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>ClecCRF/DHR2-CLECO00652

MPTYDEPAENCPWSWDGALCWPSFPPGKNASLPCFEELKGIKYDTSQNASRYCFPNGTWSTYTNYNACQATVPENMVP
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NYFWMFVEGLYLYMLVAVTFTRENIKLRVYLGIGWGKCFFIGIISTASEELDRNCSWLT PHWSDWIDQSAALLVGVNLIF
LFMIMLVLITKLRSSNNVETQQYRKASKALLVLIPLLGVTYIFFLVGP KTDIYEYIRAILLSTQGF SVALFYCFLNTEVQNTFRH H
LRWKESRDIGHRRYTSKDWSPNTRTESIR

>HhaCRF/DHR2a-XP_024216523.1

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SLTVQVSIHTDSISCLVFLTHYFLLTNFFWMFVEGLYLYMLV VETFTRENIGL RAYLAIGWGSPIVIVWIIARTTVQDPNA
VTIMGVPETMNQCTMMYTSMTDWIYIIPVLVLLVNLFLCMIMWVLITKLSANNAETEYRKGSKALLVLIPLLGITYILL
IAGPNASVYHNIRALLSTQGLTVGLLYCFLNTEVQNTLRHRWQRWREERSLPHRTYTKDSSPNTRTESIRLYSKHEVVPYRK
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>HhaCRF/DHR2b-XP_024216523.1

MEDQELTSNFSYHIREECLQRWSYHYQEGWCPAVFDGALCWGPTGPAVLASQPCREEIHGVLYDTSKNATKYCHESGI
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SMHTDSVSLIFLTHYFILTFFWMFVEGLYLYMLV VETFTRENIGL RAYLAIGWGLPVAVIIVWVIARFNASDMPEVPPG
TKQCTWMNQSWSDWIYQVPAIVLAINLLFLVRIMWVLITKLSANNAETEYRKGSKALLVLIPLLGITYILFIAGPQSAVYS
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MTLVHSSRLSNGPRSSFLQPPSEPV

>ApisCRF/DHR2-XP_001944842.2

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CRPLDTNPNLYPDPSIVYSYFYYGGYTISLVALVA AVSIFVYFKDLRCLRNTIHTNLMCTYILSDFTWILTSTLQEWLSASNNA
CVLFTFSLHYFVLTNFFWMFVEGLYLYLVVETFTRENIKLRVYMF IGWGFPLVIMIVWGVSKITPIEVEERSDSCSWMTPHP
VHDWIYQGPAIIVLVINLVFLSKIMWVLITKLSANSAETQQYRKASKALLVLIPLLGVTYILTMVGPTESGTYANYYSYGRATL
LSMQGFMAIFYCFVNSEVKNTFKHHFIRWNDARNLRTGGSRRFTYSKDWSPNTRSDSVRLARPSIIADTMNKGKRAST
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>ApisCRF/DHR1-XP_008183744.1

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QITYERYCPLMASVYVDDWIYQSPIVIVLLINSIFLVKIMRVLITKIRSTKSAETHNYKKATKALLVLIPLLGITFCLDMINPSSGLL
VNIYKFSKVVIISTQGFTVSLLYCFNNEVQNTLKYHITRWQTKRKF LASKYGRSWLSVKQNNIICDHQLDPKELMPWIPA
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>AmelCRF/DHR-LOC413829

MLRIQRELR CIRNNIHTNLMFTYILADFMWILNNVMQVSMQPDVPTCVAFSLFHYFQLTNYFWMFVEGLYLYLLVVKFTFT
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KLWSATNVETQQYRKASKALLVLIPLLGVTYVLVLTGPTEGQVANAFSYARAVLLSSQGLFVALFYCFLNTEVRNTVKSHIER
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>TcasCRF/DHR1-TC007104

MDQGESEVVYARHEDIVRILNRLNETQAELACELKKTLSPPSNGCAVDFDTVLCWPQTAPNSLAVLPCFDQLNGIKYDTRE
NATRLCFANGTWDQYSNYTSCKELSPLEVPEVELTTTTIYFIGYTVSLVALLFAVYIFWKFKDLRCLRNTIHMNLMCSYLADFM
WIFVYSLQVPLQTNKAFICIFLIILLHYFHLTNFFWWMFVEGLYLYLVVKTFTGENIKPRIYAVIGWGGPILFVLVWGIKSAFTLPL
EDQQAGEMFRSCPWTPHPFDWIYQGPAIAVLIINVFLLCIIMWVLITKLSANNVETQQYRKAALKALLVLIPLLVGTYLVIVG
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STLKY

>TcasCRF/DHR2-TC012799

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NLMWSYMLMYIMWILTTLVLSKGGTGASIACIFVITLLHYFHISTFFWWMFVEGLYLYLVVETLTRENYKLRVYVCIGWGLP
MIFILVWVIVKSFIPAAGDPATCTWFNSHDVDWIFQGPMLVLLLNLAFLAIMWVLITKLSANTVETQQYHKAALKALLVL
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>AgamCRF/DHR1-AGAP005464

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TFSGDTLRFRKYAIIIGWGGPLIFVGAWAIAKPFVGSVSNLEHPSKLEIECSWMRESHIDWIIQGPSCAVLVINLIFLLRIMWVLI
TKLSANTVETRQYRKASKALLVLIPLLGITYLIVYGPVEGVGSHIFAITRAILLSTQGFVVSLLYCFLNSEVRQTLRHHFYRWR
DERNILSGKVNHHRRPTFSKDNSPRSRTESTRLVLVKECASSVPAKHVLYCRLQVVVAFIHVCLFVFWCVCVSLFVFLY
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>AgamCRF/DHR2-AGAP005465

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DVTQNA TRYCHPNGRWDNYSHYAACHHVNEPPDIVEISSIIYTYGILSLVALSLAVIVFVYFKDLRCLRNTHANLFITYILSA
LLWIIILTLQLSSGSSTGMTSCVIFVTLHYFTLTNFFWMLVEGLYLYMLVVETFSGDNLRFNMYAAIGWGKCSRASLEIECS
WMRESVVDWIFQGPVCAVLIINLVFLIRIMWVLITKLSANTVETRQYRKASKALLVLIPLLGITYLVVLAAPAEGVVSDFIFAIA
RALLSTQGLSVSLFYCFLNSEVRLALRHRLERWRDERNIRLGQVRQSRMEKGPSKPESEPIHHATESLKGFIPLPFSSAG
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>AaegCRF/DHR1-AAEL008292

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HVNLVFTYIMSSSLWIIILSQQLAAKQGLVDCIFLVTLFHYFSTTNFFWMLVEGLYLYMLVVQTFSGDYLRFWKYSIIGWGGP
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ALLVLIPLLGITYLVVYGPHEGVSRIFAVTRAVLLSTQGLVVSLLYCFLNSEVRGTLRLHYRWRDERNIRLGIISKHRRPTISG
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>AaegCRF/DHR2-AAEL019757

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>DmelCRF/DHR1-CG8422

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GLEENSV

>DmelCRF/DHR2-CG12370

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LP A I I Y A G G Y F L S F A T L V V A L I I F L S F K D L R C L R N T I H A N L F L T Y I T S A L L W I L T L F L Q V I T T E S S Q A G C I T L V I M F Q Y F Y L T N F F W M
F V E G L Y L Y T L V V Q T F S S D N I S F I I Y A L I G W G C P A V C I L V W S I A K A F A P H L E N E H F N G L E I D C A W M R E S H I D W I F K V P A S L A L L V
N L V F L I R I M W V L I T K L R S A H T L E T R Q Y Y K A S K A L L V L I P L F G I T Y L L V L T G P E Q G I S R N L F E A I R A F L I S T Q G F F V A L F Y C F L N S E V R
Q T L R H G F T R W R E S R N I H R N S S I K N R R H R A S K D Y S L R S R T E S L R L T S T S P I P T G H Y E

>DmelGlutR

M K Q K N N N G T I L V V M V L S W S R V V D L K S P S N T H T Q D S V S V S L P G D I I L G G L F P V H E K G E G A P C G P K V Y N R G V Q R L E A M L Y
A I D R V N N D P N I L P G I T I G V H I L D T C S R D T Y A L N Q S L Q F V R A S L N N L D T S G Y E C A D G S S P Q L R K N A S S G P V F G V I G G S Y S S V S L
Q V A N L L R L F H I P Q V S P A S T A K T L S D K T R F D L F A R T V P P D T F Q S V A L V D I L K N F N W S Y V S T I H S E G S Y G E Y G I E A L H K E A T E R N V
C I A V A E K V P S A A D D K V F D S I S K L Q K K P N A R G V V L F T R A E D A R R I L Q A A K R A N L S Q P F H W I A S D G W G K Q Q K L L E G L E D I A E G
A I T V E L Q S E I I A D F D R Y M M Q L T P E T N Q R N P W F A E Y W E D T F N C V L T S L S V K P D T S N S A N S T D N K I G V K A K T E C D D S Y R L S E K
V G Y E Q E S K T Q F V V D A V Y A F A Y A L H N L H N D R C N T Q S D Q T T E T R K H L Q S E S V W Y R K I S T D T K S Q A C P D M A N Y D G K E F Y N N Y
L L N V S F I D L A G S E V K F D R Q G D L A R Y D I L N Y Q R Q E N S S G Y Q Y K V I G K W F N G L Q L N S E T V V W N K E T E Q P T S A C S L P C E V G M I
K K Q Q G D T C C W I C D S C E S F E Y Y D E F T C K D C G P G L W P Y A D K L S C Y A L D I Q Y M K W N S L F A L I P M A I A I F G I A L T S I V I V L F A K N H
D T P L V R A S G R E L S Y T L L F G I L V C Y C N T F A L I A K P T I G S C V L Q R F G I G V G F S I I Y S A L L T K T N R I S R I F H S A S K S A Q R L K Y I S P Q S Q V V I
T T S L I A I Q V L I T M I W M V V E P P G T R F Y Y P D R R E V I L K C K I Q D M S F L S Q L Y N M I L I T I C T I Y A I K T R K I P E N F N E S K F I G F T M Y T T C I I
W L A F V P I Y F G T G N S Y E V Q T T T L C I S I S L S A S V A L V C L Y S P K V Y I L V F H P D K N V R K L T M N S T V Y R R S A A V A Q G A P T S S G Y S R T H
A P G T S A L T G G A V G T N A S S T L P T Q N S P H L D E A S A Q T N V A H K T N G E F L P E V G E R V E P I C H I V N K

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Nuclear receptor sequences

>DmelHR51

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V D V N I I I A A H S Q R R R I G L V R F H Q R E S E D R P L A V A S P R L Q I N M E P T A M N P K K L H S P Q R H C Y T P P P A P M H G Q A P P P T S T G V A P
P T Q P P P P H A A P N V P N G R L L S W N H S A A A A A A A A A A Q A A A N S M N H S S A A E G S S M T R I K G Q N L G I C V V C G D T S S G K H Y G
I L A C N G C S G F F K R S V R R K L I Y R C Q A G T G R C V V D K A H R N Q C Q A C R L K K C L Q M G M N K D D D S I D V T N D N E P H A V S R S D S S F I
M P Q F M S P N L Y T H Q H E T V Y E T S A R L L F M A V K W A K N L P S F A R L S F R D Q V I L L E E S W S E L F L L N A I Q W C I P L D P T G C A L F S V A E
H C N N L E N N A N G D T C I T K E E L A A D V R T L H E I F C K Y K A V L V D P A E F A C L K A I V L F R P E T R G L K D P A Q I E N L Q D Q A H H T K T Q F T A
Q I A R F G R L L L M L P L L R M I S S H K I E S I Y F Q R T I G N T P M E K V L C D M Y K N

>DmelII

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D K T H R N Q C R A C R L R K C F E V G M N K D A V Q H E R G P R N S T L R R H M A M Y K D A M M G A G E M P Q I P A E I L M N T A A L T G F P G V P
M P M P G L P Q R A G H P A H M A A F Q P P P S A A A V L D L S V P R V P H P V H Q G H H G F F S P T A A Y M N A L A T R A L P P T P P L M A A E H I
K E T A A E H L F K N V N W I K S V R A F T E L P M P D Q L L L L E E S W K E F F I L A M A Q Y L M P M N F A Q L L F V Y E S E N A N R E I M G M V T R E V H A
F Q E V L N Q L C H L N I D S T E Y E C L R A I S L F R K S P P S A S T E D L A N S S I L T G S G S P N S S A S A E S R G L L E S G K V A A M H N D A R S A L H N Y I
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>Dmel dsf

M G T A G D R L L D I P C K V C G D R S S G K H Y G I Y S C D G C S G F F K R S I H R N R I Y T C K A T G D L K G R C P V D K T H R N Q C R A C R L A K C F Q S A
M N K D A V Q H E R G P R K P K L H P Q L H H H H H A A A A A A A H H A A A H H H H H H H A H A A A A H H A A V A A A A S G L H H H H H
A M P V S L V T N V S A S F N Y T Q H I S T H P P A P A A P P S G F H L T A S G A Q Q G P A P P A G H L H H G G A G H Q H A T A F H H P G H G H A L P A P H
G G V I S N P G G N S S A I S G S G P G S T L P F P S H L L H H N L I A E A S K L P G I T A T A V A A V S S T S T P Y A S A A Q A S S P S N N H N Y S P S P S N
S I Q S I S S I G S R S G G G E E G L S L G S E S P R V N V E T E T P S P S N S P L S A G S I S P A P T L T T S S G S P Q H R Q M S R H S L S E A T T P P S H A S L M I
C A S N N N N N N N N N N N N N G E H K Q S S Y T S G S P T P T P P P P R S G V G S T C N T A S S S G F L E L L S P D K C Q E L I Q Y Q V Q H N T L
L F P Q Q L L D S R L L S W E M L Q E T T A R L L F M A V R W V K L M P F Q T L S K N D Q H L L L Q E S W K E L F L L N L A Q W T I P L D L T P I L E S P L I R E
R V L Q D E A T Q T E M K T I Q E I L C R F R Q I T P D G S E V G C M K A I A L F A P E T A G L C D V Q P V E M L Q D Q A Q C I L S D H V R L R Y P R Q A T R F G
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>DmelHR78

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Y Q Q G R G K G H S V K A E S A A T P P V H S A P A T A F N L N E N I F P M G L N F A E L T Q T L M F A T Q Q Q Q Q Q H Q Q S G S Y S P D I P K A D P
E D E D D S M D N S S T L C L Q L L A N S A S N N N S Q H L N F N A G E A P T A L P T T S T M G L I Q S S L D M R V I H K G L Q I L Q P I Q N Q L E R N G N L
S V K P E C D S E A E D S G T E D A V D A E L H M E L D F E C G G N R S G G S D F A I N E A V F E Q D L L T D V Q C A F H V Q P P T L V H S Y L N I H Y V C E T
G S R I I F L T I H T L R K V P V F E Q L E A H T Q V K L L R G V W P A L M A I A L A Q C Q G Q L S V P T I I G Q F I Q S T R Q L A D I D K I E P L K I S K M A N L T R T
L H D F V Q E L Q S L D V T D M E F G L L R L I L L F N P T L L Q R K E R S L R G Y V R R V Q L Y A L S S L R R Q G G I G G G E E R F N V L V A R L L P L S S L D A E
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>DmelKni

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>DmelKnrl

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>Dmelea

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>DmelHR3

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>DmelEcR

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>DmelHR96

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>DmelHNF4

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>DmelHR83

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>Dmelsvp

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>DmelERR

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>DmelHR38

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>DmelFtz

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>DmelHR39

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>DmeIHR4

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>Ph516230-ERR

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>Ph596250-dsf

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>Ph494010-PNR

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>Ph477600-HNF4

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>Ph475840-Ftz

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>Phknr1

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>Phknr2

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>PhEcR

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>Ph460980-HR96

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>Ph411130-HR38

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>Ph331460-tII

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>Ph318510-HR39

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>Ph301950-HR78

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>Ph234430-Eip78C

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>Ph233230-Eip75b

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>Ph195250-HR4

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VYTCVADGNCEITKAQRNRCQYCRFKKICIEQGMVLQAVREDRMPGGRNSGAVYNYKVLNRERDNKFLNVIFNNNEKG
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HKSDLSEKLCQIGDSIVYKLVQWTKRPFYLELPEVHTRLLTHKWHELLVLTTSAYQAIHGVHKLSTSTAGQEAFTQEV
NNLVTLQCLTSMGRPITMDQLRQDVGLMVEKITHVTLMFRRVKLRMEEYVCLKVITMLNQGRGGSNELEAIQDRYM
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>Ph164330-usp

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PIDTFLMDMLGSSSDS*

>Ph053030-HR3

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>Ph039420-HR51

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VESSPLFSVNEHAATVPNGKSSQTAADIRVLNDMLLRYKAVGVDPAEFACLKAIVLFKSETRGLKDPLQVENLQDQAQVML
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>Phumsvp

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>Phumea

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>ClecKnr1

MNQLCRVCGEPAAGFHFGAFTCEGCKSFFGRTYNNLSSISECKNNGECVINKKNRTSCKACRLRKCLLVGMSKSGSRYGRR
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>ClecHR6

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VRVYLVNPNPSQVEPILIEIFDLKTH*

>ClecEcR

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VPEYQCAVKRKEKKAQKDKDKPVSTTNGSPEAIKVEPEPHRVSYTSSLFQSMIKESQTQSTEGELAKVAVNGIKQVSAEQEE
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>ClecHR39

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>ClecHNF4

MFVRDVEDGEMGEGSLVGGNTVPVNFPOSCAICGDRATGKHYGASSCDGCKGFFRRSVRKNHLYNCRFSRTCVDKDK
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>ClectII

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>Clecusp

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>ClecHR38

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>ClecPNR

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>ClecHR4

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>ClecKnrI3

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>ClecKnrI2

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DGRLGAQIASINRKEELMLLGLLEDYKTYSPSTSSPGSDTSEEKCRREPPYFGFPIIPQMFLPQPFPHPAFLPSPYLYQNRTWD
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>ClecHR3

MVKHPSGTYNRRNDSTPLECPGCDPSLLEYAFPNSQWSASRGTVKGRTPVATPRSHPAAAVPSLEQSVGGVIGVISWVR
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VDSTTSRQSEDVSPKESESNSNSYSSLIDPAQISELLSKTIADAHARTCLYSIEHIHNMFRKPQDLSKLIFYKNMAHEELWLEC

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>Clecdfs

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>ClecE75B

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>Clecsvp

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>ClecFtz

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HSWSDMLVLDHMHQRMHNSLPDETTLPNGQKFDLLSLGLLGVPSLSEPFTEITKLQDLKFDLSDYICIKLLLLNPEVRGL
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>ClecHR51

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>ClecHR78

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FSLQDFVGSMAVALNVDDEHYAYLKLIALFSPDNPSLHIRRQLSELQEAFQELREQIGDVNSNRFARLLRLPLRALNRHIM
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>ClecE78C

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EDL

>Ph460980-HR96

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DLKPH*