

LBD Features	SIGNATURE																																																																																	
	h	hh	AK	hP	F	L	DQ	LL	h	hh																																																																								
HsRARg	D	K	F	S	E	L	A	T	K	C	I	I	K	I	V	E	F	A	K	R	L	P	G	F	T	G	L	S	I	A	D	Q	I	T	L	L	K	A	A	C	L	D	I	L	M	L	R	I	C	T	R	Y	T	P	E	Q	D	T	M	T	F	S	D	G	L	T	L	N	R	T	Q	M	H	N	A	G	---	76				
CbFAX1	D	S	L	Q	E	S	A	L	S	H	M	E	S	I	L	Q	W	A	Q	Q	F	R	L	F	A	V	L	T	E	S	E	K	R	Q	I	I	L	T	Q	W	P	R	L	L	C	I	A	L	C	E	Q	S	E	D	A	S	L	D	---	58																						
CeFAX1	D	S	L	Q	E	T	T	M	S	Q	L	E	S	V	L	Q	W	A	Q	Q	F	R	L	F	T	V	L	T	N	S	E	K	R	Q	I	I	L	T	Q	W	P	R	L	L	C	I	S	L	C	E	Q	A	E	D	V	S	F	D	---	58																						
CeNHR111	---	---	---	---	S	V	L	V	H	L	K	N	A	L	Q	W	V	Q	Q	F	S	L	F	A	V	L	S	D	V	E	K	S	Q	I	I	L	T	Q	W	P	H	L	L	C	I	A	L	F	E	N	S	E	K	I	F	I	D	---	53																							
BmFAX1	E	N	V	Q	E	A	S	T	R	L	L	E	L	A	I	K	W	A	K	N	L	P	S	F	A	S	L	S	R	D	Q	L	K	L	K	E	N	W	C	D	L	F	L	L	S	V	F	Q	W	S	L	P	M	D	K	---	69																									
PpFAX1	---	H	S	H	A	L	L	R	K	Y	A	G	C	A	V	S	A	V	L	S	Q	P	D	S	T	S	L	L	P	S	D	E	D	A	S	P	L	S	E	E	S	K	L	E	T	L	R	S	I	L	A	G	N	A	G	V	C	E	A	P	P	A	---	62																		
DmUNF	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	---	80
AaHR51	E	T	I	Y	E	T	S	A	R	L	L	F	M	A	V	K	W	A	K	N	L	P	S	F	A	S	L	T	F	R	D	Q	V	I	L	L	E	E	S	W	S	E	L	F	L	L	N	A	I	Q	W	C	M	P	I	D	T	S	A	C	T	L	F	S	L	N	E	H	C	S	S	V	N	N	S	G	---	76				
TcHR51	E	T	I	Y	E	T	S	A	R	L	L	F	M	A	V	K	W	A	K	N	L	P	S	F	A	S	L	P	F	R	D	Q	V	I	L	L	E	E	A	W	S	E	L	F	L	L	N	A	I	Q	W	C	M	P	L	D	V	S	A	S	P	L	F	N	V	N	E	H	V	K	N	G	H	S	---	74						
SpNR2E3	D	S	I	Y	E	S	A	R	L	L	F	M	A	V	K	W	A	K	T	L	P	S	F	S	G	L	P	F	R	D	Q	V	I	L	L	E	E	A	W	S	E	L	F	L	L	C	A	L	Q	W	S	M	P	L	D	S	---	74																								
SkNR2E3	E	N	I	Y	E	S	A	R	L	L	F	M	A	V	K	W	A	K	N	L	P	S	F	S	A	L	P	F	R	D	Q	V	I	L	L	E	E	A	W	S	E	L	F	L	L	C	A	I	Q	W	S	M	P	L	E	S	---	77																								
DrNR2E3	E	S	V	Y	E	T	S	A	R	L	L	F	M	S	V	K	W	A	K	N	L	P	V	F	S	H	L	P	F	R	D	Q	V	I	L	L	E	E	A	W	S	E	L	F	L	L	C	A	I	Q	W	S	L	P	L	D	N	---	75																							
XlNR2E3	E	G	V	Y	E	T	S	A	R	L	L	F	M	A	V	K	W	A	K	N	L	P	V	F	S	N	L	P	F	R	D	Q	V	I	L	L	E	E	A	W	S	E	L	F	L	L	C	A	I	Q	W	S	M	P	L	D	S	---	75																							
GgNR2E3	E	N	V	Y	E	T	S	A	R	L	L	F	M	A	V	K	W	A	K	N	L	P	V	F	S	N	L	P	F	R	D	Q	V	I	L	L	E	E	A	W	S	E	L	F	L	L	C	A	I	Q	W	S	M	P	L	E	S	---	72																							
MmPNR	D	G	I	H	E	T	S	A	R	L	L	F	M	A	V	K	W	A	K	N	L	P	V	F	S	N	L	P	F	R	D	Q	V	I	L	L	E	E	A	W	N	E	L	F	L	L	G	A	I	Q	W	S	L	P	L	D	S	---	75																							
HsPNR	D	S	I	H	E	T	S	A	R	L	L	F	M	A	V	K	W	A	K	N	L	P	V	F	S	S	L	P	F	R	D	Q	V	I	L	L	E	E	A	W	S	E	L	F	L	L	G	A	I	Q	W	S	L	P	L	D	S	---	77																							
CbNHR67	D	S	V	V	G	T	A	A	R	I	F	F	A	L	V	G	Y	C	Q	N	---	A	L	T	G	V	P	R	E	Q	Q	L	A	I	F	Q	Q	H	W	A	T	L	L	L	L	H	A	T	E	S	R	A	I	T	S	R	Q	I	R	N	E	V	T	S	G	T	S	K	L	R	---	69										
CeNHR67	D	T	V	A	G	T	A	A	R	I	F	F	A	L	V	G	F	C	Q	N	---	P	L	N	G	V	P	K	E	R	Q	M	T	M	F	Q	Q	N	W	A	A	L	L	V	L	H	A	T	E	T	R	A	I	T	S	K	Q	I	R	T	E	T	I	S	G	S	E	Q	R	---	69											
BmNHR67	---	T	T	R	D	A	A	A	R	L	F	F	Q	I	L	H	W	S	K	S	L	I	A	F	A	C	L	S	P	Q	E	V	A	A	F	T	S	S	W	G	V	L	F	L	L	S	A	V	E	N	R	F	L	Q	S	S	---	65																								
DmT11	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	---	75					
AgT11	D	A	I	R	E	S	A	A	Q	L	L	F	M	N	V	N	F	L	K	S	L	T	P	F	T	Q	L	P	M	A	D	Q	L	V	L	F	E	E	S	W	R	E	F	F	I	L	A	V	A	Q	Y	L	A	P	I	N	F	S	Q	L	L	I	A	Y	E	Y	L	N	N	R	G	E	T	G	T	V	S	D	---	79		
TcTL1	S	A	I	C	E	S	A	A	Q	L	L	F	M	N	V	Q	W	V	R	S	I	P	A	F	T	C	L	P	L	S	D	Q	L	L	L	L	E	E	S	W	L	D	L	F	V	L	G	A	A	Q	F	L	P	L	M	D	F	S	V	L	V	E	A	C	G	V	L	Q	Q	E	P	H	R	R	D	---	75					
SpNR2E1	D	A	I	C	E	T	A	A	R	L	L	F	M	S	I	R	W	V	K	N	V	P	A	F	I	G	L	P	Y	S	D	Q	L	T	L	L	E	E	G	W	R	E	L	F	I	L	G	A	A	Q	W	M	T	V	D	G	---	72																								
SkNR2E1	E	A	I	C	E	T	A	A	R	L	L	F	M	S	V	K	W	A	K	N	V	P	A	F	L	S	L	P	F	R	D	Q	L	L	L	L	E	E	G	W	R	E	L	F	V	L	G	A	A	Q	W	M	C	M	E	I	---	72																								
DrNR2E1	E	S	V	C	E	S	A	A	R	L	L	F	M	S	I	K	W	A	K	S	V	P	A	F	S	T	L	P	L	P	D	Q	L	I	L	L	E	D	A	W	R	E	L	F	V	L	G	I	A	Q	W	A	I	P	V	D	S	---	72																							
XlNR2E1	E	S	V	C	E	S	A	A	R	L	L	F	M	S	I	K	W	A	K	S	V	P	A	F	S	T	L	S	L	Q	D	Q	L	M	L	L	E	D	A	W	R	E	L	F	V	L	G	I	A	Q	W	A	I	P	V	D	A	---	72																							
GgNR2E1	E	S	V	C	E	S	A	A	R	L	L	F	M	S	I	K	W	A	K	S	V	P	A	F	S	T	L	S	L	Q	D	Q	L	M	L	L	E	D	A	W	R	E	L	F	V	L	G	I	A	Q	W	A	I	P	V	D	A	---	72																							
MmT1x	E	S	V	C	E	S	A	A	R	L	L	F	M	S	I	K	W	A	K	S	V	P	A	F	S	T	L	S	L	Q	D	Q	L	M	L	L	E	D	A	W	R	E	L	F	V	L	G	I	A	Q	W	A	I	P	V	D	A	---	72																							
HsT1x	E	S	V	C	E	S	A	A	R	L	L	F	M	S	I	K	W	A	K	S	V	P	A	F	S	T	L	S	L	Q	D	Q	L	M	L	L	E	D	A	W	R	E	L	F	V	L	G	I	A	Q	W	A	I	P	V	D	A	---	72																							
CbNHR239	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	L	R	C	I	T	I	P	R	I	N	N	L	N	S	F	K	Y	D	M	I	F	S	K	A	V	S	L	T	G	---	29																														
CeNHR239	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	L	R	C	L	Q	L	K	H	T	N	N	P	I	S	F	K	Y	D	S	I	F	S	K	S	V	I	L	T	S	---	29																														
DmHR83	A	L	H	F	Q	I	L	A	Q	I	L	V	T	C	L	R	Q	A	K	A	N	E	Q	F	A	L	L	D	R	C	Q	Q	D	A	I	F	Q	V	V	W	S	E	I	F	V	L	R	A	S	H	W	S	L	D	I	S	A	---	64																							
AgHR83	G	L	S	V	Q	I	L	S	Q	V	L	M	A	C	I	R	Q	V	R	H	N	E	H	F	A	I	F	S	R	A	Q	Q	N	E	I	L	R	H	V	W	Y	E	C	F	L	L	R	V	A	N	S	I	D	I	S	S	---	64																								
TcHR83	---	P	I	Q	E	L	A	A	Q	I	L	L	V	A	I	K	Q	A	R	C	N	S	G	F	G	L	L	N	R	A	S	Q	N	L	I	L	S	H	L	W	A	P	L	F	L	L	R	A	A	H	P	S	E	S	A	D	---	56																								
SpGA10225	S	A	I	E	E	A	A	T	Q	I	I	I	H	A	L	R	T	S	K	S	V	Q	P	F	R	A	L	D	P	W	D	Q	N	S	L	L	Q	E	C	W	A	E	L	F	L	L	H	A	A	Y	W	P	P	---	76																											
SkXP2740657	E	M	L	H	E	I	A	A	Q	I	L	F	T	S	I	K	R	A	R	S	V	Q	T	F	Q	T	L	S	F	S	D	Q	I	L	L	L	E	D	C	W	G	E	L	F	L	L	H	A	A	Y	W	P	---	73																												

LBD Features

E h h Lh

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HsRARg	-----FGPLTDLVFFAFAGQLLPLEMDDTETGLLSAICLICG-----	DRMDLEEPE	121
CbFAX1	-----EHLGSIMLKFRRLDVSPAEFNCKMAITIFMKRTIG-----	WRSKHHYRIPQTTCTVP	109
CeFAX1	-----DHLTSLIMLKFRRLDVSPAEFNCKMAITIFMKRELSL-----	WRAGWDNRASIIITVYP	110
CeNHR111	-----EKFAQLAEKFKSLELSAQDYFLLKGIIIFTET-----	-----KDG	88
BmFAX1	-----SFRYLNDLFFRIRISYGDHGEFACLKAIVLFRP-----	ETRGLKNLV	111
PpFAX1	-----PVERIVRASFDWARGLPSEFAALP-----	-----KDDQ	89
DmUNF	CITKEELAADVRTLHEIFCKYKAVLVDPAEFACLKAIVLFRP-----	ETRGLKDP	131
AaHR51	VFKPGQLAQDLRVLNDTLCRFKSVMVDPAEFACMKAIIVLFRS-----	EARGLKDPV	127
TcHR51	-----ATDVRILADTLMRFKAIHVDPAEFACLKAIVLFRS-----	ETRGLKDPS	118
SpNR2E3	-----TCVSDIRLLQEIMSRFRGLRVDPAEFACLKAIVLFKP-----	ETRGLKDPQ	120
SkNR2E3	-----AMLSDIRVLQEIMARFKAMNVDPAEFACMKAIIVLFKP-----	DTRGLKDPQ	123
DrNR2E3	-----PSASDVRVLQEVFSRFKPLQVDPTEFACLKAIVLFKP-----	ETRGLKDPE	121
XlNR2E3	-----SSTIDVRILQETISRFKSLNVDPTFACLKAVLLFKP-----	ETRGLKDPE	121
GgNR2E3	-----PAAVDVRALQETLGRFKALAVDPTFACMKAVVLFKP-----	ETRGLKDPE	118
MmPNR	-----LASAETRFLQETISRFRALAVDPTFACLKALVLFKP-----	ETRGLKDPE	121
HsPNR	-----LASMETRVLQETISRFRALAVDPTFACMKALVLFKP-----	ETRGLKDPE	123
CbNHR67	-----NEVAAAFEMIEGLHLDTREYSLIKIMTLMRA-----	-----	100
CeNHR67	-----NAVANAFEIIERLQLDNREYMLKHFTMWRD-----	-----	100
BmNHR67	-----IQMRMKLLSAVSQLEQLRLDSTEYNQLRLSLIKG-----	-----	100
DmT11	-----MVTREVHAFQEVNLQCHLNIDSTEYECLRAISLFRKSPPSASTEDLANSSILTGSGSPNSSASAE	SRGLLESG	150
AgT11	-----FLVKEVEIFQEIILAQLAALRVPNEYVYLRAIVLYKSEFDAETSISSVSSD---	GSDVTTASSAGSAKSIGEIA	150
TcTLL	-----AFLKEVADFQETLKKISQFQLDAHEFACLRAIVLFKTSFEKPS-----	SSSNQEKTTTESA	131
SpNR2E1	AEKLAAISSELRLVQELIAKFRQLNVDDTEFACLKGIVIFK-----	TDISGIKETS	123
SkNR2E1	PEKIVAIMSEMRTFQEIIAKFKQMQVDATEYACLKGIIIFKS-----	VFPDSPQEIIRGVDFH	130
DrNR2E1	SQRLNKIISEIQALQEVVTRFRQLRLDATEFACLKCIVTFKA-----	VPTHSGSELRSFRNAS	130
XlNR2E1	SPKLNKIISEIQALQDVVSRFRQLRLDATEFACLKCIVTFKAG-----	VSTHSGSELRNFRNAA	131
GgNR2E1	SQKLNKIISEIQALQEVVARFRQLRLDATEFACLKCIVTFKA-----	VPTHSGSELRSFRNAA	130
MmT1x	SQKLNKIISEIQALQEVVARFRQLRLDATEFACLKCIVTFKA-----	VPTHSGSELRSFRNAA	130
HsT1x	SQKLNKIISEIQALQEVVARFRQLRLDATEFACLKCIVTFKA-----	VPTHSGSELRSFRNAA	130
CbNHR239	-----KCILLNFMISE-----	-----Q	41
CeNHR239	-----KCILLNFMISQ-----	-----E	41
DmHR83	-----EQLKRLICEAHQLRADVLELNFMESLILCRK-----	ELAINAEY	103
AgHR83	-----GHLRSVMEDIKALRVDLIELSLLETILILCRK-----	EFALSARE	103
TcHR83	-----LFPGVKGTFRVVRQLKLNLTLEIVENILLCRA-----	DIILDDV	95
SpGA10225	KGATRRKSEVVDDIQEITVRLTLNLSTHEFAFLEAIVLFKPD-----	T-----KGTLREKS	128
SkXP2740657	-----FDSLKVNFKEG-----	LGNTQ	89

LBD Features	h	h	L	Φ	L	h	h	h	AF-2																																																									
HsRARγ	KVDKLQEP	LL	LEALRLYARRRR	PSQPYM	FF	PM	L	MKIT-DLRGISTKGAERAITL	KMEIPGPMPP	LIREMLENPEM	194																																																							
CbFAX1	KRDEKRRH	DV	VALCRRFCRLMGFN	-	CVIPLALVSFLPKCEMQPRHAIN	SL	PTACVPGGSSAHP	ELGCSIEP	---		179																																																							
CeFAX1	AGERGARL	VAAAL	LLAEH	SVMGFGNC	VIPLALVFSTKSRYVIQRHAIN	SLP	-ACVPGGTAHP	VL	RCSMGS	---	180																																																							
CeNHR111	TDLKFD	RQ	L	D	I	CIGLLNQLHLESSKS	SGRLL	FLLG-EL	KS	SYSTRQLES	LLDL	KACEIVISFL	-----	150																																																				
BmFAX1	QIEDLQ	DQAQ	Q	T	LAKHTMNSS	PAR	---	FG	RLL	LL	LLP	-LL	RTISA	EKIERM	FF	MAIFGNTSIDQI	ICKMYNG	---	178																																															
PpFAX1	TALLSS	KW	TS	LYL	LHC	VEAALGS	EKCP	AL	EH	CGGS	-REN	LD	RS	RV	LF	SL	SDADRGEI	ACL	K	AITL	FHNVPQD	162																																												
DmUNF	QIENLQ	DQ	AH	V	M	L	SQHTKTQ	FTAQ	IAR	FGR	LL	LL	MLP	-LL	R	MIS	SHK	IESI	YFQ	T	IGNT	PMEK	VLC	DMYKN	---	201																																								
AaHR51	QIENLQ	DQ	AQ	V	M	L	AQHSRTQ	FP	GOIAR	FGR	LL	LL	MLP	-LL	R	I	IN	SHK	IESI	YFQ	T	IGNT	PMEK	VLC	DMYKN	---	197																																							
TcHR51	QIENLQ	DQ	AQ	V	M	L	WQHCR	TQ	LP	GQ	VAR	FGR	LL	LL	MLP	-LL	R	I	V	PAS	R	VEA	VFF	Q	T	IGNT	PMEK	VLC	DMYKN	---	188																																			
SpNR2E3	QVEILQ	DQ	AH	M	M	L	TQH	IRAHQ	PAQ	TAR	FGR	LL	LL	MLP	-SL	R	F	V	T	S	DQ	VER	LFF	R	C	T	I	G	D	T	P	M	E	R	L	L	C	D	M	F	K	N	---	190																						
SkNR2E3	QVENLQ	DQ	AQ	L	M	L	GQ	H	T	R	-NH	P	TQ	P	T	R	FGR	LL	LL	MLP	-SL	R	F	V	T	P	N	R	I	E	N	L	F	F	H	T	I	G	N	T	P	M	E	R	L	L	C	D	M	F	K	N	---	192												
DrNR2E3	QVENLQ	DQ	SQ	V	L	L	AQ	H	I	H	T	L	Y	P	SQ	VAR	FGR	LL	LL	MLP	-SL	H	F	V	S	S	E	R	I	E	H	L	F	F	Q	T	I	G	N	T	P	M	E	K	L	L	C	D	M	F	K	N	---	191												
XlNR2E3	QIENLQ	DQ	SQ	M	M	L	AQ	H	T	R	NQ	YPAQ	P	V	R	FGR	LL	LL	MLP	-SL	R	F	I	S	S	E	R	I	E	L	L	F	F	H	R	T	I	G	N	T	P	M	E	K	L	L	C	D	M	F	K	N	---	191												
GgNR2E3	QVENLQ	DQ	SQ	V	M	L	GQ	H	R	S	H	Y	P	GQ	P	V	R	FGR	LL	LL	MLP	-AL	R	F	L	S	S	E	R	V	E	L	L	F	F	R	T	I	G	N	T	P	M	E	K	L	L	C	D	M	F	K	N	---	188											
MmPNR	HVEALQ	DQ	SQ	V	M	L	SQ	H	S	K	AH	HPSQ	P	V	R	FGR	LL	LL	MLP	-SL	R	F	L	T	A	E	R	I	E	L	L	F	F	R	K	T	I	G	N	T	P	M	E	K	L	L	C	D	M	F	K	N	---	191												
HsPNR	HVEALQ	DQ	SQ	V	M	L	SQ	H	S	K	AH	HPSQ	P	V	R	FGR	LL	LL	MLP	-SL	R	F	I	T	A	E	R	I	E	L	L	F	F	R	K	T	I	G	N	T	P	M	E	K	L	L	C	D	M	F	K	N	---	193												
CbNHR67	--TPNG	QQ	I	A	Y	Q	L	M	T	L	Q	A	V	T	H	R	T	D	Q	L	R	F	W	K	C	Y	T	A	T	T	---	TT	P	T	S	A	I	D	V	L	F	R	P	S	I	G	S	A	S	M	T	R	L	I	E	D	M	F	K	P	P	K	P	168		
CeNHR67	--TPSA	IQ	I	V	F	Q	L	A	S	I	Q	N	F	T	H	R	T	E	P	T	R	I	Y	I	Q	C	I	N	A	I	A	---	AI	P	T	T	S	I	D	V	L	F	R	P	S	I	G	S	A	S	M	P	R	L	I	Q	D	M	F	K	P	P	Q	168		
BmNHR67	RNPQME	Q	L	T	A	F	N	F	A	Q	H	Q	I	T	Y	P	CQ	P	L	R	Y	I	S	C	M	V	L	E	---	TM	P	Q	E	A	I	L	S	E	L	Y	F	K	R	S	I	G	N	A	S	M	S	A	L	V	A	D	I	L	L	P	K	D	L	171		
DmT11	KVAAMH	N	D	A	R	S	A	L	H	N	Y	I	Q	R	T	H	P	SQ	P	M	R	F	-Q	T	L	G	V	V	Q	L	M	K	V	S	S	F	T	I	E	E	L	F	F	R	K	T	I	G	D	I	T	I	V	R	L	I	S	D	M	Y	S	Q	R	K	I	223
AgT11	TVRALE	E	S	A	K	E	A	L	A	S	Y	I	S	T	C	R	P	G	S	N	R	Y	-R	T	L	L	Q	L	L	P	A	L	R	N	V	S	S	Y	T	I	E	E	L	F	F	R	N	I	G	P	A	P	L	L	K	L	L	D	F	Y	R	Q	K	--	221	
TcTLL	KISVIQ	D	D	AQ	M	R	L	N	K	H	V	T	T	T	Y	P	KQ	P	L	R	F	G	K	I	L	L	V	S	S	T	F	R	T	I	S	G	R	T	I	E	D	L	F	F	K	K	V	I	R	D	T	P	I	V	A	I	S	N	M	Y	K	N	Q	I	L	205
SpNR2E1	SVVTLQ	DQ	SQ	L	A	L	S	K	Y	I	T	V	R	H	Q	TQ	P	Y	R	FGR	LL	LL	LL	MLP	-SV	R	A	I	R	P	T	T	L	E	Q	I	F	F	W	K	A	V	G	S	T	P	F	H	T	L	L	D	L	Y	K	K	N	E	H	196						
SkNR2E1	GVATLQ	DQ	AQ	L	T	L	S	K	Y	I	H	T	K	Y	P	TQ	P	F	R	FGR	LL	LL	MLP	-QL	R	A	I	R	P	S	T	I	E	E	L	F	F	R	K	T	I	G	N	I	P	I	E	R	L	L	C	D	M	Y	K	A	N	D	F	203						
DrNR2E1	AIAALQ	D	E	AQ	L	T	L	N	S	Y	I	H	T	R	Y	P	TQ	P	C	R	FGR	LL	LL	MLP	-AL	R	S	V	G	P	S	T	I	E	E	V	F	F	K	K	T	I	G	N	V	P	I	T	R	L	L	S	D	M	Y	K	S	S	D	I	203					
XlNR2E1	AISALQ	D	E	AQ	L	T	L	N	S	Y	I	H	T	R	Y	P	TQ	P	C	R	FGR	LL	LL	MLP	-AL	R	S	I	N	P	S	T	I	E	E	V	F	F	K	K	T	I	G	N	V	P	I	T	R	V	L	S	D	M	Y	K	S	S	D	I	204					
GgNR2E1	AIAALQ	D	E	AQ	L	T	L	N	S	Y	I	H	T	R	Y	P	TQ	P	C	R	FGR	LL	LL	MLP	-AL	R	S	I	S	P	S	T	I	E	E	V	F	F	K	K	T	I	G	N	V	P	I	T	R	L	L	S	D	M	Y	K	S	S	D	I	203					
MmTlx	AIAALQ	D	E	AQ	L	T	L	N	S	Y	I	H	T	R	Y	P	TQ	P	C	R	FGR	LL	LL	MLP	-AL	R	S	I	S	P	S	T	I	E	E	V	F	F	K	K	T	I	G	N	V	P	I	T	R	L	L	S	D	M	Y	K	S	S	D	I	203					
HsTlx	AIAALQ	D	E	AQ	L	T	L	N	S	Y	I	H	T	R	Y	P	TQ	P	C	R	FGR	LL	LL	MLP	-AL	R	S	I	S	P	S	T	I	E	E	V	F	F	K	K	T	I	G	N	V	P	I	T	R	L	L	S	D	M	Y	K	S	S	D	I	203					
CbNHR239	RREVVE	EN	CQ	M	I	F	A	L	L	L	L	L	N	G	D	Q	T	T	I	R	R	F	T	T	N	E	N	V	P	---	SG	V	S	C	D	P	EQL	R	L	L	V	C	I	L	S	Q	S	S	E	F	Q	-----	102													
CeNHR239	RREVVE	EN	CQ	I	F	A	L	L	I	L	A	S	G	D	E	A	V	L	S	R	F	P	V	S	F	W	V	S	---	Q	R	I	L	P	-----	82																														
DmHR83	AVILG	S	H	S	K	A	A	L	I	S	L	A	R	Y	T	L	Q	S	N	Y	L	R	F	G	Q	L	L	L	G	L	R	T	V	A	L	R	F	N	E	F	A	V	R	A	M	L	R	E	V	I	S	D	E	G	L	A	E	T	I	L	T	K	L	-----	165	
AgHR83	ATQLE	Q	F	A	E	R	A	L	V	A	L	E	P	-T	A	A	L	P	A	P	A	R	L	G	K	L	L	L	G	L	R	T	V	A	L	R	F	N	E	F	A	V	R	A	M	L	R	E	V	I	S	D	E	G	L	A	E	T	I	L	T	K	L	-----	171	
TcHR83	EQITL	A	L	N	V	L	T	R	A	L	D	E	L	A	V	R	T	V	L	E	R	R	R	F	A	D	I	L	L	A	L	P	-V	L	F	V	P	S	A	V	V	L	H	S	L	L	F	K	P	V	I	G	A	V	P	I	E	T	V	I	S	T	I	-----	162	
SpGA10225	KVEFFR	DQ	SQ	V	V	L	AQ	Y	E	N	I	V	H	P	E	S	P	A	R	FGR	K	L	L	T	M	P	-AL	K	R	V	G	T	E	N	L	E	E	L	F	F	R	R	T	L	G	K	V	Q	I	E	K	I	L	E	R	M	-----	195								
SkXP2740657	QVEFLQ	DQ	AQ	L	I	L	AQ	Y	V	N	S	K	T	PQ	N	P	A	R	FGR	K	L	L	L	T	L	A	-SL	R	T	Y	K	S	E	I	E	E	L	F	F	R	K	T	I	G	K	V	P	I	E	A	I	F	G	S	V	-----	156									

FIGURE S2. Alignments of LBD regions of NR2E proteins.

Multiple alignments were performed using CLUSTAL W using a BLOSUM matrix and a pairwise gap penalty of 10 with 0.1 extension penalty and a multiple alignment gap penalty of 10 with 0.2 extension penalty (Thompson et al., 1994). Numbers at right margin identify amino acid positions relative to the first residue after the DBD. The alignment was colorized using the Color Align utility of the Sequence Manipulation Suite (Stothard, 2000; <http://www.bioinformatics.org/>). Key LBD features were annotated following the analysis of critical conserved LBD features from structures of vertebrate LBDs (Wurtz et al., 1996).

Weber et al., 2012.

Key:

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

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