

A. DNA-binding domain

PXR_human	QICRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNARLRCPFKRGACEITRKTRRQCQACR
PXR_chicken	KVCAVCGDRATGYHFHVMSCGCKGFFRRSILKGVHFTCPF-TRSCPITKAKRRQCQACR
PXR_fugu	RACGVCGDQAKGYHFNAWTCEGCKGFFRAIKRTPPLPCQF-LNKCSITKKNRRQCQDCR
VDR_human	RICGVCGDRATGFHFNAMTCEGCKGFFRRSMKRKALFTCPFN-GDCRITKDNRRHCQACR
VDR_mouse	RICGVCGDRATGFHFNAMTCEGCKGFFRRSMKRKALFTCPFN-GDCRITKDNRRHCQACR
VDR_x_laevis	RICGVCGDKATGFHFNAMTCEGCKGFFRRSMKRKAMFTCPFN-GDCRITKDNRRHCQSCR
VDR_zebrafish	PICGVCGDKATGFHFNAMTCEGCKGFFRRSMKRKASFTCPFN-GNCTITKDNRRHCQACR
VDR_lamprey	KVCGVCGDKATGYHFNAMTCEGCKGFFRRSMKRKASFTCPFE-GKCNITKDNRRHCQACR
VDR_PXR_Ciona	-----MHFGAITCEGCKGFFRRSVKKNASFSCAF-EKKCEINKNNRKHQCQACR
CAR_human	RNCVVCGDQATGYHFNALTCEGCKGFFRRTVSKSIGPTCPF-AGSCEVSKTQRRHCPACR

PXR_human	LRKCLESGM
PXR_chicken	LQKCLDVGM
PXR_fugu	LRKCQAIGM
VDR_human	LKRCVDIGM
VDR_mouse	LKRCVDIGM
VDR_x_laevis	LKRCVDIGM
VDR_zebrafish	LKRCIDIGM
VDR_lamprey	LKRCRDIGM
VDR_PXR_Ciona	FNACLAAGM
CAR_human	LQKCLDAGM

B. Ligand-binding domain

		<u>Helix-1</u>	
PXR_human	141	QGLTEEQRMMIRELMDAQMKTFTDFTTSHFKNFRLPGVLSGGCELPELQAP-SREEA-AK	
PXR_chicken		GGLTAEQQELISILIAAHKRTFDSSFSQFQHYQPAVRLC----IPGPCSQS-PPGPG-VP	
PXR_fugu		IHLSSQQEETIRELLYGHRKTFDLEFYRFSSFRVRTSTTLFDLSKLSERL-NIFAV-RG	
VDR_human	118	PKLSEEQQRIIAAILLDAHHTYDPTYSDFCQFRPPVRVNDGGGSHPSRPNRHTPSF-SG	
VDR_mouse		PKLSEEQQHIIAAILLDAHHTYDPTYADFRDFRPPPIRADVSTGYSYSPR-----TLSF-SG	
VDR_x_laevis		PKISDEQQKMIDILLEAHRKTFDFTTYSDFNKFPPVRENVDPFRITRSSSVHTQGSPSE	
VDR_zebrafish		PRLSDEQMQUIINSLVEAHHKTYDSDYSDFVFRPPVREGPVTRSASRAASLHSLSDA-SS	
VDR_lamprey		PQLLEEQRERLIATLIEAHRKTYDASYSDFSQFRPPKRGDGSPECRNATNPFMLSLLN-SD	
VDR_PXR_Ciona		TRMTMDEKLLVKTLKGRDSDYDFAYVEYDTFRGREDGQOEIGNNTENPNG---LDA-AT	
CAR_human	103	VQLSKEQEELIRTLGATHRMGMTMFEQFVQFRPPAHLFIHHQPL-----	

			<u>Helix-3</u>
PXR_human	199	WSQVRKDLCSLKVSLQL-RGEDGSVWNYKPP-----ADSGGKEIFSLPHMADMSTYMFK	
PXR_chicken		SASLSPQLDCLDEDVL-----PDVFSILPHFADLSTFMIQ	
PXR_fugu		SSPSGPASSDV--SSLS-TSARLRGRPETPQTQGGENARRGC-VFTALPHVTDLATCMIH	
VDR_human	181	DSSSSCDHCITSSDM-MDSSSFSNLDLSEEDSDDPVTLLELSQLSMLPHLADLVSYSIQ	
VDR_mouse		DSSSNS-DLYTPSLDM-MEPASFSTMDLNEEGSDDPSVTLDLSPLSMLPHLADLVSYSIQ	
VDR_x_laevis		DSDVFTSSPDSSEHGFFSASLFGQFEYSSMGGKSGELS-----MLPHIADLVSYSIQ	
VDR_zebrafish		DSFNHSPESVDTKLNFSNLLMMYQDSG-SPDSSEEDQQS----RLSMLPHLADLVSYSIQ	
VDR_lamprey		MD-----ELPKASASGAEAAAGDELSMLPHLADLVSYSIQ	
VDR_PXR_Ciona		AVEAQSTTEDSGKQLHL-MLLFQHFLPIYP-----FSFDPKA-QQLFQHFCDIMTWGIR	
CAR_human	149	-----PTLAPVPLVTHFADINTFMVL	

		<u>Helix-3</u>	<u>Helix-4</u>	<u>Helix-5</u>	
PXR_human	253	GIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAET-GTWECGR--LSY---			
PXR_chicken		QVIKFAKEIPAFRGLPIDDQISLLKCATLGICQIQFNTVFNEET-NAWECGQ--HCF---			

PXR_fugu		DI IAFSKSLTDFKSL LIGDQ IALLKGATFEVMEIRFNMVFNTKT-GLWECGH--ATY---
VDR_human	240	KVIGFAKMIPGFRDLTSEDQIVLLKSSAIEVIMLRSNESFTMDD-MSWTCGNQDYKY---
VDR_mouse		KVIGFAKMIPGFRDLTSDQIVLLKSSAIEVIMLRSNQSFTMDD-MSWDCGSQDYKY---
VDR_x_laevis		KIIGFAKMIPGFRDLIAEDQ IALLKSSVIEVIMLRSNQSFSLDD-MSWTCGSEDFKYKVD
VDR_zebrafish		KVIGFAKMIPGFRDLTAEDQ IALLKSSAIEIIMLRSNQSFSLED-MSWSCGGPDFKYCIN
VDR_lamprey		KVIGFAKMIPGFKELCTEDQISLLKASAIEIIILRSNESFTMED-NSWTCGSNEFKYQIG
VDR_PXR_Ciona		KVIDYCKGIPQFVQLSIVDQIVLLRGGCLEMLVLRSYFAFSCNE-NKYMSDK--FQY---
CAR_human	171	QVIKFTKDLPVFRSLPIEDQISLLKGAAVEICHIVLNTTFCLOT-QNFLCGP--LRY---
		<u>Helix-7</u> <u>Helix-8</u> <u>Helix-9</u>
PXR_human	308	CLEDT-AGGF----QQLLLEPMLKFHYMLKKLQLHEEEYVLMQAI SLFSPDRPGVLQHRV
PXR_chicken		TIKDGALAGF----QIYLEPLLKFHISLKKLRLHEAEYVLLVAMLLFSPDHASVTQRDF
PXR_fugu		CIEDAVRAGF----QPLFLEPLLKFHHTLRNLGLEEEYVLMQALS LFS PDRPGVQQHSV
VDR_human	297	RVSDVTKAGH----SLELIEPLIKFQVGLKKNLHHEEHVLLMAICIVSPDRPGVQDAAL
VDR_mouse		DITDVSRAGH----TLELIEPLIKFQVGLKKNLHHEEHVLLMAICIVSPDRPGVQDAKL
VDR_x_laevis		D---VTQAGH----NMELLEPLVKFQVGLKKNLHHEEHVLLMAICILSPDRPGLQDKAL
VDR_zebrafish		D---VTKAGH----TLELLEPLVKFQVGLKKNLHHEEHVLLMAICLLSPDRPGVDHVR
VDR_lamprey		D---VMQAGH----KLELLEPLVKFQVNMKKDLHHEEHVLLMAICLFS PDRPGVQDRCR
VDR_PXR_Ciona		KPSDFLQAGG----NKEFVEKYNSLHIRMRKMKLQVEEICLLLALVLFSPDRPGLEDQAK
CAR_human	226	TIEDGARVGF----QVEFLELLFHFGHTLRKLQLQEPEYVLLAAMALFSPDRPGVTQRDE
		<u>Helix-9</u> <u>Helix-10</u>
PXR_human	363	IDQLQEQAIFAITLKS YIECNR-PQPAHRFLFLKIMAMLTELRSINAQHTQRLRLRIQDIHPFA
PXR_chicken		VDQLQEKVALTLKSYIDHRH-PMPEGRFLYAKLLLLLTELQTLKMENTRQILHIQDLSSM-
PXR_fugu		IDKIHENLALALKTRIELKR-TGPEKHMLYPKVL SCLTEMRTMNEEYSKQVLQIQDIPNV
VDR_human	353	IEAIQDRLSNTLQTYIRCRH-PPPGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECS
VDR_mouse		VEAIQDRLSNTLQTYIRCRH-PPPGSHQLYAKMIQKLADLRSLNEEHSKQYRSLSFQPECS
VDR_x_laevis		VESIQDRLSSTLQTYILCKH-PPPGSRLLYAKMIQKLADLRSLNEEHSKQYRSISFLPEHS
VDR_zebrafish		IEALQDRLCDVLAQYIRIQH-P--GGRLLYAKMIQKLADLRSLNEEHSKQYRSLSFQPEHS
VDR_lamprey		IEEVQEHLTETLRAYIACRH-PLSCKHMLYTKMVEKLTTELRS LNEEHSKQYLQISQDAV NK
VDR_PXR_Ciona		VEQMQDCVANTLQAYEYTHK-PPNESSFLQARTMYCLPILRTINMLFAQNIMSLQTNKDM
CAR_human	282	VDQLQEEMALTLQSYIKGQQ-RRPRDRFLYAKLLGLLAELRSINEAYGYQIQHIQGLSAMM
PXR_human	422	ATPLMQELFGITGS
PXR_chicken		-TPLLSEIIS
PXR_fugu		VIPPLLMEMVS
VDR_human	412	SMKLTPLVLEVFGNEIS
VDR_mouse		SMKLTPLVLEVFGNEIS
VDR_x_laevis		SMKLTPLMLEVFSDEIP
VDR_zebrafish		SMQLTPLVLEVFGSEVS
VDR_lamprey		KEDLPPLLEVFGNPTA
VDR_PXR_Ciona		N-PLILEVNNSADDED
CAR_human	341	MPLLQEICS

Additional file 1: Sequence alignment of (A) DNA-binding domain and (B) ligand-binding domain of three PXR, five VDR, *Ciona intestinalis* VDR/PXR, and human CAR. The ligand-binding domain is annotated with the α -helices [1]. Accession numbers are: human PXR [Genbank:AF061056], chicken PXR [Genbank:AF276753], takifugu PXR [Ensembl,<http://www.ensembl.org:NEWSINFRUT00000171584>], human VDR [Genbank:NM_00376], mouse VDR [Genbank:NM_008504], *Xenopus laevis* VDR [Genbank:U91849], zebrafish VDR [Genbank:AF164512], sea lamprey VDR [Genbank:AY249863], *Ciona intestinalis* VDR/PXR [Genbank:BR000137], and human

CAR [Genbank:NM_005122]. Note that some N-terminal sequence is unavailable for the *Ciona* VDR/PXR.

Reference

1. Moore LB, Maglich JM, McKee DD, Wisely B, Willson TM, Kliewer SA, Lambert MH, Moore JT: **Pregnane X receptor (PXR), constitutive androstane receptor (CAR), and benzoate X receptor (BXR) define three pharmacologically distinct classes of nuclear receptors.** *Mol Endocrinol* 2002, **16**:977-986.