ANTP class

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            ______I______     ____II____     ________III________
            10        20        30        40        50        60
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	Consensus	KRRKRTTFTKEQLLELEKEFAKNPYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE	**Accession**	**ML bs**	**NJ bs**
HOXL subclass					
Cdx	**Hs CDX1**	KDKYRVVYTDHQRLELEKEFHYSRYITIRRKSELAANLGLTERQVKIWFQNRRAKERKVN	NP_001795	100	80
	Hs CDX2	KDKYRVVYTDHQRLELEKEFHYSRYITIRRKAELAATLGLSERQVKIWFQNRRAKERKIN	NP_001256		
	Hs CDX4	KEKYRVVYTDHQRLELEKEFHCNRYITIQRKSELAVNLGLSERQVKIWFQNRRAKERKMI	NP_005184		
	Dm cad	KDKYRVVYTDFQRLELEKEYCTSRYITIRRKSELAQTLSLSERQVKIWFQNRRAKERKQN	NP_476954		
Evx	**Hs EVX1**	MRRYRTAFTREQIARLEKEFYRENYVSRPRRCELAAALNLPETTIKVWFQNRRMKDKRQR	NP_001980	100	100
	Hs EVX2	VRRYRTAFTREQIARLEKEFYRENYVSRPRRCELAAALNLPETTIKVWFQNRRMKDKRQR	NP_001073927		
	Dm eve	VRRYRTAFTRDQLGRLEKEFYKENYVSRPRRCELAAQLNLPESTIKVWFQNRRMKDKRQR	NP_523670		
Gbx	**Hs GBX1**	SRRRRTAFTSEQLLELEKEFHCKKYLSLTERSQIAHALKLSEVQVKIWFQNRRAKWKRIK	NP_001092304	99	100
	Hs GBX2	NRRRRTAFTSEQLLELEKEFHCKKYLSLTERSQIAHALKLSEVQVKIWFQNRRAKWKRVK	NP_001476		
	Dm unpg	SRRRRTAFTSEQLLELEREFHAKKYLSLTERSQIATSLKLSEVQVKIWFQNRRAKWKRVK	NP_477146		
Gsx	**Hs GSX1**	SKRMRTAFTSTQLLELEREFASNMYLSRLRRIEIATYLNLSEKQVKIWFQNRRVKHKKEG	NP_663632	98	100
	Hs GSX2	GKRMRTAFTSTQLLELEREFSSNMYLSRLRRIEIATYLNLSEKQVKIWFQNRRVKHKKEG	NP_573574		
	Dm ind	SKRIRTAFTSTQLLELEREFSHNAYLSRLRRIEIANRLRLSEKQVKIWFQNRRVKQKKGG	NP_996087		
Hox1	**Hs HOXA1**	PNAVRTNFTTKQLTELEKEFHFNKYLTRARRVEIAASLQLNETQVKIWFQNRRMKQKKRE	NP_005513	98	99
	Hs HOXB1	PSGLRTNFTTRQLTELEKEFHFNKYLSRARRVEIAATLELNETQVKIWFQNRRMKQKKRE	NP_002135		
	Hs HOXD1	SSAIRTNFSTKQLTELEKEFHFNKYLTRARRIEIANCLHLNDTQVKIWFQNRRMKQKKRE	NP_078777		
	Dm lab	NNSGRTNFTNKQLTELEKEFHFNRYLTRARRIEIANTLQLNETQVKIWFQNRRMKQKKRV	NP_476613		
Hox2	**Hs HOXA2**	SRRLRTAYTNTQLLELEKEFHFNKYLCRPRRVEIAALLDLTERQVKVWFQNRRMKHKRQT	NP_006726	92	100
	Hs HOXB2	ARRLRTAYTNTQLLELEKEFHFNKYLCRPRRVEIAALLDLTERQVKVWFQNRRMKHKRQT	NP_002136		
	Dm pb	PRRLRTAYTNTQLLELEKEFHFNKYLCRPRRIEIAASLDLTERQVKVWFQNRRMKHKRQT	NP_476669		
Hox3	**Hs HOXA3**	SKRARTAYTSAQLVELEKEFHFNRYLCRPRRVEMANLLNLTERQIKIWFQNRRMKYKKDQ	NP_109377	69	68
	Hs HOXB3	SKRARTAYTSAQLVELEKEFHFNRYLCRPRRVEMANLLNLSERQIKIWFQNRRMKYKKDQ	NP_002137		
	Hs HOXD3	SKRVRTAYTSAQLVELEKEFHFNRYLCRPRRVEMANLLNLTERQIKIWFQNRRMKYKKDQ	NP_008829		
	Sm Hox3b	NKRSRTAYTQSQLVELEKEFHFNRYLCRPRRVELASMLNLTERQIKIWFQNRRMKNKKIK	ABN42908		
Hox4	**Hs HOXA4**	PKRSRTAYTRQQVLELEKEFHFNRYLTRRRRIEIAHTLCLSERQVKIWFQNRRMKWKKDH	NP_002132	n/a	39
	Hs HOXB4	PKRSRTAYTRQQVLELEKEFHYNRYLTRRRRVEIAHALCLSERQIKIWFQNRRMKWKKDH	NP_076920		
	Hs HOXC4	PKRSRTAYTRQQVLELEKEFHYNRYLTRRRRIEIAHSLCLSERQIKIWFQNRRMKWKKDH	NP_055435		
	Hs HOXD4	PKRSRTAYTRQQVLELEKEFHFNRYLTRRRRIEIAHTLCLSERQIKIWFQNRRMKWKKDH	NP_055436		
	Dm Dfd	PKRQRTAYTRHQILELEKEFHYNRYLTRRRRIEIAHTLVLSERQIKIWFQNRRMKWKKDN	NP_477201		
Hox5	**Hs HOXA5**	GKRARTAYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLSERQIKIWFQNRRMKWKKDN	NP_061975	n/a	28
	Hs HOXB5	GKRARTAYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLSERQIKIWFQNRRMKWKKDN	NP_002138		
	Hs HOXC5	GKRSRTSYTRYQTLELEKEFHFNRYLTRRRRIEIANNLCLNERQIKIWFQNRRMKWKKDS	NP_061826		
	Dm Scr	TKRQRTSYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKEH	NP_524248		

Hox6-8	**Hs HOXA6**	GRRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIANALCLTERQIKIWFQNRRMKWKKEN	NP_076919	20	39
	Hs HOXB6	GRRGRQTYTRYQTLELEKEFHYNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKES	NP_061825		
	Hs HOXC6	RRRGRQIYSRYQTLELEKEFHFNRYLTRRRRIEIANALCLTERQIKIWFQNRRMKWKKES	NP_004494		
	Hs HOXA7	RKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKEH	NP_008827		
	Hs HOXB7	RKRGRQTYTRYQTLELEKEFHYNRYLTRRRRIEIAHTLCLTERQIKIWFQNRRMKWKKEN	NP_004493		
	Hs HOXB8	RRRGRQTYSRYQTLELEKEFLFNPYLTRKRRIEVSHALGLTERQVKIWFQNRRMKWKKEN	NP_076921		
	Hs HOXC8	RRSGRQTYSRYQTLELEKEFLFNPYLTRKRRIEVSHALGLTERQVKIWFQNRRMKWKKEN	NP_073149		
	Hs HOXD8	RRRGRQTYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQNRRMKWKKEN	NP_062458		
	Dm Antp	RKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALCLTERQIKIWFQNRRMKWKKEN	NP_996172		
	Dm Ubx	RRRGRQTYTRYQTLELEKEFHTNHYLTRRRRIEMAHALCLTERQIKIWFQNRRMKLKKEI	NP_536752		
	Dm Abd-A	RRRGRQTYTRFQTLELEKEFHFNHYLTRRRRIEIAHALCLTERQIKIWFQNRRMKLKKEL	NP_476693		
Hox9-13	**Hs HOXA9**	TRKKRCPYTKHQTLELEKEFLFNMYLTRDRRYEVARLLNLTERQVKIWFQNRRMKMKKIN	NP_689952	66	61
	Hs HOXB9	SRKKRCPYTKYQTLELEKEFLFNMYLTRDRRHEVARLLNLSERQVKIWFQNRRMKMKKMN	NP_076922		
	Hs HOXC9	TRKKRCPYTKYQTLELEKEFLFNMYLTRDRRYEVARVLNLTERQVKIWFQNRRMKMKKMN	NP_008828		
	Hs HOXD9	TRKKRCPYTKYQTLELEKEFLFNMYLTRDRRYEVARILNLTERQVKIWFQNRRMKMKKMS	NP_055028		
	Hs HOXA10	GRKKRCPYTKHQTLELEKEFLFNMYLTRERRLEISRSVHLTDRQVKIWFQNRRMKLKKMN	NP_061824		
	Hs HOXC10	GRKKRCPYTKHQTLELEKEFLFNMYLTRERRLEISKTINLTDRQVKIWFQNRRMKLKKMN	NP_059105		
	Hs HOXD10	GRKKRCPYTKHQTLELEKEFLFNMYLTRERRLEISKSVNLTDRQVKIWFQNRRMKLKKMS	NP_002139		
	Hs HOXA11	TRKKRCPYTKYQIRELEREFFFSVYINKEKRLQLSRMLNLTDRQVKIWFQNRRMKEKKIN	NP_005514		
	Hs HOXC11	TRKKRCPYSKFQIRELEREFFFNVYINKEKRLQLSRMLNLTDRQVKIWFQNRRMKEKKLS	NP_055027		
	Hs HOXD11	SRKKRCPYTKYQIRELEREFFFNVYINKEKRLQLSRMLNLTDRQVKIWFQNRRMKEKKLN	NP_067015		
	Hs HOXC12	SRKKRKPYSKLQLAELEGEFLVNEFITRQRRRELSDRLNLSDQQVKIWFQNRRMKKKRLL	NP_776272		
	Hs HOXD12	ARKKRKPYTKQQIAELENEFLVNEFINRQKRKELSNRLNLSDQQVKIWFQNRRMKKKRVV	NP_067016		
	Hs HOXA13	GRKKRVPYTKVQLKELEREYATNKFITKDKRRRISATTNLSERQVTIWFQNRRVKEKKVI	NP_000513		
	Hs HOXB13	GRKKRIPYSKGQLRELEREYAANKFITKDKRRKISAATSLSERQITIWFQNRRVKEKKVL	NP_006352		
	Hs HOXC13	GRKKRVPYTKVQLKELEKEYAASKFITKEKRRRISATTNLSERQVTIWFQNRRVKEKKVV	NP_059106		
	Hs HOXD13	GRKKRVPYTKLQLKELENEYAINKFINKDKRRRISAATNLSERQVTIWFQNRRVKDKKIV	NP_000514		
	Dm Abd-B	VRKKRKPYSKFQTLELEKEFLFNAYVSKQKRWELARNLQLTERQVKIWFQNRRMKNKKNS	NP_650577		
Mnx	**Hs MNX1**	CRRPRTAFTSQQLLELEHQFKFNKYLSRPKRFEVATSLMLTETQVKIWFQNRRMKWKRSK	NP_005506	90	99
	Dm exex	TRRPRTAFTSQQLLELEKQFKQNKYLSRPKRFEVASGLMLSETQVKIWFQNRRMKWKRSK	NP_648164		
Meox	**Hs MEOX1**	ARKERTAFTKEQLRELEAEFAHHNYLTRLRRYEIAVNLDLSERQVKVWFQNRRMKWKRVK	NP_004518	95	100
	Hs MEOX2	PRKERTAFTKEQIRELEAEFAHHNYLTRLRRYEIAVNLDLTERQVKVWFQNRRMKWKRVK	NP_005915		
	Dm btn	NRKERTAFSKTQLKQLEAEFCYSNYLTRLRRYEIAVALELTERQVKVWFQNRRMKCKRIK	NP_732768		
Pdx	**Hs PDX1**	NKRTRTAYTRAQLLELEKEFLFNKYISRPRRVELAVMLNLTERHIKIWFQNRRMKWKKEE	NP_000200	89	100
	Ps Xlox	NKRTRTAYTRAQLLELEKEFHFNKYISRPRRIELAAMLNLTERHIKIWFQNRRMKWKKDE	AAK77134		

NKL subclass

Barhl	**Hs BARHL1**	PRKARTAFTDHQLAQLERSFERQKYLSVQDRMELAASLNLTDTQVKTWYQNRRTKWKRQT	NP_064448	95	94
	Hs BARHL2	PRKARTAFSDHQLNQLERSFERQKYLSVQDRMDLAAALNLTDTQVKTWYQNRRTKWKRQT	NP_064447		
	Dm B-H1	QRKARTAFTDHQLQTLEKSFERQKYLSVQERQELAHKLDLSDCQVKTWYQNRRTKWKRQT	NP_523387		
	Dm B-H2	QRKARTAFTDHQLQTLEKSFERQKYLSVQDRMELANKLELSDCQVKTWYQNRRTKWKRQT	NP_523386		
Barx	**Hs BARX1**	GRRSRTVFTELQLMGLEKRFEKQKYLSTPDRIDLAESLGLSQLQVKTWYQNRRMKWKKIV	NP_067545	prot/cnid homolog not found	
	Hs BARX2	PRRSRTIFTELQLMGLEKKFQKQKYLSTPDRLDLAQSLGLTQLQVKTWYQNRRMKWKKMV	NP_003649		
Bsx	**Hs BSX**	RRKARTVFSDSQLSGLEKRFEIQRYLSTPERVELATALSLSETQVKTWFQNRRMKHKKQL	NP_001091639	89	100
	Dm bsh	RRKARTVFSDPQLSGLEKRFEGQRYLSTPERVELATALGLSETQVKTWFQNRRMKHKKQL	NP_477350		

Dbx	**Hs DBX1**	GMLRRAVFSDVQRKALEKMFQKQKYISKPDRKKLAAKLGLKDSQVKIWFQNRRMKWRNSK	EAW68342	94	96
	Hs DBX2	GILRRAVFSEDQRKALEKMFQKQKYISKTDRKKLAINLGLKESQVKIWFQNRRMKWRNSK	NP_001004329		
	Dm CG12361	GMMRRAVFSDSQRKGLEKRFQQQKYISKPDRKKLAERLGLKDSQVKIWFQNRRMKWRNSK	NP_647677		
Dlx	**Hs DLX1**	IRKPRTIYSSLQLQALNRRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLM	NP_835221	100	100
	Hs DLX2	VRKPRTIYSSFQLAALQRRFQKTQYLALPERAELAASLGLTQTQVKIWFQNRRSKFKKMW	NP_004396		
	Hs DLX3	VRKPRTIYSSYQLAALQRRFQKAQYLALPERAELAAQLGLTQTQVKIWFQNRRSKFKKLY	NP_005211		
	Hs DLX4	LRKPRTIYSSLQLQHLNQRFQHTQYLALPERAQLAAQLGLTQTQVKIWFQNKRSKYKKLL	NP_612138		
	Hs DLX5	VRKPRTIYSSFQLAALQRRFQKTQYLALPERAELAASLGLTQTQVKIWFQNKRSKIKKIM	NP_005212		
	Hs DLX6	IRKPRTIYSSLQLQALNHRFQQTQYLALPERAELAASLGLTQTQVKIWFQNKRSKFKKLL	NP_005213		
	Dm Dll	MRKPRTIYSSLQLQQLNRRFQRTQYLALPERAELAASLGLTQTQVKIWFQNRRSKYKKMM	NP_523857		
Emx	**Hs EMX1**	PKRIRTAFSPSQLLRLERAFEKNHYVVGAERKQLAGSLSLSETQVKVWFQNRRTKYKRQK	NP_004088	92	100
	Hs EMX2	PKRIRTAFSPSQLLRLEHAFEKNHYVVGAERKQLAHSLSLTETQVKVWFQNRRTKFKRQK	NP_004089		
	Dm ems	PKRIRTAFSPSQLLKLEHAFESNQYVVGAERKALAQNLNLSETQVKVWFQNRRTKHKRMQ	NP_731868		
	Dm E5	PKRVRTAFSPTQLLKLEHAFEGNHYVVGAERKQLAQGLSLTETQVKVWFQNRRTKHKRMQ	NP_524825		
En	**Hs EN1**	DKRPRTAFTAEQLQRLKAEFQANRYITEQRRQTLAQELSLNESQIKIWFQNKRAKIKKAT	NP_001417	97	99
	Hs EN2	DKRPRTAFTAEQLQRLKAEFQTNRYLTEQRRQSLAQELSLNESQIKIWFQNKRAKIKKAT	NP_001418		
	Dm en	EKRPRTAFSSEQLARLKREFNENRYLTERRRQQLSSELGLNEAQIKIWFQNKRAKIKKST	NP_523700		
	Dm inv	DKRPRTAFSGTQLARLKHEFNENRYLTEKRRQQLSGELGLNEAQIKIWFQNKRAKLKKSS	NP_725055		
Hhex	**Hs HHEX**	RKGGQVRFSNDQTIELEKKFETQKYLSPPERKRLAKMLQLSERQVKTWFQNRRAKWRRLK	NP_002720	88	85
	Dm CG7056	RKGGQIRFTSQQTKNLEARFASSKYLSPEERRHLALQLKLTDRQVKTWFQNRRAKWRRAN	NP_650938		
Hlx	**Hs HLX**	RSWSRAVFSNLQRKGLEKRFEIQKYVTKPDRKQLAAMLGLTDAQVKVWFQNRRMKWRHSK	NP_068777	n/a	n/a
	Dm H2.0	KRKRSWSRAVFSNLQRKGLEIQQKYITKPDRRKLAARLNLTDAQVKVWFQNRRMKWRHTR	NP_523488		
Lbx	**Hs LBX1**	RRKSRTAFTNHQIYELEKRFLYQKYLSPADRDQIAQQLGLTNAQVITWFQNRRAKLKREL	NP_006553	95	94
	Hs LBX2	RRKSRTAFTAQQVLELERRFVFQKYLAPSERDGLATRLGLANAQVVTWFQNRRAKLKRDV	NP_001009812		
	Dm lbe	KRKSRTAFTNHQIFELEKRFLYQKYLSPADRDEIAASLGLSNAQVITWFQNRRAKQKRDI	NP_524435		
	Dm lbl	KRKSRTAFTNQQIFELEKRFLYQKYLSPADRDEIAGGLGLSNAQVITWFQNRRAKLKRDM	NP_524434		
Msx	**Hs MSX1**	NRKPRTPFTTAQLLALERKFRQKQYLSIAERAEFSSSLSLTETQVKIWFQNRRAKAKRLQ	NP_002439	98	100
	Hs MSX2	NRKPRTPFTTSQLLALERKFRQKQYLSIAERAEFSSSLNLTETQVKIWFQNRRAKAKRLQ	NP_002440		
	Dm Dr	NRKPRTPFTTQQLLSLEKKFREKQYLSIAERAEFSSSLRLTETQVKIWFQNRRAKAKRLQ	NP_477324		
Nanog	**Hs NANOG**	KQKTRTVFSSTQLCVLNDRFQRQKYLSLQQMQELSNILNLSYKQVKTWFQNQRMKSKRWQ	NP_079141	prot/cnid	homolog not found
Nk1	**Hs NKX1-1**	PRRARTAFTYEQLVALENKFKATRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN	XP_931434	100	100
	Hs NKX1-2	PRRARTAFTYEQLVALENKFRATRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN	XP_372331		
	Dm slou	PRRARTAFTYEQLVSLENKFKTTRYLSVCERLNLALSLSLTETQVKIWFQNRRTKWKKQN	NP_476657		
Nk2-1	**Hs NKX2-1**	RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA	NP_001073136	62	79
	Hs NKX2-4	RRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQA	CAH71494		
	Dm scro	RRKRRVLFTQAQVYELERRFKQQRYLSAPEREHLASLIHLTPTQVKIWFQNHRYKCKRQA	NP_001015473		
Nk2-2	**Hs NKX2-2**	KRKRRVLFSKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKMKRAR	NP_002500	84	62
	Hs NKX2-8	RKKRRVLFSKAQTLELERRFRQQRYLSAPEREQLASLLRLTPTQVKIWFQNHRYKLKRAR	NP_055175		
	Dm vnd	KRKRRVLFTKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKTKRAQ	NP_476786		
Nk3	**Hs NKX3-1**	QKRSRAAFSHTQVIELERKFSHQKYLSAPERAHLAKNLKLTETQVKIWFQNRRYKTKRKQ	NP_006158	79	88
	Hs NKX3-2	KKRSRAAFSHAQVFELERRFNHQRYLSGPERADLAASLKLTETQVKIWFQNRRYKTKRRQ	NP_001180		
	Dm bap	KKRSRAAFSHAQVFELERRFAQQRYLSGPERSEMAKSLRLTETQVKIWFQNRRYKTKRKQ	NP_732637		

Nk4	**Hs NKX2-3**	RRKPRVLFSQAQVFELERRFKQQRYLSAPEREHLASSLKLTSTQVKIWFQNRRYKCKRQR	NP_660328	n/a	60
	Hs NKX2-5	RRKPRVLFSQAQVYELERRFKQQRYLSAPERDQLASVLKLTSTQVKIWFQNRRYKCKRQR	NP_004378		
	Hs NKX2-6	RRKPRVLFSQAQVLALERRFKQQRYLSAPEREHLASALQLTSTQVKIWFQNRRYKCKRQR	XP_070619		
	Pd NK4	KRKPRVLFSQAQVYELERRFKQQRYLSAPEREQLASMLKLTSTQVKIWFQNRRYKMKRQR	ABQ10640		
Nk5/Hmx	**Hs HMX1**	KKKTRTVFSRSQVFQLESTFDLKRYLSTAERAGLAASLQLTETQVKIWFQNRRNKWKRHV	NP_061815	99	100
	Hs HMX2	KKKTRTVFSRSQVYQLESTFDMKRYLSSSERACLASSLQLTETQVKTWFQNRRNKWKRQL	NP_005510		
	Hs HMX3	KKKTRTVFSRSQVFQLESTFDMKRYLSSSERAGLAASLHLTETQVKIWFQNRRNKWKRQL	XP_291716		
	Dm Hmx	KKKTRTVFSRAQVFQLESTFDLKRYLSSSERAGLAASLRLTETQVKIWFQNRRNKWKRQL	NP_524951		
Nk6	**Hs NKX6-1**	RKHTRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKH	NP_006159	100	100
	Hs NKX6-2	KKHSRPTFSGQQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKRH	NP_796374		
	Hs NKX6-3	KKHTRPTFTGHQIFALEKTFEQTKYLAGPERARLAYSLGMTESQVKVWFQNRRTKWRKKS	EAW63251		
	Dm HGTX	KKHTRPTFSGQQIFALEKTFEQTKYLAGPERAKLAYALGMSESQVKVWFQNRRTKWRKRH	NP_652614		
Noto	**Hs NOTO**	QKRVRTMFNLEQLEELEKVFAKQHNLVGKKRAQLAARLKLTENQVRVWFQNRRVKYQKQQ	XP_292889	prot/cnid homolog not found	
Tlx	**Hs TLX1**	KKKPRTSFTRLQICELEKRFHRQKYLASAERAALAKALKMTDAQVKTWFQNRRTKWRRQT	NP_005512	98	100
	Hs TLX2	RKKPRTSFSRSQVLELERRFLRQKYLASAERAALAKALRMTDAQVKTWFQNRRTKWRRQT	NP_057254		
	Hs TLX3	RKKPRTSFSRVQICELEKRFHRQKYLASAERAALAKSLKMTDAQVKTWFQNRRTKWRRQT	NP_066305		
	Dm C15	RKKPRTSFTRIQVAELEKRFHKQKYLASAERAALARGLKMTDAQVKTWFQNRRTKWRRQT	NP_476873		
Vax	**Hs VAX1**	PKRTRTSFTAEQLYRLEMEFQRCQYVVGRERTELARQLNLSETQVKVWFQNRRTKQKKDQ	CAI14825	prot/cnid homolog not found	
	Hs VAX2	PKRTRTSFTAEQLYRLEMEFQRCQYVVGRERTELARQLNLSETQVKVWFQNRRTKQKKDQ	NP_036608		
Ventx	**Hs VENTX**	APRVRTAFTMEQVRTLEGVFQHHQYLSPLERKRLAREMQLSEVQIKTWFQNRRMKHKRQM	NP_055283	prot/cnid homolog not found	

PRD class

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         10        20         30        40        50        60
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	Consensus	KRRKRTTFTKEQLLELEKEFAKN-PYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE	Accession	ML bs	NJ bs
Alx	**Hs ALX1**	KRRHRTTFTSLQLEELEKVFQKT-HYPDVYVREQLALRTELTEARVQVWFQNRRAKWRKRE	NP_008913	n/a	79
	Hs ALX3	KRRNRTTFSTFQLEELEKVFQKT-HYPDVYAREQLALRTDLTEARVQVWFQNRRAKWRKRE	NP_006483		
	Hs ALX4	KRRNRTTFTSYQLEELEKVFQKT-HYPDVYAREQLAMRTDLTEARVQVWFQNRRAKWRKRE	NP_068745		
	Nv CART1	KRRNRTTFTAYQLEEMERVFQKT-HYPDVYTREQLALRCALTEARVQVWFQNRRAKWRKRE	ABB83749		
Argfx	**Hs ARGFX**	RHKERTSFTHQQYEELEALFSQT-MFPDRNLQEKLALRLDLPESTVKVWFRNRRFKLKKQQ	NP_001012677	prot/cnid homolog not found	
Arx	**Hs ARX**	QRRYRTTFTSYQLEELERAFQKT-HYPDVFTREELAMRLDLTEARVQVWFQNRRAKWRKRE	NP_620689	23	28
	Dm al	QRRYRTTFTSFQLEELEKAFSRT-HYPDVFTREELAMKIGLTEARIQVWFQNRRAKWRKQE	NP_722629		
	Dm Pph13	QRRYRTTFNTLQLQELERAFQRT-HYPDVFFREELAVRIDLTEARVQVWFQNRRAKWRKQE	NP_477330		
Dmbx	**Hs DMBX1**	QRRSRTAFTAQQLEALEKTFQKT-HYPDVVMRERLAMCTNLPEARVQVWFKNRRAKFRKKQ	NP_671725	50	49
	Hv manacle	HRRVRTAFTHHQLTTLERTFETS-HYPDVVLRERLASFTGLAESRIQVWFKNRRAKYRKHQ	AAD30998		
Dprx	**Hs DPRX**	SHRKRTMFTKKQLEDLNILFNEN-PYPNPSLQKEMASKIDIHPTVLQVWFKNHRAKLKKAK	NP_001012746	prot/cnid homolog not found	

Drgx	**Hs DRGX**	QRRNRTTFTLQQLEALEAVFAQT-HYPDVFTREELAMKINLTEARVQVWFQNRRAKWRKTE	NP_001073989	90	97
	Dm IP09201	QRRNRTTFTLQQLEELETAFAQT-HYPDVFTREDLAMKINLTEARVQVWFQNRRAKWRKAE	ABK30908		
Dux	**Hs DUXA-I**	HRRCRTKFTEEQLKILINTFNQK-PYPGYATKQKLALEINTEESRIQIWFQNRRARHGFQK	NP_001012747	prot/cnid homolog not found	
	Hs DUXA-II	ARRCRTTYSASQLHTLIKAFMKN-PYPGIDSREELAKEIGVPESRVQIWFQNRRSRLLLQR	NP_001012747		
	Hs DUXB-I	FWRNRIQYNQSQKDILQSWFQHD-PFPDKAAREQLAKEIGVPESNIQVWFKNYRVKQRKLD	unassigned		
	Hs DUXB-II	ARQKQTFITWTQKNRLVQAFERN-PFPDIATRKKLAEQTGLQESRIQMWFQKQRSLYLKKS	unassigned		
Esx	**Hs ESX1**	KRRRRTAFTQFQLQELENFFDES-QYPDVVARERLAARLNLTEDRVQVWFQNRRAKWKRNQ	NP_703149	prot/cnid homolog not found	
Gsc	**Hs GSC**	KRRHRTIFTDEQLEALENLFQET-KYPDVGTREQLARKVHLREEKVEVWFKNRRAKWRRQK	NP_776248	74	77
	Hs GSC2	TRRHRTIFSEEQLQALEALFVQN-QYPDVSTRERLAGRIRLREERVEVWFKNRRAKWRHQK	NP_005306		
	Dm Gsc	KRRHRTIFTEEQLEQLEATFDKT-HYPDVVLREQLALKVDLKEERVEVWFKNRRAKWRKQK	NP_476949		
Hesx	**Hs HESX1**	GRRPRTAFTQNQIEVLENVFRVN-CYPGIDIREDLAQKLNLEEDRIQIWFQNRRAKLKRSH	NP_003856	prot/cnid homolog not found	
Hopx	**Hs HOPX**	SAETASGPTEDQVEILEYNFNKVDKHPDSTTLCLIAAEAGLSEEETQKWFKQRLAKWRRSE	NP_115884	prot/cnid homolog not found	
Isx	**Hs ISX**	KRRVRTTFTTEQLHELEKIFHFT-HYPDVHIRSQLAARINLPEARVQIWFQNQRAKWRKQE	NP_001008494	prot/cnid homolog not found	
Leutx	**Hs LEUTX**	YRRPRTRFLSKQLTALRELLEKT-MHPSLATMGKLASKLQLDLSVVKIWFKNQRAKWKRQQ	XP_001129035	prot/cnid homolog not found	
Mix	**Hs MIXL**	QRRKRTSFSAEQLQLLELVFRRT-RYPDIHLRERLAALTLLPESRIQVWFQNRRAKSRRQS	NP_114150	prot/cnid homolog not found	
Nobox	**Hs NOBOX**	RKKTRTLYRSDQLEELEKIFQED-HYPDSDKRREIAQTVGVTPQRIMVWFQNRRAKWRKME	O60393	prot/cnid homolog not found	
Otp	**Hs OTP**	QKRHRTRFTPAQLNELERSFAKT-HYPDIFMREELALRIGLTESRVQVWFQNRRAKWKKRK	NP_115485	100	99
	Dm otp	QKRHRTRFTPAQLNELERCFSKT-HYPDIFMREEIAMRIGLTESRVQVWFQNRRAKWKKRK	NP_523799		
Otx	**Hs OTX1**	QRRERTTFTRSQLDVLEALFAKT-RYPDIFMREEVALKINLPESRVQVWFKNRRAKCRQQQ	NP_055377	91	98
	Hs OTX2	QRRERTTFTRAQLDVLEALFAKT-RYPDIFMREEVALKINLPESRVQVWFKNRRAKCRQQQ	NP_068374		
	Hs CRX	QRRERTTFTRSQLEELEALFAKT-QYPDVYAREEVALKINLPESRVQVWFKNRRAKCRQQR	NP_000545		
	Dm oc	QRRERTTFTRAQLDVLEALFGKT-RYPDIFMREEVALKINLPESRVQVWFKNRRAKCRQQL	NP_511091		
Pax2/5/8	**Hs PAX2**	KHLRADTFTQQQLEALDRVFERP-SYPDVFQASE---------------------------	NP_003981	partial homeodomain	
	Hs PAX5	KQMRGDLFTQQQLEVLDRVFERQ-HYSDIFTTTE---------------------------	NP_057953		
	Hs PAX8	KHLRTDAFSQHHLEPLECPF RQ-HYPEAYASPS---------------------------	NP_003457		
Pax3/7	**Hs PAX3**	QRRSRTTFTAEQLEELERAFERT-HYPDIYTREELAQRAKLTEARVQVWFSNRRARWRKQA	NP_852122	78	79
	Hs PAX7	QRRSRTTFTAEQLEELEKAFERT-HYPDIYTREELAQRTKLTEARVQVWFSNRRARWRKQA	NP_002575		
	Dm prd	QRRCRTTFSASQLDELERAFERT-QYPDIYTREELAQRTNLTEARIQVWFSNRRARLRKQH	NP_523556		
	Dm gsb	QRRSRTTFSNDQIDALERIFART-QYPDVYTREELAQSTGLTEARVQVWFSNRRARLRKQL	NP_523863		
	Dm gsb-n	QRRSRTTFTAEQLEALERAFSRT-QYPDVYTREELAQTTALTEARIQVWFSNRRARLRKHS	NP_523862		
Pax4/6	**Hs PAX4**	GHRNRTIFSPSQAEALEKEFQRG-QYPDSVARGKLATATSLPEDTVRVWFSNRRAKWRRQE	NP_006184	28	29
	Hs PAX6	LQRNRTSFTQEQIEALEKEFERT-HYPDVFARERLAAKIDLPEARIQVWFSNRRAKWRREE	NP_001595		
	Dm ey	LQRNRTSFTNDQIDSLEKEFERT-HYPDVFARERLAGKIGLPEARIQVWFSNRRAKWRREE	NP_524628		
	Dm eyg	FRRNRTTFSPEQLEELEKEFDKS-HYPCVSTRERLSSRTSLSEARVQVWFSNRRAKWRRHQ	NP_524042		
	Dm toy	LQRNRTSFSNEQIDSLEKEFERT-HYPDVFARERLADKIGLPEARIQVWFSNRRAKWRREE	NP_524638		
	Dm toe	FRRNRTTFSPEQLDELEKEFDKS-HYPCVNTREKLAARTALSEARVQVWFSNRRAKWRRHQ	NP_524041		
Phox	**Hs PHOX2A**	QRRIRTTFTSAQLKELERVFAET-HYPDIYTREELALKIDLTEARVQVWFQNRRAKFRKQE	NP_005160	75	71
	Hs PHOX2B	QRRIRTTFTSAQLKELERVFAET-HYPDIYTREELALKIDLTEARVQVWFQNRRAKFRKQE	NP_003915		
	Dm PHDP	QRRIRTTFTSNQLNELEKIFLET-HYPDIYTREEIASKLHLTEARVQVWFQNRRAKFRKQE	NP_523834		

Pitx	**Hs PITX1**	QRRQRTHFTSQQLQELEATFQRN-RYPDMSMREEIAVWTNLTEPRVRVWFKNRRAKWRKRE	NP_002644	100	100
	Hs PITX2	QRRQRTHFTSQQLQELEATFQRN-RYPDMSTREEIAVWTNLTEARVRVWFKNRRAKWRKRE	NP_000316		
	Hs PITX3	QRRQRTHFTSQQLQELEATFQRN-RYPDMSTREEIAVWTNLTEARVRVWFKNRRAKWRKRE	NP_005020		
	Dm Ptx1	QRRQRTHFTSQQLQELEHTFSRN-RYPDMSTREEIAMWTNLTEARVRVWFKNRRAKWRKRE	NP_733410		
Prop	**Hs PROP1**	RRRHRTTFSPVQLEQLESAFGRN-QYPDIWARESLARDTGLSEARIQVWFQNRRAKQRKQE	NP_006252	52	n/a
	Dm CG32532	RRRHRTTFTQEQLAELEAAFAKS-HYPDIYCREELARTTKLNEARIQVWFQNRRAKYRKQE	NP_608318		
Prrx	**Hs PRRX1**	QRRNRTTFNSSQLQALERVFERT-HYPDAFVREDLARRVNLTEARVQVWFQNRRAKFRRNE	NP_073207	92	81
	Hs PRRX2	QRRNRTTFNSSQLQALERVFERT-HYPDAFVREELARRVNLSEARVQVWFQNRRAKFRRNE	NP_057391		
	Dm CG9876	PRRNRTTFSSAQLTALEKVFERT-HYPDAFVREELATKVHLSEARVQVWFQNRRAKFRRNE	NP_611756		
Rax	**Hs RAX**	HRRNRTTFTTYQLHELERAFEKS-HYPDVYSREELAGKVNLPEVRVQVWFQNRRAKWRRQE	NP_038463	94	99
	Hs RAX2	HRRNRTTFTTYQLHQLERAFEAS-HYPDVYSREELAAKVHLPEVRVQVWFQNRRAKWRRQE	NP_116142		
	Dm Rx	HRRNRTTFTTYQLHELERAFEKS-HYPDVYSREELAMKVNLPEVRVQVWFQNRRAKWRRQE	NP_726006		
Rhox	**Hs RHOXF1**	PRTRRTKFTLLQVEELESVFRHT-QYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQ	NP_644811	prot/cnid homolog not found	
	Hs RHOXF2	QQPNVHAFTPLQLQELERIFQRE-QFPSEFLRRRLARSMNVTELAVQIWFENRRAKWRRHQ	NP_115887		
	Hs RHOXF2B	QQPNVHAFTPLQLQELECIFQRE-QFPSEFLRRRLARSMNVTELAVQIWFENRRAKWRRHQ	NP_001093155		
Sebox	**Hs SEBOX**	HRRKRTTFSKGQLLELERAFAAW-PYPNISTHEHLAWVTCLPEAKVQVWFQKRWAKIIKNR	NP_001074306	prot/cnid homolog not found	
Shox	**Hs SHOX**	QRRSRTNFTLEQLNELERLFDET-HYPDAFMREELSQRLGLSEARVQVWFQNRRAKCRKQE	NP_000442	100	100
	Hs SHOX2	QRRSRTNFTLEQLNELERLFDET-HYPDAFMREELSQRLGLSEARVQVWFQNRRAKCRKQE	NP_006875		
	Dm IP17602	QRRSRTNFTLDQLNELERLFEET-HYPDAFMREELSQRLGLSEARVQVWFQNRRAKCRKHE	ABM92832		
Tprx	**Hs TPRX1**	QRQERTVYTESQQKVLEFYFQKD-QYPNYDQRLNLAEMLSLREQQLQVWFKNRRAKLARER	EAW57514	prot/cnid homolog not found	
	Hs TPRXL	QRQDRTIYNWKQQEVLENHFKEE-QYPDYDTRQELAEMLNLREYQVQVWFKNRRAKRSRER	unassigned		
Uncx	**Hs UNCX**	RRRTRTNFTGWQLEELEKAFNES-HYPDVFMREALALRLDLVESRVQVWFQNRRAKWRKKE	NP_001073930	90	85
	Dm unc-4	RRRSRTNFNSWQLEELERAFSAS-HYPDIFMREALAMRLDLKESRVAVWFQNRRAKVRKRE	NP_573242		
	Dm OdsH	KRRGRTNFNSWQLRELERVFQGS-HYPDIFMREALATKLDLMEGRIAVWFQNRRAKWRKQE	NP_523389		
Vsx	**Hs VSX1**	KRRHRTVFTAHQLEELEKAFSEA-HYPDVYAREMLAVKTELPEDRIQVWFQNRRAKWRKRE	NP_055403	97	100
	Hs VSX2	KRRHRTIFTSYQLEELEKAFNEA-HYPDVYAREMLAMKTELPEDRIQVWFQNRRAKWRKRE	NP_878314		
	Dm CG33980	RRHSRTIFTSYQLEKLEEAFKEA-HYPDVYAREMLSLKTELPEDRIQVWFQNRRAKWRKTE	NP_001033832		
	Dm CG4136	RRHGRTIFTSSQLEELEKAFKEA-HYPDVSARELLSMKTGLAEDRIQVWYQNRRAKWRKTE	NP_572232		

LIM class

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        ______I_______    ____II_____   _______III________
         10        20        30        40        50        60
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	Consensus	KRRKRTTFTKEQLLELEKEFAKNPYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE	**Accession**	**ML bs**	**NJ bs**
Isl	**Hs ISL1**	TTRVRTVLNEKQLHTLRTCYAANPRPDALMKEQLVEMTGLSPRVIRVWFQNKRCKDKKRS	NP_002193	100	100
	Hs ISL2	TTRVRTVLNEKQLHTLRTCYAANPRPDALMKEQLVEMTGLSPRVIRVWFQNKRCKDKKKS	NP_665804		
	Dm tup	PTRVRTVLNEKQLHTLRTCYNANPRPDALMKEQLVEMTSLSPRVIRVWFQNKRCKDKKKT	NP_476775		

Lhx1/5	**Hs LHX1**	RRGPRTTIKAKQLETLKAAFAATPKPTRHIREQLAQETGLNMRVIQVWFQNRRSKERRMK	NP_005559	96	89
	Hs LHX5	RRGPRTTIKAKQLETLKAAFAATPKPTRHIREQLAQETGLNMRVIQVWFQNRRSKERRMK	NP_071758		
	Dm Lim1	RRGPRTTIKAKQLEVLKTAFNQTPKPTRHIREQLAKETGLPMRVIQVWFQNKRSKERRMK	NP_572505		
Lhx2/9	**Hs LHX2**	TKRMRTSFKHHQLRTMKSYFAINHNPDAKDLKQLAQKTGLTKRVLQVWFQNARAKFRRNL	NP_004780	98	100
	Hs LHX9	TKRMRTSFKHHQLRTMKSYFAINHNPDAKDLKQLAQKTGLTKRVLQVWFQNARAKFRRNL	NP_064589		
	Dm ap	TKRMRTSFKHHQLRTMKSYFAINHNPDAKDLKQLSQKTGLPKRVLQVWFQNARAKWRRMM	NP_724428		
Lhx3/4	**Hs LHX3**	AKRPRTTITAKQLETLKSAYNTSPKPARHVREQLSSETGLDMRVVQVWFQNRRAKEKRLK	NP_055379	94	99
	Hs LHX4	AKRPRTTITAKQLETLKNAYKNSPKPARHVREQLSSETGLDMRVVQVWFQNRRAKEKRLK	NP_203129		
	Dm Lim3	NKRPRTTITAKQLETLKTAYNNSPKPARHVREQLSQDTGLDMRVVQVWFQNRRAKEKRLK	NP_476606		
Lhx6/8	**Hs LHX6**	AKRARTSFTAEQLQVMQAQFAQDNNPDAQTLQKLADMTGLSRRVIQVWFQNCRARHKKHT	NP_055183	58	54
	Hs LHX8	AKRARTSFTADQLQVMQAQFAQDNNPDAQTLQKLAERTGLSRRVIQVWFQNCRARHKKHV	NP_001001933		
	Dm Awh	TKRVRTTFTEEQLQVLQANFQIDSNPDGQDLERIASVTGLSKRVTQVWFQNSRARQKKHI	NP_523907		
Lmx	**Hs LMX1A**	PKRPRTILTTQQRRAFKASFEVSSKPCRKVRETLAAETGLSVRVVQVWFQNQRAKMKKLA	NP_796372	100	100
	Hs LMX1B	PKRPRTILTTQQRRAFKASFEVSSKPCRKVRETLAAETGLSVRVVQVWFQNQRAKMKKLA	NP_002307		
	Dm CG32105	PKRPRTILTSQQRKQFKASFDQSPKPCRKVREALAKDTGLSVRVVQVWFQNQRAKMKKIQ	NP_729801		
	Dm CG4328	PKRPRTILNTQQRRAFKASFEVSPKPCRKVRENLAKDTGLSLRIVQVWFQNQRAKVKKIQ	NP_648567		

POU class

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             _____I_____       ___II___   ______III______
             10        20             30        40        50        60
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	Consensus	KRRK----RTTFTKEQLLELEKEFAKNPY----PSREEREELAASLGLTERQVKVWFQNRRAKWKKQE	**Accession**	**ML bs**	**NJ bs**
Hdx	**Hs HDX**	SRKRALQDRTQFSDRDLATLKKYWDNGMTSLGSVCREKIEAVATELNVDCEIVRTWIGNRRRKYRLMG	NP_653258	prot/cnid	homolog not found
Pou1	**Hs POU1F1**	KRKR----RTTISIAAKDALERHFGEQNK----PSSQEIMRMAEELNLEKEVVRVWFCNRRQREKRVK	NP_000297	94	90
	Nv POU1	RRKR----RTTIGLAAKEALENHFMKQTK----PSSPEIVRIADGLRLDKEVVRVWFCNRRQREKRVK	ABB86471		
Pou2	**Hs POU2F1**	RRKK----RTSIETNIRVALEKSFLENQK----PTSEEITMIADQLNMEKEVIRVWFCNRRQKEKRIN	NP_002688	83	79
	Hs POU2F2	RRKK----RTSIETNVRFALEKSFLANQK----PTSEEILLIAEQLHMEKEVIRVWFCNRRQKEKRIN	NP_002689		
	Hs POU2F3	KRKK----RTSIETNIRLTLEKRFQDNPK----PSSEEISMIAEQLSMEKEVVRVWFCNRRQKEKRIN	NP_055167		
	Dm nub	RRKK----RTSIETTIRGALEKAFLANQK----PTSEEITQLADRLSMEKEVVRVWFCNRRQKEKRIN	NP_476659		
	Dm pdm2	RRKK----RTSIETTVRTTLEKAFLMNCK----PTSEEISQLSERLNMDKEVIRVWFCNRRQKEKRIN	NP_523558		
Pou3	**Hs POU3F1**	KRKK----RTSIEVGVKGALESHFLKCPK----PSAHEITGLADSLQLEKEVVRVWFCNRRQKEKRMT	NP_002690	83	93
	Hs POU3F2	KRKK----RTSIEVSVKGALESHFLKCPK----PSAQEITSLADSLQLEKEVVRVWFCNRRQKEKRMT	NP_005595		
	Hs POU3F3	KRKK----RTSIEVSVKGALESHFLKCPK----PSAQEITNLADSLQLEKEVVRVWFCNRRQKEKRMT	NP_006227		
	Hs POU3F4	KRKK----RTSIEVSVKGVLETHFLKCPK----PAAQEISSLADSLQLEKEVVRVWFCNRRQKEKRMT	NP_000298		
	Dm vvl	KRKK----RTSIEVSVKGALEQHFHKQPK----PSAQEITSLADSLQLEKEVVRVWFCNRRQKEKRMT	NP_523948		
Pou4	**Hs POU4F1**	KKRK----RTSIAAPEKRSLEAYFAVQPR----PSSEKIAAIAEKLDLKKNVVRVWFCNQRQKQKRMK	NP_006228	95	100
	Hs POU4F2	KKRK----RTSIAAPEKRSLEAYFAIQPR----PSSEKIAAIAEKLDLKKNVVRVWFCNQRQKQKRMK	NP_004566		
	Hs POU4F3	RKRK----RTSIAAPEKRSLEAYFAIQPR----PSSEKIAAIAEKLDLKKNVVRVWFCNQRQKQKRMK	NP_002691		
	Dm acj6	KKRK----RTSIAAPEKRSLEAYFAVQPR----PSGEKIAAIAEKLDLKKNVVRVWFCNQRQKQKRIV	NP_524876		

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Pou5      Hs POU5F1     RKRK----RTSIENRVRGNLENLFLQCPK----PTLQQISHIAQQLGLEKDVVRVWFCNRRQKGKRSS                NP_002692        prot/cnid homolog not found
          Hs POU5F2     GKWR----RASRERRIGNSLEKFFQRCPK----PTPQQISHIAGCLQLQKDVVRVWFYNRSKMGSRPT                NP_694948

Pou6      Hs POU6F1     KRKR----RTSFTPQAIEALNAYFEKNPL----PTGQEITEIAKELNYDREVVRVWFCNRRQTLKNTS                NP_002693        89        92
          Hs POU6F2     KRKR----RTSFTPQALEILNAHFEKNTH----PSGQEMTEIAEKLNYDREVVRVWFCNKRQALKNTI                NP_009183
          Dm pdm3       KRKR----RTSFTPQALELLNAHFERNTH----PSGTEITGLAHQLGYEREVIRIWFCNKRQALKNTV                NP_610377
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HNF class

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                                 ______I_______    _____II____                        _______III________
                                 10        20        30                             40        50        60
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          Consensus     KRRKRTTFTKEQLLELEKEFAKNPYPSREEREELAASLG---------------------LTERQVKVWFQNRRAKWKKQE   Accession        ML bs      NJ bs

Hmbox     Hs HMBOX1     RRGSRFTWRKECLAVMESYFNENQYPDEAKREEIANACN--AVIQK---PGKKLS-DLERVTSLKVYNWFANRRKEIKRRA   NP_078843        prot/cnid homolog not found

Hnf1      Hs HNF1A      GRRNRFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGLGSNLVTEVRVYNWFANRRKEEAFRH   NP_000536        99        98
          Hs HNF1B      MRRNRFKWGPASQQILYQAYDRQKNPSKEEREALVEECNRAECLQRGVSPSKAHGLGSNLVTEVRVYNWFANRRKEEAFRQ   NP_000449
          Nv HNF        SRRNRFKWGPASTNILYQSYEQQRNPSKEEREALVEACNRAECEQRGVSYNNVEGLGFNLVTESRVYNWFANRRKEETFRM   ABB86496
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SINE class

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                                 ______I_______    _____II____   _______III________
                                 10        20        30        40        50        60
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          Consensus     KRRKRTTFTKEQLLELEKEFAKNPYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE                        Accession        ML bs      NJ bs

Six1/2    Hs SIX1       GEETSYCFKEKSRGVLREWYAHNPYPSPREKRELAEATGLTTTQVSNWFKNRRQRDRAAE                        NP_005973        81        100
          Hs SIX2       GEETSYCFKEKSRSVLREWYAHNPYPSPREKRELTEATGLTTTQVSNWFKNRRQRDRAAE                        NP_058628
          Dm so         GEETSYCFKEKSRSVLRDWYSHNPYPSPREKRDLAEATGLTTTQVSNWFKNRRQRDRAAE                        NP_476733

Six3/6    Hs SIX3       GEQKTHCFKERTRSLLREWYLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRAAA                        NP_005404        100       99
          Hs SIX6       GEQKTHCFKERTRNLLREWYLQDPYPNPSKKRELAQATGLTPTQVGNWFKNRRQRDRAAA                        NP_031400
          Dm Optix      GEQKTHCFKERTRSLLREWYLQDPYPNPTKKRELAKATGLNPTQVGNWFKNRRQRDRAAA                        NP_524695

Six4/5    Hs SIX4       GEETVYCFKEKSRNALKELYKQNRYPSPAEKRHLAKITGLSLTQVSNWFKNRRQRDRNPS                        NP_059116        90        91
          Hs SIX5       GEETVYCFKERSRAALKACYRGNRYPTPDEKRRLATLTGLSLTQVSNWFKNRRQRDRTGA                        NP_787071
          Dm Six4       GEETVYCFKEKSRNALKDCYLTNRYPTPDEKKTLAKKTGLTLTQVSNWFKNRRQRDRTPQ                        NP_649256
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TALE class

		______I______ ____II____ _______III_______			
		10 20 30 40 50 60			
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	Consensus	KRRKRTTFTKEQLLELEKEFAKN---PYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE	**Accession**	**ML bs**	**NJ bs**
Irx	**Hs IRX1**	DPGRPKNATRESTSTLKAWLNEHRKNPYPTKGEKIMLAIITKMTLTQVSTWFANARRRLKKEN	NP_077313	97	38
	Hs IRX2	DPAYRKNATRDATATLKAWLNEHRKNPYPTKGEKIMLAIITKMTLTQVSTWFANARRRLKKEN	NP_150366		
	Hs IRX3	DPSRPKNATRESTSTLKAWLNEHRKNPYPTKGEKIMLAIITKMTLTQVSTWFANARRRLKKEN	NP_077312		
	Hs IRX4	SGTRRKNATRETTSTLKAWLQEHRKNPYPTKGEKIMLAIITKMTLTQVSTWFANARRRLKKEN	NP_057442		
	Hs IRX5	DPAYRKNATRDATATLKAWLNEHRKNPYPTKGEKIMLAIITKMTLTQVSTWFANARRRLKKEN	NP_005844		
	Hs IRX6	GAGRRKNATRETTSTLKAWLNEHRKNPYPTKGEKIMLAIITKMTLTQVSTWFANARRRLKKEN	NP_077311		
	Dm ara	LAARRKNATRESTATLKAWLNEHKKNPYPTKGEKIMLAIITKMTLTQVSTWFANARRRLKKEN	NP_524045		
	Dm caup	LAARRKNATRESTATLKAWLSEHKKNPYPTKGEKIMLAIITKMTLTQVSTWFANARRRLKKEN	NP_524046		
	Dm mirr	NGARRKNATRETTSTLKAWLNEHKKNPYPTKGEKIMLAIITKMTLTQVSTWFANARRRLKKEN	NP_524047		
Meis	**Hs MEIS1**	RHKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIVQPM	NP_002389	69	93
	Hs MEIS2	RQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIVQPM	NP_733777		
	Hs MEIS3	RNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIVQPM	NP_001009813		
	Dm hth	NQKKRGIFPKVATNILRAWLFQHLTHPYPSEDQKKQLAQDTGLTILQVNNWFINARRRIVQPM	NP_476578		
Mkx	**Hs MKX**	KVRHKRQALQDMARPLKQWLYKHRDNPYPTKTEKILLALGSQMTLVQVSNWFANARRRLKNTV	NP_775847	n/a	n/a
	Dm CG11617	SRATKRLFTPDIKRMLKDWLIRRRENPYPSREEKKQLAAETGLTYTQICNWFANWRRKLKNSE	NP_608502		
Pbx	**Hs PBX1**	ARRKRRNFNKQATEILNEYFYSHLSNPYPSEEAKEELAKKCGITVSQVSNWFGNKRIRYKKNI	NP_002576	100	100
	Hs PBX2	ARRKRRNFSKQATEVLNEYFYSHLSNPYPSEEAKEELAKKCGITVSQVSNWFGNKRIRYKKNI	NP_002577		
	Hs PBX3	ARRKRRNFSKQATEILNEYFYSHLSNPYPSEEAKEELAKKCSITVSQVSNWFGNKRIRYKKNI	NP_006186		
	Hs PBX4	ARRKRRNFSKQATEVLNEYFYSHLNNPYPSEEAKEELARKGGLTISQVSNWFGNKRIRYKKNM	NP_079521		
	Dm exd	ARRKRRNFSKQASEILNEYFYSHLSNPYPSEEAKEELARKCGITVSQVSNWFGNKRIRYKKNI	NP_523360		
Pknox	**Hs PKNOX1**	SKNKRGVLPKHATNVMRSWLFQHIGHPYPTEDEKKQIAAQTNLTLLQVNNWFINARRRILQPM	NP_004562	97	94
	Hs PKNOX2	SKNKRGVLPKHATNIMRSWLFQHLMHPYPTEDEKRQIAAQTNLTLLQVNNWFINARRRILQPM	NP_071345		
	Am Prep	GRQKRGVLPKQATSIMRTWLFEHLVHPYPTEDEKRQIASQTNLTLLQVNNWFINARRRILQPM	XP_001120618		
Tgif	**Hs TGIF1**	KRRRRGNLPKESVQILRDWLYEHRYNAYPSEQEKALLSQQTHLSTLQVCNWFINARRRLLPDM	NP_733796	100	88
	Hs TGIF2	KRKRRGNLPKESVKILRDWLYLHRYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLLPDM	NP_068581		
	Hs TGIF2LX	KKKRKGNLPAESVKILRDWMYKHRFKAYPSEEEKQMLSEKTNLSLLQISNWFINARRRILPDM	NP_620410		
	Hs TGIF2LY	KKKRKGNLPAESVKILRDWMYKHRFKAYPSEEEKQMLSEKTNLSLLRISNWFINARRRILPDM	NP_631960		
	Dm achi	LRKRRGNLPKTSVKILKRWLYEHRYNAYPSDAEKFTLSQEANLTVLQVCNWFINARRRILPEM	NP_725182		
	Dm vis	LRKRRGNLPKSSVKILKRWLYEHRYNAYPSDAEKFTLSQEANLTVLQVCNWFINARRRILPEM	NP_523714		

CUT class

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                                ______I______     ____II____    _______III_______
                                10        20         30        40        50        60
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             Consensus KRRKRTTFTKEQLLELEKEFAK-NPYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE                          Accession        ML bs      NJ bs

Cux       Hs CUX1      LKKPRVVLAPEEKEALKRAYQQ-KPYPSPKTIEDLATQLNLKTSTVINWFHNYRSRIRREL                          NP_853530        90         n/a
          Hs CUX2      IKKPRVVLAPEEKEALRKAYQL-EPYPSQQTIELLSFQLNLKTNTVINWFHNYRSRMRREM                          NP_056082
          Dm ct        SKKQRVLFSEEQKEALRLAFAL-DPYPNVGTIEFLANELGLATRTITNWFHNHRMRLKQQV                          NP_524764

Onecut    Hs ONECUT1   PKKPRLVFTDVQRRTLHAIFKE-NKRPSKELQITISQQLGLELSTVSNFFMNARRRSLDKW                          NP_004489        99         96
          Hs ONECUT2   QKKSRLVFTDLQRRTLFAIFKE-NKRPSKEMQITISQQLGLELTTVSNFFMNARRRSLEKW                          NP_004843
          Hs ONECUT3   PKKQRLVFTDLQRRTLIAIFKE-NKRPSKEMQVTISQQLGLELNTVSNFFMNARRRCMNRW                          NP_001073957
          Dm onecut    PKKPRLVFTDLQRRTLQAIFKE-TKRPSKEMQVTIARQLGLEPTTVGNFFMNARRRSMDKW                          NP_524842

Satb      Hs SATB1     KTRPRTKISVEALGILQSFIQDVGLYPDEEAIQTLSAQLDLPKYTIIKFFQNQRYYLKHHG                          NP_002962        prot/cnid homolog not found
          Hs SATB2     KPRSRTKISLEALGILQSFIHDVGLYPDQEAIHTLSAQLDLPKHTIIKFFQNQRYHVKHHG                          NP_056080
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PROS class

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                                ______I______    ____II____      _______III_______
                                10        20        30        40            50       60
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             Consensus KRRKRTTFTKEQLLELEKEFAKNPYPSREEREELAASLGLT---ERQVKVWFQNRRAKWKKQE                        Accession        ML bs      NJ bs

Prox      Hs PROX1     GSAMQEGLSPNHLKKAKLMFFYTRYPSSNMLKTYFSDVKFNRCITSQLIKWFSNFREFYYIQM                        NP_002754        100        99
          Hs PROX2     LVHIQEGLNPGHLKKAKLMFFFTRYPSSNLLKVYFPDVQFNRCITSQMIKWFSNFREFYYIQM                        NP_001073877
          Dm pros      MAPTSSTLTPMHLRKAKLMFFWVRYPSSAVLKMYFPDIKFNKNNTAQLVKWFSNFREFYYIQM                        NP_731565
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ZF class

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                                ______I______    ____II____    _______III_______
                                10        20        30        40        50        60
                       ....|....|....|....|....|....|....|....|....|....|....|....|
             Consensus KRRKRTTFTKEQLLELEKEFAKNPYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE                           Accession        ML bs      NJ bs

Adnp      Hs ADNP      PKGHEDDSYEARKSFLTKYFNKQPYPTRREIEKLAASLWLWKSDIASHFSNKRKKCVRDC                           NP_056154        prot/cnid homolog not found
          Hs ADNP2     PKKYEGRSYEEKKQFLKDYFHKKPYPSKKEIELLSSLFWVWKIDVASFFGKRRYICMKAI                           NP_055728
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                                ______I______                ____II____    _______III_______
                                10        20                   30        40        50        60
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          Consensus    KRRKRTTFTKEQLLELEKEFAKNPYPS-----------REEREELAASLGLTERQVKVWFQNRRAKWKKQE             Accession        ML bs     NJ bs

Tshz      Hs TSHZ1     RKGRQSNWNPQHLLILQAQFASSLRETTEGKYIMSDLGPQERVHISKFTGLSMTTISHWLANVKYQLRRTG             NP_005777        no homeodomain in Dm tsh
          Hs TSHZ2     RKGRQSNWNPQHLLILQAQFASSLFQTSEGKYLLSDLGPQERMQISKFTGLSMTTISHWLANVKYQLRKTG             NP_775756
          Hs TSHZ3     RKGRQSNWNPQHLLILQAQFAASLRQTSEGKYIMSDLSPQERMHISRFTGLSMTTISHWLANVKYQLRRTG             NP_065907


                                 ______I______     ____II____    _______III_______
                                 10        20        30        40        50        60
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          Consensus    KRRKRTT-FTKEQLLELEKEFAKNPYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE                       Accession        ML bs     NJ bs

Zeb       Hs ZEB1      GNLSPSQPPLKNLLSLLKAYYALNAQPSAEELSKIADSVNLPLDVVKKWFEKMQAGQISVQ                       NP_110378        n/a       n/a
          Hs ZEB2      GMTSPIN-PYKDHMSVLKAYYAMNMEPNSDELLKISIAVGLPQEFVKEWFEQRKVYQYSNS                       NP_055610
          Dm zfh1      KVRVRTA-INEEQQQQLKQHYSLNARPSRDEFRMIAARLQLDPRVVQVWFQNNRSRERKMQ                       NP_733402


                                ______I______     ____II____    _______III_______
                                10        20        30        40        50        60
                       ....|....|....|....|....|....|....|....|....|....|....|....|

          Consensus    KRRKRTTFTKEQLLELEKEFAKNPYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE                        Accession        ML bs     NJ bs

Zfhx      Hs ZFHX3-I   NKRPRTRITDDQLRVLRQYFDINNSPSEEQIKEMADKSGLPQKVIKHWFRNTLFKERQRN                        NP_008816        99        98
          Hs ZFHX4-I   FKRPRTRITDDQLKILRAYFDINNSPSEEQIQEMAEKSGLSQKVIKHWFRNTLFKERQRN                        NP_078997
          Dm zfh2-I    QKRARTRITDDQLKILRAHFDINNSPSEESIMEMSQKANLPMKVVKHWFRNTLFKERQRN                        NP_524623

          Hs ZFHX2-I   RRFSRTKFTEFQTQALQSFFETSAYPKDGEVERLASLLGLASRVVVVWFQNARQKARKNA                        NP_207646        97        92
          Hs ZFHX3-II  KRSSRTRFTDYQLRVLQDFFDANAYPKDDEFEQLSNLLNLPTRVIVVWFQNARQKARKNY                        NP_008816
          Hs ZFHX4-II  KRSSRTRFTDYQLRVLQDFFDTNAYPKDDEIEQLSTVLNLPTRVIVVWFQNARQKARKSY                        NP_078997
          Dm zfh2-II   KRANRTRFTDYQIKVLQEFFENNSYPKDSDLEYLSKLLLLSPRVIVVWFQNARQKQRKIY                        NP_524623

          Hs ZFHX2-II  DKRLRTTILPEQLEILYRWYMQDSNPTRKMLDCISEEVGLKKRVVQVWFQNTRARERKGQ                        NP_207646        91        95
          Hs ZFHX3-III DKRLRTTITPEQLEILYQKYLLDSNPTRKMLDHIAHEVGLKKRVVQVWFQNTRARERKGQ                        NP_008816
          Hs ZFHX4-III DKRLRTTITPEQLEILYEKYLLDSNPTRKMLDHIAREVGLKKRVVQVWFQNTRARERKGQ                        NP_078997
          Dm zfh2-III  NKRLRTTILPEQLNFLYECYQSESNPSRKMLEEISKKVNLKKRVVQVWFQNSRAKDKKSR                        NP_524623

          Hs ZFHX2-III QRRYRTQMSSLQLKIMKACYEAYRTPTMQECEVLGEEIGLPKRVIQVWFQNARAKEKKAK                        NP_207646
          Hs ZFHX3-IV  QKRFRTQMTNLQLKVLKSCFNDYRTPTMLECEVLGNDIGLPKRVVQVWFQNARAKEKKSK                        NP_008816
          Hs ZFHX4-IV  HKRFRTQMSNLQLKVLKACFSDYRTPTMQECEMLGNEIGLPKRVVQVWFQNARAKEKKFK                        NP_078997
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                                  ______I______     ____II____    _______III_______
                                  10        20        30        40        50        60
                        ....|.. ..|....|....|....|....|....|....|....|....|....|....|
           Consensus    KRRKRTT-FTKEQLLELEKEFAKNPYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE    Accession        ML bs     NJ bs

Zhx/       Hs ZHX1-I    NSIPTYN-AALDNNPLLLNTYNKFPYPTMSEITVLSAQAKYTEEQIKIWFSAQRLKHGVSW    NP_001017926     prot/cnid homolog not found
Homez      Hs ZHX2-I    LNTTKYN-SALDTNATMINSFNKFPYPTQAELSWLTAASKHPEEHIRIWFATQRLKHGISW    NP_055758
           Hs ZHX3-I    SSIPTYN-AAMDSNSFLKNSFHKFPYPTKAELCYLTVVTKYPEEQLKIWFTAQRLKQGISW    NP_055850
           Hs HOMEZ-I   WTQAAQT-SELDSNEHLLKTFSYFPYPSLADIALLCLRYGLQMEKVKTWFMAQRLRCGISW    NP_065885

           Hs ZHX1-II   SFGIRAK-KTKEQLAELKVSYLKNQFPHDSEIIRLMKITGLTKGEIKKWFSDTRYNQRNSK    NP_001017926
           Hs ZHX2-II   TPASDRK-KTKEQIAHLKASFLQSQFPDDAEVYRLIEVTGLARSEIKKWFSDHRYRCQRGI    NP_055758
           Hs ZHX3-II   ASIYKNK-KSHEQLSALKGSFCRNQFPGQSEVEHLTKVTGLSTREVRKWFSDRRYHCRNLK    NP_055850

           Hs ZHX1-III  TPQKFKE-KTAEQLRVLQASFLNSSVLTDEELNRLRAQTKLTRREIDAWFTEKKKSKALKE    NP_001017926
           Hs ZHX2-III  APQKFKE-KTQGQVKILEDSFLKSSFPTQAELDRLRVETKLSRREIDSWFSERRKLRDSME    NP_055758
           Hs ZHX3-III  TPTKYKE-RAPEQLRALESSFAQNPLPLDEELDRLRSETKMTRREIDSWFSERRKKVNAEE    NP_055850

           Hs ZHX1-IV   STGKICK-KTPEQLHMLKSAFVRTQWPSPEEYDKLAKESGLARTDIVSWFGDTRYAWKNGN    NP_001017926
           Hs ZHX2-IV   SPSPAIA-KSQEQVHLLRSTFARTQWPTPQEYDQLAAKTGLVRTEIVRWFKENRCLLKTGT    NP_055758
           Hs ZHX3-IV   PGKVSCK-KTAQQRHLLRQLFVQTQWPSNQDYDSIMAQTGLPRPEVVRWFGDSRYALKNGQ    NP_055850
           Hs HOMEZ-II  RQRKTKR-KTKEQLAILKSFFLQCQWARREDYQKLEQITGLPRPEIIQWFGDTRYALKHGQ    NP_065885

           Hs ZHX1-V    DRGPSLI-KFKTGTAILKDYYLKHKFLNEQDLDELVNKSHMGYEQVREWFAERQRRSELGI    NP_001017926
           Hs ZHX3-V    FPPGLLV-IAPGNRELLQDYYMTHKMLYEEDLQNLCDKTQMSSQQVKQWFAEKMGEETRAV    NP_055850
           Hs HOMEZ-III TPPLPIP-PPPPDIQPLERYWAAHQQLRETDIPQLSQASRLSTQQVLDWFDSRLPQPAEVV    NP_065885
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CERS class

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                                 ______I______      ____II____    _______III_______
                                  10        20        30        40        50        60
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           Consensus    KRRKRTTFTKEQLLELEKEFAK-NPYPSREEREELAASLGLTERQVKVWFQNRRAKWKKQE    Accession        ML bs     NJ bs

Cers       Hs CERS2     NIKEKTRLRAPPNATLEHFYLTSGKQPKQVEVELLSRQSGLSGRQVERWFRRRRNQDRPSL    NP_859530        87        78
           Hs CERS3     GIKETV-RKVTPNTVLENFFKHSTRQPLQTDIYGLAKKCNLTERQVERWFRSRRNQERPSR    NP_849164
           Hs CERS4     GVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLAAQCGLTLQQTQRWFRRRRNQDRPQL    NP_078828
           Hs CERS5     GIEDSGPYQAQPNAILEKVFISITKYPDKKRLEGLSKQLDWNVRKIQCWFRHRRNQDKPPT    NP_671723
           Hs CERS6     NIQANGPQIAPPNAILEKVFTAITKHPDEKRLEGLSKQLDWDVRSIQRWFRQRRNQEKPST    NP_982288
           Dm Lag1      GIRSSRPKKAANVPILEKTYAKSTRLDKKK-LVPLSKQTDMSEREIERWWRLRRAQDKPST    NP_727075
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