Multiple sequence alignment (protein), residue positions 1–260+.

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                                             1         10        20        30        40        50        60        70        80
Hsap1_4AWN  ..................MRGMKL.LGALLALA.........LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQD.A..PDTYHYVVSEPLGRN.SYKERY
Hsap1       ...........MRGMKL.LGALLALA.........LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQD.A..PDTYHYVVSEPLGRN.SYKERY
Ggal1       ...........MARL.VLELLAAA.LLLRVAATLRISAFNIRTFGDSKMSNQTVAGFIVSILVQYDITLVQEVRDADLSSVKKLVSQLNSA.S...SYPYSFLSSIPLGRN.SYKEQY
Drer1       ...........MKF.IITLGVLL.VSVHIGSSFLIGAFNIKSFGNSKVSNATLLDIITKVVHRYDIILIQEVRDSDLSATSKLMDSVNGGSS..PYQYDYIASEPLGRN.TYKERY
Scan1       ...........MHQ.LITALTLACLLSAAYSIQISAFNIRTFGDKKMSNVTIANIIVHLIERNDIILIQEVRDADLSAVKILMNKLQSS.S...AQTYSYIVSDPLGHS.SYKERY
Pmar1       ...........MKL.LLAATLLAVAMGMAESIRIAAFNIQTFGDAKMSKPDVAKVIVDVISLFDIVVVQEVRDSDLSAVKLLMSQLNSA.S..AHHYEYLASDQLGSS.TYTERY
Scan1L5     MRISDNPSGFPGFTTMAF.LLLMVLIGCFMQGSQGLKISAFNIQRFDQTKVNDPVTLDILIQILQRYDLITIEEVMDSDNSAMTELVKELNRS.T..KLHYNYIISDHLGRS.SYREKY
Hsap1L2     ...........MGGPRA.LLA.ALWALEAAGTAALRIGAFNIQSFGDSKMVSDPACGSIIAKILAGYDLALVQEVRDPDLSAVSALMEQINSV.S..EHEYSFVSSQPLGRD.QYKEMY
Ggal1L2     ...........MGTVVL.ALSSLLSTALLCPATAVLRIGAFNIQAFGDSKMSDESVADVIINILRRYDIVLVQEVRDSDLSAVTELLEQLNSV.S..SSPYDYEISGPLGRD.NYKEMY
Hsap1L1     ...........MHYPTALLFLPLILANGAQAFRICAFNAQRLTLAKVAREQVMDTLVRILARCDIMVLQEVVDSSGSAIPLLLRELNRFDG..SGPYSTLSSQPLGRS.TYMETY
Drer1L1     ...........MRMTIRRILLSIFLLSGLLTCYGFRICAFNVQSFGDSKSADAKIMNSLSRIVARCDICLLQEVRDQKNKAIPRLLEAVNKIG..DNDFQYVASRLGRTQTYQEQY
Drer1L1L    ...........MRPPLLLCFIGLCLWTCVISLKICAFNVQSFGNSKVSNATLLDIITKVVHRYDIILIQEVRDSRGEAISALLMSLNRFDK..SHIYAHLESKRLGKK.TYKEQY
Scan1L1L    ...........MRWFLFLCTLASSRCFRICSFNIQCFGESKGAKPVVMEIITKIVARCDICLLMEVRDSSGAIVDQLLQDLNSYDQ..HHQYVYLASRLGER.RYKEQY
Pmar1L1L    .......MCEGRTTRGHAGALWLSLLLSLVCCGASSDLKICSFNIQTFGQAKASKPHVMEIIVKIISRCDVTLVMEIRDCKNCTLPRLMEQLNNQHR..GHPYSYVASKRLGRG.SYREQY
Hsap1L3     ...........MSRELAPLLLLLLSIHSALAMRIGSFNVRSFGESKQEDKNAMDVIVKVIKRCDIILVMEIKDSNNRICPILMEKLNRNSR.RGITYNYVISRLGRN.TYKEQY
Ggal1L3     ...........MLLFALFSLLCFNPSLSLRICSFNVRSFGEAKIGRAEVLDAVVKIISRCDIMLLMEIKENKNRMCPLLVQQLAGQTKGNREEYSCVVSGRLGRK.SYKEQY
Scan1L3     ...........MVNMLFLHGVLLASFHEIQSLKICSFNVRTFGKSKVAKEGILDVLVRIISRCDLLLMMEIKDSSNKAFPILMTSLNNQSN..RNEYKFIISKRLGRG.NYKEQY
Pmar1L3     ...........MRSLLSLLLLLAVCSCAVNALKICSFNIQSFGETKAAKGHIMAIITKVTSRCDIMLVMEVKDSTGSSLVSLVNELNRGDR.R.KPYTYIISDRLGRK.SYKEQY
Drer1L4     ...........MKVASFNVQKFGKSKLSDPAVLQTLIKIVSRYDIIVILEVVDSKGRAMDNFLKELNKFDK..KAHYTMELSTRLGRG.NYKEQY
Scan1L4     ...........MKIAAFNIRRLGISKISKPEVVSTIVNILLRYDITLIMEVTDKTGTATKKLLEELNKQA...ESHYSFELSKPLGRG.TYKEQY
Drer1L4-2   ...........MKIAAFNIQRMGPSKLSDKKVVKTLIKIFSRYSIVIVLEVVDKQGKAINQFLNELNKTGANKNSPFKMVGSSRLGRT.LYKEQY

                          90        100       110       120                        130       140       150       160       170
Hsap1_4AWN  LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFT....................EVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPS
Hsap1       LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFT....................EVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPS
Ggal1       VFIYRSDIVSVLESYYYDDGCESCGTDIFSREPFIVKFSSPTT....................QLDEFVIVPLHAAPSDAVAEINALTDVYTDVINKWETNNIFFMGDFNADCSYVTAE
Drer1       LFVYRSESVSAVNSFHYDDGCEPCGTDTFNREPFVVMFSSKT....................AVRDFALVQHTSPEVAVQEIDALHDVVLDTRQRLNTNNIMLLGDFNAGCRYVSNS
Scan1       LFIYRNSAVSVVNSYLYNDASKNTGQDSFNREPFLVKFYSRYS....................VIHEFVIMPMHTSPSAAVKEIDALYDVFLDAKKKLGTDNMLIMGDLNADCSYVKPT
Pmar1       VYIYRDKVVSVSSSYHFDDGCESCGTDTFSREPFLVRFNIPSS...................AVPQLVLVPLHTSPEDLAVREIDALYDVYADVRQRWGTDNVMLLGDLNADCSYVTAS
Scan1L5     AFVYNENILKPMAWYHFDDGCEKCGTDTFSREPFIVHFHSLTT....................IVKDFVLVAIHTSPSYAVREVDALYDVWADARNMFNTENILILGDYNAAACNYVTDN
Hsap1L2     LFVYRKDAVSVVDTYLYPDP....EDVFSREPFVVKFSAPGTGERAPPLPSRRALTPPPLPAAAQNIVLIPLHAAPHDQAVREIDALYDVYLDVIDKWGTDDMLFLGDFNADCSYVRAQ
Ggal1L2     LFIYRTDAVSVVDTYQYEDP....QDIFSREPFVLRVSAPHS....................KAEEFVMVPLHSAPHDAVAEIDALYDVYLAVVNKWGTDNIVFLGDFNADCSYVKQS
Hsap1L1     VYFYRSHKTQVLSSYVYNDE.D....DVFAREPFVAQFSLPSN...................VLPSLVLVPLHTTPKAVEKELNALYDVFLEVSQHWQSKDVILLLGDFNAGCASLTKK
Drer1L1     VFFYRKSTAILKGQYQYPDT.QTGDIDAFSREPFVVYFQAPKT...................LAKEFVLIPQHTIPSNATKEIDELYDVFVDVKVRWETENVMFLGDFNAACCNYVAKK
Drer1L1L    VYIYRKDMLQVQEQYEHPEV.NESASEVFSREPFIILVHSPTT...................LVKNFVLIGQHTSPKSAMKEMDSLYEVFQTVKKKWKTENVMFLGDLNAACNYVTNK
Scan1L1L    VFIYRSDMVKITSSYQYKGG.KKGL.QTFAREPLIVRFVSSPRT..................AIKDFVLIPLHAPPGEAVNEIDQLYNVFLDVRAKWDIEDIMILGDLNADCRYVSAK
Pmar1L1L    AFLYRSNLVKLRDSHQYKEN.DAQGPCVFSREPFSVRFHSPKT...................AVQDLILVGQHTSPKSAVSELQKLHIVFEYLSQHWQNQNVMLLGDFNAACCYVSAT
Hsap1L3     AFLYRNLVSVKQTYQYPDT.QPGDEDAFSREPFVVWFSSPHT...................AVKDFVIIPLHTIPETSVKEIDELVEVYTDVKHRWKAENFIFMGDFNAGCSYVPEK
Ggal1L3     AFIYRPKLLSVKESYQYPDD.Q....TDVFAREPFVVWFSSPLT..................TVKDFVIIPQHTSPDSSVSEINALYDVYTEVKAWRAKYFILMGDFNACDYVRKK
Scan1L3     AFIYRQTMVSVLDRYQYMDE.QVGDVDAFSREPFVVWFSSPTT...................DIKEFLILPQHTPEASVKELDELYDVYMDVKNRWKAENMIFLGDFNAGCTYVTRK
Pmar1L3     VYFYRSHKTQVLSSYVYNDE.DVFAREPFVIQFKSQTT........................VMKDLVLIPVHTKPKDSQKELDELYDVFVEVRDKWKTDNVMILGDFNADGAYVSKK
Drer1L4     MFLYREDVVELVCGSYQYKDD.QPGDEDAFAREPYILRFKCPNA...................VLEDLVLMPVHTRPEDSVKEIDELYDVFQDVRKWKTDNIMILGDGSYVSDK
Scan1L4     LFIYRDDVVQVERRFQYKDM.QPGDEDAFSREPFVIQFKSQTT...................AVQDFVLIPQHTGPDDSVKEIDELYDVFLKIKKEWHIENIMILGDFNADGRYVSKK
Drer1L4-2   VCFYREADAKLLNTYQYEDN.QVGDEDAFSREPFILRFQCKNT...................VMKDLVLIPVHTKPKDSQKELDELYDVFVEVRDKWKTDNVMILGDFNADGAYVSKK

                        180       190       200       210       220       230       240       250       260
Hsap1_4AWN  QWSSIRLWTSPTFQWLIPDSADTTAT.PTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYGLSDQLAQAISDHYPVEVMLK....
Hsap1       QWSSIRLWTSPTFQWLIPDSADTTAT.PTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYGLSDQLAQAISDHYPVEVMLK....
Ggal1       QWPSIRLRSLSSCEWLIPDSADTTVT.STDCAYDRIVACGSALRQAVEYGSATVNFQEIIRIQNKDALASIDHFPVEVTLKAR...
Drer1       AWANIRLRTDQSYTWLIPDSADTTVT.HTNCPYDRIVATPGDMM.RGVAPGSAQVFDFMEAHGLSQDWALAVSDHFPVEVKLM...
Scan1       DWPHIRIRKDTQFQWLIPDTADTTTTISTKCAYDRIIAVGSALNAVAIDGSAAINFQEIKHRKSLASIDHFPVEVIRAA......
Pmar1       DWGRIRLRSDSRFSWLIGDEVDTTVG.TTNCAYDRIVVAGSALQGAVASGSARILNFQSYMYGLSLEKAKEVSDHFPVEVTIN...
Scan1L5     DWPHIRLRQHKNFHWLIDDAIDTVSKYTHCAYDRFVVTTKGLLKTIVPGSVKTHFQEEGFLPYYTVKEVSDHFPIELELEKDPNTIGAKYGTESSIGINGGISGGPCSCEGVDFTSC
Hsap1L2     DWAAIRLRSSEVEFKWLIPDSADTTVG.NSDCAYDRIVACGARLRRSLKPQSATVHDFQEEFGLDQTQALAISDHFPVEVTLKFHR..
Ggal1L2     DWAAIRLRSSDVEFKWLIPDSADTTVG.KSDCAYDRIVVCGKKLKRSIVPNSATVFNFQEEEALGLDQTQALAISDHFPVEVKLMA..
Hsap1L1     RLDKLELRTEPGFHWVIADGEDTTVRASTHCTYDRVVLHGERCRSLL..HTAAAFDFPTSFQLTEEEALNISDHYPVEVELELSQAHSVQPLSLTVLLLLSLLSPQLCPAA.......
Drer1L1     NRKNIRLYTDPSFTWLIDDNVDTTVKESTDCAYDRIVVHGEPFLRSLKPFSAQPFNFKQEFNLSEEEALEVSDHFPIEVVLEVDLKVKSRMSTRYSEAPCLLPAVFVLNALLLMQMIV....
Drer1L1L    GLRNVRLRSDPKFHWLIRDEQDTTVREKTRCAYDRIIIHGKELISGIVPESAQPFNFKQEFNLSEEEALEVSDHFPVEVDLKANHRYLLRHEL..
Scan1L1L    DWETIRLRNKPGFWLIGDNDTTASARTDCAYDRIIVHGWNFKALVPGSAKVFNVQEEFKLTEKEAVEVSDHYPVEVKLKLEAVHYEL..
Pmar1L1L    NWSHVRIR.DPSFHWAIGDDVDTTVKNKTDCAYDRIIVHGTELRSALVAGSARAFNFQKKYGLSNEKALEVSDHYPVEVKLKVPVHHHEL..
Hsap1L3     AWKNIRLRTDPRFEWLIGDQEDTTVKKSTNCAYDRIVVRGQEIVSSVVPKSAKVFKLTEEEALDVSDHFPVEFKLQSSRAFTNSKKSVTLRKKTKSKRS.
Ggal1L3     HWKNIRLRTSSEFAWLIGDTNDTTVRRSTSCPYDRIVVSGEQLSQAVVPHSATIFDFQTAFQMSEEQALGVSDHFPVEFELKARGGFFDWIKSKFSKKGRARKSRRSGS..
Scan1L3     EWPNIRLRNDTNFTWLIEDNNDTTVDTTRCAYDRIVLRGEKLVKEAYGMTEAQAVEVSDHFPVEVDLQESHGYFYWLRSFKGLKG....
Pmar1L3     KWSQIRIRMEEGFHWLIGDETDTTVNTNTRCAYDRIVVKGEPLYRAVVPGSAKPFNFQAAYGLSETEALEVSDHFFPIEVELK....
Drer1L4     KMKQIRIRSDPEFHWLISDDEDTTASTHNDNTYDRIVIYGDDMMQAVVPGSAKPFQTAFSLTEEDALKVSDHDKSKKKRKVK......
Scan1L4     KMKTIRLRKDKDFHWLIGDDEDTMASLKTDEAYDRIVVYGGDTFYQGIVPNSAKPFNFQEAWKLTEQQALEVSDHYPIEVELRLIE....
Drer1L4-2   KMKAIRIRTDTDFHWLIGDDVDTVKTTNDNTYDRIVVYKEDMLEAVVPRSAKPFNFQEAYKLTEEEALDVSDHYPVEVTLKKKPAAKATGKTKKPQKRRKA.......
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Scan1L5     AGRCGAYSPTMPCTCTASCSKYNDCCADYGNYC
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