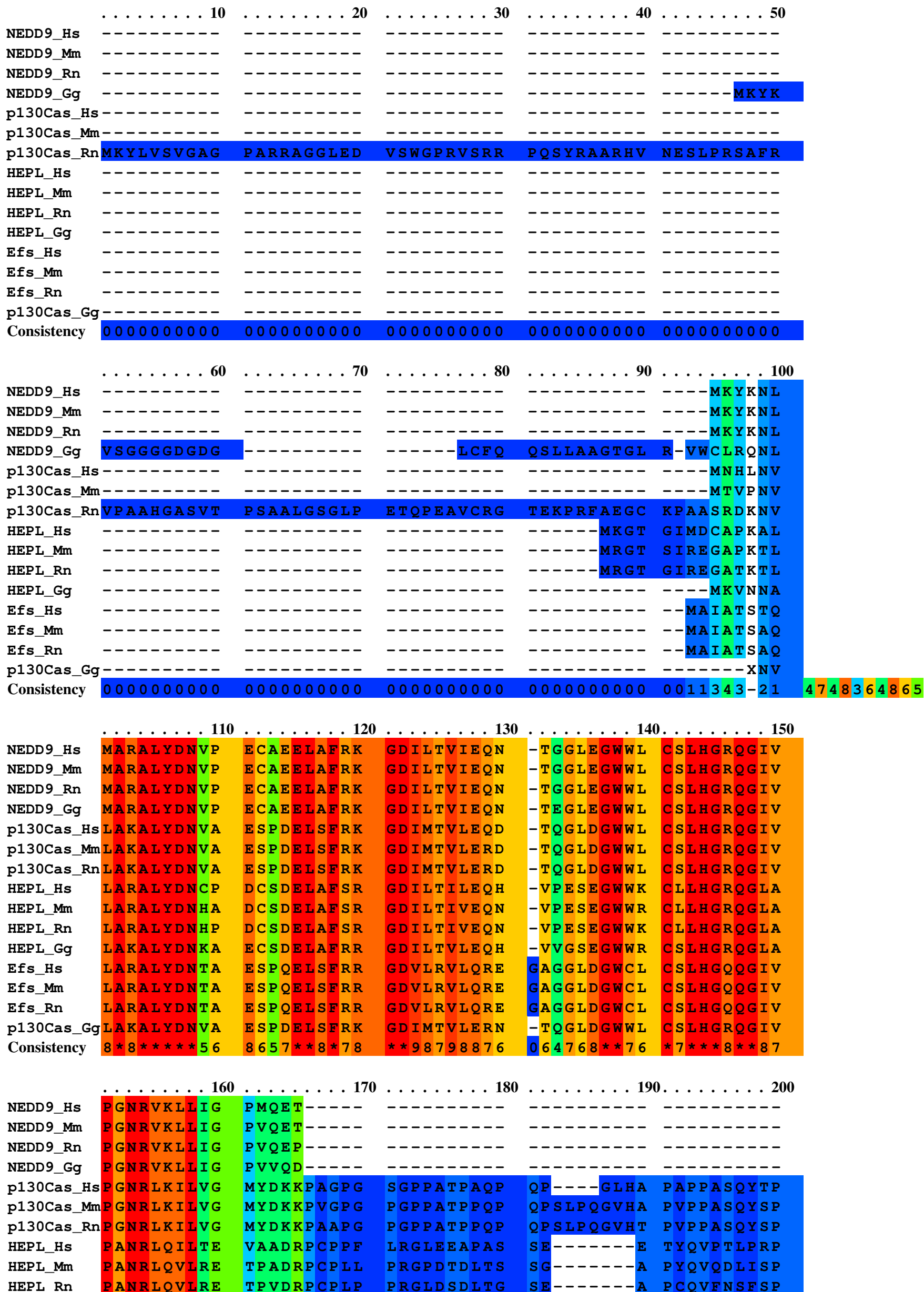


Results colour-coded for amino acid conservation

The current colourscheme of the alignment is for **amino acid conservation**.

The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position. The colour assignments are:

Unconserved 0 1 2 3 4 5 6 7 8 9 10 Conserved



HEPL_Gg	PANRLQLLAG	-PQALPPP	AI	PSDAPEPPVA	PQ	-----	N	IYQVPSVPKG
Efs_Hs	PANRVKLLPA	GPAPK	-----	-----	-----	-----	-----	-----
Efs_Mm	PANRVKLLPA	GPAPK	-----	-----	-----	-----	-----	-----
Efs_Rn	PANRVKLLPA	SPAPK	-----	-----	-----	-----	-----	-----
p130Cas_Gg	PGNRLKILVG	MYDKK	-----	-----	-----	-----	-----	-----
Consistency	*7**888*45	34445	20100	1000011000	1000000001	1011010011		

 210 220 230 240 250
NEDD9_Hs	-----ASSHE	QPASGLMQQT	FGQQKLYQVP	NPQAAPRDTI	YQVPP-----
NEDD9_Mm	-----PGHE	QPTPGPMHQT	FGQQKLYQVP	NSQAASRDTI	YQVPP-----
NEDD9_Rn	-----SSHE	QPTPGPMHQN	FGQQKLYQVP	NSQAAPRDTI	YQVPP-----
NEDD9_Gg	-----GPSSQD	MSNSGLTHQS	FNQQKIYQVP	SSHASARDPV	YQVPP-----
p130Cas_Hs	MLPNTYQPQP	DSVYLVPTPS	KAQQGLYQVP	GPSPOFQSP	AKQTSTFSKQ
p130Cas_Mm	MLPTAYQPQS	DNVYLVPTPS	KTQQGLYQAP	GPNPQFQSP	AKQTSTFSKQ
p130Cas_Rn	MLPTAYQPQP	DNVYLVPTPS	KTQQGLYQAP	GPNPQFQSP	AKQTSTFSKQ
HEPL_Hs	PTPGPVYEQM	RSWAEGPQP	T--AQVYEF	DPPTSARIIC	EKTL-----
HEPL_Mm	PPQGPVYEP	RSWVEGSPA	T--AQVYEL	ESPSSARIIC	EKTL-----
HEPL_Rn	PTPGPVYEP	KSWVEGSPA	T--AQVYEL	DSPSSARIIC	EKTL-----
HEPL_Gg	TASSSTYEKM	EGWVTSPARA	ATLPAQGVYQ	VPALAAQLLS	ERTR-----
Efs_Hs	-----	PSLSPASPA	QPG-SPYPAP	DHSN-----	-----
Efs_Mm	-----	PSLCPASPT	QPG-SSCPTP	ERGC-----	-----
Efs_Rn	-----	PSLCPAPPT	QPGCSSCPTP	ERGC-----	-----
p130Cas_Gg	-----QQQ	QQQQQQQAAG	PGQGQAPPVP	QPTLP-----	-----
Consistency	0010112232	3533334455	3233555559	4534324221	2322100000

 260 270 280 290 300
NEDD9_Hs	-----SYQN	QGIYQVPTGH	GTQEQEYVQV	PPSVQR-----	-----SIG
NEDD9_Mm	-----SYQN	QGIYQVPTGH	GTPEQDVYQV	PPSVQR-----	-----NIG
NEDD9_Rn	-----SYQN	QGIYQVPTGH	GTPEQDVYQV	PPSVQR-----	-----NIG
NEDD9_Gg	-----SHTN	QGIYQIPTGH	GVAGQDIYQV	PPSTQR-----	-----CLD
p130Cas_Hs	TPHHPFPSPA	TDLYQVPPGP	GGPAQDIYQV	PPSAGMGHDI	YQVPPSMDTR
p130Cas_Mm	TPHHSFPSPA	TDLYQVPPGP	GSPAQDIYQV	PPSAGIGHDI	YQVPPSLDTR
p130Cas_Rn	TPHHSFPSPA	TDLYQVPPGP	GSPAQDIYQV	PPSAGTGHDI	YQVPPSLDTR
HEPL_Hs	-----SFPK	QAILTLRPRV	RASLPTLPSQ	VYDVPT-----	-----
HEPL_Mm	-----SFPK	QALSVLPRPT	RASLPTLPSQ	VYDVPV-----	-----
HEPL_Rn	-----NFPK	QALFVLPRPT	RASLPTLPSQ	VYDVPV-----	-----
HEPL_Gg	-----CSTQ	QHLFTLPRAC	RASVPNITSE	LYDVPSMQSR	ESLLTQSGAT
Efs_Hs	-----ED	QEVYVPPPA	RPCPTSGPPA	GPCPPS-----	-----
Efs_Mm	-----EE	QEVYVPPPA	RPCSASGLPA	RSCSPS-----	-----
Efs_Rn	-----EE	QEVYVPPPA	RPCSASGLPA	RSCSPS-----	-----
p130Cas_Gg	-----YH	HQGGYAPLSP	ASQYTPMHPS	YVPQGD-----	-----
Consistency	0000002244	747657*453	5443555455	3455440000	0000000111

 310 320 330 340 350
NEDD9_Hs	GTSGPHVGKK	VITP-VRTGH	GYVYEYPSRY	QKDVDYDIPP	--SHTTQGVY
NEDD9_Mm	GTNGPLLSKK	VITP-VRTGH	GYVYEYPSRY	QKDVDYDIPP	--SHSTQGVY
NEDD9_Rn	STNGPHLGKK	VITP-VRVGH	GYVYEHPSRY	QKDVDYDIPP	--SHTTQGVY
NEDD9_Gg	GPPLT---NK	VITP-VRSGQ	GYVYEFPSKY	QKDTYDIPP	--VRPLQGIY
p130Cas_Hs	SWEGTKPPAK	VVVP-TRVGQ	GYVYEAAQPE	Q-DEYDIPRH	LLAPGPQDIY
p130Cas_Mm	GWEGTKPPAK	VVVP-TRVGQ	GYVYEAAQTE	Q-DEYDTPRH	LLAPGPQDIY
p130Cas_Rn	SWEGTKPPAK	VVVP-TRVGQ	GYVYEASQAE	Q-DEYDTPRH	LLAPGSQDIY
HEPL_Hs	---QHRGPVV	LKEP---EK	QQLYDIPASP	KKAG-----	--LHPPDSQA
HEPL_Mm	---QRQGFST	LERL---EK	QQFYDIPTSS	QKAL-----	--LHSSTSQA
HEPL_Rn	---QRQVSST	LERP---EK	QQFYDIPTSS	QKAV-----	--F--HISTS
HEPL_Gg	PPAARKGSVL	LRSPRCFQEE	QQFYNVPSSS	EKAGAVIQDS	AVGNLYDVPS
Efs_Hs	-----	-----P	DLIYKIPRAS	-----	-----GTQL
Efs_Mm	-----	-----S	DSIYKVPRVN	-----	-----GMQL
Efs_Rn	-----	-----S	DSIYKVPRVN	-----	-----GIQL
p130Cas_Gg	-----	-----	NVYLMVPG	K-----	-----
Consistency	1012221123	4224012134	447*547544	5232221210	0022124344

 360 370 380 390 400
NEDD9_Hs	DIPPSSAKGP	VFSVPVGEIK	PQGVYDIP--	--PTKGVYAI	PPSACRDEA-
NEDD9_Mm	DIPPSSVKGP	VFSVPVGEIK	PQGVYDIP--	--PTQGVYAI	PPSACRDEA-
NEDD9_Rn	DIPPSSVKGP	VFSVPVGEIK	PQGVYDIP--	--PTQGVYAI	PPSACRDEA-
NEDD9_Gg	DIPPTSAGKT	AHSVPTGDAK	ALGVYDVP--	--PAKGMYAT	PPSTCRDDV-
p130Cas_Hs	DVPPVRGLLP	SQYGQEVYDT	PPMAVKGPNG	RDPLLEVYDV	PPSVEKGLPP
p130Cas_Mm	DVPPVRGLLP	NQYGQEVYDT	PPMAVKGPNG	RDPLLDVYDV	PPSVEKGLLS
p130Cas_Rn	DVPPVRGLLP	NQYGQEVYDT	PPMAVKGPNG	RDPLLDVYDV	PPSVEKGLPP
HEPL_Hs	SGQGVPLISV	TTLRRGGYST	-LPNPQ----	--KSEWIYDT	PVSPGKASV-
HEPL_Mm	SGRDVTLAPT	MAFRQGGGYN	PLSSPQ----	--KSERIHDT	PVLLKADV-
HEPL_Rn	QPGVTLAPT	TAFRQGGGYN	PLSSPQ----	--KSDWIHDT	PVSLGADV-
HEPL_Gg	KRETDASKKK	SQKKYWGHCN	TLPNPR----	--KSEWIYDI	PISPEKTGL-
Efs_Hs	AAPR-----	-----	-----	--DALEVYDV	PPTALRV--
Efs_Mm	TASR-----	-----	-----	--DVAEVYDV	PPNILRA--

Efs_Rn	TAPR	-----	-----	-----	-----	DVGEVYDV	PPNILRA	----	
p130Cas_Gg	-----	-----	-----	-----	-----	GQQGHYSG	SAPS	----	
Consistency	4453222212	2221213212	3222220200	0045437866	9664273220				
	410	420	430	440	
NEDD9_Hs	GLR	EKYDFP	PPMRQAGRPD	L	RPEGV	---	YDIPPTCT	KPAGKDLHVK	
NEDD9_Mm	GLREKEYDFP	PPMKQDGKPD	T	RPEGV	---	YDIPPTST	KTAGKDLHIK		
NEDD9_Rn	GLREKEYDFP	PPMKQDGKLD	T	RPEGV	---	YDIPPTST	KTVGKDLHTK		
NEDD9_Gg	GLRDNLQDFS	SPAGHN	---	A	RQEGV	---	YDIPPPIT	KATGKELIKK	
p130Cas_Hs	SNHHAVIDVP	PSVSKDVPDG	PL	REET	---	YDVPPAFA	KAKPFDPART		
p130Cas_Mm	SSHHSVIDVP	PSVSKDVPDG	PL	REET	---	YDVPPAFA	KPKPFDPTRH		
p130Cas_Rn	SNHHSVIDVP	PSVSKDVPDG	PL	REET	---	YDVPPAFA	KPKPFDPTRH		
HEPL_Hs	RNTPLTSFAE	ESRPHALPSS	S	STFYNP	PSG	RS	RSRLTPQLN	NNVPMQKKLS	
HEPL_Mm	RNVSMTSFTK	DSGSRAIPGS	S	AVHTGA	---	VALSPQLG	NTVQRKNSLP		
HEPL_Rn	RNASMTSFTK	ESCSNTIPGS	S	VVRIGA	---	VTLSPQLG	NAVQKSSPP		
HEPL_Gg	KQNSSVHSME	NQVLYDIPP	---	ARYKALT	TNA	EAN	VVNPQLY	DIPPTQRKLT	
Efs_Hs	-----	-----	---	PSSGP	---	YDCPASFS	HPLTRVAPQP		
Efs_Mm	-----	-----	---	PSSCP	---	YDSPASFS	CPVAPVVPQP		
Efs_Rn	-----	-----	---	PSNCP	---	YDSPASFS	CPATPVVPQP		
p130Cas_Gg	-----	-----	---	---	---	GQFPAPA	KQPPAY	----	
Consistency	2221222222	2322222211	2033434000	0056567545	4444343333				
	460	470	480	490	
NEDD9_Hs	YNCDIPGAAE	---	PVA	RRHQ	SLSPNHPPPQ	LGQSV	---	GS	QNDAYDVPRG
NEDD9_Mm	FPCDAPGGVE	---	PMA	RRHQ	SFSLHHAPSQ	LGQSG	---	DT	QSDAYDVPRG
NEDD9_Rn	FPCDAPGGAE	---	PMA	RRHQ	SLSLHHAPSQ	VGPSG	---	DT	QSDAYDVPRG
NEDD9_Gg	FSSEGLALTD	G	APHK	QSVY	DIPVNHQNH	LGQQI	---	AP	QKDVDYDTPRG
p130Cas_Hs	PLVLAAPPPD	S	PPA	EDVY	DVPPPAPDLY	DVPPGLRRPG	PG	TLYDVPRE	
p130Cas_Mm	PLILAAPPPD	S	PAA	EDVY	DVPPPAPDLY	DVPPGLRRPG	PG	TLYDVPRE	
p130Cas_Rn	PLILAAPPPD	S	PPA	EDVY	DVPPPAPDLY	DVPPGLRRPG	PG	TLYDVPRE	
HEPL_Hs	LPEIPSYGFL	V	PRGT	FPLDE	DVSYKVPSSF	LIPRVEQONT	KP	NIYDIPKA	
HEPL_Mm	EEPTYAFPTS	R	D	L	PSDA	GGSYKVPSRF	LIPRVEQONT	MP	NIYDTPKA
HEPL_Rn	EETSAYFLTP	R	GDSL	PSDA	GSSYKVPSRF	LIPRVERQNT	KP	NIYDTPKA	
HEPL_Gg	FPDVPLYDVP	S	SKDV	LLQQ	NGSCDVPPSL	PAPNAENQIS	GG	NVYDIPKG	
Efs_Hs	PGEDD	---	---	---	---	---	---	AP	YDVPLT
Efs_Mm	PREDE	---	---	---	---	---	---	AP	YDVPLA
Efs_Rn	PGEDE	---	---	---	---	---	---	AP	YDVPLA
p130Cas_Gg	-----	---	---	---	---	---	---	PK	QTPP
Consistency	3223321122	1031302212	2231223222	2232201112	2244897*54				
	510	520	530	540	
NEDD9_Hs	VQF	---	L	EPPAETSEKA	NPQERDGVYD	VPLHNPDAK	GS	RDLVDGIN	
NEDD9_Mm	VQF	---	L	EVPTETSEKA	NPEERDGVYD	VPLHNPDAK	GS	RDVVDGIN	
NEDD9_Rn	VQF	---	L	EVPTESSEKA	NLEERDGVYD	VPLHNPDAK	GS	RDVVDGIN	
NEDD9_Gg	IAF	---	P	GQQTGLNESL	ASEGREGVYD	VPPPVLQDTK	GL	QDVTDGMN	
p130Cas_Hs	---	---	R	VLPPEVADGG	VVD	SGVYA	VPPP	---	AEREAPAEK
p130Cas_Mm	---	---	R	VLPPEVADGS	VVD	DGVYA	VPPP	---	AEREAPTDGK
p130Cas_Rn	---	---	R	VLPPEVADGS	VID	DGVYA	VPPP	---	AEREAPTDGK
HEPL_Hs	TSS	---	V	S	QAGKELEKAK	EVSEN	SAGH	NSSWFSR	---
HEPL_Mm	MQGVSHNAPK	A	M	QGVSLAGK	ELERGREAPE	NSPWISG	---	QTSFLSPDSD	
HEPL_Rn	MQGVFQNTSK	A	T	QGVSLAGK	ELERGREAPE	NSPWVSR	---	QTNFLSPDSD	
HEPL_Gg	LPT	---	A	M	QPKKEMEKN	SNHSGNQAYH	I	PTQLSR	---
Efs_Hs	PKP	---	P	A	ELEPDLEWEG	GREPGPIYA	APS	---	---
Efs_Mm	LKP	---	P	A	ELERDPEWEG	GREPGPLYA	APS	---	---
Efs_Rn	LKS	---	P	A	EMEPDLEWEG	GREPGPLYA	APS	---	---
p130Cas_Gg	---	---	H	A	FPSAQOE	---	I	YQ	VP
Consistency	331000004	4454544443	3352234664	5731111000	2232222212				
	560	570	580	590	
NEDD9_Hs	RLSFS	---	S	TGS	TRSNMSTSST	SSKESLSAS	PAQD	KRLFL	DPDTAIERLQ
NEDD9_Mm	RLSFS	---	S	TGS	TRSNMSTSST	SSKESLSAS	PSQD	KRLRL	DPDTAIEKLY
NEDD9_Rn	RLSFS	---	S	TGS	TRSNMSTSST	SSKESLSAS	PSQD	KRLLL	DPDTAIGKLY
NEDD9_Gg	RLSFS	---	S	TGS	TRSNMSTSST	TSKDSFSAS	TTQD	KRLIL	DPDTAIERLY
p130Cas_Hs	RLSAS	---	S	TGS	TRSSQSASSL	EVAGP	---	GREPL	ELEVAVEALA
p130Cas_Mm	RLSAS	---	S	TGS	TRSSQSASSL	EVVVP	---	GREPL	ELEVAVESLA
p130Cas_Rn	RLSAS	---	S	TGS	TRSSQSASSL	EVVVP	---	GREPL	ELEVAVETLA
HEPL_Hs	RLSGS	---	S	SDS	RASIVSSCST	TSTDSSSSS	SEESAKELS	DL	VDVAKETVM
HEPL_Mm	RLSVA	---	S	SDS	RASVVSSCSS	ISMDSSSGSS	SEDSVKELWM	DV	DFAKETAV
HEPL_Rn	RLSVA	---	S	SDS	RASVVSSCSS	LSTDSSPGSS	SEDSVKELWM	DL	DFAKETAV
HEPL_Gg	MCGHDNSADS	K	N	S	TLSMSSN	SSSESSSASS	S	DEPDKEIKL	DLEVAIETLT
Efs_Hs	---	---	---	---	---	---	---	NL	KRASALLNLY
Efs_Mm	---	---	---	---	---	---	---	NL	KRASALLNLY
Efs_Rn	---	---	---	---	---	---	---	NL	KRASALLNLY
p130Cas_Gg	---	---	---	---	---	---	---	---	PSLSQAA
Consistency	4442405335	3352353352	2322321122	1111033327	5354965574				

	610	620	630	640	650
NEDD9_Hs	RLQQALEMGV	SSLMALVTTD	-----WRCY-	GYMERHINEI	RTAVDKVELF
NEDD9_Mm	RLQQTLEMGV	CSLMSLVTTD	-----WRCY-	GYMERHINEI	RTAVDKVELF
NEDD9_Rn	WLQQTLETGI	CSLMSLVTTD	-----WRSY-	GYMERHINEI	RTAVDKVELF
NEDD9_Gg	RLQQMVETAV	NNLMAFATAD	-----WRSY-	SYMEKHINEI	HTAVDKVEQS
p130Cas_Hs	RLQQGVSATV	AHLLDLAGSA	GATGSWRSPS	EPQEPLVQDL	QAAVAAVQSA
p130Cas_Mm	RLQQGVSTTV	AHLLDLVGSA	SGPGGWRGTS	EPQEPPAQDL	KAAVA AVHGA
p130Cas_Rn	RLQQGVSTTV	AHLLDLVGSA	SGPGGWRSTS	EPQEPPVQDL	KAAVA AVHGA
HEPL_Hs	ALQHKVVSSV	AGLMLFVSRK	-----WRFK-	DYLEANIDAI	HRSTDHIEES
HEPL_Mm	SLQHKVASSA	AGLLLFVSRK	-----WRFK-	DSLETNIHRI	RRAADHVEES
HEPL_Rn	ALQSRVASSV	AGLLLFVSRK	-----WRFK-	DSLETNVNRI	RGADRVEES
HEPL_Gg	RLQHSVSSSV	ASLMIFVSSK	-----WRLQ-	EHLEKNIEEI	HRAIDHIKVS
Efs_Hs	EAPEELLADG	EG-----	-----	GGTDEGIYDV	PLLGPEAPPS
Efs_Mm	EAPEELLANG	ES-----	-----	RDADEGIYDV	PLLGPEPPSP
Efs_Rn	EAPEELLANG	ES-----	-----	RDADEGIYDV	PLLGPEPPSP
p130Cas_Gg	DAYPVGSAS-	-----	-----	--PPQDIYQV	PPSVAQAQDI
Consistency	4765374655	4454234322	0000055210	4347438468	4475546534

	660	670	680	690	700
NEDD9_Hs	LKEYLHFVKG	AVANAACLPE	LILHNKMKRE	LQRVEDSHQI	LSQTS HDLNE
NEDD9_Mm	LREYLHFVKG	ALANASCLPE	LVLHNKMKRE	LQRVEDSHQI	LSQTS HDLNE
NEDD9_Rn	LREYLHFARG	ALANASCLPE	PVLLNKMNRE	LQRVDDSHQI	LSQTS HDLNE
NEDD9_Gg	LLEYLQFAKG	SAANASFLSE	ISLHNKMRRE	VQRLED SHQI	LTQTS HDLNS
p130Cas_Hs	VHELLEFARS	AVGNAHTSD	RALHAKLSRQ	LQKMEDVHQT	LVAHGQALDA
p130Cas_Mm	VHELLEFARG	AVSNATHSD	RTLHAKLSRQ	LQKMEDVYQT	LVVHGQVLD S
p130Cas_Rn	VHELLEFARS	AVSSATHSD	RTLHAKLSRQ	LQKMEDVYQT	LVVHGQVLD S
HEPL_Hs	VREFLDFARG	VHGTACNLTD	SNLQNRIRDQ	MQTISNSYRI	LLETKESLDN
HEPL_Mm	VREFLDFARG	VGGTACNLTD	SYLQARIRDQ	LQTISSSYQT	LLDAKGS LDR
HEPL_Rn	LREFLDFARG	VGGTACNLTD	SYLQARVRDQ	LQTISSSYQT	LLDAKGS LDR
HEPL_Gg	LGEFLAFARA	LKVNASYLTD	NNLQIRIKKQ	LEILMNSFQI	LTETREALNN
Efs_Hs	PEPPGALASH	DQDTLAQLLA	RSPPPPHRPR	LPSAESLSRR	PLPALPVPEA
Efs_Mm	EPPVASSST-	DLDTVAQLPT	RSSPPQHRPR	LPSTESLSRR	PLPALPVSEA
Efs_Rn	EPPAASSSA-	DPDTVAQLLT	RSPPPQHRPR	LPSTESLSRR	PLPALPVSEA
p130Cas_Gg	YQVPPSLDAR	SWEGP----	KPSGKVL LPT	RVGQVYVYDS	PKGEQDEYDF
Consistency	5464646754	4345753645	4464465546	8645655574	6545444664

	710	720	730	740	750
NEDD9_Hs	CSWSLNILAI	NKPQNKDDL	DRFVMVAKTV	PDDAKQLTTT	INTNAEALFR
NEDD9_Mm	CSWSLNILAI	NKPQNKDDL	DRFVMVAKTV	PDDAKQLTTT	ISTYAETLFR
NEDD9_Rn	CSWSLNVLAI	NKPQNKDDL	DRFVMVAKTV	PDDAKQLTTT	ISTYAETLFR
NEDD9_Gg	YNWSLNVLAV	NRLQNKDDL	DRFVMVAKTV	PDDAKQLTTT	ISVNAELLFK
p130Cas_Hs	GRGSGGAT--	-----LEDL	DRLVACSRAV	PEDAKQLASF	LHGNASLLFR
p130Cas_Mm	GRGSPGFT--	-----PEDL	DRLVACSRAV	PEDAKQLASF	LHGNASLLFR
p130Cas_Rn	GRGGPGFT--	-----LDDL	DRLVACSRAV	PEDAKQLASF	LHGNASLLFR
HEPL_Hs	RNWPLEV LVT	DSVQNSPDDL	ERFVMVARM L	PEDIKRFASI	VIANGRL LFK
HEPL_Mm	CNWSLEV LVT	DKVQNSLDDL	ERFVATARI V	PEDVKRFTSI	VIANGKLLFK
HEPL_Rn	CNWSLEV LVV	DKAQSSVDDL	ERFVQVARV V	PEDVKRFTSI	VVANGKLLFK
HEPL_Gg	CNWSLEALVL	KKPYSNPDDL	DRFVMVARTI	PDDLKR FVSI	IIANGKLLFR
Efs_Hs	PSPSPVPS--	-----PAPG	RKGSIQDRPL	PPPPPR LPGY	GGPKVEGDPE
Efs_Mm	PAPSPAPS--	-----PAPG	RKGSIQDRPL	PPPPPC LPGY	GGLKPEGDPE
Efs_Rn	PAPSPAPS--	-----PAPG	RKGSIQDRPL	PPPPPC LPGY	GGLKPEGDPE
p130Cas_Gg	-----	-----	-----	SRHLLSLGS-	-----
Consistency	2436434511	1212213565	5746445747	9565657564	4335454556

	760	770	780	790	800
NEDD9_Hs	PGPGSLHLKN	GPESIMNSTE	YPHGGSQGQL	LHPGDHKAQA	HNKALP--PG
NEDD9_Mm	ADPANSHLKN	GPNSIMNSSE	YTHPGSQMQP	LHPGDYKAQV	HSKPLP--PS
NEDD9_Rn	VDPGNSHLKN	GPDSITNSIE	YTHTGSQMOP	LRPGDYKGQV	HNKPLP--PT
NEDD9_Gg	QVSGSSRFRS	VPENMNA---	-PDYAYNSPH	MQRHGKQPQN	HFSSLP--PL
p130Cas_Hs	RTKATAPGP-	-----	---EGGGTLH	PNPTDKTSSI	QSRPLPSPPK
p130Cas_Mm	RTKAPGPGP-	-----	---EGSSSLH	PNPTDKASSI	QSRPLPSPPK
p130Cas_Rn	RTKAPGPGP-	-----	---EGSSSLH	LNPTDKASSI	QSRPLPSPPK
HEPL_Hs	RNCEKEE---	-----	---TVQLT	PNAEFKCEKY	IOPP-----
HEPL_Mm	QNCEKGE---	-----	---M-DLK	CERCIRPPQR	ET-----
HEPL_Rn	QNCERGE---	-----	---V-DWR	CERC IQPPQR	EAESH-----
HEPL_Gg	KNEKEQE---	-----	---MKQPR	VSPGYKMPKQ	ITSP-----
Efs_Hs	GR-----	-----	---EME	DDPAGHNEY	EGIP-----
Efs_Mm	CR-----	-----	---EVA	NDPAGPHNEY	EGIP-----
Efs_Rn	CR-----	-----	---EVD	SDSGGPHNEY	EGIP-----
p130Cas_Gg	-----	-----	-----	-----	-----
Consistency	3312222010	0000000000	0000121433	2453333353	4435220020

	810	820	830	840	850
NEDD9_Hs	LSKEQAPDCS	SSDGSE RSWM	DDYDYVHLQG	KEEFERQOKE	LLEKENIMKQ

NEDD9_Mm	LSKDQPPDCG	SSDGSEERSWM	DDYDYVHLQG	KEEFERQOKE	LLEKENIMKQ	
NEDD9_Rn	LSKEQPPDCS	SSDGSEERSWM	DDYDYVHLQG	KEEFERQOKE	LLEKENIMKQ	
NEDD9_Gg	LSKGQPPHST	ASESSEKSWM	DDYDYVHLQG	KEEFERQOKE	LLEKENI IKQ	
p130Cas_Hs	FTSQDSPD-G	QYENSEGGWM	EDYDYVHLQG	KEEFEKTQKE	LLEKGSITRQ	
p130Cas_Mm	FTSQDSPD-G	QYENSEGGWM	EDYDYVHLQG	KEEFEKTQKE	LLERGNIMRQ	
p130Cas_Rn	FTSQDSPD-G	QYENSEGGWM	EDYDYVHLQG	KEEFEKTQKE	LLEKGNIVRQ	
HEPL_Hs	-----	-----QRET	ESHQKSTPST	KQREDE---	-----	
HEPL_Mm	-----	-----	ESYQESSPFD	RQPTTE---	-----	
HEPL_Rn	-----PER	SSPFHKQPAA	EHSLELAKKS	RGDVC GQKSP	NLQ-----	
HEPL_Gg	-----	-----RRIEI	DSL PVSAPDK	PNPSQGS---	-----	
Efs_Hs	-----	-----MA	EEYDYVHLKG	MDKAQGSRPP	D-----	
Efs_Mm	-----	-----MA	EEYDYVHLKG	VDTAQGSRPL	D-----	
Efs_Rn	-----	-----MA	EEYDYVHLKG	VDKAQGSRPL	D-----	
p130Cas_Gg	-----	-----Q	EIXDVPPVRG	ALPSQVSQGT	KFNH-----F	
Consistency	1111112101	1111222134	85-2147483	6486565556	5554644433	2322112112

 860 870 880 890 900
NEDD9_Hs	NKMQLEHHQL	SQFOLLEQEI	TKPVENDISK	WKPSQSL-PT	TNSG-VSAQD
NEDD9_Mm	SKAQLEHHQL	SQFOLLEQEI	TKPVENDISK	WKPSQSL-PT	TNNS-VGAQD
NEDD9_Rn	SKAQLEHHQL	SQFOLLEQEI	TKPVENDISK	WKPSQSL-PT	TNNS-VGAQD
NEDD9_Gg	SKTELEHHQI	NQFQRLEQEI	TKPVENDISK	WKPPQAL-QT	ANST-IAFHD
p130Cas_Hs	GKSQLELQQL	KQFERLEQEV	SRPIDHDLAN	WTPAQPLAPG	RTGG-LGPSD
p130Cas_Mm	GKGQLELQQL	KQFERLEQEV	SRPIDHDLAN	WTPAQPLVPG	RTGG-LGPSD
p130Cas_Rn	GKGQLELQQL	KQFERLEQEV	SRPIDHDLAN	WTPAQPLVPG	RTGG-LGPSD
HEPL_Hs	-----	HSSELLKKNR	-----ANICG	QNP G-----PL	IPQP-SSQQT
HEPL_Mm	-----	HSFELARKNR	-----VNVCW	QSPP-----PL	TSPS-PSGQN
HEPL_Rn	-----KKGK	NTMEGKS NEN	-----QDFCG	TSPT-----PL	PSPS-PSGQN
HEPL_Gg	-----NET	TKENVSEDCE	-----YVQLQ	VLPS-----TK	KNAV-RSQQD
Efs_Hs	-----QACT	GDPELPERGM	-----	PAPQEALSPG	EPLV-VSTGD
Efs_Mm	-----KAFP	VDPELLERGL	-----	AERKEALSPE	EPLV-LSTGD
Efs_Rn	-----NAFP	ADPELLERGL	-----	VEQKEALSPE	EPLV-LSTGD
p130Cas_Gg	YVTPPIYSTQK	KQPERREQEE	KRPKDTDGSK	GSPPQQYGPE	RGGGALCAAD
Consistency	1212222333	4647558654	1221224332	3484424083	4434056357

 910 920 930 940 950
NEDD9_Hs	RQLLCFYDQ	CETHFISLLN	AIDALFSCVS	SAQPPRIFVA	HSKFVILSAH
NEDD9_Mm	RQLLCFYDQ	CETHFISLLN	AIDALFSCVS	SAQPPRIFVA	HSKFVILSAH
NEDD9_Rn	RQLLCFYDQ	CETHFISLLN	AIDALFSCVS	SAQPPRIFVA	HSKFVILSAH
NEDD9_Gg	RQPLLFYSDQ	YETHFN SLLN	TIDAFFSCVS	ASQPPRIFVA	HSKLVILSAH
p130Cas_Hs	RQLLLFYLEQ	CEANLTTLTN	AVDAFFTAVA	TNQP PKIFVA	HSKFVILSAH
p130Cas_Mm	RQLLLFYLEQ	CEANLTTLTD	AVDAFFTAVA	TNQP PKIFVA	HSKFVILSAH
p130Cas_Rn	RQLLLFYLEQ	CEANLTTLTD	AVDAFFTAVA	TNQP PKIFVA	HSKFVILSAH
HEPL_Hs	PERKPRLSEH	CRLYFGALFK	AISAFHG SLS	SSQPAE-IIT	QSKLVIMVGQ
HEPL_Mm	TERKIHL SKH	SRLYFGALFK	AISVFASSLS	NGQPPEVFIT	QSKLVITVGQ
HEPL_Rn	VERKIRLSEH	SRLYFGALFK	AIGVFASSLS	NSQPPEVFIT	QSKLAITIGQ
HEPL_Gg	SAKKVVIPEQ	CRLCFGALHK	AIAVFN S SLS	SKQPPEVFIS	HSKLIIMVGQ
Efs_Hs	LQLLYFYAGQ	CQSHYSALQA	AVAALMSSTQ	ANQP PRLFVP	HSKR VVVA AH
Efs_Mm	LQLLHFYAGQ	CQSHYSALQA	AVAALVASTQ	ANQP PCLFVP	HGKR VVVA AH
Efs_Rn	LQLLHFYAGQ	CQSHYSALQT	AVAALMSSTQ	ANQP PCLFVP	HGKR VVVA AH
p130Cas_Gg	RQLLLFYLEQ	CEANLTTLTN	AIDAFFTAIS	TNQP PKIFVA	HSKF IILSAH
Consistency	4856467457	7755646*45	9958747667	65**957996	78*5996677

 960 970 980 990 1000
NEDD9_Hs	KL VFI GDTLT	RQVTAQDIRN	KVMNSSNQLC	EQLKTIVMAT	KMAALHYPST
NEDD9_Mm	KL VFI GDTLT	RQVAAQDIRN	KVRNSSNQLC	EQLKTIVMAT	KMAALHYPST
NEDD9_Rn	KL VFI GDTLT	RQVAAQDIRN	KVRNSSNQLC	EQLKTIVMAT	KMAALHYPST
NEDD9_Gg	KL VFI GDTLT	RQLTSQDIRN	RVRNSSDQLC	EL LKSIVMAT	KMAALHYPHT
p130Cas_Hs	KL VFI GDTLS	RQAKAADVRS	QVTHYSNLLC	DL LRGIVATT	KAAALQYPS P
p130Cas_Mm	KL VFI GDTLS	RQAKAADVRS	QVTHYSNLLC	DL LRGIVATT	KAAALQYPS P
p130Cas_Rn	KL VFI GDTLS	RQAKAADVRS	KVTHYSNLLC	DL LRGIVATT	KAAALQYPS P
HEPL_Hs	KL V---DTLC	METQERDVRN	EILRGSSHL C	SL LK DVALAT	KNAVLTYPSP
HEPL_Mm	KL V---DTLC	SETQEKDERN	EILCGSSHL C	GL LK DLALAT	KSAVIQYPS P
HEPL_Rn	KL V---DTLC	SETQERDERN	EILCGSSHL C	GL LK DLALAT	KNAVIQYPS P
HEPL_Gg	KIV---DSL C	QDTQLREARS	DVLHSSSRFC	SL LK NLALAT	KNAAIQYPNA
Efs_Hs	RLV FVGD TLG	RLAASAPLRA	QVRAAGTALG	QALRATVLAV	KGAALGYPS S
Efs_Mm	RLV FVGD TLG	RLAASAALRA	QVGAAGTMLA	QTLRATVLAV	KGAALGYPS D
Efs_Rn	RLV FVGD TLG	RLAASAPLRA	QVGAAGTVLA	QTLRATVLAV	KGAALGYPS D
p130Cas_Gg	KL VFI GDTLS	RQAKAQDVRH	KVTHYSNLLC	EL LKEIVVST	KAAALHYPSP
Consistency	89*545*9*4	75656566*5	6944486497	55*8477678	*4*894**85

 1010 1020 1030
NEDD9_Hs	TALQEMVHQV	TDLSRNAQLF	KRSLLEMATF
NEDD9_Mm	TALQEMVHQV	TDLSRNAQLF	KRSLLEMATF
NEDD9_Rn	TALQEMVHQV	TDLSRNAQLF	KRSLLEMATF
NEDD9_Gg	AALQEMVNRV	TELSYHAQLF	KL SLVQMASL

p130Cas_Hs	S	A	A	Q	D	M	V	E	R	V	K	E	L	G	H	S	T	Q	Q	F	R	R	V	L	G	Q	L	A	A	A
p130Cas_Mm	S	A	A	Q	D	M	V	D	R	V	K	E	L	G	H	S	T	Q	Q	F	R	R	V	L	G	Q	L	A	A	A
p130Cas_Rn	S	A	A	Q	D	M	V	D	R	V	K	E	L	G	H	S	T	Q	Q	F	R	R	V	L	G	Q	L	A	A	A
HEPL_Hs	A	A	L	G	H	L	Q	A	E	A	E	K	L	E	Q	H	T	R	Q	F	R	G	T	L	G	-	-	-	-	-
HEPL_Mm	S	A	L	S	L	L	Q	S	E	V	E	R	L	E	H	H	S	R	K	F	R	D	T	L	E	-	-	-	-	-
HEPL_Rn	S	A	L	G	L	L	Q	S	E	L	E	K	L	E	Y	H	S	R	K	F	R	G	T	L	E	-	-	-	-	-
HEPL_Gg	D	A	M	R	E	L	Q	N	K	N	D	E	L	Y	K	Y	T	Q	Q	F	R	A	M	L	E	-	-	-	-	-
Efs_Hs	P	A	I	Q	E	M	V	Q	C	V	T	E	L	A	G	Q	A	L	Q	F	T	T	L	L	T	S	L	A	P	-
Efs_Mm	T	A	V	Q	E	M	A	R	C	V	A	E	L	A	G	Q	A	L	R	F	T	T	L	L	A	G	L	L	P	-
Efs_Rn	T	A	V	Q	E	M	A	R	C	V	A	E	L	A	G	Q	A	L	R	F	T	T	L	L	A	G	L	L	P	-
p130Cas_Gg	A	A	S	K	D	M	V	E	R	V	K	D	L	A	N	S	T	Q	Q	F	R	M	V	L	G	Q	L	A	A	M
Consistency	6	*	6	6	5	8	6	4	4	7	5	6	*	5	4	5	6	6	5	*	6	4	5	*	3	3	4	4	2	1