

SATB1 protein alignment

SATB1	MDHLNEATQGKEHSEMSNNVSDPKGPPAKIARLEQNGSP	60
SATB1_new	-----	

SATB1	GHLMKTNLRKGTMLPVFCVVEHYENAIEYDCKEEHAEFVLVRKDMLFNQLIEMALLSLGY	120
SATB1_new	-----MLPVFCVVEHYENAIEYDCKEEHAEFVLVRKDMLFNQLIEMALLSLGY	48

SATB1	SHSSAAQAKGLIQVGKWNPVPLSYVTDAPDATVADMLQDVYHVVTLKIQLHSCPKELEDLP	180
SATB1_new	SHSSAAQAKGLIQVGKWNPVPLSYVTDAPDATVADMLQDVYHVVTLKIQLHSCPKELEDLP	108

SATB1	PEQWSHTTVRNALKDLLKDMNQSSLAKECPLSQSMISSIVNSTYYANVSAAKCQEFGRWY	240
SATB1_new	PEQWSHTTVRNALKDLLKDMNQSSLAKECPLSQSMISSIVNSTYYANVSAAKCQEFGRWY	168

SATB1	KHFKKTKDMMVEMDSLSELSQQGANHVNFQQPVPGNTAEQPPSPAQLSHGSQPSVRTPL	300
SATB1_new	KHFKKTKDMMVEMDSLSELSQQGANHVNFQQPVPGNTAEQPPSPAQLSHGSQPSVRTPL	228

SATB1	PNLHPGLVSTPISPQLVNQQQLVMAQLLNQQYAVNRLLAQQSLNQQYLNHPPPVSRSMNKP	360
SATB1_new	PNLHPGLVSTPISPQLVNQQQLVMAQLLNQQYAVNRLLAQQSLNQQYLNHPPPVSRSMNKP	288

SATB1	LEQQVSTNTEVSSEIYQWVRDELKRAGISQAVFARVAFNRTQGLLSEILRKEEDPKTASQ	420
SATB1_new	LEQQVSTNTEVSSEIYQWVRDELKRAGISQAVFARVAFNRTQGLLSEILRKEEDPKTASQ	348

SATB1	SLLVNLRAMQNFLQLPEAERDRIYQDERERSLNAASAMGPAPLISTPPSRPPQVKTATIA	480
SATB1_new	SLLVNLRAMQNFLQLPEAERDRIYQDERERSLNAASAMGPAPLISTPPSRPPQVKTATIA	408

SATB1	TERNGKPENNTMNINASIYDEIQQEMKRAKVSQALFAKVAATKSQGWLCELLRWKEDPSP	540
SATB1_new	TERNGKPENNTMNINASIYDEIQQEMKRAKVSQALFAKVAATKSQGWLCELLRWKEDPSP	468

SATB1	ENRTLWENLSMIRRFSLPQPERDAIYEQESNAVHHGDRPPHIIHVPAEQIQQQQQQQQ	600
SATB1_new	ENRTLWENLSMIRRFSLPQPERDAIYEQESNAVHHGDRPPHIIHVPAEQIQQQQQQQQ	528

SATB1	QQQQQQQAPPPPQPQQQPQTGPRLP RPQPTVASPAESDEENRQKTRPRTKISVEALGILQ	660
SATB1_new	QQQQQQQAPPPPQPQQQPQTGPRLP RPQPTVASPAESDEENRQKTRPRTKISVEALGILQ	588

SATB1	SFIQDVGLYPDEEAIQTLSAQLDLPKYTIKFFQNQRYYLKHGKLDNSGLEVDVAEYK	720
SATB1_new	SFIQDVGLYPDEEAIQTLSAQLDLPKYTIKFFQNQRYYLKHGKLDNSGLEVDVAEYK	648

SATB1	EEELLKDLEESVQDKNTNTLFSVKLEEELSVEGNTDINTDLKD	763
SATB1_new	EEELLKDLEESVQDKNTNTLFSVKLEEELSVEGNTDINTDLKD	691

ELF2 protein alignment

ELF2	MTSAVVDSGGTILELSSNGVENQEESEKVSEYPVIVPEVPSARLEQGYAAQVLVYDDDET	60
ELF2_new	-----	
ELF2	YMQDVAAEEQEVETENVETVEASVHSSNAHCTDKTIEAAEALLHMESPTCLRDSRSPVEV	120
ELF2_new	-----MESPTCLRDSRS----	12

ELF2	FVPPCVSTPEFIHAAMRPDVITETVVEVSTEESEPMDTSPIPTSPDSHEPMKKKKVGRKP	180
ELF2_new	-----PEFIHAAMRPDVITETVVEVSTEESEPMDTSPIPTSPDSHEPMKKKKVGRKP	64

ELF2	KTQQSPIISNGSPELGIKKKPREGKGNTTYLWEFLDLLQDKNTCPRIKWTQREKGIFKL	240
ELF2_new	KTQQSPIISNGSPELGIKKKPREGKGNTTYLWEFLDLLQDKNTCPRIKWTQREKGIFKL	124

ELF2	VDSKAVSKLWGKHKNKPD MN YETMGRALRYYYQRGILAKVEGQRLVYQFKDMPKNIVVID	300
ELF2_new	VDSKAVSKLWGKHKNKPD MN YETMGRALRYYYQRGILAKVEGQRLVYQFKDMPKNIVVID	184

ELF2	DDKSETCNEDLAGTTDEKSLERVSLSAESLLKAASSVRSGKNSSPINC SRAEKGVARVVN	360
ELF2_new	DDKSETCNEDLAGTTDEKSLERVSLSAESLLKAASSVRSGKNSSPINC SRAEKGVARVVN	244

ELF2	ITSPGHDASSRSPTTTASVSATAAPRTVRVAMQVPVVM TSLGQKISTVAVQSVNAGAPLI	420
ELF2_new	ITSPGHDASSRSPTTTASVSATAAPRTVRVAMQVPVVM TSLGQKISTVAVQSVNAGAPLI	304

ELF2	TSTSPTTATSPKVVIQTIPTVMPASTENGDKITMQPAKIIITIPATQLAQCQLQTKSNLTG	480
ELF2_new	TSTSPTTATSPKVVIQTIPTVMPASTENGDKITMQPAKIIITIPATQLAQCQLQTKSNLTG	364

ELF2	SGSINIVGTPLAVRALTPV SIAHGTPVMRLSMPTQQASGQTPPRVISAVIKGPEVKSEAV	540
ELF2_new	SGSINIVGTPLAVRALTPV SIAHGTPVMRLSMPTQQASGQTPPRVISAVIKGPEVKSEAV	424

ELF2	AKKQEHVDVKTLQLVEEKPADGNKTVTHV VVSAPS AIALPVTMKTEGLVTCEK	593
ELF2_new	AKKQEHVDVKTLQLVEEKPADGNKTVTHV VVSAPS AIALPVTMKTEGLVTCEK	477

■ Transactivation Domain

SP140L protein alignment

SP140L	MAGGGSDLSTRGLNGGVSQVANEMNHLPAHSQSLQRLFTEDQDVDEGLVYDTVFKHFKRH	60
SP140L_new	MAGGGSDLSTR-----LFTEDQDVDEGLVYDTVFKHFKRH	35
	*****	*****
SP140L	KLEISNAIKKTFFPLEGLRDRELITNKMFEDESDSCRNLVPVQRVVYNVLSELEKTFNLS	120
SP140L_new	KLEISNAIKKTFFPLEGLRDRELITNKMFEDESDSCRNLVPVQRVVYNVLSELEKTFNLS	95

SP140L	VLEALFSEVNMQEYPDLIHIYKSFKNAIQDKLSFQESDRKEREERPDIKLSLKQGEVPES	180
SP140L_new	VLEALFSEVNMQEYPDLIHIYKSFKNAIQDKLSFQESDRKEREERPDIKLSLKQGEVPES	155

SP140L	PEARKESEDQACGKMDTVDIANNSTLGKPKRKRKKKGHWGSRMGTRTQKNNQQNDNSKAD	240
SP140L_new	PEARKESEDQACGKMDTVDIANNSTLGKPKRKRKKKGHWGSRMGTRTQKNNQQNDNSKAD	215

SP140L	GQLVSSEKKANMNLKDLSKIRGRKRGKPGTHFTQSDRAPQKRVRSRASRKHKDETVDFQA	300
SP140L_new	GQLVSSEKKANMNLKDLSKIRGRKRGKPGTHFTQSDRAPQKRVRSRASRKHKDETVDFQA	275

SP140L	PLLPVTCGGVKGILHKEKLEQGTAKCIQTEDGKWFTPMEFEIKGGYARSKNWRLSVRCG	360
SP140L_new	PLLPVTCGGVKGILHKEKLEQGTAKCIQTEDGKWFTPMEFEIKGGYARSKNWRLSVRCG	335

SP140L	GWPLRRLMEEGSLPNPPRIYYRNKKRILKSQNNSSVDPCMRNLDECEVCRDGGELFCCDT	420
SP140L_new	GWPLRRLMEEGSLPNPPRIYYRNKKRILKSQNNSSVDPCMRNLDECEVCRDGGELFCCDT	395

SP140L	CSRVFHEDCHIPPVESEKTPWNCIFCRMKESPGSQCCQSEVLERQMCPEEQLKCEFL	480
SP140L_new	CSRVFHEDCHIPPVESEKTPWNCIFCRMKESPGSQCCQSEVLERQMCPEEQLKCEFL	455

SP140L	LKVYCCSESSFFAKIPYYYYIREACQGLKEPMWLDKIKKRLNEHGYPQVEGFVQDMRLIF	540
SP140L_new	LKVYCCSESSFFAKIPYYYYIREACQGLKEPMWLDKIKKRLNEHGYPQVEGFVQDMRLIF	515

SP140L	QNHASYKYKDFGQMGLRLEAEFEKDFKEVFQAIQETNGNS	580
SP140L_new	QNHASYKYKDFGQMGLRLEAEFEKDFKEVFQAIQETNGNS	555

ARID5B protein alignment

ARID5B	MEPNSLQWVGSPCGLHGPIFYKAFQFHLEGKPRILSLGDFFFVRCTPKDPICIAELQLL	60
ARID5B_new	MEPNSLQWVGSPCGLHGPIFYKAFQFHLEGKPRILSLGDFFFVRCTPKDPICIAELQLL	60

ARID5B	WEERTSRQLLSSSKLYFLPEDTPQGRNSDHGEDEVIAVSEKVIKLEDLVKQVHSDFSKW	120
ARID5B_new	WEERTSRQLLSSSKLYFLPEDTPQGRNSDHGEDEVIAVSEKVIKLEDLVKQVHSDFSKW	120

ARID5B	RCGFHAGPVKTEALGRNGQKEALLKYRQSTLNSGLNFKDVLKEKADLGEDEEETNVIVLS	180
ARID5B_new	RCGFHAGPVKTEALGRNGQKEALLKYRQSTLNSGLNFKDVLKEKADL-----	167

ARID5B	YPQYCRYRSMKRIQDKPSSILTDQFALALGGIAVVSARNPQILYCRDTFDHPTLIENESI	240
ARID5B_new	-----	
ARID5B	CDEFAPNLKGRPRKKKPCPQRRDSFSGVKDSNNNSDGKAVAKVKCEARSALTKPKNNHNC	300
ARID5B_new	---APNLKGRPRKKKPCPQRRDSFSGVKDSNNNSDGKAVAKVKCEARSALTKPKNNHNC	223

ARID5B	KKVSNEEKPKVAIGEEGRADEQAFVLALYKMKERKTPIERIPYLGFQKQINLWTFQAAQ	360
ARID5B_new	KKVSNEEKPKVAIGEEGRADEQAFVLALYKMKERKTPIERIPYLGFQKQINLWTFQAAQ	283

ARID5B	KLGGYETITARRQWKHIYDELGGNPGSTSAATCTRRHYERLILPYERFIKGEEDKPLPPI	420
ARID5B_new	KLGGYETITARRQWKHIYDELGGNPGSTSAATCTRRHYERLILPYERFIKGEEDKPLPPI	343

ARID5B	KPRKQENSSQENENKTKVSGTKRIKHEIPKSKKEKENAPKPQDAAEVSSEQEKEQETLIS	480
ARID5B_new	KPRKQENSSQENENKTKVSGTKRIKHEIPKSKKEKENAPKPQDAAEVSSEQEKEQETLIS	403

ARID5B	QKSIPEPLPAADMKKKIEGYQEFSAPKLASRVDPEKDNETDQGSNSEKVAEEAGEKGPTP	540
ARID5B_new	QKSIPEPLPAADMKKKIEGYQEFSAPKLASRVDPEKDNETDQGSNSEKVAEEAGEKGPTP	463

ARID5B	PLPSAPLAPEKDSALVPGASKQPLTSPSALVDSKQESKLCCFTESPESEPEASFPSPPT	600
ARID5B_new	PLPSAPLAPEKDSALVPGASKQPLTSPSALVDSKQESKLCCFTESPESEPEASFPSPPT	523

ARID5B	TQPPLANQNETEDDKLPAMADYIANCTVKVDQLGSDDIHNALKQTPKVLVVQSFD MFKDK	660
ARID5B_new	TQPPLANQNETEDDKLPAMADYIANCTVKVDQLGSDDIHNALKQTPKVLVVQSFD MFKDK	583

ARID5B	DLTGPMNENHGLNYTPLLYSRGNPGIMSPAKKKLLSQVSGASLSSSYPYGSPPLISKK	720
ARID5B_new	DLTGPMNENHGLNYTPLLYSRGNPGIMSPAKKKLLSQVSGASLSSSYPYGSPPLISKK	643

ARID5B	KLIARDDLCSSLSQTHHGQSTDHMAVSRPSVIQHVQSFRSKPSEERKTINDIFKHEKLSR	780
ARID5B_new	KLIARDDLCSSLSQTHHGQSTDHMAVSRPSVIQHVQSFRSKPSEERKTINDIFKHEKLSR	703

ARID5B	SDPHRCFSFSKHHLNPLADSYVLKQEIQEGKDKLLEKRALPHSHMPSFLADFYSSPHLHSL	840
ARID5B_new	SDPHRCFSFSKHHLNPLADSYVLKQEIQEGKDKLLEKRALPHSHMPSFLADFYSSPHLHSL	763

ARID5B	YRHTEHHLHNEQTSKYPSRDMYRESENSSFPSHRHQEKLHVNYLTSLHLQDKKSAAAEAP	900
ARID5B_new	YRHTEHHLHNEQTSKYPSRDMYRESENSSFPSHRHQEKLHVNYLTSLHLQDKKSAAAEAP	823

ARID5B	TDDQPTDLSLPKNPHKPTGKVLGLAHSTTGPQESKGISQFQVLGSQSRDCHPKACRVSPM	960
ARID5B_new	TDDQPTDLSLPKNPHKPTGKVLGLAHSTTGPQESKGISQFQVLGSQSRDCHPKACRVSPM	883

ARID5B	TMSGPKKYPESLSRSGKPHHVRLNFRKMEGMVHPILHRKMSPQNIGAARPIKRSLEDLD	1020
ARID5B_new	TMSGPKKYPESLSRSGKPHHVRLNFRKMEGMVHPILHRKMSPQNIGAARPIKRSLEDLD	943

ARID5B	LVIAGKKARAVSPLDPSKEVSGKEKASEQESEGSKAAHGGHSGGGSEG HKLPLSSPIFPG	1080
ARID5B_new	LVIAGKKARAVSPLDPSKEVSGKEKASEQESEGSKAAHGGHSGGGSEG HKLPLSSPIFPG	1003

ARID5B	LYSGSLCNSGLNSRLPAGYSHSLQYLKNQTVLSPLMQPLAFHSLVMQRGIFTSPTNSQQL	1140
ARID5B_new	LYSGSLCNSGLNSRLPAGYSHSLQYLKNQTVLSPLMQPLAFHSLVMQRGIFTSPTNSQQL	1063

ARID5B	YRH LAAATPVGSSYGDLLHNSIYPLAAINPQA AFPSSQLSSVHPSTKL	1188
ARID5B_new	YRH LAAATPVGSSYGDLLHNSIYPLAAINPQA AFPSSQLSSVHPSTKL	1111

NCOA2 protein alignment

NCOA2	MSGMGENTS DPSRAET RKRKECPDQLGPSPKRNTEKRNREQENKYIEELAELIFANFNDI	60
NCOA2_new	MSGMGENTS DPSRAET RKRKECPDQLGPSPKRNTEKRNREQENKYIEELAELIFANFNDI	60

NCOA2	DNFNFKPDKCAILKETVKQIRQIKEQEKA AAAANIDEVQKSDVSSTGQGVIDKDALGPMML	120
NCOA2_new	DNFNFKPDKCAILKETVKQIRQIKEQEKA AAAANIDEVQKSDVSSTGQGVIDKDALGPMML	120

NCOA2	EALD GFFV VV NLEGNV V FVSENV TQYLRYNQEELMNKSVYSILHVG DHT E FVKNLLPKSI	180
NCOA2_new	EALD GFFV VV NLEGNV V FVSENV TQYLRYNQEELMNKSVYSILHVG DHT E FVKNLLPKSI	180

NCOA2	VNGGSWSGEPPRRNSHTFNC RMLVKPLPDSEEEGH DNQEAHQKYETMQCFAVSQPKSIKE	240
NCOA2_new	VNGGSWSGEPPRRNSHTFNC RMLVKPLPDSEEEGH DNQEAHQKYETMQCFAVSQPKSIKE	240

NCOA2	EGEDLQ SCLICVARRVPMKERPVLP SSEFTTRQDLQ GKITS LDTSTMRAAMKPGWEDLV	300
NCOA2_new	EGEDLQ SCLICVARRVPMKERPVLP SSEFTTRQDLQ GKITS LDTSTMRAAMKPGWEDLV	300

NCOA2	RRCIQKFHAQH EGESVS YAKRHHHEVLRQGLAFS QIYRFS LSDGTLVAAQTKSKLIRSQT	360
NCOA2_new	RRCIQKFHAQH EGESVS YAKRHHHEVLRQGLAFS QIYRFS LSDGTLVAAQTKSKLIRSQT	360

NCOA2	TNEPQLVISLHMLHREQNVCMNPDLTGQTMGKPLNPIS SNSPA HQALCSGNPGQDMTSL	420
NCOA2_new	TNEPQLVISLHMLHREQNVCMNPDLTGQTMGKPLNPIS SNSPA HQALCSGNPGQDMTSL	420

NCOA2	SNINF PINGPKEQMGM PMGRFGGSGGMNHVSGMQATTPQGSNYALKMNSPSQSSPGMNPG	480
NCOA2_new	SNINF PINGPKEQMGM PMGRFGGSGGMNHVSGMQATTPQGSNYALKMNSPSQSSPGMNPG	480

NCOA2	QPTSM LSPRHRMSPGVAGSPRIPPSQFSPAGSLHSPVGVCSSTGNSHSYTNSSLNALQAL	540
NCOA2_new	QPTSM LSPRHRMSPGVAGSPRIPPSQFSPAGSLHSPVGVCSSTGNSHSYTNSSLNALQAL	540

NCOA2	SEGHGVSLGSSLASPD LKMGNLQNSPVNMNPPPLSKMGS LDKDCFGLYGEPSEGT TGQA	600
NCOA2_new	SEGHGVSLGSSLASPD LKMGNLQNSPVNMNPPPLSKMGS LDKDCFGLYGEPSEGT TGQA	600




NCOA2	ESSCHPGEQKETNDPNLPPAVSSERADGQSRLHDSKGQTKLLQLLTTKSDQMEPSPLASS	660
NCOA2_new	ESSCHPGEQKETNDPNLPPAVSSERADGQSRLHDSKGQTKLLQLLTTKSDQMEPSPLASS	660

NCOA2	LSDTNKDSTGSLPGSGSTHGTS LKEKHKILHRL LQDSSSPVDLAKLTAEATGKDLSQESS	720
NCOA2_new	LSDTNKDSTGSLPGSGSTHGTS LKEKHKILHRL LQDSSSPVDLAKLTAEATGKDLSQESS	720

NCOA2	STAPGSEVTIKQEPVSPKKKENALLRYLLDKDDTKDIGLPEITPKLERLDSKTDPASNTK	780
NCOA2_new	STAPGSEVTIKQEPVSPKKKENALLRYLLDKDDTKDIGLPEITPKLERLDSKTDPASNTK	780

NCOA2	LIAMKTEKEEMSFEPGDQPGSELDNLEEILDDLQNSQLPQLFPDTRPGAPAGSVDKQAI I	840
NCOA2_new	LIAMKTEKEEMSFEPGDQE-----	799

NCOA2	NDLMQLTAENSPVTPVGAQKTALRISQSTFNNPRPGQLGRLLPNQNLPLDITLQSPTGAG	900
NCOA2_new	-----	
NCOA2	PFPPIRNSSPYSVIPQPGMMGNQGMIGNQGNLGNSSTGMIGNSASRPTMPSGEWAPQSSA	960
NCOA2_new	-----	
NCOA2	VRVTCAATTSAMNRPVQGGMIRNPAASIPMRPSSQPGQRQTLQSQVMNIGPSELEMNMG	1020
NCOA2_new	-----	
NCOA2	PQYSQQQAPPNQ TAPWPESILPIDQASFASQNRQPFQSSPDDLCPHPAAESPSDEGALL	1080
NCOA2_new	-----	
NCOA2	DQLYLALRNFDGLEEIDRALGIPELVSQSQA VDPEQFSSQDSNIMLEQKAPVFPQQYASQ	1140
NCOA2_new	-----	
NCOA2	AQMAQGSYSQPMQDPNFHTMGQRPSYATLRMQPRPGLRPTGLVQNQPNQLRLQLQHRLQAQ	1200
NCOA2_new	-----	
NCOA2	QNRQPLMNQISNVSNVNLTLRPGVPTQAPINAQMLAQ RQREILNQHLRQRQMHQQQQVQQ	1260
NCOA2_new	-----	
NCOA2	RTLMMRGQGLNMTPSMVAPSGMPATMSNPRI PQANAQQFPFPPNYGISQQPDPGFTGATT	1320
NCOA2_new	-----	
NCOA2	PQSPLMSPRMAHTQSPMMQQSQANPAYQAPSDINGWAQGNMGGNSMFSQQSPPHFGQQAN	1380
NCOA2_new	-----	
NCOA2	TSMYSNNMNINVS MATNTGGMSSMNQMTGQISMTSVTSVPTSGLSMSGPEQVNDPALRGG	1440
NCOA2_new	-----	
NCOA2	NLFPNQLPGMDMIKQEGDTTRKYC	1464
NCOA2_new	-----	

-  LXXLL motif 4
-  LLXXLXXXL motif
-  Poly-Gln

ZNF266 protein alignment

ZNF266	-----	
ZNF266_new	MAATDLSYGLYRDPVCLQEKTEVERVVADCLTNCYQDSVTFDDLAVDFTPEEWTLLDPTQ	60
ZNF266	-----MLENYKNLATVGYQLFKPSLISWLEQEEERTVQRGDFQASEWKVQLKTKEAL	53
ZNF266_new	RNLYRDVMLENYKNLATVGYQLFKPSLISWLEQEEERTVQRGDFQASEWKVQLKTKEAL	120

ZNF266	QQDVLGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQNSSENTFECYLYGV	113
ZNF266_new	QQDVLGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQNSSENTFECYLYGV	180

ZNF266	DFLTLHKKTSTGEQRSVFSQCGKAFSLNPDVVCQRTCTGEKAFDCSDSGKSFINHSHLQG	173
ZNF266_new	DFLTLHKKTSTGEQRSVFSQCGKAFSLNPDVVCQRTCTGEKAFDCSDSGKSFINHSHLQG	240

ZNF266	HLRTHNGESLHEWKECGRGFIHSTD LAVRIQTHRSEKPYKCKEKGKGFYSAYLNIHMGT	233
ZNF266_new	HLRTHNGESLHEWKECGRGFIHSTD LAVRIQTHRSEKPYKCKEKGKGFYSAYLNIHMGT	300

ZNF266	HTGDNPYECKEKGKAFTRSCQLTQHRKTHTGKPYKCKDCGRAFTVSSCLSQHMKIHVGE	293
ZNF266_new	HTGDNPYECKEKGKAFTRSCQLTQHRKTHTGKPYKCKDCGRAFTVSSCLSQHMKIHVGE	360

ZNF266	KPYECKEKGIAFTRSSQLTEHLKTH TAKDPFECKICGKSFRNSSCLSDHFRIHTGIKPYK	353
ZNF266_new	KPYECKEKGIAFTRSSQLTEHLKTH TAKDPFECKICGKSFRNSSCLSDHFRIHTGIKPYK	420

ZNF266	CKDCGKAFTQNSDLTKHARTHSGERP YECKEKGKAFARSSRLSEHTRTHTGKPFECVKC	413
ZNF266_new	CKDCGKAFTQNSDLTKHARTHSGERP YECKEKGKAFARSSRLSEHTRTHTGKPFECVKC	480

ZNF266	GKAFAISSNLSGHLRIHTGKPFECLECGKAFTHSSSLNNHMRTHSAKKPFTCMECGKAF	473
ZNF266_new	GKAFAISSNLSGHLRIHTGKPFECLECGKAFTHSSSLNNHMRTHSAKKPFTCMECGKAF	540

ZNF266	KFPTCVNLHMRIHTGKPYKCKQCGKSFSYSNSFQLHERHTHTGKPYECKEKGKAFSSSS	533
ZNF266_new	KFPTCVNLHMRIHTGKPYKCKQCGKSFSYSNSFQLHERHTHTGKPYECKEKGKAFSSSS	600

ZNF266	SFRNHERRHADERLSA	549
ZNF266_new	SFRNHERRHADERLSA	616
