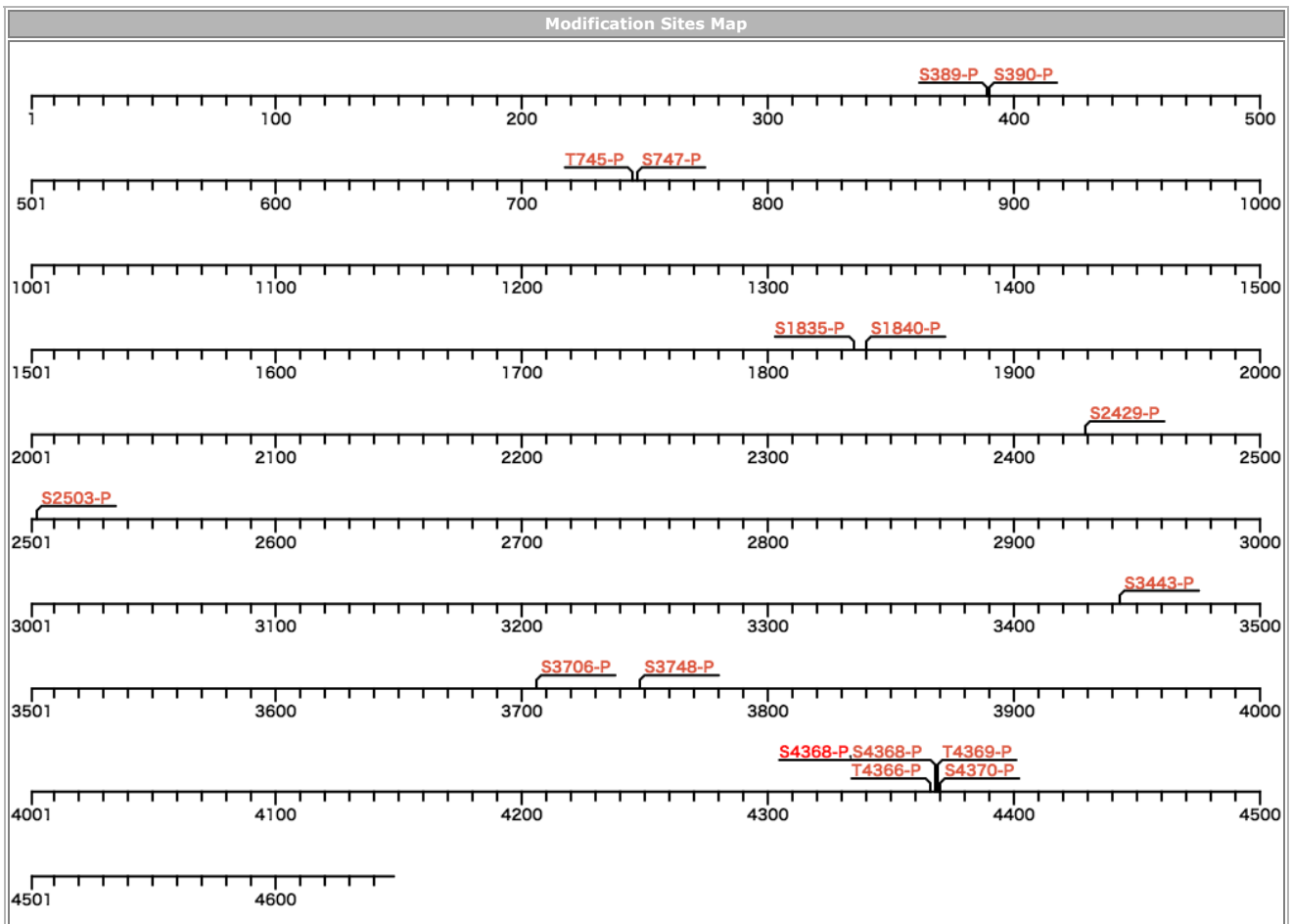


ID	Accession	GeneName	Chr.No.	Description
DYHC1_HUMAN	Q14204	DYNC1H1	14q32.31 102430865..102517129	Cytoplasmic dynein 1 heavy chain 1



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
4368	S	P	Lab	130327_HEK_ME_pphos.mgf[F015008]
4368	S	P	Lab	140320_OVISE_ME_.mgf[F017429]
4368	S	P	Paper	Sci Signal 2011, 4(179), rs5

Protein Sequence

MSEPGGGGGS DGSAGLEVSA VQNVADVSVL QKHLRKLVL LLEDGGEAPA ALEAALEEKSA ALEQMRKFLS DPQVHTVLVE RSTLKEDVGD EGEEEFKES YNINIDIHYG VK SINSLAFIK RTPVIDADKP VSSQLRVLTL SEDSPYETLH SFISNAVAPF FKSUIRESGK ADRDGDGKMAP SVEKIAELE MGLLHLQQNI EPEISLPIH PMITNVAQCQ YERGEKPK VT DFGDKVEDPT FLNQLQSGVN RWIREIQKVT KLRDRPASGT ALQEISFWLN LERALYRIQE KRESPEVLLT LDILKHGKRF HATVVSFDTDT GLKQALETVN DYNPLMKDFP L NDLLSATEL DKIRQALVAI FTHLRKIRNT KYPIQRALRL VEASIRDLSS QLLKVLGTRK LMHVAYEEFE KVMVACFEV FQWVDEYEKL QVLLRDIVKR KREENLKMVM RINPA HRKLQ ARLDQMRKFR RQHEQLRAVI VRVLRPQVTA VAQQNQGEVP EPQDMKVAEV LFDAADANAI EEVNLAYENV KEVDGLDVSK EGTEAWAAM KRYDERIDRV ETRITA RLRD QLTAKNANE MFRIFSRFNA LFRVPHIRGA IREYQTQLIQ RVKDDIESLH DKFKVQYPQS QACKMSHVRD LPPVSGSIW AKQIDRQLTA YMKRVEDVLG KGWENHVE GQ KLVKQDGSFR MKNLTQEIFD DWARKVQQRN LGVSGRIFTI ESTRVGRGTG NVLKLKVNFL PEITLSS KEV RNLKWLGRFR PLAINVKAHQ ANQLYPFAIS LIESVRYTER T CEKVEERN ISLLVAGLKK EVQALIAEGI ALVWESYKLD PYVQRLAETV FNFQEKVDDL LIEEKIDLE VRSLETQMYD HKTFSLEINR LHSYSNLPIWV NKLDME IERI LGVRLQAGLR AWTQVLLGQA EDKAEVMDMT DAPQVSHKPG GEPKIKNVVH ELRITNQVIY LNPPIEECRY KLYQEMFAWK MVVLSLPRIQ SQRYQVGVHY ELTEEEKFY R NALTRMPDGP VALEESYSAV MGIVSEVEQY VKVWLQYQCL WDMQAENIYN RLGEDLNKQW ALLVQIRKAR GTFDQNAETK EFGPVVIDYG KVQSKVNLYK DSWHKEVLS K FGQMLGSNMT EFHSQISKR QLEQHSVDT ASTSDAVTFI TYVQSLKRKI KQFEKQVELY RINGRLLLEKQ RFQFPPSWLY IDNIEGEWGA FNDIMRRKDS AIQQQVANLQ MKIVQEDRAV ESRTDLLTD WEKTKPVTGN LRPEEALQAL TIYEGKFGRL KDDREKCAKA KEALELDTG LLSGSEERVQ VALEELQDLK GVVSELSKVV EQIDQMKEQ W VSVQPRKLR QNLDALLNQL KSFPARLRQY ASYEFVQRL KGYMKNMVL IELKSEALKD RHWKQLMKRL HVNWWVVELT LGQIWDVDLQ KNEAIVKDLV LVAQGEAL EFL KQIREVW NTEYLDLVNY QNKRLIRGW DDLFNKVKHEH INSVSAMKLS PYYKVFEEA LSWEDKLNRI MALFDVWIDV QRRWVYVLEGI FTGSADIKHL LPVETQRFQS ISTEFL LALMK KVSQSPVLMV VLNIQGVQRS LERLADLLGK IQKALGEYLE RERSSPRFY FVGDEDLLE IGNSKNVAKL QKHFKMFAG VSSIILNEDN SVVLGSSRE GEEVFMKTP V SITEHPKINE WLTLEKEMR VTLAKLAE VTEVEIFGKA TSIDPNTYIT WIDKYQAQLV VLSAQIAWSE NVETALSSMG GGGDAAPLHS VLSNVEVTLN VLADSVLMEQ PP LRRRKLH LITELVHQD VTRSLIKSI DNAKSFEWLS QMRFYFDPKQ TDVLQQLSIQ MANAKVNYGF EYLGVDKLV QTLPLDRCYL TMTQALEARL GGSPFGPAGT GKTES VKALG HQLGRFVLV NCDETFDFQA MGRIFVGLCQ VGAWGCFDEF NRLEERMLSA VSQQVQCIQE ALREHNSPNY DKTSAPITCE LLNKQVKVSP DMAIFITMNP GYAGRS NLPD NLKLFRLSLA MTKPDRQLA QVMYLSQGF R TAEVLANKIV PFFKLCDLQL SSQSHYDFGL RALKSVLVA GNVKREIRIQ IKREKEERGE AVDEGEIAEN LPEQEILIQS VCETMPKLV AEDIPFLFSL LSDVFPVQY HRGEMTALRE ELKVKCQEM Y LTYGDGEEV GMWVEKVLQL YQITQINHGL MMVPSGSGG SMAWRVLLKA LERLEGVEG A HIIDPKAIS KDHLVGTLDP NTREWTDGLF THVLRKIIDS VRGELQKRQW IVFDGVDPE WVENLNSVLD DNKLLTPNG ERLSLPPNVR IMFEVQDLKY ATLATVSRCG MWW FSEVLS TDMIFNNFLA LRSIPLDEG EDEAQRRRKG KEDEGEEAAS PMLQIQRDAA TIMQPYFTS N GLVTKALEHA FQLEHIMDLT RLRLGSLFS MLHQACRNVA QYNAN HPDFP MQIEQLERYI QRYLVYAILV SLSDGSRSLM RAELEGEYRR ITTVPLTAP NIPIDYEVS ISGEWSPWA KVPQIEVETH KVAAPDWWV TLDTVRHEAL LYTWLAHKP LVLGCGPPSGS KTMTLFSALR ALPDMVVGL NFSSATPEL LLKTFDHYCE YRRTPNGVVL APVQLGKWL V LFCDEINLPD MDKYGTQRVI SFIRQMVEHG GFYRTSDQTV VKL ERIQFVG ACNPPDPRG KLSHRFLRH VPVVYDYPG PASLTQYGT FNRAMLRLIP SLRTYAELT AAMVEFYTMS QERFTQDTQP HYIYSPREMT RWRVGIFEAL RPLETLPV EG LIRIWAHEAL RLFQDRLED EERRWTDENI DTVALKHFPN IDREKAMSRP ILYSNWLSKD YIPVDQEELR DYVKARLKV FEEELDVPLV LFNEVLDHVL RIDRIFRQPQ GH LLLIGVSG AGKTTLSRFV AWMNGLSVYQ IKVHRKYTGE DFDEDLRVL RYSGCKNEKI AFIMDES NVL DSGFLERMNT LLANGEVPL FEGDEYATLM TQCKEGAQKE GLML DSHEEL YKWFQTSQVIR NLHVFTMNP SEGLKDRAA TSPALFNRCV LNWFGDWSTE ALYQVKEFT SKMDLEKPNY IVPDYPVYV DKLPPPSHR EAIVNSCVFV HQTLL QANAR LAKRGGRTMA ITPRHVLDPI NHYANLFHEK RSELEEQMH LNVGLRRIKE TVDQVEELRR DLRIKSQLE VKNAAANDKL KKMVKDQGEA EKKKVMSQEI QEQLHK QQEV IADKQMSVKE DLDKVEPAVI EAQNAVSIK QHILVEVRS M ANPPAAVKLA LESICLLLGE STTDWKQIRS IIMRENFIPT IVNFSAEIS DAIREMKKN YMSNPSYNYE

IVNRSALACG PMVKWAIQQL NYADMLKRVE PLRNLQKLE DDAKDNQQKA NEVEQMIRDL EAS^YIARYKEE YAVLISEAQA IKADLAAVEA KVNRS^TTALLK SLSAERERWE KT
SETFKNQ^M STIAGDCLLS AAFIAYAGYF DQQMRQNLFT TWSHHLQQAN IQFR^TDIART EYLSNADERL RWQASSLPAD DLCTENAIML KRFNRYPLII DPSGQATEFI MNEYK
DRKIT RTSFLDDAFR KNLESALRFG NPLL^VQDVES YDPVLPV^LN REVRRTGGRV LITLGDQDID LSPSFVIFLS TRDPTVEFPP DLCSRVT^FVN FTVTR^SSLQS QCLNEVLKAE
RPDVDEKRS^D LLLQGEFQL RLRQLEK^SLL QALNEVKGRI LDDDTIITTL ENLKREAAEV TRKVEETDIV MQEVETVSQQ YLPLSTACSS IYFTMESLKQ IHFLYQYSLQ FFLDIY
HNVL YENPNLKGVT DHTQRLSIIT KDLFQVAFNR VARGMLHQDH ITFAMLLARI KLKGTVGEPT YDAEFQHFLR GNEIVLSAGS TPRIQGLTVE QAEAVVRLSC LPAFKDLIAK
VQADEQFGIW LDSS^SPEQTV PYLWSEETPA TPIGQAIHRL LLIQAFRPDR LLAMAHMFVS TNLGESFMSI MEQPLDLTHI VGTEVKPNT^P VLMCSVPGYD ASGHVEDLAA EQN
TQITSIA IGSAEGFNQA DKAIN^TAVKS GRWVMLKNVH LAPGWL^MQLE KKLHSLQPHA CFRLFLTMEI NPKVPV^NLLR AGRIFVFEPP PGVKANMLRT FSSIPVSRIC KSPNERA
RLY FLLAWFHAI^I QERLRYAPLG WSKKYEFGES DLRSACDTVD TWLDDTAKGR QNISPDKIPW SALKTLMAQS IYGG^RVDNEF DQRL^LNTFLE RLFTTRS^FDS EFKLACKVDG
HKDIQMPDGI RREFVQWVE LLPDTQTPSW LGLP^NNAERV LLTTQGVDMI SKMLKMQMLE DEDDLAYAET EKKTR^TD^STS DGRPAWMRTL HTTASNWLHL IPQTL^SHLKR T
VENIKDPLF RFFEREVKMG AKLLQDVRQD LADV^VQCEG KKKQTNYLRT LINELVKGIL PRSWSHYTVP AGMTVIQWVS DFSERIKQLQ NISLAAASGG AKELKNIHVC LGG
LFVPEAY ITATRQYVAQ ANSWSLEELC LEVNV^TTSQG ATLDACSFGV TGLKLQGATC NNNKLSLSNA ISTALPLTQL RWWVKQT^NTEK KASV^VTLPVY LNFTRADLIF TVDFEIA
TKE DPRSFYERGV AVLCTE

Backcolor of amino acid : Yellow -> site of modification, gray -> in front of processing