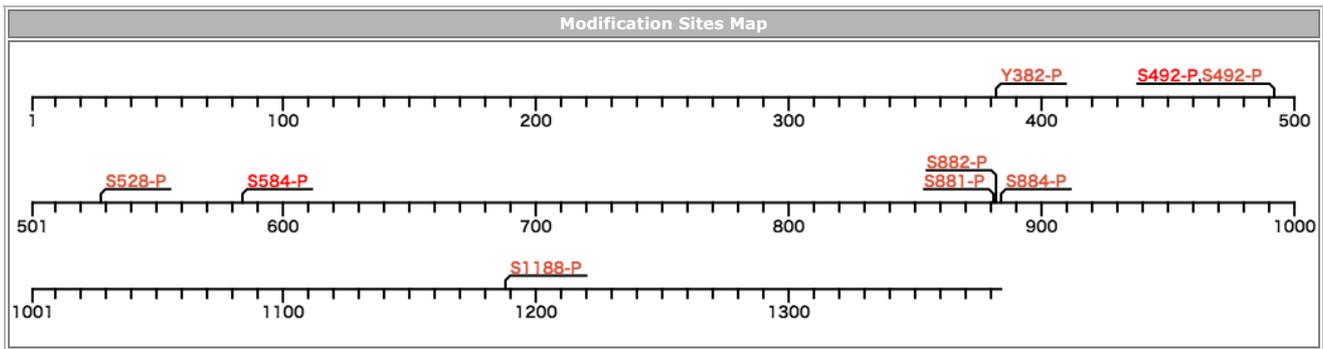


ID	Accession	GeneName	Chr.No.		Description
EIF3A_HUMAN	Q14152	EIF3A	10q26.11	120794356..120840316	Eukaryotic translation initiation factor 3 subunit A



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
492	S	P	Lab	130415_HEK_CE_tphos.mgf[F015009]
492	S	P	Lab	140320_tita_C18_.mgf[F017426]
492	S	P	Lab	140320_tita_SDB_.mgf[F017430]
492	S	P	Lab	140320_OVISE_SCE_.mgf[F017431]
492	S	P	Paper	Sci Signal 2009, 2(84), ra46

Protein Sequence

MPAYFQRPEN ALKRANEFLE VGKKQPALDV LYDVMKSKKH RTWQKIHEPI MLKYLELCVD LRKSHLAKEG LYQYKNICQQ VNIKSLEDVV RAYLKMEEK TEAAKEESQQ MV LDIEDLDN IQTPESVLLS AVSGEDTQDR TDRLLLPWW KFLWESYRQC LDLLRNNSRV ERLYHDIAQQ AFKFCQYTR KAEFRKLCDN LRMHLSQIQR HHNQSTAINL NNPES QSMHL ETRLVQLDSA ISMELWQEAF KAVEDIHGLF SLSKPPKPKQ LMANYYNKVS TVFWKSGNAL FFASTLHRLY HLSREMRKNL TQDEMQRMSR RVLLATLSIP ITPERTDI AR LLDMDGIIVE KQRRLATLLG LQAPPTRIGL INDMVRFNVL QYVVEPKDL YNWLEVEFNP LKLCERVTKV LNWVREQPEK EPELQYVVPQ LQNNILRLL QVVSQIYQSI EF SRLTSLVP FVDAFQLERA IVDAARHCDL QVRIDHTSRT L SFGSDLNIA TREDAPIGPH LQSMPEQIR NQLTAMS SVL AKALEVIKPA HILQEKEEQH QLAVTAYLKN SRKEH QRILA RRQTIEERKE RLE S LNIQRE KEELEQREAE LQKVRKAEAE RLRQEAKERE KERILQEHEQ IKKKTVRERL EQIKKTELGA KAFKDDIDIED LEELDPDFIM AKQVEQLEKE KKEQLERLKN QEKKIDYFER AKRLEEIPLI KSAYEEQRIK DMDLWEQEE ERITTMQLER EKALEHKNRM SRMLEDRDLF VMRLKAARQS VYEEKLKQFE ERLAEERHNR LEE RKRQRKE ERRITYYREK EEEEEQRAEE QMLKEREERE RAERAKREEE LREYQERVKK LEEVERKKRQ RELEIEERER RREEERRLGD S S LSRKDSRW GDRDSEGTWR KGPEA DSEWR RGPPEKEWRR GEGRDEDSSH RRDEERPRRL GDEDEDREPSL RPDDDRVPRR GMDDDRGPRR GPEEDRFSRR GADDDRPSWR NTDDDRPPRR IADEDGRNWR HA DDDDRPPRR GLDEDGRSWR TADEDGRPRR GMDDDRGPRR GGADDERSSW RNADDDRGPRR RGLDDDRGPRR RGMDDDRGPRR RGMDDDRGPRR RGMDDDRGPRR RGLDDD RGPW RNADDDRIPR RGAEDDRGPW RNMDDDRSLR RADDDRFPRR GDDSRPGPWR PLVKPGGWRE KEKAREE S WG PPRESRPEE REWDREKERD RDNQDREEND KD PERERDRE RDVDREDFR RPRDEGGWRR GPAEESSSWR DSSRRDDRDR DRRRRERDDR RDLRERRDLR DDRDRRGPPL RSEREVESSW RRADDRKDDR VEERDPPRRV PPPALSRDRE RDRDREREKE KEKASWRAEK DRESLRRTKN ETDEDGWTTV RR

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