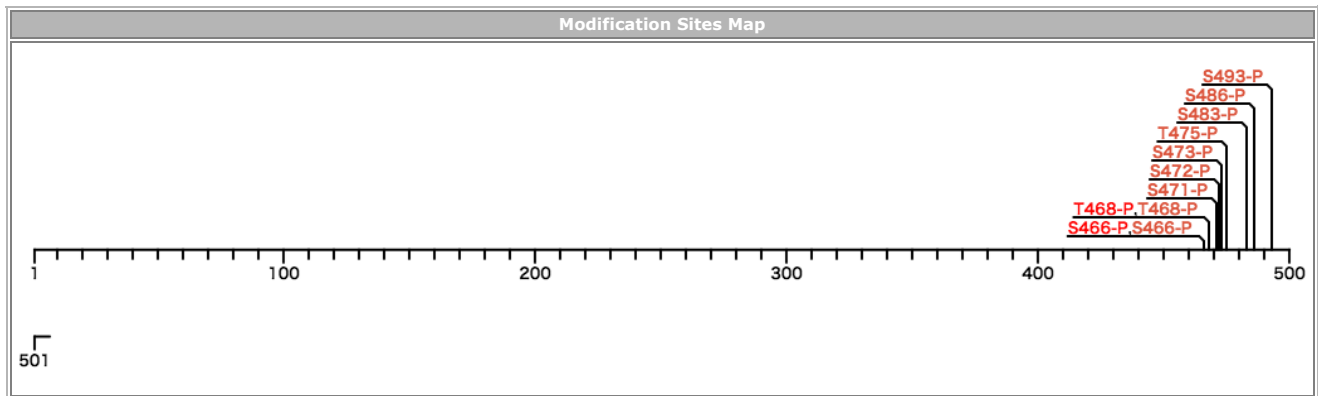


ID	Accession	GeneName	Chr.No.	Description
F262_HUMAN	O60825	PFKFB2	1q32.2 207222801...207254369	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
468	T	P	Lab	110218_pOVKATE_3.mgf[F017465]
468	T	P	Lab	110218_pOVMANA_2.mgf[F017467]
468	T	P	Lab	110218_pOVMANA_3.mgf[F017468]
468	T	P	Lab	110218_pOVSAYO_1.mgf[F017469]
468	T	P	Lab	110218_pOVSAYO_2.mgf[F017470]
468	T	P	Lab	110218_pOVSAYO_3.mgf[F017471]
468	T	P	Lab	110218_pRMG1_3.mgf[F017474]
468	T	P	Lab	110218_pRMG2_1.mgf[F017475]
468	T	P	Lab	110218_pRMG2_3.mgf[F017477]
468	T	P	Lab	110218_pRMG2_4.mgf[F017478]
468	T	P	Lab	100628_akimura_pMCAS_1.mgf[F017454]
468	T	P	Lab	100628_akimura_pOVCAR3_3.mgf[F017459]
468	T	P	Paper	Sci Signal 2011, 4(179), rs5

Protein Sequence
MSGASSEQN NNSYETKTPN LRMSEKKCSW ASYMTNSPTL IVMIGLPARG KTYVSKLTR YLNLWIGVPTK VFNLGVYRRE AVKSYKSYDF FRHDNEEAMK IRKQCALVAL ED VKAYLTEE NGQIAVFDAT NTRRERRDMI LNFAEQNSFK VFFVESVCDD PDVIAANILE VKVSSPDYPE RNRENVMEDF LKRIECYKVT YRPLDPDNYD KDLSFIKVIN VGQRFL VNRV QDYIQSKIVY YLMNIHVQPR TIYLCRHGES EFNLLGKIGG DSGLSVRGKQ FAQALRKFL EQEITDLKVV TSQKRTIQT AESLGVPEQ WKILNEIDAG VCEEMTYAEI EKRYPEEFAL RDQEKYLRYR PGGESYQDLV QRLEPVMEL ERQGNLVIS HQAVMRCLLA YFLDKGADEL PYLRCPLHTI FKLTPVAYGC KVETIKLNVE AVNTHRDKPT NNFPK NQTPV RMRRNSFTPL SSSNTIRRP NYSVGSRPLK PLSPLRAQDM QEGAD

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