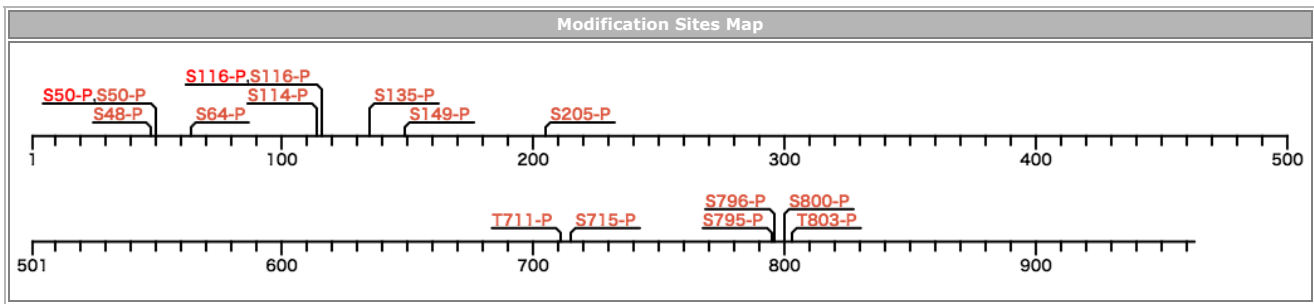


ID	Accession	GeneName	Chr.No.	Description
FGD1_HUMAN	P98174	FGD1	Xp11.22 54471887..54522599	FYVE, RhoGEF and PH domain-containing protein 1



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
50	S	P	Lab	130415_HEK_CE_tphos.mgf[F015009]
50	S	P	Lab	130415_HEK_ME_tphos.mgf[F015010]
50	S	P	Paper	Sci Signal 2011, 4(179), rs5

Protein Sequence	
MHGHRAPGGA GPSEPEHPAT NPPGAAPPAC ADSDPGASEP GLLARRGSGS ALGGPLDPQF VGPSTSLGA APGHRVLPCG PSPQHHRALR FSYHLEGSQP RPGLHQGNRI L VKSLSDPG QSLEPHPEGP QRLRSDPGPP TETPSQRPSP LKRAPGPKPQ VPPKPSYLQM PRMPPPLEPI PPPSRPLPA DPRVAKGLAP RAEASPSSAA VSSLIEKFER EPVIVA SDRP VPGSPGPPE PVMLPQPTSQ PPVPQLPEGE ASRCLFLLAP GPRDGEKVPN RDSGIDSISS PSNSEETCFV SDDGPPSHSL CPGPPALASV PVALADPHRP GSQEVSDSL E EEDDEEEEE KREIPVPLM ERQESVELTV QQKVFHIANE LLQTEKAYVS RLHLLDQVFC ARLLSEARNR SSFPADVHVG IFSNICSIYC FHQQFLPEL EKRMEEWDY PRI GDILQKL APFLKMYGEY VKNFDRVEL VNTWTERSTQ FKVIIHEVQK EEACGNLTQ HHMLEPVQRI PRYELLKDY LLKLPHGSPD SKDAQKSLEL IATAAEHSNA AIRKMER MHK LLKVYELGG EEDIVSPTKE LIKEGHILKL SAKNGTTQDR YLILFNDRL YCVPRLRLG QKFSVRARID VDGMEKESS NLNLPRTFLV SGKQRSLELQ ARTEEEKDW V QAINSTLLK HEQTLETFLK LNSTNREDED TPNSPNVDL GKRAPTPIRE KEVTMCMRCQ EPFNSITKRR HHKACGHV VCGKCEFRAR LVYDNNRSNR VCTDCYVALH GVP GSSPAC S QHTPQRRRSI LEKQASVAEE NSVICFLHY MEKGGGWKH AWFVVPENEP LVLYIYGAPQ DVKAQRLPL IGFEVGPPEA GERPDRRHVF KITQSHLSWY FSPET EELQR RWMVAVLGRAG RGDFTCPGPT LSEDREEMEA PVAALGATAE PPESPQTRDK T	

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