

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
P10586	PTPRF_HUMAN	Homo sapiens	Receptor-type tyrosine-protein phosphatase F	5.558779	NaN	S1305	35138101;34019948;33214551	MAPEPAPGRMTMVPLVPALVMLGLVA GAHGDSKPVFIKVPEDQTGLSGGVA SFVCQATGEPKPRITWMKKGKKVSS QRFEVIEFDDGAGSVLRIQPLRVQRD EAIYECTATNSLGEINTSAKLSVLEE EQLPPGFPSIDMGPQLKVVEKARTA TMLCAAGGNPDPEISWFKDFLPVDP ATSNGRIKQLRSGALQIESSESDQG KYECVATNSAGTRYSAPANLYVRVR RVAPRFSIPPSSQEVMPGGSVNLTC VAVGAPMPYVKWMMGAEELTKEDE MPVGRNVLELSNVVRSANYTCVAIS SLGMIEATAQVTVKALPKPIDLVVT ETTATSVTLTWDSGNSEPVTYYGIQY RAAGTEGPFQEVGDVATTRYSIGGLS PFSEYAFRVLAVNSIGRGPPEAVRA RTGEQAPSSPPRRVQARMLSASTML VQWEPPEEPNGLVRGYRVYYTPDSR RPPNAWHKHNTDAGLLTTVGSLLPG ITYSLRVLAFTAVGDGPPSPTIQVKTQ QGVPAQPADFQAEVESDTRIQLSWL LPPQERIIMYELVYWAAEDEDQQHK VTFDPTSSYTLEDLKPDTLYRFQLAA RSDMGVGVFTPTIEARTAQSTPSAPP QKVMCVSMGSTTVRVSWVPPADS RNGVITQYSVAYEAVDGEDRGRHVV DGISREHSSWDLVGLEKWTEYRVW VRAHTDVGPGPESSPVLVRTDEDVP SGPPRKVEVEPLNSTAVHVYWKLPV PSKQHGQIRGYQVTVRLENGEPRG LPPIQDVMLAEAQRPEESEDYETTI SGLTPETYSVTVAAYTTKGDGARSK PKIVTTTGAVPGRPTMMISTTAMNT ALLQWHPPKELPGELLYRLQYCRA DEARPNTIDFGKDDQHFTVTGLHKG TTYIFRLAAKNRAGLGEEFEKEIRTP EDLPSGFQNLHVTGLTTSTTELAW DPPVLAERNGRISYTVVFRDINSQQ ELQNITTDTRFTLTGLKPDTTYDIKV RAWTSKSGPLSPSIQSRTMPVEQV FAKNFRVAAAMKTSVLLSWEVPDSY KSAVPFKILYNGQSVEVDGHSMRKL IADLQPNTEYSFVLMNRGSSAGGLQ HLVSIRTAPDLLPHKPLPASAYIEDG RFDLSMPHVQDPSLVRWFYIVVVPI DRVGGSMMLTPRWSTPEELELDELLE AIEQGEEQRRRRRQAERLKPYVAA QLDVLPETFTLGDKKNYRGFYNRPL SPDLSYQCFVLASLKEPMDQKRYAS

SPYSDEIVVQVTPAQQQEPEMLWV  
TGPVLAVILILIVIAILLFKRKRTHSPS  
SKDEQSIGLKDSL LAHSSDPVEMRR  
LNYQTPGMRDHPPITDLADNIERL  
KANDGLKFSQEYESIDPGQQFTWEN  
SNLEVNKPKNRYANVIAYDHSRVILT  
SIDGVPGSDYINANYIDGYRKQNAYI  
ATQGPLPETMGDFWRMVWEQRTAT  
VMMTRLEEKSRVKCDQYWPARGT  
ETCGLIQVTLTDTVELATYTVRTFAL  
HKSGSSEKRELRFQFMAWPDHGV  
PEYTPILAFRRVKACNPLDAGPMV  
VHCSAGVGR TGCFIVIDAMLERMKH  
EKTVDIYGHVTCMRSQRNYMVQTE  
DQYVFIHEALLEAATCGHTEVPARN  
LYAHIQKLGQVPPGESVTAMELEFK  
LLASSKAHTSRFISANLPCNKFKNRL  
VNIMPYELTRVCLQPIRGVEGSDYIN  
ASF LDGYRQQKAYIATQGPLAESTED  
FWRMLWEHNSTIIVMLTKLREMGR  
EKCHQYWPAERSARYQYFVVDPMA  
EYNMPQYILREFKVT DARDGQSRTI  
RQFQFTDWPEQGVPKTGEGFIDFIG  
QVHKTKEQFGQDGPITVHCSAGVGR  
TGVFITLSIVLERMRYEGVDMFQTV  
KTLRTQR PAMVQTEDQYQLCYRAAL  
EYLG SFDHYAT