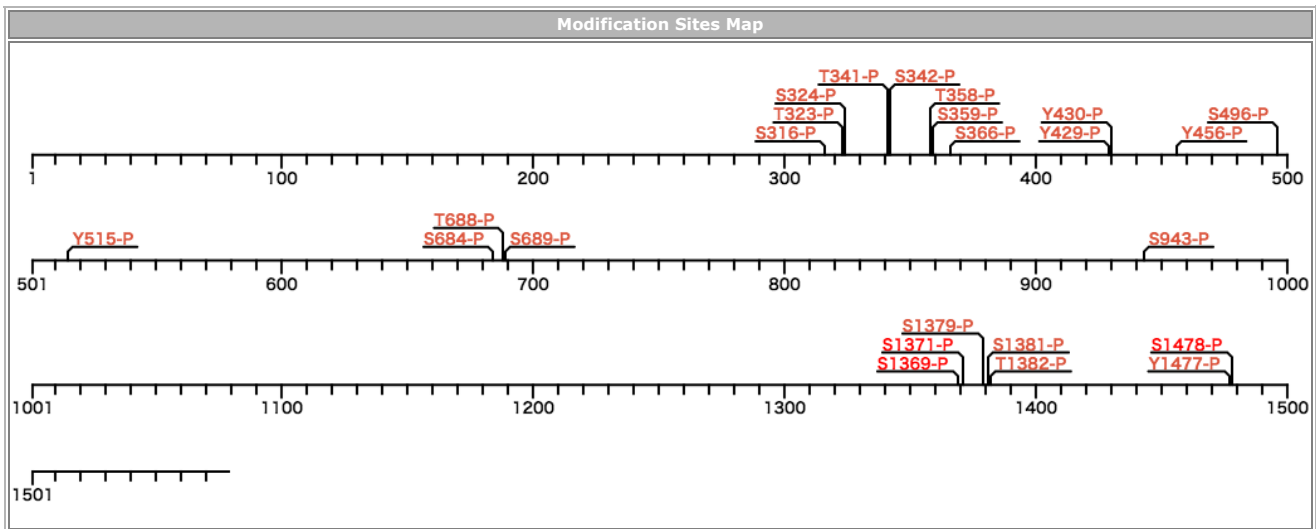


ID	Accession	GeneName	Chr.No.	Description
DNMBP_HUMAN	Q6XZF7	DNMBP	10q24.2   101635334..101769676	Dynamamin-binding protein



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
1478	S	P	Lab	100626-nagata-pRMG1-10mg.mgf[F015003]
1478	S	P	Lab	100626-nagata-pMCAS-10mg.mgf[F014995]

**Protein Sequence**

MEAGSVVRAI FDFCPSVSEE LPLFVGDII E VLAVVDEFWL LGKKEDVTGQ FPSSFVEIVT IPSLKEGERL FVCICEFTSQ ELDNPLHRG DLVILDGIPT AGWLQGRSCW GARG  
 FFSSC VRELCLSSQS RQWHSQALF QIPEYSMGQA RALMGLSAQL DEELDFREGD VITIIGVPEP GWFEGELEGR RGIFPEGFVE LLGPLRTVDE SVSSGNQDDC IVNGEV  
 DTPV GEEIIGPDED EEEPGTYGVA LYRFQALEPN ELDFEVGDKI RILATLEDGW LEGSLKGRGT IFPYRFVKLC PDTRVEETMA LPQEGSLARI PETSLDCLN TLGVEEQRHE  
 TSDHEAEEPDI CIIEAP TSP LGHLT SEYDT DRNSYQDEDT AGGPPRSPGV EWEMPLATDS PTSDPTEVVN GISSQPQVPF HPNLKQSQYY STVGGSHPHS EQYPDLLPLE AR  
 TRDYASLP PKRMYSQ LKT LQKPVLP L YR GSSVSASRVV KPRQSSQLH NLAASYTKKHH TSSVYSISER LEMKPGPQAQ GLVM EAATHS QGDGSTD L DS KLTQQLIEFE KSLA  
 GPGTEP DKILRHFSIM DFNSEKDIVR GSKLITEQE LPERRKALRP PPRPCTPVS TSPHLLVDQN LKPAPPLVVR PSRPAPLPPS AQRRTNAVSP KLLSRHRPTC ETLKEKGG  
 H MGRSLDQ TSP CPLVLVRIEE MERDLDMYSR AQEELNLMLE EKQDESSRAE TLEDLKFCE S NIESLNMELQ QLREMTLLSS QSSSLVAPSG SVSAENPEQR MLEKRAKVIE E  
 LLQTERDYI RDLEMCIERI M VPMQQAQVP NIDFEGFLGN MQMVIKVSQ LLAAL EISDA VGPVFLGHRD ELEGTYKIYC QNHDEAIAL L EIEKDEKIQ KHLQDSLADL KSLYN  
 EWGCT NYINLGSFLI KPVQRVMRYP LLLMELLNST PE SHDPKVPL TNAVLA VKEI NVNINEYKRR KDLVLKYRKG DEDSLMEKIS KLNHSI I KK SNRVSSH LKH LTGFAPQIKD  
 EVFEETKFN RMQERLIKSF IRDLSLYLQH IRESACVKVV AAVSMWDVCM ERGHRDLEQF ERVHRYISDQ LFTNFKERTE RLVISPLNQL LSMFTGPHKL VQKRFDKLLD FYN  
 CTERAEK LKDKK TLEEL QSARNNYEAL NAQLLDEL PK FHQYAQGLFT NCVHGYAEAH CDFVHQALEQ LKPLLSLLKV AGREGNLIAT FHEEHSRVLQ QLQVFTFFPE SLPATKK  
 PFE RKTIDRQSAR KPLLGLPSYM LQSEELRASL LARYPPEKLF QAERNFNAAQ DLDVSLLEGD LVGVIKK KDP MGSQNRWLID NGVTKGFVYS SFLKPYNPRR SHSDASVGS  
 H SSTESEHGS S SPRFRQNSG STLTFNPSM AVSFTSGSQ KQPQDASPPP KECQGTLSA SLNPSNSESS PSRCPSDPDS TSQPRSGDSA DVARVVKQPT ATPRSYRNFR  
 HPEIVGYSVP GRNGQSQDLV KGCARTAQAP EDRSTEPDGS EAEGNQVYFA VYTFKARNPN ELSVSANQKL KILEFKDVTG NTEWWLAEVN GKKGYVPSNY IRKTEYT

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