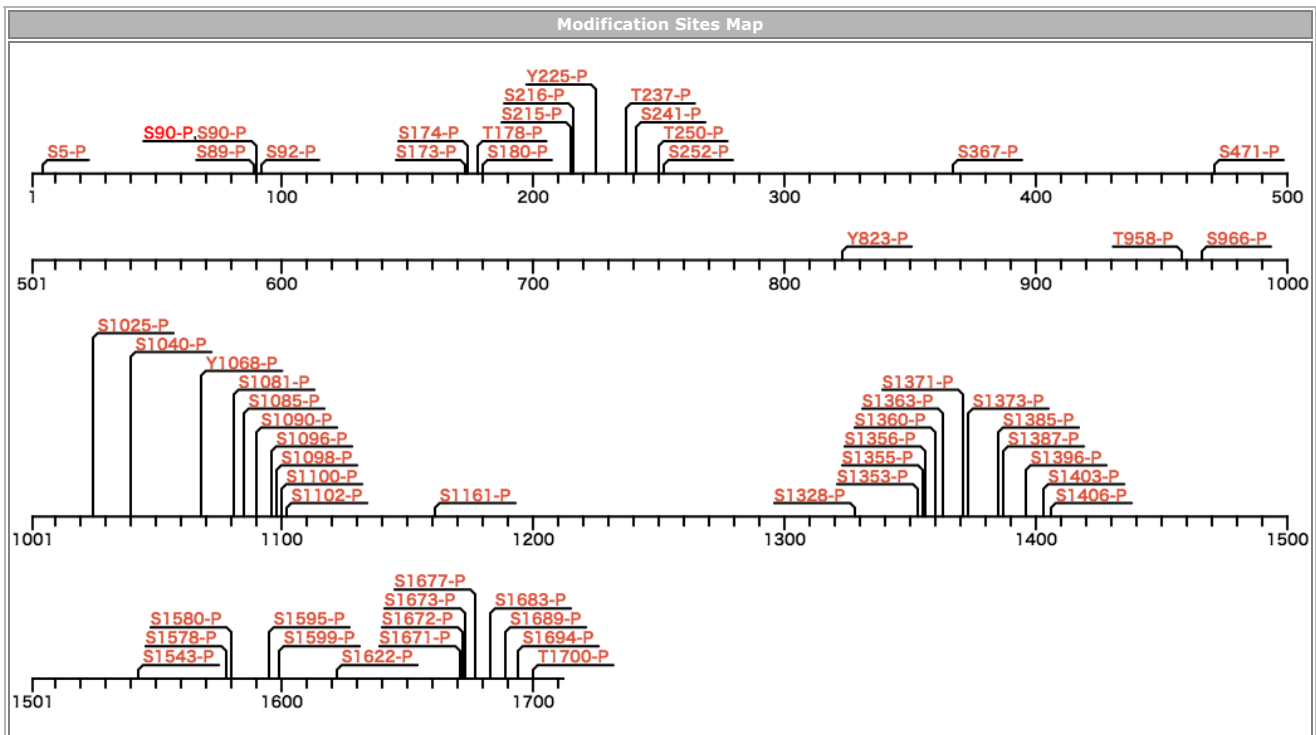


ID	Accession	GeneName	Chr.No.	Description
CHD1_HUMAN	O14646	CHD1	5q15 98190908..98262240	Chromodomain-helicase-DNA-binding protein 1



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
90	S	P	Lab	140326_OVISE_NES_tita_3_.mgf[F017523]
90	S	P	Paper	Cancer Res 2009, 69(6), 2663-2668
90	S	P	Paper	Cell Rep 2014, 8(5), 1583-1594
90	S	P	Paper	Sci Signal 2009, 2(84), ra46
90	S	P	Paper	Sci Signal 2010, 3(104), ra3
90	S	P	Paper	Science 2011, 332(6034) 1317-1322

Protein Sequence

MNGH SDEESV RNSSGESSQS DDDSGSASGS GSGSSSGSSS DGSSSQSGSS DSDSGSESGS QSESESDTSR ENKVQAKPPK VDGAEFWK SS P SILAVQRSA ILKKQQQQ
 QQ QQHQASSNS GSEEDSSSE DSDSSSEVKK RKKHKDEDWG MSGSGSPSQS GSDSESEER EKSSCDETES DYEPKNKVK RKPQNRSKK NGKKILGQKK RQID S
 SEEDD DEED YNDKR SSRQATVNV SYKEDEEMK T DSDLLLEVCG EDVPQPEEE FETIERFMD RIGRKGATGA TTTIYAVEAD GPNAGFEKN KEPGEIQYLI KWKGWS
 HIHN TWETEELKQ QNVRGMKKLD NYKKKQETK RWLKNASPED VEYNCQQL TDDLHKYQI VERIAHSNQ KSAAGYPDY CKWQGLPYSE CSWEDGALIS KKFQAC
 IDEY FSRNQSKTTP FKDCKVLKQR PRFVALKKQP SYIGGHEGLE LRDYQLNGLN WLAHSWCKGN SCILADEMGL GKTITQISFL NYLFHEHQY GPFLLVVPLS TLTSWQREI
 Q TWASQMNAV YLGDINSRNM IRTHEWTHHQ TKRLKFNILL TTYEILLKDK AFLGGLNWAF IGVDEAHLK NDDSLLYKTL IDFKSNHRL ITGTPLQNSL KELWSLLHFI MP
 EKFSWED FEEHGGKRE YGYASLHKEL EPFLRRVKK DVEKSLPAK EQILRMEMSA LQKQYKWL TRNYKALSKG SKGSTSGFLN IMELKCCN HCYLIKPPDN NEFYN
 KQEA QHLIRSSGK ILLDKLLRL RERGNRVLF SQMVRMLDIL AEYLKYRQFP FQRLDGSIK ELRKQALDHF NAEGSEDFCF LLSTRAGGLG INLASADTV IFDSWNPQ
 N DLQAQARAH IGQKKQVNIY RLVTKGSVEE DILERAKKKM VLDHLVIQRM DTTGKTVLHT GSAPSS TPF NKEEL SAILK FGAELFKPE EGEEQEPQEM DIDEILKRAE TH
 ENEPGLT VGDILLSQFK VANF SNMDED DIELEPERNS KNWEEIIPED QRRRLEEEER QKELEEYML PRMRNCAKQI SFNGSEGRRS RSRRYSGSDS DSISEGKRPK KRGR
 PRTIPR ENIKGFSDAE IRRFIKSYK FGGLERLDA IARDAELVDK SETDLRRLGE LVHNGCIKAL KDSSSGTERT GGRLGKVKGP TFRISGVQVN AKLVISHEEE LIPLHKSIPS
 DPEERKQYTI PCHTKAAHFD IDWKGEDDSN LLIGIYEGY GSWEMIKMDP DLSLTHKILP DDPDKKPAK QLQTRADYLI KLLSRDLAKK EALSAGS SSK RRKARAKNNK AM
 KSIKVKEE IKSDSSPLS EKSDDDDKL SESKSDGRER SKKSVDAP VHITASGEPV PISEESEL QKTFICKER MRPVKAALKQ LDRPEKGLSE REQLEHTRQC LIKIGD
 HITE CLKYETNPQ IKQWRKNLWI FVSKFTEFDA RKLHKLYKHA IKKRQESQSN SDQNSLNPV VIRNPDVERL KENTNHDDSS RDSYSSDRHL TQYHDHKKDR HQGDSY
 KKSD SRKRPYSFS NGKDRDWDH YKQDSRYSD REKRLKDDH RSRDHRSNLE GSKLDRSHSD HRSHSDHRLH SDHRSSSEYT HHKSSRDYRY HSDWQMDHRA SSS
 GPRSPLD QRS PYGSRSP FEHSVEHKST PEHTWSSRKT

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