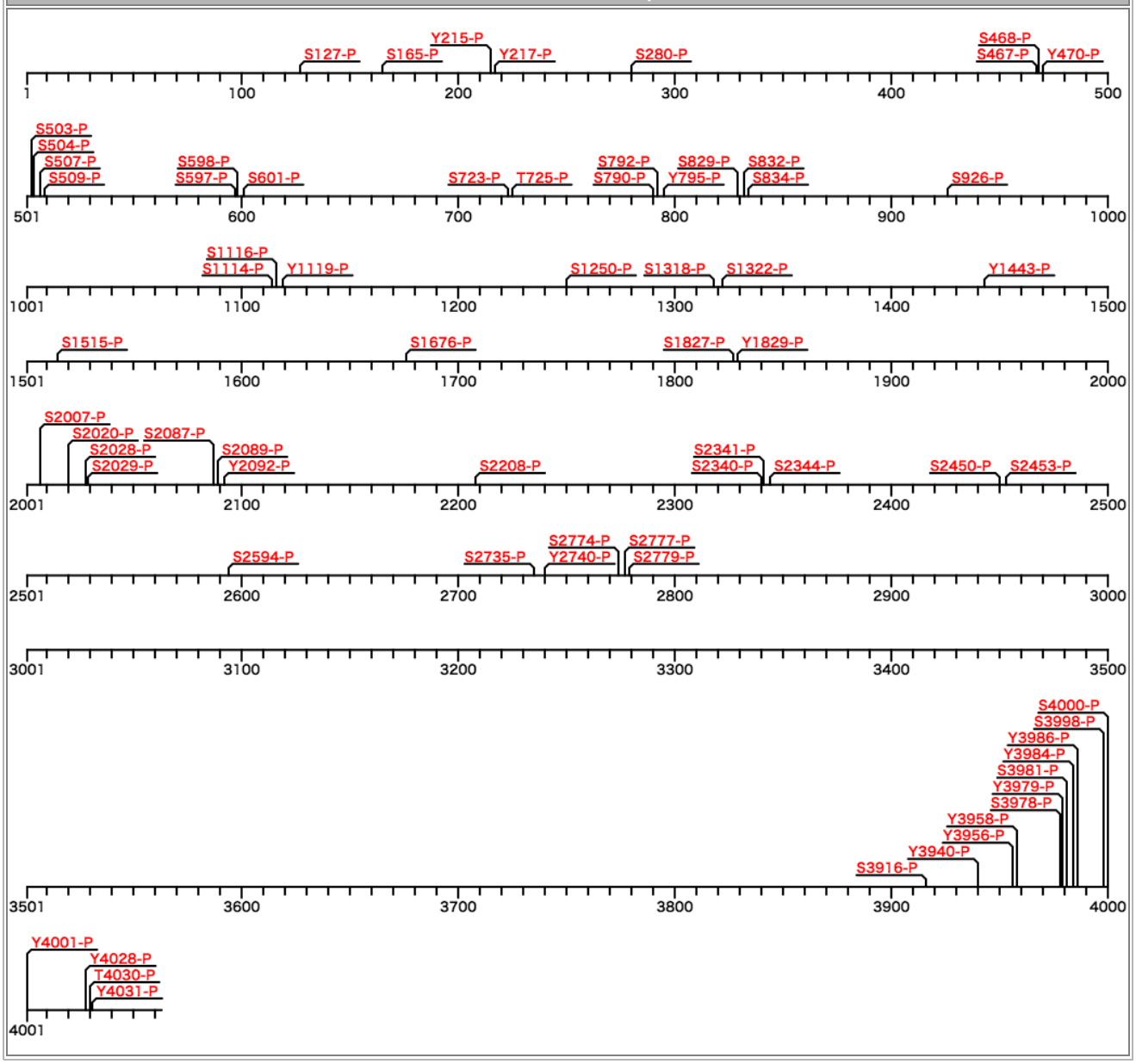
ID	Accession	GeneName	Chr.No.		Description
FILA_HUMAN	P20930	FLG	1q21.3	152274651..152297679	Filaggrin

Modification Sites Map



Click a modification site to display the information in detail.

Site no	Amino acid	Type	Division	Detail
4031	Y	P	Lab	100407-nagata-pOVCAR3-10mg-MGF.mgf[F014985]
4031	Y	P	Lab	100407-nagata-pOVHO-10mg.mgf[F014986]
4031	Y	P	Lab	100407-nagata-pOVISE-10mg.mgf[F014987]
4031	Y	P	Lab	100407-nagata-pOVKATE-10mg.mgf[F014988]
4031	Y	P	Lab	100626-nagata-pOVCAR3-10mg.mgf[F014996]
4031	Y	P	Lab	100626-nagata-pOVHO-10mg.mgf[F014997]
4031	Y	P	Lab	100626-nagata-pOVKATE-10mg.mgf[F014999]

Protein Sequence

MSTLLENIFA IINLFKQYSK KDKNTDTLSK KELKELLEKE FRQILKNPDD PDMVDVFMDH LDIDHNKKID FTEFLLMVFK LAQAYYESTR KENLPISGHK HRKHSHHDKH EDNK QEENKE NRKRPSSLER RNNRKGNKGR SKSPRETGGK RHESSSEKKE RKGYSPTHRE EEYGKNHHNS SKKEKNKTEN TRLGDNRKRL SERLEEKEDN EEGVYDYENT GRMT QKWIQS GHIATYYTIQ DEAYDTTDSL LEENKIYERS RSSDGKSSSQ VNRSRHENTS QVPLQESRTR KRRGSRVSQD RDSEGHSEDS ERHSGSASRN HHGSAWEQSR DGS RHPRSHD EDRASHGHSA DSSRQSGTRH AETSSRGQTA SSHEQARSSP GERHGSGHQQ SADSSRHSAT GRGQASSAVS DRGHRGSSGS QASDSEGHSE NSDTQSVSGH GKAGLRQQSH QESTRGRSGE RSGRSGSSLY QVSTHEQPDS AHGRTGTSTG GRQGSHHEQA RDSSRHSASQ EGQDTIRGHP GSSRGGRQGS HHEQSVNRSG HSGSHHS HTT SQGRSDASHG QSGSRSASRQ TRNEEQSGDG TRHSGSRHHE ASSQADSSRH SQVGQGQSSG PRTSRNQGSS VSQDSDSQGH SEDSERWSGS ASRNHHGSAQ EQ SRDGSRHP RSHHEDRAGH GHSADSSRKS GTRHTQNSSS GQAASSHEQA RSSAGERHGS RHQLQSADSS RHSGTGHGQA SSAVRDSGHR GSSGSQATDS EGHSEDSD TQ SVSGHGQAGH HQQSHQESAR DRSGERSRRS GSFLYQVSTH KQSESSHGWT GPSTGVRQGS HHEQARDNSR HSASQDGQDT IRGHPGSSRR GRQGSHHEQS VDRS GHSGSH HSHTTSQGRS DASRGQSGSR SASRTTRNEE QSRDGSRHSG SRHHEASSHA DISRHSQAGQ GQSEGSRTSR RQGSSVSQDS DSEGHSEDSE RWSGSASRNH RGSAQEQSRH GSRHPRSHHE DRAGHGHSAD SSRQSGTPHA ETSSGGQAAS SHEQARSSPG ERHGSRHQQS ADSSRHSGIP RRQASSAVRD SGHWGSSGSQ ASDSEG

HSEE SDTQSVSGHG QDGPHQQSHQ ESARDWSGGR SGRSGSFIYQ VSTHEQSESA HGRTRTSTGR RQGSHHEQAR DSSRHSASQE GQDTIRAHPG SRRGGRQGSH HE
QSVDRSGH SGSHHSHTTS QGRSDASHGQ SGSRSASRQT RKDKQSGDGS RHSGSRHHEA ASWADSSRHS QVGQEQSSGS RTSRHQGSSV SQDSDSERHS DDSERLSG
SA SRNHHGSSRE QSRDGSRHPG FHQEDRASHG HSADSSRQSG THHTESSSHG QAVSSHEQAR SSPGERHGSR HQQSADSSRH SGIGHRQASS AVRDSGHRGS SGSQ
VTNSEG HSEDSDTQSV SAHGQAGPHQ QSHKESARGQ SGESSGRSRS FLYQVSSHEQ SESTHGQTAP STGGRQGSRH EQARNSSRHS ASQDGQDTIR GHPGSSRGGR Q
GSYHEQSVD RSGHSGYHHS HTTPQGRSDA SHGQSGPRSA SRQTRNEEQS GDGSRHSGSR HHEPSTRAGS SRHSQVGQGE SAGSKTSRRQ GSSVSQDRDS EGHSEDSE
RR SESASRNHYG SAREQSRHGS RNPRSHQEDR ASHGHSAESS RQSGTRHAET SSGGQAASSQ EQARSSPGER HGSRHQQSAD SSTDSGTGRR QDSSVVGDSG NRGS
SGSQAS DSEGHSEESD TQSVSAHGQA GPHQQSHQES TRGQSGERSG RSGSFLYQVS THEQSESAHG RTGPSTGGRQ RSRHEQARDS SRHSASQEGQ DTIRGHPGSS R
GGRQGSHYE QSVDSSGHSG SHHSHTTSQE RSDVSRGQSG SRSVSRQTRN EKQSGDGSRH SGSRHHEASS RADSSRHSQV GQGQSSGPRT SRNQGSSVSQ DSDSQGH
SED SERWSGSASR NHLGSAWEQS RDGSRHPGSH HEDRAGHGHS ADSSRQSGTR HTESSSRGQA ASSHEQARSS AGERHGSHHQ LQSADSSRHS GIGHGQASSA VRD
SGHRGYS GSQASDSEGH SEDSDTQSVS AQGKAGPHQQ SHKESARGQS GESSGRSGSF LYQVSTHEQS ESTHGQSAPS TGGRQGSHYD QAQDSSRHSA SQEGQDTIRG
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SDSE GHSEDSERRS GSASRNHHGS AQEQSRDGSR HPRSHHEDRA GHGHSAESSR QSGTHHAENS SGGQAASSHE QARSSAGERH GSHHQQSADS SRHSGIGHGQ AS
SAVRDSGH RGSSGSQASD SEGHSEDSDT QSVSAHGQAG PHQQSHQEST RGRSAGRSGR SGSFLYQVST HEQSESAHGR TGTSTGGRQG SHHKQARDSS RHSTSQEGQ
D TIHGHPGSSS GGRQGSHYEQ LVDRSGHSGS HHSHTTSQGR SDASHGHSGS RSASRQTRND EQSGDGSRHS GSRHHEASSR ADSSGHSQVG QGQSEGPRTS RNWG
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SASQ DGQDTIRGHP GSSRGGRQGY HHEHSVDSSG HSGSHHSHTT SQGRSDASRG QSGSRSASRT TRNEEQSGDG SRHSGSRHHE ASTHADISRH SQAVQGQSEG SR
RSRRQGSS VSQDSDSEGH SEDSERWSGS ASRNHHGSAQ EQLRDGSRHP RSHQEDRAGH GHSADSSRQS GTRHTQTSSG GQAASSHEQA RSSAGERHGS HHQQSADS
SR HSGIGHGQAS SAVRDSGHRG YSGSQASDNE GHSEDSDTQS VSAHGQAGSH QQSHQESARG RSGETSGHSG SFLYQVSTHE QSESSHGWTG PSTRGRQGSR HEQA
QDSSRH SASQYGQDTI RGHPGSSRGG RQGYHHEHSV DSSGHSGSHH SHTTSQGRSD ASRGQSGSRS ASRTTRNEEQ SGDSSRHSVS RHHEASTHAD ISRHSQAVQG Q
SEGSRRSRR QGSSVSQDSD SEGHSEDSER WSGSASRNHR GSVQEQSRHG SRHPRSHHED RAGHGHSADR SRQSGTRHAE TSSGGQAASS HEQARSSPGE RHGSRHQ
QSA DSSRHSGIPR GQASSAVRDS RHWGSSGSQA SDSEGHSEES DTQSVSGHGQ AGPHQQSHQE SARDRSGGRS GRSGSFLYQV STHEQSESAH GRTRTSTGRR QGS
HHEQARD SSRHSASQEG QDTIRGHPGS SRRGRQGSHY EQSVDRSGHS GSHHSHTTSQ GRSDASRGQS GSRSASRQTR NDEQSGDGSR HSWSHHHEAS TQADSSRHS
Q SGQGQSAGPR TSRNQGSSVS QDSDSQGHSE DSERWSGSAS RNHRGSAQEQ SRDGSRHPTS HHEDRAGHGH SAESSRQSGT HHAENSSGGQ AASSHEQARS SAGE
RHGSHH QQSADSSRHS GIGHGQASSA VRDSGHRGSS GSQASDSEGH SEDSDTQSVS AHGQAGPHQQ SHQESTRGRS AGRSGRSGSF LYQVSTHEQS ESAHGRAGPS
TGGRQGSRHE QARDSSRHSA SQEGQDTIRG HPGSRRGGRQ GSYHEQSVDR SGHSGSHHSH TTSQGRSDAS HGQSGSRSAS RETRNEEQSG DGSRHSGSRH HEASTQA
DSS RHSQSGQGES AGSRRSRRQG SSVSQDSDSE AYPEDSERRS ESASRNHHGS SREQSRDGSR HPGSSHRDTA SHVQSSPVQS DSSTAKEHGH FSSLSQDSAY HSGI
QSRGSP HSSSSYHYQS EGTERQKGQS GLVWRHGSYG SADYDYGESG FRHSQHGSVS YNSNPVVFKE RSDICKASAF GKDHPRYYAT YINKDPGLCG HSSDISKQLG FSQ
SQRYYYY E

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