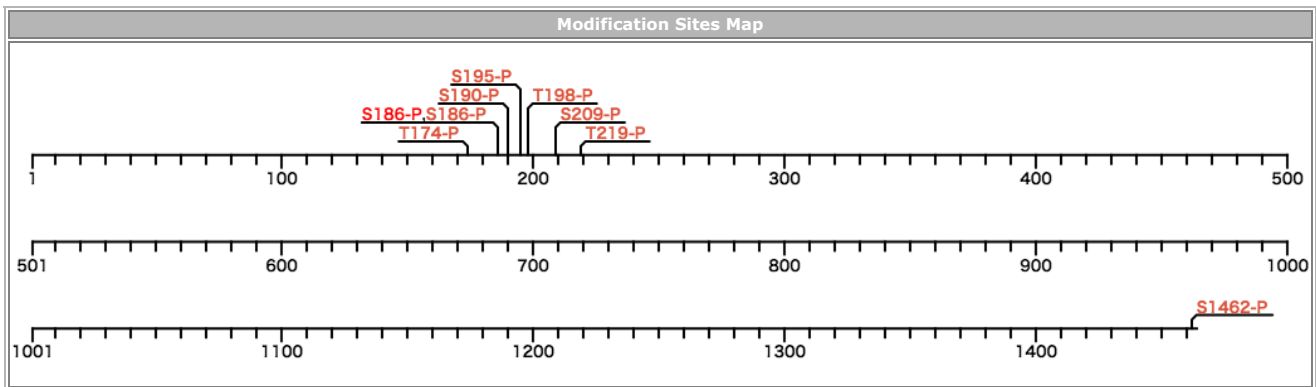


| ID | Accession | GeneName | Chr.No. | Description |
|-------------|-----------|----------|---------------------------|--|
| DPOLA_HUMAN | P09884 | POLA1 | Xp21.3 24712036..25015103 | DNA polymerase alpha catalytic subunit |



Click a modification site to display the information in detail.

| Site no | Amino acid | Type | Division | Detail |
|---------|------------|------|----------|----------------------------------|
| 186 | S | P | Lab | 130415_HEK_CE_tphos.mgf[F015009] |
| 186 | S | P | Lab | 130415_HEK_ME_tphos.mgf[F015010] |
| 186 | S | P | Paper | Sci Signal 2009, 2(84), ra46 |
| 186 | S | P | Paper | Sci Signal 2011, 4(179), rs5 |

| Protein Sequence | |
|---|--|
| MAPVHGDDSL SDGSGFVSSR ARREKSKKG RQEALERLKK AKAGEKYKYE VEDFTGVYEE VDEEQYSKLV QARQDDDWIV DDDGIGYVED GREIFDDLE DDALDADEKG KD GKARNKDK RNVKKLAVTK PNNIKSMFIA CAGKKTADKA VDLSKDGLLG DILQDLNTEP PQTTPPPVMI LKKKR SIGA S PNPFSVHTAT AVPSGKIASP VSRKEPPLTP VPLK RAEFAG DDVQVESTEE EQESGAMEFE DGD FDEPMEV EEVDLEPMAA KAWDKESPA EEVKQ EADSG KGTVS YLGSF LPDVSCWDID QEGDSSFSVQ EVQVDSHLP LVK GADEEQV FHFYWLDAYE DQYNQPGVV F LFGKVVIESA ETHVSCVMV KNIERTLYFL PREMKIDLNT GKETGTPISM KDVEEFDEK IATKYKIMKF KSKPVEKNYA FEIPDV PEKS EYLEVKYSAE MPQLPQDLKG ETFSHVFGTN TSSLEFLMN RKIKGPCWLE VKSPQLLNQP VSWCKVEAMA LKPDLVNVIK DVSPPLVVM AFMKTMQNA KNHQNEII AM AALVHHSFAL DKAAPKPPFQ SHFCVSKPK DCIFPYAFKE VIEKKNVKE VAATERTLLG FFLAKVHKID PDIIVGHNIY GFELEVLQR INVCKAPHWS KIGRLKRSNM PK LGGRSGFG ERNATCGRMI CDVEISAKEL IRCKSYHLE LVQQILKTER VVIPMENIQN MYSESSQLLY LLEHTWKDAK FILQIMCELN VLPLALQITN IAGNIMSRTL MGRSE RNEF LLLHAFYENN YIVPDKQIFR KPQKQLGDED EEIDGDTNKY KGRKKAAYA GGLVLPKVG FYDKFILLD FNSLYPSIIQ EFNICFTTVQ RVASEAQKVT EDGEQEIQPE LPDPSLEMG I LPREIRKLV E RRRKQVQLMK QDNLNPD LIL QYDIRQKALK LTANS MYGCL GFSYSRFYAK PLAALV TYKG REILMHTKEM VQKMNLEVIY GDTDSIMINT NSTN LEEVFK LGNKVKSEVN KLYKLEIDI DGVFKSLLL KKKKYAALVV EPTSDGNYVT KQELKGLDIV RRDWCDLAKD TGNFVIGQIL SDQSRDTIVE NIQKRLIEIG ENVLNGSVP V SQFEINKALT KDPQDYPDKK SLPHVHVALW INSQGRKVK AGDTSVYVIC QDGSNLTASQ RAYAPEQLQK QDNLITDQY YLAQQIHPVV ARICEPIDGI DAVLIATWLG L DPTQFRVHH YHKDEENDAL LGGPAQLTDE EKYRDCERFK CPCPTCGTEN IYDNVFDGSG TDMEPSLYRC SNIDCKASPL TFTVQLSNKL IMDIRRFIKK YYDGLICEE PTCR NRTRHL PLQFSRTGPL CPACMKATLQ PEYSKSLYT QLCFYRYIFD ACALEKLT DHEKDKLKKQ FFTPKVLQDY RKLKNTAEQF LSRSGYSEVN LSKLFAGCAV KS | |

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