

MASCOT Search Results

Protein View: Q02880

DNA topoisomerase 2-beta OS=Homo sapiens OX=9606 GN=TOP2B PE=1 SV=3

Database: Uniprot_Proteome_Human
Score: 19255
Monoisotopic mass (M_r): 184122
Calculated pI: 8.14

Sequence similarity is available as [an NCBI BLAST search of Q02880 against nr.](#)

Search parameters

MS data file: File Name: Z:\SN22\SN221364_deTOP2B_Erk2_lul.raw; File Path: ; File Time: 3/1/2023 12:45:59 PM; File Size: 347857146 [Byte]
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: **Carbamidomethyl (C)**
Variable modifications: **Acetyl (Protein N-term), Oxidation (M), Phospho (ST), Phospho (Y)**

Protein sequence coverage: 62%

Matched peptides shown in **bold red**.

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1 MAKSGGCGAG AGVGGGNGAL TWVTLFDQNN AAKKEESETA NKNDSSKKLS
51 VERVYQKKTQ LEHILLRPDT YIGSVEPLTQ FMWVYDEDVG MNCREVTFVFP
101 GLYKIFDEIL VNAADNKQRD KNMTCIKVSI DPESNIISIW NNGKGIPVVE
151 HKVEKVVYVPA LIFGQLLTSS NYDDDEKKVT GGRNGYGAKL CNIFSTKFTV
201 ETACKEYKHS FKQTWMNNM KTSEAKIKHF DGEDYTCITF QPDLSKFKME
251 KLDKDIVALM TRRAYDLAS CRGVKVMFNG KKLPVNGFRS YVDLYVKDKL
301 DETGVALKVI HELANERWDV CLTLSEKGFQ QISFVNSIAT TKGGRHVDYV
351 VDQVVGLKIE VVKKKNKAGV SVKPFQVKNH IWVFNCLIE NPTFDSQTKE
401 NMTLQPKSFG SKCQLSEKFF KAASNCGIVE SILNWVKFKA QTQLNKKCSS
451 VKYSKIKGIP KLDDANDAGG KHSLECTLIL TEGDSAKSLA VSGLGVIGRD
501 RYGVFPLRKG ILNVREASHK QIMENAEINN IIKIVGLQYK KSYYDAESLK
551 TLRYGKIMIM TDQDQDQSHI KGLLINFIIH NWPSLLKHGF LEEFITPIVK
601 ASKNKQELSF YSIPEFDEWK KHIENQKAWK IKYYKGLGTS TAKEAKEYFA
651 DMERHRILFR YAGEPDDAAI TLAFSKKKID DRKEWLTNFM EDRRQRRLHG
701 LPEQFLYGTA TKHLTYNDFI NKELILFSNS DNERSIPSLV DGFKPGQRKV
751 LFTCFKRNDK REVKVAQLAG SVAEMSAYHH GEQALMMTIV NLAQNFEVGSN
801 NINLLQPIGQ FGTRLHGKGD AASPRYIFTM LSTLARLLFP AVDDNLLKFL
851 YDDNQRVEPE WYIPIIPMVL INGAEGIGTG WACKLPNYDA REIVNNVRRM
901 LDGLDPHML PNYKNFKGTI QELGQNYAV SGEIFVVDRN TVEITELPVR
951 TWTQVYKEQV LEPMLNGTDK TPALISDYKE YHTDTTVKFV VKMTEEKLAQ
1001 AEAAGLHKVF KLQTTLTCSN MVLFDMHGCL KKYETVQDIL KEFFDLRLSY
1051 YGLRKEWLVG MLGAESTKLN NQARFILEKI QGKITIENRS KKDLIQMLVQ
1101 RGYESDPVKA WKEAQEKAAE EDETQNQHDD SSSDSGTSPG PDFNYILNMS
1151 LWSLTKEKVE ELIKQRDAKG REVNDLKRKS PSDLWKEDLA AFVEELDQVE
1201 SQEREDVLAG MSGKAIKGKV GKPKVKLQQL EETMPSPYGR RIIPEITAMK
1251 ADASKKLLKK KKGDLDTAAV KVEFDEEFSG APVEGAGEEA LTPSVPINKG
1301 PKPKREKKEP GTRVRKTPTS SGKPSAKVKV KRNPSWDES KESDLEETE
1351 PVVIPRDSLL RRAAAERPKY TDFSEEEEDD DADDDDDNN DLEELVKAS
1401 PITNDGEDEF VPSDGLDKDE YTFSPGSKA TPEKSLHDKK SQDFGNLFSF
1451 PSYSQKSEDD SAKFSNEED SASVFSPSFG LKQTDKVPK TVAACKGKPS
1501 SDTVPKPKRA PKQKVVVEAV NSDSDSEFGI PKKTTTPKGG GRGAKKRRAS
1551 SENEGDIYNP GRKTSKTSK KPKKTSFDQD SDVDIFPSDF PTEPPSLRPT
1601 GRARKEVKYF AESDEEEDDV DFAMFN
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Unformatted sequence string: **1626 residues** (for pasting into other applications).

Sort by residue number increasing mass decreasing mass
Show matched peptides only predicted peptides also

Query	Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Score	Expect	Rank	U	Peptide
1755	34 - 42	518.2515	1034.4884	1034.4880	0.46	1	37	0.012	1	U	K.KEESETANK.N
6141	34 - 47	522.9126	1565.7159	1565.7169	-0.62	2	24	0.02	1	U	K.KEESETANKNDSSK.K
6142	34 - 47	783.8665	1565.7184	1565.7169	0.96	2	55	4.1e-05	1	U	K.KEESETANKNDSSK.K
6143	34 - 47	783.8665	1565.7184	1565.7169	0.96	2	54	2.6e-05	1	U	K.KEESETANKNDSSK.K
7142	34 - 48	565.6111	1693.8114	1693.8118	-0.27	3	25	0.017	1	U	K.KEESETANKNDSSK.L
7143	34 - 48	565.6115	1693.8127	1693.8118	0.51	3	34	0.0022	1	U	K.KEESETANKNDSSK.L
2777	95 - 104	576.8185	1151.6225	1151.6227	-0.15	0	14	0.045	1	R	EVTFPVGLYK.I
2779	95 - 104	576.8187	1151.6228	1151.6227	0.11	0	18	0.026	1	R	EVTFPVGLYK.I
2780	95 - 104	576.8188	1151.6230	1151.6227	0.30	0	19	0.026	1	R	EVTFPVGLYK.I
2781	95 - 104	576.8188	1151.6230	1151.6227	0.32	0	21	0.018	1	R	EVTFPVGLYK.I
5070	105 - 117	487.9233	1460.7482	1460.7511	-2.00	0	30	0.005	1	K	IFDEILVNAADNK.Q
5071	105 - 117	731.3821	1460.7496	1460.7511	-0.98	0	50	0.00025	1	K	IFDEILVNAADNK.Q
5072	105 - 117	487.9240	1460.7502	1460.7511	-0.62	0	46	0.00075	1	K	IFDEILVNAADNK.Q
5073	105 - 117	731.3824	1460.7502	1460.7511	-0.61	0	51	0.00011	1	K	IFDEILVNAADNK.Q
5075	105 - 117	731.3824	1460.7503	1460.7511	-0.56	0	68	3.1e-06	1	K	IFDEILVNAADNK.Q

Query	Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M Score	Expect	Rank	U	Peptide
<input checked="" type="checkbox"/> 9741	1609 - 1626	1094.9130	2187.8115	2187.8103	0.55	0	27	0.0035	1	U K.YFAESDEEEDDVFAMFN.- + Oxidation (M)

