

MATRIX SCIENCE MASCOT Search Results

Protein View: ENPL_HUMAN

Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1

Database: SwissProt
Score: 71
Expect: 0.0015
Monoisotopic mass (M_r): 92696
Calculated pI: 4.76
Taxonomy: Homo sapiens

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

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Mass values searched: 12
Mass values matched: 9

Protein sequence coverage: 9%

Matched peptides shown in **bold red**.

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1 MRALWVLGLC CVLLTFGSVR ADDEVDVDGT VEEDLGKSRE GSRTDDEVVQ
51 REEEAIQLDG LNASQIRELR EKSEKFAFQA EVNRMMKLII NSLYKNKEIF
101 LRELISNASD ALDKIRLISL TDENALSGNE ELTVKIKCDK EKNLLHVTDT
151 GVGMTR EELV KNLGTIAKSG TSEFLNKMTE AQEDGQSTSE LIGQFGVGFY
201 SAFLVADKVI VTSKHNDTQ HIWESDSNEF SVIADPRGNT LGRGTTITLV
251 LKEEASDYLE LDTIKNLVKK YSQFINFPIY VWSSKTETVE EPMEEEEAAK
301 EEKEESDDEA AVEEEEEEEK PKTKKVEKTV WDWELMNDIK PIWQRPSKEV
351 EEDEYKAFYK SFSKESDDPM AYIHFTAEGE VTFKSILFVP TSAPRGLFDE
401 YGSKKSDYIK LYVRRVFITD DFHDMMPKYL NFVKGVDSD DLPLNVSRET
451 LQQHKLLKVI RKKLVRKTL DMIKKIADDKY NDTFWKEFGT NIKLGVIEDH
501 SNRTRLAKLL RFQSSHHPTD ITSLDQYVER MKEKQDKIYF MAGSSRKEAE
551 SSPFVERLLK KGYEVIYLTE PVDEYCIQAL PEFDGKRFQN VAKEGVKFDE
601 SEKTESREA VEKEFEPLLN WMKDKALKDK IEKAVVSQRL TESPCALVAS
651 QYGWSGNMER IMKAQAYQTG KDISTNYYAS QKKTFEINPR HPLIRDMLRR
701 IKEDEDDKTV LDLAVVLFET ATLRSGYLLP DTKAYGDRIE RMLRLSLNID
751 PDAKVEEEPE EEPEETAEDT TEDTEQDEDE EMDVGTDEEE ETAKESTAEK
801 DEL

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Unformatted sequence string: **803 residues** (for pasting into other applications).

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