

Peptidyl-prolyl cis-trans isomerase A Recombinant Protein | PPIA recombinant protein

Recombinant Human Peptidyl-prolyl cis-trans isomerase A

CATALOG # AAA81588	HOST E Coli or Yeast or Baculovirus or Mammalian Cell
------------------------------	---

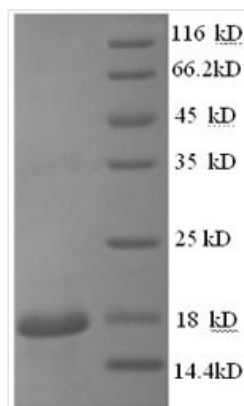
PRODUCT SYNONYMS

Peptidyl-prolyl cis-trans isomerase A; Recombinant Human Peptidyl-prolyl cis-trans isomerase A; Cyclophilin A; Cyclosporin A-binding protein; Rotamase A; PPIA recombinant protein

PRODUCT SPECIFICATIONS

Host	E Coli or Yeast or Baculovirus or Mammalian Cell
Purity/Purification	Greater or equal to 85% purity as determined by SDS-PAGE.
Form/Format	Lyophilized or liquid (Format to be determined during the manufacturing process)
Sequence Positions	2-165aa; Full Length of Mature Protein
Sequence	VNPTVFFDIA VDGEPLGRVS FELFADKVPK TAENFRALST GEKGFGYKGS CFHRIIPGFM CQGGDFTRHN GTGGKSIYGE KFEDENFILK HTGPGILSMA NAGPNTNGSQ FFICTAKTEW LDGKHVVFGK VKEGMNIVEA MERFGSRNGK TSKKITIADC GQLE
Preparation and Storage	Store at -20 degree C, for extended storage, conserve at -20 degree C or -80 degree C.

IMAGES



SDS-PAGE

ADDITIONAL INFORMATION

Related Product Information for PPIA recombinant protein	PPIases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides.
Product Categories/Family for PPIA recombinant protein	Immunology

References

Complementary DNA for human T-cell cyclophilin.Haendler B., Hofer-Warbinek R., Hofer E.EMBO J. 6:947-950(1987) Characterization of the human cyclophilin gene and of related processed pseudogenes.Haendler B., Hofer E.Eur. J. Biochem. 190:477-482(1990) Complete sequencing and characterization of 21,243 full-length human cDNAs.Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.Nat. Genet. 36:40-45(2004) Lys-N and trypsin cover complementary parts of the phosphoproteome in a refined SCX-based approach.Gauci S., Helbig A.O., Slijper M., Krijgsveld J., Heck A.J., Mohammed S.Anal. Chem. 81:4493-4501(2009) Lysine acetylation targets protein complexes and co-regulates major cellular functions.Choudhary C., Kumar C., Gnad F., Nielsen M.L., Rehman M., Walther T.C., Olsen J.V., Mann M.Science 325:834-840(2009) Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis.Olsen J.V., Vermeulen M., Santamaria A., Kumar C., Miller M.L., Jensen L.J., Gnad F., Cox J., Jensen T.S., Nigg E.A., Brunak S., Mann M.Sci. Signal. 3:RA3-RA3(2010) Initial characterization of the human central proteome.Burkard T.R., Planyavsky M., Kaupe I., Breitwieser F.P., Buerckstuemmer T., Bennett K.L., Superti-Furga G., Colinge J.BMC Syst. Biol. 5:17-17(2011) Comparative large-scale characterisation of plant vs. mammal proteins reveals similar and idiosyncratic N-alpha acetylation features.Bienvenut W.V., Sumpton D., Martinez A., Lilla S., Espagne C., Meinel T., Giglione C.Mol. Cell. Proteomics 11:M111.015131-M111.015131(2012) N-terminal acetylome analyses and functional insights of the N-terminal acetyltransferase NatB.Van Damme P., Lasa M., Polevoda B., Gazquez C., Elosegui-Artola A., Kim D.S., De Juan-Pardo E., Demeyer K., Hole K., Larrea E., Timmerman E., Prieto J., Arnesen T., Sherman F., Gevaert K., Aldabe R.Proc. Natl. Acad. Sci. U.S.A. 109:12449-12454(2012) An enzyme assisted RP-RPLC approach for in-depth analysis of human liver phosphoproteome.Bian Y., Song C., Cheng K., Dong M., Wang F., Huang J., Sun D., Wang L., Ye M., Zou H.J. Proteomics 96:253-262(2014) Structure of human cyclophilin and its binding site for cyclosporin A determined by X-ray crystallography and NMR spectroscopy.Kallen J., Spitzfaden C., Zurini M.G.M., Wider G., Widmer H., Wuethrich K., Walkinshaw M.D.Nature 353:276-279(1991) Crystal structure of recombinant human T-cell cyclophilin A at 2.5-A resolution.Ke H., Zydowsky L.D., Liu J., Walsh C.T.Proc. Natl. Acad. Sci. U.S.A. 88:9483-9487(1991) X-ray structure of a decameric cyclophilin-cyclosporin crystal complex.Pfuegl G., Kallen J., Schirmer T., Jansonius J.N., Zurini M.G.M., Walkinshaw M.D.Nature 361:91-94(1993) X-ray structure of a monomeric cyclophilin A-cyclosporin A crystal complex at 2.1-A resolution.Mikol V., Kallen J., Pfluegl G., Walkinshaw M.D.J. Mol. Biol. 234:1119-1130(1993) Crystal structure implies that cyclophilin predominantly catalyzes the trans to cis isomerization.Zhao Y., Ke H.Biochemistry 35:7356-7361(1996) Crystal structure of cyclophilin A complexed with a binding site peptide from the HIV-1 capsid protein.Vajdos F.F., Yoo S., Houseweart M., Sundquist W.I., Hill C.P.Protein Sci. 6:2297-2307(1997) X-ray structures and analysis of 11 cyclosporin derivatives complexed with cyclophilin A.Kallen J., Mikol V., Taylor P., Walkinshaw M.D.J. Mol. Biol. 283:435-449(1998) Crystal structure of calcineurin-cyclophilin-cyclosporin shows common but distinct recognition of immunophilin-drug complexes.Huai Q., Kim H.Y., Liu Y., Zhao Y., Mondragon A., Liu J.O., Ke H.Proc. Natl. Acad. Sci. U.S.A. 99:12037-12042(2002) Crystal structure of human calcineurin complexed with cyclosporin A and human cyclophilin.Jin L., Harrison S.C.Proc. Natl. Acad. Sci. U.S.A. 99:13522-13526(2002) Solution structure of the cyclosporin A/cyclophilin complex by NMR.Theriault Y., Logan T.M., Meadows R., Yu L., Olejniczak E.T., Holzman T.F., Simmer R.L., Fesik S.W.Nature 361:88-91(1993) The NMR solution conformation of unligated human cyclophilin A.Ottiger M., Zerbe O., Guentert P., Wuethrich K.J. Mol. Biol. 272:64-81(1997) Acetylation regulates cyclophilin A catalysis, immunosuppression and HIV isomerization.Lammers M., Neumann H., Chin J.W., James L.C.Nat. Chem. Biol. 6:331-337(2010)

NCBI AND UNIPROT INFORMATION

NCBI GI #	665821274
NCBI GeneID	5478

NCBI Accession #	NP_001287910.1
NCBI GenBank Nucleotide #	NM_001300981.1
UniProt Accession #	P62937 ; P05092 ; Q3KQW3 ; Q567Q0 ; Q6IBU5 ; Q96IX3 ; Q9BRU4 ; Q9BTY9 ; Q9UC61 ; A8K220
Molecular Weight	17.9 kDa
NCBI Official Full Name	peptidyl-prolyl cis-trans isomerase A isoform 2
NCBI Official Synonym Full Names	peptidylprolyl isomerase A
NCBI Official Symbol	PPIA
NCBI Official Synonym Symbols	CYPA; CYPH; HEL-S-69p
NCBI Protein Information	peptidyl-prolyl cis-trans isomerase A
UniProt Protein Name	Peptidyl-prolyl cis-trans isomerase A
UniProt Gene Name	PPIA
UniProt Synonym Gene Names	CYPA; PPlase A
UniProt Entry Name	PPIA_HUMAN

For Research Use Only. Not for use in diagnostic or therapeutic procedures. Small volumes of product may become entrapped in the seal of the vial during shipment and storage; if necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the cap.

AAA Biotech | Tel: +1 (619) 604-9440 | Fax: +1 (619) 604-9441 | contact@aaabiotech.com
Online datasheet: <https://www.aaabiotech.com/ppia-recombinant-protein-e-coli/81588>