

Methylenetetrahydrofolate reductase Recombinant Protein | MTHFR recombinant protein

Recombinant Human Methylenetetrahydrofolate reductase

CATALOG # AAA113903	HOST E Coli or Yeast or Baculovirus or Mammalian Cell
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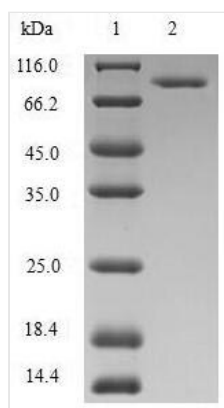
PRODUCT SYNONYMS

Methylenetetrahydrofolate reductase; Recombinant Human Methylenetetrahydrofolate reductase; MTHFR 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	1-656aa; Full Length
Sequence	MVNEARGNSS LNPCLEGSAS SGSESSKDSS RCSTPGLDPE RHERLREKMR RRLESGDKWF SLEFFPPRTA EGAVNLISRF DRMAAGGPLY IDVTWHPAGD PGSDKETSSM MIASTAVNYC GLETILHMT C CRQRLEEITG HLHKAKQLGL KNIMALRGDP IGDQWEEEEE GFNYAVDLVK HIRSEFGDYF DICVAGYPKG HPEAGSFEAD LKHLKEK VSA GADFIITQLF FEADTFFRFV KACTDMGITC PIVPGIFPIQ GYHSLRQLVK LSKLEVPQEI KDVIEPIKDN DAAIRNYGIE LAVSLCQELL ASGLVPGLHF YTLNREMATT EVLKRLGMWT EDPRRPLPWA LSAHPKRREE DVRPIFWASR PKSIIYRTQE WDEFPNGRWG NSSSPAFGEL KDYYLFY LKS KSPKEELLKM WGEELTSEES VFEVFLYLS GEPNRNGHKV TCLPWNDEPL AAETSLLEE LLRVNRQGIL TINSQPNING KPSSDPIVGW GPSGGYVFQK AYLEFFTSRE TAEALLQVLK KYELRVNYHL VNVKGENITN APELQNAV T WGIFPGREII QPTVDPVSF MFWKDEAFAL WIERWGKLYE EESPSRTIIQ YIHDNYFLVN LVDNDFPLDN CLWQVVEDTL ELLNRPTQNA RETEAP
Sequence Length	656
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 MTHFR recombinant protein	Catalyzes the conversion of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, a co-substrate for homocysteine rethylation to methionine.
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Product Categories/Family for MTHFR recombinant protein	Metabolism
References	cDNA for human methylenetetrahydrofolate reductase.Rozen R., Goyette P.Patent number WO9533054, 07-DEC-1995Gene structure of human and mouse methylenetetrahydrofolate reductase (MTHFR) .Goyette P., Pai A., Milos R., Frosst P., Tran P., Chen Z., Chan M., Rozen R.Mamm. Genome 9:652-656(1998) Revised translation initiation site of the human methylenetetrahydrofolate reductase (MTHFR) .Homberger A., Linnebank M., Winter C., Rapp B., Koch H.G.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., Nagahari 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) NIEHS SNPs programThe DNA sequence and biological annotation of human chromosome 1.Gregory S.G., Barlow K.F., McLay K.E., Kaul R., Swarbreck D., Dunham A., Scott C.E., Howe K.L., Woodfine K., Spencer C.C.A., Jones M.C., Gillson C., Searle S., Zhou Y., Kokocinski F., McDonald L., Evans R., Phillips K., Atkinson A., Cooper R., Jones C., Hall R.E., Andrews T.D., Lloyd C., Ainscough R., Almeida J.P., Ambrose K.D., Anderson F., Andrew R.W., Ashwell R.I.S., Aubin K., Babbage A.K., Bagguley C.L., Bailey J., Beasley H., Bethel G., Bird C.P., Bray-Allen S., Brown J.Y., Brown A.J., Buckley D., Burton J., Bye J., Carder C., Chapman J.C., Clark S.Y., Clarke G., Clee C., Cobley V., Collier R.E., Corby N., Coville G.J., Davies J., Deadman R., Dunn M., Earthrowl M., Ellington A.G., Errington H., Frankish A., Frankland J., French L., Garner P., Garnett J., Gay L., Ghorri M.R.J., Gibson R., Gilby L.M., Gillett W., Glithero R.J., Grafham D.V., Griffiths C., Griffiths-Jones S., Grocock R., Hammond S., Harrison E.S.I., Hart E., Haugen E., Heath P.D., Holmes S., Holt K., Howden P.J., Hunt A.R., Hunt S.E., Hunter G., Isherwood J., James R., Johnson C., Johnson D., Joy A., Kay M., Kershaw J.K., Kibukawa M., Kimberley A.M., King A., Knights A.J., Lad H., Laird G., Lawlor S., Leongamornlert D.A., Lloyd D.M., Loveland J., Lovell J., Lush M.J., Lyne R., Martin S., Mashreghi-Mohammadi M., Matthews L., Matthews N.S.W., McLaren S., Milne S., Mistry S., Moore M.J.F., Nickerson T., O'Dell C.N., Oliver K., Palmeiri A., Palmer S.A., Parker A., Patel D., Pearce A.V., Peck A.I., Pelan S., Phelps K., Phillimore B.J., Plumb R., Rajan J., Raymond C., Rouse G., Saenphimmachak C., Sehra H.K., Sheridan E., Shownkeen R., Sims S., Skuce C.D., Smith M., Steward C., Subramanian S., Sycamore N., Tracey A., Tromans A., Van Helmond Z., Wall M., Wallis J.M., White S., Whitehead S.L., Wilkinson J.E., Willey D.L., Williams H., Wilming L., Wray P.W., Wu Z., Coulson A., Vaudin M., Sulston J.E., Durbin R.M., Hubbard T., Wooster R., Dunham I., Carter N.P., McVean G., Ross M.T., Harrow J., Olson M.V., Beck S., Rogers J., Bentley D.R.Nature 441:315-321(2006)

NCBI AND UNIPROT INFORMATION

NCBI GI #	87240000
NCBI GeneID	4524
NCBI Accession #	NP_005948.3
NCBI GenBank Nucleotide #	NM_005957.4
UniProt Accession #	P42898; Q5SNW6; Q5SNW9; Q7Z6M6; Q8IU73; Q9UQR2; B2R7A6
Molecular Weight	76.6 kDa
NCBI Official Full Name	methylenetetrahydrofolate reductase
NCBI Official Synonym Full Names	methylenetetrahydrofolate reductase (NAD(P)H)
NCBI Official Symbol	MTHFR

NCBI Protein Information	methylenetetrahydrofolate reductase
UniProt Protein Name	Methylenetetrahydrofolate reductase
UniProt Gene Name	MTHFR
UniProt Entry Name	MTHR_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.

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Online datasheet: <https://www.aaabiotech.com/mthfr-recombinant-protein-e-coli/113903>