

Product datasheet

Recombinant Human EZH2 + EED + SUZ12 + AEBP2 + RBBP4 (mutated Y646F) protein ab198129

1 Image

Description

Product name	Recombinant Human EZH2 + EED + SUZ12 + AEBP2 + RBBP4 (mutated Y646F) protein	
Purity	>= 90 % SDS-PAGE. Affinity purified.	
Expression system	Baculovirus infected Sf9 cells	
Accession	<u>Q15910</u> <u>O75530</u> <u>Q15022</u> <u>Q6ZN18-2</u> <u>Q09028</u>	
Protein length	Full length protein	
Animal free	No	
Nature	Recombinant	
Amino Acid Sequence 1		
Species	Human	
Sequence	GQTGKKSEKGPVCWRKRVKSEYMRLRQLKRFRRRADEVK SMFSSNRQKILE RTEILNQEWKQRRIQPVHILTSVSSLRGTTRECSVTSDLDFP TQVIPLKTL NAVASVPIMYSWSPLQQNFMVEDETVLHNIPYMGDEVLD QDGTFFIELIK NYDGKVHGDRECGFINDEIFVELVNALGQYNDDDDDDDG DDPEEREKQK DLEDHRDDKESRPPRFPSDKIFEAISSMFPDKGTAEELK EKYKELTEQQ LPGALPPECTPNIDGPNKSVQREQLHSFHTLFCRRCFK YDCFLHRKCN YSFHATPNTYKRKNTETALDNKPCGPQCYQHLEGAKEFA AALTAERIKTP PKRPGGRRRGRLPNSSSRPSTPTINVLESKDTSDREAG TETGGENNCKE EEEEKDETSSSSEANSRCQTPIKMKPNIEPPENVEWSGA EASMFRLIGT	

YDNFCAIARLIGTKCRQVYEFVRVKESSIAPAPAEDVDTP
 PRKKKRKH
 RLWAAHCRKIQLKKDGSSNHVYNYQPCDHRQPCDSSC
 PCVIAQNFCEKF
 CQCSSECQNRFPGCRCKAQCNTKQCPCYLAVRECDPDL
 CLTCGAADHWDS
 KNVSCKNCSIQRGSKKHLLAPSDVAGWGIFIKDPVQKNE
 FISEFCGEII
 SQDEADRRGKVYDKYMCSFLFNLNDFVVDATRKGNKIR
 FANHSVNPNCY
 AKVMMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKYV
 GIEREMEIP

Predicted molecular weight 86 kDa including tags

Amino acids 2 to 751

Modifications mutated Y646F

Tags His tag N-Terminus

Additional sequence information EZH2; NM_004456. [This mutation is often cited as Y641F in variant 3 (GenBank Accession No. NM_001203247)].

Amino Acid Sequence 2

Species Human

Sequence

SEREVSTAPAGTDMPPAAKKQKLSSDENSNPDLSGDEND
 DAVSIESGTNTE
 RPDTPTNTPNAPGRKSWGKWKWSKCKYKFCVNSLK
 EDHNQPLFGVQF
 NWHSKEGDPLVFATVGSNRVTLYECHSQGEIRLLQSYVD
 ADADENFYTCA
 WTYDSNTSHPLLAVAGSRGIIRIINPITMQCIKHVGHGNAIN
 ELKFHPR
 DPNLLLSVSKDHALRLWNIQTDTLVAIFGGVEGHRDEVLS
 ADYDLLGEKI
 MSCGMDHSLKLWRINSKRMMNAIKESYDYNPNKTNRPFIS
 QKIHFPDFST
 RDIHRNYVDCVRWLGDLLSKSCENAMCWKPGKMEDDID
 KIKPSESNT
 ILGRFDYSQCDWYMRFSMDFWQKMLALGNQVGLKYWD
 LEVEDPHKAKC TTLTHHKCGAAIRQTSFSRD
 SSILIAVCDDASIRWDRLR

Predicted molecular weight 51 kDa including tags

Amino acids 2 to 441

Tags DDDDK tag N-Terminus

Additional sequence information EED; NM_003797.

Amino Acid Sequence 3

Species Human

Sequence

APQKHGGGGGGSGPSAGSGGGGFGGSAAVAAATASG
 GKSGGGSCGGGGS
 YSASSSSSAAAAAAGAAVLPVKKPKMEHVQADHELFLQAF
 EKPTQIYRFLR

TRNLIPIFLHRTLTYMSHRNSRTNIKRTFKVDDMLSKEVEK
 MKGEQESH
 SLSAHLQLTFTGFFHKNDKPSNSENEQNSVTLEVLLVKV
 CHKKRKDVSC
 PIRQVPTGKKQVPLNPDLNQTKPGNFPSLAVSSNEFEPS
 NSHMVKSYSLL
 FRVTRPGRREFNGMINGETNENIDVNEELPARRKRNRREDG
 EKTFVAQMTV
 FDKNRRLQLLDGEYEVAMQEMEECPISKKRATWETILDGK
 RLPPFETFSSQ
 GPTLQFTLRWTGETNDKSTAPIAKPLATRNSSESLHQENKP
 GSVKPTQTIA
 VKESLTTDLQTRKEKDPNENRQKLRFYQFLYNNNTRQQT
 EARDDLHCP
 WCTLNCRKLYSLLKHLKLCHSRFIFNYVYHPKGARIDVSINE
 CYDGSYAG
 NPQDIHRQPGFAFSRNGPVKRTPIHILVCRPKRTKASMSE
 FLESEDGEV
 EQQRTYSSGHNRLYFHSDTCLPLRPQEMEVDSEDEKDPE
 WLREKTTIQIE
 EFSDVNEGEKEVMKLVNLHVMKHGFIADNQMNHACMLF
 VENYGQKIKN
 LCRNFMLHLVSMHDFNLISIMSIDKAVTKLREMQQKLEKGE
 SASPANEEI
 TEEQNGTANGFSEINSKEKALETDSVSGVSKQSKKQKL

Predicted molecular weight 87 kDa including tags
Amino acids 2 to 739
Tags His tag N-Terminus
Additional sequence information SUZ12; NM_015355.
Amino Acid Sequence 4
Species Human
Sequence

AAAITDMADLEELSRLSPLPPGSPGSAARGRAEPEEEEE
 EEEEEEEEA
 EAVAALLLNGSGGGGGGGGGVGGGEAETMSEPSPE
 SASQAGEDEDEEE
 DDEEEDESSSSGGGEEESSAESLVGSSGGSSSDETR
 LSPGAASSSSGD
 GDGKEGLEEPPKGRGSQGGGGGGSSSSSVSSGGDEG
 YGTGGGGSSATSG
 GRRGSLEMSSDGEPLSRMDSSESSISSTIMDVSTISSGRS
 TPAMMNGQGS
 TTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQR
 GGVFVCLWKG
 CKVYNTPTSQSWLQRHMLTHSGDKPFKCVVGGCNASF
 ASQGGLARHVPT
 HFSQQNSSKVSSQPKAKEESPSKAGMNRKRRLKNKRRR
 SLPRPHDFFDAQ
 TLDAIRHRAICFNLSAHIESLGKGHSVVFHSTVIKRKEDSG
 KIKLLLHW

MPEDILPDVWVNESERHQLKTKVVHLSKLPKDTALLLDPN
YRTMPQKRL KR

Predicted molecular weight 53 kDa including tags

Amino acids 2 to 503

Tags His tag N-Terminus

Additional sequence information AEBP2; NM_153207.

Amino Acid Sequence 5

Species Human

Sequence

ADKEAAFDDAVEERVINEEYKIWKKNTPFLYDLVMTHALE
WPSLTAQWLP
DVTRPEGKDFSIHRLVLGHTSDEQNHLVIASVQLPNDDA
QFDASHYDSE
KGEFGFGSVSGKIEIEIKINHEGEVNRARYMPQNPCIATK
TPSSDVLV
FDYTKHPSKPDPSGECNPDLRLRGHQKEGYGLSWNPNL
SGHLLSASDDHT
ICLWDISAVPKEGKVVDAKTIFTGHTAVVEDVSWHLLHES
LFGSVADDQK
LMWDTRSNNTSKPSHSVDAHTAEVNCLSFNPYSEFILAT
GSADKTVALW
DLRNLKLLKLSFESHKDEIFQVQWSPHNETILASSGTD RR
LNVWDL SKIG
EEQSPEDAEDGPPELLFIHGGHTAKISDFSWNPNEPWVIC
SVSEDNIMQV WQMAENYNDEDPEGSVDPEGQGS

Predicted molecular weight 48 kDa including tags

Amino acids 2 to 425

Tags His tag N-Terminus

Additional sequence information RBBP4; NM_005610.

Specifications

Our **Abpromise guarantee** covers the use of **ab198129** in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications SDS-PAGE

Form Liquid

Additional notes Mutant version of EZH2 5-member complex but with a Tyr-to-Phe mutation on aa646 of the EZH2 protein. Complex of Human EZH2 (NM_004456), aa2-end, Y646F*, with N terminal His tag, MW= 86 kDa, Human EED (NM_003797), aa2-end with N terminal DDDDK tag, MW= 51 kDa, Human SUZ12 (NM_015355), aa2-end with N terminal His tag, MW = 87 kDa, Human AEBP2 (NM_153207), aa2- end with N terminal His tag, MW = 53 kDa, and Human RBBP4 (NM_005610), aa2-end with N terminal His tag, MW = 48 kDa, co-expressed in a baculovirus expression system.

Preparation and Storage

Stability and Storage Shipped on Dry Ice. Store at -80°C. Avoid freeze / thaw cycle.

pH: 8.00

Constituents: 0.4% Tris HCl, 0.8% Sodium chloride, 0.05% Tween, 10% Glycerol (glycerin, glycerine)

General Info

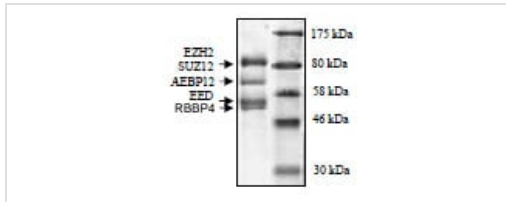
Relevance

EED: Polycomb group (PcG) protein. Component of the PRC2/EED-EZH2 complex, which methylates 'Lys-9' and 'Lys-27' of histone H3, leading to transcriptional repression of the affected target gene. The PRC2/EED-EZH2 complex may also serve as a recruiting platform for DNA methyltransferases, thereby linking two epigenetic repression systems. Genes repressed by the PRC2/EED-EZH2 complex include HOXC8, HOXA9, MYT1 and CDKN2A. RBBP4: Core histone-binding subunit that may target chromatin assembly factors, chromatin remodeling factors and histone deacetylases to their histone substrates in a manner that is regulated by nucleosomal DNA. Component of several complexes which regulate chromatin metabolism. These include the chromatin assembly factor 1 (CAF-1) complex, which is required for chromatin assembly following DNA replication and DNA repair; the core histone deacetylase (HDAC) complex, which promotes histone deacetylation and consequent transcriptional repression; the nucleosome remodeling and histone deacetylase complex (the NuRD complex), which promotes transcriptional repression by histone deacetylation and nucleosome remodeling; the PRC2/EED-EZH2 complex, which promotes repression of homeotic genes during development; and the NURF (nucleosome remodeling factor) complex. SUZ12: Polycomb group (PcG) protein. Component of the PRC2/EED-EZH2 complex, which methylates 'Lys-9' (H3K9me) and 'Lys-27' (H3K27me) of histone H3, leading to transcriptional repression of the affected target gene. The PRC2/EED-EZH2 complex may also serve as a recruiting platform for DNA methyltransferases, thereby linking two epigenetic repression systems. Genes repressed by the PRC2/EED-EZH2 complex include HOXC8, HOXA9, MYT1 and CDKN2A. EZH2: Polycomb group (PcG) protein. Catalytic subunit of the PRC2/EED-EZH2 complex, which methylates 'Lys-9' (H3K9me) and 'Lys-27' (H3K27me) of histone H3, leading to transcriptional repression of the affected target gene. Able to mono-, di- and trimethylate 'Lys-27' of histone H3 to form H3K27me1, H3K27me2 and H3K27me3, respectively. Compared to EZH2-containing complexes, it is more abundant in embryonic stem cells and plays a major role in forming H3K27me3, which is required for embryonic stem cell identity and proper differentiation. The PRC2/EED-EZH2 complex may also serve as a recruiting platform for DNA methyltransferases, thereby linking two epigenetic repression systems. Genes repressed by the PRC2/EED-EZH2 complex include HOXC8, HOXA9, MYT1, CDKN2A and retinoic acid target genes. EZH2 can also methylate non-histone proteins such as the transcription factor GATA4. AEBP2: DNA-binding transcriptional repressor. May interact with and stimulate the activity of the PRC2 complex, which methylates 'Lys-9' and 'Lys-27' residues of histone H3.

Cellular localization

Chromosome Nucleus

Images



10% gradient SDS-PAGE analysis of ab198129 (4 μ g complex).

SDS-PAGE - Recombinant Human EZH2 + EED +
SUZ12 + AEBP2 + RBBP4 (mutated Y646F) protein
(ab198129)

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