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- Mindermengenzuschlag
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SZABO-SCANDIC HandelsgmbH

Quellenstraße 110, A-1100 Wien

T. +43(0)1 489 3961-0

F. +43(0)1 489 3961-7

mail@szabo-scandic.com

www.szabo-scandic.com

[linkedin.com/company/szaboscandic](https://www.linkedin.com/company/szaboscandic) 

Data Sheet

EZH2 (E740K) /EED/SUZ12/RbAp48/AEBP2

Human, recombinant
Catalog #: 51032
Lot #: 120514 **Conc.:** 0.38 mg/ml

Formulated in: 40 mM Tris-HCl, pH 8.0, 110 mM NaCl, 2.2 mM KCl, 200 mM imidazole, and 20% glycerol.

Stability: >6 months at -70°C. Avoid freeze/thaw cycles.

References:

1. Varambally, S. *et al. Science* **322 (5908)**: 1695-1699 (2008).
2. Rakotobe, D. *et al., Virol. J.* **5** : 32 (2008).

Application Reference:

Morin, R.D., *et al. Nat Genet.* 2010 February; **42(2)**: 181-185.

Description: Mutant version of BPS's regular EZH2 5-member complex (Cat. # 51004), but with a Glu-to-Lys mutation on a.a. 745 of the EZH2 protein.* Complex of human EZH2 (GenBank Accession No. NM_004456), (a.a. 2-end ; E745K) with N-terminal His-tag, MW= 86 kDa, human EED (NM_003797) (a.a. 2-end) with N-terminal FLAG-tag, MW= 51 kDa, human SUZ12 (NM_015355) (a.a. 2-end) with N-terminal His-tag, MW = 87 kDa, Human AEBP2 (NM_153207) (a.a. 2-end) with N-terminal His-tag, MW= 53 kDa, and human RbAp48 (NM_005610) (a.a. 2-end) with N-terminal His-tag, MW = 48 kDa, co-expressed in a baculovirus expression system. *This mutation is equivalent to E740K in variant 3 (GenBank Accession No. NM_001203247).

Application: Useful for the study of enzyme kinetics, screening inhibitors, and selectivity profiling.

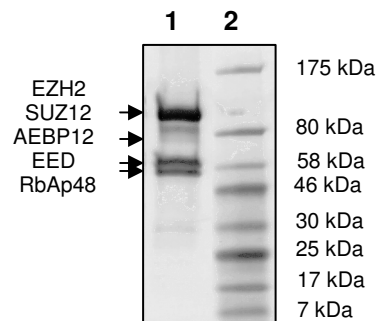
Quality Assurance

4-20% gradient SDS-PAGE
Coomassie staining

Lane 1:
 6.4 µg enzyme complex

Lane 2:
 Protein Marker

Purity: ≥81%





6044 Cornerstone Court West, Suite E
San Diego, CA 92121
Tel: 1.858.829.3082
Fax: 1.858.481.8694
Email: info@bpsbioscience.com

Protein Sequence:

MHHHHHHGQTGKKSEKGPVCWRKRVKSEYMRLRQLKRFRRRADEVKSMFSSNRQKI
LERTEILNQEWKQRRRIQPVHILTSVSSLRGTTRECSVTSDLDFPTQVIPLKTLNAVASVPI
MYSWSPLQQNFMVEDETVLHNIPYMGDEVLDQDGTFFIEELIKNYDGKVHGDRECGFIN
DEIFVELVNALGQYNDGDDDDDDGDDPEEREKQKDLEDHRDDKESRPPRKFPSPDKIF
EAISSMFPDKGTAEELKEKYKELTEQQLPGALPPECTPNIDGPNKSVQREQSLHSFH
TLFCRRCFKYDCFLHRKCNYSFHATPNTYKRKNTETALDNKPCGPQCYQHLEGAKEF
AAALTAERIKTPPKRPGRRRRGRLPNSSRPSTPTINVLESKDTDSREAGTETGGE
NNDKEEEEEKDETSSEANSRCQTPIKMKPNIEPPENVEWSGAEASMFRLVIGTYID
NFCAIARLIGTKTCRQVYEFVKESSIIAPAPAEDVDTPPRKKKRKHLWAAHCRKIQL
KKGSSNHVYNYQPCDHPRQPCDSSPCVIAQNFCEKFCQCSSECQNRFPGCRCKA
QCNTKQCPCYLAVRECDPDLCLTCGAADHWDSKNVSKNCSIQRGSKKHLHLLAPSD
VAGWGIFIKDPVQKNEFISEYCGEISQDEADRRGKVYDKYMCSFLFNLNDFVVDAT
RKGKIRFANHSVNPNCYAKVMMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKY
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