

Data Sheet

EZH2 (H689Y) /EED/SUZ12/RbAp48/AEBP2

Human, recombinant
Catalog #: 51023
Lot #: 111213 **Conc.:** 0.17 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 His-to-Tyr mutation on a.a. 694 of the EZH2 protein.* Complex of human EZH2 (GenBank Accession No. NM_004456), (a.a. 2-end ; H694Y) 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 H689Y in variant 3 (GenBank Accession No. NM_001203247).

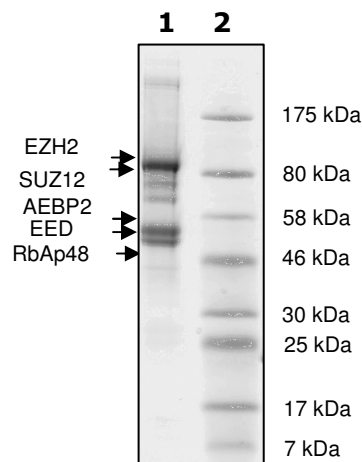
Application: Useful for the study of enzyme kinetics, screening inhibitors, and selectivity profiling.

Quality Assurance

4-20% gradient SDS-PAGE
Coomassie staining

Lane 1: 4 µg enzyme complex
Lane 2: Protein Marker

Purity: ≥ 87%



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Sequence:

MHHHHHHGQTGKKSEKGPVCWRKRVKSEYMRLRQLKRFRRRADEVKSMFSSNRQKI
LERTEILNQEWKQRRRIQPVHILTSVSSLRGTRECSVTSDLDFPTQVIPLKTLNAVASVPI
MYSWSPLQQNFMVEDETVLHNIPYMGDEVLDQDGTFFIEELIKNYDGKVHGDRECGFIN
DEIFVELVNALGQYNDDDDDDDGDDPEEREKQKDLEDHRDDKESRPPRKFPSPDKIF
EAISSMFPDKGTAEELKEKYKELTEQQLPGALPPECTPNIDGPNKSVQREQSLHSFH
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AAALTAERIKTPPKRPGRRRRLPNSSRPSTPTINVLESKDTDSREAGTETGGE
NNDKEEEEKKDETSSSEANSRCQTPIKMKPNIEPPENVEWSGAEASMFRLVIGTYID
NFCAIARLIGTKTCRQVYEFVRVKESSIIAPAPAEDVDTPPRKKRKHRLWAAHCRKIQL
KKGSSNHVYNYQPCDHPRQPCDSSCPCVIAQNFCEKFCQCSSECQNRFPGCRCKA
QCNTKQCPCYLAVRECDPDLCLTCGAADHWDSKNVSKNCSIQRGSKKHLLLAPSD
VAGWGIFIKDPVQKNEFISEYCGEISQDEADRRGKVYDKYMCSFLFNLNDFVVDAT
RKGNKIRFANYSVNPNCYAKVMMVNGDHRIGIFAKRAIQTGEELFFDYRYSQADALKY
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