

Division of Signal Transduction Therapy

Standard Operation Procedure

Preparation of His-USP8 C786S

<u>Enzyme description:-</u>	His-USP8 C786S
<u>Clone number:-</u>	DU22208
<u>Source:-</u>	Sf21 Recombinant
<u>Tag:-</u>	N-terminal His ₆ -tag
<u>Purification method:-</u>	Ni ⁺⁺ -Sepharose
<u>Expression level:-</u>	5 mg/L
<u>Calculated molecular mass:-</u>	
Monoisotopic	130695 Da
Average Mass	130772 Da
[cysteines reduced, methionines have not been oxidised]	
<u>Theoretical pI:-</u>	8.91
<u>Purity:-</u>	80%
<u>Enzyme storage buffer:-</u>	
50 mM HEPES pH 7.5, 10% glycerol, 150mM NaCl, 1mM DTT	
<u>Storage temperature:-</u>	-80°C

Assay:-

Ub-Rho110-Gly cleavage assay monitored by Ex/Em 485/535 nm

Assay buffer:-

40 mM Tris pH 7.5, 100 mM NaCl, 5 mM DTT, 0.01% Triton X-100, 0.005% Ovalbumin, 0.5 µM Ub-Rho110-Gly

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Clone Data Sheet

His-USP8 C786S

<u>Protein</u>	His-USP8 C786S
<u>Synonyms</u>	UBPY
<u>Clone Number</u>	DU22208
<u>Species</u>	Human
<u>Accession Number</u>	Protein: P40818 DNA: NM_005154.3
<u>Tags</u>	N-terminal His ₆ -tag
<u>Amino acid sequence of expressed protein</u>	MSYYHHHHHDYDIPTTENLYFQGAMGSM PAVASVPKELYLSSSLKDL NKKTEVKPEKISTKSYVHSALKIFKTAEECRLDRDEERAYVLYMKYVT VYNLIKRPDPFKQQQDYFHSILGPGNIKKAVEEAERLSESLKLRYEAA EVRKKLEEKDRQEEAQRLQQKRQETGREDGGTLAKGSLENVLDSDKDT QKSNGEKNEKCETKEKGAITAKELYTMMTDKNISLIIMDARRMQDYQD SCILHSLSVPEEAI SPGVTASWIEAHL PDDSKDTWKKRGNVEYVLLD WFSSAKDLQIGTTLRSLKDALFKWESKTVLRNEPLVLEGGYENWLLCY PQYTTNAKVTPPPRRQNEEVSISLDF TYP SLEESIPSKPAAQTPPASI EVDENIELISGQNERMGPLNISTPVEPVAASKSDVSPIIQPVP SIKNV PQIDRTKKPAVKLP EEHRIKSESTNHEQQSPQSGKVIPDRSTKPVVFS PTLMLTDEEKARIHAETALLMEKNKQEKELRERQQEEQKEKL RKEEQE QKAKKKQEAEE NEITEKQQKAKEEMGKKESEQAKKEDKETS AKRGKEI TGVKRQSKSEHETSDAKKSVEDRGKRCPTPEIQKKSTGDPHTSVTGD SGSGKPFKIKGQPESGILRTGT FREDTDDTERNKAQREPLTRARSEEM GRIVPGLPSGWAKFLDPITGTFRYYHSPTNTVHMYPP EMAPSSAPPST PPTHKAKPQIPAERDREPSKLKRSYSSPDITQAIQEE EKRPKPTVTPTV NRENKPTCYPKAEISRLSASQIRNLNPVFGGSGPALTGLRNLGNTSYM NSILQCLCNAPHLADYFNRNCYQDDINRSNLLGHKG E VAE EFGIIMKA LWTGQYRYISP KDFKITIGKINDQFAGYSQQDSQELLLFLMDGLHEDL NKADNRKRYKEENNDHLDDFKAAEHAWQKHQQLNESIIVALFQGGQFKS TVQCLTCHKKSRAFEAFMYLSLPLASTSKCTLQDCLRLFSKEEKLTDN NRFYCSHCRRARDSLKKIEIWKLPPVLLVHLKRFSYDGRWKQKLQTSV DFPLENLDLSQYVIGPKNNLKKYNLFSVSNHYGGLDGGHYTAYCKNAA RQRWFKFDDHEVSDISVSSVKSSAAYILFYTSLGPRVTDVAT
<u>Native sequence</u>	in bold
<u>Protease cleavage</u>	TEV site underlined
<u>Cloning sites</u>	BamH1 / Not1

**DNA sequence of
insert**

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