

Product datasheet for **SC323452**

TrkC (NTRK3) (NM_002530) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	TrkC (NTRK3) (NM_002530) Human Untagged Clone
Tag:	Tag Free
Symbol:	TrkC
Synonyms:	gp145(trkC); GP145-TrkC; TRKC
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)



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Fully Sequenced ORF: >OriGene ORF within SC323452 sequence for NM_002530 edited (data generated by NextGen Sequencing)

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ATGGATGTCTCTCTTTGCCAGCCAAGTGTAGTTTCTGGCGGATTTTCTTGCTGGGAAGC
GTCTGGCTGGACTATGTGGGCTCCGTGCTGGCTTGCCTGCAAATTGTGTCTGCAGCAAG
ACTGAGATCAATTGCCGGCGCCGGACGATGGGAACCTTCCCCCTCCTGGAAGGGCAG
GATTCAGGGAACAGCAATGGGAACGCCAGTATCAACATCACGGACATCTCAAGGAATATC
ACTTCCATACACATAGAGAAGTGGCGCAGTCTTACACGCTCAACGCCGTGGACATGGAG
CTCTACACCGGACTTCAAAGCTGACCATCAAGAACTCAGGACTTCGGAGCATTAGCCC
AGAGCCTTTGCCAAGAACCCCCATTTGCGTTATATAAACCTGTCAAGTAACCGGCTCACC
ACACTCTCGTGGCAGCTTCCAGACGCTGAGTCTCGGGAATTGCAGTTGGAGCAGAAC
TTTTTCAACTGCAGCTGTGACATCCGCTGGATGCAGCTCTGGCAGGAGCAGGGGAGGCC
AAGCTCAACAGCCAGAACCTCTACTGCATCAACGCTGATGGCTCCAGCTTCTCTCTTC
CGCATGAACATCAGTCAGTGTGACCTTCTGAGATCAGCGTGAGCCAGTCAACCTGACC
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GTGGTCATTGGCATGACTCGCATCCCTGTATTGAGAACCCCACTTCCGTCAGGGA
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AAGCGAGAAGTGGTGGAGGAGCCTTTGGAAAGTCTTCTGCGCCGAGTGTACAACCTC
AGCCCGACCAAGGACAAGATGCTTGTGGCTGTGATGGCCCTGAAGGATCCACCCTGGCT
GCCCGGAAGGATTTCCAGAGGGAGGCCGAGCTGCTCACCAACCTGCAGCATGAGCACATT
GTCAAGTTCTATGGAGTGTGCGGCGATGGGGACCCCTCATCATGGTCTTTGAATACATG
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AGTCAGATCGCCTCGGTATGGTGTACCTGGCCTCCCAGCACTTTGTGCACCGAGACCTG
GCCACCAGGAAGTGCCTGGTGGAGCGAATCTGCTAGTGAAGATTGGGGACTTCGGCATG
TCCAGAGATGTCTACAGCACGGATTATTACAGGGTGGGAGGACACACCATGCTCCCCATT
CGCTGGATGCCTCCTGAAAGCATCATGTACCGGAAGTTCCTACAGAGAGTGTATGG
AGCTTCGGGGTGATCCTCTGGGAGATCTTACCTATGAAAGCAGCCATGGTTCCAACTC
TCAAACACGGAGGTCACTGAGTGCATTACCAAGGTCGTGTTTTGGAGCGCCCCGAGTC
TGCCCCAAAGAGGTGTACGATGTATGCTGGGGTGTGGCAGAGGGAACACAGCAGCGG
TTGAACATCAAGGAGATCTACAAAATCCTCCATGCTTTGGGGAAGGCCACCCCAATCTAC
CTGGACATTCTTGCTAG

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Clone variation with respect to NM_002530.3
1715 a=>t

5' Read Nucleotide Sequence:	>OriGene 5' read for mutant NM_002530 unedited ACGCCGTTGAGCAATGGGCGGTAGGCGGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAAC CGTCAGAATTTTGTAAATACGACTCACTATAGGGCGGCCGGAATTCGGCACGAGGCTCCTCTTTTTAGA AGCAGCGATCGGAGATGGATGTCTCTTTGCCAGCCAAGTGTAGTTTCTGGCGGATTTCTTGTCTGGG AAGCGTCTGGCTGGACTATGTGGGCTCCGTGCTGGCTTGCCTGCAAATTGTGTCTGCAGCAAGACTGAG ATCAATTGCCGGCGCCGACGATGGGAACCTCTCCCCCTCCCTGGAGGGCAGGATTCAGGGGAACA GCGCAATGGGGACCGGCCAGTATCCAACATTCACGGGACAATCTTCAGGGAAATATCACCTTCCTTACAC CTTAAAAAACTTGGCCGATCCCTTCCCCCCTCACCCCTTGAACCTTGGGAGCTTCTACCCGGGAC TCAAAAACCTGACCTTCAAAAACCTAGGGACTTCGAACCTTTCCCCAAAAACCTTTTCCAAAACCCCC CTTTTGGCTTTAAAAACCGTGCCATTTAACGGGTAAAAAATTTTTGGGGCACCTTTTCCAAAACCCG GATTTTGGGAATTGGCTTTGGGACAAAATTTTTAAATGGCCCGTGGGAACCCCGGGGGAGCCCC CTTTCGCAACACCAGAAAACCCCAACCTCAACCCCAAAAACCTTTTGGGGACACCCGGTGGGGGCAACA TCTTTCTTTTTTCGCGAAAAACACTCAGTGGGGGGCCCTCTCCAATAAACCGGGGGCCCTCCCTCC CTCCGTCCAAAAAGGGGACACACTGCTTTTATCTTCGTTGGGGGGCGGGGAGACCCCTCTCTTAGT GGGAGCAGAGAGAATATGGGGTGGGTGCTACACACTCCAGCAAAAACCTTGATCTGTGCCGGCGTGTG TGCTTACATTACTGGCGTGATGAGGACAGAGAGAACGCGAAGATCGTCCCTACGCGTTACGATGCT CTACAGACAGAGAA
Kinase Domain Sequence:	>SC323452 kinase domain raw sequence. By performing BLASTX analysis with this sequence against NCBI reference protein database, you can confirm the presence of the kinase-deficient mutation AGGTGAGGAGCTTTGGAAGKCTTCTGGCCGAGTGTACAACCTCAGCCCGACCAAGGACAAGATGCTTG TGCTGTGATGGCCCTGAAGATCCACCTGGCTGCCCGGAAGGATTTCCAGAGGGAGGCCGAGCTGCT CACCAACCTGCAGCATGAGCACATTGTCAAGTTCTATGGAGTGTGCGGGATGGGGACCCCTCATCATG GTCTTTGAATACATGAAGCATGGAGACCTGAATAAGTTCTCAGG
Restriction Sites:	Please inquire
ACCN:	NM_002530
Insert Size:	2800 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
OTI Annotation:	This kinase-deficient mutant clone was generated by created by site-directed mutagenesis from the corresponding wild-type clone. See details in "Application of active and kinase-deficient kinome collection for identification of kinases regulating hedgehog signaling." Cell, 2008 May p536-548.
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	<ol style="list-style-type: none"> 1. Centrifuge at 5,000xg for 5min. 2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. 3. Close the tube and incubate for 10 minutes at room temperature. 4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.

RefSeq:	NM_002530.2 , NP_002521.2
RefSeq Size:	2818 bp
RefSeq ORF:	2478 bp
Locus ID:	4916
UniProt ID:	Q16288
Cytogenetics:	15q25.3
Domains:	LRRNT, LRRCT, pkinase, TyrKc, LRR, S_TKc, ig, IG
Protein Families:	Druggable Genome, Protein Kinase, Transmembrane
Protein Pathways:	Neurotrophin signaling pathway
Gene Summary:	<p>This gene encodes a member of the neurotrophic tyrosine receptor kinase (NTRK) family. This kinase is a membrane-bound receptor that, upon neurotrophin binding, phosphorylates itself and members of the MAPK pathway. Signalling through this kinase leads to cell differentiation and may play a role in the development of proprioceptive neurons that sense body position. Mutations in this gene have been associated with medulloblastomas, secretory breast carcinomas and other cancers. Several transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jul 2011]</p> <p>Transcript Variant: This variant (2) lacks an alternate in-frame exon, compared to variant 1, resulting in a shorter protein (isoform b) compared to isoform a. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.</p>