

Product datasheet for **SC109694**

RAC1 (NM_018890) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: RAC1 (NM_018890) Human Untagged Clone
Tag: Tag Free
Symbol: RAC1
Synonyms: MIG5; MRD48; p21-Rac1; Rac-1; TC-25
Mammalian Cell Selection: None
Vector: [pCMV6-XL5](#)
E. coli Selection: Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene sequence for NM_018890 edited
 GTGGTGGCCGCTGCCGGCATCGGCTTCCAGTCCGCGGAGGGCGAGGCGGCGTGGACAGC
 GGCCCCGGCACCCAGCGCCCCGCCGCCGCAAGCCGCGCGCCCGTCCGCCGCGCCCCGAG
 CCGCGCGTTCCTATCTCAGCGCCTGCCGCCGCCGCCGCGGCCAGCGAGCGGCCCTGA
 TGCAGGCCATCAAGTGTGTGGTGGTGGGAGACGGAGCTGTAGGTA AAACTGCCTACTGA
 TCAGTTACACAACCAATGCATTTCTGGAGAATATATCCCTACTGTCTTTGACAATTATT
 CTGCCAATGTTATGGTAGATGGAAAACCGTGAATCTGGGCTTATGGGATACAGCTGGAC
 AAGAAGATTATGACAGATTACGCCCCCTATCCTATCCGCAAACAGTTGGAGAAACGTACG
 GTAAGGATATAACCTCCCGGGGCAAAGACAAGCCGATTGCCGATGTGTTCTTAATTTGCT
 TTTCCCTTGTGAGTCCTGCATCATTGAAAATGTCCGTGCAAAGTGGTATCCTGAGGTGC
 GGCACCCTGTCCCAACTCCCATCATCTAGTGGAACTAACTTGATCTTAGGGATG
 ATAAAGACACGATCGAGAACTGAAGGAGAAGAAGCTGACTCCCATCACCTATCCGAGG
 GTCTAGCCATGGCTAAGGAGATTGGTGCTGTAATAACCTGGAGTGCTCGGCGCTCACAC
 AGCGAGGCCTCAAGACAGTGTGGACGAAGCGATCCGAGCAGTCTCTGCCCGCCTCCC
 TGAAGAAGAGGAAGAGAAAATGCCTGCTGTTGTAATGTCTCAGCCCCTCGTTCTTGTC
 CTGTCCCTTGAACCTTTGTACGCTTTGCTCAAAAAAAAAA

Restriction Sites: Please inquire

ACCN: NM_018890

Insert Size: 900 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).



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OTI Annotation:	The ORF of this clone has been fully sequenced and found to be a perfect match to NM_018890.2.
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_018890.2 , NP_061485.1
RefSeq Size:	2412 bp
RefSeq ORF:	636 bp
Locus ID:	5879
UniProt ID:	P63000
Cytogenetics:	7p22.1
Domains:	ras
Protein Families:	Druggable Genome
Protein Pathways:	Adherens junction, Amyotrophic lateral sclerosis (ALS), Axon guidance, B cell receptor signaling pathway, Chemokine signaling pathway, Colorectal cancer, Epithelial cell signaling in Helicobacter pylori infection, Fc epsilon RI signaling pathway, Fc gamma R-mediated phagocytosis, Focal adhesion, Leukocyte transendothelial migration, MAPK signaling pathway, Natural killer cell mediated cytotoxicity, Neurotrophin signaling pathway, Pancreatic cancer, Pathways in cancer, Regulation of actin cytoskeleton, Renal cell carcinoma, Toll-like receptor signaling pathway, VEGF signaling pathway, Viral myocarditis, Wnt signaling pathway
Gene Summary:	<p>The protein encoded by this gene is a GTPase which belongs to the RAS superfamily of small GTP-binding proteins. Members of this superfamily appear to regulate a diverse array of cellular events, including the control of cell growth, cytoskeletal reorganization, and the activation of protein kinases. Two transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Mar 2009]</p> <p>Transcript Variant: This variant (Rac1b) includes the alternatively spliced 57 bp region (exon 3b) that is missing in transcript variant Rac1. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p>