

# Product datasheet for SC328215

# NKAIN2 (NM\_153355) Human Untagged Clone

### **Product data:**

#### OriGene Technologies, Inc.

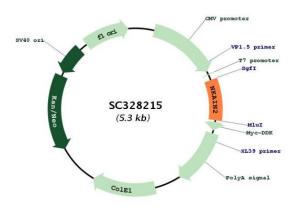
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| Product Type:                | Expression Plasmids   |
|------------------------------|---|
| Product Name:                | NKAIN2 (NM_153355) Human Untagged Clone   |
| Tag:                         | Tag Free  |
| Symbol:                      | NKAIN2  |
| Synonyms:                    | FAM77B; NKAIP2; TCBA; TCBA1   |
| Mammalian Cell<br>Selection: | Neomycin  |
| Vector:                      | pCMV6-Entry (PS100001)  |
| E. coli Selection:           | Kanamycin (25 ug/mL)  |
| Fully Sequenced ORF:         | >SC328215 representing NM_153355.<br>Blue=Insert sequence <mark>Red=</mark> Cloning site Green=Tag(s)   |
|                              | GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG<br>GATCCGGTACCGAGGAGATCTGCCGCCGCGCGCGCC<br>ATGGGTTATTGCAGTGGCAGGTGCACGCTTATCTTTATCTGTGGCATGCAACTGGTTTGTGTGCTGGAG<br>AGGCAAATATTTGACTTCCTTGGATATCAGTGGGCACCTATCCTGGCAAATTTTGTACATATTATTATC<br>GTCATTCTTGGTTTGTTTGGAACTATTCAATATAGACCTCGTTACATAACAGGATATGCTGTCTGGCTA<br>GTCCTCTGGGTTACGTGGAATGTGTTTGTTATCTGCTTCTATTTGGAGGCTGGGGACCTCTCAAAGCTG<br>GCAGGTTTCATCTACGCCGTGTTATGTTGTGAAATGTATAACTGAAGAAGAGGACAGCTTTGATTTCATA<br>GGTGGCTTTGACTCTTATGGCTATCAAGGGCCTCAGAAGACATCTCATTTACAACTACAGCCTATGTAC<br>ATGTCAAAATAA<br>ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT<br>TACAAGGATGACGACAATAAGGTTTAAACGGCCGGC |
| <b>Restriction Sites:</b>    | Sgfl-Mlul   |



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### Plasmid Map:



| ACCN:           | NM_153355  |
|-----------------|--|
| Insert Size:    | 426 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 TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.   |
| 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).   |

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# **CRIGENE** NKAIN2 (NM\_153355) Human Untagged Clone – SC328215

| Reconstitution Method: | <ol> <li>Centrifuge at 5,000xg for 5min.</li> <li>Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>Close the tube and incubate for 10 minutes at room temperature.</li> <li>Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>   |
|------------------------|--|
| RefSeq:                | <u>NM 153355.4</u>   |
| RefSeq Size:           | 3192 bp  |
| RefSeq ORF:            | 426 bp   |
| Locus ID:              | 154215   |
| UniProt ID:            | <u>Q5VXU1</u>  |
| Cytogenetics:          | 6q22.31  |
| Protein Families:      | Transmembrane  |
| MW:                    | 16.3 kDa   |
| Gene Summary:          | This gene encodes a transmembrane protein that interacts with the beta subunit of a sodium/potassium-transporting ATPase. A chromosomal translocation involving this gene is a cause of lymphoma. Alternative splicing results in multiple transcript variants encoding distinct isoforms. [provided by RefSeq, Jul 2014]<br>Transcript Variant: This variant (2) lacks an alternate in-frame exon compared to variant 1. The resulting isoform (2) has the same N- and C-termini but is shorter compared to isoform 1.<br>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. |

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