

Toxin A (TcdA), Purified from *Clostridium difficile*, Strain VPI 10463

Catalog No. NR-41658

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Contributor and Manufacturer:

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Product Description:

Toxin A (TcdA) was purified from culture supernatant of *Clostridium difficile* (*C. difficile*), strain VPI 10463. It was purified by ion exchange and gel filtration chromatography and dehydrated.

C. difficile (sometimes referred to as *Peptoclostridium difficile*) is a Gram-positive, spore-forming, obligate anaerobe that commonly inhabits the intestinal tract of various mammalian species, reptiles and birds, and may also be found in the environment. Pathogenic strains of *C. difficile* generally produce a 308 kDa enterotoxin (TcdA) and a 270 kDa cytotoxin (TcdB).¹ Both toxins are glucosyltransferases and function by inactivating the Ras superfamily of small GTPases in target cells. Production of these toxins in the gut leads to pseudomembranous colitis (PMC) and *C. difficile* associated diarrhea (CDAD).² The symptoms of PMC include fluid accumulation, inflammation and cell damage, and are inducible in animal models with TcdA. TcdA also induces cytokine production *in vivo* resulting in aggravated inflammation.³

Material Provided:

Each vial contains approximately 2 µg of dehydrated TcdA. It is recommended that the material be rehydrated with 0.1 mL of distilled water as the original material contained 20 mM Tris, pH 7.4. The concentration, expressed as mg/mL is shown on the Certificate of Analysis.

Packaging/Storage:

NR-41658 was packaged aseptically in plastic cryovials. The product is provided at 2°C to 8°C and should be stored immediately upon arrival.

Functional Activity:

NR-41658 has been shown to react with a mouse antibody to TcdA (E64E). NR-41658 does not exhibit cytotoxicity in Vero cells.

Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH:

Toxin A (TcdA), Purified from *Clostridium difficile*, Strain VPI 10463, NR-41658."

Biosafety Level: 2

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. Biosafety in Microbiological and Biomedical Laboratories. 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see www.cdc.gov/biosafety/publications/bmb15/index.htm.

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References:

1. Rupnik, M., M. H. Wilcox and D. N. Gerding. "Clostridium difficile Infection: New Developments in Epidemiology and Pathogenesis." Nat. Rev. Microbiol. 7 (2009): 526-536. PubMed: 19528959.
2. Kelly, C. P. and J. T. LaMont. "Clostridium difficile - More Difficult than Ever." N. Engl. J. Med. 359 (2008): 1932-

1940. PubMed: 18971494.
 3. Voth, D. E. and J. D. Ballard. "Clostridium difficile Toxins: Mechanism of Action and Role in Disease." *Clin. Microbiol. Rev.* (2005): 247-263. PubMed: 15831824.

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Table 1 – Predicted Protein Sequence

1	MSLISKEELI	KLAYSIRPRE	NEYKTILTNL	DEYNKLTNN	NENKYLQLKK
51	LNESIDVFMN	KYKTSSRNRA	LSNLKKDILK	EVILIKNSNT	SPVEKNLHFV
101	WIGGEVSDIA	LEYIKQWADI	NAEYNIKLWY	DSEAFVNTL	KKAIVESSTT
151	EALQLLEEEI	QNPQFDNMKF	YKKRMEFIYD	RQKRFINYYK	SQINKPTVPT
201	IDDIKSHLV	SEYNRDETVL	ESYRTNSLRK	INSNHGIDIR	ANSLFTEQEL
251	LNIYSQELLN	RGNLAAASDI	VRLALKNFG	GVYLDVDMLP	GIHSDLFKTI
301	SRPSSIGLDR	WEMIKLEAIM	KYKKYINNYT	SENFDKLDQQ	LKDNFKLIIE
351	SKSEKSEIFS	KLENLNVSDL	EIKIAFALGS	VINQALISKQ	GSYLTNLVIE
401	QVKNRYQFLN	QHLNPAIESD	NNFTDTTKIF	HDSLFNSATA	ENSMFLTKIA
451	PYLQVGFMP	ARSTISLSGP	GAYASAYYDF	INLQENTIEK	TLKASDLIEF
501	KFPENNLSQL	TEQEINSLWS	FDQASAKYQF	EKYVRDYTGG	SLSEDNGVDF
551	NKNTALDKNY	LLNNKIPSN	VEEAGSKNYV	HYIIQLQGDD	ISYEATCNLF
601	SKNPKNIII	QRNMNESAKS	YFLSDDGESI	LELNKYRIPE	RLKNKEKVKV
651	TFIGHGKDEF	NTSEFARLSV	DSLSNEISSF	LDTIKLDISP	KNVEVNLLGC
701	NMFSYDFNVE	ETYPGKLLLS	IMDKITSTLP	DVNKNSITIG	ANQYEVRLNS
751	EGRKELLAHS	GKWINKEEAI	MSDLSKEYI	FFDSIDNKLK	AKSKYVPLGA
801	SISEDIKTLL	LDASVSPDTK	FILNNLKLNI	ESSIGDYIYY	EKLEPVKNII
851	HNSIDDLIDE	FNLENVSD	LYELKLNLL	DEKYLISFED	ISKNNSTYSV
901	RFINKSNGES	VYVETEKEIF	SKYSEHITKE	ISTIKNSIIT	DVNGNLLDNI
951	QLDHTSQVNT	LNAAFFIQSL	IDYSSNKDVL	NDLSTSVKVQ	LYAQLFSTGL
1001	NTIYDSIQLV	NLISNAVNDT	INVLPTITEG	IPIVSTILDG	INLGAAIKEL
1051	LDEHDPLLK	ELEAKVGVLA	INMSLSIAAT	VASIVGIGAE	VTIFLLPIAG
1101	ISAGIPSLVN	NELILHDKAT	SVVNYFNHLS	ESKKGPLKT	EDDKILVPID
1151	DLVISEIDFN	NNSIKLGTCN	ILAMEGGSGH	TVTGNIDHFF	SSPSISSHIP
1201	SLSIYSAIGI	ETENLDFSKK	IMMLPNAPSR	VFWWETGAVP	GLRSLNDGT
1251	RLLDSIRDLY	PGKFYWRFYA	FFDYAITTLK	PVYEDTNIKI	KLDKDRNFI
1301	MPTITTNEIR	NKLSYSFDGA	GGTYSLLLS	YPISTNINLS	KDDLWIFNID
1351	NEVREISIEN	GTIKKGKLIK	DVLSKIDINK	NKLIIGNQTI	DFSGDIDNKD
1401	RYIFLTCELD	DKISLIIIEIN	LVAKSYSLLL	SGDKNYLISN	LSNTIEKINT
1451	LGLDSKNIA	NYTDESNNKY	FGAISKTSQK	SIIHYKKDSK	NILEFYNDST
1501	LEFNSKDFIA	EDINVMKDD	INTITGKYYV	DNNTDKSIDF	SISLVSKNQV
1551	KVNGLYLNE	VYSSYLDFVK	NSDGHHTSN	FMNLFLDNIS	FWKLFGFENI
1601	NFVIDKYFTL	VGKTNLGYVE	FICDNNKNID	IYFGEWKTSS	SKSTIFSGNG
1651	RNVVVEPIYN	PDTGEDISTS	LDFSYEPLYG	IDRYINKVLI	APDLYTSLIN
1701	INTNYSNEY	YPEIIVLNP	TFHKKVNINL	DSSSFYKWS	TEGSDFILVR
1751	YLEESNKKIL	QKIRIKGILS	NTQSFNKMSI	DFKDIKLSL	GYMSNFKSF
1801	NSENELDRDH	LGFKIIDNKT	YYDEDKSLV	KGLININNSL	FYFDPIEFNL
1851	VTGWQTINGK	KYYFDINTGA	ALTSYKIING	KHFYFNNDGV	MQLGVFKGPD
1901	GFEYFAPANT	QNNNIEGQAI	VYQSKFLTLN	GKKYYFDNNS	KAVTGWRIIN
1951	NEKYFNPNN	AIAAVGLQVI	DNNKYFNPDP	TAISKGWQT	VNGSRYYFDT
2001	DTAIAFNGYK	TIDGKHFYFD	SDCVVKIGVF	STSNGFEYFA	PANTYNNNIE
2051	GQAIYVQSKF	LTLNGKYYF	DNNSKAVTGL	QTIDSKYYF	NTNTAEAATG
2101	WQTIDGKKYY	FNTNTAEAAT	GWQTIDGKKY	YFNTNTAIAS	TGYTIINGKH
2151	FYFNTDGMQ	IGVFKGPNFG	EYFAPANTDA	NNIEGQAILY	QNEFLTLNGK
2201	KYYFGSDSKA	VTGWRIINNK	KYYFNPNNAI	AAIHLCTINN	DKYYFSYDGI

2251	LQNGYITIER	NNFYFDANNE	SKMVTGVFKG	PNGFEYFAPA	NTHNNNIEGQ
2301	AIVYQNKFLT	LNGKKYYFDN	DSKAVTGWQT	IDGKKYYFNL	NTAEAATGWQ
2351	TIDGKKYYFN	LNTAEAATGW	QTIDGKKYYF	NTNTFIASTG	YTSINGKHFY
2401	FNTDGIMQIG	VFKGPNGFEY	FAPANTDANN	IEGQAILYQN	KFLTLNGKKY
2451	YFGSDSKAVT	GLRTIDGKKY	YFNTNTAVAV	TGWQTINGKK	YYFNTNTSIA
2501	STGYTIISGK	HFYFNTDGIM	QIGVFKGPDG	FEYFAPANTD	ANNIEGQAIR
2551	YQNRFLYLHD	NIYYFGNNSK	AATGWVTIDG	NRYYFEPNTA	MGANGYKTID
2601	NKNFYFRNGL	PQIGVFKGSN	GFEYFAPANT	DANNIEGQAI	RYQNRFLHLL
2651	GKIYYFGNNS	KAVTGWQTIN	GKVYYFMPDT	AMAAAGGLFE	IDGVIYFFGV
2701	DGVKAPGIYG				