

| UniprotKB ID | Entry name | organism | full name | oglnacscore | oglnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|-------------|--------------|--|-------------|--------------|---|-------------------------------------|---|
| Q14573 | ITPR3_HUMAN | Homo sapiens | Inositol 1,4,5-trisphosphate receptor type 3 | 11.971014 | T1668;T2651 | S916;S934;S1813;S1832;S1834;S2609;S2670 | 34019948;30379171;21383013;30620550 | MSEMSFLHIGDIVSLYAEGSVNGFI STLGLVDDRCVVEPAAGDLDNPPKK FRDCLFKVCPMNRYSAQKQYWKAK QTKQDKEKIADVLLQKLQHAAQME QKQNDTENKKVHGDVVKYGSVIQLL HMKSNKYLTVNRKLPALLEKNAMR VTLDATGNEGSWLFIQPFWKLRSNG DNVVVGDKVILNPVNAGQPLHASNY ELSDNAGCKEVNSVNCNTSWKINL FMQFRDHLEEVKGGDVVRLFHAE QEKFLTCDEYKGLQVFLRRTLRS ATSATSSNALWEVEVVHHDPCRGG AGHWNGLYRFKHLATGNYLAAEEN PSYKGDASDPAAGMGAQGRTGRR NAGEKIKYCLVAVPHGNDIASLFELD PTTLQKTDSFVPRNSYVRLRHLCTN TWIQTNPIDIEEERPIRLMLGTCP TKEDKEAFAIVSVPVSEIRDLDFAND ASSMLASAVEKLNQGFISQNDRRFV IQLLEDLVFFVSDVPNNGQNVLDIM VTKPNRERQKLMREQNILKQVFGIL KAPFREKGGGGLVRLLEELSDQKNA PYQHMFRLCYRVLRHSQEDYRKNQ EHIAKQFGMMQSQIGYDILAEDTTA LLHNNRKLLEKHITKTEVETVSLVR KNREPRFLDYLSDLCVSNHIAIPVTQ ELICKCVLDPKNSDILIRTELRPVKE MAQSHEYLSIEYSEEEVWLTWTDKN NEHHEKSVRQLAQEARAGNAHDEN VLSYYRYQLKLFARMCLDROYLAIDE ISQQLGVDLIFLCMADEMLPFDLRA SFCHLMLHVHVDRDPQELVTPVKFA RLWTEIPTAITIKDYDSNLNASRDDK KNKFANTMEFVEDYLNNAVSEAVP FANEKKNLTFEVVSLAHNLIYFGFY SFSELLRLTRTLGIIDCVQGPAML QAYEDPGGKNVRRSIQGVGHMMST MVL SRKQSVFSAPSL SAGASAAEPL DRSKFEENEDIVVMETKLKILEILQFI LNVRLDYRISYLLSVFKKEFVEVFP QDSGADGTAPAFDSTTANMNLDRIG EQAEAMFGVGTSSMLEVDDEGGR MFLRVLIHLMHDYAPLVSGALQLL FKHFSQRQEAMHTFKQVQLLISAQD VENYKVIKSELDRRTMVEKSELWV DKKGSKGEEVEAGA AKDKKERPTD EEGFLHPPGEKSENYQIVKGILERL NKMCGVGEQMRKKQORLLKNMDA HKVMLDLLQIPYDKGDAKMMELRY THQFLQKFCAGNPGNQALLHKHLH LFLTPGLLEAETMQHIFLNNYQLCS EISEPVLQHFVHLLATHGRHVQYLD FLHTVIKAEGKYVKKCQDMIMTELT NAGDDVVVFYNDKASLAHLLDMMK AARDGVEDHSPLMYHISLVDLLAAC AEGKNVYTEIKCTSLPLEDVVSVVT |

HEDCITEVKMAYVNFVNHCYVDTEV
EMKEIYTSNHIWTLFENFTLDMARV
CSKREKRVADPTLEKYVLSVVLDTIN
AFFSSPFSENSTSLQTHQTIVVQLLQ
STTRLLECPWLQQQHKSVEACIRT
LAMVAKGRAILLPMDLDAHISSMLS
SGASCAAAAQRNASSYKATTRAFFPR
VTPANQWDYKNIEKLQDIITALEE
RLKPLVQAELSVLVDVLHWPELLFL
EGSEAYQRCESGGFLSKLIQHTKDL
MESEEKLCIKVLRTLQOMLLKTKY
GDRGNQLRKMLLQNYLQNRKSTSR
GDLDPDPIGTGLDPDWSAIAATQCRL
DKEGATKLVCDLITSTKNEKIFQESI
GLAIHLLDGGNTEIQKSFHNLMMSD
KKSERFFKVLHDRMKRAQQUETKSTV
AVNMNDLGSQPHEHEDREPVDPTTKG
RVASFVIPGSSSRYSLGPLRRGHEV
SERVQSSEMGTSLVIMQPIRLRFLQLL
CENHNRLQNFRLRCQNNKTNYNLV
CETLQFLDIMCGSTTGGGLLLGLYIN
EDNVGLVIQTLETLTEYCQGPCHEN
QTCIVTHESNGIDIITALILNDISPLCK
YRMDLVLQLKDNASKLLALMESR
HDSENAERILISLRPQELVDVIKKAY
LQEEERENSEVSPREVGHNIIYILALQ
LSRHNKQLQHLLKPKVRIQEEEAEG
ISSMLSLNNKQLSQMLKSSAPAE
EEDPLAYYENHTSQIEIVRQDRSME
QIVFPVPGICQFLTEETKHLRFTTTE
QDEQGSKVSDFFDQSSFLHNEMEW
QRKLRSMPLIYWFRRMTLWGSISF
NLAVFINIIIAFFYPYMEGASTGVLD
PLISLLFWILICFSIAALFTKRYRPLI
VALILRSIYLGIGPTLNILGALNLTN
KIVFVVSFVGNRGTFFIRGYKAMVMD
MEFLYHVGYILTSVLGLFAHELFSI
LLFDLIYREETLFNVIKSVTRNGRSIL
LTALLALILVYLFVIVGFLFLKDDFILE
VDRLPNNHSTASPLGMPHGAAAFV
DTCSGDKMDCVSGLSVPEVLEEDRE
LDSTERACDTLLMCIVTVMNHGLRN
GGGVGDILRKPSKDESLFPARVVYDL
LFFFIVIIIIVLNLI FGVIIDTFADLRSEK
QKKEEILKTTFCICGLERDKFDNKTV
SFEHILEHNMWNYLYFIVLVRVK
NKTDYTGPEYVAQMIKNKNDWFP
RMRAMSLVSNEGEGEQNEIRILQDK
LNSTMKLVSHLTAQLNELKEQMTE
QRKRRQLGFVDVQNCISR