

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|------------|--------------|-------------------|--------------|-------------------|---|----------|---|
| F6ZDS4 | TPR_MOUSE | Mus musculus | Nucleoprotein TPR | 15.818779 | S1730;T1731;S1746 | S453;S596;S597;S706;S1259;T1762;S1963;S2102;S2105;S2116;S2118;S2141;T2184;T2205;S2223 | 36852467 | MTSGGSASRSGHRGVPMTSRGFDG SRRGSLRRAGARETASEAADGAAPA AGLRASPCSLASPSAAAAVAIPADM AAVLQQVLERPELNKLPKSTQNKLE KFLAEQQSEIDCLKGRHEKFKVESE QQYFEIEKRLS QSQERLVTETRECQ NLRLELEKLNNOVKVLETKTKELET AQDRNLGIQSQFTRAKEELEAEKRD LIRTNERLSQEVEYLTEDVKRLNEKL KESNTTKGELQLKLDLQASDVAVK YREKRLEQEKELHNSWLNTEL KTKTDELLALGREKGNIELEKCNLE NKKEEVLRLLEEQMNGLKTSNEHLQ KHVEDLLTKLKEAKEQQASMEEF HNELNAHIKLSNLYKSAADDSEAKS NELTRAVDELHKLLKEAGEANKTIQ DHLLQVEESKDQMEKEMLEKIGKL EKELNANDLLSATKRKGAILSEEEL AAMSPTAAAVAKIVKPGMKLTELYN AYVETQDQLLEKQENKRINKYLDEI VKEVEAKAPILKQREERYERAQKAVA SLSAKLEQAMKEIQRLQEDTDKANK HSSVLERDNQRMEIQIKDLSQQIRV LLMELEEARGNHVIRDEEVSSADISS SSEVISQHLVSYRNIEELQQNQRL FALRELGETREREEQETTSSKIAELQ HKLENSLAELEQLRESRQHQMQLV DSIVRQRDMYRILLSQTTGMAIPLQA SSLDDISLLSTPKRSSTSQTVSTPAPE PVIDSTEAIKAKAALKQLQEIFENYK EKIDSEKLQNEQLEKLEQVTDLRS QNTKISTQLDFASKRYEMLQDNVEG YRREITSLQERNQKLTATTQKQEQII NTMTQDLRGANEKLVAEVRANL KKEKEMKLSSEVRLSQQRESLLAEQ RGQNLLLTNLQTIQGILERSETETKQ RLNSQIEKLEHEISHLKKKLENEVE QRHTLTRNLDVQLLDTKRQLDTEIN LHLNTKELLKNAQKDIATLKQHLNN MEAQLASQSTQRTGKGQPGDRDDV DDLKSQLRQAEQVNDLKERLKTST SNVEQYRAMVTSLEDSLNEKQVTE EVHKNIEVRLKESAEFQTQLEKLM EVEKEKQELQDDKRKAIESMEQQLS ELKKTLSVQNEVQEALQRASTALS NEQQARRDCQEQAIAVEAQNKYER ELMLHAADVEALQAAKEQVSKMSTI RQHLEETTQKAESQLLECKASWEER ERVVKDEVSKSVSRCEDLEKQNRL HDQIEKLSKVVVTSMKDAVQAPLNV |

SLNEEGKSQEQILEILRFIRREKEIAE
TRFEVAQVESLRYRQRVELLERELQ
ELQDSLNVEREKVQVTAKTMAQHE
ELMKKTETMNVVMETNKMLREEKE
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ANAELSEKSGMLQAEKKLLEEDVKR
WKARNQQLINQQKDPDTEEYRLLS
EKEIHTKRIQQLNEEVGRLKAEIARS
NASLTNNQNLIQSLREDLSKARTEK
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GRRYKTQFEELKAQQNKAMETSTQS
SGDHQEQHISVQEMQELKDTLSQS
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RSLQEQTVQLQSELSRLRQDLQDKT
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PTTQVESQEQAMQSEGPEHVPVFG
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SATPSSSLPKRTREEEEDSTMEAGD
QVSEDTVEMPLPKKLMVTPVGTTEE
EVMAEESTDGEAETQAYNQDSQDSI
GEGVTQGDYTPMEDSEETSQSLQID
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DDDDEEDDTGMGDEGEDSNEGTS
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VAAPVTVFTESTTSDASEHASQSVP
MVTTSTGTLSTNETAAGDDGDEVF
VEAESEGISSEAGLEIDSQQEEEPVQ
ASDESDLPSTSQDPPSSSSVDTSSSQ
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RGISHAMGGRGINRGNIN