

MATRIX SCIENCE MASCOT Search Results

Protein View: P18872

Guanine nucleotide-binding protein G(o) subunit alpha OS=Mus musculus OX=10090 GN=Gnao1 PE=1 SV=3

Database: UP589_M_musculus
Score: 105
Monoisotopic mass (M_r): 40059
Calculated pI: 5.34

Sequence similarity is available as [an NCBI BLAST search of P18872 against nr](#).

Search parameters

MS data file: masA7A.tmp
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications: [Carbamidomethyl \(C\)](#), [Oxidation \(M\)](#)

Protein sequence coverage: 24%

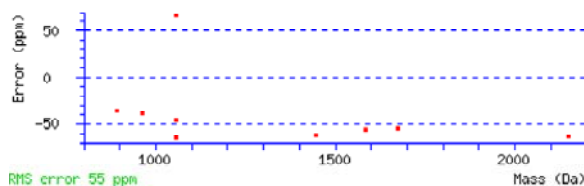
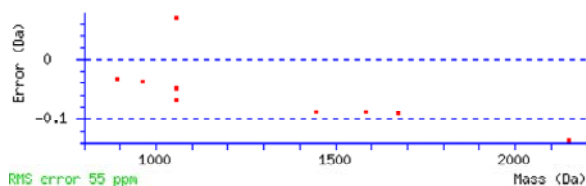
Matched peptides shown in **bold red**.

1 MGCTLSAEER AALERSKAIE KNLKEDGISA AKDVK**LLLLG AGESGK**STIV
51 KQMK**I IHEDG FSGEDVKQYK PVVYSNTIQS LA**AIVRAMDT LGVEYGDKER
101 KTD**S KMVC**DV VSRMEDTEPF SAELLSAMMR LWGDSGIQEC FNRSREYQLN
151 DSAKYILDSL DR**IGAGDYQP TEQDIL**RTRV KTTGIVETHF TFKNLHFR**LF**
201 **DVGGQR**SERK KWIHCFEDVT AIIFCVALS G YDQVLHEDET TNRMHESLML
251 FDSICNNKFF IDTSIILFLN KKDLFGEKIK KSPLTICFPE YPGSNTYEDA
301 AAYIQTFES KNRSPNKEIY CHMTCATDTN NIQVVFDAVT DIIANNLRG
351 CGLY

Unformatted sequence string: [354 residues](#) (for pasting into other applications).

Sort by ☒ residue number ☐ increasing mass ☐ decreasing mass
Show ☒ matched peptides only ☐ predicted peptides also

Query	Start - End	Observed	Mr(expt)	Mr(calc)	Delta M	Score	Expect	Rank	U	Peptide
316	36 - 46	529.2820	1056.5494	1056.6179	-0.0685	0 56	0.00047	1	U	K.LLLLGAGESGK.S
317	36 - 46	529.2919	1056.5692	1056.6179	-0.0487	0 48	0.003	1	U	K.LLLLGAGESGK.S
318	36 - 46	529.3511	1056.6876	1056.6179	0.0697	0 14	5.8	1	U	K.LLLLGAGESGK.S
421	55 - 67	482.5388	1444.5945	1444.6834	-0.0889	0 38	0.018	1	U	K.IIHEDGFSGEDVK.Q
461	68 - 86	717.3583	2149.0531	2149.1895	-0.1364	0 20	1.1	1	U	K.QYKPVVYSNTIQSLAAIVR.A
438	87 - 100	528.5538	1582.6396	1582.7297	-0.0901	1 35	0.035	1	U	R.AMDTLGVEYGDKER.K
261	106 - 113	483.2123	964.4100	964.4470	-0.0371	0 34	0.059	1	U	K.MVCDVVS.R.M + Carbamidomethyl (C)
441	163 - 177	838.3725	1674.7304	1674.8213	-0.0909	0 20	1.1	1	U	R.IGAGDYQPTQDILR.T
215	199 - 206	446.2216	890.4286	890.4610	-0.0324	0 30	0.17	1	U	R.LFDVGGQR.S



ID GNAO_MOUSE Reviewed; 354 AA.
AC P18872; P18873;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 23-JAN-2007, sequence version 3.
DT 08-NOV-2023, entry version 215.
DE RecName: Full=Guanine nucleotide-binding protein G(o) subunit alpha;
GN Name=Gnao1; Synonyms=Gna0, Gnao;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae;
OC Murinae; Mus; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS ALPHA-1 AND ALPHA-2).
RC TISSUE=Brain, and Spermatid;
RX PubMed=1697681; DOI=10.1073/pnas.87.17.6477;
RA Strathmann M., Wilkie T.M., Simon M.I.;
RT "Alternative splicing produces transcripts encoding two forms of the alpha
subunit of GTP-binding protein Go.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6477-6481(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA-1).
RC STRAIN=C57BL/6J; TISSUE=Brain;

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RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA project:
RT the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127(2004).
RN [3]
RP PROTEIN SEQUENCE OF 22-32; 36-46; 55-100; 106-143; 146-177; 182-193;
RP 199-206 AND 244-272, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC STRAIN=C57BL/6J; TISSUE=Brain, and Hippocampus;
RA Lubec G., Klug S., Kang S.U.;
RL Submitted (APR-2007) to UniProtKB.
RN [4]
RP FUNCTION, AND INTERACTION WITH RGS14.
RX PubMed=10926822; DOI=10.1042/bj3500019;
RA Traver S., Bidot C., Spassky N., Baltauss T., De Tand M.F., Thomas J.L.,
RA Zalc B., Janoueix-Lerosey I., Gunzburg J.D.;
RT "RGS14 is a novel Rap effector that preferentially regulates the GTPase
RT activity of galphao.";
RL Biochem. J. 350:19-29(2000).
RN [5]
RP SUBCELLULAR LOCATION.
RX PubMed=15585744; DOI=10.1124/mol.104.003913;
RA Nakata H., Kozasa T.;
RT "Functional characterization of Galphao signaling through G protein-
RT regulated inducer of neurite outgrowth 1.";
RL Mol. Pharmacol. 67:695-702(2005).
RN [6]
RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RC TISSUE=Brain, Brown adipose tissue, Heart, Kidney, Liver, Lung, and
RC Testis;
RX PubMed=21183079; DOI=10.1016/j.cell.2010.12.001;
RA Huttlin E.L., Jedrychowski M.P., Elias J.E., Goswami T., Rad R.,
RA Beausoleil S.A., Villen J., Haas W., Sowa M.E., Gygi S.P.;
RT "A tissue-specific atlas of mouse protein phosphorylation and expression.";
RL Cell 143:1174-1189(2010).
RN [7]
RP HISTAMINYLATION AT GLN-205.
RX PubMed=23022564; DOI=10.1016/j.febslet.2012.09.027;
RA Vowinckel J., Stahlberg S., Paulmann N., Bluemlein K., Grohmann M.,
RA Ralser M., Walther D.J.;
RT "Histaminylation of glutamine residues is a novel posttranslational
RT modification implicated in G-protein signaling.";
RL FEBS Lett. 586:3819-3824(2012).
CC -!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are involved
CC as modulators or transducers in various transmembrane signaling
CC systems. Stimulated by RGS14. The G(o) protein function is not clear.
CC {ECO:0000269|PubMed:10926822}.
CC -!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and gamma. The
CC alpha chain contains the guanine nucleotide binding site. Forms a
CC complex with GNB1 and GNG3 (By similarity). Interacts with RGS14.
CC Interacts with RGS19 (By similarity). {ECO:0000250|UniProtKB:P09471,
CC ECO:0000269|PubMed:10926822}.
CC -!- INTERACTION:
CC P18872-1; P97428: Rgs16; NbExp=2; IntAct=EBI-1018790, EBI-643424;
CC -!- SUBCELLULAR LOCATION: Cell membrane {ECO:0000269|PubMed:15585744}.
CC Membrane {ECO:0000250|UniProtKB:P09471}; Lipid-anchor
CC {ECO:0000250|UniProtKB:P09471}.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha-1;
CC IsoId=P18872-1; Sequence=Displayed;
CC Name=Alpha-2;
CC IsoId=P18872-2, P18873-1; Sequence=VSP_031251;
CC -!- PTM: Histaminylated at Gln-205 residues by TGM2.
CC {ECO:0000269|PubMed:23022564}.
CC -!- SIMILARITY: Belongs to the G-alpha family. G(i/o/t/z) subfamily.
CC {ECO:0000305}.
CC -----
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CC -----
DR EMBL; M36777; AAA37645.1; -; mRNA.
DR EMBL; M36778; AAA74566.1; -; mRNA.
DR EMBL; BC051989; AAH51989.1; -; mRNA.
DR CCDS; CCDS22532.1; -. [P18872-1]
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DR PIR; A36038; RGMSO1.
DR PIR; B36038; RGMSO2.
DR RefSeq; NP_001106855.1; NM_001113384.1. [P18872-2]
DR RefSeq; NP_034438.1; NM_010308.3. [P18872-1]
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DR PDBsum; 3C7K; -.
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DR SMR; P18872; -.
DR BioGRID; 199970; 46.
DR DIP; DIP-29921N; -.
DR IntAct; P18872; 13.
DR MINT; P18872; -.
DR STRING; 10090.ENSMUSP000000114144; -.
DR GlyGen; P18872; 2 sites, 1 O-linked glycan (2 sites).
DR iPTMnet; P18872; -.
DR PhosphoSitePlus; P18872; -.
DR SwissPalm; P18872; -.
DR jPOST; P18872; -.
DR MaxQB; P18872; -.
DR PaxDb; 10090-ENSMUSP000000114144; -.
DR PeptideAtlas; P18872; -.

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DR ProteomicsDB; 271021; -. [P18872-1]
DR ProteomicsDB; 271022; -. [P18872-2]
DR Pumba; P18872; -.
DR Antibodypedia; 3649; 283 antibodies from 34 providers.
DR DNASU; 14681; -.
DR Ensembl; ENSMUST00000034198; ENSMUSP00000034198; ENSMUSG00000031748. [P18872-1]
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DR VEuPathDB; HostDB:ENSMUSG00000031748; -.
DR eggNOG; KOG0082; Eukaryota.
DR GeneTree; ENSGT00940000155883; -.
DR HOGENOM; CLU_014184_6_0_1; -.
DR InParanoid; P18872; -.
DR OMA; RIGQANY; -.
DR OrthoDB; 2897309at2759; -.
DR PhylomeDB; P18872; -.
DR TreeFam; TF300673; -.
DR Reactome; R-MMU-4086398; Ca2+ pathway.
DR BioGRID-ORCS; 14681; 2 hits in 77 CRISPR screens.
DR ChITaRS; Gnaol; mouse.
DR EvolutionaryTrace; P18872; -.
DR PRO; PR:P18872; -.
DR Proteomes; UP000000589; Chromosome 8.
DR RNAct; P18872; Protein.
DR Bgee; ENSMUSG00000031748; Expressed in perirhinal cortex and 233 other tissues.
DR ExpressionAtlas; P18872; baseline and differential.
DR Genevisible; P18872; MM.
DR GO; GO:0044297; C:cell body; IDA:MGI.
DR GO; GO:0030425; C:dendrite; IDA:MGI.
DR GO; GO:0005834; C:heterotrimeric G-protein complex; IBA:GO_Central.
DR GO; GO:0016020; C:membrane; TAS:MGI.
DR GO; GO:0043209; C:myelin sheath; HDA:UniProtKB.
DR GO; GO:0005886; C:plasma membrane; ISO:MGI.
DR GO; GO:0051430; F:corticotropin-releasing hormone receptor 1 binding; ISO:MGI.
DR GO; GO:0031821; F:G protein-coupled serotonin receptor binding; ISO:MGI.
DR GO; GO:0031683; F:G-protein beta/gamma-subunit complex binding; IBA:GO_Central.
DR GO; GO:0005525; F:GTP binding; IMP:MGI.
DR GO; GO:0032794; F:GTPase activating protein binding; ISO:MGI.
DR GO; GO:0003924; F:GTPase activity; IDA:UniProtKB.
DR GO; GO:0046872; F:metal ion binding; IEA:UniProtKB-KW.
DR GO; GO:0031852; F:mu-type opioid receptor binding; ISO:MGI.
DR GO; GO:0005102; F:signaling receptor binding; ISO:MGI.
DR GO; GO:0007188; P:adenylate cyclase-modulating G protein-coupled receptor signaling pathway; IBA:GO_Central.
DR GO; GO:0007212; P:dopamine receptor signaling pathway; IMP:MGI.
DR GO; GO:0007186; P:G protein-coupled receptor signaling pathway; IMP:MGI.
DR GO; GO:0007626; P:locomotory behavior; IMP:MGI.
DR GO; GO:0051926; P:negative regulation of calcium ion transport; ISO:MGI.
DR GO; GO:0046676; P:negative regulation of insulin secretion; IMP:MGI.
DR GO; GO:0008016; P:regulation of heart contraction; IMP:MGI.
DR GO; GO:0010243; P:response to organonitrogen compound; ISO:MGI.
DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IMP:MGI.
DR CDD; cd00066; G-alpha; 1.
DR Gene3D; 1.10.400.10; GI Alpha 1, domain 2-like; 1.
DR Gene3D; 3.40.50.300; P-loop containing nucleotide triphosphate hydrolases; 1.
DR InterPro; IPR001408; Gprotein_alpha_I.
DR InterPro; IPR001019; Gprotein_alpha_su.
DR InterPro; IPR011025; GproteinA_insert.
DR InterPro; IPR027417; P-loop_NTPase.
DR PANTHER; PTHR10218; GTP-BINDING PROTEIN ALPHA SUBUNIT; 1.
DR PANTHER; PTHR10218:SF355; GUANINE NUCLEOTIDE-BINDING PROTEIN G(O) SUBUNIT ALPHA; 1.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR PRINTS; PR00441; GPROTEINAI.
DR SMART; SM00275; G_alpha; 1.
DR SUPFAM; SSF52540; P-loop containing nucleoside triphosphate hydrolases; 1.
DR SUPFAM; SSF47895; Transducin (alpha subunit), insertion domain; 1.
DR PROSITE; PS51882; G_ALPHA; 1.
PE 1: Evidence at protein level;
KW 3D-structure; Alternative splicing; Cell membrane;
KW Direct protein sequencing; GTP-binding; Lipoprotein; Magnesium; Membrane;
KW Metal-binding; Myristate; Nucleotide-binding; Palmitate;
KW Reference proteome; Transducer.
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Mascot: http://www.matrixscience.com/
