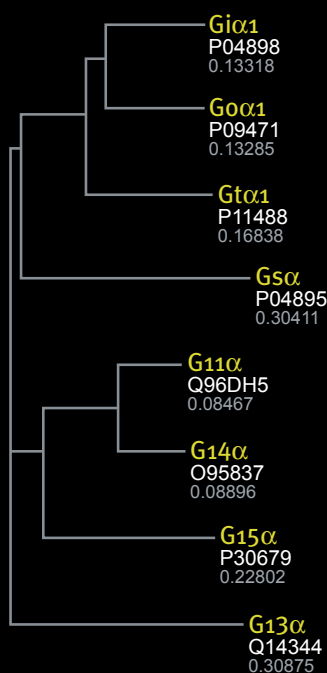




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Rat G Protein $G\alpha 1$
(Residues 1-353)
PDB: 1A50

G Protein Alpha Subunits



Sequence alignment of G protein alpha subunits. The alignment shows residues 1-353 for each subunit, with gaps indicated by dashes. Conserved residues are highlighted in yellow.

Residue numbers: 33, 40, 43, 49, 94, 94, 90, 117, 101, 97, 104, 110, 185, 186, 181, 209, 191, 187, 254, 208, 245, 246, 241, 269, 251, 247, 254, 268, 292, 293, 288, 318, 298, 294, 301, 315.

Subunits: $G_i\alpha 1$, $G\alpha 1$, $G_t\alpha 1$, $G_s\alpha$, $G_{11}\alpha$, $G_{14}\alpha$, $G_{15}\alpha$, $G_{13}\alpha$.

Conserved residues (yellow):

- 33: VKLLLLGAGESGKSTIVKQMKIIHEAGYSEEECKQYKAVVYSNT
- 40: LKLLLLGTGESGKSTIVKQMKRIIHGAGYSEEDKRGFTKL VYQNI
- 43: LKLLLLGPESGKSTIVKQMKRIIHGAGYSEEDKRGFTKL VYQNI
- 49: VKLLLLGAGESGKSTIVKQMKRIIHGAGYSEEDKRGFTKL VYQNI
- 94: [34 aa]-KRLWKDSGVQACFNRSREYQLNDSAAYYLNDLDRIAQPNVIPTQDDVLRVKTGIV
- 94: [35 aa]-MRLWGDGSGIQECFNRSREYQLNDSAAYYLNDLDRIAQPNVIPTQDDVLRVKTGIV
- 90: [34 aa]-QRLWKDSGIVQACFNRSREYQLNDSAAYYLNDLDRIAQPNVIPTQDDVLRVKTGIV
- 117: [34 aa]-KALWEDEGVVACYSNEYQLIDCAQYFLDKIDVIAQADYVPSDQDLRLCRVLTSGIF
- 101: [32 aa]-KTLWEDPGIQECYDRRREYQLSDSAKYLLTDVDRATLGLVPTQDDVLRVKTGIV
- 97: [32 aa]-KQLWDPGIVQECYDRRREYQLSDSAKYLLTDVDRATLGLVPTQDDVLRVKTGIV
- 104: [32 aa]-QWLWRDAGIRACYSNEYQLIDCAQYFLDKIDVIAQADYVPSDQDLRLCRVLTSGIF
- 110: [40 aa]-RALWADSGIQNAYDRRREFQLGESVKYFLNDLNDLKDLPEDYIPSQDILLARRPTKGTH
- 185: ETHFTFKDLHFKMFVGGQSRERKWIHCFEGVTAIIFCVALS DYDLVLADEEMNRMHE
- 186: ETHFTFKDLHFKMFVGGQSRERKWIHCFEGVTAIIFCVALS DYDLVLADEEMNRMHE
- 181: ETQFSKDLNFRMFVGGQSRERKWIHCFEGVTAIIFCVALS DYDLVLADEEMNRMHE
- 209: ETQFSKDLNFRMFVGGQSRERKWIHCFEGVTAIIFCVALS DYDLVLADEEMNRMHE
- 191: EYFPDLNFIIRFMDVGGQSRERKWIHCFENVSTIIFLVALSEYDQVLAECDNENRMHE
- 187: EYFPDLNFIIRFMDVGGQSRERKWIHCFENVSTIIFLVALSEYDQVLAECDNENRMHE
- 254: EYCFVQKTLNRIIDVGGQSRERKWIHCFENVSTIIFLVALSEYDQVLAECDNENRMHE
- 208: EYDFEIKNVFPMVDFVGGQSRERKWIHCFENVSTIIFLVALSEYDQVLAECDNENRMHE
- 245: SKMLFDSICNNKWFDTISILFLNKKDLFEKIK--KSPLTICFPEYAG
- 246: SKMLFDSICNNKWFDTISILFLNKKDLFEKIK--KSPLTICFPEYAG
- 241: SLHLFNSICNNHRYFATTSIVLFLNKKDLFEKIK--KAHLSTICFPEYAG
- 269: ALNLFKSIWNNRWLTISVILFLNKKDLFEKIK--KAHLSTICFPEYAG
- 251: SKALFRITITYPWFQNSVILFLNKKDLFEKIK--KAHLSTICFPEYAG
- 247: SKALFRITITYPWFQNSVILFLNKKDLFEKIK--KAHLSTICFPEYAG
- 254: SLALFGTILELPWFKSTSVILFLNKKDLFEKIK--KAHLSTICFPEYAG
- 268: SLNLFETIVNNRVFNVSVILFLNKKDLFEKIK--KAHLSTICFPEYAG
- 292: [29 aa]-HFTCATDTKNVQVFDAVTDVIDK 344
- 293: [28 aa]-HFTCATDTNNIQVVFDAVTDVIDK 344
- 288: [29 aa]-HFTCATDTQNVKVFDAVTDVIDK 340
- 318: [43 aa]-HFTCAVDTENIRVFNDCRDIIQR 385
- 298: [29 aa]-HFTCATDTENIRVFVAVKDTIIQ 350
- 294: [29 aa]-HFTCATDTNIRVFVAVKDTIIQ 346
- 301: [41 aa]-HYTCTTDTNIRKVFQVDRSVIA 365
- 315: [30 aa]-HFTTTINTENIRLVFRDVKDTIIH 368