

hcGAS 1 MQPWHGKAMQRASEAGATAPKASARNARGAPMDPTESPAAPEAALPKAGKF GPARKSGSR 60
 mcGAS 1 MEDPRRRRT - - - - - TAPRAKKPSAKRAPTQPSRTRAHAESC - - - - - GPQRGARSR 44

hcGAS 61 QKKSAPDTQERPPVVRATGARAK - - KAPQRAQDTQPSDATSAPGAEG - - - - - LE 106
 mcGAS 45 RAERDGDITTEKP - - RAPGPRVHPARATELTKDAQPS - AMDAAGATARPAVRVPQQQA I LD 101

hcGAS 107 P - - PAAREP - - - ALSRA - - - - - GSCRQRGARCSTKPRPPPGPWDVPSGLPVSAPI LVRR 156
 mcGAS 102 PELPAVREPQPPADPEARKVVRGSPSHRRGARSTGQPRAPRGRSKE - - - - - 146

Enzymatic domain
 hcGAS 157 DAAPGAS¹⁷³KLRAVLEK¹⁷⁴KLKLS¹⁷⁶RDDIS¹⁸⁰TAAGMV¹⁸¹KGVVDHLL¹⁹⁵LRL - KCDSAFRQVGLLNTGSYY 215
 mcGAS 147 PD - - - - - KLKVL¹⁷³DKLRL¹⁷⁴KR¹⁷⁶KDIS¹⁸⁰EAAETV¹⁸¹NK¹⁸⁷VVERLL¹⁹⁵RRMQKRESEFKGVEQLNTGSYY 201
 hcGAS Strx

hcGAS 216 EHVKISAPNEFDVMFKLEVPRI²¹⁷QLEEYSNTRAYYFVKFKRNPKENPLSQFLEGEILSASK 275
 mcGAS 202 EHVKISAPNEFDVMFKLEVPRI²³⁶ELQEYYETGAFYLVKFKRIPRGNPLSHFLEGEVLSATK 261
 hcGAS Strx

hcGAS 276 MLSKFRKIIKEEINDIKD³²⁸TDVIMKRKRGGSPAVTLLIS - - EKISVDITLALLESK³²⁸SWPAS 333
 mcGAS 262 MLSKFRKIIKEEVKEIKDIDVSVEKEKPGSPAVTLLIRNPEEISVDIILALLESK³²⁸SWPIS 321
 hcGAS Strx

hcGAS 334 TQEGLRIQNWL³⁴⁶SAKVR³⁴⁷KQL³⁵⁰RLKPFYLVPHAKEGNGFQEETWRLSFSHIE³⁵³ILNNHGKS 393
 mcGAS 322 TKEGLPIQGWLG³⁴⁶TKVR³⁴⁷TNLR³⁵³REPFYLVPHAKDGN³⁵⁴SFQGETWRLSFSHTE³⁸⁴KYILNNHGE 381
 hcGAS Strx

hcGAS 394 KTCCE³⁹⁷NKEEK⁴⁰³CCR⁴⁰⁷KDCL⁴¹¹KLMKYLLLEQLKERFKDKKHLDFSSYHVKTAFHHVCTQNPQDS 453
 mcGAS 382 KTCCE³⁹⁷SSGAK⁴⁰³CCR⁴⁰⁷KECL⁴¹¹KLMKYLLLEQLKKEFQE - - LDAFCSYHVKTAFHFWTQDPQDS 438
 hcGAS Strx

hcGAS 454 QWDRKDLGLCFDNCVTYFLQCLRTEKLENYFIPEFNLFSSNLIDKRSKEFLTKQIEYERN 513
 mcGAS 439 QWDPRNLSSCFDKLLAFFLECLRTEKLDHYFIPKFNLFSSQELIDKRSKEFLSKKIEYERN 498
 hcGAS Strx

hcGAS 514 NEFPVFDEF 522
 mcGAS 499 NGFPIFDKL 507
 hcGAS Strx