




Trafficking of the glutamate transporter is impaired in LRRK2-related Parkinson's disease

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Abstract

The Excitatory Amino Acid Transporter 2 (EAAT2) accounts for 80% of brain glutamate clearance and is mainly expressed in astrocytic perisynaptic processes. EAAT2 function is finely regulated by endocytic events, recycling to the plasma membrane and degradation. Noteworthy, deficits in EAAT2 have been associated with neuronal excitotoxicity and neurodegeneration. In this study, we show that EAAT2 trafficking is impaired by the leucine-rich repeat kinase 2 (LRRK2) pathogenic variant G2019S, a common cause of late-onset familial Parkinson's disease (PD). In LRRK2 G2019S human brains and experimental animal models, EAAT2 protein levels are significantly decreased, which is associated with elevated gliosis. The decreased expression of the transporter correlates with its reduced functionality in mouse LRRK2 G2019S purified astrocytic terminals and in *Xenopus laevis* oocytes expressing human LRRK2 G2019S. In LRRK2 G2019S knock-in mouse brain, the correct surface localization of the endogenous transporter is impaired, resulting in its interaction with a plethora of endo-vesicular proteins. Mechanistically, we report that pathogenic LRRK2 kinase activity delays the recycling of the transporter to the plasma membrane via Rab5 inactivation, causing its intracellular re-localization and degradation. Taken together, our results demonstrate that pathogenic LRRK2 interferes with the physiology of EAAT2, pointing to extracellular glutamate overload as a possible contributor to neurodegeneration in PD.

Keywords LRRK2 · Glt-1 · EAAT2 · Glia · Astrocytes · Parkinson's disease

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Introduction

The concentration of extracellular glutamate in the central nervous system is finely tuned by specific excitatory amino acid transporters (EAATs) [56, 91], which remove the neurotransmitter from the extracellular synaptic milieu and prevent the dramatic consequences of glutamate accumulation [8, 13, 20, 44, 52, 69, 75]. Impaired glutamate uptake entails neuropathological consequences such as alteration of synaptic neurotransmission, neuronal excitotoxicity, as well as astrocyte and microglia reactivity and neurodegeneration [29, 33]. Among EAATs, EAAT2 (corresponding to glutamate transporter type 1, Glt-1 in rodents) is the predominant glutamate transporter in the adult mammalian brain and accounts for the removal of most of the extracellular glutamate [71, 84]. Approximately 80 to 90% of EAAT2 is localized on astrocytes, and 5 to 10% on the axonal terminal of neurons [8, 13, 20, 52, 69, 75].

Regulation of EAAT2 function occurs by protein expression and protein distribution. Indeed, both lateral diffusion and endocytic trafficking ensure a dynamic turnover of the receptor at the synaptic terminals that reflects the shuffling activity of neighboring cells [2, 44, 46, 57]. EAAT2 is constitutively internalized into recycling endosomes via a clathrin-dependent pathway, which relies on the reversible ubiquitination of specific lysine residues located in the cytoplasmic C-terminus [25]. The ubiquitin ligase Nedd4-2 has been identified as a mediator of EAAT2 endocytosis [101]. The activation of protein kinase C (PKC) promotes the phosphorylation of Nedd4-2, its association with EAAT2, and the subsequent ubiquitination of the transporter [21]. Importantly, a ubiquitination/de-ubiquitination cycle enables a reversal translocation of EAAT2 from the recycling endosomes back to the plasma membrane. Therefore, a strict regulation of this bidirectional trafficking is crucial to guarantee an appropriate exposure of EAAT2 at the cell surface [25, 47]. Interference with EAAT2 trafficking has been often associated with the re-routing of the transporter to the cellular degradative systems [74, 82, 90, 93].

Parkinson's disease (PD) is a progressive neurodegenerative disorder clinically characterized by severe motor disability and cognitive impairment [1]. The pathological hallmarks of PD include the selective loss of dopaminergic neurons in the *Substantia nigra pars compacta* (*SNpc*) that project to the dorsal striatum, the presence of Lewy Bodies in neuronal and glial cells, as well as signs of extended neuroinflammation [30, 77, 78]. Despite decades of research, the mechanisms underlying the selective degeneration of dopaminergic neurons in PD remain unclear [14]. Recent hypotheses support the idea that chronic, subtle dysfunctions proceed years before the

clinical symptoms and the dopaminergic death [86]. Perturbation of glutamate homeostasis is one of the earliest events in the pathophysiology of PD and contributes to the exacerbation of later clinical impairments [18, 33, 37, 59, 98]. In addition, deficits in glutamate transporters have been consistently reported upon acute neurotoxin injection in rodents [9, 10, 101] as well as in genetic models of PD [11, 28, 37], and selective ablation of nigral and striatal astrocytic Glt-1 expression induces a parkinsonian-like phenotype in mice [66, 102].

Monogenic mutations with Mendelian transmission have been identified in about 10% of PD cases [34], and mutations in the leucine-rich repeat kinase 2 (LRRK2) account for up to 40% of familial PD forms. Specifically, the most common LRRK2 G2019S mutation leads to the expression of a hyperactive form of the LRRK2 kinase and appears in approximately 1% of apparently sporadic PD cases, with much higher prevalence in specific ethnic groups [87]. Although LRRK2 G2019S animal models do not show clear signs of neurodegeneration, aberrant cortico-striatal glutamatergic neurotransmission has been observed, thus comprising a valuable model system to study the early stages of the disease [7, 42, 48, 49, 89, 92].

Here, we report that the PD-linked LRRK2 G2019S mutation decreases the functionality of EAAT2 in astrocytes by impairing Rab-mediated recycling to the plasma membrane. Overall, our results point to glutamatergic dysregulation as a key pathological event in PD.

Materials and methods

Human samples

Post-mortem human caudate and putamen were lysed in RIPA buffer (20 mM Tris-HCl pH 7.5, 150 mM NaCl, 1 mM EDTA, 2.5 mM sodium pyrophosphate, 1 mM β -glycerophosphate, and 1 mM sodium orthovanadate) containing protease and phosphatase inhibitors (Roche) derived from four LRRK2 G2019S-linked patients, five idiopathic PD patients, and five age-matched controls were obtained from Queen Square Brain Bank (London, UK). *Post-mortem* human brains were collected under human tissue authority license n° 12198. Limited sample demographics are listed in Table 1 and detailed in [45].

Animals

C57Bl/6J LRRK2 wild-type (WT) and LRRK2 G2019S knock-in homozygous mice were used. LRRK2 G2019S knock-in mice were obtained from Prof. Michele Morari and Novartis Institutes for BioMedical Research, Novartis Pharma AG (Basel, Switzerland) [41]. Housing and handling

Table 1 Sample demographics of the human cases used in this study

Cases	Sex (F/M)	Age	Post-mortem dissection (hours)
LRRK2 G2019S 1	F	72	24.55
LRRK2 G2019S 2	F	84	32.2
LRRK2 G2019S 3	F	81	15
LRRK2 G2019S 4	F	80	44.4
Healthy Control 1	M	71	42.3
Healthy Control 2	F	82	55
Healthy Control 3	M	83	35.4
Healthy Control 4	F	80	66.2
Healthy Control 5	M	69	49.3
iPD 1	M	78	22.3
iPD 2	F	74	57.5
iPD 3	M	80	62.5
iPD 4	M	80	34.5
iPD 5	F	76	44.2

The table illustrates sex, age, and *Post-Mortem* Dissection (expressed in hours) characteristics of LRRK2 G2019S ($n=4$), Healthy Controls ($n=5$), and idiopathic PD (iPD; $n=5$) patients employed in the study

of mice were done in compliance with national guidelines. All procedures performed in mice were approved by the Ethical Committee of the University of Padova and the Italian Ministry of Health (license 1041/2016, 200/2019 and 105/2019). All procedures performed in *Xenopus laevis* were approved and experiments carried out according to the Ethical Committee of the University of Insubria (license no. 02_15) and the Italian Ministry of Health (1011/2015).

Immunoblotting

Human caudate and putamen samples as well as dissected striata or primary astrocytes derived from LRRK2 WT and LRRK2 G2019S knock-in mice were lysed in RIPA buffer containing 1% protease inhibitor cocktail (Sigma-Aldrich). Protein concentration was measured using the Pierce[®] BCA Protein Assay Kit following the manufacturer's instructions (Thermo Scientific). 25 μ g protein samples were resolved by electrophoresis on pre-cast 4–20% tris–glycine polyacrylamide gels (Biorad) and transferred to polyvinylidene difluoride membranes using a semi-dry Bio-Rad transfer machine (Trans-Blot[®] Turbo TM Transfer System) with the 1X Transfer Buffer (Bio-Rad) at 25 V for 20 min. Membranes were incubated in Tris-buffered saline plus 0.1% Tween (TBS-T) plus 5% skimmed milk for 1 h at room temperature (RT), and then incubated overnight with primary antibodies diluted in TBS-T plus 5% skimmed milk. The following primary antibodies were used: guinea pig anti-glutamate transporter (Glt-1/EAAT2; AB1783, EMD Millipore, 1:500), mouse anti-GAPDH (CSB-MA000195,

Cusabio, 1:3000), mouse anti- β -actin (A1978, Sigma-Aldrich, 1:10,000), mouse anti-HSP70 (H5147; Sigma-Aldrich, 1:5000), mouse anti-Flag-HRP (A8592; Sigma-Aldrich, 1:5000), rabbit anti-glial fibrillary acidic protein (GFAP; Z0334, Dako, 1:20,000/1:100,000), rabbit anti-glutamine synthetase (GS; GTX109121, GENETEX, 1:1000), rabbit anti-Tyrosine Hydroxylase (TH; AB152, EMD Millipore, 1:1000), rabbit anti-Rab8A (ab188574; Abcam, 1:2500), rabbit anti-Rab10 (ab104859; Abcam, 1:1400), rabbit anti-phospho-Rab8A T72 (ab230260; Abcam, 1:1000), rabbit anti-phospho Rab10 T73 (ab230261; Abcam, 1:400), rabbit anti-LRRK2 (MJFF2 c41-2; Abcam, 1:300), rabbit anti-pS935 LRRK2 (ab133450; Abcam, 1:300), and rabbit anti-pS1292 LRRK2 (ab203181; Abcam, 1:500). Membranes were subsequently rinsed and incubated for 1 h at RT with the appropriate HorseRadish-Peroxidase (HRP)-conjugated secondary antibodies (Invitrogen). The visualization of the signal was conducted using Immobilon[®] Forte Western HRP Substrate (Millipore) and the VWR[®] Imager Chemi Premium. Images were acquired and processed with ImageJ software to quantify total intensity of each single band.

Human caudate and putamen immunofluorescence and immunohistochemistry analysis

Paraffin-embedded sections (8 μ m) from caudate and putamen were cut using a microtome (Thermo Scientific). To remove paraffin wax, 8 μ m slices were washed in xylene and rehydrated in 100% ethanol. Slices were treated for 15 min with a quenching solution containing 50 mM NH₄Cl in phosphate buffer saline (PBS) for immunofluorescence analysis, or 100% methanol and 3% H₂O₂ for immunohistochemistry studies. Slices were then washed in TBS-T and incubated at 90 °C for 15 min with a citrate buffer (10 mM sodium citrate and 0.1 M citric acid dissolved in distilled water; pH 7.0) to perform epitope retrieval. Subsequently, slices were saturated for 1 h at RT in a blocking solution containing 1% bovine serum albumin (BSA), 15% goat serum, 0.25% gelatin, 0.20% glycine, and 0.5% Triton. Slices were then incubated overnight at 4 °C with the following primary antibodies diluted in blocking solution: guinea pig anti-EAAT2 (1:200) and/or rabbit anti-GFAP (1:400). The following day, slices were washed in TBS-T and incubated for 1 h at RT with a mixture of the following secondary antibodies diluted 1:200 in blocking solution: anti-guinea pig Alexa Fluor 488 (Life Technologies) and anti-rabbit Alexa Fluor 568 (Life Technologies) fluorophores. Upon washes in TBS-T, slices were incubated for 5 min with Hoechst (1:10,000; Invitrogen) to visualize the nuclei and mounted with Mowiol (Calbiochem).

For immunohistochemistry analysis, sections processed with rabbit anti-GFAP were incubated for 1 h at RT using secondary HRP-conjugated anti-rabbit antibody (1:200).

Slices were then washed and developed for 2–3 min using 3,3'-diaminobenzidine (DAB) staining kit (Abcam; #ab64238;). Nuclei were counterstained using Haematoxylin (MHS32-Sigma) for 5 min. Finally, sections were dehydrated in graded ethanol (70%, 90% and 100%), transferred in xylene, and mounted using a Eukitt Mounting resin (Kirkker Biotech).

Plasmids

The pCMV-hEAAT2 plasmid encoding the human excitatory amino acid transporter type 2 (EAAT2) was a gift from Susan Amara (Addgene plasmid # 32814; <http://n2t.net/addgene:32814>; RRID:Addgene_32814). The cDNA was subcloned into pcDNA3 between KpnI and XbaI restriction sites and under the T7 promoter for expression in *Xenopus laevis* oocytes. The pDESTN-SF-TAP LRRK2 plasmids encoding the human WT and G2019S variant were described in [3]. The pCMV6-mGLT-1 (Myc-DDK-tagged) plasmid encoding the mouse glial high-affinity glutamate transporter member 2 (Slc1a2), transcript variant 1, was purchased from OriGene Technologies Inc (Cat. MR226166). For the pEGFP-rat Glt1 plasmid, the 99–1820 bp fragment of the Rat Glt-1 plasmid (GenBank™ accession number X67857.1) was subcloned between the EcoRI and XbaI restriction sites of pEGFP vector (Clontech). GFP-Rab4, GFP-Rab11, and GFP-Lamp1 plasmids were generated as previously described [24, 68]. RFP-Rab8A WT or Q67L and RFP-Rab10 WT or Q68L plasmids were generated as previously described [39, 43].

Electrophysiological recordings in *Xenopus laevis* oocytes

pcDNA3_hEAAT2 and pDESTN-SF-TAP-LRRK2 WT and G2019S plasmid vectors were linearized by HindIII and SmaI, respectively. Corresponding cRNAs were transcribed in vitro and capped using T7 RNA polymerase. Oocytes were obtained by laparotomy from adult female *Xenopus laevis* (Envigo). Frogs were anesthetized by immersion in MS222 1 g/L solution in tap water adjusted at final pH 7.5 with bicarbonate. After the treatment with an antiseptic agent (povidone-iodine 0.5%), the frog abdomen was incised, and the portions of the ovary removed. Oocytes were treated with 1 mg/mL collagenase IA (Sigma Collagenase from *Clostridium histolyticum*) in calcium-free ND96 [96 mM NaCl, 2 mM KCl, 1 mM MgCl₂, 5 mM 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES); pH 7.6] for at least 1 h at 18 °C. Healthy and fully grown oocytes were selected and manually separated in NDE solution (ND96 plus 2.5 mM pyruvate, 0.05 mg/mL gentamicin sulfate, and 1.8 mM CaCl₂). After 24 h, healthy looking stage V and VI oocytes were collected and co-injection of cRNA EAAT2

(25 ng) + cRNA LRRK2 WT (25 ng) or cRNA EAAT2 (25 ng) + LRRK2 G2019S (25 ng) was carried out using a manual microinjection system (Drummond Scientific Company). Oocytes were subsequently incubated at 18 °C for 2–3 days in NDE solution [5]. Transport currents (I) were recorded from voltage-clamped oocytes using two microelectrodes filled with 3 M KCl (Oocyte Clamp OC-725C, Warner Instruments). Bath electrodes were connected to the experimental oocyte chamber via agar bridges (3% agar in 3 M KCl). The external control solution had the following composition: 98 mM NaCl, 1 mM MgCl₂, 1.8 mM CaCl₂, 5 mM HEPES, adjusted to pH 7.6 with NaOH. Signals were filtered at 0.1 kHz and sampled at 200 Hz or 0.5 kHz and at 1 kHz. Transport-associated currents were calculated by subtracting the traces in the absence of substrate from those in its presence. To measure the apparent affinity for glutamate (the concentration of glutamate that yields one-half of the maximal transport current), oocytes were exposed to different neurotransmitter concentrations (10 μM, 25 μM, 100 μM, 500 μM, and 1 mM). Clampex and Clampfit 10.7 (Molecular Devices) were used to run the experiments, and acquire and analyze the data.

Immunodetection in *Xenopus laevis* oocytes

Injected oocytes were fixed in ice-cold 4% paraformaldehyde (PFA) in PBS pH 7.5, for 15 min at 4 °C. Oocytes were subsequently washed using ND96 in mild agitation (5 min at RT, three times), included in Polyfreeze tissue freezing medium (Polysciences, Eppenheim) and frozen in liquid nitrogen. Oocyte cryosections (10 μm thickness) were obtained with a cryostat (Leica Biosystems) and preserved at –20 °C. Before use, oocyte slices were washed in PBS for 10 min at RT and incubated in blocking solution [2% BSA (w/v), 0.1% Tween in PBS] for 45 min. Slices were then incubated overnight at 4 °C with the primary antibody guinea pig anti-EAAT2 (1:200) diluted in blocking solution. The following day, oocyte sections were washed in PBS and incubated with the secondary antibody anti-guinea pig Alexa Fluor 488 fluorophore diluted 1:200 in blocking buffer for 1 h. Sections were washed and mounted using Mowiol. Images were acquired at 8-bit intensity resolution over 1024 × 1024 pixel on a Leica SP5 confocal microscope using an HC PL FLUOTAR 40x/0.70 oil objective. Using ImageJ, the integrated fluorescence density (IntDen, area × mean fluorescence) of EAAT2 was measured by defining an ROI (8 × 10^{–3} mm² area). All quantifications were applied at the animal pole of the oocytes.

Free-floating mouse brain slice immunofluorescence

Mice were anesthetized with xylazine (Rompun®) and ketamine (Zoletil®) and transcardially perfused with

physiological solution (0.9% NaCl in PBS) followed by ice-cold 4% PFA dissolved in PBS at pH 7.4. Brains were post-fixed at 4 °C for 18 h in 4% PFA and then moved in two different solutions of sucrose (20% and 30% sucrose in PBS) for 18 h each. Coronal striatal sections (30 µm thickness) were sliced using a vibratome (Campden Instruments Ltd.). Slices were stored at 4 °C in a solution containing 18% sucrose, 0.01% NaN₃ dissolved in PBS. Before staining, murine slices were rinsed in PBS and treated with 50 mM NH₄Cl dissolved in PBS for 15 min at RT to quench intrinsic autofluorescence. Sections were then washed in PBS followed by permeabilization and saturation for 1 h at RT in a blocking solution containing 2% BSA, 15% goat serum, 0.25% gelatin, 0.2% glycine and 0.5% Triton. Slices were then incubated overnight with primary antibodies diluted in blocking solution. The following primary antibodies were used: guinea pig anti-Glt-1 (1:200) and rabbit anti-GFAP (1:400). The following day, slices were washed and incubated for 1 h at RT with the appropriate secondary antibodies diluted in blocking solution: anti-guinea pig Alexa Fluor 488 or 568 fluorophores and anti-rabbit Alexa Fluor 568 or 633 fluorophores. Upon incubation, slices were washed with PBS and nuclei were counterstained with Hoechst 1:10,000 and mounted on a glass microscope slide (ThermoFisher) using Mowiol.

Images were acquired at 8-bit intensity resolution over 1024 × 1024 pixel on a Leica SP5 confocal microscope using an HC PL FLUOTAR 40x/0.70 oil objective. Using ImageJ, the IntDen of GFAP signal upon setting scale and threshold were measured. The number of GFAP⁺ cells was manually counted using the same software.

Gliosome purification

Glial perisynaptic processes (gliosomes [6, 58, 79]) derived from 4 month old LRRK2 WT and LRRK2 G2019S mouse striata were used. Gliosomes were prepared as previously described [61]. Briefly, striata were homogenized in 0.32 M sucrose, buffered at pH 7.4 with Tris-HCl, using a glass-teflon tissue grinder (clearance 0.25 mm—Potter-Elvehjem VWR International). The homogenate was centrifuged (5 min, 1000 g) to remove nuclei and debris, and the supernatant was gently layered on a discontinuous Percoll gradient (2%, 6%, 10%, and 20% v/v in Tris-buffered 0.32 M sucrose; Sigma-Aldrich). After centrifugation at 33'500 g for 5 min, the layer between 2 and 6% Percoll (gliosomal fraction) was collected and washed with a physiological medium having the following composition: 140 mM NaCl, 3 mM KCl, 1.2 mM MgSO₄, 1.2 mM NaH₂PO₄, 5 mM NaHCO₃, 1.2 mM CaCl₂, 10 mM HEPES, 10 mM glucose, and pH 7.4, and centrifuged at 20,000 g for 15 min. The pellet was resuspended in a physiological medium. All the above procedures were conducted at 4 °C. Protein concentration was

measured using the Pierce[®] BCA Protein Assay Kit following the manufacturer's instructions.

Glutamate uptake assay in gliosomes

Glutamate uptake was measured in striatal gliosomes derived from LRRK2 WT and LRRK2 G2019S mice as previously described [54]. Briefly, aliquots of the gliosomal suspensions (500 µL, corresponding to 10–15 µg protein per sample) were incubated for 10 min at 37 °C in the presence of 10 µM 2-amino-5,6,7,8-tetrahydro-4-(4-methoxyphenyl)-7-(naphthalen-1-yl)-5-oxo-4H-chromene-3-carbonitrile (UCPH-101; Abcam 120,309, UK), a specific excitatory amino acid transporter 1 (EAAT1/Glast) inhibitor [15]. Then, 20 µL of a solution of [³H]D-Aspartate ([³H] D-Asp; specific activity: 16.5 Ci/mmol; Perkin Elmer) and non-radioactive D-Aspartate (Sigma-Aldrich) was added to each sample to obtain the final concentrations of 0.03, 0.1, 1, 3, 30, and 100 µM. Incubation was continued for further 2 min. Gliosomal samples were exposed to the above [³H] D-Aspartate concentrations for 2 min at 0–4 °C, in the presence of 50 µM of the broad spectrum glutamate transporter blocker DL-threo-beta-benzyloxyaspartate (DL-TBOA; Tocris Bioscience; [76]), to determine the non-specific binding to gliosome membranes. After the 2-min exposure to [³H] D-Aspartate, uptake was blocked by rapid vacuum filtration (GF-B filters, Millipore) and filters were washed three times with 5 mL of physiological medium to remove the excess of radioactivity. Radioactivity was determined by liquid scintillation counting. The specific uptake was calculated by subtracting non-specific binding from the total filter radioactivity.

Primary striatal astrocytes

Mouse primary striatal astrocytes were obtained from postnatal animals between day 1 and day 3 as described in [81]. Brains were removed from their skull and placed in a dish containing cold Dulbecco's Phosphate-Buffered Saline (DPBS, Biowest). Olfactory bulbs and cortices were removed under an optic microscope and striata were transferred to a separate dish containing cold DPBS. After the dissection, Basal Medium Eagle (BME, Biowest), supplemented with 10% Fetal Bovine Serum (FBS, Corning) and 100 U/mL Penicillin + 100 µg/mL Streptomycin (Pen-Strep; Life Technologies), was added to the tissues. Striata were then sifted through a 70-µm cell strainer (Sarstedt) using a syringe plunger. The cell suspension was centrifuged (300 × g, 15 min) and the pellet was washed twice with 25 mL of supplemented medium. Cells were seeded at a density of 5 × 10⁶ cells/10 mL in cell culture T75 flasks. The culture medium was changed after 7 days and again after additional 3–4 days. When cell confluency reached

about 80%, microglia were detached by shaking the flask (800 rpm) for 2 h at RT. After shaking, the medium containing microglia was replaced with fresh medium. Cells were maintained in BME supplemented with 10% FBS and Pen-Strep at 37 °C in a controlled 5% CO₂ atmosphere. After 14 days, astrocytes were used for the experiments. Each experiment has been performed in triple using at least two independent cell cultures derived from different pups.

Cell transfection

Astrocytes were seeded at a density of 1×10^5 cells on 12 mm glass coverslips (VWR) coated with poly-L-lysine. Once 80% of confluency was reached, cells were transfected using Lipofectamine 2000 (Thermo Scientific) (1:3 DNA/Lipofectamine ratio). For single transfection experiments, 1 µg Myc-DDK-tagged-GLT-1 plasmid was used per each well; for double transfection experiments, 0.5 µg Myc-DDK-tagged-GLT-1 was combined with either 0.5 µg GFP-Rab4, GFP-Rab11 or GFP-Lamp1 plasmids; for triple transfection experiments, 0.3 µg Myc-DDK-tagged-GLT-1 was combined with 0.3 µg GFP-Rab4 and 0.3 µg RFP-Rab8/10 WT or QL plasmids. For TIRFM experiments, astrocytes were seeded at a density of 4×10^5 cells in 24 mm glass coverslips (VWR) coated with poly-L-lysine. Once at 80% confluence, cells were transfected with 2.5 µg GFP-GLT-1 plasmid using Lipofectamine 3000 (Invitrogen) (1:2 DNA/Lipofectamine ratio). All experiments were carried out 48 h after transfection.

Immunostaining of cultured astrocytes

Cells were fixed using 4% PFA for 20 min at RT and washed in PBS. Astrocytes were subsequently permeabilized for 20 min in PBS containing 0.1% Triton and blocked for 1 h at RT in a blocking solution containing 5% FBS in PBS. For experiments with endogenous Glt-1, astrocytes were incubated with the guinea pig anti-Glt1 (1:200) primary antibody diluted in blocking solution. To stain transfected GFP-Glt-1, astrocytes were incubated with rabbit anti-Glt-1 (1:100) primary antibody [62], whereas transfected Flag-Glt-1 cells were incubated overnight with a mouse anti-Flag® primary antibody (1:200-Sigma-Aldrich; #F1804) that recognized the DKK sequence. Co-stainings were performed with a rabbit (1:400) or mouse anti-GFAP (Sigma-Aldrich, Cat. SAB5600060-RM246) or a rat anti-Lamp1 (1:300-Abcam; #ab25245) antibody diluted in blocking solution, respectively. The next day, cells were incubated for 1 h at RT with a mixture of anti-guinea pig Alexa Fluor 488 and anti-rabbit Alexa Fluor 568 or 544 secondary antibodies, or with a mixture of anti-mouse Alexa Fluor 568 (1:200) and anti-rat Alexa Fluor 633 in blocking solution. Nuclei were

counterstained for 5 min with Hoechst (1:10,000), and after washing, coverslips were mounted using Mowiol.

Organotypic slice culture preparation

Organotypic coronal slices were prepared from 6- to 8-day-old postnatal pups from C57BL/6J mice as in [72] following the Stoppini's method [80]. Briefly, pups were anesthetized by hypothermia, and the brains were removed from the skull and separated into two hemispheres. Each hemisphere was cut into coronal slices of 400-µm thickness under sterile conditions using an McIlwain tissue chopper. The selected slices were cultured to air–fluid interface-style making use of Millicell culture inserts (30 mm diameter, 0.4 µm; Millipore) at 37 °C and 5% CO₂ for up to 14 days in vitro, changing the medium three times a week.

Biolistic transfection of organotypic slices

Organotypic coronal slices were transfected using a biolistic approach [36]. At 5 DIV, organotypic cultures were treated with 5 µM Cytosine Arabinoside (C1768; Sigma-Aldrich) overnight to reduce glial reaction following transfection. The following day, 1.5 mg of 1 µm-gold microparticles (Biorad) were coated with 15 µg GFP-Rab4 plasmid and slices were transfected making use of the DNA transformation apparatus ADNGun (Beambio). After the shot, the medium was replaced, and the slices were cultured for additional 7 days before visualization.

Fluorescence microscopy techniques

GFP-Glt-1-transfected astrocytes were imaged by Total internal reflection fluorescence microscopy (TIRFM). TIRFM was achieved with a Carl Zeiss inverted microscope equipped with an Argon laser at 37 °C using a 100× 1.45 numerical aperture (NA) oil immersion objective. Green fluorescence was excited using the 488 nm laser line and imaged through a band-pass filter (Zeiss) onto a Retiga SRV CCD camera. Images (12 bit, 696×520 pixel) were recorded with the same acquisition parameters (laser power, exposure time, and binning) [12]. After setting the threshold, the mean intensity of the GFP signal in three randomly selected regions of interest (ROIs) was measured using ImageJ. Data were expressed as fold changes over GFP-Glt-1 intensity signal measured in LRRK2 WT animals.

Flag-Glt-1 transfected astrocytes were imaged at 8-bit intensity resolution over 1920×1440 pixel using a Leica 5000B microscope HC PL FLUOTAR 40x/0.75 dry objective. Three ROIs/cell were defined, and the number of Glt-1 positive clusters (diameter > 1 µm) was counted manually using ImageJ.

Co-transfected Flag-Glt-1 astrocytes were imaged at 8-bit intensity resolution over 2048 × 2048 pixel, using a Leica SP5 confocal microscope and an HC PL FLUOTAR 40x/0.70 oil objective. After setting the threshold, ROIs were identified as the area of Lamp1, Rab11, and Rab4, and visualized in the green channel (GFP). Therefore, Lamp1, Rab11, and Rab4 IntDen were calculated for each ROI. The JACoP plugin (ImageJ) was applied for the quantification of co-localization between Flag-Glt-1 signal and the Lamp1, Rab11, and Rab4-positive structures, graphically displayed as the Pearson's Correlation Coefficient.

For the characterization of the recycling compartment, the number of GFP-Rab4-positive dots as well as the area of Rab4-positive vesicles was measured using ImageJ.

Transfected organotypic slices were imaged at 8-bit intensity resolution over 2048 × 2048 pixel, using Zeiss LSM 900 with Airyscan2 and an EC PLAN-Neofluar 40X/1.30 Oil DIC M27 objective.

Transmission electron microscopy analysis

Primary striatal astrocytes from LRRK2 WT and LRRK2 G2019S mice were seeded in 35 mm dishes containing a 14 mm Gridded Coverslip (MatTek, Life Science) and co-transfected with Flag-Glt-1 and GFP-Rab4. After 48 h of transfection, cells were fixed using 4% PFA dissolved in PBS and GFP-Rab4 was imaged on a Leica SP5 confocal microscope. Subsequently, cells were incubated in 2.5% glutaraldehyde dissolved in 0.1 M sodium cacodylate buffer for 1 h at 4 °C and post-fixed in 1% osmium tetroxide plus 1% potassium ferrocyanide in 0.1 M sodium cacodylate buffer for 1 h at 4 °C. Finally, cells were embedded in the epoxy resin (Epoxy Embedding Medium kit—Sigma-Aldrich) and 70 nm-ultrathin sections were obtained using an Ultratome V (LKB) ultramicrotome, before being processed using a Tecnai G2 transmission electron microscope (TEM) operating at 100 kV. To identify Rab4-positive structures by TEM, confocal and electron images were overlaid using nucleus shape to improve cell relocation. The diameter and area of endosomal-like structures were measured using ImageJ.

Pharmacological treatments

The following compounds were used: dibutyryl cAMP (dbcAMP; 500 μM; 10 days, ChemCruz; #B0218) was exclusively applied to primary striatal LRRK2 WT and G2019S astrocytes to stimulate Glt-1 expression [103]; LRRK2 kinase inhibitor rel-3-[6-[(2R,6S)-2,6-dimethyl-4-morpholinyl]-4-pyrimidyl]-5-[(1-methylcyclopropyl)oxy]-1H-indazole (MLi-2; 200 nM, 90 min application for the experiments on transfected cells; 120 min application for electrophysiological recordings in oocytes, Tocris; Cat. #5756) [16, 40]; PKC activator phorbol 12-myristate

13-acetate (TPA; 400 nM, 20 min, Sigma-Aldrich; Cat. #SLBX8889) [103]; PKC inhibitor Go 6976 (10 μM, 1, 10 and 90 min, Selleckchem) [26, 96]; recycling inhibitor monensin (35 μM, 40 min; Sigma-Aldrich; Cat. #M5273) [47]; proteasome inhibitor MG132 (20 μM, 8 h; Sigma-Aldrich; Cat. #M5273 [74]); vacuolar H⁺-ATPase inhibitor bafilomycin A1 (Baf A1; 100 nM, 60 min, Selleck.EU; Cat. #S1413 [63]). For the investigation of Glt-1 recycling kinetics, MLI-2 (200 nM) was acutely applied to LRRK2 WT and LRRK2 G2019S astrocytes 90 min prior to further pharmacological manipulations. For TIRFM experiment and for the treatment of organotypic slices, MLI-2 (200 nM) was acutely dissolved into the medium 90 min prior to immunofluorescence experiments.

Image preparation and statistical analysis

All images were prepared for illustration using Adobe Illustrator CS6. Statistical analyses were performed in Prism 7 (GraphPad). Data are expressed as median with interquartile range. An outlier test was applied before the statistical analysis. Gaussian distribution was assessed by D'Agostino & Pearson omnibus and Shapiro–Wilk normality tests. Data including three conditions were analyzed by one-way ANOVA test followed by Tukey's multiple comparisons test (Gaussian distribution) or Kruskal–Wallis test (non-Gaussian distribution) followed by Dunn's multiple comparisons test. To compare the effects of different drugs on groups, we used the two-way ANOVA test followed by Tukey's multiple comparisons test. Statistical analysis on data including two independent groups was performed with the unpaired *t* test (Gaussian distribution) or Mann–Whitney test (non-Gaussian distribution). A paired *t* test (Gaussian distribution) was applied for the comparison of co-injected EAAT2 + LRRK2 G2019S oocytes before and after MLI-2 application. ANOVA F and P values are noted in figure legends; post hoc p values are reported in the main text. Levels of significance were defined as *, \$, #, $p \leq 0.05$; **, \$\$, ##, $p \leq 0.01$; ***, \$\$\$, ### $p \leq 0.001$.

Results

Severe deficits in EAAT2 levels and increased gliosis in post-mortem caudate and putamen of LRRK2 G2019S PD patients

To investigate the role of EAAT2 in the pathophysiology of LRRK2-PD, we first examined the presence of the glutamate transporter protein in the caudate and putamen of LRRK2 G2019S PD patients and age-matched controls by western blot (Fig. 1a). Consistent with the previous reports, the EAAT2 antibody recognized multiple bands corresponding

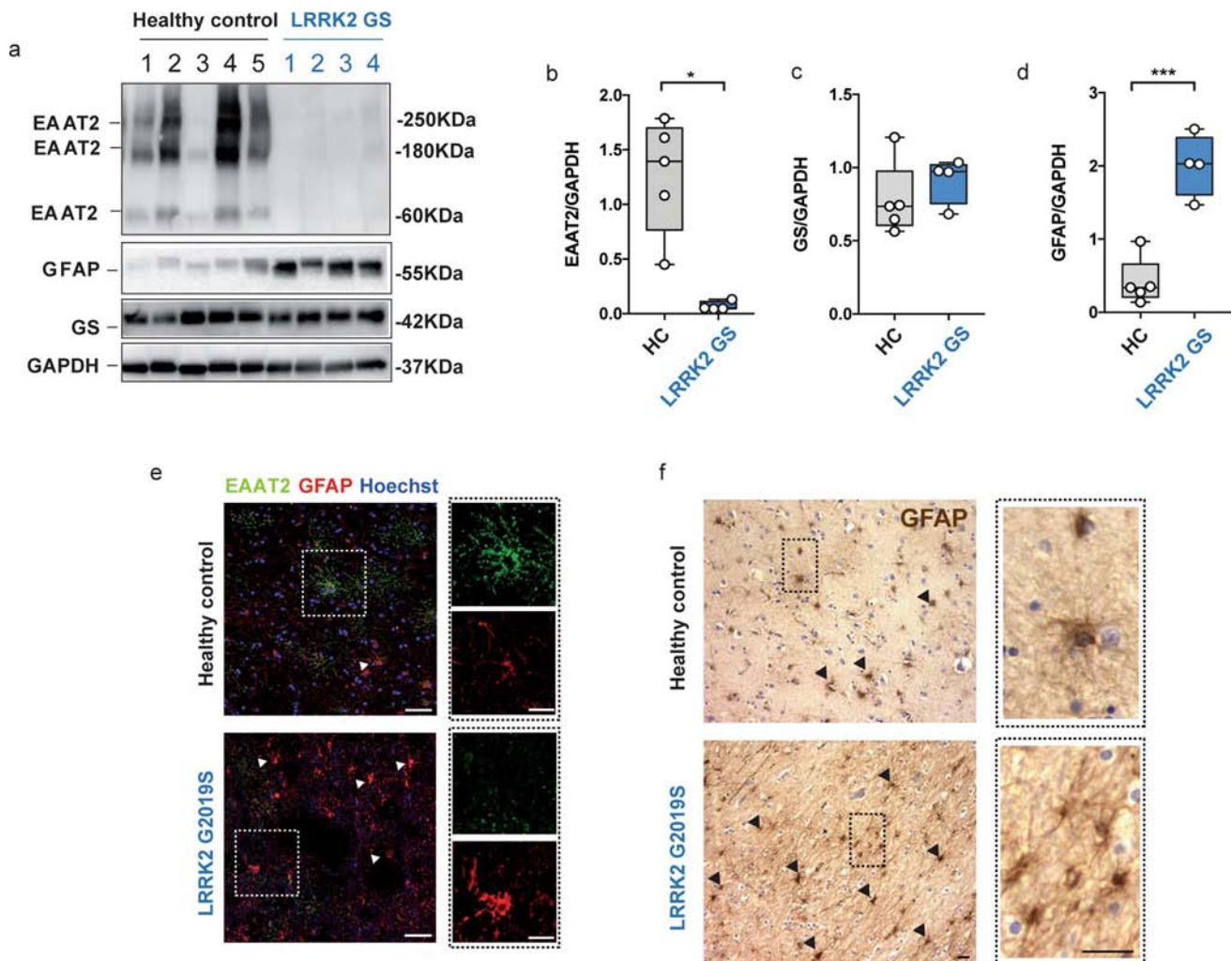


Fig. 1 EAAT2 levels are decreased in human LRRK2 G2019S brains. **a** Western blot analysis of human LRRK2 G2019S caudate and putamen lysates and healthy controls using anti-EAAT2, anti-GS, and anti-GFAP antibodies; **b–d** relative quantification of band intensity was performed using ImageJ and normalized to the housekeeping protein GAPDH ($n=5$ age-matched control samples and $n=4$ LRRK2 G2019S caudate and putamen samples); **e** representative double-labeling images for EAAT2 (green) and GFAP (red) in

LRRK2 G2019S human caudate and putamen and age-matched control; scale bar 50 μm , insets 20 μm ; **f** representative images of DAB-immunostaining for GFAP in LRRK2 G2019S human caudate and putamen and age-matched control; scale bar 25 μm , insets 10 μm ; arrowheads in (**e** and **f**) indicate the presence of GFAP-positive cells. Statistical analysis in (**b**) was performed using Mann–Whitney test and in (**c**, **d**) using unpaired *T* test

to the monomeric (60 KDa), and multimeric, SDS-resistant (180 KDa) conformations [22, 51, 105]. An additional 250 KDa band was detected which is compatible with EAAT2 multimers [23, 85] (Fig. 1a). We determined the total amount of the transporter by combining the densitometry of the three bands (Fig. 1b), and we also quantified the three bands separately (Supplementary Fig. 1a–c, online resource). In all cases, band intensity was normalized to the housekeeping protein GAPDH. We observed that EAAT2 protein was nearly absent in the caudate and putamen of LRRK2 G2019S PD patients as compared to healthy controls (Fig. 1a, b; LRRK2 G2019S PD patient cases vs age-matched controls; $p=0.01$), and this difference affected both the multimeric

and monomeric fractions (Supplementary Fig. 1a–c, online resource; LRRK2 G2019S PD patients vs age-matched controls: a, $p=0.004$; b, $p=0.006$; c, $p=0.012$). To assess whether EAAT2 downregulation was specifically linked to LRRK2-related pathology, we compared the expression of the transporter in the caudate and putamen of age-matched controls, LRRK2 G2019S and idiopathic Parkinson’s disease (iPD) patients (Supplementary Fig. 1d, online resource). The total EAAT2 expression showed a modest but non-significant decrease in the iPD group (Supplementary Fig. 1e, online resource—LRRK2 G2019S PD cases vs age-matched controls; $p=0.001$; LRRK2 G2019S PD cases vs iPD cases; $p=0.07$; age-matched controls vs iPD cases; $p>0.99$). The

quantification of the monomeric (60 KDa) and multimeric (180 and 250 KDa) EAAT2 bands also confirmed a subtle but non-significant EAAT2 deficit in the iPD samples (Supplementary Fig. 1f–h, online resource; iPD cases versus age-matched controls; $p > 0.05$).

EAAT2 is highly expressed by astrocytes [20]. To determine whether the decreased expression of EAAT2 was due to a lower number of astrocytes in LRRK2 G2019S PD patients, we assessed the amount of the cytosolic marker glutamine synthetase (GS), since its expression is restricted to astrocytes and does not depend on their activation status (Fig. 1a). GS expression levels in the caudate and putamen were comparable between LRRK2 G2019S PD patients and age-matched controls (Fig. 1c; LRRK2 G2019S PD patients vs controls, $p = 0.37$). However, expression levels of GFAP (a marker for astrogliosis) were significantly increased in the caudate and putamen of LRRK2 G2019S PD patients, as shown in Fig. 1d–f (d, LRRK2 G2019S PD patients vs age-matched controls; $p = 0.0003$). Moreover, immunohistochemical detection of GFAP-positive cells (Fig. 1e, f, arrows) and the quantification of both GFAP IntDen and GFAP⁺ cells (Supplementary Fig. 1i, j, online resource) showed that astrocytes in caudate and putamen of LRRK2 G2019S PD patients were abundant and adopted the typical morphology of hyperactive cells, with enlarged and densely stained cytoplasm (Fig. 1e–f, insets). Taken together, these data show a significant decrease in the expression of the glutamate transporter EAAT2 in the caudate and putamen of LRRK2 G2019S PD patients, and the reduction of EAAT2 levels is associated with increased astrogliosis.

Glutamate transporter expression and functionality are perturbed in the striatum of young LRRK2 G2019S mice

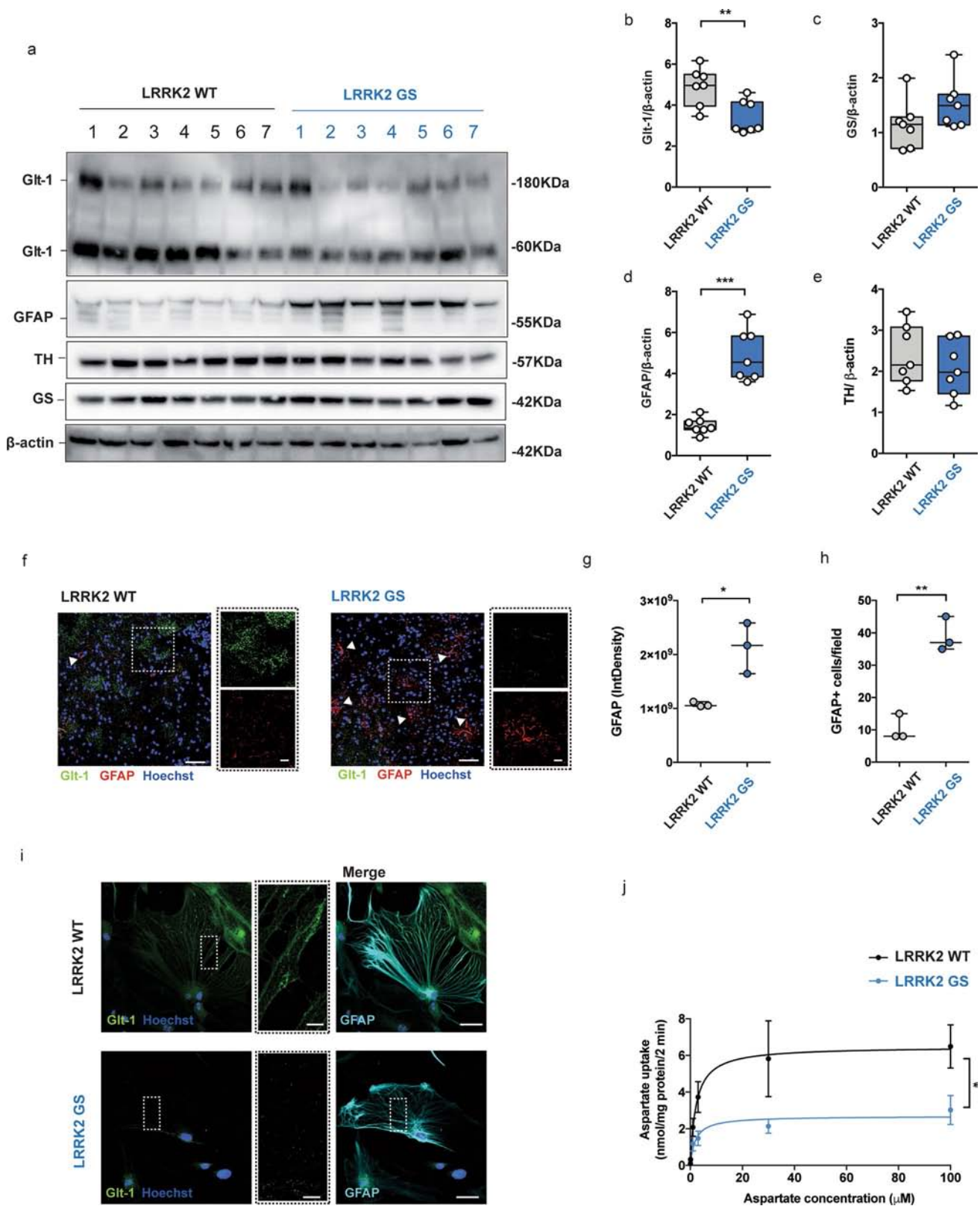
To corroborate the results obtained from a small sampling of LRRK2-PD patients in a defined mouse model, we compared the expression of Glt-1, the mouse equivalent of EAAT2, in the striatum of LRRK2 WT and LRRK2 G2019S knock-in mice. We chose 4-month-old animals, since previous studies have reported alterations in glutamatergic neurotransmission at this stage which correlate with onset of altered motor activity [42, 92]. In agreement with the previous findings [32, 94, 95], we revealed that the LRRK2 kinase activity is enhanced in G2019S LRRK2 mice, as shown by measuring pS1292 (auto-phosphorylation site) in LRRK2 (Supplementary Fig. 1k, l, online resource; $p = 0.02$). As previously reported, we confirmed the presence of two bands for Glt-1, corresponding to Glt-1 monomers (60 KDa) and Glt-1 multimers (180 KDa), respectively (Fig. 2a) [22, 51, 105]. LRRK2 G2019S mice presented a decrease in the total amount of Glt-1 as compared to LRRK2 WT controls (Fig. 2b, LRRK2 WT vs G2019S; $p = 0.008$). When

analyzing the two bands separately, the lower Glt-1 band also showed a significant decrease in the LRRK2 G2019S mice, while levels of the higher band did not reach statistical significance (Supplementary Fig. 1m, online resource—LRRK2 WT vs LRRK2 G2019S; $p = 0.0175$; Supplementary Fig. 1n, online resource—LRRK2 WT vs LRRK2 G2019S; $p = 0.07$).

We next performed qPCR analyses to explore whether the decrease in Glt-1 protein levels was attributed to a decrease of its mRNA levels in the striatum (Supplementary Fig. 1o, online resource). Importantly, no significant changes in mRNA levels between genotypes were detected for the two main glutamate transporters Glt-1 (Supplementary Fig. 1o, online resource—LRRK2 WT vs LRRK2 G2019S; $p = 0.99$) or the glutamate/aspartate transporter (Glast), which is the second most important astrocytic glutamate transporter (Supplementary Fig. 1o, online resource—LRRK2 WT vs LRRK2 G2019S; $p = 0.6575$). Similar to what we observed in human samples, GS protein levels were comparable between the genotypes (Fig. 2c, LRRK2 WT vs LRRK2 G2019S, $p = 0.1411$), while there was an increase in the levels of GFAP (Fig. 2d, LRRK2 WT vs LRRK2 G2019S; $p < 0.0001$), suggesting enhanced gliosis in young LRRK2 G2019S mice. Immunofluorescence imaging confirmed a reduction of Glt-1 staining in the striatum of LRRK2 G2019S mice compared to controls (Fig. 2f). Quantifications of the IntDen of GFAP (Fig. 2g; LRRK2 WT vs LRRK2 G2019S, $p = 0.0001$) and of the number of GFAP-positive astrocytes (Fig. 2h; LRRK2 WT vs LRRK2 G2019S, $p = 0.0017$) further indicate that decreased Glt-1 levels correlate with an intense astrogliosis in LRRK2 G2019S mice. According with previous reports [32, 41, 100], Tyrosine Hydroxylase (TH) levels as quantified by western blot from the same mice revealed no signs of dopaminergic cell loss (Fig. 2e, LRRK2 WT vs LRRK2 G2019S, $p = 0.39$).

To dissect the LRRK2-mediated effects on glial Glt-1 levels, we isolated primary striatal astrocytes from LRRK2 WT and LRRK2 G2019S mice (Fig. 2i). Astrocytes were treated with dbcAMP to stimulate endogenous Glt-1 expression [83] (Fig. 2i). Consistent with published data [73], qPCR analysis showed a more than tenfold increase in Glt-1 mRNA levels upon dbcAMP treatment (Supplementary Fig. 1p, online resource). Immunocytochemistry revealed that Glt-1 was diffusely expressed in LRRK2 WT astrocytes, while LRRK2 G2019S astrocytes displayed a less pronounced staining, almost restricted to discrete dots (Fig. 2i).

To evaluate whether the Glt-1 deficits and impaired Glt-1 localization may functionally affect glutamate re-uptake in astrocytes, we purified striatal mouse gliosomes from LRRK2 WT and LRRK2 G2019S mice. Gliosomes constitute pure subcellular *ex vivo* preparations that resemble most of the molecular and functional features of astrocytes in vivo [61, 79]. [³H]D-Asp, a non-metabolizable analogue



of glutamate used to mimic the endogenous neurotransmitter [64], was applied to assess Glt-1 activity, and experiments were conducted in the presence of 10 μ M UCPH-101 to

exclude [3 H]D-Asp uptake by Glast. To calculate the K_m and the V_{max} of [3 H]D-Asp uptake, radioactivity was determined in gliosomes in the presence of different concentrations of

Fig. 2 Glutamate transporter is downregulated in the striatum of LRRK2 G2019S mice. **a** Western blot analysis of LRRK2 WT and LRRK2 G2019S striatal lysates using anti-Glt-1, anti-GS, anti-GFAP, and anti-TH antibodies; **b–e** relative quantification of band intensity was performed using ImageJ and normalized to β -actin ($n=7$ striatal samples for both LRRK2 WT and LRRK2 G2019S 4-month-old mice); **f** representative confocal double-labeling images for Glt-1 (green) and GFAP (red) in LRRK2 WT and G2019S striatal slices; scale bar 50 μm , insets 20 μm ; **g** quantification of GFAP IntDen and GFAP⁺ cells (**h**) in the dorsal striatum of LRRK2 WT and G2019S mice. Three different fields per animal were collected, $n=3$ animals for each genotype; **i** representative confocal images of the cellular distribution of the endogenous Glt-1 (green) in primary striatal astrocytes stained for GFAP (cyan) derived from LRRK2 WT and LRRK2 G2019S mice treated with dbcAMP (500 μM) for 10 days; scale bars 20 μm , inserts 5 μm ; **j** striatal gliosomes from LRRK2 WT and LRRK2 G2019S 4-month-old mice were exposed for 2 min at 37 °C to increasing concentration of [³H]D-Asp (0.03, 0.1, 1, 3, 30, and 100 μM) in the presence of 10 μM UCPH to exclude [³H]D-Asp uptake by Glst. The specific [³H]D-Asp uptake is expressed as nmol/mg protein/2 min; the kinetic parameters V_{max} and K_m were obtained by fitting data with the Michaelis–Menten equation ($n=4$ independent experiments for each group). Statistical analysis in (**b**, **e**, **h**, and **j**) was performed using unpaired T test; statistical analysis in **g** was performed using Mann–Whitney test

[³H]D-Asp. As shown in Fig. 2j, LRRK2 G2019S-derived gliosomes displayed a lower V_{max} of aspartate uptake as compared to age-matched LRRK2 WT mice (Fig. 2j, V_{max} [LRRK2 WT]: 6.7 ± 1.37 nmol/mg/2 min, V_{max} [LRRK2 G2019S]: 2.73 ± 0.59 nmol/mg/2 min, $p=0.036$), while no significant difference was registered in the K_m values (Fig. 2j; K_m [LRRK2 WT] 2.56 ± 0.16 mM, K_m [LRRK2 G2019S] 2.05 ± 0.14 mM, $p=0.054$). Altogether these findings show that astrocytes from LRRK2 G2019S mice present a reduced expression of Glt-1, which results in reduced glutamate uptake and is associated with increased gliosis.

Human pathogenic G2019S LRRK2 mutation impacts on EAAT2 electrophysiological properties

To confirm that the reduced glutamate uptake observed in LRRK2 G2019S gliosomes also applies to the human EAAT2 protein, we used *Xenopus laevis* oocytes, an excellent model system to study transport processes at a cellular level [97]. Human glutamate transporter EAAT2 mRNA was co-injected with human LRRK2 WT or LRRK2 G2019S mRNA into oocytes (Supplementary Fig. 1q, online resource), and two-electrode voltage-clamp was performed to record the transport current elicited by glutamate through EAAT2 (Experimental design in Fig. 3a). The inward transport-associated-current (I_{EAAT2}) obtained upon the application of glutamate to oocytes injected with LRRK2 G2019S mRNA was significantly reduced as compared to the one obtained from oocytes injected with LRRK2 WT mRNA (Fig. 3b; EAAT2 + LRRK2 WT: mean amplitude 43 ± 3 nA vs EAAT2 + LRRK2 G2019S: mean amplitude 25 ± 2

nA; $p < 0.0001$). We also measured the maximal transport current (I_{max}) and the apparent affinity for glutamate (aK_m). We found that the expression of LRRK2 G2019S mRNA significantly decreased the I_{max} but not the aK_m of the transporter as compared to the WT counterpart (Fig. 3c; EAAT2 + LRRK2 G2019S, aK_m : 51 ± 27 μM , I_{max} : 28 ± 3 nA vs EAAT2 + LRRK2 WT, aK_m : 89 ± 32 μM , I_{max} : 52 ± 5 nA; aK_m , $p=0.05$; I_{max} , $p < 0.001$).

We next imaged EAAT2 in oocyte slices to understand the reduction of transport current observed in the presence of LRRK2 G2019S. Fluorescence images and IntDen quantification revealed that the transporter was mainly found at the plasma membrane in oocytes injected with LRRK2 WT, while it was sparsely localized there upon pathogenic LRRK2 G2019S expression (Fig. 3d, e EAAT2 + LRRK2 WT vs EAAT2 + LRRK2 G2019S, $p=0.006$). Importantly, short-term incubation of LRRK2 G2019S-injected oocytes with the LRRK2 kinase inhibitor MLI-2 restored both the localization (Fig. 3d, e; EAAT2 + LRRK2 G2019S vs EAAT2 + LRRK2 G2019S + MLI-2, $p=0.002$) and the activity of the transporter (Fig. 3f; EAAT2 + LRRK2 G2019S, mean amplitude 17 ± 1 nA vs EAAT2 + LRRK2 G2019S + MLI-2 mean amplitude 37 ± 3 nA; $p < 0.0001$; EAAT2 + LRRK2 WT: mean amplitude 34 ± 4 vs LRRK2 G2019S + MLI-2; $p=0.715$). Together with our findings on mouse gliosomes, these observations suggest that the presence of pathogenic human LRRK2 G2019S does not alter the catalytic properties of the glutamate transporter. However, the mutation affects the amount of glutamate transporter functionally trafficked to/from the plasma membrane in a manner mediated by the LRRK2 kinase activity.

Glt-1 displays an altered localization in LRRK2 G2019S astrocytes

To gain insights into the mechanism behind the mutant LRRK2-dependent Glt-1 mislocalization and reduced protein levels, we first performed an unbiased protein–protein interaction screen. Endogenous Glt-1 was immunoprecipitated from homogenized WT and LRRK2 G2019S mouse striata (Supplementary Fig. 2a, online resource). As negative control, only magnetic beads were incubated with WT and LRRK2 G2019S solubilized brain extracts, respectively. Glt-1 interactors were revealed using liquid-chromatography coupled with tandem mass spectrometry (LC–MS/MS) (Supplementary file 1, online resource). The two interactome datasets were compared to highlight significant differences in protein abundances (Supplementary file 2, online resource). Common and divergent Glt-1 binders between the LRRK2 WT and G2019S genetic environments were identified upon filtering hits with fold-change > 3.5 with respect to the relative control. As shown in the Supplementary Fig. 2b (online resource), 40 interactors were present

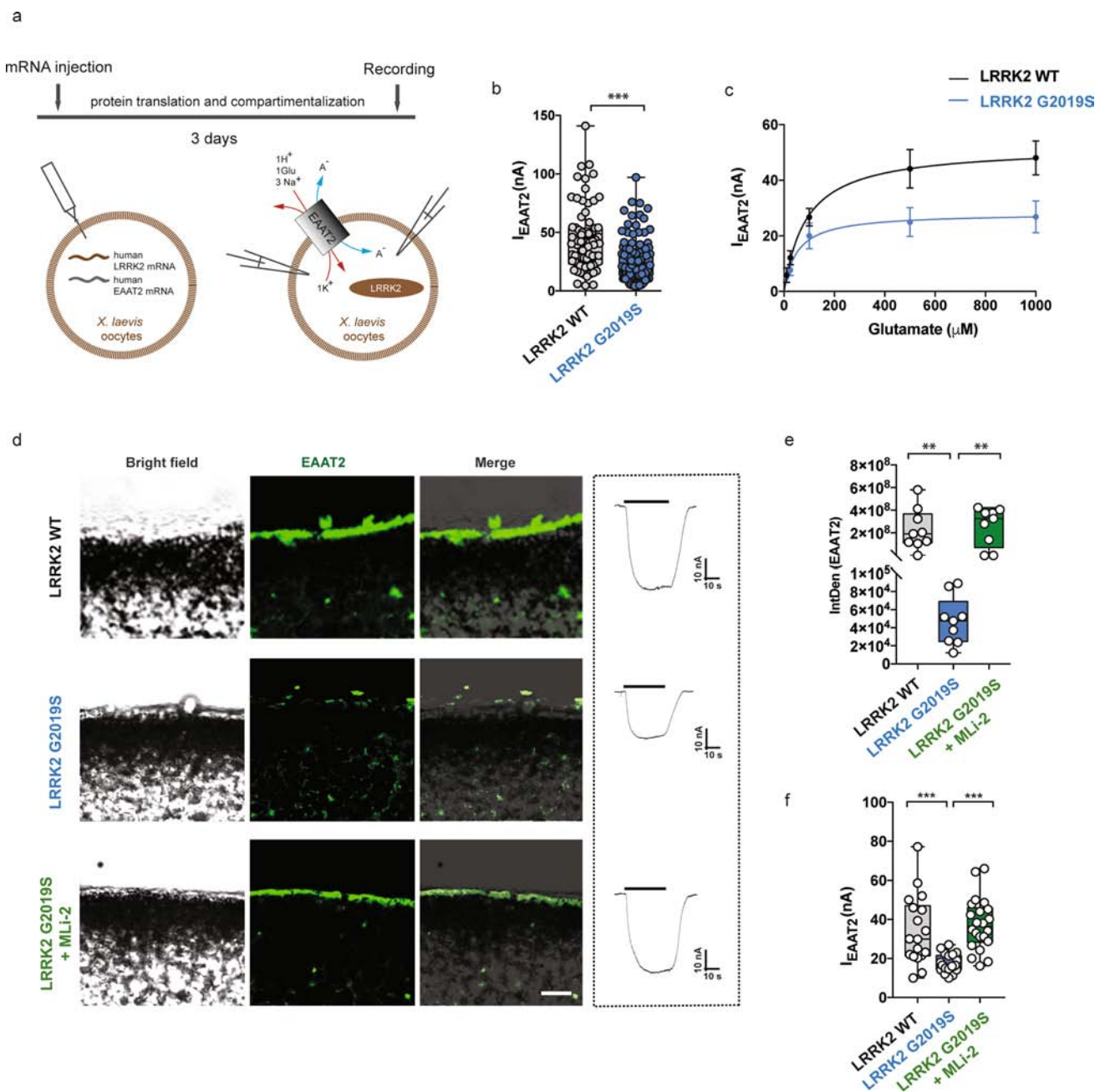


Fig. 3 LRRK2 G2019S alters EAAT2 electrophysiological properties. **a** Schematic outline of the experimental setup. Oocytes were co-injected with mRNA of EAAT2 and human LRRK2 (WT or G2019S) and glutamate transport-associated currents were recorded using the two-electrode voltage-clamp technique; **b** the bar graph represents current amplitudes elicited in oocytes co-expressing EAAT2 and LRRK2 WT ($n=79$ oocytes, 12 frogs) or G2019S ($n=122$ oocytes, 12 frogs). Glutamate application was at 1 mM and the holding potential at -60 mV; **c** transport-associated currents in oocytes co-expressing EAAT2 and LRRK2 WT or G2019S as a function of glutamate concentration. The kinetic parameters I_{\max} and aK_m were obtained by fitting data with the Michaelis–Menten equation ($n=6$ oocytes; 2 frogs); **d** representative bright-field (left column) or fluorescence (middle column, on the right column) images of oocyte slices co-expressing EAAT2 (green) and LRRK2 WT or G2019S, with or

without 90 min MLI-2 (200 nM) treatment; scale bar 20 μm . Representative traces of the recorded transport current in all the three groups are shown on the right; **e** quantitative analysis of the IntDen of the EAAT2 signal at the oocyte membrane was performed in three different fields for each oocyte; $n=3$ oocytes for each group; **f** the bar graph represents current amplitudes elicited in oocytes co-expressing EAAT2 and LRRK2 WT ($n=18$ oocytes, 6 frogs), G2019S ($n=22$ oocytes, 6 frogs), or G2019S+MLI-2 ($n=22$ oocytes, 6 frogs). Statistical analysis in **b** was performed using Mann–Whitney test, in **e** using one-way ANOVA test ($F=8.891$, $P=0.001$) followed by Tukey’s multiple comparison test. Statistical analysis in (**f**) was performed using unpaired T test to compare EAAT2+LRRK2 WT to EAAT2+G2019S-injected oocytes and with paired T test to compare EAAT2+G2019S oocytes before and after LRRK2 inhibition

in both datasets, 14 were unique to Glt-1 immunoprecipitated from LRRK2 WT background, and 10 were unique to LRRK2 G2019S background. Gene Ontology (GO) analysis was employed to identify discrete functional enrichments, and data relative to the Cellular Component (CC) biological domain were analyzed in detail (Supplementary file 3, online resource). In both datasets, Glt-1 was in contact with membrane domains (GO:0045121; GO:0098857), synaptic and vesicular components (GO:0045202; GO:0043232), cytoskeletal scaffolds (GO:0,005,856; GO:0,005,874), and mitochondrial elements (GO:0,005,743; GO:0031966; GO:0005740) (Supplementary Fig. 2c, online resource) as already reported [22]. Components of the plasma membrane region associated with sodium–potassium exchanging ATPase complexes were represented in the LRRK2 WT genotype only (GO:0098796; GO:0098590; GO:0005890) (Supplementary Fig. 2c, online resource). Among the GO terms that characterize the transporter in the LRRK2 G2019S genotype, we indeed observed several unique categories associated with internalized vesicles and clathrin-mediated endocytosis (GO:0030119; GO:0030128) (Supplementary Fig. 2c, online resource). Overall, the pathogenic LRRK2 G2019S mutation changes the interactome of endogenous striatal Glt-1 toward specific components of the endo-vesicular pathways.

To investigate the localization of Glt-1 in the genotypes, we acutely transfected primary striatal astrocytes with a GFP-Glt-1 construct. TIRFM imaging was performed to selectively visualize Glt-1 localization within thin regions of the plasma membrane [12]. We observed that GFP-Glt-1 localized in or immediately below the plasma membrane in LRRK2 WT astrocytes, showing a sparse ‘patchy’ pattern (Fig. 4a—WT inset). Although showing a similar membrane distribution, Glt-1 was less detectable on the cell surface of LRRK2 G2019S astrocytes (Fig. 4a—GS inset). The quantification of Glt-1 mean fluorescence using TIRFM confirmed a lower presence of Glt-1 at the plasma membrane of LRRK2 G2019S astrocytes as compared to LRRK2 WT astrocytes (Fig. 4b; LRRK2 WT vs LRRK2 G2019S, $p < 0.0001$). However, the application of the LRRK2 inhibitor MLI-2 in G2019S astrocytes completely rescues the expression of Glt-1 at the plasma membrane, as confirmed by the mean fluorescence quantification (Fig. 4b, LRRK2 G2019S vs LRRK2 G2019S + MLI-2, $p = 0.01$; LRRK2 G2019S + MLI-2 vs LRRK2 WT, $p = 0.004$). Conversely, MLI-2 application in LRRK2 WT astrocytes did not alter Glt-1 membrane distribution (Fig. 4b, LRRK2 WT vs LRRK2 WT + MLI-2, $p > 0.99$). We then studied the overall Glt-1 distribution in primary astrocytes transfected with Flag-Glt-1 using epifluorescence microscopy. Despite the equal ectopic expression of the transporter (Supplementary Fig. 3a, b, online resource:

LRRK2 WT vs LRRK2 G2019S, $p > 0.05$), we detected a clear accumulation of Glt-1 in round intracellular clusters along with the spotted membrane distribution in LRRK2 G2019S astrocytes (Fig. 4d). Glt-1 was present within two distinct populations of clusters, namely a larger cluster of $\sim 1.8 \mu\text{m}$ diameter and a smaller cluster of $\sim 0.8 \mu\text{m}$ diameter, respectively (Supplementary Fig. 3c–f, online resource). In contrast, a unique population of dots with an average diameter of $0.6 \mu\text{m}$ was present in the LRRK2 WT background, perhaps reflecting clusters in the plasma membrane (Supplementary Fig. 3c, d, online resource). Using intracellular cluster formation as a readout (diameter $> 1 \mu\text{m}$), we detected a significant increase of Glt-1 clusters in LRRK2 G2019S astrocytes as compared to the LRRK2 WT genotype (Fig. 4d, e LRRK2 WT vs LRRK2 G2019S, $p < 0.0001$). Noteworthy, 90 min MLI-2 application restored the number of Glt-1-positive clusters to control values in LRRK2 G2019S astrocytes (Fig. 4d, e; LRRK2 G2019S vs LRRK2 G2019S + MLI-2, $p < 0.0001$; LRRK2 G2019S + MLI-2 vs LRRK2 WT, $p > 0.99$). Conversely, LRRK2 inhibition did not change the number of clusters in LRRK2 WT astrocytes (Fig. 4d–e LRRK2 WT vs LRRK2 WT + MLI-2, $p = 0.9692$). To investigate a possible role for LRRK2 in PKC-mediated internalization of Glt-1, we used the PKC activator TPA, as well as the PKC inhibitor Go 6976 (Fig. 4c). In agreement with published data [21, 103], the application of TPA enhanced Glt-1 intracellular clusters in LRRK2 WT astrocytes (Fig. 4d, e; LRRK2 WT vs LRRK2 WT + TPA, $p < 0.0001$). Of note, the distribution of cluster diameters in this condition peaked at $\sim 1.9 \mu\text{m}$, which is similar to that observed in LRRK2 G2019S astrocytes (Supplementary Fig. 3c, f, online resource). No significant changes were observed in the number of Glt-1-positive puncta in LRRK2 G2019S astrocytes upon TPA treatment, suggesting that the majority of Glt-1 was localized to the intracellular compartment already under basal conditions (Fig. 4d, e; LRRK2 G2019S vs LRRK2 G2019S + TPA, $p = 0.9741$). Furthermore, to unravel whether LRRK2 acts upstream of PKC, we applied MLI-2 to TPA-treated LRRK2 WT astrocytes. Interestingly, the application of MLI-2 did not restore the number of Glt-1 clusters to basal values (Fig. 4d–f; LRRK2 WT vs LRRK2 WT + TPA + MLI-2, $p < 0.0001$). Moreover, PKC inhibition using Go 6976 did not prevent Glt-1 clustering in LRRK2 G2019S astrocytes (Fig. 4d–g; LRRK2 G2019S vs LRRK2 G2019S + Go 6976, $p = 0.1645$). These data demonstrate that LRRK2 G2019S reduces Glt-1 localization at the plasma membrane in a PKC-independent manner in primary astrocytes. Moreover, the correction of the pathogenic phenotype observed upon application of MLI-2 indicates that the LRRK2 kinase activity is crucial for the relocation of Glt-1.

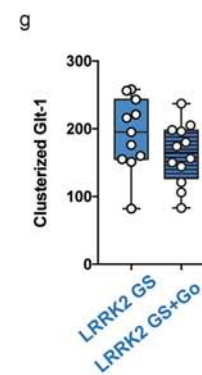
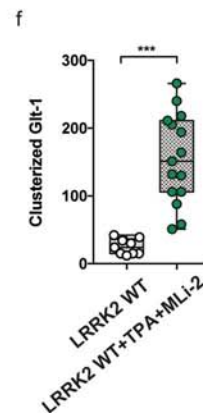
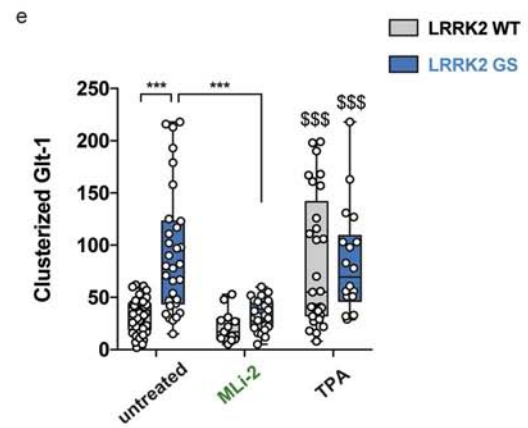
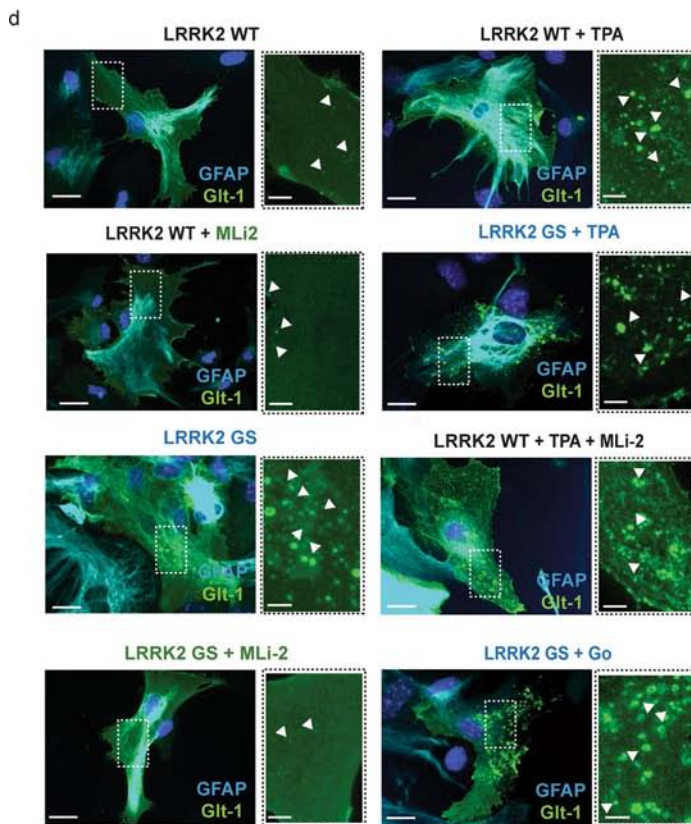
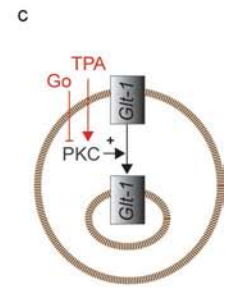
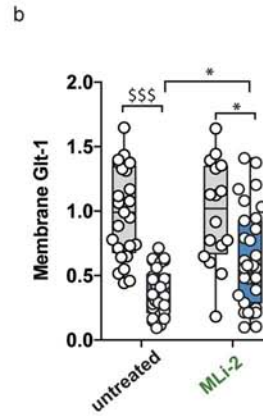
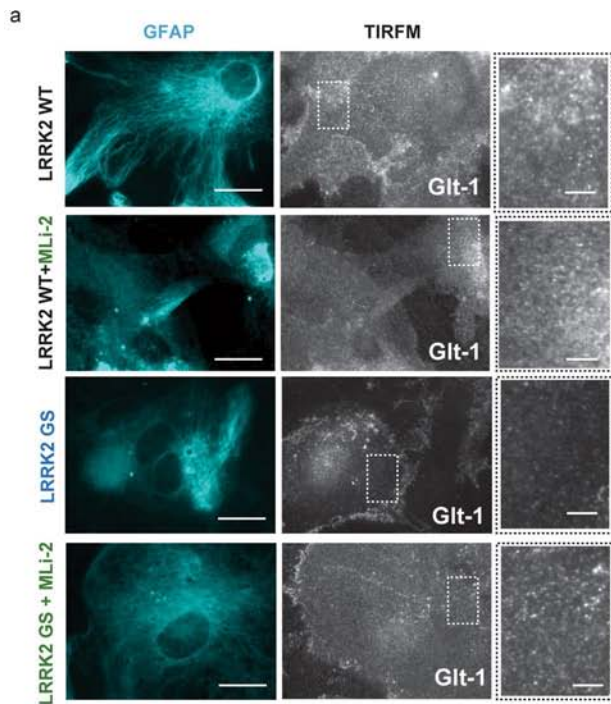


Fig. 4 Astroglial Glt-1 is mislocalized in the presence of LRRK2 G2019S mutation. **a** Representative TIRFM images of Glt-1 localization in LRRK2 WT and LRRK2 G2019S astrocytes (untreated or treated with MLI-2) transfected with GFP-Glt1 (gray) and stained with GFAP (cyan). Scale bar 20 μ m; insets 10 μ m; **b**) quantification of the GFP-Glt-1 mean fluorescence performed in TIRFM images ($n=25$ cells from LRRK2 WT, $n=16$ cells from LRRK2 WT+MLi-2; $n=30$ cells from LRRK2 GS and $n=31$ cells from LRRK2 GS+MLi-2, experiments performed at least in triple); **c** schematic representation of TPA and Go 6976 effects on PKC activity; **d** representative epifluorescence images of Glt-1 intracellular clusters in LRRK2 WT and LRRK2 G2019S astrocytes transfected with Flag-Glt-1 (green) and stained with GFAP (cyan) under basal condition and after pharmacological treatment; Scale bar 20 μ m, insets 5 μ m; **e** quantification of the number of Glt-1-positive clusters per cell in LRRK2 WT and G2019S astrocytes under basal condition and after pharmacological treatment using LRRK2 inhibitor MLI-2 (90 min) and the PKC activator TPA (20 min). Number of cells analyzed: LRRK2 WT ($n=40$ cells), LRRK2 WT+MLi-2 ($n=13$ cells), LRRK2 G2019S ($n=31$ cells), LRRK2 G2019S+MLi-2 ($n=26$ cells), LRRK2 WT+TPA ($n=29$ cells), and LRRK2 G2019S+TPA ($n=18$ cells); **f** quantification of the number of Glt-1-positive clusters per cell under basal condition and after pharmacological co-treatment with TPA and MLI-2 in LRRK2 WT astrocytes. Number of cells analyzed: LRRK2 WT ($n=9$ cells) and WT+TPA+MLi-2 ($n=15$ cells); **g** quantification of the number of Glt-1-positive clusters per cell under basal condition and after pharmacological treatment with the PKC inhibitor Go 6976 in LRRK2 G2019S astrocytes. Number cells analyzed: LRRK2 GS ($n=11$ cells) and LRRK2 GS+Go ($n=12$ cells). Experiments performed at least in triple. Three cells were analyzed for each independent cell culture. Statistical analysis in (**b** and **e**) was performed using two-way ANOVA (**b** treatment $F=0.06$ and $p=0.06$; genotypes $F=53.01$ and $p<0.0001$; **e** treatment: $F=16.53$ and $p<0.0001$; genotypes $F=10.67$ and $p=0.001$) test followed by Tukey's multiple comparisons test. (\$ vs LRRK2 WT and * versus LRRK2 G2019S). Statistical analysis in (**f** and **g**) was performed using unpaired *T* test

Glt-1 is retained at the Rab4-positive compartment in LRRK2 G2019S striatal astrocytes

To determine the identity of the Glt-1 clusters, we co-transfected LRRK2 WT and LRRK2 G2019S astrocytes with Flag-Glt-1 together with GFP-Lamp1 (lysosomal marker), GFP-Rab11 (marker of slow-recycling endocytosis), or GFP-Rab4 (marker of fast-recycling endocytosis) (Fig. 5a). Quantification showed that there was no significant difference in the amount of Lamp1, Rab11, or Rab4 fluorescence between the two genotypes (Fig. 5b–f; all comparisons $p>0.05$). We then quantified the co-localization of Glt-1 with the three markers. There were no significant changes in the amount of the transporter in the Lamp1- or Rab11-positive compartments in LRRK2 G2019S astrocytes as compared to LRRK2 WT astrocytes (Fig. 5c, e; $p>0.05$). However, there was a significant increase in the amount of Glt-1 co-localizing with the Rab4-positive fast-recycling vesicles in LRRK2 G2019S astrocytes as compared to control (Fig. 5g; LRRK2 WT vs LRRK2 G2019S, $p<0.0001$). Z-stack orthogonal projections confirmed that Glt-1 co-localized with Rab4-positive vesicles in LRRK2 G2019S primary astrocytes (Supplementary

Fig. 4a, online resource). Interestingly, short-term application of MLI-2 reverted the LRRK2 G2019S-mediated pathogenic phenotype as shown by the loss of co-localization between Glt-1 and Rab4-positive vesicles (Fig. 5g, LRRK2 G2019S vs LRRK2 G2019S+MLi-2, $p=0.0001$; LRRK2 G2019S+MLi-2 vs LRRK2 WT, $p=0.89$). Conversely, MLI-2 application in LRRK2 WT astrocytes did not influence Glt-1 co-localization with the Rab4-positive vesicles (Supplementary Fig. 4b, online resource- LRRK2 WT+MLi2 vs LRRK2 WT, $p=0.87$).

Since pathogenic LRRK2 did not influence the expression of Rab4 protein per se, we investigated the impact of the kinase on Rab4-positive vesicle morphology using both confocal fluorescence microscopy and TEM (Supplementary Fig. 4c–e, online resource, and Fig. 5h). Fluorescence analysis demonstrated that the LRRK2 G2019S mutation did not alter the total amount of Rab4-positive vesicles (Supplementary Fig. 4c, d, online resource: LRRK2 WT vs LRRK2 G2019S, $p>0.05$). Rather, the area of Rab4-positive fast-recycling endosomes appeared increased in the presence of the pathogenic LRRK2 mutation (Supplementary Fig. 4e, online resource: LRRK2 WT vs LRRK2 G2019S, $p=0.003$). By overlapping fluorescence images with TEM ultrathin sections, we were able to identify and define the Rab4-positive recycling vesicles (Supplementary Fig. 4f, online resource-asterisks). Rab4-positive endosomes presented an irregular shaped vacuole (0.2–0.5 μ m diameter) characterized by an electron-lucent lumen [17, 38]. TEM analysis confirmed that the LRRK2 G2019S mutation markedly increased the area of Rab4-positive vesicles (Fig. 5h–i; LRRK2 WT vs LRRK2 G2019S, $p<0.0001$) as compared to controls.

To validate these observations in intact tissue, we employed organotypic coronal cultures derived from LRRK2 WT and LRRK2 G2019S mice. Slices were transfected with the GFP-Rab4 plasmid to visualize the fast-recycling compartment. As shown in Fig. 5j–l, the endogenous expression of Glt-1 was reduced in LRRK2 G2019S organotypic slices as compared to control samples (Fig. 5k). Moreover, astrocytic endogenous Glt-1 abundantly accumulated in Rab4-positive vesicles in the presence of the G2019S mutation (Fig. 5k) compared to the WT counterpart (Fig. 5j). A representative 3D image confirming the Glt-1 co-localization with Rab4-positive vesicles in the pathogenic compartment is shown in Supplementary Files 4 (online resource). Intriguingly, short-term application of the LRRK2 kinase inhibitor MLI-2 restored the phenotype (Fig. 5l). Overall, here, we show that in LRRK2 G2019S astrocytes, the transporter is predominantly confined to enlarged Rab4-positive recycling vesicles not only in primary astrocytes but also in organotypic slices. In both cases, the rescuing effect of MLI-2 suggests that dysregulation of the LRRK2 kinase activity is sufficient to impair Glt-1 trafficking.

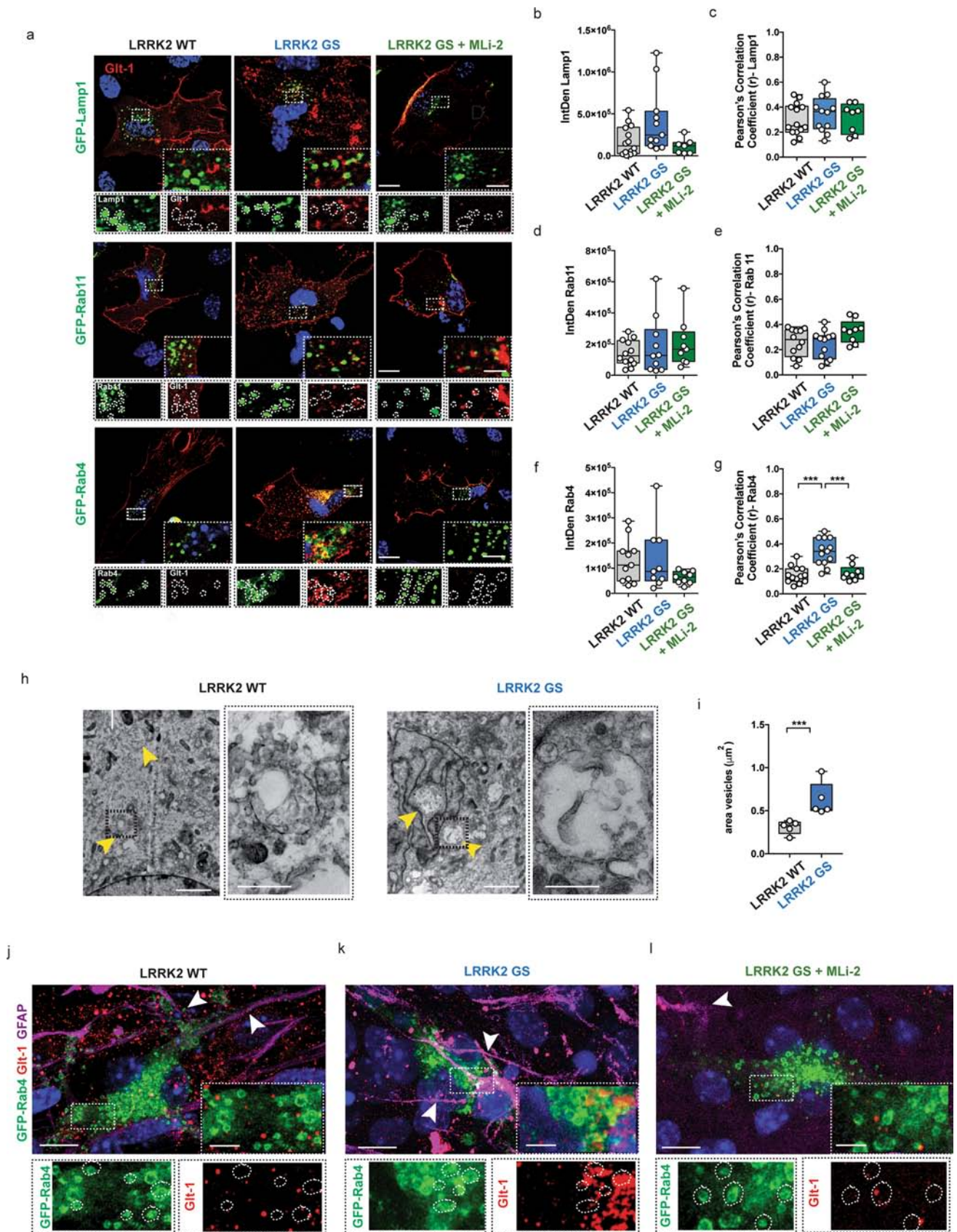


Fig. 5 LRRK2 G2019S enhances Glt-1 accumulation in Rab4-positive organelles. **a** Representative z-stack confocal images of primary astrocytes from LRRK2 WT and LRRK2 G2019S mice transfected with Flag-Glt-1 and GFP-Lamp1, GFP-Rab11, or GFP-Rab4 under basal conditions or upon treatment with MLI-2 inhibitor. Insets show Lamp1-, Rab11-, or Rab4-positive area and the localization of Glt-1 in the indicated ROIs. Scale bars: 20 μm ; insets 5 μm ; **b, c** quantitative analysis of Lamp1 IntDen ($n=14$ cells for LRRK2 WT, $n=11$ cells for LRRK2 GS and $n=7$ cells for LRRK2 GS+MLi2, experiments performed at least in triple) and of the Pearson's correlation coefficient of Glt-1 co-localizing with the Lamp1-positive compartment ($n=14$ cells for LRRK2 WT, $n=12$ cells for LRRK2 GS and $n=8$ cells for LRRK2 GS+MLi2, experiments performed at least in triple); **d–e** quantitative analysis of Rab11 IntDen ($n=12$ cells for LRRK2 WT, $n=10$ cells for LRRK2 GS and $n=9$ cells for LRRK2 GS+MLi2, experiments performed at least in triple) and of the Pearson's correlation coefficient of Glt-1 co-localizing with the Rab11-positive compartment ($n=12$ cells for LRRK2 WT, $n=12$ cells for LRRK2 GS and $n=10$ cells for LRRK2 GS+MLi2, experiments performed at least in triple); **f, g** quantitative analysis of Rab4 IntDen ($n=11$ cells for LRRK2 WT, $n=9$ cells for LRRK2 GS and $n=9$ cells for LRRK2 GS+MLi2, experiments performed at least in triple) and of the Pearson's correlation coefficient of Glt-1 co-localizing with the Rab4-positive vesicles ($n=13$ cells for LRRK2 WT, $n=13$ cells for LRRK2 GS and $n=9$ cells for LRRK2 GS+MLi2, experiments performed at least in triple). **h** Representative TEM images of LRRK2 WT and G2019S endosomal-like structures (yellow arrowheads) in primary striatal astrocytes transfected with GFP-Rab4 and Flag-Glt-1 (scale bars: 5 μm ; insets: scale bars: 500 nm); **i** Quantification of the area of endosomal-like structures ($n=5$ cells analyzed for each group, ten independent fields were analyzed for quantification). **j–l** Representative z-stack confocal images of coronal organotypic LRRK2 WT, LRRK2 G2019S, and LRRK2 G2019S treated with MLI-2 slices transfected with the GFP-Rab4 plasmid and stained for the endogenous proteins Glt-1 (red) and GFAP (magenta). Insets show Rab4-positive area and the localization of Glt-1 in the indicated ROIs. Scale bars: 20 μm ; insets 2 μm ; Statistical analysis in b–g was performed using one-way ANOVA test (**b**) $F=3.77$ and $p=0.04$; **c** $F=0.36$ and $p=0.69$, **d** $F=0.53$ and $p=0.59$, **e** $F=2.77$ and $p=0.08$, **f** $F=1.76$ and $p=0.19$, and **g** $F=19.04$ and $p<0.0001$) followed by Tukey's multiple comparison test. Statistical analysis in i was performed using unpaired t tests

G2019S LRRK2 alters the endocytic Rab4-positive compartment via Rab8A/Rab10

Multiple reports indicate that LRRK2 regulates recycling and secretory trafficking pathways via the phosphorylation and inactivation of its substrates Rab8A and Rab10 [31, 67, 68]. We first evaluated the levels and activity of endogenous LRRK2 in WT and G2019S LRRK2 astrocytes by monitoring two different phosphosites: pS935 (CK1 α /PKA/IKKs phosphorylation site), used to detect on-target effects of LRRK2 kinase inhibitor treatment, and pS1292 (auto-phosphorylation site) (Fig. 6a). In agreement with the previous reports, G2019S LRRK2 decreased the levels of pS935-LRRK2 [32, 60, 95] and increased the levels of pS1292-LRRK2 [32, 94, 95] (Fig. 6a). Total Rab8A and Rab10 levels were not different between genotypes, while pT72-Rab8A and pT73-Rab10 levels were increased in the G2019S LRRK2 astrocytes (Fig. 6a). As expected, acute

application of the LRRK2 kinase inhibitor MLI-2 to G2019S LRRK2 astrocytes reverted the increased phosphorylation levels of Rab8A, Rab10, and pS1292-LRRK2, and abolished the levels of pS935-LRRK2 (Fig. 6a).

To test whether the LRRK2-mediated alterations of the Rab4-positive recycling compartment are modulated by Rab8A or Rab10, we transfected primary astrocytes with Flag-Glt-1 and GFP-Rab4 along with either RFP-tagged wild-type Rab8A or Rab10, or with variants mimicking the GTP-bound active state (Rab8A-Q67L or Rab10-Q68L) (Fig. 6b, d). Overexpression of wild-type Rab8A or wild-type Rab10 did not alter the G2019S LRRK2-mediated increase in the size of the Rab4-positive recycling endosomes (Fig. 6c–e; LRRK2 WT+Rab8A WT vs LRRK2 G2019S+Rab8A WT, $p<0.0001$; LRRK2 WT+Rab10 WT vs LRRK2 G2019S+Rab10 WT, $p=0.0003$). In contrast, overexpression of the active variants of RFP-Rab8A or RFP-Rab10 completely reverted the G2019S LRRK2-mediated morphological alterations of the Rab4 recycling compartment (Fig. 6c–e; LRRK2 G2019S+Rab8A-Q67L vs LRRK2 WT+Rab8A-Q67L, $p=0.91$; LRRK2 G2019S+Rab8A-Q67L vs LRRK2 G2019S+Rab8A WT, $p=0.0003$; LRRK2 G2019S+Rab10-Q68L vs LRRK2 WT+Rab10-Q68L, $p>0.99$; LRRK2 G2019S+Rab10-Q68L vs LRRK2 G2019S+Rab10 WT, $p=0.04$). Together, analyzing the distribution of Rab4-positive vesicles dimension (Supplementary Fig. 5a, b, online resource), we confirmed that the overexpression of Rab8A-Q67L or Rab10-Q68L variants in LRRK2 G2019S astrocytes shifted vesicle dimension range from $\sim 1\text{--}0.8\ \mu\text{m}^2$ to $\sim 0.5\text{--}0.2\ \mu\text{m}^2$, sizes similar to wild-type organelles (Supplementary Fig. 5a, b, online resource). Altogether, these data suggest that the aberrant kinase activity of pathogenic LRRK2 causes enlargement of the Rab4-positive compartment through Rab8A and Rab10 inactivation.

LRRK2 G2019S perturbs Glt-1 recycling and favors its degradation

We next examined whether Glt-1 accumulation in the Rab4-positive compartment in the LRRK2 G2019S astrocytes was due to a delay in recycling. First, we applied the recycling inhibitor Monensin on primary striatal LRRK2 WT and G2019S astrocytes, and investigated the co-localization of Glt-1 with Rab4 (Fig. 7a). In untreated cells, Glt-1 accumulated in Rab4-positive recycling vesicles in the presence of the LRRK2 pathogenic mutation as compared to controls (Fig. 7b; untreated LRRK2 WT vs untreated LRRK2 G2019S, $p=0.04$). Monensin application induced a significant accumulation of Glt-1 in Rab4-positive vesicles in LRRK2 WT cells (Fig. 7b; untreated LRRK2 WT vs LRRK2 WT+Monensin, $p=0.001$), thereby phenocopying the distribution of the transporter observed in untreated LRRK2 G2019S astrocytes (Fig. 7b; LRRK2 WT+Monensin vs

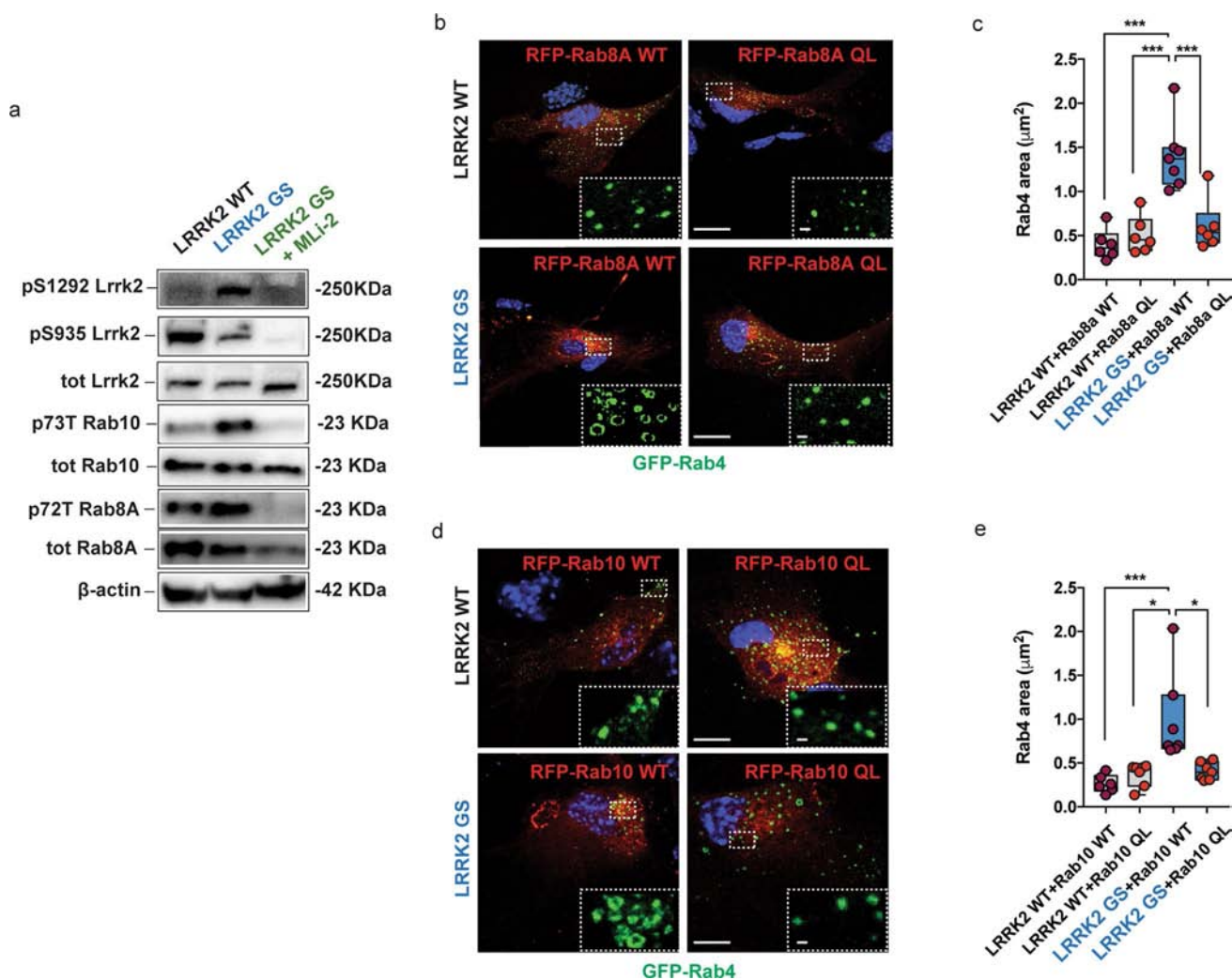


Fig. 6 LRRK2 G2019S mutation enhances Rab4-positive organelles dimension via Rab8A and Rab10 phosphorylation. **a** Western blot analysis of extracts from primary striatal astrocyte cultures from LRRK2 WT, LRRK2 G2019S mice with or without MLI-2 treatment, and blotted with the following antibodies: anti-pS1292 LRRK2, anti-pS935 LRRK2, anti-total LRRK2, anti-p73T Rab10, anti-total Rab10, anti-p72T Rab8A, and anti-total Rab8A antibodies; **b, d** Representative *z*-stack confocal images of primary astrocytes from LRRK2 WT and LRRK2 G2019S mice transfected with GFP-Rab4 and Rab8A WT/QL or Rab10 WT/QL. Insets show the area of the

untreated LRRK2 G2019S, $p=0.73$). Conversely, Monensin treatment did not induce further Glt-1 accumulation in Rab4-positive vesicles in the LRRK2 G2019S astrocytes (Fig. 7b; untreated LRRK2 G2019S vs LRRK2 G2019S + Monensin, $p=0.70$), suggesting that the transporter was almost completely incorporated in the fast-recycling compartment under basal conditions in those cells.

We next studied the recycling kinetics by measuring Glt-1 localization in Rab4-positive vesicles after TPA-induced internalization. To isolate the unique contribution of the recycling pathway, the subsequent basal internalization was

blocked using Go 6976. We again confirmed that under basal conditions, Glt-1 accumulated as clusters in Rab4-positive vesicles in LRRK2 G2019S but not in LRRK2 WT astrocytes (Fig. 7c, d; LRRK2 WT vs LRRK2 G2019S, $p=0.01$), and that the application of MLI-2 reverted this phenotype (Fig. 7c, d; LRRK2 G2019S vs LRRK2 G2019S + MLI-2, $p=0.01$; LRRK2 G2019S + MLI-2 vs LRRK2 WT, $p>0.99$). Upon TPA stimulation, there was an overall increase of Glt-1 in Rab4-positive vesicles in LRRK2 WT and LRRK2 G2019S + MLI-2 astrocytes (LRRK2 WT vs LRRK2 WT + TPA, $p=0.01$; LRRK2 G2019S + MLI-2

vs LRRK2 G2019S + MLI-2 + TPA, $p = 0.003$), reaching values of Glt-1/Rab4 co-localization similar to those observed in LRRK2 G2019S astrocytes (Fig. 7c, d; LRRK2 WT + TPA vs LRRK2 G2019S + TPA, $p > 0.99$; LRRK2 G2019S + TPA vs LRRK2 G2019S + MLI-2 + TPA, $p = 0.99$; LRRK2 WT + TPA vs LRRK2 G2019S + MLI-2 + TPA, $p = 0.95$). Conversely, the amount of Glt-1 co-localizing with Rab4-positive vesicles in LRRK2 G2019S astrocytes did not increase upon TPA stimulation (Fig. 7 c-d; LRRK2 G2019S + TPA vs LRRK2 G2019S, $p > 0.99$). Both *Lrrk2* WT and *Lrrk2* G2019S + MLI-2 astrocytes displayed a decrease of Glt-1 in Rab4-positive vesicles already 1 min after Go 6976 application, with a most prominent effect 10 min after Go 6976 application (Fig. 7c-d; LRRK2 WT + Go T10' vs LRRK2 G2019S + Go T10', $p = 0.03$; LRRK2 G2019S + MLI-2 + Go T10' vs LRRK2 G2019S + Go T10', $p = 0.02$; LRRK2 WT + Go T10' vs LRRK2 G2019S + MLI-2 + Go T10', $p > 0.99$; LRRK2 WT + Go T10' vs LRRK2 WT, $p = 0.99$; LRRK2 G2019S + MLI-2 + Go T10' vs LRRK2 G2019S + MLI-2, $p > 0.99$). Although not reaching statistical significance, the overall amount of the transporter at the Rab4-positive organelles progressively decreased in the pathogenic LRRK2 astrocytes upon 10 min Go treatment (Fig. 7c-d; LRRK2 G2019S + Go T10' vs LRRK2 G2019S, $p = 0.89$). Of note, this phenomenon was not associated with a relocation of Glt-1 to the plasma membrane in the G2019S background (Fig. 7c, arrowheads).

Therefore, we examined whether Glt-1 incorporated into Rab4-positive vesicles was targeted for degradation in the LRRK2 G2019S astrocytes. As Glt-1 can be degraded through both the proteasome [74, 93] and the lysosome [82, 101], we monitored the presence of Glt-1 in the fast recycling and lysosomal compartments in the presence of either MG132 or Bafilomycin to block proteasomal or lysosomal function, respectively [63, 74]. LRRK2 G2019S astrocytes were co-transfected with Flag-Glt-1 and GFP-Rab4 and stained for the endogenous lysosomal protein Lamp1 to measure Glt-1 localization in the Rab4- and Lamp1-positive organelles (Fig. 7e). Upon MG132 application, the fraction of Glt-1 co-localizing with the Rab4-positive compartment was significantly enhanced in LRRK2 G2019S astrocytes (Fig. 7f; LRRK2 G2019S vs LRRK2 G2019S + MG132; $p = 0.02$). In the same condition, MG132 also promoted increases of Glt-1 localization in the Lamp1-positive vesicles in LRRK2 G2019S astrocytes (Fig. 7g; LRRK2 G2019S vs LRRK2 G2019S + MG132; $p = 0.012$). Furthermore, we demonstrated that lysosomal inhibition by Bafilomycin caused a significant increase of Glt-1 in the Rab4-positive compartment (Fig. 7f; LRRK2 GS and LRRK2 G2019S + Bafilomycin; $p = 0.004$) and dramatically accentuated Glt-1 accumulation in Lamp1-positive vesicles (Fig. 7g; LRRK2 G2019S vs LRRK2 G2019S + Bafilomycin;

$p < 0.0001$). The efficacy of the treatments to block the Glt-1 degradative pathways has been evaluated by measuring the total Glt-1 IntDen in these cells (Fig. 7h; LRRK2 G2019S vs LRRK2 G2019S + MG132; $p = 0.06$; LRRK2 G2019S vs LRRK2 G2019S + Bafilomycin; $p = 0.005$). Similar accumulation of Glt-1 upon pharmacological manipulations was measured in the wild-type background confirming the involvement of both the degradative pathways in Glt-1 degradation (Supplementary Fig. 6a–c, online resource). These results indicate that pathogenic LRRK2 profoundly perturbs Glt-1 recycling to the cell membrane, possibly associated with the re-routing of the transporter for lysosomal degradation (Fig. 7i).

Discussion

In the present study, we report severe deficits of EAAT2 in *post-mortem* caudate and putamen from Parkinson's disease (PD) patients carrying the LRRK2 G2019S mutation. Previous clinical data have shown alterations in the glutamate content in the brain as well as in the plasma of idiopathic PD (iPD) patients, suggesting that glutamate dyshomeostasis might be a common feature in PD [18, 27, 35, 59, 98]. However, our data indicate that the EAAT2 phenotype is clearly exacerbated in the presence of the LRRK2 pathogenic mutation as compared to iPD, suggesting a specific involvement of LRRK2 in EAAT2 biology. Striatal EAAT2 downregulation correlated with increased expression of the reactive marker GFAP in caudate and putamen glial cells of LRRK2-linked PD patients. Although impaired glutamate buffering is often found accompanied by astroglial reactivity and neuroinflammation in several disease models [29, 55, 104], conflicting results have been published in the context of PD patients. Enhanced GFAP reactivity has been clearly documented in *Substantia Nigra pars compacta* (*SNpc*) and olfactory bulbs [19, 50, 88]. However, one report suggested astrocytic atrophy (instead of reactivity) in PD brains, since low levels of astrocyte markers were observed in the *SNpc* and the striatum [88], and studies in human iPS-derived astrocytes from LRRK2 G2019S-PD patients suggested a similar mechanism [65]. Our study suggests an absence of astrocytic degeneration or atrophy, since the levels of the astrocyte marker GS were not perturbed in the context of disease. The presence of astrocyte reactivity has been reported in different transgenic mice overexpressing the LRRK2 G2019S kinase [32, 99]. Accordingly, LRRK2 G2019S knock-in mice display an evident phenotype characterized by a significant downregulation of striatal Glt-1 protein levels and extensive astrogliosis, which recapitulates the human disease in *post-mortem* samples. Thus, the knock-in G2019S LRRK2 mouse is an outstanding model system to unravel the mechanism that links pathogenic LRRK2 to transporter

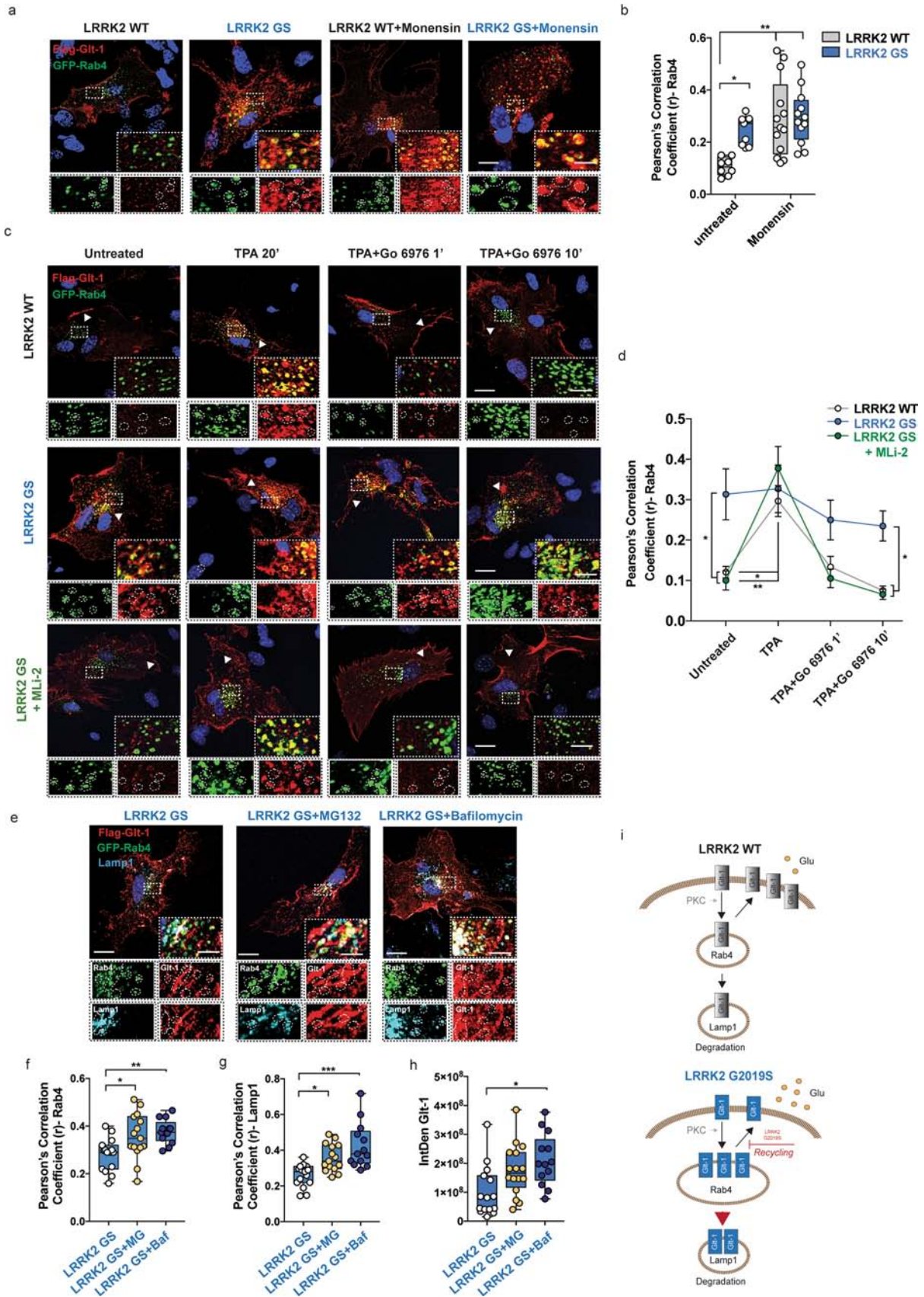


Fig. 7 G2019S pathogenic LRRK2 mutation impacts on Glt-1 recycling and turnover. **a** Representative confocal images of primary striatal LRRK2 WT and G2019S astrocytes under basal conditions and treated with the recycling blocker Monensin (35 μ M, 40 min). Insets show the Rab4-positive area and the localization of Glt-1 in the indicated ROIs. Scale bars: 20 μ m; insets 5 μ m; **b** quantitative analysis of the Pearson's correlation coefficient of Glt-1 co-localizing with the Rab4-positive compartment; $n=8$ cells for LRRK2 WT, $n=13$ cells for LRRK2 WT + Monensin, $n=9$ cells for LRRK2 G2019S and $n=12$ cells for LRRK2 G2019S + Monensin, experiments performed at least in triple; **c** Representative z-stack confocal images of primary LRRK2 WT and G2019S (with or without MLI-2) striatal astrocytes transfected with Flag-Glt-1 (red) and GFP-Rab4 (green). The insets show Rab4-positive area and the localization of Glt-1 in these ROIs; scale bar 20 μ m; insets 5 μ m; **d** quantitative analysis of the Pearson's correlation coefficient of Glt-1 co-localizing with the Rab4-positive compartment in the four selected experimental time points. At least $n=6$ cells have been analyzed for each experimental group and the experiments have been performed in triple; **e** representative z-stack confocal images of primary striatal LRRK2 G2019S astrocytes transfected with GFP-Rab4 and Flag-Glt-1 (red) and labeled for endogenous Lamp1 (far red, pseudocolored in blue). Insets show Rab4- and Lamp1-positive area and the localization of Glt-1 in these ROIs. Scale bar 20 μ m; insets 5 μ m; **f** Quantitative analysis of the Pearson's correlation coefficient of Glt-1 co-localizing with the Rab4-positive vesicles in LRRK2 G2019S astrocytes under basal conditions ($n=15$ cells) or upon MG132 ($n=15$ cells) or Bafilomycin application ($n=13$ cells); **g** quantitative analysis of the Pearson's Correlation Coefficient of Glt-1 co-localizing with the Lamp1-positive structures in LRRK2 G2019S astrocytes under basal conditions ($n=15$ cells) or upon MG132 ($n=15$ cells) or Bafilomycin ($n=13$ cells) application; experiments performed at least in triple; **h** Quantitative analysis of Glt-1 IntDen in LRRK2 G2019S astrocytes, under basal condition or after application of MG132 or Bafilomycin A1 ($n=15$ cells for untreated LRRK2 GS, $n=16$ cells for LRRK2 GS + MG132 and $n=13$ LRRK2 GS + Bafilomycin; experiments performed at least in triple); **i** schematic representation of Glt-1 trafficking in LRRK2 WT and LRRK2 G2019S astrocytes. Statistical analysis in **b** was performed using two-way ANOVA test (treatment: $F=12.86$ and $p=0.0009$; Genotypes $F=4.672$ and $p=0.03$) followed by Tukey's multiple comparisons test; statistical analysis in **d** was performed using two-way ANOVA test (treatment: $F=16.17$ and $p<0.0001$; group: $F=13.87$ and $p<0.0001$) followed by Tukey's multiple comparison test; statistical analysis in (**f–h**) was performed using one-way ANOVA test (**f** $F=6.68$ and $p=0.003$); **g** $F=12.07$ and $p<0.0001$; **h** $F=5.79$ and $p=0.006$) followed by Tukey's multiple comparisons test (*LRRK2 WT vs LRRK2 G2019S, #LRRK2 G2019S vs LRRK2 G2019S + MLI-2)

deficiencies. In agreement with the downregulation of Glt-1 protein, an enhanced glutamatergic cortico-striatal neurotransmission has been described in LRRK2 animal model [7, 48, 49, 89, 92]. All together, these findings suggest that striatal glutamatergic imbalance and correlated glutamate-induced excitotoxicity intervene in PD pathophysiology.

LRRK2 is expressed in glial cells and plays a relevant role in astrocyte physiology both in humans and mice [4, 53, 81]. In this context, we specifically dissected the contribution of the pathogenic LRRK2 mutation to Glt-1 functionality in astrocytes at endogenous levels in cultured cells, in pure subcellular astrocytic ex vivo preparations, and in organotypic coronal slices. We confirmed a reduced level of the

transporter, in agreement with our observations in human and murine striatal lysates. These observations fit with the functional analysis carried out on isolated mouse striatal gliosomes, which reveal a decreased ability of the transporter to re-uptake glutamate. By comparing the kinetic values, we find that LRRK2 G2019S impinges on Glt-1 transport velocity without affecting substrate affinity. Similarly, the expression of human LRRK2 G2019S induces a decrease of the EAAT2 transport current without modifying the biophysical properties of the transporter in *Xenopus* oocytes. Therefore, the EAAT2/Glt-1 functional impairment can be ascribed to a reduced localization of the transporter at the plasma membrane mediated by pathogenic LRRK2. Importantly, the effects of G2019S LRRK2 on EAAT2 are restored upon acute inhibition of the G2019S kinase activity by MLI-2, indicating that pathogenic LRRK2 impairs proper EAAT2 homeostasis.

It has been consistently reported that Glt-1 continuously exchanges between a diffuse and spotted localization at the surface, shaping synaptic transmission [2, 57]. Moreover, Glt-1 undergoes basal PKC-mediated endocytosis and intracellular cluster formation in astrocytic processes to regulate glutamate uptake activity [103]. In our system, only the amount of the transporter, but not the spotted distribution at the plasma membrane, was affected by pathogenic LRRK2. Conversely, LRRK2 G2019S astrocytes exhibited the presence of large intracellular Glt-1 clusters resembling, in terms of dimension, those found upon pharmacological stimulation of PKC-mediated endocytosis of Glt-1. However, our data exclude the involvement of LRRK2 in the PKC-mediated internalization pathway. Indeed, the inhibition of LRRK2 kinase activity was not able to revert the PKC-induced clusterization in control astrocytes, and PKC inhibition failed to reduce Glt-1 clusters in G2019S LRRK2 astrocytes. PKC activation was also not able to induce a further increase in Glt-1 clusters in LRRK2 G2019S astrocytes, suggesting that most of the transporter is internalized in the pathogenic LRRK2 background. Endogenous Glt-1 interacts with partially different protein environments in the two backgrounds, as revealed by mass spectrometry data. On the one hand, striatal Glt-1 immunoprecipitated from LRRK2 WT mice mainly interacts with plasma membrane proteins. In agreement with the previous findings, we identified the Na^+ - K^+ pump as a Glt-1 interactor in an LRRK2 WT background, confirming that Glt-1 and Na^+ - K^+ -ATPases are part of the same macromolecular complex and operate as a functional unit to regulate physiological glutamatergic neurotransmission [70]. On the other hand, Glt-1 almost exclusively interacts with intracellular proteins in presence of the G2019S LRRK2 mutation. Indeed, we identified proteins involved in the endo-vesicular pathway, suggesting a different subcellular compartmentalization of the transporter in the presence of the LRRK2 G2019S mutation. Along these lines, we

demonstrate that LRRK2 operates in Glt-1 recycling to the plasma membrane. In the LRRK2 G2019S astrocytes, Glt-1 is preferentially engulfed in fast-recycling endosomes, which are recognized by overexpression of the marker Rab4. Pharmacological LRRK2 inhibition reduces the amount of Glt-1 co-localizing with the Rab4-positive marker and promotes Glt-1 redistribution to the plasma membrane, which allows for the functional recovery of the transporter as assessed by electrophysiological recordings in oocytes. These findings have been corroborated in a more complex and robust physiological system represented by the *ex vivo* organotypic coronal slices. Here, endogenous Glt-1 accumulates in enlarged Rab4-positive vesicles and the acute application of the LRRK2 inhibitor MLI-2 reverts this phenotype.

By combining confocal and TEM ultrastructural analysis, we show that the LRRK2 G2019S mutation profoundly affects the architecture of the fast-recycling Rab4-positive organelles in astrocytes, promoting an enlargement of the area of these vesicles. Coherently with previous studies [32, 68, 95], we report that G2019S LRRK2 aberrantly phosphorylates Rab8A/Rab10 proteins at the endogenous level in cultured astrocytes. The Rab hyperphosphorylation has been reported to promote defects in the recycling of the EGFR and its accumulation in Rab4-positive recycling structures [67, 68]. In line with these reports, we observed that the overexpression of the active Rab8A or Rab10 mutants in LRRK2 G2019S astrocytes restored the dimension of the Rab4-positive vesicles, pointing to the LRRK2-mediated phosphorylation and inactivation of Rab8A/Rab10 as the pathogenic mechanism causing the Glt-1 trafficking defects in G2019S LRRK2 astrocytes. The role of LRRK2 in Glt-1 recycling was further dissected by pharmacological approaches. The accumulation of Glt-1 in the Rab4-positive compartment observed in LRRK2 G2019S astrocytes was phenocopied by blocking the recycling of Glt-1 in control astrocytes. In LRRK2 G2019S astrocytes, the same treatment did not induce further increases in Glt-1 co-localization with Rab4 vesicles, confirming that almost the totality of the transporter is localized to this subcellular compartment under basal conditions. Moreover, our observations on the kinetics of the process confirm that when internalized, Glt-1 is re-routed to early endosomes, as previously reported [25]. While Glt-1 repopulates the plasma membrane in LRRK2 wild-type astrocytes, Glt-1 is basally captured and persists in the Rab4 compartment in the pathogenic LRRK2 context. In addition, a tendential decrease in the amount of Glt-1 co-localizing with the Rab4-positive marker not associated with plasma membrane re-localization indicates that the persistent delay in Glt-1 recycling might promote the degradation of the protein. Accordingly, the blockade of the degradative systems promoted an increase in the amount of Glt-1 co-localizing with a Lamp1-positive compartment especially upon lysosomal inhibition.

In conclusion, our work reveals that the LRRK2 G2019S mutation profoundly affects Glt-1 recycling to the plasma membrane by impinging on the early endosomal fast-recycling compartment in striatal astrocytes. Although additional mechanistic investigations are needed, we propose that the cellular degradative system may eventually promote Glt-1 turnover by sensing the overload of the transporter in the Rab4-positive compartment (Fig. 7h). In this manner, a chronic, subtle LRRK2-mediated impairment of the recycling machinery in brain cells might cause a progressive depletion of Glt-1 with a consequent reduction of extracellular glutamate clearance. In a broader context, our work supports a novel pathogenic mechanism by which the nigro-striatal synapses might be affected at the early stage of the neurodegenerative process. Indeed, the LRRK2-mediated impairment of the astrocytic glutamate re-uptake capacity could induce a premature striatal glutamate accumulation, anticipating subsequent irreversible consequences on the integrity of dopaminergic connections.

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Author contribution LI and LC designed the study, performed and optimized experiments, interpreted data, and wrote the manuscript; VG performed imaging experiments and helped in preparing primary astrocyte cultures; FP and GP performed qPCR experiments; EG and NP contributed to data analysis; AM, TB, and GB performed gliosomes' experiments; IB and GA performed mass spec experiments; ADI, CR, and EB performed electrophysiological experiments; AM and CP performed TIRFM experiments; R.B. provided human samples; EG, LB, EG, and SH have contributed to manuscript editing and optimization. All authors have read and approved the final manuscript.

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Data availability Data supporting the findings of the present study are available from the corresponding author, upon reasonable request.

Declarations

Conflict of interest The authors have no conflicts of interest to declare.

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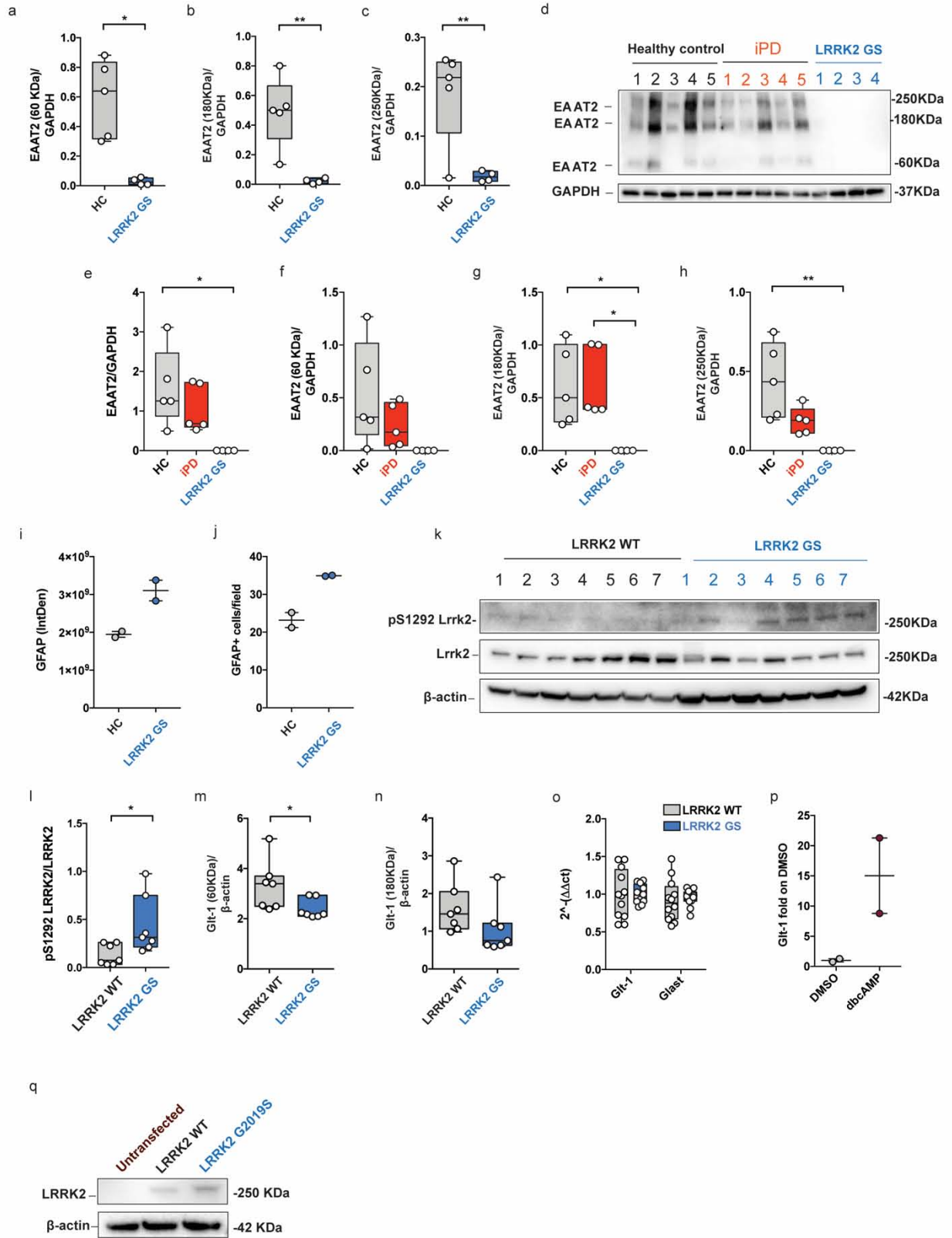
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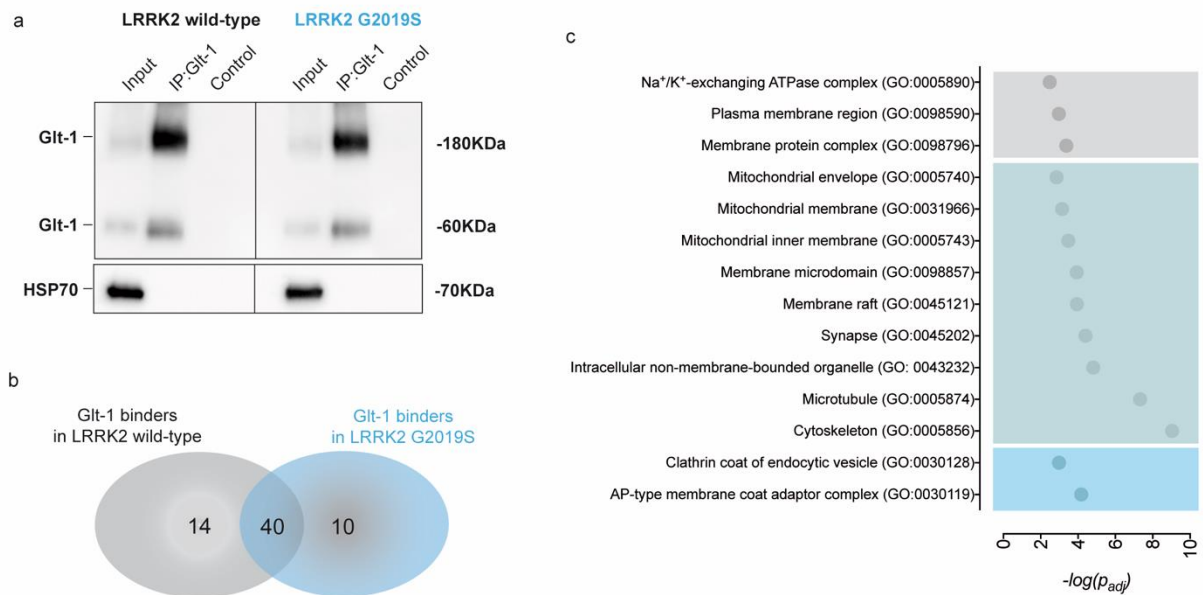
Supplementary Figure 1



Supplementary Figure 1

a-c) Western blot quantification of the monomeric fractions (60 KDa) as well as of the multimeric fractions (180 KDa and 250 KDa) of EAAT2 in LRRK2 G2019S PD patients (n=4) compared to healthy controls (n=5); d) Western blot analysis of healthy controls, idiopathic PD patients (iPD) and LRRK2 G2019S caudate and putamen lysates using an anti-EAAT2 antibody; e-h) Relative quantification of the total EAAT2 as well as of the monomeric fractions (60 KDa) and multimeric fractions (180 KDa and 250 KDa) of EAAT2 in the healthy controls (n=5), iPD patients (n=5) and LRRK2 G2019S PD patients (n=4). The band intensity was performed using ImageJ and normalized to the housekeeping protein GAPDH; i-j) Quantification of GFAP IntDen and of GFAP⁺ positive cells in the caudate and putamen of healthy controls (n=2) and LRRK2 G2019S PD patients (n=2); k) Western blot analysis of LRRK2 WT and LRRK2 G2019S striatal lysates blotted with the following antibodies: anti-pS1292 LRRK2, anti-total LRRK2 and the housekeeping β -actin; l) Quantification of Ser1292 phosphorylation (pS1292 LRRK2/total LRRK2) was performed using ImageJ (n=7 striatal samples for both LRRK2 WT and LRRK2 G2019S 4-month old mice; m-n) Quantification of the 60 KDa and 180 KDa Glt-1 bands in LRRK2 WT and LRRK2 G2019S mice; n=7 animals for each genotype; o) qPCR analysis of Glt-1 and Glast mRNA in the striatum of LRRK2 WT and LRRK2 G2019S mice; n=12 animals for each genotype; p) qPCR analysis of Glt-1 mRNA in primary LRRK2 WT striatal astrocytes untreated or treated with dbcAMP for 10 days; experiment performed twice on n=2 independent cell cultures; q) Western blot analysis of oocytes co-injected with the mRNA of the excitatory amino acid transporter 2 and the mRNA of the human LRRK2 WT or G2019S, blotted with the antibodies against the total LRRK2 and the housekeeping β -actin. Statistical analysis was performed in a-c, o using Unpaired T-test and in k-l using Mann-Whitney test. Statistical analysis was performed in e, g using Kruskal-Wallis test (e: P=0.006; g: P=0.007) followed by Dunn's multiple comparisons test and in f, h using One-way ANOVA test (f: F=3.07 and P=0.08; h: F=9.49 and P=0.004) followed by Tukey's multiple comparisons test.

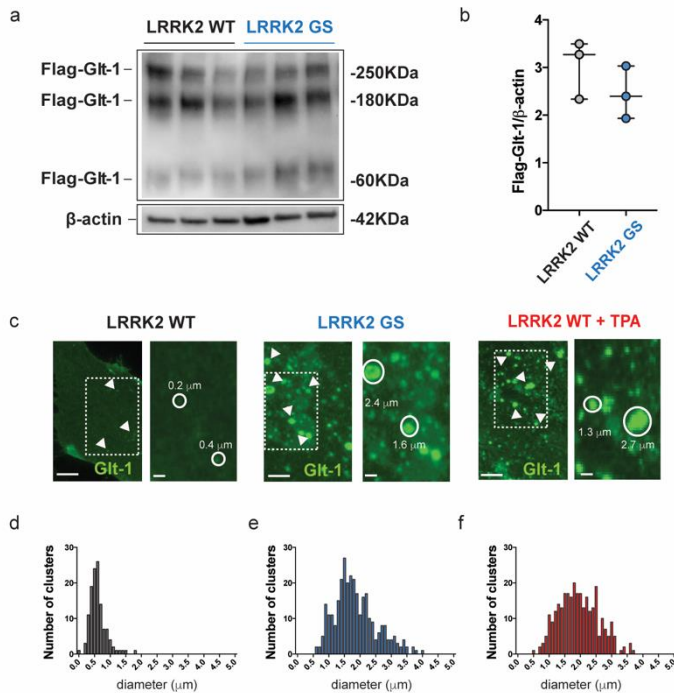
Supplementary Figure 2



Supplementary Figure 2- Screening of Glt-1 protein-protein interactions

a) Striatal Glt-1 immunoprecipitated from LRRK2 WT and G2019S brains was resolved by immunoblotting. Anti-HSP70 was applied to normalize for protein content; b) Venn diagram summary of interacting proteins, colored for different background (grey for LRRK2 WT, light blue for LRRK2 G2019S, dark blue for LRRK2 WT and G2019S shared interacting proteins); c) Selected GO term enrichments from CC categories using gProfiler were plotted using $-\log(P_{adj})$ values.

Supplementary Figure 3



Supplementary Figure 3

a) Western blot analysis of transfected Flag-Glt-1 expression in primary striatal LRRK2 WT and G2019S astrocytes using an anti-Flag-HRP antibody; b) Relative quantification of band intensity was performed using ImageJ and normalized to β-actin; experiment performed in triple; c) Representative epifluorescence images of Glt-1 clusters in Flag-Glt-1 transfected primary striatal astrocytes from LRRK2 WT (untreated or treated with TPA) and from LRRK2 G2019S astrocytes. Scale bars 5 μm; insets 1 μm. d) Frequency distribution of Glt-1 cluster diameter in untreated LRRK2 WT (grey bars); e) Frequency distribution of Glt-1 cluster diameter in LRRK2 G2019S (blue bars); f) Frequency distribution of Glt-1 cluster diameter in LRRK2 WT treated with TPA (d; red bars); n=5 cells analyzed for each group. Statistical analysis in b was performed using Mann-Whitney test.

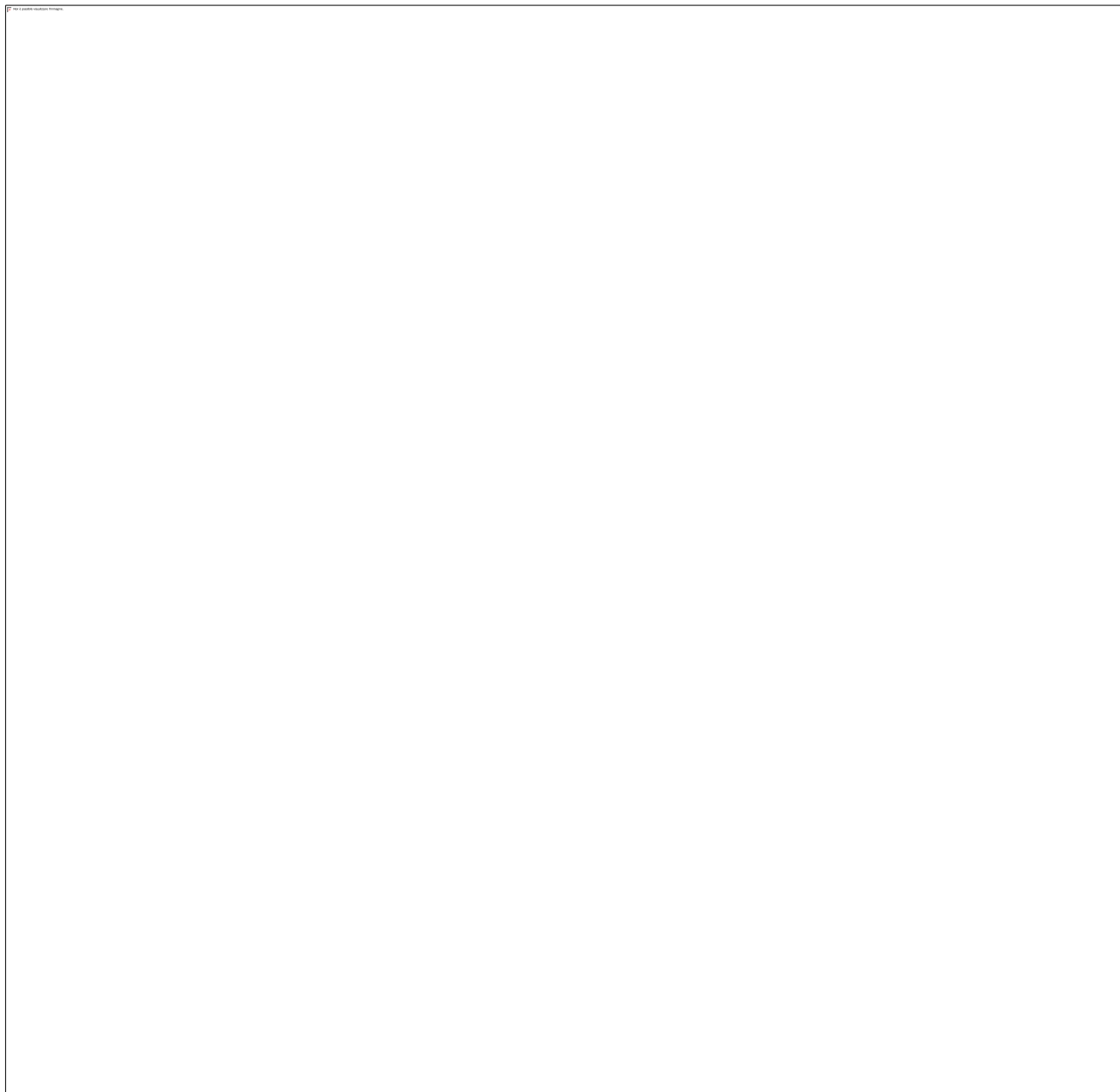
Supplementary Figure 4



Supplementary Figure 4

a) Orthogonal z-stack projections of LRRK2 G2019S astrocytes co-transfected with Flag-Glt-1 (red) and GFP-Lamp1, GFP-Rab11 or GFP-Rab4 (green). Scale bar 20 μm ; b) Quantitative analysis of the Pearson's Correlation Coefficient of Glt-1 colocalizing with the Rab4-positive vesicles in LRRK2 WT and G2019S astrocytes under basal conditions or upon MLI-2 application; at least n=6 cells analyzed for each group; c) Representative confocal microscopy images of LRRK2 WT and G2019S primary striatal astrocytes transfected with GFP-Rab4 and Flag-Glt-1. Scale bars: 2 μm ; d,e) Quantification of Rab4-positive vesicle number and area; at least n=9 cells analyzed for each group and experiments performed at least in triple; f) Representative confocal (left panel), electron microscopy (middle panel) and merge (right panel) image of a LRRK2 WT primary astrocyte transfected with Rab4-GFP (green). The image reveals the co-localization of early endosomal structures identified by transmission microscopy with the GFP-Rab4-positive vesicles identified by confocal microscopy; scale bar: 1 μm . Statistical analysis in b was performed using Two-way ANOVA test (Treatment F=15.79 and P=0.004; Genotypes F=16.38 and P =0.004) followed by Tukey's multiple comparisons test. Statistical analysis in d, e was performed using Unpaired t-tests.

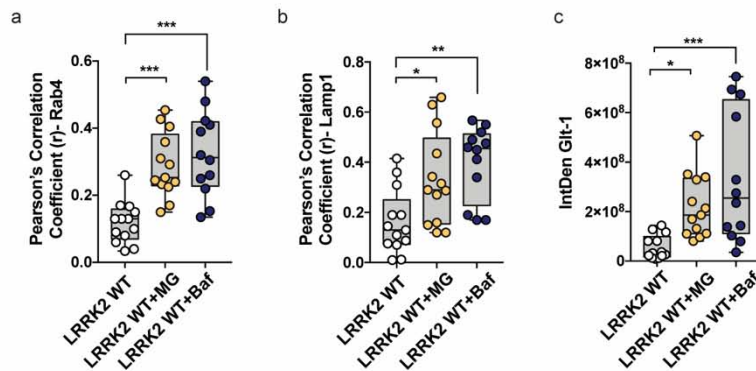
Supplementary Figure 5



Supplementary Figure 5

a,b) Frequency distribution of Rab4-positive vesicles area in LRRK2 WT and LRRK2 G2019S astrocytes. At least n=6 cells analyzed for each group and experiments performed at least in triple.

Supplementary Figure 6



Supplementary Figure 6

a) Quantification of Glt-1 IntDen in the Rab4-positive vesicles in LRRK2 WT astrocytes under basal conditions (n=13 cells) or upon MG132 (n=13 cells) or Bafilomycin application (n=12 cells); b) Quantification of Glt-1 IntDen in the endogenous Lamp1-positive structures in LRRK2 WT astrocytes under basal conditions (n=13 cells) or upon MG132 (n=13 cells) or Bafilomycin (n=12 cells) application; experiments performed at least in triple; c) Quantitative analysis of Glt-1 IntDen in LRRK2 WT astrocytes, under basal condition or after application of MG132 or Bafilomycin A1 (n=13 cells for untreated LRRK2 WT, n=13 cells for LRRK2 WT+MG132 and n=12 LRRK2 WT+Bafilomycin; experiments performed at least in triple; Statistical analysis in a-c was performed using One-way ANOVA test (a: $F=16.06$ and $P<0.0001$; b: $F=7.79$ and $P=0.001$; c: $F=8.76$ and $P=0.0008$) followed by Tukey's multiple comparisons test.

Supplementary materials and methods

Quantitative Polymerase Chain Reaction (qPCR)

Total RNA was extracted from mice striata or from primary striatal astrocytes with the Total RNA Purification kit (NORGEN Biotek) and quantified by absorbance in a NanoDrop 2000c UV-Vis spectrophotometer (ThermoFisher Scientific). cDNA was synthesized with the All-in-One Cdna Synthesis SuperMix (Bimake) following manufacturer's instructions. Gene expression was quantified by qPCR in real-time PCR reactions with Sybr Green technology in a CFX96 Touch Real-Time PCR Detection System (Bio-Rad). 30 ng cDNA were used in iTaq Universal SYBR Green Supermix (Bio-Rad) at the following conditions: stage 1: 95 °C, 5 min; stage 2: 39 x (95 °C, 15 s; 60 °C, 30 s).

The primers were as follows: mSLC1A2 fw: GGTGGAAAGCCGGGACGTGGATTA; mSLC1A2 rev: GCTTGGGCATATTGTTGGCACCCCT; SLC1A3 fw: ATCCGGGAGGAGATGGTGCCCGT; SLC1A3 rev: AGGATGCCAGAGGCGCATAACCACA; ACTIN fw: TACCACCATGTACCCAGGCATT; ACTIN rev: ACTCATCGTACTCCTGCTTGCTGA; mGAPDH fw: GAGAGTGTTTCCTCGTCCCG; mGAPDH rev: ACTGTGCCGTTGAATTTGCC; TRANSFERRIN RECEPTOR fw: TATAAGCTTTGGGTGGGAGGCA; TRANSFERRIN RECEPTOR rev: AGCAAGGCTAAACCGGGTGTATGA;

Primers for Slc1a2, Slc1a3, β -Actin and Transferrin were purchased from Sigma Aldrich while primers for GAPDH were purchased from Metabion International AG. The quantification of the gene relative expression was carried out by the Delta-Delta Ct method [4] by normalizing to the reference genes GAPDH, β -Actin and Transferrin receptor. A dissociation curve was built in the 60-95 °C range to confirm the specificity of the amplification product.

Western blot on injected oocytes

Western blot analysis on injected oocytes was performed as in [3]. Briefly, oocytes were homogenized in 20 mM HEPES solution (pH 7.3), supplemented with phosphatase and protease inhibitors. To remove the abundant yolk platelets, samples were centrifuged at 800g for 5 minutes RT. Then, protein concentration was measured using the Pierce® BCA Protein Assay Kit. Oocytes samples were resolved by electrophoresis on pre-cast 4–20 % tris-glycine polyacrylamide gels and transferred to polyvinylidene difluoride membranes using a semi-dry Biorad transfer machine with the 1X Transfer Buffer at 25 V for 20 min. Membranes were incubated in TBS-T plus 5 % skimmed milk for 1 h RT, and then incubated overnight with primary antibodies diluted in TBS-T plus 5 % skimmed milk. The following primary antibodies were used: a mouse anti- β -actin (A1978, Sigma-Aldrich, 1:10000) and a rabbit anti-LRRK2 (MJFF2 c41-2; Abcam, 1:300). Membranes were

subsequently rinsed and incubated for 1h at RT with the appropriate HRP-conjugated secondary antibodies. The visualization of the signal was conducted using Immobilon® Forte Western HRP Substrate and the VWR® Imager Chemi Premium.

Liquid-chromatography mass spectrometry (LC-MS) analysis

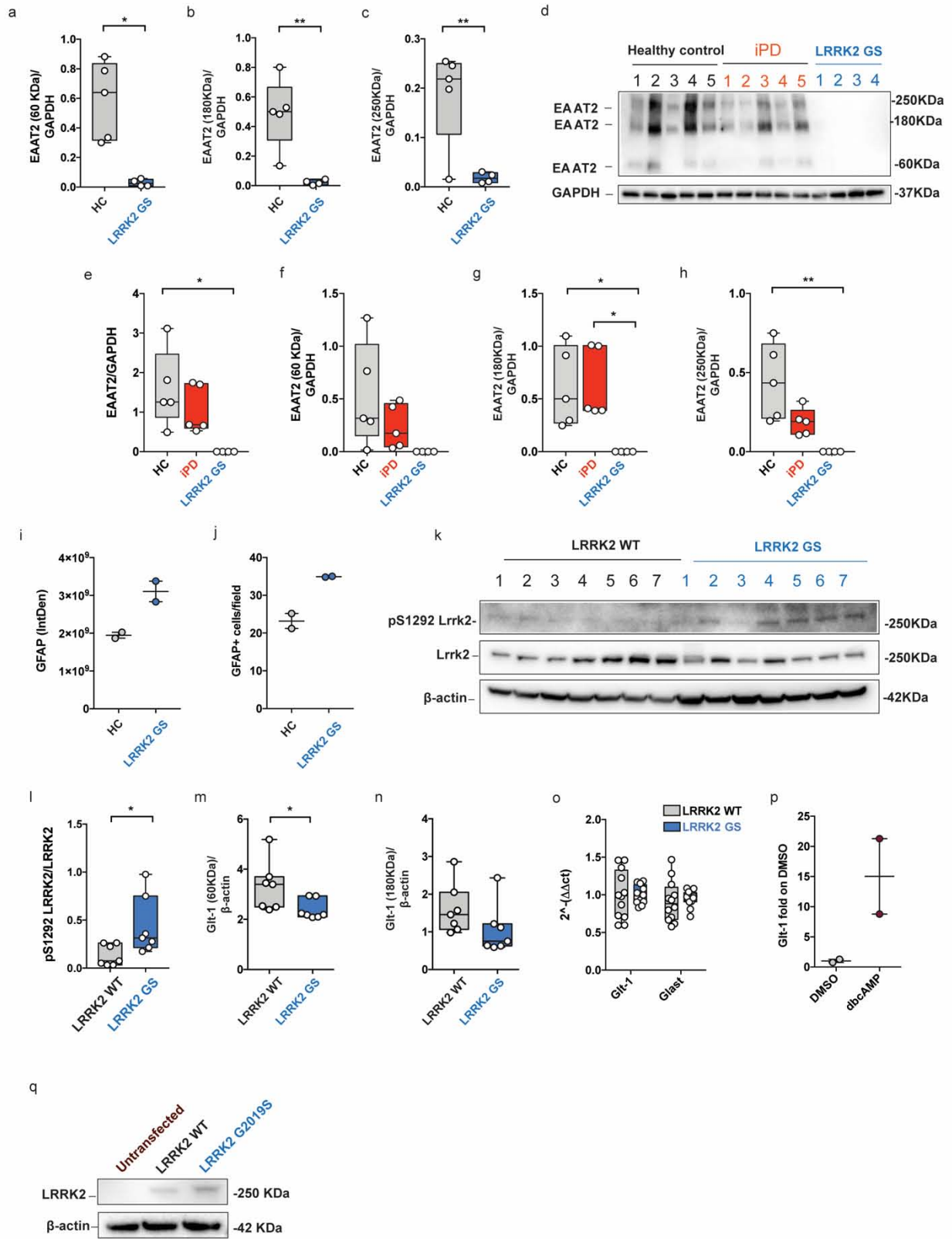
Endogenous Glt-1 was immunoprecipitated from homogenized WT and LRRK2 G2019S mouse striata using 5 µg of a rabbit anti-Glt-1 antibody (Abcam; ab205248) in RIPA buffer (1.5 mg of total protein each). Magnetic beads (Protein A/G Magnetic Beads, BioTool) (50 µL) were used to pre-clear and precipitate the transporter. Beads were then washed three times using 1 ml of RIPA buffer and proteins loaded on pre-cast 4–20 % tris-glycine polyacrylamide gels (Biorad). Gel bands were excised, cut into small pieces and destained with a solution of 60 % NH₄HCO₃ 200 mM/40 % acetonitrile (ACN) at 37 °C. Disulfide bridges were reduced with 2 mM Tris (2-carboxyethyl)phosphine hydrochloride (TCEP) in 50 mM NH₄HCO₃ at 56 °C for 1 h, and cysteine residues were alkylated with 4 mM methyl methanethiosulfonate (MMTS) with 50 mM NH₄HCO₃ in the dark at room temperature for 45 min. Gel samples were washed twice with 50 mM NH₄HCO₃ and ACN alternatively and vacuum-dried. Samples were incubated with 12.5 ng/µL trypsin (Sequencing Grade Modified Trypsin, Promega) in 50 mM (NH₄)₂HCO₃ and protein digestion was carried out overnight at 37 °C. Peptides were extracted with three changes of 50 % ACN/ 0.1 % formic acid (FA). Samples were vacuum-dried and stored at –20 °C. Samples were analyzed using a LTQ Orbitrap XL mass spectrometer (Thermo Fisher Scientific) coupled to a HPLC Ultimate 3000 (Dionex - Thermo Fisher Scientific) through a nanospray source (NSI), as described previously [1]. Samples were resuspended in 30 µL of 3 % ACN/0.1 % FA and each sample was acquired twice. Raw data files were analyzed with MaxQuant [2] software (v. 1.5.1.2) interfaced with Andromeda search engine. Protein search was performed against the mouse section of the UniProt database (*Mus musculus*, version 2020-09-30, 55494 entries). Enzyme specificity was set to trypsin with up to one missed cleavage allowed, while methylthio-cysteine and oxidized methionine were set as fixed and variable modifications, respectively. A minimum of two peptides was required for protein identification, and a false discovery rate (FDR) ≤ 0.01, both at the peptide and protein level, was used to filter the results. To estimate the relative protein abundance across samples, the intensity values calculated by the software were used. The datasets were compared to highlight significant differences in the protein abundances: common and unique Glt-1 binders between the LRRK2 WT and G2019S genetic environments were identified performing a Z-test on the log-transformed values of the IP/CTRL ratios and considering only proteins with p < 0.05 and Fold Changes (FC) ≥ 3.5. Gene Ontology (GO) terms were employed to identify discrete functional enrichments in order to extract

information about novel networks of interactors in relationship to the different subcellular localization of the transporter. G:profiler (<https://biit.cs.ut.ee/gprofiler/gost>) was used for enrichment analysis. Glt-1-related protein networks in LRRK2 G2019S pathogenic background were ranked based on the fold-change affinity over the control (≥ 3.5).

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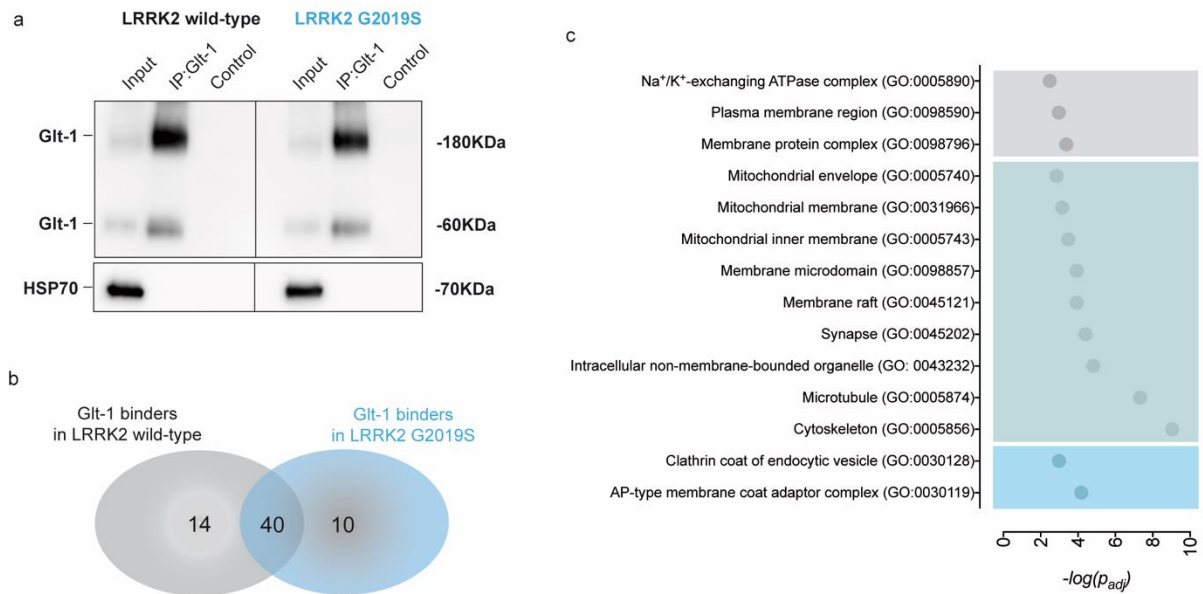
Supplementary Figure 1



Supplementary Figure 1

a-c) Western blot quantification of the monomeric fractions (60 KDa) as well as of the multimeric fractions (180 KDa and 250 KDa) of EAAT2 in LRRK2 G2019S PD patients (n=4) compared to healthy controls (n=5); d) Western blot analysis of healthy controls, idiopathic PD patients (iPD) and LRRK2 G2019S caudate and putamen lysates using an anti-EAAT2 antibody; e-h) Relative quantification of the total EAAT2 as well as of the monomeric fractions (60 KDa) and multimeric fractions (180 KDa and 250 KDa) of EAAT2 in the healthy controls (n=5), iPD patients (n=5) and LRRK2 G2019S PD patients (n=4). The band intensity was performed using ImageJ and normalized to the housekeeping protein GAPDH; i-j) Quantification of GFAP IntDen and of GFAP⁺ positive cells in the caudate and putamen of healthy controls (n=2) and LRRK2 G2019S PD patients (n=2); k) Western blot analysis of LRRK2 WT and LRRK2 G2019S striatal lysates blotted with the following antibodies: anti-pS1292 LRRK2, anti-total LRRK2 and the housekeeping β -actin; l) Quantification of Ser1292 phosphorylation (pS1292 LRRK2/total LRRK2) was performed using ImageJ (n=7 striatal samples for both LRRK2 WT and LRRK2 G2019S 4-month old mice; m-n) Quantification of the 60 KDa and 180 KDa Glt-1 bands in LRRK2 WT and LRRK2 G2019S mice; n=7 animals for each genotype; o) qPCR analysis of Glt-1 and Glast mRNA in the striatum of LRRK2 WT and LRRK2 G2019S mice; n=12 animals for each genotype; p) qPCR analysis of Glt-1 mRNA in primary LRRK2 WT striatal astrocytes untreated or treated with dbcAMP for 10 days; experiment performed twice on n=2 independent cell cultures; q) Western blot analysis of oocytes co-injected with the mRNA of the excitatory amino acid transporter 2 and the mRNA of the human LRRK2 WT or G2019S, blotted with the antibodies against the total LRRK2 and the housekeeping β -actin. Statistical analysis was performed in a-c, o using Unpaired T-test and in k-l using Mann-Whitney test. Statistical analysis was performed in e, g using Kruskal-Wallis test (e: P=0.006; g: P=0.007) followed by Dunn's multiple comparisons test and in f, h using One-way ANOVA test (f: F=3.07 and P=0.08; h: F=9.49 and P=0.004) followed by Tukey's multiple comparisons test.

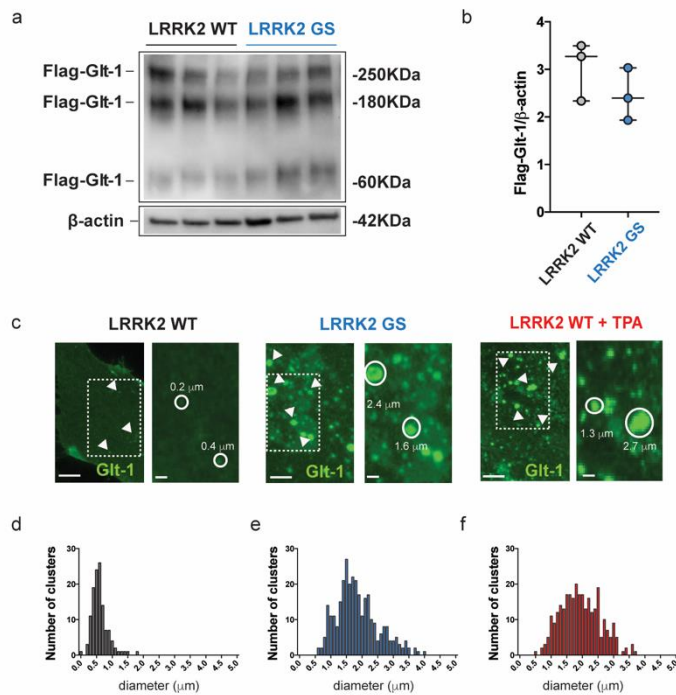
Supplementary Figure 2



Supplementary Figure 2- Screening of Glt-1 protein-protein interactions

a) Striatal Glt-1 immunoprecipitated from LRRK2 WT and G2019S brains was resolved by immunoblotting. Anti-HSP70 was applied to normalize for protein content; b) Venn diagram summary of interacting proteins, colored for different background (grey for LRRK2 WT, light blue for LRRK2 G2019S, dark blue for LRRK2 WT and G2019S shared interacting proteins); c) Selected GO term enrichments from CC categories using gProfiler were plotted using $-\log(P_{adj})$ values.

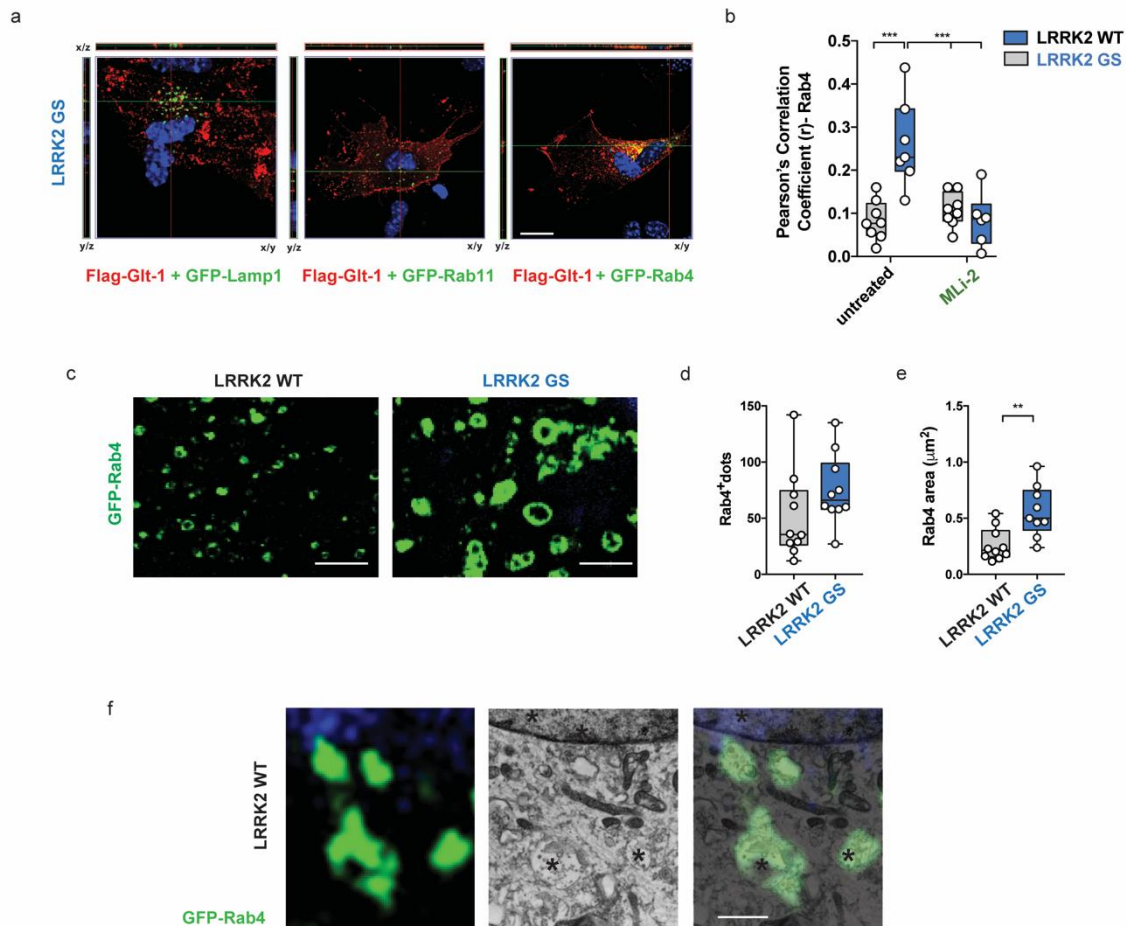
Supplementary Figure 3



Supplementary Figure 3

a) Western blot analysis of transfected Flag-Glt-1 expression in primary striatal LRRK2 WT and G2019S astrocytes using an anti-Flag-HRP antibody; b) Relative quantification of band intensity was performed using ImageJ and normalized to β -actin; experiment performed in triple; c) Representative epifluorescence images of Glt-1 clusters in Flag-Glt-1 transfected primary striatal astrocytes from LRRK2 WT (untreated or treated with TPA) and from LRRK2 G2019S astrocytes. Scale bars 5 μ m; insets 1 μ m. d) Frequency distribution of Glt-1 cluster diameter in untreated LRRK2 WT (grey bars); e) Frequency distribution of Glt-1 cluster diameter in LRRK2 G2019S (blue bars); f) Frequency distribution of Glt-1 cluster diameter in LRRK2 WT treated with TPA (d; red bars); n=5 cells analyzed for each group. Statistical analysis in b was performed using Mann-Whitney test.

Supplementary Figure 4

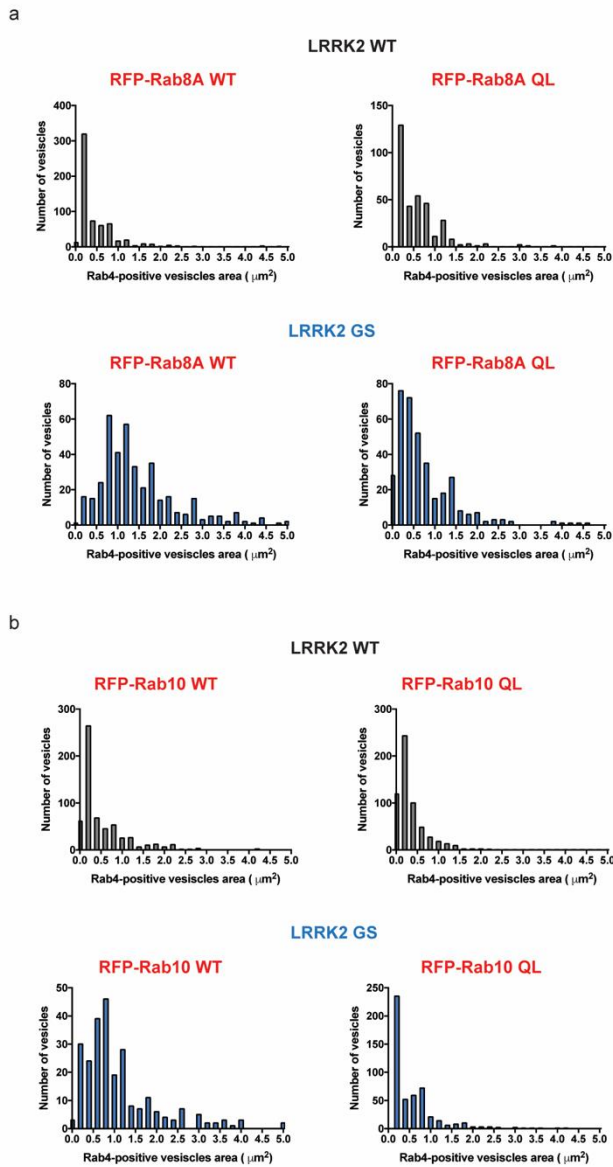


Supplementary Figure 4

a) Orthogonal z-stack projections of LRRK2 G2019S astrocytes co-transfected with Flag-Glt-1 (red) and GFP-Lamp1, GFP-Rab11 or GFP-Rab4 (green). Scale bar 20 μm; b) Quantitative analysis of the Pearson's Correlation Coefficient of Glt-1 colocalizing with the Rab4-positive vesicles in LRRK2 WT and G2019S astrocytes under basal conditions or upon MLI-2 application; at least n=6 cells analyzed for each group; c) Representative confocal microscopy images of LRRK2 WT and G2019S primary striatal astrocytes transfected with GFP-Rab4 and Flag-Glt-1. Scale bars: 2 μm; d,e) Quantification of Rab4-positive vesicle number and area; at least n=9 cells analyzed for each group and experiments performed at least in triple; f) Representative confocal (left panel), electron microscopy (middle panel) and merge (right panel) image of a LRRK2 WT primary astrocyte transfected with Rab4-GFP (green). The image reveals the co-localization of early endosomal structures identified by transmission microscopy with the GFP-Rab4-positive vesicles identified by confocal microscopy; scale bar: 1 μm. Statistical analysis in b was performed using Two-way

ANOVA test (Treatment $F=15.79$ and $P=0.004$; Genotypes $F=16.38$ and $P=0.004$) followed by Tukey's multiple comparisons test. Statistical analysis in d, e was performed using Unpaired t-tests.

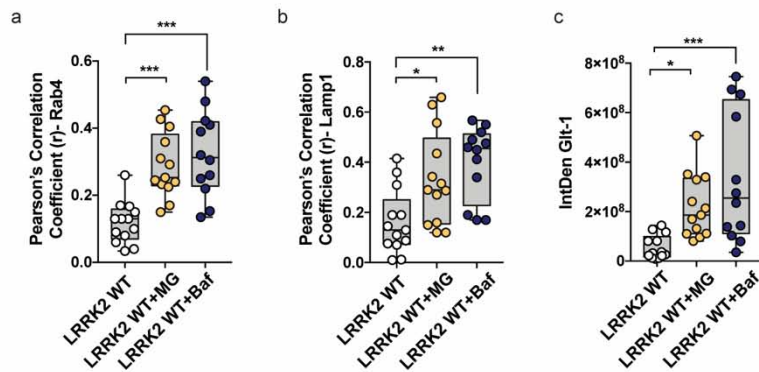
Supplementary Figure 5



Supplementary Figure 5

a,b) Frequency distribution of Rab4-positive vesicles area in LRRK2 WT and LRRK2 G2019S astrocytes. At least $n=6$ cells analyzed for each group and experiments performed at least in triple.

Supplementary Figure 6



Supplementary Figure 6

a) Quantification of Glt-1 IntDen in the Rab4-positive vesicles in LRRK2 WT astrocytes under basal conditions (n=13 cells) or upon MG132 (n=13 cells) or Bafilomycin application (n=12 cells); b) Quantification of Glt-1 IntDen in the endogenous Lamp1-positive structures in LRRK2 WT astrocytes under basal conditions (n=13 cells) or upon MG132 (n=13 cells) or Bafilomycin (n=12 cells) application; experiments performed at least in triple; c) Quantitative analysis of Glt-1 IntDen in LRRK2 WT astrocytes, under basal condition or after application of MG132 or Bafilomycin A1 (n=13 cells for untreated LRRK2 WT, n=13 cells for LRRK2 WT+MG132 and n=12 LRRK2 WT+Bafilomycin; experiments performed at least in triple; Statistical analysis in a-c was performed using One-way ANOVA test (a: $F=16.06$ and $P<0.0001$; b: $F=7.79$ and $P=0.001$; c: $F=8.76$ and $P=0.0008$) followed by Tukey's multiple comparisons test.

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cell junction	GO:0030054	0,020007571
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1,500909182	6339	14	11
1,446316421	515	14	4
1,367920208	540	14	4

effective_domain_size

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intersections

A0A1L1SU37,D3YYN7,A0A0N4SUX5,A0A0J9YUE9,Q99KI0,P56480,Q8VDN2,P18872,Q64332,P60202

D3YYN7,A0A0J9YUE9,P56480,Q8VDN2,P18872,Q64332,P60202

E9PZW0,D3YYN7,Q8VDN2

E9PZW0,Q8VDD5,D3YYN7,A0A0N4SUX5,P11499,A0A0J9YUE9,Q8VDN2

A0A1L1SU37,A0A0N4SUX5,A0A0J9YUE9

E9PZW0,D3YYN7,Q8VDN2

D3YYN7,Q8VDN2

D3YYN7,Q8VDN2

A0A1L1SU37,Q8VDD5,D3YYN7,A0A0N4SUX5,P11499,A0A0J9YUE9,P56480,Q8VDN2,P18872,Q64332,

A0A1L1SU37,Q8VDD5,D3YYN7,A0A0N4SUX5,P11499,A0A0J9YUE9,Q8VDN2,P18872

D3YYN7,Q8VDN2

A0A1L1SU37,Q8VDD5,D3YYN7,A0A0N4SUX5,P11499,A0A0J9YUE9,Q8VDN2,P18872

E9PZW0,A0A1L1SU37,Q8VDD5,D3YYN7,A0A0N4SUX5,P11499,A0A0J9YUE9,P56480,Q8VDN2,P18872

D3YYN7,A0A0N4SUX5,P56480,Q8VDN2

D3YYN7,A0A0N4SUX5,P56480,Q8VDN2

E9PZW0,Q8VDD5,D3YYN7,A0A0N4SUX5,A0A0J9YUE9,Q8VDN2,Q64332

Q8VDD5,D3YYN7,A0A0N4SUX5,A0A0J9YUE9,Q8VDN2,Q64332

Q8VDD5,P11499

E9PZW0,Q8VDD5,D3YYN7,A0A0N4SUX5,P11499,A0A0J9YUE9,P56480,Q8VDN2,P18872,Q64332,P60202

E9PZW0,Q8VDD5,D3YYN7,Q8VDN2

D3YYN7,Q8VDN2,P18872,P60202



,Q64332,P60202

Sequence	N-term cle	C-term cle	Amino aci	First amin	Second am	Second las	Last amin	Amino aci	A Count
AAAEVNQIQAFGILKRRQEYGLDPK			R	A	A	P	K	I	3
AADELEAFPPRSKEQKGGGAPGSI			K	A	A	S	R	H	4
AAEAGVTEYVMAVADGYLGTSAK			K	A	A	A	K	Q	4
AAGAEEYATKFCDYGKYAQQEVVI			K	A	A	V	K	R	4
AAGAEEYATKFCDYGKAQQEVVKI			K	A	A	K	R	S	4
AAIAAAAA PKKAAVAKAAAAAAAI			K	A	A	A	K	A	11
AAIDWFDG FDDPPSAK EFSGNPIK			K	A	A	I	K	V	2
AAMIVNQIEDPVVVTKMIVNQLSK			K	A	A	S	K	K	2
AANAAENIERQVESLKSQAEVSSR			K	A	A	S	R	Q	5
AAVPSGASYTAKGLFRIYEALERD			R	A	A	L	R	D	4
AAYFGIYDVQGIHYRAFGIYDTAK			R	A	A	A	K	G	3
AAYFGVYDVQGIHYRACFGVYDTAK			R	A	A	A	K	G	3
ADFSEAYKYKIIPGSRAADFSEAYKI			R	A	D	Y	K	R	2
ADFSEAYKYKIIPGSRAADFSEAYKRI			R	A	D	K	R	L	2
ADIGIAMGNDSPALKKISGSDVSKC			K	A	D	S	K	Q	2
ADIGVAMGNDSPALKKIAGSDVSKC			K	A	D	S	K	Q	3
ADLEMQIELDELTLTKATEELAYLKK			K	A	D	L	K	K	2
ADLEMQIELDELTLTKATEELAYLKKI			K	A	D	K	K	N	2
ADLINNLGDTGIGMTIANNLGTIAK			K	A	D	A	K	S	2
ADMEDLVERQNKQLFMEDLMSSI			R	A	D	S	K	D	1
ADTLTDEIINKVELQAKTDEINFLRA			K	A	D	L	R	A	1
AEAESLYQEDIAQKSKAESLYQSK			K	A	E	S	K	Y	2
AEAESLYQEDIAQKSKELQITAGRI			K	A	E	G	R	H	3
AEAESWYCEEIAQRSRAESWYQTI			R	A	E	T	K	Y	2
AEFVEVTKRLSQKFKPAEFVEVTKI			K	A	E	T	K	L	1
AENSSLNLI NSQVAFEK SSLNLIGKA			K	A	E	G	K	A	1
AESFFQTKVAEKKRPKAESFFQTK			K	A	E	T	K	A	1
AETECQNT EEQLQQIR YQQLLDIKI			R	A	E	I	K	I	1
AFVHWYVFDLMYAKFEGEFSEARI			R	A	F	A	R	E	2
AGAGSATLGTEVVKAKSMAYAGAI			K	A	G	A	R	F	6
AGAYDFPSHKLYQQIKDTVTPREAK			K	A	G	A	K	N	3
AGETVLGSAPGLR				A	G	L	R		2
AGFAGDDDNGSGMCFAGDDAPF			K	A	G	P	R	A	3
AGIPKEEVI AIQGAIEK/ GIPKEEVKE			K	A	G	V	K	E	1
AGIPKEEVI AIQGAIEK/ GEGQAPTF			K	A	G	T	R	Q	2
AGQENISVLCNRAVFKQENISVSKI			K	A	G	S	K	R	1
AGQVFLEEKSSETLRKALEELGNHK			K	A	G	H	K	A	1
AGVLAHLEGQSKIFFR/ LAHLEERI			R	A	G	E	R	D	2
AGYTDQVLLKTAIAKAAVAASEFYR			K	A	G	Y	R	S	3
AHGGYSVVELINNVAKVFAGVGEF			K	A	H	E	R	T	2
AIAELGIYPDATTVLSRDPLDSTSRI			R	A	I	S	R	I	3
AIEMFHFRCHAHPTLKAEMFHFR			K	A	I	F	R	G	1
AIEQSIEQENKVRSKLKEQEGLNR			K	A	I	N	R	S	1
AIFHEEEPF ESEDEKPK/ IFHEEEPRF			K	A	I	P	R	H	1
AIFTGYYGI LTKKMEVKIFTGYYGKC			K	A	I	G	K	G	1
AIGGGLSSGFSSSSGRGGGSSTIK			R	A	I	I	K	Y	1
AIGNIELGIVTEEHLRRGNIELGIRS			R	A	I	I	R	S	1
AILVDLEPCAGNKYVPFPGTMDSVI			R	A	I	V	R	S	1
AITGASLAI RRAVKFQFSLADIMAK			R	A	I	A	K	R	4

ALAAAGYC VSLAALKK/ AAGYDVEK	K	A	L	E	K	N	4
ALAAAGYC VSLAALKK/ DVEKNNSF	K	A	L	S	R	I	4
ALALVPGT SLAFSGDR/ LVPGTPTR	R	A	L	T	R	T	2
ALDLLYGV KDESIRLR/ LLYGMVSK	R	A	L	S	K	K	1
ALDVSASD AESFFQTK/ DEEMARPI	K	A	L	P	K	K	3
ALEEANAD ASYLDKVR/ ANADLEVK	R	A	L	V	K	I	3
ALEESNYEI ASYLDKVR/ SNYELEGKI	R	A	L	G	K	I	1
ALELDPNL/ QACERMIF ELDPNLYRI	R	A	L	Y	R	I	1
ALEQQVEE HELEKSKR/ EQQVEEM	R	A	L	M	R	T	1
ALIAAQYS/ PENWRAF/ QYSGAQVI	K	A	L	V	R	V	4
ALLQAILQ/ LNSLCSVR/ LQTEDMLK	R	A	L	L	K	V	2
ALMGSPQ/ SKKEASRR/ QLVAAVVF	R	A	L	V	R	T	3
ALQGASQ/ KEAADMLI/ SQIIAEIRET	K	A	L	I	R	E	3
ALQHMTD MEMNFT/ DFAIQFNK	K	A	L	N	K	N	2
ALTVPELT/ SRGSQQYF/ TQQMFDA	R	A	L	A	K	N	2
ALTVPELT/ SRGSQQYF/ TQQMFDS	R	A	L	S	K	N	1
ALTVPELT/ SRGSQQYF/ TQQVFDAL	R	A	L	A	K	N	2
ALVGDEAE IGPYPIRA/ DEAELPCR	R	A	L	C	R	I	2
ALYDAELS/ TDEINFLR/ VLSMDNN	R	A	L	N	R	N	2
ALYDYDGC DAKGVRV/ EQDELSFK/	R	A	L	F	K	A	1
AMDTLGV/ QSLAAIVR/ VEYGDKER	R	A	M	E	R	K	1
AMPQSPEI TVADFFIK/ QSPENIAKI	K	A	M	A	K	E	2
ANFTPQET SANLKSDK/ NFTPQETR	K	A	N	T	R	G	1
ANVTPQSS KGGKANPA/ LGSGQEAKE	K	A	N	A	K	K	4
APAPAAPA/ EAPSSAAK/ EQSVAVKE	K	A	P	K	E	-	14
APDFVFYA VIKPIDKKA/ DFVIFYAPR	K	A	P	P	R	L	2
APDSGAEV EDKGSKNF/ DSGAEVER	R	A	P	E	R	E	2
APEHIIPQF KVLVLEDR/ PQPTQTDI	R	A	P	D	R	A	1
APQVYILP/ SKIKGLVR/ PPAEQLSR	R	A	P	S	R	K	2
APSLDSSLF DEYLEVTK/ PLLSNLPRF	K	A	P	P	R	P	2
APSTYGGC VLAGGSCR/ GGLSVSSRI	R	A	P	S	R	F	1
APSTYGGC VLAGGSCR/ GLSVSSSRF	R	A	P	S	R	F	1
AQASAPAC/ AGAKAPAI/ SAPAQAPK	K	A	Q	P	K	G	5
AQLEEASS/ QRELRELR/ LEEASSAR/	R	A	Q	A	R	A	3
AQMVQEC EAVEWQQ/ MVQEDLEI	K	A	Q	E	K	T	1
AQWGENL LDALLEGK/ THDTEVTR	K	A	Q	T	R	E	1
AQWGSNN LDALLEGK/ THDSEVMI	K	A	Q	M	R	E	1
AQYEDIAQ DSIIAEVKA/ QYEDIAQK	K	A	Q	Q	K	S	2
AQYEEIAN DSIIAEVKA/ QYEEIANR/	K	A	Q	N	R	S	2
AQYEEIAQ DSIIAEVKA/ QYEEIAQR/	K	A	Q	Q	R	S	2
ARFEELNA DFYTSITRA/ ELNADLFR/	R	A	R	F	R	G	2
ASAELALG/ GGLAEFCK/ GENNEVLK	K	A	S	L	K	S	3
ASAELDIK/ CSEEKELK/ IKDVSDERI	K	A	S	E	R	L	2
ASGPPVSE KPAGVRRK/ PVSELITKA	K	A	S	T	K	A	1
ASLEGNLA LQSQLSMK/ NLAETENR	K	A	S	N	R	Y	2
ASLENSLEE LQSQLSMK/ ENSLEETKC	K	A	S	T	K	G	1
ASLENSLEE LQSQLSMK/ SLEETKGR/	K	A	S	G	R	Y	1
ASLSPMDE EAKDENER/ DSESPVEK/	R	A	S	E	K	V	1
ASMQQQC QPMPVNIF/ QQQLASAI	R	A	S	A	R	N	3
ASVTVGGC AVVQRVTF/ EQISAIGRC	R	A	S	G	R	G	2

ATENDIAN HMRGLPFI FSPLNPIRV	R	A	T	I	R	V	2
ATGGGLSS GFSSSSGR, GGGSSTIK)	R	A	T	I	K	Y	1
ATSVLPR MDGSRRV RATSVLPR)	R	A	T	P	R	Y	1
AVAIETQP, PALAPPSR, GESDAVAF	R	A	V	A	R	A	5
AVAQGNL, NAAYNQV SADVQAAI	K	A	V	A	K	N	5
AVCMLSN, GDLAKVQI AIAEAWAF	R	A	V	A	R	L	5
AVDSLVPIC EPMQTGIK DSLVPIGR	K	A	V	G	R	G	1
AVFPSIVGI FAGDDAPI VFPSIVGR	R	A	V	G	R	P	1
AVFPSIVGI FAGDDAPI PSIVGRPR	R	A	V	P	R	H	1
AVFVDLEP GAGKHVPI PTVIDEIRN	R	A	V	I	R	N	1
AVFVDLEP GAGKHVPI PTVIDEVR	R	A	V	V	R	T	1
AVIYNPATI ERYLFVDR, TQADWTA	R	A	V	A	K	K	4
AVLDALLE, PAAEEPSR, LDALLEGK	R	A	V	G	K	A	2
AVLVDLEP TGGKYVPR PGTMDSVI	R	A	V	V	R	S	1
AVMDDFA KATKEQLK DFAAFVEK	K	A	V	E	K	C	3
AVSIVGNE, DPKTIHKK, IVGNEVFRI	K	A	V	F	R	F	1
AVTEQGA, DDMATCM AELSNEERI	K	A	V	E	R	N	2
AVVFETGE QLLPEQDK GSLPGEVR	K	A	V	V	R	T	5
AVVVNAA, GCIPTMAR LASYSQSK	R	A	V	S	K	Q	4
AWGAMM PQYGSLER SELHQEVK	R	A	W	V	K	N	3
AWQGTAC GRRLEDDF ADGGMMI	R	A	W	E	R	D	2
AWTVEQLI MAAAVPQ AWTVEQLI	R	A	W	L	R	S	1
AYAQQLTI QERAKIEK, QQLTDWA	K	A	Y	A	K	R	3
AYGENIGY, TEIRVECKA ENIGYSEK	K	A	Y	E	K	D	1
AYHEQLSV APVISAEK, EPANQMV	K	A	Y	V	K	C	4
CATILLQGI, APERILDR, ATILLQKE	R	C	A	G	K	E	1
CCTESLVNI PVSEKVTI, CTESLVNRI	K	C	C	N	R	R	0
CEKEFKLSK KLRKELARI EKEFKLSKS	R	C	E	S	K	S	0
CEMEQQN EEQLAQLR EQQNQEYI	R	C	E	Y	K	I	0
CLEDNLGII GTLPVTFRI EDNLGIDK	R	C	L	D	K	R	0
CLEDNLGII GTLPVTFRI DNLGIDKR	R	C	L	K	R	V	0
DAAEAWFN QLAEQNRI AEAWFNEI	K	D	A	E	K	S	2
DAETWFLS QMAEKNR AETWFLSK	R	D	A	S	K	T	1
DAFLGSFL, CKNYQEA, SFLYEYSRR	K	D	A	S	R	R	1
DAGMQLC GNHTPIFR GMQLQGY	R	D	A	Y	R	Y	1
DAGTIAGL DSQRQATI IAGLNLVRI	K	D	A	L	R	I	2
DAQEMAD AFDVRIERI MADSLGVI	R	D	A	V	R	I	2
DATNVGDI VIKEKYGKI APNILENKI	K	D	A	N	K	E	2
DAVTYTEH VFLENVIRI VTYTEHAK	R	D	A	A	K	R	2
DDNPNLPI NECFLQHK DDNPNLPI	K	D	D	P	R	L	0
DDPHACYS TLECCA, KI CYSTVFDKI	K	D	D	D	K	L	1
DDSPDLPK NECFLSHK, DDSPDLPK	K	D	D	P	K	L	0
DFHVDEQ, EMKHTTEF VDEQTTVK	R	D	F	V	K	V	0
DFLAGGVA, DAAVSAK, GVAAAISK,	K	D	F	S	K	T	4
DFSALESQ, SKSSKLTKE ELLQEENR,	K	D	F	N	R	Q	1
DGLTDVYN KLEDLIVKE GLTDVYNK	K	D	G	N	K	I	0
DGMDNQ, SGMGGYG GGYGSGVI	R	D	G	G	R	M	0
DHTEIVFAI EQLDEILRE HTEIVFART	R	D	H	A	R	T	1
DIEAMDPS KLFGLLVKI AMDPSILK	K	D	I	L	K	G	1
DIENQYET, QLIAKNRK QEVQSSAK	K	D	I	A	K	E	1

DIGAIAQVI YEVLSVIRD IIAEEQQR	R	D	I	Q	R	I	4
DIKPQLELI AEEIDVAKI ELIEDEEKL	K	D	I	E	K	L	0
DKPLKDVII ESTKTDSRI VIIVDSGKII	R	D	K	G	K	I	0
DLAAGAVF RYPVATQK PANLKPSKI	K	D	L	S	K	I	4
DLDVAVLV DKEEIAFKI VLVGSMPFI	K	D	L	P	R	R	1
DLEAQIEA KKMEIDLK AQIEAANK	K	D	L	N	K	A	3
DLEQKDEF RARAQEHF KDEHLELRI	R	D	L	L	R	D	0
DLEVVAR CGKIIAIKD KDLEVVAR	K	D	L	A	R	Q	1
DLFDPIIEEI EESYDVFKI FDPPIEERH	K	D	L	E	R	H	0
DLGEEHFK SEIAHRFKI DLGEEHFK	K	D	L	F	K	G	0
DLPEHAVL KKAEEVEGK LPEHAVLKI	K	D	L	L	K	M	1
DLQSAEKE GHVTEEW AEKEEQEK	R	D	L	E	K	L	1
DLTDYLMK LRLDLAGR DLTDYLMK	R	D	L	M	K	I	0
DLTGQVPT KQPLATQK QVPTPPVK	K	D	L	V	K	Q	0
DLYANTVL KCDVDIRK MYPGIADF	K	D	L	D	R	M	2
DMGGYST KAGKVRTR STTTDFIKS	R	D	M	I	K	S	0
DMPIQAFI KAVPYPQF EPVLGPVR	R	D	M	V	R	G	1
DNDFLNEC AKDLPTFKI DFLNEGQK	K	D	N	Q	K	L	0
DNIQGITKI KRHRKVLK GITKPAIRR	R	D	N	I	R	R	1
DNPQTHY VAEFHGTY YAVAVVK	K	D	N	V	K	K	2
DNSTMGY IMKAQALF TMGYMMI	R	D	N	A	K	K	1
DQIVDLTV YNTIDDLKI DLTVGNNI	K	D	Q	N	K	T	0
DQYEQMA SRILNEMR QYEQMAE	R	D	Q	E	K	N	1
DRDITLQQ EQEVRYW LQQDAYW	R	D	R	W	K	E	1
DSTYSMSS SWTDQDS SSTLTLTKD	K	D	S	T	K	D	0
DSYVGDEA VMVGMGI VGDEAQS	K	D	S	S	K	R	1
DSYVGDEA VMVGMGI GDEAQS	K	D	S	K	R	G	1
DTAPVLDS GHTEENYK GSYFIYSKI	K	D	T	S	K	L	1
DTAVELGK KGRDLDDK LGKGPEPK	K	D	T	P	K	G	1
DTGILDSIG HGFLPRHR GILDSIGRF	R	D	T	G	R	F	0
DVAGDASI DNIPVLKRI ASESALLKC	R	D	V	L	K	C	3
DVDAAYM NEFVTLKKI VDAAYMN	K	D	V	N	K	V	2
DVDGAYM NEFVTIKKI VDGAYMT	K	D	V	T	K	V	1
DVDNAYM NDFVTLKK VDNAYMI	K	D	V	I	K	V	1
DVEFLAQL NFLEKLRKI VEFLAQLKI	R	D	V	L	K	I	1
DVFLGMFI CKNYAEAK MFLYEYAR	K	D	V	A	R	R	1
DVLMISLTI FIFPPNIKD LMISLTPKI	K	D	V	P	K	V	0
DVNAAIAA YRGDVVPK NAAIAAIKT	K	D	V	I	K	T	4
DVNAAIAT YRGDVVPK NAAIATIKT	K	D	V	I	K	T	3
DVQFAVQI NVGHQDV QEEHFDAF	K	D	V	A	R	R	2
DYQELMN EDLARLLRI YQELMNTI	R	D	Y	T	K	L	0
DYQELMN EDLARLLRI YQELMNVI	R	D	Y	V	K	L	0
DYTYEELLI TAWAGSEI TYEELLNRI	R	D	Y	N	R	V	0
EAELTPENI TWEERKPF PENIAAARI	R	E	A	A	R	E	4
EAFQNAYL QPLDEEMI ELGGLGER	K	E	A	E	R	V	2
EAMEHPYI HQSRLTAR PYFYTVVKI	R	E	A	V	K	D	1
EAVQLLED FVTEKRLRI VQLLEDYK	R	E	A	Y	K	H	1
EAYPGDVF LLRPPGRI DVFYLHSRI	R	E	A	S	R	L	1
EDAANNYI PEQLITGKI DAANNYAI	K	E	D	A	R	G	3
EDMAALEI EGEFSEARI EDMAALEI	R	E	D	E	K	D	2

EDSPQSHV YQLSIHERE QSHVLVMI	R	E	D	M	K	G	0
EEAAPPTP RRSPPRKR PDDLAQLK	R	E	E	L	K	N	4
EEMSQLTC MALKKNH APGKDLTK	K	E	E	T	K	T	1
EEQSQITSC IKSQHQTK VTGQIGWI	K	E	E	W	R	R	0
EEREQIKTL PTIQRVRKI QIKTLNCKI	K	E	E	N	K	F	0
EEVKEVYM IEKAGIPKE GEGQAPTF	K	E	E	T	R	Q	1
EGEGGAG YRKAEGER DSSSFSSKV	R	E	G	S	K	V	2
EGLVMVEI DVGLGLVK GLVMVEVI	K	E	G	V	R	K	0
EHALLAYTI ISKNGQTR LAYTLGVKI	R	E	H	V	K	Q	2
EHANIDAC ELEDLVRRI STTISPCKS	R	E	H	G	K	S	3
EIDQEAAY FVRHRTKK AVEVSQLR	K	E	I	L	R	D	2
EIETYHNLL SIKMRLEKI FESSGAGK	K	E	I	G	K	I	1
EIIDLVLDL RGHYTIGK IIDLVLDLRF	K	E	I	D	R	I	0
EIKIEISELN GRHGDSLK IEISELNRVI	K	E	I	N	R	V	0
EITALAPST GIADRMQ ALAPSTMK	K	E	I	M	K	I	2
EIVHIQAG _____ CGNQIGTK	R	E	I	T	K	F	1
EIVHLQAG _____ CGNQIGAK	R	E	I	A	K	F	2
EKADMPLI TQLSLQAR PLEVSVRKI	R	E	K	R	K	E	1
EKLELVSYF FIGDEPKE ELVSYFGKI	K	E	K	G	K	R	0
ELDDATEA ASRRKLQR EANEGLSR	R	E	L	S	R	E	2
ELISNASDZ SNKEIFLRE NASDALDK	R	E	L	D	K	I	2
ELLTTDGN SVLKEGGK GNEPVGLK	K	E	L	L	K	K	0
ELPDPQES IPMAKLYK DPQESIQR	K	E	L	Q	R	A	0
ELQVGIPV NIPLMRQF VTDEAGQF	R	E	L	Q	R	L	1
ELTAPDEN ITLQQQLKI PDENVPAK	K	E	L	A	K	I	2
ELTTEIDNN AWFNEKSI IEQISSYKSI	K	E	L	Y	K	S	0
EMLSSTTYI QTFYPNHK TTYPVVVK	K	E	M	V	K	M	0
EMLTLPTFI QTYYPNHF PTFPVVVK	R	E	M	V	K	I	0
EMQFLMC LNPVKDSK EMQFLMC	K	E	M	Q	K	W	0
EMQYFMC LNPVKSSKI QQWTGTM	K	E	M	N	K	D	0
EMSLYASL LSDVPPR YASLASEKI	R	E	M	E	K	V	2
EQAADTEZ YASILQQKI VTQLLVERI	K	E	Q	E	R	L	4
EQDVVQG EQEEKYWI QDVVQGM	K	E	Q	W	R	E	0
EQGFLSFA DCVVRIPKI QGFLSFWF	K	E	Q	W	R	G	0
EQIMVLNN QRIKTQER QIMVLNNI	R	E	Q	N	K	F	0
ESAPFAVIC KQQDRELK SNTVVEAK	K	E	S	A	K	G	3
ESLKPATKF LKQRADSR ATKPVASK	R	E	S	S	K	S	2
ESMIISR		E	S	S	R		0
ESSPLYSPG DISPLTPRE SDSTSAAKI	R	E	S	A	K	E	2
ESTFLDEGI RPRYSEERI TPLQHTPR	R	E	S	P	R	S	0
ESTLHLVLF LSDYNIQKI STLHLVLRL	K	E	S	L	R	L	0
ETAAAHQZ SDSTSAAK TAEPYGFR	K	E	T	F	R	S	7
ETPAASEA AEPAPSSKI EAPSSAAK	K	E	T	A	K	A	5
EVAFAAQF KLELAQYR ATQQLLSR	R	E	V	S	R	G	5
EVASNSEL SKTEELNKI SELVQSSR	K	E	V	S	R	S	1
EVATNSEL TKTEELNRI SELVQSGK	R	E	V	G	K	S	1
EVDEQML FRGRMSM QMLAIQSK	K	E	V	S	K	N	1
EVDEQMLI FRGRMSM QMLNVQNI	K	E	V	N	K	N	0
EVDEQML' FRGRMSM QMLSVQSI	K	E	V	S	K	N	0
EVFTSSSSS SGQSYSSR SSSSSSR	R	E	V	S	R	Q	0

EVMIVGVC AALTAAGK MIVGVGEK	K	E	V	E	K	I	0
EVYMGNV GIPKEEVKE GEGQAPTF	K	E	V	T	R	Q	1
EWYQETHI THDSEVMI WYQETHEI	R	E	W	E	K	Q	0
EYQELMN QDMARLLI YQELMNTI	R	E	Y	T	K	L	0
EYQELMN QDLARLLK YQELMNVI	K	E	Y	V	K	L	0
FANLNEQA AEEWYKSK NLNEQAAF	K	F	A	A	R	S	3
FASEITPITI KEAWDAG TPITISVKGI	K	F	A	V	K	G	1
FASFIDK QIKTLNKK KFAFIDKV	K	F	A	D	K	V	1
FASFIDKVF QIKTLNKK ASFIDKVR	K	F	A	V	R	F	1
FDAGELITC ILKSVMARF AGELITQRI	R	F	D	Q	R	E	1
FDGALNVC SSITASLRFI TNLVPYPR	R	F	D	P	R	I	1
FDLMYAK AWARLDH KFDLMYAK	K	F	D	A	K	R	1
FEMEQLNF TLDDFRIKF FEMEQLNF	K	F	E	L	R	Q	0
FFGPGFEFD GNLLSFPRI SVDVYAMI	R	F	F	M	K	S	1
FGDSNTVM QDSLESMI GDSNTVM	K	F	G	M	R	F	0
FGGFGGPG GGGFGGG LLQPLNVK	R	F	G	V	K	V	0
FGIDDQDF VFRNLRRER DFQNSLTR	R	F	G	T	R	S	0
FKDLGEEH HKSEIAHRI DLGEEHFK	R	F	K	F	K	G	0
FLEQQNK ASFIDKVRF RFLEQQNK	R	F	L	N	K	V	0
FLEQQNQ ASFIDKVRF QNQVLETK	R	F	L	T	K	W	0
FLEQQNQ ASFIDKVRF QNQVLQTI	R	F	L	T	K	W	0
FLEQQNQ ASFIDKVRF QQVDTSTF	R	F	L	T	R	T	0
FLGDYVEN VVADLLNR DYVENLNK	R	F	L	N	K	S	0
FLQDHGSC LPKKDIIKFI DSFLAEHKI	K	F	L	H	K	L	1
FLSQPFQV SRARKIQRI VFTGHMG	R	F	L	G	K	L	1
FLVPDHVN LPVLDKTKI VNMSELIK	K	F	L	I	K	I	0
FPGQLNAC SGVTTCLRI GQLNADLF	R	F	P	L	R	K	1
FPTSTYDLS DERPAPPR AVPASSSK	R	F	P	S	K	T	4
FQILEGPPF PLEELYKRF GPPESMGI	R	F	Q	G	R	G	0
FQMPDQC GGIDVHTR DDFQGTK	R	F	Q	T	K	A	1
FQNALLVR FEQLGEYK FQNALLVR	K	F	Q	V	R	Y	1
FSKPDLPKPI DTKPELKKI KPFTPEVRI	K	F	S	V	R	K	0
FSNSSSSNI HEYGSCGR SSSNEFSKC	R	F	S	S	K	C	0
FSSCGGGC RSGGGGG AGGGFGSF	R	F	S	S	R	S	1
FSSSSGYG GGRGGGG GYGGGSSF	R	F	S	S	R	V	0
FTASAGIQ DDWGAW DLTVTNPK	K	F	T	P	K	R	2
FTQAGSEV LFIDNIFRF EVSALLGRI	R	F	T	G	R	I	2
FVEGLPINI VIKNKTWK LPINDFSRE	K	F	V	S	R	E	0
FVTVQTISC NEVLKSGR ISGTGALRI	R	F	V	L	R	V	1
FWEVISDE CGNQIGAK DSDLQLER	K	F	W	E	R	I	0
FWEVISDE CGNQIGAK DSDLQLER	K	F	W	E	R	I	0
FWEVISDE CGNQIGAK DSDLQLDR	K	F	W	D	R	I	0
FWEVISDE CGNQIGAK DSDLQLER	K	F	W	E	R	I	0
GAALQQTC KDKALEQR QTQAPEPF	R	G	A	P	R	A	3
GAAQNIIP GKLWRDG PASTGAAK	R	G	A	A	K	A	5
GAAVNLTL EGYFGMYI LTLVTPEKA	R	G	A	E	K	A	2
GADAQED RELEQAIRI ADAQEDLF	R	G	A	L	R	W	2
GAILTTML FNARRKLLK LTTMLATR	K	G	A	T	R	N	2
GATPYGGI NVPYVMSI KLEDLIVKC	R	G	A	V	K	D	1
GDATVSYE DKETGKPK YEDPPTAK	K	G	D	A	K	A	2

GDSTLQVS VSNFKSGK STLQVSSRI	K	G	D	S	R	L	0
GEATVSFD DRETGKLK FDDPPSAK	K	G	E	A	K	A	2
GEFITTVQC LKDDSWLK FITTVQQR	K	G	E	Q	R	G	0
GELASYDM IYTPMEYKI ASYDMQLI	K	G	E	L	R	R	1
GFAFVTFE! DRETNKSR FESPADAK	R	G	F	A	K	D	3
GFFDPNTE SDPSDDTK NLTYLQLKI	K	G	F	L	K	E	0
GFGFVTFD DRQSGKKF DDHDPVDI	R	G	F	D	K	I	0
GFNEGLW YGKPNKRK WEIDNNPI	K	G	F	P	K	V	0
GFSSGSAV GGGGGGF AVVSGGSR	R	G	F	S	R	R	1
GGGGGGY TISGGGSR! GGGGGGG	R	G	G	G	R	G	0
GGGGNFG NFGFGDSF PGPGSNFR	R	G	G	F	R	G	0
GGGGSFG! GSSRVCGR GGFGGGSF	R	G	G	S	R	G	1
GGLSDGEC GAPLAGVF GEGPPGGF	R	G	G	G	R	G	0
GGNFGFGI VQSSRSGR NFGFGDSF	R	G	G	S	R	G	0
GGPNIITLA IKILENLRG IVKDPVSR!	R	G	G	S	R	T	1
GGSGGGG GGRQSGSI SGGGSGGI	R	G	G	G	R	Y	0
GGSGGSH! YGGGSGSF GYGGGSGI	R	G	G	G	K	S	1
GGSGGSYC GSYGRGRS YGGGSGSF	R	G	G	S	R	G	0
GGSISGGG YGSGGGS! GYSGGGGI	K	G	G	G	K	H	0
GGSQGEA! LDILQVVK EAVGELPR	K	G	G	P	R	G	1
GGSSSGGC HSSGGGSF GGGSSSVK	R	G	G	V	K	G	0
GHQLLSAD HIHTARMF LSADVDIKE	R	G	H	I	K	E	1
GHYTEGAE GAGNNW! DSVLDVVR	K	G	H	V	R	K	1
GHYTEGAE GAGNNW! SVLDVVRK	K	G	H	R	K	E	1
GICVLLGIS EQISAIGRC ISMEDSQK	R	G	I	Q	K	E	0
GIHETTFN! SFLGIESRG TTFNSIMK!	R	G	I	M	K	C	0
GIRPAINVC LETELFYKC NVGLSVSR	K	G	I	S	R	V	1
GISPVPINL DRVGTGNI SPVPINLRV	K	G	I	L	R	V	0
GISQTNLIT TGQYATTK ITTVTPEKK	K	G	I	E	K	K	0
GIVDQSQC VAAGDDKI QEAFEISKK	K	G	I	S	K	K	2
GKPDVVV! TPITISVKG VKEDEEYK!	K	G	K	Y	K	R	0
GLCGAIHS! IIGVSSDRG AIHSSVAKC	R	G	L	A	K	Q	2
GLEISGFTT WLPVAKAI ISGTFTHRC	K	G	L	H	R	Q	0
GLSATVTG YKTTICGKC ATVTGGQI	K	G	L	Q	K	G	1
GMGGAFFV GAWSNVL VLYDEIKKY	R	G	M	K	K	Y	1
GMQDLVE GRLDSELRI QDLVEDFK	R	G	M	F	K	N	0
GMSLNLEF VEFSSGLK! VVVFGNDF	K	G	M	D	K	L	0
GNPTVEVC AREIFDSRC EVDLYTAK!	R	G	N	A	K	G	1
GPMQLSA! RRPQSQEF MQLSADA!	R	G	P	A	R	D	2
GPQYGSLE RWRQLIEK PQYGSLE	K	G	P	E	R	A	0
GPSSVEDII! EKTPKTPKI PSSVEDIKA	K	G	P	I	K	A	0
GPVFAPPY KWKFLEHK EPLPESVKF	K	G	P	V	K	F	1
GPYESGSG GSGRSSR GLGHQESF	R	G	P	S	R	S	0
GPYESGSG GSGWSSSF HSSGLGHR	R	G	P	H	R	E	0
GQTGGDV EEEMLALR APGVDLSR	R	G	Q	S	R	I	2
GQVGGDV EEEMNALF APGVDLSR	R	G	Q	S	R	I	2
GQVGGEI! EEEMNALF APGVDLSR	R	G	Q	S	R	I	2
GSALDPEP QKSKNRKK LDPEPQVK	K	G	S	V	K	L	1
GSCGIGGG FTSSSSMK! GIGGGSSR	K	G	S	S	R	I	0
GSETLGGG GKAAEEAR GGGGAAGTI	R	G	S	T	R	E	2

GSGGLGG/ SVSVRSR/ GGAGFGSF	R	G	S	S	R	S	2
GSLGGGFS SLRISSSKG FSGGSFSR/	K	G	S	S	R	G	0
GSPLVVISC IFEGMECR LVVISQGI	R	G	S	G	K	I	0
GSSGGGCF FSGGSFSR/ GFGGGSFF	R	G	S	F	R	G	0
GSSSGGGY AFGGSGGI SSYGSGGR	R	G	S	G	R	Q	0
GSTASQVL VSVLNKEK TASQVLQR	K	G	S	Q	R	L	1
GTGGVDT/ KRLRLQKR FDVSNADF	R	G	T	D	R	L	3
GTQGATA(KKKDQIGK SSELDASK/	K	G	T	S	K	A	4
GTVLLSGPI ALESPKGR/ TVLLSGPRI	R	G	T	P	R	K	0
GVAPLWV EGLNAFYK GVAPLWV	K	G	V	M	R	Q	1
GVEQQDG QKSPEKAK QDGAVPEI	K	G	V	E	K	T	1
GVGASGSF TGVLKQTK VGASGSFR	K	G	V	F	R	L	1
GVGIISEGM ITAKAIKAG TVEDIAARI	K	G	V	A	R	L	2
GVNLPGA/ GGSLSGSK DLPAVSEKI	K	G	V	E	K	D	3
GVSQAVEF DKTRFMGI QAVEHINK	K	G	V	N	K	T	1
GVVDESDL PEYLNFIK DLPLNISRE	R	G	V	S	R	E	0
GYLDKLEP/ AVIYAGVR LDKLEPSKI	R	G	Y	S	K	I	0
GYSFTTTAI LMKILTER/ SFTTTAERE	R	G	Y	E	R	E	1
HALIYDDL EYFRDNGK IYDDLKQ	K	H	A	S	K	Q	1
HALLETAL/ GSSKIAARI LLETALTRV	R	H	A	T	R	V	2
HDIIGEFK YDFDRFSK HDIIGEFKV	K	H	D	F	K	V	0
HEMPPHIY EMYRGKKI AISESAYRC	R	H	E	Y	R	C	2
HFEATDIL/ ESPKMFGE ATDILVSKI/	R	H	F	S	K	I	1
HFISGDEPI KAFKKELRI FISGDEPKE	R	H	F	P	K	E	0
HFISGDEPI KAFKKELRI SGDEPKEK	R	H	F	E	K	L	0
HFTEDIQTI GNACWV/ FTEDIQTR/	K	H	F	T	R	Q	0
HGAGAEIS AHAAKTV/ VNPEQYSK	K	H	G	S	K	R	2
HGDSLKEI/ ELQVTVGR GDLSLKEIKI	R	H	G	I	K	I	0
HGFEAASII LVWIPSER/ AASIKEERC	R	H	G	E	R	G	2
HGGGGGG SSFCLSRH GGGGFGSI	R	H	G	S	R	S	0
HGSGSGH/ GQSPSRGF GWSSSSGF	R	H	G	G	R	H	0
HGVQELEI/ AKEVTQLR ELQSLSKI	R	H	G	S	K	K	0
HGVQELEI/ AKEVTQLR LQSLSKK/	R	H	G	K	K	A	0
HIQKEDVP VPNSVEQ/ KEDVPSER/	K	H	I	E	R	Y	0
HLDLSNVA EVLLEVQ/ KLSNVASYK	K	H	L	Y	K	T	1
HLEINPDH MGYMMA HPIVETLRC	K	H	L	L	R	Q	0
HLIIGVSSD KAPEDKKK IIGVSSDRG	K	H	L	D	R	G	0
HLNLAENS EVLLDIKRI/ SSYMHVYF	R	H	L	Y	R	E	1
HLPSSDSM EKAKALSKI SSDSMSLK	K	H	L	L	K	V	0
HLQAQGV ARAEVTLR QGVEVPSK	R	H	L	S	K	D	1
HLQDLME/ LNTGILNKI LMEGLTAK	K	H	L	A	K	V	1
HLTDAYFK ISDVKIPKH HLTDAYFK	K	H	L	F	K	K	1
HLVDEPQ/ STVFDKLI DEPQNLIK/	K	H	L	I	K	Q	0
HMDPPPA TDKTVTYK PPAPMQD	K	H	M	D	R	S	1
HNLQDFIN WKNSNLD LQDFINIKL	R	H	N	I	K	L	0
HNNLDLVI SLPGYKTRI NLDLVIIRE/	R	H	N	I	R	E	0
HPEAEMA/ ALRHLSRI EMAQNSV	R	H	P	V	R	L	2
HPEYAVSV FLYEYSRR/ YAVSVLLRI	R	H	P	L	R	L	1
HPFAQAV/ AVFETGAR PFAQAVGF	R	H	P	G	R	N	2
HQAQVDC TLPVVYVKI DQYGLVLR	K	H	Q	V	R	T	1

HQGLPQE\ _____ VLNENLLRI	K	H	Q	L	R	F	0
HQGVMOV PSIVGRPRI VMVGMG	R	H	Q	Q	K	D	0
HQQLLEEK ELEEMERK HQQLLEEK	K	H	Q	E	K	N	0
HRDTGILD ARHGFLPR GILDSIGRF	R	H	R	G	R	F	0
HSGIGHGC LQSADSSR GQASSAVF	R	H	S	V	R	D	2
HSPGEITGI SALSGDRK TSDSSLTKS	K	H	S	T	K	S	0
HSPTEDDE NASGSASK AEADVHLK	K	H	S	L	K	E	3
HTFSGVAS HRAHYDLF GEAFHVGK	R	H	T	G	K	T	2
HTLNQIDS KHLPRGYK LNQIDSVK	K	H	T	V	K	V	0
HVMSVHA ETILVEERH GDASHTAF	R	H	V	A	R	D	3
HWSDMLA NSTGAELR SDMLANPI	R	H	W	P	R	R	1
HYGPGWV PDENFKLK VSMANAG	K	H	Y	G	K	D	2
IAAFADAA LNVKPLAR APAYAVPK	R	I	A	P	K	V	8
IAATILTSPI NPPLNGAF ILTSPDLRK	R	I	A	L	R	K	2
IAEFAFEYA ITEEASKRI EFAFEYARI	R	I	A	A	R	N	3
IAELEER INSMQLQRK IAELEERS	K	I	A	E	R	S	1
IALTDNSLI YGKINKKRI TDNSLIARS	R	I	A	A	R	S	2
IAQLEEQLI SIAALEAKI EQLDNETK	K	I	A	T	K	E	1
IASSFTIGLF GHNPRRRI SSFTIGLRG	R	I	A	L	R	G	1
IATLASGLE GDRTVMG ASGLEVGK	R	I	A	G	K	T	2
IDASKNEEI SAEAEGAK GHSNSSPR	K	I	D	P	R	H	1
IDTIEITDR DYFEYEGK TIEITDRQS	K	I	D	D	R	Q	0
IEEELGSK AKYNQILRI IEEELGSKA	R	I	E	S	K	A	0
IEEIEREIK YVREEDK EIEREIKQE	K	I	E	I	K	Q	0
IEISELNR GDSLKEIKI IEISELNRVI	K	I	E	N	R	V	0
IETIEVMEC DYFEKYGK TIEVMEDR	K	I	E	D	R	Q	0
IFVGGLNPI MKKDPVKI NPEATEEK	K	I	F	E	K	I	1
IFVGGLSPI KTKEPVKK SPDTPEEKI	K	I	F	E	K	I	0
IGAEVYHN SSFREAMR AEVYHNLK	R	I	G	L	K	N	1
IGAGDYQF YYLDSLDR I PTEQDILRI	R	I	G	L	R	T	1
IGEHTPSAI AKWRCVLI ENANVLAF	K	I	G	A	R	Y	4
IGGIGTVP LPLQDVYK IGTVPVGR	K	I	G	G	R	V	0
IGLFGGAG APYAKGGK FGGAGVGI	K	I	G	G	K	T	1
IGQLEEQLI TISALEAKI EQLEQEA	K	I	G	A	K	E	1
IGSTTNPFL THPKTISR I DPNAAVYK	R	I	G	Y	K	S	2
IHFPLATYA TNLVYPR APVISAEEK	R	I	H	E	K	A	3
IHMGNCAI GLTDVYNK NCAENTAK	K	I	H	A	K	K	2
IHPMAYQL VPRLYGFK LQAASNFK	K	I	H	F	K	S	3
IIAATIENA TIEDLRNKI ILQIDNARL	K	I	I	A	R	L	4
IIAIKDLEV IACLICGKII KDLEVVAR	K	I	I	A	R	Q	2
IIHEDGFSG STIVKQMK GFSGEDVK	K	I	I	V	K	Q	0
IINEPTAAA IAGLNLVRI AIAYGLDKI	R	I	I	D	K	K	4
IINEPTAAA IAGLNLVRI IAYGLDKI	R	I	I	K	K	V	4
IITHPNFNC EQFINAAK DNDIMLIKI	K	I	I	I	K	L	0
IITHPNFNC EQFINAAK SPATLNSR	K	I	I	S	R	V	1
IITITGTQDI PLEGSEDR YLLQNSVKI	R	I	I	V	K	Q	1
IKEWYEK SNYELEGK KIKEWYEK	K	I	K	E	K	H	0
IKFEMEQN RMTLDDFI FEMEQLNF	R	I	K	L	R	Q	0
ILGADTSVI MSSILEERI VDLEETGR	R	I	L	G	R	V	1
ILGPQGNT PKFNFVVGK GPQGNTIK	K	I	L	I	K	R	0

ILIEDSDQN QLCVQKLR EDSQNLK	R	I	L	L	K	Y	0
ILIGNSPPLGR		I	L	G	R		0
ILLENLGEA DDLTVLMI QYAQEAAI	K	I	L	A	R	V	4
ILMVGLDA LFGKKEMF VGLDAAGI	R	I	L	G	K	T	2
ILNEMRDC APGVDLR QYEQMAE	R	I	L	E	K	N	1
ILPLDGLQ/ NNLIGQR DGLQAGYI	R	I	L	Y	R	H	1
ILTATVDN/ TIEELQNKI LLQIDNARI	K	I	L	A	R	L	3
ILTATVDN/ TIEDLRNKI LLQIDNARI	K	I	L	A	R	L	3
ILTFDQLAL RILKAGGKI QLALESPKI	K	I	L	P	K	G	1
ILVAGDTM AFAGEIPKI GDTMDSV	K	I	L	V	K	Q	1
ILVDQVTG YGRIITSRIL DQVTGVSF	R	I	L	S	R	G	0
IMDPNIVG DPLDSTSRI NEHYDVAI	R	I	M	A	R	G	1
IMGIPEDI QETMEAM DEQMGLLI	R	I	M	L	R	V	0
IMNTFSVM IREEYPDRI FSVMPSPK	R	I	M	P	K	V	0
IMNTFSVV IREEYPDRI FSVVPSPK	R	I	M	P	K	V	0
IMNVIGEP VGPETLGR IGEPIDERG	R	I	M	E	R	G	0
INQTVEILK KLLSAEERI NQTVEILKI	R	I	N	L	K	H	0
INVYYNEA DSDLQLER YNEAAGNI	R	I	N	N	K	Y	2
INVYYNEA DSDLQLER YNEATGGK	R	I	N	G	K	Y	1
INVYYNEA DSDLQLER TGGNYVPF	R	I	N	P	R	A	1
INVYYNEA DSDLQLER YNEATGNK	R	I	N	N	K	Y	1
IPGMLIIDT NFDRENVF HESFSNLRI	R	I	P	L	R	N	0
IPIHNEDIT QLGEDIRR ELVLMMQ	R	I	P	Q	R	V	0
IPSAVGYQ EVSALLGRI DMGMTMQI	R	I	P	E	R	I	2
IPVGPETLC LDSGAPIKI VGPETLGR	K	I	P	G	R	I	0
IPVIER IREQHPTKI KIPVIERYK	K	I	P	E	R	Y	0
IQDWYDKI ANNDLENI IQDWYDKI	K	I	Q	K	K	G	0
IQEAGTEV QLATLTGR EAGTEVVK	R	I	Q	V	K	A	1
IQMSNLM KQIEQQKK SNLMNQA	K	I	Q	A	R	L	1
IQTQPGYA PMEAAKVI PGYANTLR	R	I	Q	L	R	E	1
IRLENEIQT YQQLLDIKI ENEIQTYS	K	I	R	Y	R	S	0
ISEQFTAM AIQELFKRI EQFTAMFF	R	I	S	F	R	R	1
ISEQTYQLS SKPERKERI EQTYQLSR	R	I	S	S	R	W	0
ISGLIYEETF ARRGGVKI GLIYEETRC	R	I	S	T	R	G	0
ISIGGGSCA YGLGGSKR ISGGYGSR	R	I	S	S	R	A	1
ISISTSGGSI YNLGGSKR STSGGSFRI	R	I	S	F	R	N	0
ISNSSEFSA SHRSKSMK NSSEFSAKI	K	I	S	A	K	E	1
ISSVLAGGSI GIGGGSSR VLAGGSCR	R	I	S	C	R	A	1
ISVYYNEAS DSDLQLER YNEASSHK	R	I	S	H	K	Y	1
ISVYYNEAT DSDLQLDR YNEATGGK	R	I	S	G	K	Y	1
ITQYLDAGI SACIAYIRIT LDAGGIPR	R	I	T	P	R	T	1
ITSFPESES YSYETTEKI YSYETSTKT	K	I	T	T	K	T	0
IVGLDQVT ELWKDVDI TAFGSAYK	R	I	V	Y	K	T	2
IVLEDGTLF LVVISQGKI HVTEGSGR	K	I	V	G	R	Y	0
IVNDDQSF RLLIKGGKI YMEDGLIK	K	I	V	I	K	Q	1
IVNTSDVSI DSKGEPLR VSDGILLKL	R	I	V	L	K	L	0
IVQAEGEA AKQEQRQ EGAEAAK	K	I	V	A	K	M	4
IVSNASCTI EKYDNSLK NCLAPLAK	K	I	V	A	K	V	3
IVYGHLEDD RPLTLSEKI PANQEIER	K	I	V	E	R	G	1
IWHHTFYN TNWDDMI HTFYNELR	K	I	W	L	R	V	0

IYELAAGG`RIKAAMP`R VGTGLNTR	R	I	Y	T	R	I	3
IYTPMEYK NKVAIIGKI IYTPMEYK	K	I	Y	Y	K	G	0
IYVDDGLIS KVVVEVGSK GLISLQVKE	K	I	Y	V	K	E	0
KADIGVAN VNDSPALK IAGSDVSK	K	K	A	S	K	Q	3
KAEGATLS AKKEKQPK STSQAGDF	K	K	A	D	R	G	5
KAGQVFLE KKSSETLRK LEELGNHK	R	K	A	H	K	A	1
KASGPPVS KKPAGVRF PVSELITKA	R	K	A	T	K	A	1
KDAEAWFI EQLAEQNF AEAWFNEI	R	K	D	E	K	S	2
KDDEENYL KIQKGESKI YLDFLSHKI	K	K	D	H	K	N	0
KDLYANTV MKCDVDIF MYPGIADF	R	K	D	D	R	M	2
KDVDGAYI ENFVTIK VDGAYMT	K	K	D	T	K	V	1
KDVDNAYI ENDFVTLK VDNAYMIH	K	K	D	I	K	V	1
KEEELQGA ELKVQLTKI ELQGALAR	K	K	E	A	R	G	2
KFSRPLLP`PAAIGSQK LLPATTTKL	K	K	F	T	K	L	1
KGFNEGLV KYGKPNKR WEIDNNPI	R	K	G	P	K	V	0
KGIELIPQV LGSGQEAK IELIPQVRIE	K	K	G	V	R	I	0
KLAVNMV`GQLNADLF VNMVPPFI	R	K	L	P	R	L	1
KLGGDVSP SALALDERI GSFKEDTKI	R	K	L	T	K	M	0
KLLEGEECF DVEIATYRI LLEGEECRI	R	K	L	C	R	M	0
KMDVGGI ILEAKNLK GLSDPYVK	K	K	M	V	K	I	0
KNDEVSSL KKQLGPGK DAFDLIRN	K	K	N	I	R	N	1
KNHEEEMI KEELAYLR EEEMLALR	R	K	N	L	R	G	1
KQEEQME KEAGDRK METEHFAL	R	K	Q	A	L	-	1
KQEQANN LARRREAR ANNPFIK	R	K	Q	I	K	S	1
KQISNLQQ RSEIDNVKI SISDAEQR	K	K	Q	Q	R	G	1
KQTALVEL PDTEKQIKI TALVELLK	K	K	Q	L	K	H	1
KQTALVEL`SEKERQIKI TALVELVKI	K	K	Q	V	K	H	1
KTGQPMI`_____MINLYTDR	K	K	T	D	R	E	0
KTLNPVFN KFETKVHR FNEQFTFK	R	K	T	F	K	V	0
KTSGPPVS KAAGGAKI PVSELITKA	R	K	T	T	K	A	0
KTTLQVDT ELLNDRFR NTELAER	R	K	T	E	R	S	2
KVNVEEQI IAPALVSK VNVVEEQI	K	K	V	E	K	I	0
KVNVEEQI IAPALVSK VEQEKIDKI	K	K	V	D	K	L	0
KVPQVSTP ALIVRYTRK PTLVEVSR	R	K	V	S	R	S	0
KYEDEINKI DLVEDYKK YEDEINKR	K	K	Y	K	R	T	0
KYQVDLSK LSLDELGR KYQVDLSK	R	K	Y	S	K	G	0
LAELEEALC ALKDARN ELEEALQK	K	L	A	Q	K	A	2
LAFIAHPK PKGPKLKR LAFIAHPKL	R	L	A	P	K	L	2
LAFLTNTT`CLKKHWM FLTNTTGKI	K	L	A	G	K	I	1
LALDLEIAT YQELMNTI DLEIATYRT	K	L	A	Y	R	T	2
LALDVEIAT YQELMNV DVEIATYRH	K	L	A	Y	R	K	2
LALDVEIAT YQELMNV VEIATYRKL	K	L	A	R	K	L	2
LAMQEFM GGSHAGN PVGAESFR	K	L	A	F	R	D	2
LAMQEFM GGSHAGN PVGASSFR	K	L	A	F	R	E	2
LAPDYDAL GEKKAYVR DALDVANH	R	L	A	N	K	I	3
LAQAYYES`EFLLMVFK QAYYESTR	K	L	A	T	R	K	2
LASPIHPD`AVCGLLR FPGDILMR	R	L	A	M	R	M	2
LASYLDKVI`TMQELNSI ANNDLENI	R	L	A	N	K	I	3
LASYLDKVI`TMQNLND ASYLDKVR	R	L	A	V	R	A	1
LATPTYGD DICFRTLKL SGVTTSRIF	K	L	A	L	R	F	2

LATQLTGP DSSAEELKI TGPVMPIR	K	L	A	I	R	N	1
LAVEALSSI GERRAIEKI LDGDLSGR	K	L	A	G	R	Y	2
LAVNMVPI QLNADLRK VNMVPPFI	K	L	A	P	R	L	1
LCVLHEK YLSLILNRL RLCVLHEK	R	L	C	E	K	T	0
LCYVALDFI IVRDIKEKL ASSSSLEKS	K	L	C	E	K	S	4
LDEDLAGY DFSEAYKR EDLAGYCR	R	L	D	C	R	R	1
LDHKFDLM AIAEAWAF KFDLMYAK	R	L	D	A	K	R	1
LDHYAIK KSAPRRNK LDHYAIKF	K	L	D	I	K	F	1
LDIDSAPIT TFLEHMCF DSAPITARI	R	L	D	A	R	N	2
LDKSQIHD EKALRDAK VLVGGSTR	K	L	D	T	R	I	0
LDLIAQQM VSNTLESRI QQMMPEV	R	L	D	V	R	G	1
LDMYVLNF FHKMGVG MYVLNPVI	R	L	D	V	K	D	0
LDMYVLNF FHKMGVG LNPVKDSK	R	L	D	S	K	E	0
LDQLFEM DTNHEREF QVVLEPK	R	L	D	P	K	T	1
LDSELKNM QLKSDQSR QDMVEDY	R	L	D	Y	R	N	0
LEDLIVK ATPYGGVK KLEDLIVKC	K	L	E	V	K	D	0
LEDLIVK ATPYGGVK GLTDVYNK	K	L	E	N	K	I	0
LEGQMGE VREPSAPK GEDGNSIK	K	L	E	I	K	V	0
LEKPAKYD SVVDLTCR PAKYDDIKI	R	L	E	I	K	K	1
LELAQYR KQVAGTM KLELAQYRI	K	L	E	Y	R	E	1
LELVSYFGK SGDEPKEK ELVSYFGK	K	L	E	G	K	R	0
LEMYVLNF FQKMGVG MYVLNPVI	K	L	E	V	K	S	0
LENEIQTYF QLLDIKIRLI ENEIQTYR	R	L	E	Y	R	S	0
LENIIVTDV KKQSLFAR IVTDVDPK	R	L	E	P	K	T	0
LEQEIATYF ILLDVKTRL EQEIATYRF	R	L	E	Y	R	R	1
LEQQQAID LLIEMEQR DDLMPAQ	R	L	E	Q	K	-	2
LEQMMEA NLSLSTSKL QMMEASV	K	L	E	V	R	D	1
LEVNMQA ATEDAKLR EVNMQAN	R	L	E	M	K	A	1
LFGTSPAAI QRRSIISRL PALEAPAR	R	L	F	A	R	V	6
LFIGGLNTE VEADRPVK LNTETNEK	K	L	F	E	K	A	0
LFIGGLSFE REKEQFRK ETTEESLRN	K	L	F	L	R	N	0
LFTFHADIC VPKAFDEK CTLPDTEK	K	L	F	E	K	Q	1
LGAEVYHT ESFRDAMF AEVYHTLK	R	L	G	L	K	G	1
LGDICFSLR AEKEEQEK GDICFSLR	K	L	G	L	R	Y	0
LGEHNIDV YKSRIQVRI EQFINAAK	R	L	G	A	K	I	2
LGEHNINV YKSRIQVRI EQFVNSAK	R	L	G	A	K	I	1
LGEYGFQN QNCDQFEI FQNALIVR	K	L	G	V	R	Y	1
LGFSEVEL FDVSNADF QMVVDGV	R	L	G	V	K	L	0
LGGSAVISI DRCTLAEK ISLEGKPL_	K	L	G	P	L	-	1
LGIQAEPLY LTLQLHLNR IQAEPLYR	R	L	G	Y	R	V	1
LGTAAIQG LASQPATK AIQGAIEK	K	L	G	E	K	A	3
LHFFMPGF VNMVPPFI GFAPLTAR	R	L	H	A	R	G	2
LHFFMPGF VNMVPPFI GFAPLTSR	R	L	H	S	R	G	1
LIETYFSK EALTGTEKI LIETYFSKN	K	L	I	S	K	N	0
LIFDNLKK VTGVEEGF LIFDNLKKS	R	L	I	K	K	S	0
LIGQIVSSIT PTYTNLNR SSITASLRFI	R	L	I	L	R	F	1
LIIVEGCQR ARTSPQQK IIVEGCQRC	K	L	I	Q	R	Q	0
LISQIVSSIT PTYTNLNR SSITASLRFI	R	L	I	L	R	F	1
LISWYDNE ALNDNFVK NEYGYSNR	K	L	I	N	R	V	0
LKECCDKP NQDTISSKI CDKPLLEK	K	L	K	E	K	S	0

LKEGDTIIV DVILINGRL GPIVTQIRC	R	L	K	I	R	G	0
LKETQPG E ELIEDEEKL GEAYVIQK	K	L	K	Q	K	E	1
LKGEATVSI YTDRETGK FDDPPSAK	K	L	K	A	K	A	2
LKYENEVA RLAADDFR YENEVALR	R	L	K	L	R	Q	1
LLDSLEPPC ELRNKVN R ENDTV DGI	R	L	L	G	R	E	0
LLEAQIATC IEKGHGIRL TGGIIDPKE	R	L	L	P	K	E	2
LLEGEDAH QEIATYRRI SGQSYSSRI	R	L	L	S	R	E	2
LLEGEDAH QEIATYRRI SSGSQSSRI	R	L	L	S	R	D	1
LLEGE ECR VEIATYRKL LLEGE ECR	K	L	L	C	R	M	0
LLESE ECR MEIATYRK LLESE ECR	K	L	L	C	R	M	0
LLESGLDLS M CYSDAF AK DLSMNSIK	K	L	L	I	K	V	0
LLIEMEQR QMVVDG L LLIEMEQR	K	L	L	Q	R	L	0
LLLIGNSSV QNF D YMF IGNSSV GK	K	L	L	G	K	T	0
LLLLGAGE S ISAAKDVKI LGAGES GK	K	L	L	G	K	S	1
LLLQVQHA VAPIERVKI LQVQHASK	K	L	L	S	K	Q	1
LLNDEDPV RALPELTKI EDPVVVTK	K	L	L	T	K	A	0
LLNQPNQ L YGIPAIVKL PNQWPLV	K	L	L	V	K	A	0
LLRDYQELI QAKEDLAF YQELMNTI	R	L	L	T	K	L	0
LLRDYQELI QAKEDLAF YQELMNVI	R	L	L	V	K	L	0
LLSNDEVTI MQRVFRG SNDEVTIK	K	L	L	I	K	Y	0
LMDYLLV VEFLAQLK VGIHDVER	K	L	M	E	R	A	0
LMIEMDG VEQEKIDKI EMDGTEN	K	L	M	N	K	S	0
LMMDPLS AGPIWDLF DPLSGQNF	R	L	M	N	R	G	0
LMMDPLT AGPIWDLF DPLTGLNR	R	L	M	N	R	G	0
LNDLEDAL ALKDAKN EDALQQA	K	L	N	A	K	E	2
LNDLEDAL ALKDAKN QAKEDLAR	K	L	N	A	R	L	3
LNDLEEAL ALKDARNK EEALQQA	K	L	N	A	K	E	2
LNIPVNQV TVEDIAARI PVNQVNPI	R	L	N	P	R	D	0
LNIPVSQVI TVEDIAARI PVSQVNP	R	L	N	P	R	D	0
LPLQDVYK RPTDKPLR LPLQDVYK	R	L	P	Y	K	I	0
LPQFVQSA VTQLLVER ADLEVQER	R	L	P	E	R	A	1
LPRPPPPEI DSVKVFYFR PEMPEL	R	L	P	L	K	K	0
LPSYLDK QGIPSKSRI RLPSYLDK	R	L	P	D	K	V	0
LQGEIAHV ELNRVIQRI QGEIAHV	R	L	Q	V	K	K	1
LQLWDTA YLEDRTVR WDTAGQE	R	L	Q	E	R	F	1
LQNNNVY NADTVSSK NNVYTIKI	K	L	Q	A	K	R	1
LQQLPADF KLDLSKNK QLPADFG	K	L	Q	G	R	L	1
LQTAPVPM SPSASKSRI PVPMPDL	R	L	Q	L	K	N	1
LRAEIDNVI EMNRMIQ AEIDNVKK	R	L	R	K	K	Q	1
LRSEIDHV EINRMIQR SEIDHVKK	R	L	R	K	K	Q	0
LRSEIDNV ELNRVIQRI RSEIDNVK	R	L	R	V	K	K	0
LRSEIDNV ELNRVIQRI SEIDNVKK	R	L	R	K	K	Q	0
LSGPGGSG DSSRLSARI PGGSGSFR	R	L	S	F	R	S	0
LSISALFVTI RSYGKAFK SALFVTPK	K	L	S	P	K	T	1
LSISETYDLI SANLHLPK ISETYDLKS	K	L	S	L	K	S	0
LSMKPEPL FTLQYLNKI MKPEPLFR	K	L	S	F	R	S	0
LSMYGVDI HFLENACK GVDLHHA	K	L	S	A	K	D	1
LSQEEQLK LLPATTTKL LSQEEQLK	K	L	S	L	K	S	0
LSQKFPK LKAWSVAI RLSQKFPK	R	L	S	P	K	A	0
LSSFATSV TSITECDKL PQTEETGK	K	L	S	G	K	S	4

LSSPATLNS DNDIMLIK SPATLNSR	K	L	S	S	R	V	1
LSSQLSEEK GWSEKSVI SSQLEEKV	K	L	S	E	K	W	0
LTGMAFR VPELNGKI KLTGMAFF	K	L	T	F	R	V	1
LTLYDIAHT KNSPLVSR DLSHIETRA	R	L	T	T	R	A	3
LTMQNLN GLLAGNEK TMQNLND	K	L	T	D	R	L	0
LTTPTYGDI DICFRTLKL SGVTTCLRI	K	L	T	L	R	F	1
LTVVILEAK RYVPTAGK TVVILEAKM	K	L	T	A	K	N	1
LVDTFLED LFINESAKL DTFLEDVKI	K	L	V	V	K	N	0
LVINGKPIT TVKAENG PITIFQERD	K	L	V	E	R	D	0
LVLEVAQH EVQGRDSF HLGESTVR	R	L	V	V	R	T	1
LVMEEAPE AIRVASPKI EEAPESYKI	K	L	V	Y	K	N	1
LVNELTEF CPFDEHVK NELTEFAK	K	L	V	A	K	T	1
LVNEVTEF CPFEDHVK NEVTEFAK	K	L	V	A	K	T	1
LVTLPVSFA HLDLLNNR PVSFAQLK	R	L	V	L	K	N	1
LVVSTQTA CFAVEGPK VSTQTALA	K	L	V	L	A	-	2
LYMNP GAI QPISASAKI PGAESLK	K	L	Y	L	K	T	1
LYMNP GAI QPISASAKI ESELKTPKL	K	L	Y	P	K	L	1
MAATFIGN DIPPRGLKI TAIQELFKR	K	M	A	F	K	R	3
MADGAPL ESGGKGER GAPLAGVF	R	M	A	V	R	G	3
MASTFIGN DIPPRGLKI TAIQELFKR	K	M	A	F	K	R	2
MATDPEN AKGLSDVK TDPENIIE	K	M	A	I	K	E	1
MAVTFIGN DIPPRGLKI TAIQELFKR	K	M	A	F	K	R	2
MDDFQLK IEGFDPKRI IVEEFVKV	R	M	D	V	K	W	0
MDENQFV DKAVVTGK VTSTNAAK	K	M	D	A	K	V	3
MDSTEPAN QLIVGVNK TEPAYSEK	K	M	D	E	K	R	1
MDSTEPPY QLIVGVNK TEPPYSQKI	K	M	D	Q	K	R	0
MDVGGLS LEAKNLKKI GLSDPYVK	K	M	D	V	K	I	0
MEEEVLLI TAEAKIKKI LLEDQNSK	K	M	E	S	K	F	0
MEEGEVY VKGGEATF ETFGSTGKI	R	M	E	G	K	G	1
MEIAELNR GDDLKNSK MEIAELNR	K	M	E	N	R	T	1
MEIGLPDE RPGRLEVK EIGLPDEKC	K	M	E	E	K	G	0
MEPLNNLC NTLGPVMI NNLQVAVI	K	M	E	V	K	N	1
MESPIILP SKLTQDSR TPDAAETEK	R	M	E	E	K	L	1
MFFDAELS MDEINFM VLSMDNN	K	M	F	N	R	N	1
MFIGGLSM AAQREEW LSWDTTKK	K	M	F	K	K	D	0
MGVVGKLEI EPVILFQKI MYVLNPVI	K	M	G	V	K	S	0
MHDSHLS MPKQVEV HLSSDEPKI	R	M	H	P	K	H	0
MIAEAIPEI KITPFEEKI AEAIPELKA	K	M	I	L	K	A	2
MIEEAGAI VHGGTILKI AGAIISTRH	K	M	I	T	R	H	2
MKGYPHM PGDLIFAKI GYPHWPA	K	M	K	A	R	V	1
MLDNLGYI QEFEALMF MLDNLGYI	R	M	L	Y	R	T	0
MLEIDPQK VVVLANIKI MLEIDPQK	K	M	L	Q	K	V	0
MLVVGIGI IAPELYHKI LVVGGIDR	K	M	L	D	R	V	0
MPCTEDYL CTKPESERI YLSLILNRL	R	M	P	N	R	L	0
MPIPVIQA KIGGATERI IQAFGILKR	R	M	P	L	K	R	1
MQAFEASI NANSHARI PMWLQDT	R	M	Q	T	K	P	2
MQEDIEM DTIDSQHR QEDIEMTK	R	M	Q	T	K	T	0
MQINAEEL LVIREGEKI VGDLEVEK	K	M	Q	V	K	G	1
MQVNAAE LVIREGEKI VGDLEVEIK	K	M	Q	I	K	G	1
MREIVHIQ _____ CGNQIGTK	-	M	R	T	K	F	1

MREIVHLC _____ CGNQIGAK	-	M	R	A	K	F	2
MSATFIGN DIPPRGLKI TAIQELFKR	K	M	S	F	K	R	2
MSDAQVC LKGLGPKR VSIGPVGK!	R	M	S	G	K	S	1
MSESLDTA LVDVICEKI DPAVTGAK	K	M	S	A	K	Q	3
MSGDLSSM LLEGEECRI ISSNVASKA	R	M	S	S	K	A	1
MSGECAPI LLEGESRI TISGGGSR	R	M	S	S	R	G	1
MSISEGTV GSFKEDTK SEGTVSDK	K	M	S	D	K	S	0
MSMKEVD VATVFRGR QMLAIQSK	R	M	S	S	K	N	1
MSMKEVD VAAVFRGF QMLNVQM	R	M	S	N	K	N	0
MSMKEVD VAAVFRGF QMLSVQSI	R	M	S	S	K	N	0
MSSTFIGN DIPPRGLKI TAIQELFKR	K	M	S	F	K	R	1
MSVEADIN YETELNLR ADINGLRR	R	M	S	R	R	V	1
MSVQPTV KVTLATLKI ITPPVVLR	K	M	S	L	R	L	0
MTLDDFR LLDIDNTRI RMTLDDFF	R	M	T	F	R	I	0
MVIGMDV DKAGYTEK VAASEFYRI	K	M	V	Y	R	D	2
MVIPGGID KTIEAHSRI GGIDVHTR	R	M	V	T	R	F	0
MVSADAYI EKYHDGTK MVSADAYI	K	M	V	Y	K	I	2
MVTGDNII QRAGITVR GDNINTAR	R	M	V	A	R	A	1
MYGVLPW GSLCADAR PWNAPFG	R	M	Y	G	K	V	1
MYKEEGLM TLREAVPKI EGLNAFYK	K	M	Y	Y	K	G	1
NADVELQC LRSDSLKI ADVELQQF	K	N	A	Q	R	A	1
NAVTQEFQ NGKANSVI GPVPDTAF	R	N	A	A	R	Y	2
NDEVSSLD KQLGPGKI DAFDLIRN	K	N	D	I	R	N	1
NDISSHPP EKLMMENM VEGSYAPR	R	N	D	P	R	R	1
NEGATYA LMELLHSR YAAAVLFR	R	N	E	F	R	I	4
NEVLMVN AKVQKLSK GSLSTGGR	K	N	E	G	R	V	0
NFDVGHVI MECSHYM DVGHVPIR	K	N	F	I	R	-	0
NFILDQTN EIAARKKRI NVSAAAQI	R	N	F	Q	R	R	3
NFSGAELE KELAVETKI AELEGLVR	K	N	F	V	R	A	1
NHEEEML EELAYLRKI EEEMLALR	K	N	H	L	R	G	1
NHEEEMN EELAYLKKI EEEMNALF	K	N	H	L	R	G	1
NHKEEMS EELMALKK APGKDLTK	K	N	H	T	K	T	1
NIPAGLQS EQAPGRDI SMNQALQ	K	N	I	Q	R	R	2
NISFTVWD NVETVEYK WDVGGQI	K	N	I	D	K	I	0
NKLDHYAII PRKSAPRR LDHYAIIKF	R	N	K	I	K	F	1
NKLEGLD EMALKDAI GLEDALQK	K	N	K	Q	K	A	1
NKLNLDLED ENALKDAK EDALQQA	K	N	K	A	K	E	2
NKLNLDLED ENALKDAK QAKEDLAR	K	N	K	A	R	L	3
NKLNLDLEE EHALKDAR EEALQQA	R	N	K	A	K	E	2
NKYEDEIN QDMVEDY KYEDEINKF	R	N	K	N	K	R	0
NKYEDEIN QDMVEDY YEDEINKR	R	N	K	K	R	T	0
NLANTVTE LVKVLVRI VTEEILEKS	R	N	L	E	K	S	1
NLATTVTEI KVKVLFVR VTEEILEKS	R	N	L	E	K	S	1
NLDIERPTY AIYDICRRN PTYTNLNR	R	N	L	N	R	L	0
NLDLDSIIA ILSMDNSR DSIIAEVKA	R	N	L	V	K	A	1
NLEAVETL ARKNCLVK TSTICSDKT	K	N	L	D	K	T	1
NLHQSGFS KQQAPPVI QIDDNIPRI	R	N	L	P	R	R	1
NLINQMLT DTVTPEAK MLTINPAK	K	N	L	A	K	R	1
NLLLSGEQ FFTVTDPR GEQLEASR	R	N	L	S	R	N	1
NLPIYSENI CVVINPYKI ENIIEMYRC	K	N	L	Y	R	G	0

NLVDSYM/ ERQVETIRI SYMAIVNK	R	N	L	N	K	T	1
NMELNVLINQSSSFLKIVLDSLNTKI	K	N	M	T	K	M	0
NMGGPYGSGNFGGSFGSGGYGGI	R	N	M	G	R	S	0
NMMAACITQQMFDA MMAACDF	K	N	M	P	R	H	2
NMQDLVEGRLDSELRIQDLVEDFK	R	N	M	F	K	N	0
NMQDMVSRLDSELKIQDMVEDY	K	N	M	Y	R	N	0
NMVPQQ/ SKIMESFKI PQQALVIR	K	N	M	I	R	E	1
NQILNLTTIYKTIDDLKILQIDNARI	K	N	Q	A	R	L	2
NQVAMNFRIGDAAKITNTVFDK	K	N	Q	A	K	R	2
NQWQLSADCAQLKEKQLSADDLK	K	N	Q	L	K	K	1
NQWQLSADCAQLKEKLSADDLKI	K	N	Q	K	K	L	1
NRAPDSG/FPEDKGSKDSGAEVER	K	N	R	E	R	E	2
NRLDYHIS/ HKAYKEVKISVQNM	K	N	R	M	R	R	0
NSLESYAFIQRDKVSSKESYAFNM	K	N	S	M	K	A	1
NSLLNEDLISELHQEVKLLNEDLEK	K	N	S	E	K	V	0
NSSYFVEWQMLNVQMEWIPNNV	K	N	S	V	K	T	0
NSVFQQGI LIICKTRRN SVFQQGM	R	N	S	M	K	N	0
NTATVLDSGRTEQNYKGSYFMYSK	K	N	T	S	K	L	1
NTDQASMNIAFKKERIPDNTAAQI	R	N	T	Q	K	V	3
NTDQASMNISFKKERIPENTVAQ	R	N	T	Q	K	L	2
NTKQEIAEIGRHGDDLIQEIAEINR	R	N	T	N	R	M	1
NTLNPYYNKKKTTIKKVPFEQIQ	K	N	T	Q	K	V	0
NVDVEFFKIPNHSNSKIVDVEFFK	K	N	V	K	R	V	0
NVEGQDNVNYTIAKRIDMLYQSLK	R	N	V	L	K	L	0
NVMSAFGKNQDEINKPSAPTEDR	K	N	V	D	R	S	2
NVQAEEMIARVHGLRVEFSSGLK	R	N	V	L	K	G	1
NVQALEIEISEITELRRNLQSQLALK	R	N	V	L	K	Q	2
NVQDAIACAHVKKQCI AIADAEQR	K	N	V	Q	R	G	3
NVQDAIACAHVKKQCIQRGEHALK	K	N	V	L	K	D	4
NVQDAIACAHVKKQCI EHALKDAR	K	N	V	A	R	N	5
NVSTGDVIEEEMKDLFTQLLNNMI	R	N	V	M	R	S	2
NVTAIQGPAPIQWEEFAIQGPGGK	R	N	V	G	K	W	1
NVTELNEPDDMAAAN EPLSNEERI	K	N	V	E	R	N	0
NYSPPYNTKGPAAIQKDLTVGNN	K	N	Y	N	K	T	0
PATKPVASADSRESLKIATKPVASK	K	P	A	S	K	S	2
PDVVVKECITISVKGKPKEDDEYKR	K	P	D	K	R	V	0
PGAHVTV/ VAREESGKPGAHVTV	K	P	G	V	K	K	1
PLAASPKPKKKGDKSKSPKPGALK	K	P	L	L	K	E	3
PLESSQVKLFVNGQPFPLESSQVK	R	P	L	V	K	Y	0
PSICSGVVAVLNSYTELM		P	S	L	M		1
QAADMILLIAGSDVSKI VTGVEEGR	K	Q	A	G	R	L	3
QATINIGTILSREISRQIGHVAHGK	R	Q	A	G	K	S	2
QATLGAGIGEGQAPTI TPCTTVNK	R	Q	A	N	K	V	2
QCANLQNAEIDNVKKAIAADAEQR	K	Q	C	Q	R	G	4
QDGQFSVIDCDIHVLKQFSVLFTK	K	Q	D	T	K	C	0
QDHPSSMYGQQSSFRFSGPGENR	R	Q	D	N	R	S	0
QDLATLDV LGQPHLSRLATLDVTKI	R	Q	D	T	K	L	1
QDLPNAMVLLVFNKNAAEITDKI	K	Q	D	D	K	L	3
QEIAEINRGDDL RNT/ QEIAEINR	K	Q	E	N	R	M	1
QEIECQNC EAQITDVR YSLLLSIKM	R	Q	E	I	K	M	0

QEPSDSPM MIAFKIIRC SPMFIINR	R	Q	E	N	R	K	0
QEQDTYAI AKKMNISR YALSSYTRS	R	Q	E	T	R	S	1
QEYDESGP FQQMWIS SGPSIVHRI	K	Q	E	H	R	K	0
QEYEQLIAI TKTLNDMI EYEQLIAK	R	Q	E	A	K	N	1
QFSSSYLSF _____ FSSSYLSRS	R	Q	F	S	R	S	0
QGAIVAVT IIVEGCQRC VNDSPALK	R	Q	G	L	K	K	3
QGAIVAVT IIVEGCQRC NDSPALKK	R	Q	G	K	K	A	3
QGVDAIDM FEMEQNLI DADINGLR	R	Q	G	L	R	Q	1
QIFLGGVD FAFKDKYK IFLGGVDRI	K	Q	I	D	R	H	0
QIGENLIVF YMEDGLIK LIVPGGVK	K	Q	I	V	K	T	0
QIPYTMMI GVAPLWM QIPYTMMI	R	Q	I	M	K	F	0
QIQDAIDM EVKQSSMI QDAIDMEI	K	Q	I	E	K	A	1
QISNLQQS SEIDNVKKI SISDAEQR	K	Q	I	Q	R	G	1
QISNLQQS SEIDNVKKI QRGENAL	K	Q	I	L	K	D	2
QISNLQQS SEIDNVKKI ENALKDAK	K	Q	I	A	K	N	3
QITTELAEF KSHESKLIK TTELAHR	K	Q	I	H	R	S	1
QLDDLKVE KKKEELLK KVELSQLR	K	Q	L	L	R	V	0
QLDSIVGEI QYINNLRR LDSIVGER	R	Q	L	E	R	G	0
QLEEAEEE ARMKQLKI EAEAEATR	R	Q	L	T	R	A	2
QLFHPEQL EVRTGTYR PEQLITGKE	R	Q	L	G	K	E	0
QLFHPEQL EVRTGTYR DAANNYAI	R	Q	L	A	R	G	3
QLITDLVIS GEHQVEDI ITDLVISM	R	Q	L	S	K	M	0
QLLQANPI NIPGELER LESFGNAK	R	Q	L	A	K	T	2
QMYMSLP SHLNKGIKI MSLPQGEI	K	Q	M	E	K	V	0
QNCDQFEI DEPQNLIK QNCDQFEI	K	Q	N	E	K	L	0
QNLEPLFEI EQGKTQVR EQYINNLRI	R	Q	N	L	R	R	0
QNPMTLG RPAFSAIRC GNVVIFDK	R	Q	N	D	K	V	0
QQPALEQF NGSLNGEK AHSTPVKR	K	Q	Q	K	R	E	4
QRPAEIKD KIRDWYQF KDYSPYFK	R	Q	R	F	K	T	1
QRPSEIKD KIRDWYQF KDYSPYFK	R	Q	R	F	K	T	0
QSLEASLAI LQSQLALK SLAETEGR	K	Q	S	G	R	Y	2
QSRPVAGC PVTQGGQ PASPSPQR	R	Q	S	Q	R	Q	5
QSSYGQQ YGSYENQK SSGGQGGI	K	Q	S	G	R	A	0
QSTQVMA AASDSSGK MSAFDPLK	K	Q	S	L	K	N	3
QSTQVMA AASDSSGK KNQDEINK	K	Q	S	N	K	N	3
QSVEADIN YENEVALR EADINGLRI	R	Q	S	L	R	R	1
QSVEADIN YENEVALR ADINGLRR	R	Q	S	R	R	V	1
QTAASAGL SLSQAVKI PAPSAASR	K	Q	T	S	R	K	7
QTVEADV YEHELALRI ADVNGLRF	R	Q	T	R	R	V	1
QVDLLSAE NYIGDLRR LLSAEQMF	R	Q	V	M	R	Q	1
QVDTEEAC GRKRKAEK AATASNK	K	Q	V	V	K	A	4
QVLALQSC EARKNLEK QSQLADTK	K	Q	V	T	K	K	2
QVLDNLTA DADINGLR LDNLTMEK	R	Q	V	E	K	S	0
QVVAVTGI DSTTGEQF TNDGPALK	R	Q	V	L	K	K	2
RAIGNIELC TVTEEHLRI GNIELGIRS	R	R	A	I	R	S	1
REEVLEEG TAMSKLAK EVLEEGAK	K	R	E	A	K	E	1
RGDIIGVE VHINNKLR GVEGNPGI	R	R	G	G	K	T	0
RHPEYAVS SFLYEYSRR YAVSVLLRI	R	R	H	L	R	L	1
RIPIHNEDI AQLGEDIR ELVLMMQ	R	R	I	Q	R	V	0
RISEQFTAI TAIQELFKF EQFTAMFF	K	R	I	F	R	R	1

RLDEDLAG ADFSEAYK EDLAGYCR	K	R	L	C	R	R	1
RMEELHN(MRRQEELI LHNQEVQI	R	R	M	Q	K	R	0
RNLDIRP1 EAIYDICRR PTYTNLNR	R	R	N	N	R	L	0
RPCFSALTF CTESLVNR PDETYVPK	R	R	P	P	K	A	1
RPPGVLHC ELVSYFGKI GVLHCTTK	K	R	P	T	K	F	0
RQLDSIVG EQYINNLR LDSIVGERC	R	R	Q	E	R	G	0
RSEGHEQT AGPAWM) GTGPEGGH	R	R	S	G	K	G	3
RVDQLKSD SFINNLRRL QLKSDQSR	R	R	V	S	R	L	0
RVIISAPSA AHLKGGAI VMGVNHE	K	R	V	E	K	Y	3
RVLDELTL1 EADINGLR LDELTLTKA	R	R	V	T	K	A	0
SAAEVIAQ, YVTKVMSK AEVIAQAR	K	S	A	A	R	K	4
SADCSVEE VTLAANGK SVEEEPWK	K	S	A	W	K	R	1
SADCSVEE VTLAANGK VEEEPWKF	K	S	A	K	R	E	1
SASSGAEG NAPRKEDF EGDVSSER	R	S	A	E	R	E	2
SASSGAEG NAPRKEDF DVSSEREP_	R	S	A	E	P	-	2
SDAAPAAS AAAGPEAK AEPAPSSKI	K	S	D	S	K	E	6
SDAAPTVP KAAKQEA FVVPQSAPR	R	S	D	P	R	N	3
SDISPLTPR EGEKLSPK! DISPLTPRE	K	S	D	P	R	E	0
SDLEMQYI LDNLTMEK QEELMALK	K	S	D	L	K	K	1
SDLEMQYI LDNLTMEK EELMALKK	K	S	D	K	K	N	1
SDLYSSGR RDSYSSSR! SDLYSSGRI	R	S	D	G	R	D	0
SDVLETVV GQKILHHR EAVSTEVRI	R	S	D	V	R	L	1
SEETLDEGI DDKPKDSK TLDEGPCK	K	S	E	P	K	Y	0
SEISELRR SELVQSGK SEISELRRTI	K	S	E	R	R	T	0
SEITELR IEQISSYKSI KSEITELRR	K	S	E	L	R	R	0
SEITELRR IEQISSYKSI SEITELRRN	K	S	E	R	R	N	0
SELDTIDSC GIVYHLSK! DTIDSQHR	K	S	E	H	R	M	0
SEQHGSSS SRSGQSSR HQSSGHGI	R	S	E	G	R	Q	0
SEVTELRR SELVQSSR! SEVTELRR\	R	S	E	R	R	V	0
SFNLPHYQD TPTEYLQR! NLPYQDAF	R	S	F	A	R	K	1
SFSTASAIT SFRSGGSR AITPSVSRT	R	S	F	S	R	T	2
SGFSSISVS ARLPGVSR FSSISVRSI	R	S	G	S	R	S	0
SGFSSVSV! ARLPGVSR FSSVSVRS	R	S	G	S	R	S	0
SGGGFSSG FSSRSGYR! AGIINYQRI	R	S	G	Q	R	R	1
SGGGGGG SKHYSSSR! GGGVSSLR	R	S	G	L	R	I	0
SGGGGGG FSSSYLSRS LGSGGSIR!	R	S	G	I	R	S	0
SGPFGQIFI PGTMDSV GAGNNW/	R	S	G	A	K	G	2
SGQSSYGC GFGQHESF GYGQHGSI	R	S	G	S	R	Q	0
SGVSLAALI AVAASKER GVSALAALKI	R	S	G	L	K	K	2
SGVSLAALI AVAASKER VSLAALKK/	R	S	G	K	K	A	2
SHCIAEVEK CDKPLLEK! HCIAEVEKI	K	S	H	E	K	D	1
SIEEACLT! DASRKAKR LTLQHLNR	R	S	I	N	R	L	1
SIQFVDWC IATIKTKRSI DWCPTGFI	R	S	I	F	K	V	0
SISHPESGL FSNRTSRK! MAEGEGYI	K	S	I	Y	R	N	1
SISISVAGG LVGLGGTK AAGGFGGI	K	S	I	G	R	G	3
SITIANQTN VEA EAVNF NCP LYVTK'	R	S	I	T	K	V	1
SKAEAESLY QNEDIAQK AESLYQSK'	K	S	K	S	K	Y	2
SKAEAESLY QNEDIAQK ELQITAGRI	K	S	K	G	R	H	3
SKEEAEALY QYEEIAQR AEALYHSK'	R	S	K	S	K	Y	2
SKEEAEALY QYEEIAQR ELQVTVGR	R	S	K	G	R	H	2

SKEEQELH MQKYEDIK LHDIHSTRS	K	S	K	T	R	S	0
SKELTTEID AEAWFNEI IEQISSYKSE	K	S	K	Y	K	S	0
SKYLATAST SQKRPSQR ASTMDHA	R	S	K	A	R	H	3
SLDGEVGT SKRYTMSR TGQYATTK	R	S	L	T	K	G	1
SLDLDSIIAI ILSMDNNF DSIIAEVKA	R	S	L	V	K	A	1
SLHTLFGDI ESHAGCEK LFGDELCK	K	S	L	C	K	V	0
SLHTLFGDI ESAENCDK LHTLFGDK	K	S	L	D	K	L	0
SLLEEGES ENEIQTYR GSSGGGGI	R	S	L	G	R	G	0
SLNNQFAS SREREQIK QFASFIDK	K	S	L	D	K	V	1
SLNNQFAS SREREQIK ASFIDKVR	K	S	L	V	R	F	1
SLVGHTVG EGLVIGVR GAAGVVSF	R	S	L	S	R	I	2
SLVGLGGT GGGGFGSI LVGLGGTK	R	S	L	T	K	S	0
SLVNLGGS AGGGFGSI LVNLGGSK	R	S	L	S	K	S	0
SLVNLGGS AGGGFGSI SISISVARG	R	S	L	A	R	G	1
SLVNLGGS GVGGYGSI YNLGGSKR	R	S	L	K	R	I	0
SMQDVVE MRQNAEV QDVVEDYH	R	S	M	Y	K	S	0
SNVNDGV EKLRGWLK DGVAQSTF	K	S	N	T	R	I	1
SPEFTHEN GESEPQTR HENPLETR	R	S	P	T	R	N	0
SPPLLGSES EKVLSPLRS DFLSADSK	R	S	P	S	K	V	1
SPSLSPSP DERLSPAK SPPSPIEKT	K	S	P	E	K	T	0
SPWASDF TPLQHTPR FQEPLPQK	R	S	P	Q	K	G	1
SQGSTSNS IAELEEERS TSNSDWM	R	S	Q	M	K	N	0
SQIHDIVLV LRDAKLDK VLVGGSTR	K	S	Q	T	R	I	0
SQYEQLAE TQLLNNM EQLAEQNF	R	S	Q	N	R	K	1
SQYEQLAE TQLLNNM QLAEQNRH	R	S	Q	R	K	D	1
SRAEAESW QYEEIAQR AESWYQTI	R	S	R	T	K	Y	2
SRTEAESW QYEEIANR AESWYQTI	R	S	R	T	K	Y	1
SSASFSTTA HYPYISTRS STTAVSAR	R	S	S	A	R	Y	3
SSGSPYGG KGGSGGGI GSGGYGSF	R	S	S	S	R	R	0
SSLLDVTV PQTEETGK VTSIPSSRT	K	S	S	S	R	T	0
SSLSGEEVI EPLEQAVR SGEEVDSK	R	S	S	S	K	V	0
SSMLFDTM TAEPYGFR QHHLALNF	R	S	S	N	R	D	1
SSRPDTLLS SWPEGAEI SSEQRPGK	R	S	S	G	K	S	0
SSVLENFV VGGQSAG VLENFVGR	K	S	S	G	R	D	0
SSYYVVSIG VEFFKVR PAAEEPSR	R	S	S	S	R	A	2
STAGDTHL EDGIFEVK GGEDFDNI	K	S	T	N	R	M	1
STESLQAN VDPRRRN SLQANVQF	K	S	T	Q	R	L	1
STGEAFVQ LTMDYQG AFVQFASK	R	S	T	S	K	E	2
STGFIPIKEI YQDKQEEI KEDFGPEK	K	S	T	E	K	K	0
STGFIPIKEI YQDKQEEI EDFGPEKK	K	S	T	K	K	T	0
STMQELNS GILTANEK TMQELNSI	K	S	T	S	R	L	0
STPSQVTSI SRALPRPR SQVTSEEKI	R	S	T	E	K	D	0
STSSFCLS VVSGGSRR SSFCLS RH	R	S	T	S	R	H	0
STTTGHLIY IGHVDSGK TTGHLIYKC	K	S	T	Y	K	C	0
STVAQLVK YVAIGQKR STVAQLVK	R	S	T	V	K	R	1
SVGNTIEP MKPELFR EPVILFQKN	R	S	V	Q	K	M	0
SVNFSLTPI EKTPLGER SLTPNEIKV	R	S	V	I	K	V	0
SVTEQGAE DDMAACN AELSNEERI	K	S	V	E	R	N	1
SVTLPTHH DPYVIALR HETPEYQR	R	S	V	Q	R	G	0
SVTQQPGS VALYSGAR SEVIAPQKI	R	S	V	Q	K	T	1

SVVTVIDVI _____ TVIDVFYKY	R	S	V	Y	K	Y	0
SWQDELA _____ QAEEGSAR	R	S	W	A	R	L	3
SYEAYVLNI SFRPNDPK AYVLNIIRF	K	S	Y	I	R	F	1
SYELPDGQ ASSSSLEKS VITIGNERF	K	S	Y	E	R	F	0
SYRPELIR SFLEQLRKS SYRPELIRD	K	S	Y	I	R	D	0
TAAENDFV YEDEINKR' ENDFVTLK	R	T	A	L	K	K	2
TAAENDFV YEDEINKR' NDFVTLKK	R	T	A	K	K	D	2
TAAENEFV YEDEINKR' ENEFVTLKI	R	T	A	L	K	K	2
TAAENEFV YEDEINKR' NEFVTLKKI	R	T	A	K	K	D	2
TADQDFFF IPNHCSGK TADQDFFF	K	T	A	F	R	R	1
TALVANTS KVESIMKR SNMPVAA	R	T	A	A	R	E	4
TAVAPIER GIAAAVSK TAVAPIER	K	T	A	E	R	V	2
TAVCDIPPI EWIPNNVI AVCDIPPR	K	T	A	P	R	G	1
TAVVVGTV KLPGRENK GTVTDDVF	K	T	A	V	R	I	1
TCVADESH NELTEFAK' ESHAGCEK	K	T	C	E	K	S	2
TDYNASVS GKNIKALR' PDSSGPER	R	T	D	E	R	I	1
TEAESWYC EEIANRSR1 AESWYQTI	R	T	E	T	K	Y	1
TEELNKEV, AETWFLSK SELVQSSR	K	T	E	S	R	S	1
TEGLSVLN1 MTTTTLER NQAMAVII	R	T	E	I	K	E	2
TEGLDLGI SVGLGFLR' LDLGLEPKI	R	T	E	P	K	R	0
TEQSVTPE1 MTREMNS SVTPEQQK	K	T	E	Q	K	K	0
TFEGVDPC NFDENDP1 DPQNTSM	K	T	F	M	R	D	0
TFITQQGIK NSETGALK FITQQGIKS	K	T	F	I	K	S	0
TGAIVDVP KEGDVVKF VGEELLGR'	R	T	G	G	R	V	1
TGQPMINI _____ MINLYTDR	K	T	G	D	R	E	0
TGTAEMSS ASNTRLQK MSSILEERI	K	T	G	E	R	I	1
TGYTLDVT KIKALLERT LDVTTGQR	R	T	G	Q	R	K	0
THDVGGY1 ESQEKTI RT VGGYYYEK	R	T	H	E	K	T	0
THINIVVIG _____ IGHVDSGK	K	T	H	G	K	S	0
THINTVVA DQYLGLVR HINTVVAK	R	T	H	A	K	I	1
THNLEPYFI QQVDTSTF ESFINNLR	R	T	H	L	R	R	0
THSDQFLV KIKGILYRTI DQFLVSFKI	R	T	H	F	K	D	0
TIAMDGTE HLGESTVR DGTEGLVR	R	T	I	V	R	G	1
TIDDLKNQ RDYSKYYY' LLQIDNARI	K	T	I	A	R	L	2
TIGGGDDS DGQMPSD FSETGAGK	K	T	I	G	K	H	1
TIPAWATL EKEKKVKK' LSASQLAR	K	T	I	A	R	A	4
TIQFVDWC IATIKTKRTI DWCPTGFI	R	T	I	F	K	V	0
TITLEVEPS FVKTLTGK' SDTIENVK	K	T	I	V	K	A	0
TKYEHELAI RLAADDFR YEHELALR	R	T	K	L	R	Q	1
TKYETELNI RLAADDFR YETELNLR	R	T	K	L	R	M	0
TLDNDIML KHPKFKKK DNDIMLIK	K	T	L	I	K	L	0
TLEVVSPTS HICASPEEK YQSPTDEK	K	T	L	E	K	S	1
TLIEAGLPC VTHTEHYK IEAGLPQK	K	T	L	Q	K	V	1
TLLDIDNTF DLTVGNNI LLDIDNTR	K	T	L	T	R	M	0
TLLEGEESF DLEIATYRT LLEGEESR	R	T	L	S	R	M	0
TLMGMSAEK		T	L	E	K		1
TLNDMRQ APGKDLTK EYEQLIAK	K	T	L	A	K	N	1
TLNPVFNE FETKVHRK FNEQFTFK'	K	T	L	F	K	V	0
TLTLVDTG IIPNPQERT DTGIGMTK	R	T	L	T	K	A	0
TLVMAIYD PYQELGGK MAIYDFDR	K	T	L	D	R	F	1

TLVMAVYI PYSELGGK MAVYDFD	K	T	L	D	R	F	1
TMQALEIE SEISELRRT LQSQLSMK	R	T	M	M	K	A	1
TMQNLEIE SEISELRRT LQSQLSMK	R	T	M	M	K	A	0
TMQNTSD QLVAAVVF TSDLDTAR	R	T	M	A	R	C	1
TMSTSDPA QEKACSLK DPAEVLIK	K	T	M	I	K	N	1
TNAENEFV YEDEINKR' ENFVTIKK	R	T	N	I	K	K	1
TNAENEFV YEDEINKR' NEFVTIKK	R	T	N	K	K	D	1
TNQELQEI LIEIICSRTN QELQEINR'	R	T	N	N	R	V	0
TNSTFNQV LYRFLARRT TFNQVVLK	R	T	N	L	K	R	0
TPALVFEH' IVKDPVSR' HVNNTDF	R	T	P	F	K	Q	1
TPEEGGY S EITEKTRT YSYEISEKT	R	T	P	E	K	T	0
TPEVSGYT' EISEKTRT VSGYTYEK'	R	T	P	E	K	T	0
TPIAAGHP' MGLKGPLI PSMNLLR	K	T	P	L	R	K	2
TPIGSFLGS VVIVSAIRT LASQPATK	R	T	P	T	K	L	2
TPIVGQPSI GEAFHVG' SIPGGPVRI	K	T	P	V	R	L	0
TPQASTYS' ETMEKITK' YSYETSDR	K	T	P	D	R	C	1
TPSPPEPEF KTSNSVEK' EPAGTAQK	K	T	P	Q	K	N	2
TPVLLMLG IKYIPQVKT LMLGQEDI	K	T	P	D	R	R	0
TQDENPV' PQKSQHG' NPVVHFFK	R	T	Q	F	K	N	0
TQSIYDDK QEDIEMTK TQSIYDDKI	K	T	Q	D	K	N	0
TQSIYDDKI QEDIEMTK IYDDKNHR	K	T	Q	H	R	E	0
TQYELIAQ' DSIIAVRT QYELIAQR'	R	T	Q	Q	R	S	1
TREGNDLY VFAGVGEF ESGVINLKI	R	T	R	L	K	D	0
TRHDEYLE' LVPGTPTR' DEYLEVTK	R	T	R	T	K	A	0
TRLEQEIAT YQILLDVKT EQEIATYRF	K	T	R	Y	R	R	1
TRLEQEIAT YQILLDVKT QEIATYRRI	K	T	R	R	R	L	1
TSASIGSLC QSIAFPSKT GSLCADAR	K	T	S	A	R	M	3
TSDVETMS EDFGPEKK SALALDERI	K	T	S	E	R	K	2
TSFTSVSR AITPSVSRT TSFTSVSRS	R	T	S	S	R	S	0
TSGPPVSEI AAGGAKRI PVSELITKA	K	T	S	T	K	A	0
TSIAIDTIIN IGDRQTGK IDTIINQKR	K	T	S	Q	K	R	1
TSQNSELN LDGLTAER' QDLVEDYK	R	T	S	Y	K	K	0
TSQNSELN LDGLTAER' DLVEDYKK	R	T	S	K	K	K	0
TSVNVVGI DWLLDRM GIVYHLSKS	R	T	S	S	K	S	1
TTAENEFV YEDEINKR' ENFVMLK	R	T	T	L	K	K	1
TTAENEFV YEDEINKR' NEFVMLK	R	T	T	K	K	D	1
TTASTQMI LKQGALSR QMNVQSS	R	T	T	S	R	S	1
TTEAAATA KVIKKEGK' IAASGPVKI	K	T	T	V	K	E	13
TTGIVETH' DILRTRVKI VETHFTFKI	K	T	T	F	K	N	0
TTGIVMDS LSLYASGR' ALPHAILRL	R	T	T	L	R	L	2
TTHFVEGG PRGGMCK NREDQINR	K	T	T	N	R	L	1
TTHYGSLP' SGKDSHTR HYGSLPQK	R	T	T	Q	K	S	0
TTLQVDTL LLNDRFRK' NTELAAER	K	T	T	E	R	S	2
TTPSYVAF' IANDQGNI VAFDTER	R	T	T	E	R	L	1
TVDNFVAL LFGKTVPK' VALATGEK	K	T	V	E	K	G	2
TVEVPEDE EKPKPNGR' VPEDEVVR	R	T	V	V	R	N	0
TVLIMELIN FGGAGVG' ELINNVAK	K	T	V	A	K	A	1
TVMENFV' KATEEQLK' NFVAFVDK	K	T	V	D	K	C	1
TVNDLEDS IRLNWDDF' QQWTYEQ	R	T	V	Q	R	K	0
TVSASSTGI SPSHDRSR' SSTGDLPK'	R	T	V	P	K	T	1

TVSLGAGA NEHQLSLR NYEGSPIK	R	T	V	I	K	V	4
TVTNAVVT IAEAYLGKI AYFNDSQF	K	T	V	Q	R	Q	2
TYATAEPFI ASVVALTKE AEPFIDAK	K	T	Y	A	K	Y	3
VADISGDT KKEVPIHR DISGDTQK	R	V	A	Q	K	A	1
VAEIPFNST LMRERNKI IPFNSTNKY	K	V	A	N	K	Y	1
VALVYGQML NLKDATSK MNEPPGA	K	V	A	A	R	A	2
VAPDEHPI HTFYNELR TEAPLNPKI	R	V	A	P	K	I	2
VAPEEHPV HTFYNELR TEAPLNPK	R	V	A	P	K	A	2
VAPPGLTC LKPTYQDR TQIPQIQKI	R	V	A	Q	K	T	1
VATVSLPR SPATLNSR VATVSLPR	R	V	A	P	R	S	1
VAVLGASC TSAQNNAI QPLSLLKN	K	V	A	L	K	N	2
VDALMDEI NKVELEAK MDEINFM	K	V	D	M	K	M	1
VDEVPDGA GYPHWPA AVKPPTNK	R	V	D	N	K	L	1
VDLLNQEII KVELQSK NQEIEFLK	K	V	D	L	K	V	0
VDNDENEI ADKDYHFK NEHQLSLR	K	V	D	L	R	T	0
VDNSSLTG IISAHGCKV GESEPQTR	K	V	D	T	R	S	0
VDSILLTHI KLIRHLDR GINSMLQF	R	V	D	Q	R	K	0
VDTLTGEV SKVDLESR TGEVNFLK	R	V	D	L	K	Y	0
VEIIANDQI VGVFQHG IANDQGNF	K	V	E	N	R	T	1
VESTSVGSI HFESSTVR SISPGGAKI	R	V	E	A	K	L	1
VETGILRPC IGTVPVGR VNITTEVK	R	V	E	V	K	S	1
VETGVLKP IGTVPVGR VNVTTEVK	R	V	E	V	K	S	1
VFDEFKPL DPHECYAK EEPQNLIK	K	V	F	I	K	Q	0
VFLLPDKK GTSDPYVK VLLPDKKI	K	V	F	K	K	K	0
VFVGYNST GKNDAI GK NSTGAELR	K	V	F	L	R	H	1
VGEGFEET EVSKKTSK GEAVISTKI	K	V	G	T	K	K	1
VGENADSC KYIKSHYK ENADSQIK	K	V	G	I	K	L	1
VGGTSDVE SDGVAVLK SDVEVNEK	K	V	G	E	K	K	0
VGINYQPP DWCP TGF VPGGDLAK	K	V	G	A	K	V	1
VGVNFGFI _____ VGVNFGFI	K	V	G	G	R	I	0
VGVVGYGI TLPQVPYK VGVVGYGI	K	V	G	G	R	L	0
VHIDIGADI FSPLNPIRV IDIGADGR	R	V	H	G	R	A	1
VHVFYIDYI EKVESPAK FYIDYGNRI	K	V	H	N	R	E	0
VIGPGYPIR CSYAGQFR IGPYPIRA	R	V	I	I	R	A	0
VIHDFNGI NCLAPLAK HAITATQK	K	V	I	Q	K	T	2
VIISAPSAD HLKGGAKF VMGVNHE	R	V	I	E	K	Y	3
VIKDFMIQ YKNSKFHR IQGGDFTR	R	V	I	T	R	G	0
VIMVTGDI KCRSAGIK GDHPITAK	K	V	I	A	K	A	1
VIQYLAHV GKTENTKK AHVASSHK	K	V	I	H	K	G	2
VITEYLNAC RKEKQFQK LNAQESAK	K	V	I	A	K	S	2
VITNANEN NQVIRFEK ANENYEPR	K	V	I	P	R	N	1
VKLLLQVQ TAVAPIER LQVQHASK	R	V	K	S	K	Q	1
VLDDGELL KWGDPVT ELLVQQTK	R	V	L	T	K	N	0
VLDELTLAF ADVNGLRF LDELTLART	R	V	L	A	R	T	1
VLDELTLTK ADINGLRR LDELTLTKA	R	V	L	T	K	A	0
VLDGAPII EGLVRGQK VGPETLGR	K	V	L	G	R	I	1
VLFPGNST NPAEKIRV NILEGLEKL	R	V	L	E	K	L	0
VLNNMEIC GMAFTFLK LYDEEGAK	K	V	L	A	K	I	1
VLNQQLTI MGTPYLQI QQLTNHIR	K	V	L	I	R	D	0
VLQETILVE PQPLSTEK ETILVEERH	K	V	L	E	R	H	0

VLQGLEIEL SEVTELRRI LQSQLSMK	R	V	L	M	K	A	0
VLSIGDGI V DLEETGR SIGDGIAR	R	V	L	A	R	V	1
VLTPELYAE SHNNHMA PELYAELR	K	V	L	L	R	A	1
VLTVINQTI VVRKSIAR TVINQQTQK	R	V	L	Q	K	E	0
VLVAPPSEI QIQTVTKK SEEANTTK	K	V	L	T	K	A	2
VLVLDDTN GYCRRDIR LDDTNHEF	R	V	L	E	R	E	0
VLVVDQLS VKKKGEWI VVDQLSMI	K	V	L	M	R	M	0
VLYDAEISC NQEIEFLK ILSMDNSR	K	V	L	S	R	N	1
VMQVLNA KDKQFVAI NADAI VVK	K	V	M	V	K	L	2
VNIHGGAI MLEIDPQK PIGMSGAF	K	V	N	A	R	I	2
VNQIGSVT SCNCLLLK TESLQACKI	K	V	N	C	K	L	1
VNTLIRPDI LYDIDVAI LIRPDGEKI	K	V	N	E	K	K	0
VPEVTESH DSSSFSSK VTESHTTRI	K	V	P	T	R	D	0
VPMNTVD HDIIGEFKV GHVTEEWI	K	V	P	W	R	D	0
VPMNTVD HDIIGEVK GQPIEEWF	K	V	P	W	R	D	0
VPQVSTPT LIVRYTRKV PTLVEVSR	K	V	P	S	R	S	0
VPSAPGQE PPEMTGQ ESPVPDTK	R	V	P	T	K	S	1
VPTPNVSV KLTGMAFF SVVDLTCR	R	V	P	C	R	L	0
VPYQELGC FNETFTFK PYQELGGK	K	V	P	G	K	T	0
VPYSELGG FNEQFTFK PYSELGGK	K	V	P	G	K	T	0
VQALEEAN RLASYLDK ANNDLENH	K	V	Q	N	K	I	2
VQISQLHQ GDRMQET QLHQEIQR	K	V	Q	Q	R	L	0
VQVEYKGE VNDAGRPI VEYKGETK	K	V	Q	T	K	S	0
VQVVVTVI VPFEQIQK VTVLDYDK	K	V	Q	D	K	I	0
VQVVVTVI IPFEQIQK LDYDKLGK	K	V	Q	G	K	N	0
VRTESSEAI EKPSKPER SEALKAEKI	R	V	R	E	K	R	2
VSAADSTC PEAMLQSF DGGTPMV	R	V	S	V	K	D	2
VSEYVPEIV LPPDVLTR EIVNFVQKI	R	V	S	Q	K	I	0
VSLAGACG GGGGGFG GVGGYGSF	R	V	S	S	R	S	2
VTMQNLN GLLSGNEK TMQNLND	K	V	T	D	R	L	0
VTMQNLN GLLSGNEK ASYLDKVR	K	V	T	V	R	A	1
VTSLVVDI FLYDWYTK LVVDIVPR	K	V	T	P	R	Q	0
VTTLPGHIC LEAMLRPK VYVQNVVI	K	V	T	V	K	L	1
VVDALGN VGEELLGR LGNAIDGK	R	V	V	G	K	G	2
VVDLMAYI NEYGYSNR LMAYMAS	R	V	V	S	K	E	2
VVDLMAYI NEYGYSNR MAYMASK	R	V	V	K	E	-	2
VVFDSVQF CWSADSQ VVFDSVQF	R	V	V	Q	R	S	0
VVLAYEPV DNVKDWS VWAIGTGI	K	V	V	G	K	T	2
VVNGPEILI MLNAREPI NGPEILNK	K	V	V	N	K	Y	0
VVSALPIQI EDYNSTIR HQDWMSI	R	V	V	G	K	E	1
VVSNTIEPL IQAEPLYR EPLTLFHKI	R	V	V	H	K	M	0
VVSSVLQF EEILSMK QFGNISFKI	K	V	V	F	K	K	0
VVTDDET FNVQMEP TDETELARI	K	V	V	A	R	Q	1
VYGTGSLA ERELKPAR GSLALYEK	R	V	Y	E	K	A	1
WELLQQVI QNQVLQT QQVDTSTF	K	W	E	T	R	T	0
WGEAGAE ERDPTNIK GVFTTMEK	K	W	G	E	K	A	2
WHVVASM AYDTRTDR VVASMSTF	R	W	H	T	R	R	1
WLAESPVC QKGLEVER EEEDKLTR	R	W	L	T	R	S	1
WMNNLLI EYLQFAFR LPLRCTIRL	R	W	M	I	R	L	0
WTLLQEQI QNKVLETK LLQEQGTK	K	W	T	T	K	T	0

YALYDATY MLPDKDCI YDATYETKI	R	Y	A	T	K	E	2
YDDYSSSR PSYGGSSR YDDYSSSR	R	Y	D	S	R	D	0
YEDEINKR LVEDYKKK YEDEINKR	K	Y	E	K	R	T	0
YEELQITAC AESLYQSK ELQITAGRI	K	Y	E	G	R	H	1
YEELQQTAE SWYQTI ELQQTAGF	K	Y	E	G	R	H	1
YEELQVTA AESWYQTI ELQVTAGR	K	Y	E	G	R	H	1
YEELQVTV AEALYHSK ELQVTVGR	K	Y	E	G	R	H	0
YEILTPNAII VFQEFRQR LTPNAIPKC	R	Y	E	P	K	G	1
YENEVALR AADDFRLK YENEVALR	K	Y	E	L	R	Q	1
YFPTQALN GNLANVIR QALNFAFK	R	Y	F	F	K	D	2
YGQQGSG SGSSQSSR GSGQSPSR	R	Y	G	S	R	G	0
YICDNQDT DDRADLAI NQDTISSKI	K	Y	I	S	K	L	0
YIDQEELNI KTKKIKEY IDQEELNK	K	Y	I	N	K	T	0
YIMLNPSSI ENIQGSIKY IMLNPSSRI	K	Y	I	S	R	I	0
YITPDQLAI KSPDDPSR DQLADLYK	R	Y	I	Y	K	S	1
YLAEVAAG KMKGDYI VAAGDDKI	R	Y	L	K	K	G	3
YLATASTM KRPSQRSK ASTMDHA	K	Y	L	A	R	H	3
YLDFAIIE VLSMDNN SSIITEVRAI	R	Y	L	V	R	A	0
YLDGLTAEI GYIDSLKRY LDGLTAER	R	Y	L	E	R	T	1
YLGLLAMS EDSQNLK LGLLAMSK	K	Y	L	S	K	I	1
YLPPELMAE VKMEPENI LPELMAEK	K	Y	L	E	K	D	1
YLTVAAIIFR ACDPRHGI LTVAAIIFR	R	Y	L	F	R	G	2
YLTVAAVFI ACDPRHGI LTVAAVFI	R	Y	L	F	R	G	2
YLTVATVFI ACDPRHGI LTVATVFR	R	Y	L	F	R	G	1
YNILGTNTI HAAENPGI GTNTIMDK	K	Y	N	D	K	M	0
YNVLGAET AKDNPERF ETVLTQMF	R	Y	N	M	R	M	1
YPIEHGIIIT KRGILTLKY TNWDDMI	K	Y	P	E	K	I	0
YQLSIHETE IPFNSTNK TEDPNDNF	K	Y	Q	N	R	Y	0
YSDMIVAA KKSTDHPK VAAIQAEK	K	Y	S	E	K	N	3
YSVDIPLDK ESCVLGFR SVDIPLDKI	R	Y	S	D	K	T	0
YVGESEAN NGPEILNK GESEANIRI	K	Y	V	I	R	K	1
YVNWIQQ GVYTKVCK IQQTIAAN	K	Y	V	A	N	-	2
YYVTIIDAP LWKFETSK IIDAPGHRI	K	Y	Y	H	R	D	1

R Count	N Count	D Count	C Count	Q Count	E Count	G Count	H Count	I Count	L Count
0	1	1	0	1	2	1	0	0	1
1	0	1	0	0	2	4	0	0	2
0	0	0	0	1	3	3	0	0	1
0	0	0	0	2	3	1	0	0	0
1	0	0	0	2	3	1	0	0	0
0	0	0	0	0	0	0	0	1	0
0	1	2	0	0	1	2	0	2	0
0	1	0	0	1	0	0	0	1	1
1	2	1	0	1	2	0	0	0	0
1	0	0	0	0	2	2	0	1	2
0	0	1	0	0	0	1	0	1	0
0	0	1	0	0	0	1	0	0	0
0	0	1	0	0	1	0	0	0	0
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0	0	0	0	1	2	0	0	0	1
1	0	0	0	2	4	1	0	1	2
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0	0	0	0	0	0	6	0	2	1
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0	2	0	0	0	3	1	0	0	3
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1	1	1	0	0	0	2	0	1	2
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0	3	2	0	0	2	3	0	1	1
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0	0	3	1	0	0	0	1	0	0
0	0	3	0	0	0	0	0	0	1
0	0	2	0	1	1	0	1	0	0
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0	0	2	0	0	1	0	0	2	1
0	1	1	0	5	5	1	1	3	0

1	1	2	0	3	3	2	1	4	0
0	0	2	0	1	4	0	0	2	2
0	0	3	0	0	0	1	0	2	1
0	1	1	0	0	0	1	0	0	2
1	0	2	0	0	0	1	0	0	2
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0	0	1	0	0	1	0	1	0	2
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K Count	M Count	F Count	P Count	S Count	T Count	W Count	Y Count	V Count	U Count
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0	0	0	0	0	1	1	1	1	0
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Length	Missed cle	Mass	Proteins	Leading ra	Start posit	End positi	Unique (G	Unique (P	Charges
14	0	1503,721	sp P97807	sp P97807	99	112	yes	yes	2
17	0	1616,779	sp Q5U3K	sp Q5U3K	699	715	yes	yes	2
19	0	1943,911	sp P14873	sp P14873	1049	1067	yes	yes	2
14	0	1491,721	sp P1633C	sp P1633C	261	274	yes	yes	2
15	1	1647,822	sp P1633C	sp P1633C	261	275	yes	yes	2;3
13	0	1040,598	sp Q9CR5	sp Q9CR5	148	160	yes	yes	2
17	1	1893,926	tr G3UXT7	tr G3UXT7	40	56	yes	no	2
10	0	1073,59	sp Q0225	sp Q0225	162	171	yes	yes	2
19	0	1951,887	sp Q6P54	sp Q6P54	268	286	yes	yes	2
18	0	1803,937	sp P17182	sp P17182	33	50	no	no	2
11	0	1218,592	sp P51881	sp P51881	189	199	yes	yes	2
11	0	1204,576	sp P48962	sp P48962	189	199	yes	yes	2
8	0	929,4131	sp P1633C	sp P1633C	94	101	yes	yes	1;2
9	1	1085,514	sp P1633C	sp P1633C	94	102	yes	yes	2
16	0	1519,755	tr D3YYN7	tr D3YYN7	725	740	yes	no	2
16	0	1489,745	sp Q6PIC6	sp Q6PIC6	718	733	yes	no	2
18	0	2095,04	CON__P13	CON__P13	267	284	yes	yes	2
19	1	2223,135	CON__P13	CON__P13	267	285	yes	yes	2;3
12	0	1241,698	sp P11495	sp P11495	96	107	yes	no	2
10	0	1125,468	sp Q6187	sp Q6187	1511	1520	yes	no	2
12	0	1406,704	CON__P02	CON__P02	288	299	no	no	2
10	0	1124,535	CON__P04	CON__P04	367	376	yes	yes	2
20	1	2285,118	CON__P04	CON__P04	367	386	yes	yes	2;3
10	0	1211,546	sp Q8BGZ	CON__P02	350	359	no	no	2
8	0	921,4808	CON__P02	CON__P02	249	256	yes	yes	2
11	0	1144,609	sp P4646C	sp P4646C	188	198	yes	no	2
8	0	956,4604	tr A0A0R4	tr A0A0R4	172	179	yes	no	2
17	0	2070,924	CON__P13	CON__P13	423	439	yes	yes	2;3
20	0	2329,011	sp P68368	sp P05213	403	422	no	no	2;3
16	0	1453,698	sp P08245	sp P08245	242	257	yes	yes	2
19	0	2079,943	tr Q5SVI9	sp P11798	228	246	no	no	2
13	0	1226,662	REV__tr D6RI90	D6RI90_MOUS			yes	no	2
10	0	975,441	sp P6326C	sp P6326C	19	28	no	no	2
9	1	969,5495	sp Q8QZT	sp Q8QZT	76	84	yes	yes	2
27	2	2856,444	sp Q8QZT	sp Q8QZT	76	102	yes	yes	3
10	0	1031,525	tr D3YYN7	tr D3YYN7	433	442	yes	no	2
13	0	1440,736	sp P1633C	sp P1633C	204	216	yes	yes	2;3
11	0	1222,631	sp Q8VDD	sp Q6187	772	782	no	no	2
20	0	2191,026	sp P17182	sp P17182	234	253	yes	no	2
14	0	1405,674	sp P5648C	sp P5648C	226	239	yes	yes	2
19	0	1987,026	sp P5648C	sp P5648C	388	406	yes	yes	2
8	0	1049,512	sp Q8VHC	sp Q8VHC	267	274	yes	no	2
14	0	1614,785	sp P61264	sp P61264	94	107	yes	yes	2
9	0	1126,541	sp O5477	sp O5477	643	651	yes	yes	2
9	0	1018,512	sp P1633C	sp P1633C	391	399	yes	yes	2
17	0	1446,768	CON__P02	CON__P02	534	550	no	no	2
10	0	1054,614	sp P14873	sp P14873	55	64	yes	yes	2
15	0	1614,829	sp Q7TMM	sp Q7TMM	63	77	no	no	2;3
13	0	1260,675	sp Q8BP6	sp Q8BP6	81	93	yes	yes	2

11	0	1106,561	sp P15864	sp P43274	65	75	no	no	2
15	1	1577,78	sp P15864	sp P43274	65	79	no	no	2
11	0	1094,645	sp Q9QYR	sp Q9QYR	2175	2185	yes	no	2
11	0	1208,648	sp O5477	sp O5477	360	370	yes	yes	2
15	1	1617,767	tr A0A0R4	tr A0A0R4	180	194	yes	no	3
12	0	1300,651	CON__P08	CON__P08	137	148	no	no	2
12	0	1380,641	CON__P13	CON__P13	166	177	yes	no	2
10	0	1202,63	sp Q6187	sp Q6187	753	762	no	no	2
10	0	1231,587	sp Q6187	sp Q6187	1536	1545	yes	no	2
13	0	1346,731	sp Q9D8N	sp Q9D8N	18	30	yes	yes	2
14	0	1585,875	tr E9PZW	tr E9PZW	784	797	yes	no	2
14	0	1410,802	sp Q0225	sp Q0225	178	191	yes	yes	2
13	0	1368,773	tr A0A2U	tr A0A2U	570	582	yes	no	2
14	0	1662,819	tr H3BKM	tr H3BKM	722	735	yes	no	2
15	0	1690,86	sp P68372	sp P68372	283	297	no	no	2
15	0	1706,855	sp Q7TMM	sp Q7TMM	283	297	no	no	2
15	0	1658,888	sp P99024	sp P99024	283	297	yes	yes	2
12	0	1317,606	tr Q29ZQ	tr Q29ZQ	43	54	yes	no	2
27	0	3037,412	CON__P02	CON__P02	300	326	no	no	3
16	0	1919,843	sp Q6164	sp Q6164	389	404	yes	no	2
14	1	1582,73	sp P18872	sp P18872	87	100	yes	no	3
11	0	1184,586	sp Q8BX7	sp Q8BX7	2062	2072	yes	yes	2
9	0	1062,509	tr F7BNZ5	tr F7BNZ5	209	217	yes	no	2
26	1	2600,304	tr V9GXQ	tr V9GXQ	883	908	yes	no	3
31	1	2857,409	sp Q91XV	sp Q91XV	196	226	yes	yes	3
10	0	1181,587	sp P26041	sp P26041	264	273	no	no	2
10	0	1029,473	sp Q9QYR	sp Q9QYR	608	617	yes	no	2
14	0	1601,816	sp Q9QYR	sp Q9QYR	1486	1499	yes	no	3
16	0	1777,973	tr A0A075	tr A0A075	234	249	yes	no	2;3
27	0	2697,434	sp Q9QYR	sp Q9QYR	2197	2223	yes	no	2
14	0	1337,658	CON__P08	CON__P08	42	55	yes	yes	2
15	0	1424,69	CON__P02	CON__P02	42	56	yes	yes	2
11	0	1038,546	sp P47915	sp P47915	135	145	yes	yes	2
10	0	1060,515	sp P4666C	sp P4666C	152	161	yes	yes	2
10	0	1189,565	sp P26041	sp P26041	449	458	yes	yes	2
21	0	2407,213	sp Q9QYR	sp Q9QYR	2718	2738	yes	no	3
21	0	2399,136	sp P14873	sp P14873	2406	2426	yes	yes	3
9	0	1064,514	sp Q3UV1	sp Q3UV1	343	351	yes	yes	2
9	0	1092,52	CON__P13	CON__P13	344	352	yes	yes	2
9	0	1106,536	CON__P35	CON__P35	360	368	no	no	2
12	1	1479,747	sp P63017	sp P63017	300	311	yes	no	2
15	0	1556,805	sp P05202	sp P05202	108	122	yes	yes	2
14	1	1546,748	sp P14873	sp P14873	1232	1245	yes	yes	2
12	0	1197,661	sp P15864	sp P15864	35	46	yes	no	2
13	0	1402,669	CON__Q0	CON__Q0	322	334	yes	yes	2
11	0	1219,593	CON__P08	CON__P08	355	365	no	no	2
13	1	1432,716	CON__P08	CON__P08	355	367	no	no	2
19	0	2012,925	sp P14873	sp P14873	1370	1388	yes	yes	2
13	0	1445,705	tr D3YZA1	tr D3YZA1	39	51	yes	no	2
15	0	1443,768	sp Q9DD1	sp Q9DD1	11	25	yes	yes	2

17	0	1917,959	tr D3YWT:tr D3YWT:	191	207	yes	no		2
17	0	1434,731	CON__P04 CON__P04	534	550	yes	yes		2
7	0	742,4337	tr Q3U5D(tr Q3U5D(9	15	yes	no		2
18	0	1811,901	tr D3Z6W:tr D3Z6W:	60	77	yes	no		2
16	0	1528,785	sp Q9DB7 sp Q9DB7	360	375	yes	yes		2
17	0	1852,863	sp P6836€ sp P0521€	374	390	no	no	2;3	
10	0	1025,587	sp Q0326! sp Q0326!	195	204	yes	no		2
9	0	944,5444	sp P6326€ sp P6326€	29	37	no	no		2
11	1	1197,698	sp P6326€ sp P6326€	29	39	no	no		2
15	0	1714,914	sp P6836€ sp P6836€	65	79	yes	no	2;3	
15	0	1700,899	sp P0521€ sp P0521€	65	79	no	no	2;3	
15	0	1647,826	sp Q6187! sp Q6187!	19	33	yes	no		2
10	0	1027,591	sp Q9QYR sp P1487€	2396	2405	no	no		2
15	0	1600,813	sp P6837€ sp P6837€	63	77	no	no		2
12	0	1341,628	CON__P02 CON__P02	570	581	yes	yes		2
11	0	1189,646	sp Q8BX7! sp Q8BX7!	1144	1154	yes	yes		2
14	0	1531,711	sp P6825€ sp P6825€	28	41	yes	yes		2
23	0	2131,055	sp Q9QYR sp Q9QYR	1090	1112	yes	no	2;3	
16	0	1634,863	tr Q5SX46 tr Q5SX46	159	174	yes	no		2
20	1	2259,066	sp Q6164! sp Q6164!	80	99	yes	no		3
13	0	1408,586	sp D3YXK! sp D3YXK!	854	866	yes	no		2
8	0	1001,529	sp Q6244! sp Q6244!	9	16	yes	no		2
11	0	1293,635	sp Q6164! sp Q6164!	52	62	yes	no		2
11	0	1229,556	sp P1409€ sp P1409€	279	289	yes	yes		2
24	0	2738,25	sp P6836€ sp P0521€	281	304	no	no		3
9	0	991,5195	sp Q6PIC€ sp Q6PIC€	508	516	yes	no		2
9	0	1115,423	CON__P02 CON__P02	499	507	no	no		2
9	2	1156,562	tr Q3U5D(tr Q3U5D(96	104	yes	no		2
11	0	1474,553	CON__P02 CON__P02	389	399	no	no		2
10	0	1164,516	sp P4300€ sp P4300€	373	382	yes	no		2
11	1	1320,617	sp P4300€ sp P4300€	373	383	yes	no	2;3	
9	0	1108,483	CON__P13 CON__P13	335	343	yes	no		2
9	0	1095,524	CON__P08 CON__P08	303	311	yes	yes		2
13	0	1566,736	CON__P02 CON__P02	347	359	yes	yes		2
10	0	1137,524	sp P0520€ sp P0520€	171	180	yes	yes		2
12	0	1198,667	sp P6301€ sp P6301€	160	171	yes	no		2
12	0	1290,587	sp Q05D4 sp Q05D4	1040	1051	yes	yes		2
19	0	1959,917	sp P1718€ sp P1718€	203	221	yes	no		2
10	0	1133,535	sp P6280€ sp P6280€	69	78	yes	yes		2
8	0	939,441	CON__P02 CON__P02	131	138	yes	yes		2
13	0	1542,612	CON__P02 CON__P02	387	399	yes	yes		2
8	0	885,408	CON__P02 CON__P02	131	138	yes	yes		2
11	0	1317,62	CON__P34 CON__P34	229	239	yes	yes		2
13	0	1218,661	sp P51881 sp P51881	11	23	yes	yes		2
21	0	2492,167	sp Q8VDD sp Q8VDD	1302	1322	yes	no	2;3	
9	0	1023,487	sp Q8QZT sp Q8QZT	179	187	yes	yes		2
14	0	1411,579	tr D3YWT:tr D3YWT:	273	286	yes	no		2
9	0	1086,546	tr D3YYN7 tr D3YYN7	681	689	yes	no		2
11	0	1230,617	sp P4646€ sp P4646€	151	161	yes	no		2
29	0	3263,507	CON__P35 CON__P35	340	368	yes	yes	3;4	

22	0	2376,167	sp O0855: sp O0855:	190	211	yes	yes	3
14	1	1697,872	sp P14873: sp P14873:	850	863	yes	yes	2
14	2	1525,872	sp P24369: sp P24369:	191	204	yes	yes	3
15	1	1450,814	sp Q9QYR sp Q9QYR	298	312	yes	no	2
13	0	1370,723	sp P14152: sp P14152:	80	92	yes	no	2
11	0	1200,599	sp Q6187: sp Q6187:	1628	1638	yes	no	2
12	1	1523,758	sp Q9QYR sp Q9QYR	1458	1469	yes	no	3
7	0	800,4392	sp P43006: sp P43006:	304	310	yes	no	2
10	0	1245,624	sp Q0444: sp Q0444:	87	96	yes	yes	2
8	0	973,4505	CON__P02 CON__P02	37	44	yes	yes	2
9	0	1020,56	sp Q8VEK: sp Q8VEK:	603	611	yes	yes	2
12	1	1432,668	sp P46096: sp P46096:	261	272	yes	yes	2
8	0	997,479	sp P6326C sp P6326C	184	191	no	no	2
12	0	1250,687	sp P14873: sp P14873:	520	531	yes	yes	2
21	0	2214,063	sp P6326C sp P6326C	292	312	yes	no	2;3
13	0	1434,634	tr Q91VA7: tr Q91VA7:	361	373	yes	no	2
19	0	2185,161	CON__P02 CON__P02	184	202	yes	yes	2
10	0	1178,52	sp Q80XI4 sp Q80XI4	240	249	yes	yes	2
12	1	1324,746	sp P62806: sp P62806:	25	36	yes	yes	2
14	0	1603,8	CON__Q2: CON__Q2:	88	101	yes	no	2
11	0	1247,499	sp P11499: sp P11499:	613	623	yes	yes	2
12	0	1314,678	CON__P35 CON__P35	213	224	yes	yes	2
9	0	1140,476	CON__P08 CON__P08	291	299	yes	no	2
13	1	1650,8	sp Q9QYR sp Q9QYR	1658	1670	yes	no	2
14	0	1533,723	tr A0A5H1: tr A0A5H1:	63	76	yes	no	2
11	0	1197,515	sp P6326C sp P6326C	51	61	no	no	2
12	1	1353,616	sp P6326C sp P6326C	51	62	no	no	2
17	0	1876,873	tr A0A075: tr A0A075:	282	298	yes	no	2
13	1	1339,698	sp Q9QYR sp Q9QYR	1404	1416	yes	no	2
10	0	1045,54	tr A0A498: tr A0A498:	33	42	yes	no	2
13	0	1274,635	sp Q6PIC6: sp Q6PIC6:	436	448	yes	no	2
9	0	1025,449	CON__P02 CON__P13	273	281	no	no	2
9	0	998,4379	CON__P04 CON__P04	290	298	yes	yes	2
9	0	1067,496	CON__P35 CON__P35	294	302	yes	yes	2
9	0	1061,576	sp Q80XI4: sp O7017:	267	275	no	no	2
13	0	1622,78	CON__P02 CON__P02	348	360	yes	yes	2
10	0	1115,626	tr A0A075: tr A0A075:	138	147	yes	no	2
10	0	984,5604	sp P6836E: sp P6836E:	327	336	yes	no	2
10	0	1014,571	sp P05213: sp P05213:	327	336	no	no	2
18	0	2158,044	tr A0A0R4: tr A0A0R4:	546	563	yes	no	2
9	0	1140,512	CON__P04 CON__P04	464	472	no	no	2
9	0	1138,533	CON__P35 CON__P35	468	476	no	no	2
10	0	1314,609	sp Q99L45: sp Q99L45:	171	180	yes	yes	2
13	0	1383,699	sp Q9QYR sp Q9QYR	629	641	yes	no	2
16	0	1765,864	sp Q6PIC6: sp Q6PIC6:	526	541	yes	no	2
13	0	1612,76	sp Q6073: sp Q6073:	317	329	yes	yes	2
10	0	1206,613	tr Q8BRQ: tr Q8BRQ:	64	73	yes	no	2
13	0	1552,731	sp Q0326: sp Q0326:	335	347	yes	no	2
9	0	1022,442	sp P6836E: sp P05213:	97	105	no	no	2
8	0	905,4164	sp P6836E: sp P05213:	423	430	no	no	2

12	0	1368,671	tr D3YYN7tr D3YYN7	494	505	yes	no		2
17	0	1761,879	sp Q80WJ sp Q80WJ	90	106	yes	no		2
28	1	2972,44	CON__P35 CON__P35	294	321	yes	yes		3
17	0	1945,949	tr A0A338tr A0A338	70	86	yes	no		2
12	2	1500,79	sp Q8BGZ sp Q8BGZ	149	160	yes	no		2
22	1	2390,154	sp Q8QZT sp Q8QZT	81	102	yes	yes		3
17	0	1568,659	sp Q9QYR sp Q9QYR	1888	1904	yes	no		2
9	0	1030,548	sp Q78PY sp Q78PY	858	866	yes	yes		2
12	0	1313,734	sp P1012€ sp P1012€	135	146	no	no		2
24	0	2406,141	tr A0A140tr A0A140	310	333	yes	no		3
14	0	1585,795	sp Q9CR6 sp Q9CR6	183	196	yes	yes		2
23	0	2509,125	CON__P35 CON__P35	450	472	yes	yes	2;3	
9	0	1084,613	sp P0521€ sp P0521€	113	121	no	no		2
11	1	1342,746	CON__P35 CON__P35	397	407	yes	yes		2
11	0	1160,611	sp P6326€ sp P6326€	316	326	no	no		2
17	0	1840,892	sp Q922F sp Q922F	3	19	yes	yes		3
17	0	1810,882	sp P6837€ sp P6837€	3	19	no	no	2;3	
13	2	1500,797	tr F8VQC2tr F8VQC2	207	219	yes	no		2
11	1	1311,708	sp P1633€ sp P1633€	233	243	yes	yes		2
14	0	1518,68	sp Q6187€ sp Q6187€	1906	1919	yes	no		2
12	0	1274,635	sp P1149€ sp P1149€	42	53	yes	no		2
14	0	1484,772	tr E9PUC5tr E9PUC5	322	335	yes	no		2
11	0	1310,647	CON__Q2€ CON__Q2€	137	147	yes	no		2
15	0	1610,826	tr Q3U4F€ tr Q3U4F€	199	213	yes	no		2
12	0	1282,641	sp Q0475€ sp Q0475€	606	617	yes	yes		2
17	0	1995,964	CON__P13 CON__P13	346	362	yes	yes	2;3	
13	0	1452,753	sp O8893€ sp O8893€	257	269	yes	yes		2
13	0	1472,831	sp Q6433€ sp Q6433€	258	270	yes	yes		2
8	0	1053,499	sp Q9QYR sp Q9QYR	211	218	yes	no		2
14	0	1790,776	sp P1487€ sp P1487€	433	446	yes	yes		2
12	0	1327,633	sp P1487€ sp P1487€	1754	1765	yes	yes		2
19	0	2100,034	sp O5477€ sp O5477€	538	556	yes	yes		2
9	0	1115,536	sp Q9QYR sp Q9QYR	1623	1631	yes	no		2
9	0	1168,567	sp P4896€ sp P4896€	64	72	yes	yes		2
9	0	1087,57	CON__Q7€ CON__Q7€	166	174	yes	yes		2
17	0	1717,889	tr A0A338tr A0A338	249	265	yes	no		2
13	2	1354,782	sp P1487€ sp P1487€	543	555	yes	yes		3
7	0	834,4269	REV__tr Q8VG87 Q8VG87_MOI			yes	yes		2
18	0	1829,832	sp P1487€ sp P1487€	1787	1804	yes	yes		2
22	0	2537,203	sp Q9QYR sp Q9QYR	1698	1719	yes	no		3
9	0	1066,614	tr A0A0A€ tr A0A0A€	64	72	yes	no		2
25	0	2544,188	sp P1487€ sp P1487€	1805	1829	yes	yes		3
14	0	1315,626	sp Q91XV sp Q91XV	182	195	yes	yes		2
22	0	2337,16	sp Q0326€ sp Q0326€	442	463	yes	no	2;3	
13	0	1404,685	CON__P08 CON__P08	318	330	yes	yes		2
13	0	1360,683	CON__P02 CON__P02	316	328	no	no		2
12	0	1389,681	sp Q9ERD sp Q9ERD	325	336	yes	yes		2
12	0	1445,682	sp Q7TMM sp P6837€	325	336	no	no	2;3	
12	0	1391,66	sp Q9D6F sp Q9D6F	325	336	yes	yes		2
12	0	1259,563	CON__P08 CON__P08	442	453	yes	yes		2

10	0	1059,563	tr A2AKV1tr A2AKV1	103	112	yes	no		2
18	0	1904,905	sp Q8QZT sp Q8QZT	85	102	yes	yes	2;3	
9	0	1248,541	sp P14873 sp P14873	2427	2435	yes	yes		2
9	0	1154,528	CON__P13 CON__P13	452	460	no	no		2
9	0	1152,549	sp Q8BGZ CON__P02	447	455	no	no		2
10	0	1132,563	sp P4666C sp P4666C	291	300	yes	yes		2
13	0	1404,786	sp Q8QZT sp Q8QZT	228	240	yes	yes		2
7	0	826,4225	CON__P35 CON__P35	195	201	no	no	1;2	
9	1	1081,592	CON__P35 CON__P35	195	203	no	no		2
10	0	1148,583	tr Q5SQG!tr Q5SQG!	134	143	yes	no		2
21	0	2408,201	sp P6836E sp P0521E	244	264	no	no	2;3	
7	0	886,4259	sp P6836E sp P0521E	395	401	no	no		2
8	0	1065,491	CON__P35 CON__P35	243	250	yes	yes		2
17	0	1904,866	sp Q80XI4 sp Q80XI4	336	352	yes	yes		2
9	0	1025,46	tr E9PZW(tr E9PZW(929	937	yes	no		2
44	0	4091,065	CON__P35 CON__P35	129	172	yes	yes	3;4	
14	0	1654,759	sp O7017: sp O7017:	105	118	yes	no		2
10	1	1248,614	CON__P02 CON__P02	35	44	yes	yes	2;3	
7	0	905,4607	sp Q8BGZ CON__P13	183	189	no	no		2
12	0	1475,762	CON__Q14 CON__Q7F	145	156	no	no		2
12	0	1474,778	CON__P35 CON__P35	204	215	no	no	2;3	
24	1	2931,509	CON__P04 CON__P04	200	223	yes	yes		3
11	0	1310,651	sp Q8BX7(sp Q8BX7(14	24	yes	no		2
15	0	1729,806	sp Q6244(sp Q6244(28	42	yes	no		3
18	0	2022,003	sp P5648C sp P5648C	463	480	yes	yes		3
14	0	1640,86	sp Q9CQV sp Q9CQV	52	65	yes	no		2
10	0	1129,588	sp Q7TMM sp P68372	242	251	no	no		2
33	0	3284,5	sp Q9QYR sp Q9QYR	767	799	yes	no		3
13	0	1459,713	sp P5039E sp P5039E	56	68	yes	no		2
19	0	2149,909	sp O0855: sp O0855:	76	94	yes	yes		2
8	0	959,5553	CON__P02 CON__P02	427	434	yes	yes		2
14	2	1659,898	sp Q9QYR sp Q9QYR	459	472	yes	no		3
12	0	1319,563	CON__Q5I CON__Q5I	404	415	yes	yes		2
20	0	1753,694	CON__P04 CON__P04	46	65	yes	yes		2
13	0	1234,521	CON__P35 CON__P35	47	59	yes	yes		2
20	0	2032,048	sp P17182 sp P17182	307	326	yes	no		2
14	0	1434,747	sp P5648C sp P5648C	311	324	yes	yes		2
12	0	1392,704	sp P14152 sp P14152	299	310	yes	no		2
14	0	1448,799	sp P05202 sp P05202	126	139	yes	yes		2
27	0	3076,405	sp Q9ERD sp Q9ERD	20	46	yes	no		3
27	0	3101,4	sp Q7TMM sp Q7TMM	20	46	no	no	3;4	
27	0	3101,4	sp P99024 sp P99024	20	46	yes	yes		3
27	0	3115,416	sp P68372 sp P68372	20	46	no	no		4
13	0	1365,7	sp Q9QYR sp Q9QYR	1438	1450	yes	no		2
15	0	1368,736	sp P1685E sp P1685E	199	213	yes	no		2
13	0	1311,74	tr V9GWS tr V9GWS	24	36	yes	no		2
9	0	973,4465	sp Q6164: sp Q6164:	274	282	yes	no		2
11	0	1146,643	tr Q5SVI9 sp P1179E	302	312	no	no		2
16	1	1658,924	sp Q8QZT sp Q8QZT	163	178	yes	yes		2
14	0	1449,662	tr Q5SUTC tr Q5SUTC	373	386	yes	no		2

10	0	1048,515	sp Q80WJ	sp Q80WJ	264	273	yes	no		2
14	0	1419,652	tr Q8BQ4	tr G3UXT7	26	39	no	no		2
10	0	1177,609	sp P14152	sp P14152	221	230	yes	no		2
11	0	1281,602	tr Q91VA7	tr Q91VA7	122	132	yes	no		2
14	0	1485,714	tr A0A2I3I	tr A0A2I3I	50	63	yes	no		2
17	0	2027,984	tr E9PZW	tr E9PZW	1827	1843	yes	no		2
15	0	1694,758	sp O8856	sp O8856	154	168	yes	no		2
14	0	1631,758	tr A2BI12	tr A2BI12	76	89	yes	no		2
14	0	1253,6	CON__P35	CON__P35	21	34	no	no		2
31	0	2382,945	CON__P04	CON__P04	519	549	yes	yes	2;3	
15	0	1376,622	sp O8856	sp O8856	214	228	yes	yes		2
32	0	2704,154	CON__P35	CON__P35	64	95	yes	yes	2;3	
13	0	1154,532	sp Q9JIS5	sp Q9JIS5	124	136	yes	yes		2
10	0	1012,436	sp O8856	sp O8856	204	213	yes	yes		2
18	1	1864,042	sp Q6073	sp Q6073	90	107	yes	yes		2
23	0	1740,741	CON__P35	CON__P35	556	578	yes	yes		2
40	0	3222,274	CON__P35	CON__P35	580	619	yes	yes	3;4	
23	0	1790,72	CON__P35	CON__P35	491	513	yes	yes	2;3	
15	0	1196,542	CON__P35	CON__P35	587	601	yes	yes		2
13	0	1255,616	sp P1633C	sp P1633C	356	368	yes	yes		2
20	0	1587,676	CON__P35	CON__P35	610	629	yes	yes		2
12	0	1294,688	sp P4646C	sp P4646C	416	427	yes	yes		2
18	0	1957,975	sp Q7TMM	sp P68372	104	121	no	no	2;3	
19	1	2086,07	sp Q7TMM	sp P68372	104	122	no	no		3
15	0	1637,783	sp Q9DD1	sp Q9DD1	26	40	yes	yes		2
12	0	1376,676	sp Q8BFZ	sp Q8BFZ	274	285	yes	yes		2
14	1	1437,842	sp Q0326	sp Q0326	403	416	yes	no		2
10	0	1064,634	tr A0A0J9	tr A0A0J9	114	123	no	no		2
15	0	1600,867	tr A0A3B2	tr A0A3B2	462	476	yes	no		2
18	0	2039,98	tr A0A2I3I	tr A0A2I3I	140	157	yes	no		2
14	2	1633,82	sp Q8QZT	sp Q8QZT	241	254	yes	yes		3
12	0	1187,579	tr A2AKV1	tr A2AKV1	77	88	yes	no		2
11	0	1216,62	tr H3BKM	tr H3BKM	698	708	yes	no		2
11	0	1017,546	sp P60202	sp P60202	112	122	yes	yes		2
16	1	1738,933	sp P48962	sp P48962	281	296	no	no	2;3	
10	0	1180,543	CON__P02	CON__P02	241	250	yes	yes		2
20	0	2103,031	sp Q0326	sp Q0326	104	123	yes	no		2
13	0	1405,709	sp P17182	sp P17182	16	28	no	no		2
10	0	1044,502	tr D3Z6W	tr D3Z6W	202	211	yes	no		2
9	0	1005,488	sp Q6164	sp Q6164	71	79	yes	no		2
9	0	930,4658	tr Q9DAY	tr Q9DAY	238	246	yes	no		2
16	0	1725,898	sp Q0475	sp Q0475	226	241	yes	yes		2
19	0	1927,841	CON__Q8	CON__Q8	572	590	yes	yes	3;4	
16	0	1583,708	CON__Q8	CON__Q8	1038	1053	yes	no	2;3;4	
21	0	2086,959	CON__P08	CON__P08	264	284	yes	no		2
21	0	2084,98	CON__P02	CON__P02	262	282	yes	no		2
21	0	2113,011	CON__Q0	CON__Q0	231	251	no	no		2
11	0	1139,582	tr Z4YKA3	tr Z4YKA3	210	220	yes	no		2
15	0	1266,545	CON__P08	CON__P08	16	30	no	no		2
16	0	1303,612	sp P3165C	sp P3165C	20	35	yes	yes		2

17	0	1412,593	CON__P02	CON__P02	43	59	no	no		2
19	0	1706,765	CON__P13	CON__P13	41	59	yes	yes		2
11	0	1083,629	sp O0855:	sp O0855:	441	451	yes	yes		2
27	0	2330,943	CON__P13	CON__P13	60	86	yes	yes	2;3	
20	0	1739,698	CON__P35	CON__P35	531	550	yes	yes		2
10	0	1045,552	sp Q8VEM	sp Q8VEM	291	300	yes	no		2
21	0	1963,924	sp Q0444:	sp Q0444:	321	341	yes	yes		2
17	0	1549,722	tr E9Q740	tr E9Q740	540	556	yes	no		2
9	0	898,5236	tr A0A1B0	tr A0A1B0	106	114	yes	no		2
8	0	928,4953	sp Q8VEM	sp Q8VEM	214	221	yes	no		2
12	0	1255,604	sp Q9QYR	sp Q9QYR	1586	1597	yes	no		2
9	0	836,4141	sp P10922	sp P10922	86	94	yes	yes		2
18	0	1828,917	sp Q6PIC6	sp Q6PIC6	620	637	no	no	2;3	
17	0	1635,883	tr A0A1L1	tr A0A1L1	208	224	yes	no		2
11	0	1180,62	sp P17182	sp P17182	61	71	yes	no	2;3	
14	0	1512,778	sp P11499	sp P11499	379	392	yes	no		2
10	1	1148,608	sp Q0326:	sp Q0326:	494	503	yes	no		2
10	0	1131,52	sp P6326C	sp P6326C	197	206	yes	no		2
11	0	1286,687	sp Q0326:	sp Q0326:	306	316	yes	no		2
10	0	1123,635	tr Q8BRQ:	tr Q8BRQ:	249	258	yes	no		2
8	0	957,492	sp P4609E	sp P4609E	237	244	yes	yes		2
16	0	1899,894	sp Q6187:	sp Q6187:	148	163	yes	no		3
11	0	1258,656	sp Q05D4	sp Q05D4	1171	1181	yes	yes		2
9	0	1028,493	sp P1633C	sp P1633C	224	232	yes	yes		2
11	1	1285,63	sp P1633C	sp P1633C	224	234	yes	yes		3
9	0	1145,547	sp O5478:	sp O5478:	533	541	yes	no		2
17	0	1786,849	sp Q80XI4	sp O7017:	389	405	no	no	2;3	
9	1	1025,551	CON__P35	CON__P35	391	399	no	no		3
12	1	1372,674	sp Q6187:	sp Q6187:	43	54	yes	no		3
16	0	1319,576	CON__P35	CON__P35	46	61	yes	yes	2;3	
26	0	2476,014	CON__Q8E	CON__Q8E	1365	1390	yes	no		4
16	0	1836,958	CON__P35	CON__P35	375	390	yes	yes	2;3	
17	1	1965,053	CON__P35	CON__P35	375	391	yes	yes		3
11	1	1336,674	CON__P02	CON__P02	80	90	yes	yes		3
11	0	1245,635	tr A0A2R8	tr A0A2R8	81	91	yes	no		2
15	0	1781,942	sp P11499	sp P11499	625	639	yes	yes		3
10	0	1095,604	tr A2AKV1	tr A2AKV1	67	76	yes	no		2
15	0	1832,863	sp Q6164:	sp Q6164:	252	266	yes	no		3
11	0	1200,581	tr E9Q740	tr E9Q740	444	454	yes	no		2
12	0	1291,688	sp Q05D4	sp Q05D4	424	435	yes	yes		2
12	0	1354,692	sp Q0475:	sp Q0475:	578	589	yes	no		2
8	0	993,492	sp P47911	sp P47911	219	226	yes	yes		2
11	0	1304,709	CON__P02	CON__P02	402	412	yes	yes	2;3	
12	0	1390,612	sp P1487E	sp P1487E	2193	2204	yes	yes	2;3	
10	0	1240,656	sp P1487E	sp P1487E	204	213	yes	yes		2
10	0	1205,688	tr Q91VA:	tr Q91VA:	154	163	yes	no		2
12	0	1367,625	sp Q0225:	sp Q0225:	466	477	yes	yes		3
11	0	1282,703	CON__P02	CON__P02	361	371	yes	yes		2
9	0	981,5145	tr Q91VA:	tr Q91VA:	308	316	yes	no		2
13	0	1525,8	tr Q7M6V	tr Q7M6V	174	186	yes	no		2

15	0	1758,938	CON__P02	CON__P02	8	22	yes	yes		3
11	0	1170,564	sp P6326C	sp P6326C	40	50	no	no	2;3	
8	0	1023,535	sp Q6187!	sp Q6187!	882	889	yes	no		2
12	1	1338,7	tr A0A498	tr A0A498	31	42	yes	no	2;3	
14	0	1362,675	CON__P20	CON__P20	2019	2032	yes	no		3
22	0	2242,032	sp Q9QYR	sp Q9QYR	1288	1309	yes	no		3
19	1	2077,955	sp P1487!	sp P1487!	966	984	yes	yes		4
21	0	2118,997	CON__P12	CON__P12	313	333	yes	yes	3;4	
10	0	1153,609	CON__P12	CON__P12	58	67	yes	yes		2
16	0	1661,769	tr A0A3B2	tr A0A3B2	626	641	yes	no		4
10	0	1225,566	sp P4609!	sp P4609!	389	398	no	no	2;3	
14	0	1473,682	sp P2436!	sp P2436!	132	145	yes	yes		3
24	0	2442,284	sp Q8QZT	sp Q8QZT	309	332	yes	yes	2;3	
12	0	1269,729	sp P0520!	sp P0520!	326	337	yes	yes		2
10	0	1215,592	sp Q9D6R	sp Q9D6R	179	188	yes	no		2
8	0	987,4873	sp P1487!	sp P1487!	328	335	yes	yes		2
11	0	1185,672	sp P1414!	sp P1414!	189	199	yes	no		2
13	0	1529,757	sp Q8VDD	sp Q8VDD	1816	1828	yes	yes		2
10	0	1063,603	sp Q8CEG	sp Q8CEG	69	78	yes	yes		3
12	0	1157,666	sp Q6PIC!	sp Q6PIC!	260	271	yes	no		2
18	1	1970,857	sp Q6066!	sp Q6066!	68	85	yes	yes		4
10	0	1187,64	sp O8856!	sp O8856!	138	147	yes	no		2
8	0	903,4549	sp P1718!	sp P1718!	413	420	yes	no		2
10	1	1270,713	tr F7C528	tr F7C528	1258	1267	yes	no		2
8	0	972,524	CON__P35	CON__P35	400	407	no	no		2
10	0	1233,591	tr A2AL12	tr A2AL12	152	161	yes	no		2
14	0	1502,762	sp Q990!	sp Q990!	161	174	yes	no		2
14	0	1487,751	sp Q6066!	sp Q6066!	184	197	yes	no		2
10	0	1142,608	sp P1718!	sp P1718!	184	193	yes	no	2;3	
15	0	1674,821	sp P1887!	sp P1887!	163	177	yes	no		2
20	0	2106,089	tr D3Z510	tr D3Z510	154	173	yes	no		3
11	0	1024,603	sp P1012!	sp P1012!	256	266	no	no		2
11	0	974,5549	sp P5648!	sp P5648!	202	212	yes	yes		2
13	0	1513,762	sp Q6187!	sp Q6187!	1823	1835	yes	no		2
21	0	2269,138	tr E9PUC5	tr E9PUC5	96	116	yes	no		3
16	0	1755,956	sp P6836!	sp P0521!	265	280	no	no	2;3	
12	0	1333,558	sp Q8QZT	sp Q8QZT	188	199	yes	yes		2
17	0	1959,004	tr G3UXG!	tr G3UXG!	141	157	yes	no		3
19	0	2063,138	CON__P08	CON__P08	178	196	yes	yes	2;3	
12	1	1338,824	sp P4300!	sp P4300!	299	310	yes	no		2
13	0	1444,683	sp P1887!	sp P1887!	55	67	yes	no	2;3	
16	0	1658,888	sp P6301!	sp P6301!	172	187	yes	no		2
17	1	1786,983	sp P6301!	sp P6301!	172	188	yes	no		3
20	0	2282,173	CON__P00	CON__P00	78	97	yes	yes	2;3	
30	1	3308,719	CON__P00	CON__P00	78	107	yes	yes		4
23	0	2588,381	tr B2M1R!	tr B2M1R!	410	432	yes	no		3
7	1	994,5124	CON__P13	CON__P13	178	184	yes	no		2
10	1	1306,67	CON__P35	CON__P35	241	250	yes	yes	2;3	
15	0	1574,779	sp Q0326!	sp Q0326!	59	73	yes	no		2
10	0	1039,603	sp Q6074!	sp Q6074!	176	185	yes	yes		2

11	0	1286,672	sp O5477	sp O5477	310	320	yes	yes		2
11	0	1135,671		REV__tr Q91XX0 Q91XX0_MOU			yes	yes		3
24	0	2572,277	sp Q8BX7	sp Q8BX7	1878	1901	yes	yes		3
11	0	1086,611	sp Q8BSL	sp Q8BSL	20	30	yes	no		2
15	1	1896,871	CON__P08	CON__P08	285	299	yes	no		3
12	0	1314,73	tr V9GXQ	tr V9GXQ	786	797	yes	no		2
19	0	2067,132	CON__Q0	CON__Q0	145	163	yes	yes		2
19	0	2053,117	CON__P02	CON__P02	176	194	yes	yes	2;3	
13	0	1473,808	tr A0A1B0	tr A0A1B0	91	103	yes	no		2
12	0	1247,643	sp P17427	sp P17427	154	165	yes	yes		2
11	0	1185,672	sp Q6170	sp Q6170	168	178	yes	yes		2
16	0	1841,873	sp P5648C	sp P5648C	407	422	yes	yes		3
14	0	1600,795	sp Q8VDD	sp Q8VDD	328	341	yes	yes		2
12	0	1350,668	sp Q7TMM	sp Q7TMM	163	174	no	no		2
12	0	1318,696	sp P68372	sp P68372	163	174	no	no		2
12	0	1384,702	sp P5648C	sp P5648C	144	155	yes	yes		2
9	0	1056,618	tr A0A338	tr A0A338	91	99	yes	no		2
12	0	1354,652	sp Q7TMM	sp Q7TMM	47	58	yes	yes		2
12	0	1327,641	sp P68372	sp P68372	47	58	yes	yes		2
16	0	1828,874	sp Q9D6F	sp Q9D6F	47	62	yes	yes	2;3	
12	0	1384,662	sp Q9CWF	sp Q9CWF	47	58	yes	yes		2
19	0	2096,073	sp Q05D4	sp Q05D4	691	709	yes	yes		3
19	0	2329,145	tr Q9Z1A1	tr Q9Z1A1	24	42	yes	no		3
21	0	2265,077	sp P5648C	sp P5648C	325	345	yes	yes	2;3	
10	0	1037,587	sp P5648C	sp P5648C	134	143	yes	yes		2
7	0	838,5276	sp Q9CQV	sp Q9CQV	31	37	no	no		2
8	1	1094,54	CON__P35	CON__P35	185	192	yes	yes		2
10	0	1072,576	sp P0824	sp P0824	230	239	yes	yes		2
11	0	1304,633	sp P5051	sp P5051	70	80	yes	no		2
12	0	1360,71	sp Q8VEM	sp Q8VEM	185	196	yes	no		2
11	1	1433,763	CON__P13	CON__P13	440	450	yes	yes	2;3	
10	0	1228,591	sp Q7TMM	sp P68372	381	390	no	no		2
10	0	1223,615	sp O0859	sp O0859	468	477	yes	yes		2
10	0	1179,614	sp P6280	sp P6280	47	56	yes	yes		2
17	0	1586,718	CON__P02	CON__P02	70	86	no	no		2
11	0	1110,567	CON__P13	CON__P13	74	84	yes	yes		2
10	0	1068,509	tr E9PUC5	tr E9PUC5	41	50	yes	no		2
11	0	1094,521	CON__P08	CON__P08	31	41	no	no		2
12	0	1396,662	sp Q9ERD	sp Q9ERD	47	58	yes	no	2;3	
12	0	1300,63	sp P99024	sp P99024	47	58	yes	yes		2
12	0	1302,693	sp P1179	sp P1179	434	445	yes	no		2
17	0	1954,868	sp P1487	sp P1487	2010	2026	yes	yes		2
20	0	2087,025	sp Q6187	sp Q6187	625	644	yes	no		2
16	0	1681,864	sp O0855	sp O0855	452	467	yes	yes	2;3	
20	0	2348,088	sp O0855	sp O0855	24	43	yes	no		2
14	0	1472,809	sp Q8BX7	sp Q8BX7	1492	1505	yes	yes		2
12	0	1214,614	tr F6QPR1	tr F6QPR1	83	94	yes	no		2
17	0	1796,829	sp P1685	sp P1685	144	160	yes	no		2
16	0	1867,906	sp Q99KI0	sp Q99KI0	69	84	yes	no		3
11	0	1514,742	sp P6326C	sp P6326C	85	95	no	no	2;3	

18	0	1762,921	sp P97807	sp P97807	266	283	yes	yes		2
8	0	1043,5	tr Q91VA7	tr Q91VA7	114	121	yes	no		2
13	0	1461,808	tr A0A1L1	tr A0A1L1	174	186	yes	no		2
17	1	1617,84	sp Q6PIC6	sp Q6PIC6	717	733	yes	no		2
23	1	2220,062	sp Q6164	sp Q6164	319	341	yes	no		3
14	1	1568,831	sp P1633C	sp P1633C	203	216	yes	yes		3
13	1	1325,756	sp P15864	sp P15864	34	46	yes	no	2;3	
10	1	1236,578	CON__P13	CON__P13	334	343	yes	no		2
14	1	1751,8	sp Q6074	sp Q6074	139	152	yes	yes		3
22	1	2342,158	sp P6326C	sp P6326C	291	312	yes	no		3
10	1	1126,533	CON__P04	CON__P04	289	298	yes	yes		2
10	1	1195,591	CON__P35	CON__P35	293	302	yes	yes		2
11	1	1242,657	sp Q6187	sp Q6187	1088	1098	yes	no		2
13	2	1458,856	tr E9PUC5	tr E9PUC5	242	254	yes	no		3
15	1	1759,853	tr A2BI12	tr A2BI12	75	89	yes	no		2
10	1	1151,703	tr V9GXQ	tr V9GXQ	909	918	yes	no		2
11	1	1270,722	sp Q7TMM	sp P68372	252	262	no	no	2;3	
24	2	2582,286	sp P14873	sp P14873	1491	1514	yes	yes		3
9	1	1121,521	CON__P35	CON__P35	488	496	no	no		2
13	1	1407,707	sp P4609	sp P4609	301	313	no	no		2
16	1	1833,947	sp P4300	sp P4300	158	173	yes	no		2
11	1	1368,682	CON__P08	CON__P08	253	263	yes	no		3
13	1	1618,73	tr A2BI12	tr A2BI12	315	327	yes	yes		2
12	1	1478,752	sp O5477	sp O5477	673	684	yes	yes		2
16	1	1843,939	CON__P04	CON__P04	417	432	yes	yes		3
10	1	1141,707	CON__P02	CON__P02	548	557	yes	yes		2
10	1	1127,691	CON__P02	CON__P02	549	558	yes	yes		2
13	1	1535,777	tr G3UXT7	tr G3UXT7	7	19	yes	no		3
14	1	1711,893	sp P4609	sp P4609	200	213	yes	yes		2
13	1	1355,766	sp P43274	sp P43274	34	46	yes	yes		2
17	1	1902,006	sp Q6187	sp Q6187	1761	1777	yes	no		3
9	1	1071,592	sp P17182	sp P17182	81	89	yes	no		2
12	2	1427,798	sp P17182	sp P17182	81	92	yes	no		3
15	1	1638,931	CON__P02	CON__P02	437	451	no	no	2;3	
9	2	1193,604	CON__P35	CON__P35	273	281	no	no	2;3	
8	1	979,5339	tr D3YYN7	tr D3YYN7	52	59	yes	no		2
10	0	1142,618	CON__P13	CON__P13	432	441	yes	yes		2
8	0	895,528	sp P47915	sp P47915	94	101	yes	no		2
10	0	1064,587	tr V9GXQ	tr V9GXQ	154	163	yes	no		2
11	0	1276,703	CON__P04	CON__P04	473	483	yes	yes		2
11	0	1262,687	CON__P35	CON__P35	477	487	no	no		2
12	1	1390,782	CON__P35	CON__P35	477	488	no	no		2
17	0	1937,974	tr A0A0N4	tr A0A0N4	120	136	yes	no		2
17	0	1895,964	sp P17182	sp P17182	163	179	yes	no		2
13	0	1403,693	sp P62751	sp P62751	140	152	yes	yes		2
10	0	1200,578	CON__P2C	CON__P2C	81	90	yes	yes		2
22	0	2404,301	sp P4300	sp P4300	66	87	yes	no	2;3	
21	1	2376,181	CON__P35	CON__P35	164	184	yes	yes	2;3	
9	1	1063,603	CON__P08	CON__P13	157	165	no	no		2
25	0	2604,322	sp Q9ERD	sp Q9ERD	217	241	yes	yes		3

13	0	1395,791	sp P47963	sp P47963	146	158	yes	yes		2
16	0	1601,826	sp Q0444	sp Q0444	157	172	yes	yes		2
10	0	1142,627	sp Q7TMM	sp P68372	253	262	no	no		2
7	0	886,4405	CON__P02	CON__P02	483	489	yes	yes		2
23	0	2538,133	sp P6326C	sp P6326C	216	238	yes	no	2;3	
10	0	1199,495	sp P1633C	sp P1633C	103	112	yes	yes		2
11	1	1379,691	sp P6836E	sp P0521E	391	401	no	no	2;3	
8	0	971,544	sp P62751	sp P62751	71	78	yes	yes		2
11	0	1170,625	tr A0A1L1	tr A0A1L1	33	43	yes	no		2
17	1	1837,006	sp P63017	sp P63017	326	342	yes	no		3
13	0	1542,79	sp P5051E	sp P5051E	200	212	yes	yes		2
10	0	1190,637	sp Q9QYR	sp Q9QYR	198	207	yes	no		2
13	1	1520,791	sp Q9QYR	sp Q9QYR	198	210	yes	no	2;3	
21	0	2555,262	sp P1633C	sp P1633C	130	150	yes	yes		2
16	1	1984,887	CON__P04	CON__P04	252	267	yes	yes	2;3	
7	0	828,4957	sp Q8QZT	sp Q8QZT	172	178	yes	yes		2
16	1	1833,972	sp Q8QZT	sp Q8QZT	172	187	yes	yes		2
13	0	1376,624	tr E9Q589	tr E9Q589	607	619	yes	no		2
11	2	1318,713	sp P1685E	sp P1685E	247	257	yes	no		3
7	0	891,4814	sp Q0326	sp Q0326	435	441	yes	no		2
9	0	1054,57	sp P1633C	sp P1633C	235	243	yes	yes		2
10	0	1204,653	sp P1487E	sp P1487E	420	429	yes	yes		2
9	0	1164,578	CON__P13	CON__P13	442	450	yes	no		2
12	0	1354,734	sp Q8BX7	sp Q8BX7	1127	1138	yes	yes		2
9	0	1121,572	CON__P08	CON__P08	410	418	no	no		2
15	0	1655,819	sp Q0444	sp Q0444	367	381	yes	yes	2;3	
10	0	1192,558	sp Q8BX7	sp Q8BX7	2138	2147	yes	yes		2
9	0	1062,52	sp Q6187	sp Q6187	1565	1573	yes	no		2
26	0	2572,317	sp Q5U3K	sp Q5U3K	373	398	yes	yes	2;3	
13	0	1434,736	tr A0A2I3	tr A0A2I3	10	22	yes	no		2
16	0	1797,915	sp O8856	sp O8856	23	38	yes	yes		2
16	0	1895,88	CON__P02	CON__P02	529	544	yes	yes		2
10	0	1129,613	tr A0A0N	tr A0A0N	141	150	yes	no		2
9	0	1068,51	sp P4609E	sp P4609E	273	281	yes	no		2
20	0	2210,097	CON__P0C	CON__P0C	58	77	yes	yes	2;3;4	
20	0	2211,092	tr Q9R0T7	tr Q9R0T7	73	92	yes	no		2
13	0	1478,788	CON__P02	CON__P02	421	433	yes	yes		2
17	0	1847,97	sp Q0444	sp Q0444	342	358	yes	yes		2
14	1	1339,771	sp P1876C	sp P1876C	153	166	yes	yes		2
10	0	1158,64	sp Q9QYR	sp Q9QYR	169	178	yes	no		2
12	0	1170,661	sp Q8QZT	sp Q8QZT	64	75	yes	yes		2
14	0	1603,833	sp Q9ERD	sp Q9ERD	263	276	no	no		2
14	0	1619,828	sp Q7TMM	sp P68372	263	276	no	no	2;3	
8	0	999,5277	sp P60202	sp P60202	46	53	yes	yes		2
8	1	989,591	sp Q6PIC6	sp Q6PIC6	757	764	no	no		2
14	0	1456,861	sp P6836E	sp P6836E	230	243	yes	no		2
9	0	1075,552	sp Q6PIC6	sp Q6PIC6	689	697	no	no		2
14	0	1486,872	sp P6836E	sp P0521E	230	243	no	no		2
14	0	1778,79	sp P1685E	sp P1685E	308	321	yes	no	2;3	
12	2	1509,706	CON__P02	CON__P02	298	309	yes	yes		3

21	1	2233,268	sp Q05D4	sp Q05D4	878	898	yes	yes		3
14	1	1602,862	sp P14873	sp P14873	864	877	yes	yes	2;3	
16	1	1660,831	tr G3UXT7	tr G3UXT7	24	39	yes	no		3
10	1	1233,672	CON__P13	CON__P13	236	245	yes	yes	2;3	
26	0	2691,288	tr Q9Z1A1	tr Q9Z1A1	119	144	yes	no	2;3	
15	0	1537,872	tr E9PZW	tr E9PZW	1780	1794	yes	no		2
22	0	2349,083	CON__P08	CON__P08	420	441	yes	yes		3
22	0	2308,057	CON__P02	CON__P02	418	439	yes	no		3
8	0	993,426	CON__P35	CON__P35	489	496	no	no		2
8	0	1023,437	CON__Q14	CON__Q14	430	437	no	no		2
13	0	1405,712	sp O54774	sp O54774	1107	1119	yes	yes		2
8	0	1030,548	sp Q0444	sp Q0444	359	366	yes	yes		2
11	0	1099,66	tr D3YWL	tr D3YWL	25	35	yes	no		2
11	0	1056,618	sp P18872	sp P18872	36	46	yes	no		2
10	0	1135,671	sp P48962	sp P48962	34	43	no	no	2;3	
12	0	1340,719	sp Q0225	sp Q0225	150	161	yes	yes		2
12	0	1448,814	sp Q0225	sp Q0225	488	499	yes	yes		2
12	1	1522,781	CON__P04	CON__P04	461	472	no	no	2;3	
12	1	1520,802	CON__P35	CON__P35	465	476	no	no		3
10	0	1130,618	tr Q9Z1A1	tr Q9Z1A1	48	57	yes	no		2
15	0	1758,898	sp O7017	sp O7017	271	285	yes	no		3
11	0	1279,579	sp P17182	sp P17182	93	103	yes	no		2
11	0	1260,596	tr Q8VHM	tr Q8VHM	196	206	yes	no		2
11	0	1259,637	tr G3UXJ6	tr G3UXJ6	193	203	yes	no		2
12	0	1356,689	CON__P04	CON__P04	444	455	yes	yes		2
17	1	1940,98	CON__P04	CON__P04	444	460	yes	yes		2
12	0	1370,704	CON__P35	CON__P35	448	459	yes	yes		2
11	0	1262,71	sp Q8VDN	sp Q8VDN	648	658	yes	yes		2
11	0	1235,699	sp Q6PIC6	sp Q6PIC6	638	648	no	no		2
8	0	974,5437	sp P10126	sp P10126	248	255	no	no		2
15	0	1757,895	sp O54774	sp O54774	557	571	yes	yes		2
14	1	1586,849	sp Q8VEM	sp Q8VEM	337	350	yes	no		3
7	0	834,4487	tr D3YW2	tr D3YW2	318	324	yes	no		2
9	0	993,5607	CON__P35	CON__P35	412	420	yes	yes	2;3	
11	0	1315,652	tr A0A1L1	tr A0A1L1	10	20	yes	no		2
11	0	1276,678	tr H3BKM	tr H3BKM	844	854	yes	no		2
10	0	1143,604	sp Q922Q	sp Q922Q	74	83	yes	yes		2
12	0	1308,711	tr B1AQW	tr B1AQW	192	203	yes	no		2
10	2	1184,688	CON__P13	CON__P13	396	405	yes	yes		3
10	2	1223,699	CON__P02	CON__P02	391	400	no	no		3
9	1	1072,588	CON__P04	CON__P04	408	416	no	no		2
10	2	1200,683	CON__P04	CON__P04	408	417	no	no	2;3;4	
11	0	1020,499	sp P4666C	sp P4666C	29	39	yes	yes		2
11	0	1174,696	sp P1633C	sp P1633C	283	293	yes	yes		2
10	0	1167,602	CON__P34	CON__P34	313	322	yes	yes		2
10	1	1216,664	sp P14873	sp P14873	391	400	yes	yes		3
12	0	1369,681	tr A0A3B2	tr A0A3B2	297	308	no	no		3
8	0	973,508	tr E9PUC5	tr E9PUC5	255	262	yes	no		2
7	1	846,4963	CON__P02	CON__P02	242	248	yes	yes		2
27	0	2753,324	sp Q9QYR	sp Q9QYR	837	863	yes	no		2

10	0	1044,556	CON__P00	CON__P00	98	107	yes	yes		2
9	0	1019,514	sp Q80WJ	sp Q80WJ	292	300	yes	no		2
7	0	794,4109	sp P1685E	sp P1685E	226	232	yes	no		2
22	0	2392,239	sp P0824C	sp P0824C	53	74	yes	no		3
9	0	1103,539	CON__P08	CON__P08	82	90	yes	yes		2
25	0	2696,297	sp Q7TMM	sp P68372	217	241	no	no		3
9	0	984,6219	sp P4609E	sp P4609E	289	297	yes	yes		2
10	0	1177,623	CON__P34	CON__P34	148	157	yes	yes		2
14	1	1626,946	sp P1685E	sp P1685E	65	78	yes	no	2;3	
15	0	1649,91	sp P5648C	sp P5648C	95	109	yes	yes	2;3	
11	0	1294,612	sp Q99LF4	sp Q99LF4	466	476	yes	yes		2
10	0	1162,623	CON__P02	CON__P02	66	75	yes	yes		2
10	0	1148,608	CON__P02	CON__P02	66	75	yes	yes		2
12	0	1314,791	sp Q922Q	sp Q922Q	97	108	yes	yes		2
10	0	1001,576	CON__P02	CON__P02	598	607	yes	yes		2
12	0	1350,649	sp Q8BX7I	sp Q8BX7I	305	316	yes	no		2
15	1	1676,844	sp Q8BX7I	sp Q8BX7I	305	319	yes	no		3
17	0	1840,939	sp Q9D6F!	sp Q9D6F!	363	379	yes	yes		2
11	0	1056,539	sp Q9JIS5	sp Q9JIS5	113	123	yes	yes		2
17	0	1856,934	sp Q922F4	sp Q922F4	363	379	yes	yes		2
10	0	1130,564	sp Q6227!	sp Q6227!	170	179	yes	yes		2
17	0	1868,971	sp P99024	sp P99024	363	379	yes	yes		2
16	2	1924,997	tr A0A0AC	tr A0A0AC	535	550	yes	no		2
16	0	1724,804	sp O0855!	sp O0855!	375	390	yes	no		2
11	0	1256,523	sp P62631	sp P62631	155	165	yes	yes		2
11	0	1281,555	sp P1012E	sp P1012E	155	165	yes	no		2
12	0	1279,612	sp P4609E	sp P4609E	302	313	no	no		2
14	0	1675,798	sp Q6187!	sp Q6187!	983	996	yes	no		2
17	0	1846,83	tr M0QW!	tr M0QW!	66	82	yes	no		2
8	0	974,4855	CON__Q7!	CON__Q7!	380	387	yes	yes		2
9	0	1030,501	sp P4646C	sp P4646C	393	401	yes	yes		2
12	0	1354,728	tr H3BKM!	tr H3BKM!	773	784	yes	no		2
19	0	2077,065	tr A0A338	tr A0A338	334	352	yes	no		2
27	0	3101,389	CON__P13	CON__P13	305	331	no	no		3
13	1	1482,754	sp Q6066!	sp Q6066!	99	111	yes	no		2
15	1	1676,899	sp P1487E	sp P1487E	415	429	yes	yes		3
12	0	1381,593	sp P4300E	sp P4300E	18	29	yes	no	2;3;4	
10	0	1113,61	sp P0824C	sp P0824C	315	324	yes	yes		2
12	0	1289,665	sp Q91V1!	sp Q91V1!	80	91	yes	no		2
10	1	1241,613	tr A2BI12	tr A2BI12	15	24	yes	no		3
8	0	980,475	tr F6V4G5	tr F6V4G5	34	41	yes	no		2
8	0	972,495	sp Q8QZT	sp Q8QZT	363	370	yes	yes		2
9	0	958,527	sp Q99MM!	sp Q99MM!	304	312	yes	no		2
14	0	1712,794	CON__P02	CON__P02	469	482	yes	yes		2
13	0	1425,842	sp P97807	sp P97807	85	97	yes	yes		2
15	0	1781,812	tr A0A140	tr A0A140	139	153	yes	no		2
9	0	1123,489	sp P4300E	sp P4300E	509	517	yes	no		2
17	0	1870,971	tr D3YYN7	tr D3YYN7	176	192	yes	no		2
17	0	1870,971	sp Q6PIC6	sp Q6PIC6	168	184	yes	no		2
19	1	2128,034	sp Q922F4	sp Q922F4	1	19	yes	yes		3

19	1	2098,023	sp P68372	sp P68372	1	19	no	no		3
17	0	1856,934	sp Q7TMM	sp P68372	363	379	no	no		2
18	0	1827,904	tr F7BNZ5	tr F7BNZ5	360	377	yes	no		2
16	0	1591,74	sp P63011	sp P63011	187	202	yes	yes		2
25	0	2457,191	CON__P35	CON__P35	497	521	yes	yes	2;3	
26	0	2553,126	CON__P04	CON__P04	493	518	yes	yes		3
11	0	1152,533	sp P14873	sp P14873	1515	1525	yes	yes		2
16	1	1866,889	sp Q9ERD	sp Q9ERD	321	336	yes	yes		3
16	1	1922,89	sp Q7TMM	sp P68372	321	336	no	no		3
16	1	1868,868	sp Q9D6F	sp Q9D6F	321	336	yes	yes		3
17	0	1872,929	sp Q9ERD	sp Q9ERD	363	379	yes	yes	2;3	
12	1	1359,693	CON__P02	CON__P02	212	223	no	no		3
21	0	2226,208	tr Q9DAY	tr Q9DAY	81	101	yes	no		2
7	0	896,4062	CON__P35	CON__P35	234	240	yes	yes		2
14	0	1587,743	tr A0A0N	tr A0A0N	197	210	yes	no		2
12	0	1293,686	sp O0855	sp O0855	64	75	yes	yes		2
8	0	883,411	sp P1633C	sp P1633C	80	87	yes	yes		2
11	0	1190,571	tr Q8C048	tr Q8C048	703	713	yes	no		2
13	0	1478,738	sp P60202	sp P60202	206	218	yes	yes		2
12	1	1491,707	sp Q8VEM	sp Q8VEM	202	213	yes	no	2;3	
9	0	1071,531	sp P17427	sp P17427	570	578	yes	no		2
15	0	1600,785	sp Q99KI0	sp Q99KI0	634	648	yes	yes		2
15	0	1705,852	sp P4300E	sp P4300E	159	173	yes	no		2
16	0	1724,812	sp Q78PY	sp Q78PY	716	731	yes	yes		3
14	0	1482,747	sp Q0225	sp Q0225	638	651	yes	yes		2
16	0	1645,846	sp Q9Z0N	sp Q9Z0N	401	416	yes	no		2
10	0	1152,604	tr M0QW	tr M0QW	97	106	yes	no		2
15	0	1646,838	sp Q8VEK	sp Q8VEK	552	566	yes	yes		2
12	0	1290,657	sp P4646C	sp P4646C	435	446	yes	yes		2
10	0	1240,587	CON__P08	CON__P08	254	263	yes	no		2
10	0	1241,546	CON__P02	CON__P02	252	261	no	no	2;3	
31	2	3351,637	CON__P35	CON__P35	291	321	yes	yes		4
15	0	1639,846	sp Q5U3K	sp Q5U3K	20	34	yes	yes		2
14	0	1564,752	sp Q8BSL	sp Q8BSL	60	73	yes	no		2
10	1	1213,682	sp P62751	sp P62751	69	78	yes	yes		3
12	1	1356,725	CON__P02	CON__P02	425	436	no	no		2
14	1	1598,826	CON__P04	CON__P04	442	455	yes	yes	2;3	
19	2	2183,118	CON__P04	CON__P04	442	460	yes	yes		3
14	1	1612,842	CON__P35	CON__P35	446	459	yes	yes	2;3	
9	1	1151,546	CON__P02	CON__P04	268	276	no	no		2
10	2	1307,647	CON__P02	CON__P04	268	277	no	no	2;3	
13	0	1472,772	tr G3UXJ6	tr G3UXJ6	230	242	yes	no		2
13	0	1459,777	tr Q8VHM	tr Q8VHM	347	359	yes	no		2
14	1	1717,875	sp P6836E	sp P0521E	216	229	no	no	2;3	
12	0	1328,719	CON__P35	CON__P35	348	359	no	no		2
18	0	1912,876	sp Q6PIC6	sp Q6PIC6	350	367	no	no		2
20	0	2168,061	sp O0855	sp O0855	533	552	yes	yes		3
13	0	1468,807	tr Q5SVI9	tr Q5SVI9	247	259	yes	no		2
13	0	1428,757	tr Q3U4FC	tr Q3U4FC	35	47	yes	no		2
14	0	1753,871	sp Q6187	sp Q6187	130	143	yes	no		2

12	0	1365,696	tr A0A0J9' tr A0A0J9'	635	646	yes	no		2
13	0	1489,745	sp O54774' sp O54774'	1009	1021	yes	yes		2
25	0	2188,898	sp O88566' sp O88566'	326	350	yes	yes	2;3	
9	0	1053,386	sp Q7TMM' sp P68372	298	306	no	no		2
10	0	1237,565	CON__P13 CON__P13	246	255	no	no		2
10	0	1299,522	CON__P04 CON__P04	258	267	yes	yes		2
11	0	1267,707	sp Q6PIC6' sp Q6PIC6'	153	163	no	no		2
21	0	2366,255	CON__P13 CON__P13	208	228	yes	yes	2;3	
15	0	1648,788	sp P63017' sp P63017'	57	71	yes	no		2
11	0	1316,636	sp P1633C' sp P1633C'	164	174	yes	yes		2
12	1	1444,731	sp P1633C' sp P1633C'	164	175	yes	yes	2;3	
12	1	1299,617	sp Q9QYR' sp Q9QYR'	606	617	yes	no		3
14	1	1775,856	sp Q9CQC' sp Q9CQC'	195	208	yes	yes		3
11	0	1302,591	sp P63017' sp P63017'	540	550	yes	no		2
10	0	1173,588	sp Q61644' sp Q61644'	100	109	yes	no		2
14	0	1695,826	sp Q7TMM' sp P68372	337	350	no	no	2;3	
9	0	1037,496	sp Q6PIC6' sp Q6PIC6'	932	940	no	no		2
17	0	1897,84	tr A0A0A6' tr A0A0A6'	281	297	yes	no		2
15	0	1590,694	sp Q8VDD' sp Q8VDD'	359	373	no	no		2
15	0	1632,741	sp Q61876' sp Q61876'	366	380	yes	no		2
11	1	1314,689	CON__P02 CON__P02	376	386	no	no		2
22	0	2693,265	sp P46096' sp P46096'	333	354	yes	yes	2;3	
9	1	1152,593	sp P14873' sp P14873'	2367	2375	yes	yes		2
13	0	1523,729	tr H3BKM' tr H3BKM'	856	868	yes	no		2
24	0	2490,133	tr Q9Z1A1' tr Q9Z1A1'	181	204	yes	no		2
15	0	1666,787	sp Q03266' sp Q03266'	89	103	yes	no		2
16	0	1796,004	CON__P13 CON__P13	371	386	yes	yes	2;3	
12	0	1328,632	CON__P35 CON__P35	425	436	yes	yes	2;3	
18	1	1963,971	CON__P35 CON__P35	425	442	yes	yes		4
21	2	2306,136	CON__P35 CON__P35	425	445	yes	yes		3
27	0	2871,386	CON__P13 CON__P13	296	322	yes	yes	2;3;4	
11	0	1040,562	sp Q9D6R' sp Q9D6R'	67	77	yes	no		2
14	0	1642,78	sp P61982' sp P61982'	29	42	yes	yes		2
25	1	2901,403	CON__P35 CON__P35	200	224	yes	yes	3;4	
9	1	897,5284	sp P14873' sp P14873'	547	555	yes	yes		2
13	2	1604,805	sp Q8QZT' sp Q8QZT'	243	255	yes	yes		3
8	0	807,4603	sp O88566' sp O88566'	105	112	yes	no		2
12	1	1148,692	sp P14873' sp P14873'	2263	2274	yes	yes		2
8	0	886,476	tr Q9Z1A1' tr Q9Z1A1'	96	103	yes	no		2
18	0	1927,909	REV__sp P16373 ZFP59_MOUSE			yes	yes		2
23	0	2463,195	sp Q6PIC6' sp Q6PIC6'	734	756	no	no	2;3	
16	0	1615,879	sp Q9Z0N' sp Q9Z0N'	39	54	yes	no		3
19	0	1916,97	sp Q8QZT' sp Q8QZT'	103	121	yes	yes		2
15	0	1689,756	CON__P13 CON__P13	406	420	no	no		2
11	0	1268,64	CON__P12 CON__P12	121	131	yes	yes		2
24	0	2479,046	tr Q5SUTC' tr Q5SUTC'	269	292	yes	no		3
10	0	1102,587	sp Q9Z0N' sp Q9Z0N'	18	27	yes	no		2
15	0	1629,767	sp Q8BSL7' sp Q8BSL7'	128	142	yes	no		2
8	0	971,5036	CON__P02 CON__P02	379	386	no	no		2
17	0	2082,997	CON__P35 CON__P35	428	444	yes	yes		2

13	0	1532,729	sp Q6149! sp Q6149!	201	213	yes	no		2
13	0	1560,706	sp Q8QZT sp Q8QZT	206	218	yes	yes		2
13	0	1515,695	sp P6326C sp P6326C	360	372	yes	no	2;3	
9	0	1120,576	CON__P35 CON__P35	328	336	yes	yes		2
9	0	1073,514	CON__P35 CON__P35	5	13	yes	yes		2
19	0	1810,943	sp Q6PIC6 sp Q6PIC6	698	716	no	no		2
20	1	1939,038	sp Q6PIC6 sp Q6PIC6	698	717	no	no		3
11	0	1156,584	CON__P35 CON__P35	251	261	yes	yes		2
9	0	1003,545	sp P48962 sp P48962	97	105	yes	yes		2
13	0	1322,756	sp O0855: sp O0855:	44	56	yes	no		2
8	0	1010,493	sp Q8VEM sp Q8VEM	222	229	yes	no		2
10	0	1189,565	sp Q9CQC sp Q9CQC	145	154	yes	no		2
15	0	1715,844	CON__P04 CON__P04	418	432	yes	yes	2;3	
21	1	2328,167	CON__P04 CON__P04	418	438	yes	yes		3
24	2	2642,326	CON__P04 CON__P04	418	441	yes	yes		3
10	0	1196,615	tr E9PUC5 tr E9PUC5	270	279	yes	no		2
13	1	1555,857	sp Q6ZWL sp Q6ZWL	20	32	yes	yes		2
9	0	1015,53	CON__P02 CON__P13	224	232	no	no		2
11	0	1303,589	sp Q6187! sp Q6187!	1885	1895	yes	no		2
12	0	1409,767	sp P6836E sp P0521E	85	96	no	no	2;3	
21	1	2414,198	sp P6836E sp P0521E	85	105	no	no	3;4	
10	0	1128,675	sp Q6433: sp Q6433:	405	414	yes	yes		2
16	0	1741,936	sp Q6187! sp Q6187!	217	232	yes	no		2
11	0	1310,6	tr D3YVK1 tr D3YVK1	15	25	yes	no		2
8	0	1056,401	CON__P02 CON__P02	413	420	yes	yes		2
15	0	1889,964	CON__P02 CON__P13	208	222	no	no		2
14	0	1574,813	sp P9808E sp P9808E	122	135	yes	yes		2
20	1	2204,134	tr A0A3B2 tr A0A3B2	45	64	yes	no		4
14	2	1740,884	CON__P02 CON__P02	154	167	yes	yes		3
14	2	1756,878	CON__P08 CON__P08	156	169	yes	yes		3
13	0	1389,674	CON__P13 CON__P13	387	399	yes	no		2
25	2	2405,268	sp O8893! sp O8893!	532	556	yes	yes		4
26	0	2746,156	tr Q8BQ4 tr Q8BQ4	75	100	yes	yes	2;3	
17	0	1810,859	tr Q9Z1A1 tr Q9Z1A1	157	173	yes	no		2
24	1	2652,252	tr Q9Z1A1 tr Q9Z1A1	157	180	yes	no		3
11	0	1200,61	CON__P13 CON__P13	246	256	no	no		2
12	1	1356,711	CON__P13 CON__P13	246	257	no	no		2
19	0	1739,88	sp Q6433: sp Q6433:	94	112	yes	yes		2
12	1	1356,711	CON__P08 CON__P08	214	225	yes	yes		3
11	0	1288,645	CON__Q7: CON__Q7:	225	235	yes	yes		2
19	0	1920,91	tr A2BI12 tr A2BI12	156	174	yes	no		2
13	0	1413,783	sp Q6187! sp Q6187!	1365	1377	yes	no		2
10	0	1189,601	CON__P35 CON__P35	262	271	yes	yes		2
17	0	1640,837	tr Q8C04E tr Q8C04E	787	803	yes	no		2
11	1	1210,715	sp P1487E sp P1487E	54	64	yes	yes		2
10	1	1158,588	sp Q9QYR sp Q9QYR	337	346	yes	no		2
13	1	1310,694	sp Q99M tr Q99M	176	188	yes	no		2
12	1	1438,805	CON__P02 CON__P02	360	371	yes	yes	2;3	
20	1	2485,246	tr Q9Z1A1 tr Q9Z1A1	23	42	yes	no		3
11	1	1384,692	sp Q7TM tr P6837E	380	390	no	no		3

11	1	1355,596	sp P1633C	sp P1633C	102	112	yes	yes		2
12	1	1539,746	sp Q99K4	sp Q99K4	327	338	yes	yes		3
15	2	1873,976	sp P6836E	sp P0521E	215	229	no	no		3
16	1	1868,88	CON__P02	CON__P02	508	523	yes	yes	2;3	
11	1	1253,637	sp P1633C	sp P1633C	244	254	yes	yes		3
10	1	1171,631	CON__P02	CON__P13	223	232	no	no		2
22	1	2201,021	tr D3Z6W	tr D3Z6W	385	406	yes	no		4
11	2	1330,695	CON__P04	CON__P04	241	251	yes	yes		3
22	1	2368,203	sp P1685E	sp P1685E	116	137	yes	no		3
10	1	1186,692	CON__P13	CON__P13	257	266	yes	yes		2
10	0	1014,546	sp O0855	sp O0855	259	268	yes	yes		2
12	0	1424,559	sp P4300E	sp P4300E	558	569	yes	yes		2
13	1	1580,66	sp P4300E	sp P4300E	558	570	yes	yes	2;3	
14	0	1337,57	sp Q9DD1	sp Q9DD1	194	207	yes	yes		2
16	1	1563,665	sp Q9DD1	sp Q9DD1	194	209	yes	yes		2
22	1	2056,955	sp Q91XV	sp Q91XV	160	181	yes	yes		3
14	0	1392,7	sp Q8BJW	sp Q8BJW	503	516	yes	yes		2
9	0	984,524	sp P1487E	sp P1487E	1778	1786	yes	yes		2
18	0	2170,017	CON__P35	CON__P35	272	289	yes	yes	2;3	
19	1	2298,112	CON__P35	CON__P35	272	290	yes	yes		3
8	0	883,4036	tr A0A2I3I	tr A0A2I3I	329	336	yes	no		2
22	0	2371,212	sp P1487E	sp P1487E	104	125	yes	yes		2
11	0	1200,551	sp Q6244E	sp Q6244E	100	110	yes	yes		2
8	1	988,5302	CON__P02	CON__P02	329	336	no	no		2
7	0	846,4447	CON__P13	CON__P13	363	369	yes	no		2
8	1	1002,546	CON__P13	CON__P13	363	370	yes	no		2
11	0	1299,606	sp P4300E	sp P4300E	498	508	yes	no	2;3	
29	0	2868,216	CON__Q8E	CON__Q8E	739	767	yes	yes		5
8	1	988,5302	CON__P08	CON__P08	331	338	yes	no		2
10	0	1209,578	sp Q6P54E	sp Q6P54E	706	715	yes	yes		2
14	0	1409,715	CON__P13	CON__P13	16	29	no	no		2
10	0	1025,514	CON__P04	CON__P48	31	40	no	no		2
10	0	1011,499	CON__P02	CON__P02	31	40	yes	yes		2
17	0	1656,786	CON__P04	CON__P04	13	29	yes	yes	2;3	
20	0	1537,636	CON__P13	CON__P13	16	35	yes	yes		2
16	0	1231,591	CON__P35	CON__P35	14	29	yes	yes		2
26	1	2797,336	sp Q7TMM	sp P6837E	78	103	no	no		3
25	0	2499,04	CON__Q5I	CON__Q5I	613	637	yes	no		4
9	0	844,5018	sp P15864	sp P43274	55	63	no	no		2
10	1	972,5968	sp P15864	sp P43274	55	64	no	no		2
9	0	1060,468	CON__P02	CON__P02	310	318	yes	yes		2
14	0	1671,807	sp Q9QYR	sp Q9QYR	155	168	yes	no		2
13	0	1572,711	sp P6836E	sp P0521E	340	352	no	no		2
20	0	2115,917	sp Q8VHC	sp Q8VHC	25	44	yes	no		3
22	0	1837,907	CON__P35	CON__P35	71	92	yes	yes	2;3	
16	0	1810,896	sp O0855	sp O0855	239	254	yes	yes		2
12	1	1339,662	CON__P04	CON__P04	365	376	yes	yes	2;3	
22	2	2500,245	CON__P04	CON__P04	365	386	yes	yes	3;4	
12	1	1390,673	CON__P35	CON__P35	369	380	yes	yes	2;3;4	
22	2	2565,271	CON__P35	CON__P35	369	390	yes	yes	3;4	

14	1	1707,818	sp P35802	sp P35802	256	269	yes	yes		4
19	1	2211,091	CON__P13	CON__P13	344	362	yes	yes	2;3	
14	1	1550,751	tr A0A498	tr A0A498	11	24	yes	no		3
15	0	1525,726	tr A0A3B2	tr A0A3B2	447	461	yes	no		2
12	0	1301,708	sp Q8BGZ	CON__P04	344	355	no	no		2
12	0	1407,653	CON__P02	CON__P02	89	100	yes	yes		2
9	0	1016,529	CON__P02	CON__P02	89	97	yes	no		2
14	0	1261,59	CON__P13	CON__P13	451	464	yes	yes		2
12	0	1382,683	CON__P04	CON__P04	186	197	no	no		2
14	1	1637,853	CON__P04	CON__P04	186	199	no	no	2;3	
16	0	1465,8	sp Q8BX7	sp Q8BX7	3460	3475	yes	no		2
9	0	830,4862	CON__P35	CON__P35	62	70	yes	yes		2
9	0	873,492	CON__P04	CON__P04	66	74	yes	yes		2
17	1	1686,963	CON__P04	CON__P04	66	82	yes	yes	2;3	
10	1	1093,588	CON__P13	CON__P13	64	73	no	no		2
10	0	1212,533	CON__Q7	CON__Q7	242	251	yes	yes		2
12	0	1246,59	tr H7BXC3	tr H7BXC3	113	124	yes	no		2
13	0	1555,727	tr D3YYN7	tr D3YYN7	226	238	yes	no		3
20	0	2138,006	sp P1487	sp P1487	1395	1414	yes	yes		2
14	0	1421,74	sp P1487	sp P1487	1251	1264	yes	yes		2
17	1	2018,974	sp Q9QYR	sp Q9QYR	1720	1736	yes	no		3
12	0	1326,551	sp P1487	sp P1487	336	347	yes	yes		2
14	0	1480,8	sp P63017	sp P63017	329	342	yes	no		2
11	0	1364,632	CON__P13	CON__P13	323	333	yes	yes	2;3	
12	1	1492,727	CON__P13	CON__P13	323	334	yes	yes	2;3	
12	1	1454,679	sp Q8BGZ	CON__P02	348	359	no	no		2
12	1	1484,69	CON__P13	CON__P13	353	364	no	no		2
13	0	1270,615	sp O0859	sp O0859	506	518	yes	yes		2
22	0	1909,783	tr A2AL12	tr A2AL12	295	316	yes	no		2
15	0	1574,852	sp Q9QYR	sp Q9QYR	864	878	yes	no		2
11	0	1136,52	sp Q9ER7	sp Q9ER7	255	265	yes	yes		2
16	0	1899,908	sp P1487	sp P1487	1830	1845	yes	yes		3
16	2	1756,907	sp Q9QYR	sp Q9QYR	2378	2393	yes	no	3;4	
10	0	1106,572	tr A0A0J9	tr A0A0J9	45	54	no	no		2
18	0	1926,86	sp P1487	sp P1487	2378	2395	yes	yes		2
16	0	1690,718	sp P63017	sp P63017	221	236	yes	no		3
11	0	1231,616	sp P4796	sp P4796	106	116	yes	yes		2
12	0	1270,619	tr D3YWT	tr D3YWT	56	67	yes	no		2
15	1	1663,846	sp P1487	sp P1487	1457	1471	yes	yes		2
16	2	1791,941	sp P1487	sp P1487	1457	1472	yes	yes	2;3	
9	0	1064,492	CON__P35	CON__P35	155	163	yes	yes		2
11	0	1191,562	sp Q9QYR	sp Q9QYR	2623	2633	yes	no		2
10	0	1119,469	CON__P35	CON__P35	36	45	yes	yes		2
10	0	1119,592	sp P1012	sp P1012	21	30	no	no		2
8	0	844,5018	sp Q0326	sp Q0326	254	261	yes	no		2
14	0	1543,861	sp P1487	sp P1487	401	414	yes	yes		2
12	0	1347,703	sp P1487	sp P1487	1271	1282	yes	yes		2
14	0	1547,706	tr A0A2I3I	tr A0A2I3I	28	41	yes	no		2
15	0	1793,87	sp Q8VHC	sp Q8VHC	510	524	yes	no		3
15	0	1567,821	tr G3UYW	tr G3UYW	93	107	yes	no		2

11	0	1268,702	CON__Q5I	CON__Q5I	7	17	yes	yes		2
16	0	1803,802	sp Q80WJ	sp Q80WJ	5	20	yes	no		2
11	0	1339,714	sp P14094	sp P14094	97	107	yes	no		2
16	0	1789,885	sp P6326C	sp P6326C	239	254	no	no	2;3	
8	1	1032,572	sp Q9DD1	sp Q9DD1	116	123	yes	yes		2
11	0	1207,609	CON__P35	CON__P35	282	292	yes	yes		2
12	1	1335,703	CON__P35	CON__P35	282	293	yes	yes	2;3	
11	0	1221,624	CON__P02	CON__P02	261	271	no	no		2
12	1	1349,719	CON__P02	CON__P02	261	272	no	no		2
8	0	998,4458	sp Q9QYR	sp Q9QYR	2679	2686	yes	no		2
15	0	1514,788	sp P5051€	sp P5051€	309	323	yes	yes		2
8	0	855,4814	sp P48962	sp P48962	24	31	no	no	1;2	
9	0	1016,478	sp Q7TMM	sp P68372	351	359	no	no		2
13	0	1330,709	tr A0A1B0	tr A0A1B0	50	62	yes	no		2
13	0	1440,514	CON__P02	CON__P02	76	88	yes	yes	2;3	
17	0	1779,791	tr B2M1R	tr B2M1R	70	86	yes	no		2
10	0	1241,556	CON__P13	CON__P13	355	364	no	no		2
19	1	2119,039	CON__P08	CON__P08	312	330	yes	yes	2;3	
15	0	1572,855	sp Q6ZWx	sp Q6ZWx	245	259	yes	yes		2
12	0	1283,697	sp Q80WJ	sp Q80WJ	34	45	yes	no		2
11	0	1273,615	sp Q6164	sp Q6164	176	186	yes	no		2
13	0	1480,662	sp P5039€	sp P5039€	157	169	yes	yes		2
9	0	1034,576	tr A0A338	tr A0A338	55	63	yes	no		2
16	0	1623,883	sp Q0326!	sp Q0326!	134	149	yes	no		2
12	0	1407,682	tr G3UXT7	tr G3UXT7	8	19	yes	no		2
13	0	1422,666	sp Q0326!	sp Q0326!	46	58	yes	no		2
12	0	1310,647	tr Q8VHM	tr Q8VHM	134	145	no	no		2
11	0	1330,583	sp P14873	sp P14873	1894	1904	yes	yes	2;3	
15	0	1587,873	sp P1012€	sp P1012€	6	20	no	no		3
9	0	981,5607	tr Q7M6V	tr Q7M6V	187	195	yes	no		2
16	0	1992,969	CON__P04	CON__P04	224	239	yes	yes	2;3	
11	0	1307,651	tr A2AKV1	tr A2AKV1	120	130	yes	no		2
12	0	1261,634	sp P5648C	sp P5648C	110	121	yes	yes		2
27	1	3051,62	CON__P13	CON__P13	202	228	yes	yes		3
20	0	2006,886	sp P05213	sp P05213	41	60	no	no	2;3	
15	0	1584,862	tr Z4YKA3	tr Z4YKA3	96	110	yes	no		2
13	0	1586,726	sp P6836€	sp P6836€	340	352	no	no		2
16	0	1786,92	tr A0A0A€	tr A0A0A€	12	27	yes	no		2
10	1	1258,667	CON__P08	CON__P08	204	213	yes	yes		3
10	1	1265,662	CON__P02	CON__P02	202	211	yes	no		2
10	0	1174,627	tr Q792Z1	tr Q792Z1	103	112	yes	yes		2
28	0	2964,399	sp P14873	sp P14873	1312	1339	yes	yes		3
10	0	1068,618	tr Q8VHM	tr Q8VHM	32	41	yes	no		2
9	0	1059,556	CON__P35	CON__P35	225	233	yes	yes		2
9	0	1032,509	CON__P04	CON__P04	484	492	no	no		2
10	0	1095,494		REV__tr H7BWZ4 H7BWZ4_MC			yes	yes		2
15	1	1850,92	CON__P35	CON__P35	322	336	yes	yes	2;3	
13	0	1583,798	sp P4609€	sp P4609€	201	213	yes	yes		2
13	0	1348,727	sp P1149€	sp P1149€	83	95	yes	yes		2
11	0	1342,659	tr A0A0R4	tr A0A0R4	224	234	yes	no		2

11	0	1328,644	sp P4609€	sp P4609€	223	233	yes	yes		2
16	0	1848,933	CON__Q0€	CON__Q0€	306	321	no	no		2
16	0	1891,938	CON__P02	CON__P02	337	352	yes	no		2
12	0	1351,604	sp Q0225€	sp Q0225€	192	203	yes	yes		2
13	0	1390,701	sp Q80WJ	sp Q80WJ	489	501	yes	no		2
11	0	1264,63	CON__P04	CON__P04	278	288	no	no		2
12	1	1392,725	CON__P04	CON__P04	278	289	no	no	2;3	
10	0	1243,616	tr B0V2N€	tr B0V2N€	136	145	yes	no		2
11	0	1249,667	tr A0A1B0	tr A0A1B0	10	20	yes	no		2
15	0	1730,863	sp Q6073€	sp Q6073€	108	122	yes	no		3
14	0	1587,694	sp P1487€	sp P1487€	1945	1958	yes	yes		2
11	0	1272,587	sp P1487€	sp P1487€	1962	1972	yes	yes		2
15	0	1589,871	sp Q9D6R	sp Q9D6R	101	115	yes	no		3
17	0	1673,899	sp Q8QZT	sp Q8QZT	47	63	yes	yes	2;3	
15	0	1473,83	CON__P12	CON__P12	334	348	yes	yes		2
14	0	1604,695	sp P1487€	sp P1487€	2047	2060	yes	yes		2
15	0	1505,736	tr F7BNZ5	tr F7BNZ5	269	283	yes	no		2
12	0	1370,723	tr A0A0R4	tr A0A0R4	649	660	yes	no		2
12	0	1459,71	tr A0A498	tr A0A498	78	89	yes	no		2
8	0	968,4451	sp P4300€	sp P4300€	518	525	yes	no		2
11	1	1375,648	sp P4300€	sp P4300€	518	528	yes	no	2;3;4	
9	0	1120,588	CON__Q7€	CON__Q7€	340	348	yes	yes		2
20	1	2317,137	sp P5648€	sp P5648€	240	259	yes	yes		3
11	1	1389,689	sp Q9QYR	sp Q9QYR	2186	2196	yes	no		3
11	1	1378,721	CON__P08	CON__P08	408	418	no	no		2
12	2	1534,822	CON__P08	CON__P08	408	419	no	no		3
13	0	1296,58	sp P6020€	sp P6020€	193	205	yes	yes		2
18	0	1938,884	sp P1487€	sp P1487€	1473	1490	yes	yes		2
8	0	883,44	CON__P13	CON__P13	30	37	no	no		2
12	0	1227,671	sp P4327€	sp P4327€	35	46	yes	yes		2
12	0	1315,735	sp Q0326€	sp Q0326€	219	230	yes	no		2
18	0	2126,943	CON__P35	CON__P35	254	271	yes	yes		2
19	1	2255,038	CON__P35	CON__P35	254	272	yes	yes	2;3	
20	0	2049,053	sp P4300€	sp P4300€	478	497	yes	no	2;3	
11	0	1281,628	CON__P13	CON__P13	266	276	no	no		2
12	1	1409,723	CON__P13	CON__P13	266	277	no	no	2;3	
13	0	1409,657	tr F8VQE2	tr F8VQE2	212	224	yes	no		2
31	0	2669,424	sp P1487€	sp P1487€	788	818	yes	yes	2;3	
12	0	1379,709	sp P1887€	sp P1887€	182	193	yes	no		2
30	0	3182,607	sp P6326€	sp P6326€	148	177	no	no	3;4	
19	1	2114,973	sp P1414€	sp P1414€	246	264	yes	yes		4
10	0	1130,572	tr A0A498	tr A0A498	63	72	yes	no	2;3	
16	0	1773,911	sp Q6187€	sp Q6187€	1762	1777	yes	no		2
13	0	1486,694	sp P6301€	sp P6301€	37	49	yes	no		2
13	0	1363,698	sp P2436€	sp P2436€	72	84	yes	yes		2
11	0	1270,641	sp Q80WJ	sp Q80WJ	131	141	yes	no		2
13	0	1456,832	sp P5648€	sp P5648€	213	225	yes	yes		2
12	0	1398,685	CON__P02	CON__P02	569	580	yes	yes		2
18	0	2230,977	sp Q6PIC6	sp Q6PIC6	884	901	yes	no		2
12	0	1161,588	sp O5478€	sp O5478€	485	496	yes	no		2

28	1	2928,454	tr Q9DAY€tr Q9DAY€	46	73	yes	no		3
18	0	1980,991	sp P63017sp P63017	138	155	yes	yes		2
12	0	1325,65	sp O8893!sp O8893!	300	311	yes	yes		2
10	0	1032,509	sp Q78PY' sp Q78PY'	504	513	yes	no		2
11	0	1218,625	sp Q6PIC6 sp Q6PIC6	467	477	no	no		2
15	0	1600,803	sp P5648C sp P5648C	265	279	yes	yes		2
18	0	1953,057	sp Q8BFZ€ sp Q8BFZ€	97	114	yes	yes		3
18	0	1953,057	sp P6326C sp P6326C	96	113	yes	no	2;3	
14	0	1488,866	sp P14094 sp P14094	72	85	yes	no		2
8	0	841,5022	CON__P0C CON__P0C	108	115	yes	yes		2
19	0	1792,082	sp P0824€ sp P0824€	27	45	yes	no		2
12	0	1424,668	CON__P13 CON__P13	293	304	no	no		2
15	1	1564,81	tr A2BI12 tr A2BI12	25	39	yes	no	2;3	
12	0	1459,792	CON__P35 CON__P35	309	320	yes	yes		2
13	0	1567,723	tr Q9DAY€tr Q9DAY€	33	45	yes	no	2;3	
15	0	1618,744	sp Q6PIC6 sp Q6PIC6	203	217	no	no		2
23	0	2520,301	sp P1487€ sp P1487€	304	326	yes	yes		3
12	0	1334,708	CON__Q7€ CON__Q7€	289	300	yes	yes		2
11	0	1227,621	sp P63017sp P63017	26	36	yes	no		2
15	0	1374,699	tr A0A3B2tr A0A3B2	720	734	yes	no		2
24	1	2570,414	sp P62631sp P62631	267	290	yes	yes		3
24	1	2514,377	sp P1012€ sp P1012€	267	290	yes	yes		3
17	1	2044,088	CON__P02 CON__P02	397	413	yes	yes		3
8	1	958,5852	sp P4609€ sp P4609€	183	190	no	no		2
13	0	1411,71	sp P4609€ sp P4609€	376	388	yes	yes		2
17	0	1764,878	sp P4666C sp P4666C	468	484	yes	yes		2
10	0	1059,52	sp P1092€ sp P1092€	60	69	yes	yes		2
12	0	1232,589	sp P6303€ sp P6303€	406	417	yes	yes		2
18	0	1823,978	sp P6836€ sp P0521€	353	370	no	no	2;3	
8	0	804,4242	sp P1685€ sp P1685€	4	11	yes	no		2
8	0	805,4446	tr D6RE19tr D6RE19	13	20	yes	no		2
10	0	1051,541	tr D3YWT' tr D3YWT'	208	217	yes	no		2
11	0	1381,678	sp Q78PY' sp Q78PY'	759	769	yes	yes		2
9	0	970,56	tr Q29ZQ€tr Q29ZQ€	34	42	yes	no		2
24	0	2594,353	sp P1685€ sp P1685€	161	184	yes	no	3;4	
21	0	2212,102	sp P1685€ sp P1685€	117	137	yes	no	2;3	
14	1	1625,824	sp P2436€ sp P2436€	96	109	yes	yes		3
13	0	1380,744	sp Q6PIC6 sp Q6PIC6	603	615	no	no	2;3	
13	0	1451,789	sp Q8VDD sp Q6187!	191	203	no	no		3
13	0	1464,746	sp Q78PY' sp Q78PY'	874	886	yes	yes		2
12	0	1418,679	sp P1410€ sp P1410€	143	154	yes	yes		2
12	1	1362,835	sp P4896€ sp P4896€	32	43	no	no		3
13	0	1456,777	sp P4646C sp P4646C	517	529	yes	yes		2
9	0	1028,587	CON__P08 CON__P08	226	234	no	no		2
9	0	1030,591	CON__P13 CON__P13	258	266	yes	yes		2
19	1	1918,089	sp P5648C sp P5648C	125	143	yes	yes		3
18	0	2021,047	sp P1487€ sp P1487€	487	504	yes	yes		2
18	0	1981,93	sp P09411sp P09411	247	264	yes	yes		2
11	0	1334,742	tr A0A0J9' tr A0A0J9'	280	290	yes	no		2
11	0	1327,735	tr A0A3B2tr A0A3B2	615	625	yes	no		2

16	0	1814,981	CON__P08	CON__P08	339	354	yes	yes		2
10	0	999,5713	sp Q0326!	sp Q0326!	74	83	yes	no		2
11	0	1302,718	sp Q0444!	sp Q0444!	33	43	yes	yes		2
10	0	1142,666	sp Q6ZW\	sp Q6ZW\	57	66	yes	yes		2
14	0	1454,762	sp P4300€	sp P4300€	195	208	yes	no		2
11	0	1309,663	sp P1633C	sp P1633C	117	127	yes	yes	2;3	
10	0	1158,643	sp O0859€	sp O0859€	30	39	yes	yes		2
27	0	3047,487	CON__P35	CON__P35	321	347	yes	yes	3;4	
13	0	1398,791	sp Q78PY!	sp Q78PY!	347	359	yes	no		2
20	0	1929	sp Q8QZT	sp Q8QZT	371	390	yes	yes	3;4	
15	0	1621,78	sp P17182	sp P17182	344	358	yes	no		2
11	1	1240,678	sp P62751	sp P62751	124	134	yes	yes		2
11	0	1254,62	sp Q9QYR	sp Q9QYR	1905	1915	yes	no	2;3	
16	0	1915,889	sp P4609€	sp P4609€	245	260	yes	yes	2;3	
16	0	1882,925	tr A0A0R4	tr A0A0R4	246	261	yes	no		2
14	0	1510,836	CON__P02	CON__P02	438	451	no	no		2
15	0	1507,752	sp Q9QYR	sp Q9QYR	1781	1795	yes	no		2
14	0	1544,769	sp P1685€	sp P1685€	233	246	yes	no		2
9	0	989,5182	tr A0A0R4	tr A0A0R4	215	223	yes	yes		2
9	0	948,4917	sp P4609€	sp P4609€	214	222	yes	yes		2
14	0	1585,758	CON__P35	CON__P35	171	184	yes	yes	2;3	
12	0	1477,8	CON__Q8!	CON__Q8!	328	339	yes	no	2;3	
10	1	1179,614	sp P63017	sp P63017	103	112	yes	no		3
12	0	1376,755	sp P4609€	sp P4609€	355	366	no	no		2
15	1	1674,956	tr A0A0R4	tr A0A0R4	356	370	yes	no		2
13	2	1446,768	sp Q9QYR	sp Q9QYR	380	392	yes	no		3
17	0	1661,793	tr A2AUK7	tr A2AUK7	571	587	yes	no		2
14	0	1649,867	sp Q9ER7!	sp Q9ER7!	324	337	yes	yes		2
15	0	1398,638	CON__P13	CON__P13	49	63	yes	yes		2
9	0	1089,524	CON__P08	CON__P13	148	156	no	no		2
18	2	2135,116	CON__P08	CON__P13	148	165	no	no		3
11	0	1196,713	tr A0A0R4	tr A0A0R4	339	349	yes	no		2
18	0	1965,105	sp O5477!	sp O5477!	511	528	yes	yes		3
12	0	1170,625	sp Q0326!	sp Q0326!	150	161	yes	no		2
11	0	1226,604	sp P1685€	sp P1685€	322	332	yes	no		2
12	1	1355,647	sp P1685€	sp P1685€	322	333	yes	no		2
8	0	948,5029	tr A0A0R4	tr A0A0R4	375	382	yes	no		2
15	0	1601,882	tr H7BXC3	tr H7BXC3	79	93	yes	no		2
10	0	1081,613	sp P4646C	sp P4646C	284	293	yes	yes		2
16	0	1794,909	tr A0A075	tr A0A075	191	206	no	no	2;3	
14	0	1596,888	sp Q9QYR	sp Q9QYR	179	192	yes	no	2;3	
14	0	1523,835	sp Q6187!	sp Q6187!	349	362	yes	no		2
12	0	1347,652	sp Q6ZW\	sp Q6ZW\	277	288	yes	yes		2
12	0	1299,671	tr A2AKV1	tr A2AKV1	44	55	yes	no		2
12	0	1474,742	CON__P04	CON__P04	212	223	yes	yes		2
21	0	2290,046	sp P1685€	sp P1685€	85	105	yes	no	2;3	
10	0	1172,576	sp Q6TDP.	sp Q6TDP.	367	376	yes	yes		2
19	1	2165,1	sp Q9QYR	sp Q9QYR	1743	1761	yes	no		3
17	2	2204,12	tr Q80VE5	tr Q80VE5	409	425	yes	no		3
10	0	1202,63	CON__P02	CON__P13	195	204	no	no		2

11	0	1336,619	sp P1876C sp P1876C	82	92	yes	no		2
8	0	991,3883	tr A0A2I3I tr A0A2I3I	307	314	yes	no		2
8	1	1065,509	CON__P35 CON__P35	274	281	no	no		2
10	0	1178,593	CON__P04 CON__P04	377	386	yes	yes		2
10	0	1193,568	CON__P13 CON__P13	365	374	no	no		2
10	0	1164,578	sp Q8BGZ CON__P02	360	369	no	no		2
10	0	1192,609	CON__P35 CON__P35	381	390	yes	yes		2
11	0	1257,697	sp Q6187I sp Q6187I	728	738	yes	no		2
8	0	992,4927	CON__P13 CON__P13	238	245	yes	yes		2
12	0	1445,734	sp P48962 sp P48962	81	92	no	no		2
14	0	1394,618	CON__Q8I CON__Q8I	649	662	yes	yes		2
12	0	1431,601	CON__P02 CON__P02	286	297	yes	yes		2
9	0	1150,551	sp P1149I sp P1149I	276	284	yes	no		2
9	0	1079,543	sp Q0475I sp Q0475I	428	436	yes	yes		2
12	0	1438,734	sp P17182 sp P17182	270	281	yes	no		2
12	1	1278,646	tr A0A2I3I tr A0A2I3I	128	139	yes	no		2
12	0	1335,624	tr A0A498 tr A0A498	13	24	yes	no	2;3	
12	0	1441,745	CON__Q8I CON__Q8I	275	286	yes	no		2
9	0	1036,519	CON__P35 CON__P35	245	253	yes	yes		2
9	0	994,5521	sp O5477I sp O5477I	321	329	yes	yes		2
9	0	1092,553	sp Q6074I sp Q6074I	103	111	yes	no		2
9	0	1052,602	sp Q7TMM sp Q7TMM	310	318	no	no		2
9	0	1038,586	sp P68372 sp P68372	310	318	no	no		2
9	0	1068,597	sp Q9ERD sp Q9ERD	310	318	no	no		2
12	0	1381,691	sp Q8VEKI sp Q8VEKI	501	512	yes	yes		2
14	0	1593,819	sp Q00PI9 sp Q00PI9	479	492	yes	yes		2
16	0	1959,904	sp P68134 sp P68134	71	86	yes	no	2;3	
15	0	1829,818	sp Q6PIC6 sp Q6PIC6	478	492	yes	no		3
13	0	1437,717	sp P10922 sp P10922	28	40	yes	yes		2
9	0	1048,544	tr A2A4QC tr A2A4QC	36	44	yes	no		2
10	0	1136,546	sp P4646C sp P4646C	294	303	yes	yes		2
12	0	1419,715	tr Q9CPNI tr Q9CPNI	236	247	yes	yes	1;2	
12	0	1403,72	sp P1012I sp P1012I	85	96	yes	no	2;3	

PEP	Score	Identificat	Identificat	Identificat	Identificat	Identificat	Identificat	Identificat	Identificat
0,000806	94,487	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By MS/MS	By MS/MS
0,00021	95,662	By MS/MS	By MS/MS	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
7,94E-24	156,29	By MS/MS	By MS/MS	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
1,72E-47	211,83	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
9,07E-17	154,13	By MS/MS	By MS/MS	By MS/MS	By matchir	By matchir	By MS/MS	By MS/MS	By MS/MS
0,001094	96,229	By MS/MS	By MS/MS	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
1,70E-07	100,69	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By matchir	By matchir
0,014351	63,624	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By MS/MS	By MS/MS
0,006464	57,045	By MS/MS	By MS/MS	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
6,45E-13	135,57	By matchir	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
2,73E-05	123,75	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By MS/MS	By matchir
0,00678	87,184	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By MS/MS	By MS/MS
0,000182	131,22	By matchir	By MS/MS	By matchir	By matchir	By matchir	By MS/MS	By MS/MS	By MS/MS
0,015768	89,355	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By matchir	By MS/MS
0,001936	64,454	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By matchir	By MS/MS
4,41E-17	151,49	By MS/MS	By matchir	By MS/MS	By MS/MS	By MS/MS	By matchir	By MS/MS	By MS/MS
2,19E-24	164,58	By matchir	By matchir	By matchir	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By matchir
3,62E-07	105,06	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By matchir	By matchir
0,014879	71,888	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By MS/MS	By matchir
0,034688	40,727	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS
7,48E-09	140,91	By MS/MS	By MS/MS	By matchir	By MS/MS	By matchir	By matchir	By matchir	By MS/MS
5,33E-50	229,82	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
0,003642	85,166	By matchir	By matchir	By MS/MS	By MS/MS	By MS/MS	By matchir	By matchir	By matchir
1,02E-06	134,57	By MS/MS	By MS/MS	By matchir	By MS/MS	By MS/MS	By matchir	By matchir	By MS/MS
0,000551	128,36	By MS/MS	By MS/MS	By matchir	By matchir	By matchir	By MS/MS	By matchir	By matchir
0,006496	87,667	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By matchir	By MS/MS
0,039328	77,318	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
4,70E-64	229,02	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
5,91E-08	109,87	By matchir	By matchir	By MS/MS	By MS/MS	By matchir	By MS/MS	By MS/MS	By MS/MS
0,000257	88,768	By matchir	By matchir	By matchir	By MS/MS	By MS/MS	By matchir	By MS/MS	By matchir
0,02933	45,347	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
0,007903	75,788	By matchir	By matchir	By matchir	By MS/MS	By matchir	By matchir	By matchir	By matchir
3,96E-07	139,43	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By matchir	By MS/MS
0,011011	114,86	By MS/MS	By MS/MS	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
0,007595	40,625	By matchir	By MS/MS	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
0,017267	76,326	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By matchir
1,92E-17	162,31	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
2,52E-05	121,9	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By MS/MS
0,004691	51,431	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
0,003855	78,615	By matchir	By matchir	By matchir	By matchir	By MS/MS	By MS/MS	By MS/MS	By MS/MS
0,00047	86,005	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
0,009143	86,794	By MS/MS	By MS/MS	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
3,45E-07	120,29	By matchir	By matchir	By MS/MS	By matchir	By MS/MS	By matchir	By matchir	By matchir
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0,005964	95,502	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By MS/MS	By MS/MS
1,78E-17	151,11	By MS/MS	By MS/MS	By MS/MS	By matchir	By MS/MS	By matchir	By matchir	By MS/MS
1,91E-18	172,56	By MS/MS	By MS/MS	By matchir	By matchir	By matchir	By matchir	By matchir	By matchir
8,40E-22	159,22	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS	By MS/MS
0,003086	75,088	By matchir	By matchir	By matchir	By matchir	By matchir	By MS/MS	By matchir	By matchir

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8,40E-10 154,85 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS
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1,06E-21 163,62 By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS By MS/MS
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0,006953 41,367 By MS/MS By matchir By matchir By matchir By matchir By matchir By matchir By matchir
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8,72E-07 99,414 By matchir By matchir By matchir By matchir By matchir By MS/MS By MS/MS By MS/MS
0,030216 72,928 By matchir By matchir By matchir By matchir By matchir By MS/MS By matchir By matchir
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By matchir	1	1					1	1	1
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By matching						1	1	1	1
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By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matchir	1			1		1	1	1	
By MS/MS	1	1	1	1	1	1	1	1	1
By matching						1		1	1
By matchir	1								1
By MS/MS		1	1	1	1	1	1	1	1
By MS/MS	2	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matching			1	1	1	1	1	1	1
By MS/MS	1							1	1
By matchir	1	1							
By MS/MS	1	1		1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	
By matchir	1	1	1	1	1	1	1	1	
By matchir	1	1							
By matching			1	1	1		1		1
By matchir	1								
By matchir	1	1							
By matchir	1	1							
By matchir	2	2	1	1	2		1	1	
By matching		1							
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	2	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matching					1	1	1	1	1
By matchir	1	1							
By matchir	1	1							
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS		1	1	1	1	1	1	1	1
By matching						1	1		
By matching					1				
By matchir	1	1							
By matchir	1	1	1	1	1		1		
By matchir	1	1	1			1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matching		1							
By matchir	1	1							
By matchir	1	1	1	1	1				
By MS/MS	1	1	1	1	1	1	1	1	1
By matching		1							
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							

By MS/MS	1	1	1	1	1		1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS					1	1	1	1	1
By MS/MS	1	1	2	2	2	2	2	2	2
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS			1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1					1	1	
By matching							1		
By matching		1	1			1	1	1	1
By matchir	1	1	1	1	1	1	1	1	
By matchir	1	1							
By MS/MS	1	1	1	2	2	1	2	2	1
By MS/MS						1			1
By MS/MS	2	2	2	2	2	2	2	2	2
By MS/MS	1	1	1	1	1	1	1	1	1
By matching		1				1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matching					1		1	1	1
By matchir	1	1				1			
By MS/MS						1	1	1	1
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1		1	1	1	1	1	1
By matchir	1	1							
By matchir	2	2							
By MS/MS	1	1		1		1	1	1	1
By matchir	1	1	1		1	1	1	1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1		1		1				
By matching						1	1	1	1
By MS/MS	1	1	1			1	1	1	1
By matchir	1	1	1						1
By matchir	1	1							
By matchir	1	1							
By matchir	1	1							
By matchir	1	1				1	1		
By MS/MS	2	2	2	2	1	2	2	2	2
By matchir	1	2		1					
By matchir	1	1							
By MS/MS						1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1			1	1		
By matchir	1	1	1		1	1	1	1	1
By MS/MS						1	1	1	1

By matching				1			1	1	1
By MS/MS	1	1	1	1	2	1	1	2	1
By matching						1	1	1	1
By MS/MS	2	2	1	1	1	2	2	2	2
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matching		1							
By matchir	2	2		1	1	1	1	1	
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1					1	1	
By matchir	2	2					1	1	
By matchir	1	1							
By matchir	2	2							
By matchir	1		1	1	1	1	1	1	1
By MS/MS					1	1		1	1
By matchir	1								
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS			1			1	1	1	1
By matching			1		1			1	
By matchir	1	1	1	1	1		1		
By matchir	1	1	1	1	1	1	1		
By MS/MS	1	1	1		1	1	1	1	1
By MS/MS	1	1	1	1	1		1	1	1
By matching			1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	2	1	2	2	2	2	2
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS		1	1	1			1		1
By MS/MS	1	1	1	1	1	1		1	1
By matching				1	1	1	1	1	1
By MS/MS			1	1		1	1	1	1
By matchir	1	1							
By MS/MS	2	2	2	2	2	2	2	2	2
By matchir	1	1							
By matchir	1	1							
By MS/MS	2	2	1	2	1	2	2	2	2
By MS/MS						1	1	1	1
By matchir	2	1	2	1	1	2	2	2	2
By matchir	1			1	1				1
By matching						1	1	1	
By MS/MS	2	2	1	2	1	2	2	2	2
By matching								1	
By matching				1		1			
By MS/MS	2	2	2	1	2	2	2	2	1
By MS/MS	1	1	2	2	1	1	1	1	1
By MS/MS	1	1		1	1	1	1	1	1

By matchir	1	1							
By matchir	1	1		1		2			
By matching				1		1			
By MS/MS		1				1	1	1	1
By MS/MS	1	1		1	1	1	1	1	1
By matchir	1	1							
By matchir	1	2							
By MS/MS	2	2	1	1	2	2	2	2	2
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matching						1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matching						1	1		
By MS/MS	1	1	1		1	1		1	1
By MS/MS	1	1	1	2	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	
By MS/MS						1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS		1	1		1	1	1	1	1
By MS/MS	1	1	2	2	1	2	2	2	2
By MS/MS	1	1		1	1				1
By matchir	1	1							
By matching						1	1		1
By MS/MS		1	1	1	1	2	2	2	2
By matching			1	1	1	1	1	1	1
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1		1	1		1
By MS/MS			1	1	1	1		1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By MS/MS	1	1	1	1	1	1		1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1				1	1	1	
By MS/MS	1	1	1	1	1		1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	2	2	2	2
By MS/MS	1		1	1	1	1	1	1	1
By matching							1	1	
By matchir	1	1							
By matching						1		1	
By MS/MS	2	1	2	1	1	2	2	2	2
By matching			1	1	1		1		1
By matchir	1		1	1	1	1	1	1	1
By MS/MS						1	1	1	1
By MS/MS						1	1	1	1
By matching		1	1	1	1	1			
By MS/MS	1	1	2	1	1	2	2	2	2

By MS/MS						1	1	1	1
By matchir	1	1			1	1	1	1	1
By matching			1	1	1		1	1	1
By MS/MS	1	1	1		1	1	1	1	1
By matchir	1	1	1	1				1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	2	2							
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1		1		
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	2		1	1
By MS/MS	1		1	1	1	1	1	1	1
By MS/MS	1					1	1	1	1
By matchir	1	1							
By matchir	1	1							
By matchir	1	1							
By MS/MS	2	2	2	2		2	2	2	2
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By MS/MS							1	1	1
By matchir	1	1	1		1	1	1	1	1
By matchir	1	1							
By matchir	1	1						1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matching			1	1	1	1	1	1	1
By MS/MS	1	1	1		1	1		1	1
By matchir	1	1							
By matchir	1	1							
By MS/MS						1	1		1
By MS/MS			1	1		1	1	1	1
By MS/MS	1					1	1	1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By MS/MS	4	4	3	4	3	4	2	3	4
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1			1	1	1	1	
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By matching		1	1	1	1	1	1	1	
By matchir	1		1	1	1	1	1	1	1
By MS/MS					1			1	1
By MS/MS			1		1	1	1	1	1
By matchir	1	1							
By matchir	1					1		1	1
By MS/MS						2	1	2	1
By MS/MS	2	2	2	2	2	1	2	2	2
By MS/MS	1	1	1		1	1	1	1	1
By MS/MS						1	1	1	2

By matching						1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By MS/MS						2	2	1	2
By MS/MS	1	1				1	1	1	1
By MS/MS	2	2	2	1	2	2	1	2	2
By matchir	1	1							
By matching			1	1	1			1	1
By matching							1		
By matching							1		
By matchir	1	1							
By matchir	2	2							
By MS/MS		1				1	1	1	1
By MS/MS	2	2	2	2	2	2	2	2	1
By matchir	1	1					1		
By matchir	1	1							
By matchir	1	1	1	1	1	1	1	1	
By matchir	1	1	1		1	1	1	1	
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS						1	1	1	1
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	2	2	2	1	1		1
By MS/MS	1		1	1	1		1	1	1
By MS/MS	1					1	1	1	1
By matchir	2	1							
By matchir	1	1	1	1		1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1		1	1		
By matchir	1		1		1	1		1	
By matchir	1	1							
By MS/MS	4	3	3	3	4	3	3	3	3
By MS/MS	1	1	1	1	1	1		2	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matching				1					
By MS/MS	1		1	1	1	1	1	1	1
By matchir	1	1	1						
By matchir	1	1				1	1		1
By MS/MS				1	1	1	1	1	1
By MS/MS	1	1	1	1	1	2	2	2	2
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	2	1	1
By MS/MS	1		1	1	1	1	1	1	1
By MS/MS	1	1	1	1		1	1	1	1
By MS/MS	1		1	1	1	1	1		1
By MS/MS	1	1	1	2	1	2	2	1	2
By matching		1							

By matchir	1	1							
By matchir	2	2					1		
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	1	2	2	2	2	2	2
By MS/MS						1		1	2
By matchir	1		1	1	1	1	1	1	1
By matchir	1	1	1	1	1		1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By MS/MS	1	1		1	1	1	1	1	1
By MS/MS					1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	2		2	1	2	1	2
By MS/MS	1	1	1			1	1	1	1
By matchir	1		1		1	1	1		1
By MS/MS	2	2	2	2	2	2	2	2	2
By matching		1	1	1	1		1		1
By MS/MS						1	1	1	1
By matchir	1	1							
By MS/MS		1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1		1
By MS/MS	1	1	1	1	1	1	1	1	1
By matching			1	1	1		1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1		1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By MS/MS	1	1				1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	1	1	1	2	1	2	2
By MS/MS						1	1	1	1
By matchir	1	1	1	1	1			1	1
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1		1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	3	3	2	3	1	3	1	3	3
By MS/MS						1	1	1	1
By MS/MS	1	1		1		1	1	1	1
By matchir	1	1		1			1		
By matchir	1	1							
By matching		1	1			1	1	1	
By matchir	1	1							
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							

By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matching						1	1	1	1
By matchir	1			1	1		1	1	1
By MS/MS		1						1	1
By MS/MS						1	1	1	2
By matchir	1	1							
By matching		1							
By MS/MS						2	1	2	2
By MS/MS	2	2	2	2	2	2	2	2	2
By matchir	1	1	1	1	1	1	1		1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS			1	1	1	1	1		1
By matchir	1	1							
By matchir	1		1	1	1				
By MS/MS	1	1			1	1	1	1	1
By matching		1	1	1	1				
By matching			1	1	1	1			
By MS/MS	1	1			1	1	1	1	1
By MS/MS						1			1
By MS/MS			1	1	1	1		1	1
By MS/MS	1	1	1	1	1	1			1
By matching								1	
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1				1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1			1	1			
By MS/MS								1	1
By matchir	1	1							
By matching			1	1	1	1			
By matching						1			
By matchir	1	1				1	1		
By MS/MS						1		1	1
By MS/MS	1	1				1	1	1	1
By matchir	1	1		1	1	1	1	1	1
By matchir	1								
By MS/MS	3	2	2	2	2	3	4	5	4
By matchir	1	1	1	1	1				
By matching					1				
By matchir	1	1							
By matchir	1	1	1		1		1	1	1
By matchir	1	1							
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By matching						1	1		1
By matchir	1	1	1	1		1		1	1
By MS/MS	2	2	1	1	1	4	4	4	4
By MS/MS			1	1	1	1	1	1	1
By matching			1	1	1	1	1		1
By matching						1		1	

By MS/MS	1	1	1		1	1	1	1	1
By MS/MS	1				1				1
By matchir	1	1	1	1	1		1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	2	2	2	1	2	2	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1					1		1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1		1	1	1	1	1	1	1
By MS/MS	2	1	2	2	2	3	3	3	2
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By MS/MS	2	2	1	1	1	2	2	2	2
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1	1			1	1	1	1
By MS/MS							1	1	1
By MS/MS	1		1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS						2	1	2	1
By matchir	1	1				1	1	1	1
By matching			1	1	1	1	1	1	1
By MS/MS						1	1		1
By matchir	1	1							
By matching		1		1			1		
By matching		1							
By matchir	1	1							
By matchir	1								
By MS/MS				1		1	1	1	1
By matchir	1	1	1	1	1		1		
By MS/MS	1	2	2	1	1	2	2	1	2
By matching		1		1	1				
By matchir	1	1							
By MS/MS							1	1	1
By matchir	1	1							
By matchir	1	1	1	1	1		1	1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By MS/MS	1		1	1	1	1	1	1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By matchir	1		1	1	1	1	1		
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	2	2	2	1	1	1	1
By MS/MS		1	1	1	1	1	1		1
By matching				1		1	1		1
By matchir	1		1	1	1	1	1	1	1
By matching		1	1		1	1	1	1	1
By MS/MS				1		1	1	1	1
By matching							1	1	1

By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	2	2
By MS/MS		1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1		1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1		1			1	2	1	2
By matchir	1	1	1	1	1	1	1	1	1
By matching		1			1	1	1	1	
By matching						1	1	1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By matching		1	1	1	1	1	1	1	1
By matching			1						
By matchir	1	1							
By matchir	1	1						1	
By matchir	1	1	2	2	2	2	2	2	1
By MS/MS		1	1	1		1	1	1	1
By MS/MS	2	2	2	2	2	2	1	2	2
By MS/MS	2	2	2	2	2	2	2	2	2
By MS/MS				1	1	1	1	1	1
By MS/MS									1
By matchir	1	1		1	1	1	1	1	
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1		1		1	1	1	
By MS/MS						1	1	1	1
By matchir	1	1					1		
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1		1	1	1	1
By MS/MS			1			1	1	1	1
By matchir	1	1	2	2	1	2	1	1	
By MS/MS						1	1	1	1
By MS/MS						1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1		1
By matchir	1	1		1	1	1	1	1	1
By matchir	1		1	1	1	1	1	1	
By matchir	1	1							
By MS/MS	1	1				1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1		1
By matchir	1	1		1	1	1	1	1	1
By matchir	1		1	1	1	1	1	1	
By matchir	1	1							
By MS/MS	1	1				1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matching						1	1	1	1
By matchir	1	1							
By matchir	1	1		1	1	1		1	
By matchir	1	1							
By MS/MS	1	2	2	1	2	1	2	2	2
By MS/MS						1	1	1	1
By matching						1	1	1	

By MS/MS	1			1		1	1	1	1
By matchir	1	1			1			1	
By MS/MS	1	1	1		1	1		1	1
By matchir	2	2		1	2	2	2	2	2
By matching			1			1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1	1		1	1	1	1	1
By matchir	1	1	1	1	1		1	1	1
By MS/MS					1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1		1
By MS/MS						1	1	1	1
By MS/MS						1	2	2	2
By matchir	1	1							
By matchir	1								
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matchir	1	1							
By MS/MS	2	2	2	2	2	2	1	1	2
By MS/MS	1	1	1				1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	2	2	2	1	2	2	2	1	1
By MS/MS	2	2	1	1	2	2	2	2	2
By MS/MS	1		1	1	1	1	1		1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matchir	1	1	1		1	1	1	1	
By matchir	1	1	1						1
By matchir	1	1			1	1	1	1	1
By MS/MS	2	2	2	2	2	2	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS				1		1		1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matchir	1	1			1		1	1	
By matchir	1	1					1		
By matchir	1	1							
By MS/MS			1	1		1	1	1	1
By matchir	1	1	1		1	1	1	1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By matching		1	1	1					1
By MS/MS	1	2		2	2	2	2	2	1
By matchir	2	1	2	2	2		1	1	1
By MS/MS	3	3	3	3	3	3	3	3	3
By matching			2	1	1				1

By MS/MS		1	1	1	1	1	1	1	1
By MS/MS	1	1	1	2	2	2	2	2	2
By MS/MS	1	1		1	1	1	1	1	1
By matchir	1	1				1			
By MS/MS		1			1	1			1
By matchir	1	1	1	1	1	1	1	1	
By matching		1	1	1	1	1	1	1	
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1		1	1	1	
By MS/MS	2	2	2	2	2	2	2	2	2
By matchir	1		1		1	1	1		
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1		1	1
By MS/MS	2	2	2	2	1	2	2	1	1
By matching					1				
By matching			1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS							1	1	1
By matchir	1	1							
By matchir	1	1							
By matchir	1	1		1					
By matchir	1								
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	2	2	2	1	2	2	2
By MS/MS	2	2	2	2	2	2	2	2	2
By matchir	1	1	1	1	1	1	1		
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matchir	1	1							
By matchir	1	1							
By matchir	2	2			1				
By MS/MS		1		1	1	1	1	1	1
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By matching						1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matchir	2	2							
By MS/MS	2	2		1		2	2	2	2
By matchir	1	1							
By matchir	1	1	1	1		1		1	
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1		1	1	1	1	1	1	1
By matchir	1	1							
By matchir	1	1			1				
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1			1	1	1	1	
By matchir	1	1							

By matching		1	1	1		1	1	1	1
By matchir	1	1							
By MS/MS	1	1		1	1	2		1	1
By MS/MS	2	1	2	2	1	2	2	2	2
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By matchir	1	1	1			1		1	1
By matchir	1	1	1	1		1		1	
By matchir	1	1							
By MS/MS	1	1	1	1	1		1	1	1
By MS/MS	1	2	2	1	1	2	2	2	2
By matching						1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	2	2	1		1	2	2	1	2
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS			1	1	1	1	1	1	1
By matchir	2	2	1	1	1	1		1	1
By matchir	1	1							
By matchir	1	1							
By matching		1			1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1				1			
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS		1	1	1	1	1	1	1	1
By matchir	2	2							
By MS/MS	1	1				1	1	1	1
By matchir	1		1		1	1	1	1	1
By MS/MS	1	1	2	2	2	2	2	2	2
By MS/MS	1	1			1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1		1	1	1	1	1		1
By MS/MS	1	1	1	1	1	2	2	2	2
By matchir	1	1							
By MS/MS				1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1				
By matchir	1	1		1		1	1	1	
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matchir	1	1		1		1	1	1	
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matching						2			1
By MS/MS	2	2	1	2	2	1	2	2	2
By matchir	1	1							
By MS/MS	1	1	2		2	2	2	2	2
By matchir	1	1							

By matchir	1								
By MS/MS	1	1	1	1	1	1	1	1	1
By matching			1		1	1	1	1	1
By matchir	1	1							
By matchir	1	1	1	1	1	1		1	1
By MS/MS	1		1	1	1	1	1	1	1
By matching			1						1
By MS/MS	2	2	1	2	2	2	2	2	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	2	2
By matching			1	1	1			1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	2	2							
By MS/MS		1		1	1	1	1	1	1
By matchir	2	2							
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1								
By matching			1	1	1	1	1		
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS						1		1	1
By MS/MS				1		1	1	1	1
By matching			1	1	1		1	1	
By matchir	1	1							
By matchir	1	1	1					1	
By MS/MS						1	1	1	1
By matchir	1	1	1	1	1				
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	2	2	2	2	2	1	2
By MS/MS						1	1	1	1
By MS/MS							1		1
By matchir	1	1	1		1	1	1	1	1
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By matching						2	1	1	
By matching		1		1		2	1	2	
By matchir	1	1							
By MS/MS	2	2	2	1	2	2	2	2	2
By matching						1	1	1	1
By matchir	1	1							
By MS/MS		1				1	1	1	1
By MS/MS			1			1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1		1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1		1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matching					1				
By matchir	1	1				1	1	1	1
By matchir	1	1	1	1			1		

By MS/MS	1	1	1	1				1	1
By MS/MS	1	1	1		1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS						1	1	1	1
By MS/MS	2	2	2	2	2	2	2	1	2
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	2	1	1	1
By matchir	1	1							
By matchir	2	2					1		
By MS/MS						1	1	1	1
By matchir	1	1							
By matchir	2	2							
By matchir	2	2		1			1		
By matchir	1	1							
By MS/MS	1	1		1	1	1	1	1	1
By matchir	1	1			1	1			
By MS/MS	1	1	1		1	1	1	1	1
By matchir	1	1							
By matching		1	1		1				
By MS/MS	2	2	2	2	2	2	1	2	2
By matching		1	2		1	2	1	2	1
By matching		1							
By matchir	1	1							
By matching		1							
By matchir	1	1							
By matchir	1	1	1						
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	1	1	1	1	1	1	1
By matchir	1	1	1	1					1
By matching						1	1	1	1
By matchir	1	1							
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS						1	1	1	1
By MS/MS				1	1	1	1	1	1
By matching				1		1	1	1	1
By matchir	2	2	2	2	2	1	1	2	2
By matchir	1	2							
By MS/MS							1	1	1
By matchir	1	1							
By MS/MS	1	1	1	1		1	1	1	1
By MS/MS	1	1	1	1		1	1	1	1
By MS/MS		1		2	2	2	2	2	2
By matchir	1	1	1	1	1	1	1	1	1
By matchir	1	1							
By matching				1			1		1
By MS/MS	1	1		1	1	1	1	1	1

By MS/MS						1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	1	2	2	2	2	2	2
By MS/MS	1	1	1	1	1		1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS						1		1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matching						1	1	1	1
By matchir	1			1					1
By MS/MS	1	2	1	1	1	1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1								
By MS/MS	1	1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	2	2	2	2	2	2	2	2	2
By matching				1					
By MS/MS	1	1		1	1	1	1	1	1
By matchir	1	1							
By matchir	1	1	1	1	1	1	1	1	1
By MS/MS	1			1		1	1	1	1
By MS/MS	1	1	1	1	1	1	1	1	1
By MS/MS		1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1	1	1	1	1
By matching		1	1	1	1		1	1	
By MS/MS	2	1	2	1	2	2	2	2	2
By matching		1	1	1	1	1	1	1	1
By matchir	1	1	1	1	1				
By matchir	1	1							
By MS/MS	1		1	1	1	1	1	1	1
By matchir	1	2	2	2	2	1	2	2	2
By MS/MS					1	2	2	2	2

2,32E+06	4,39E+05	0,00E+00	0,00E+00	2,10E+05	2,08E+05	5,16E+05	2,80E+05	3,58E+05	3,10E+05
3,51E+06	1,12E+06	1,01E+06	2,66E+05	0,00E+00	1,82E+05	0,00E+00	1,50E+05	3,59E+05	4,15E+05
7,66E+07	9,83E+06	8,81E+06	7,95E+06	5,01E+06	8,53E+06	9,71E+06	9,06E+06	8,88E+06	8,80E+06
3,15E+06	3,25E+05	2,33E+05	1,93E+05	1,06E+05	2,59E+05	6,34E+05	4,38E+05	5,53E+05	4,08E+05
2,54E+06	1,07E+05	1,20E+05	2,94E+05	1,84E+05	2,69E+05	0,00E+00	5,35E+05	5,93E+05	4,35E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,18E+07	6,16E+05	0,00E+00	0,00E+00	3,02E+05	6,26E+05	3,21E+06	3,49E+06	3,58E+06	0,00E+00
1,54E+07	0,00E+00	0,00E+00	6,16E+05	0,00E+00	0,00E+00	2,97E+06	3,51E+06	4,38E+06	3,88E+06
4,23E+07	2,21E+06	2,21E+06	1,40E+06	3,06E+05	1,41E+06	8,67E+06	8,79E+06	8,89E+06	8,45E+06
1,84E+07	3,11E+05	4,67E+05	7,22E+05	7,72E+05	6,55E+05	6,69E+05	4,18E+06	5,46E+06	5,12E+06
1,13E+08	5,22E+06	4,57E+06	4,61E+06	7,37E+06	3,46E+06	2,92E+07	3,21E+06	2,83E+07	2,71E+07
8,51E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	2,43E+05	0,00E+00	0,00E+00	6,08E+05
5,20E+06	2,70E+06	2,49E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,46E+06	3,12E+05	1,79E+05	4,20E+05	2,81E+05	0,00E+00	0,00E+00	0,00E+00	2,69E+05	0,00E+00
2,06E+06	1,79E+05	1,10E+05	2,04E+05	1,98E+05	1,42E+05	3,38E+05	3,17E+05	3,11E+05	2,66E+05
3,01E+06	1,43E+06	1,58E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,07E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	4,07E+05	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
7,14E+05	3,86E+05	3,28E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,95E+06	8,63E+05	9,37E+05	0,00E+00	0,00E+00	0,00E+00	1,49E+05	0,00E+00	0,00E+00	0,00E+00
4,34E+06	2,94E+05	2,84E+05	2,70E+05	2,02E+05	3,51E+05	8,25E+05	6,36E+05	7,77E+05	6,97E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
9,43E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,89E+05	3,67E+05	0,00E+00	1,87E+05
3,91E+06	1,28E+06	9,42E+05	0,00E+00	0,00E+00	0,00E+00	5,60E+05	6,39E+05	2,02E+05	2,83E+05
1,16E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,96E+05	2,63E+05	3,02E+05	2,01E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
6,54E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	2,08E+06	1,99E+06	1,14E+06	1,34E+06
9,66E+07	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,36E+07	3,01E+07	1,62E+07	1,67E+07
1,04E+08	6,20E+06	5,76E+06	1,86E+07	1,06E+07	0,00E+00	1,88E+07	1,85E+07	1,31E+07	1,28E+07
1,65E+06	5,07E+05	3,92E+05	1,38E+05	9,86E+04	1,36E+05	0,00E+00	0,00E+00	1,53E+05	2,26E+05
1,20E+07	4,00E+06	3,88E+06	0,00E+00	1,02E+06	5,72E+05	0,00E+00	0,00E+00	1,23E+06	1,28E+06
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,91E+06	5,63E+05	8,09E+05	3,49E+05	4,14E+05	3,96E+05	5,40E+05	8,48E+05	5,20E+05	4,74E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,32E+06	0,00E+00	0,00E+00	0,00E+00	2,07E+05	2,73E+05	8,68E+05	8,47E+05	1,14E+06	9,86E+05
1,20E+06	2,46E+05	2,41E+05	0,00E+00	0,00E+00	0,00E+00	1,80E+05	4,34E+05	0,00E+00	1,05E+05
1,73E+06	0,00E+00	0,00E+00	2,95E+05	2,60E+05	3,59E+05	1,93E+05	1,82E+05	2,29E+05	2,10E+05
5,83E+06	1,46E+06	1,60E+06	0,00E+00	5,79E+04	0,00E+00	9,68E+05	9,18E+05	4,54E+05	3,70E+05
5,29E+06	1,50E+06	1,43E+06	1,64E+05	1,08E+05	1,81E+05	6,46E+05	4,93E+05	3,70E+05	3,96E+05
5,07E+06	1,97E+06	1,64E+06	1,39E+05	0,00E+00	1,79E+05	5,73E+05	3,49E+05	9,96E+04	1,20E+05
8,22E+06	2,16E+05	2,36E+05	0,00E+00	1,63E+05	0,00E+00	1,94E+06	2,16E+06	1,64E+06	1,86E+06
6,61E+05	0,00E+00	0,00E+00	6,61E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,49E+07	6,97E+06	7,57E+06	0,00E+00	0,00E+00	0,00E+00	1,09E+05	0,00E+00	1,05E+05	1,25E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,55E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	5,54E+05	5,95E+05	3,99E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,34E+07	2,81E+06	2,41E+06	2,97E+06	4,12E+06	2,04E+06	4,67E+06	4,31E+06	5,27E+06	4,80E+06

0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,48E+06	7,01E+05	7,74E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
6,85E+05	2,64E+05	2,94E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,26E+05	0,00E+00	0,00E+00	0,00E+00
7,62E+06	4,24E+05	4,34E+05	1,25E+06	8,47E+05	1,13E+06	8,49E+05	8,40E+05	1,04E+06	8,10E+05	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,93E+06	2,30E+06	1,44E+06	0,00E+00	6,20E+04	0,00E+00	7,43E+04	0,00E+00	6,21E+04	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
6,14E+06	0,00E+00	3,22E+05	2,22E+05	0,00E+00	2,81E+05	1,55E+06	1,56E+06	1,24E+06	9,68E+05	0,00E+00
2,34E+06	2,13E+05	1,83E+05	2,78E+05	1,67E+05	2,65E+05	3,63E+05	2,81E+05	3,47E+05	2,44E+05	0,00E+00
8,81E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,00E+05	2,65E+05	3,16E+05	0,00E+00	0,00E+00
1,49E+07	6,70E+05	6,85E+05	1,49E+06	1,38E+06	1,36E+06	2,43E+06	2,13E+06	2,14E+06	2,61E+06	0,00E+00
3,38E+07	4,72E+05	5,61E+05	1,02E+06	8,18E+05	8,98E+05	7,07E+06	7,84E+06	7,72E+06	7,37E+06	0,00E+00
1,97E+06	0,00E+00	3,33E+05	0,00E+00	6,42E+05	0,00E+00	9,93E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,93E+06	8,84E+04	0,00E+00	2,05E+05	1,15E+05	3,04E+05	9,60E+05	6,94E+05	7,58E+05	8,09E+05	0,00E+00
1,64E+07	2,11E+05	0,00E+00	1,51E+05	0,00E+00	1,50E+05	4,63E+06	4,11E+06	3,68E+06	3,48E+06	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,09E+06	1,59E+05	1,73E+05	2,99E+05	1,06E+05	1,85E+05	9,25E+05	7,31E+05	6,34E+05	8,80E+05	0,00E+00
1,20E+06	0,00E+00	0,00E+00	2,86E+04	0,00E+00	0,00E+00	2,45E+05	1,11E+05	3,68E+05	4,48E+05	0,00E+00
1,38E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,38E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5,10E+05	5,10E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,64E+06	5,26E+05	6,78E+05	0,00E+00	0,00E+00	0,00E+00	3,34E+05	1,05E+05	0,00E+00	0,00E+00	0,00E+00
2,00E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	5,47E+05	5,62E+05	4,11E+05	4,77E+05	0,00E+00
1,18E+06	6,48E+05	5,35E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
6,72E+07	3,87E+06	3,44E+06	6,76E+06	5,96E+06	4,96E+06	1,19E+07	1,11E+07	1,01E+07	9,03E+06	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5,25E+05	2,56E+05	2,69E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,54E+06	8,63E+05	6,78E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,83E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,83E+05	0,00E+00	0,00E+00
5,43E+06	2,62E+06	2,81E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,97E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,97E+06	0,00E+00
2,83E+06	1,33E+06	1,50E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,54E+06	7,95E+05	7,45E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,83E+06	3,84E+05	2,70E+05	1,37E+05	3,56E+04	1,90E+05	7,88E+05	6,97E+05	6,91E+05	6,36E+05	0,00E+00
2,30E+06	1,31E+06	9,82E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,59E+06	5,20E+05	5,45E+05	8,01E+05	5,12E+05	0,00E+00	5,92E+05	5,86E+05	5,07E+05	5,32E+05	0,00E+00
1,89E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,04E+06	0,00E+00	8,52E+05	0,00E+00	0,00E+00
7,43E+06	2,16E+06	1,74E+06	3,65E+05	3,26E+05	3,78E+05	4,47E+05	4,44E+05	8,44E+05	7,23E+05	0,00E+00
4,14E+07	0,00E+00	7,75E+06	2,87E+06	2,64E+06	2,97E+06	7,40E+06	5,23E+06	6,77E+06	5,80E+06	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,60E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	5,72E+05	5,34E+05	8,37E+05	6,52E+05	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,18E+06	1,49E+06	1,28E+06	1,55E+05	1,80E+05	1,57E+05	1,21E+05	1,51E+05	3,34E+05	3,10E+05	0,00E+00

0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
9,07E+05	4,43E+05	4,64E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,64E+06	0,00E+00	0,00E+00	0,00E+00	7,76E+04	6,49E+04	8,70E+05	6,49E+05	5,57E+05	4,26E+05	
2,58E+07	1,25E+07	1,28E+07	0,00E+00	8,36E+04	0,00E+00	0,00E+00	2,51E+05	1,67E+05	0,00E+00	
1,12E+08	8,34E+06	7,44E+06	1,05E+07	4,03E+06	1,21E+07	2,14E+07	1,94E+07	1,48E+07	1,40E+07	
2,56E+07	1,69E+06	1,65E+06	6,56E+06	1,35E+06	7,54E+06	1,99E+06	2,10E+06	1,33E+06	1,41E+06	
1,22E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,39E+05	3,69E+05	2,33E+05	2,81E+05	
1,83E+07	3,13E+05	4,86E+05	7,64E+05	1,36E+06	1,02E+06	0,00E+00	4,82E+06	5,43E+06	4,08E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
4,07E+06	0,00E+00	0,00E+00	5,65E+05	1,02E+06	7,52E+05	7,86E+05	5,04E+05	0,00E+00	4,49E+05	
1,66E+06	7,40E+05	9,25E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,43E+07	7,65E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	4,87E+06	9,20E+05	5,83E+05	3,19E+05	
1,71E+07	0,00E+00	3,25E+06	1,42E+06	1,33E+06	1,74E+06	2,37E+06	1,92E+06	2,51E+06	2,54E+06	
9,12E+06	1,05E+06	8,80E+05	1,15E+06	4,37E+05	1,08E+06	1,70E+06	1,73E+06	1,10E+06	0,00E+00	
1,06E+09	1,00E+08	8,69E+07	1,41E+08	6,62E+07	1,33E+08	1,63E+08	1,48E+08	1,22E+08	1,02E+08	
1,61E+07	1,50E+06	1,41E+06	2,18E+06	2,16E+06	1,89E+06	1,65E+06	1,78E+06	1,93E+06	1,58E+06	
1,16E+06	1,71E+05	0,00E+00	1,06E+05	1,57E+05	9,48E+04	0,00E+00	2,67E+05	3,64E+05	0,00E+00	
9,61E+05	4,42E+05	5,19E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
2,85E+07	7,96E+05	6,28E+05	8,32E+05	3,65E+05	1,18E+06	6,81E+06	6,54E+06	5,89E+06	5,42E+06	
1,20E+06	5,75E+05	6,25E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
3,52E+06	0,00E+00	0,00E+00	6,58E+05	2,58E+05	7,96E+05	4,42E+05	5,52E+05	3,96E+05	4,19E+05	
3,48E+06	1,74E+06	1,74E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
9,06E+06	5,42E+05	5,40E+05	1,14E+06	1,29E+06	1,07E+06	1,17E+06	9,21E+05	1,22E+06	1,17E+06	
2,83E+07	2,62E+06	3,32E+06	1,78E+06	1,61E+06	2,99E+06	3,70E+06	4,73E+06	3,46E+06	4,05E+06	
1,03E+08	0,00E+00	0,00E+00	1,20E+07	0,00E+00	1,47E+07	2,08E+07	1,66E+07	1,89E+07	2,00E+07	
4,75E+06	0,00E+00	3,38E+05	2,89E+05	0,00E+00	2,19E+05	7,92E+05	1,11E+06	9,93E+05	1,01E+06	
4,43E+06	2,73E+05	0,00E+00	6,13E+05	0,00E+00	5,15E+05	0,00E+00	1,02E+06	9,55E+05	1,05E+06	
2,26E+06	2,12E+05	2,55E+05	4,04E+05	0,00E+00	2,82E+05	2,80E+05	2,05E+05	2,93E+05	3,24E+05	
2,84E+05	0,00E+00	0,00E+00	1,61E+05	1,24E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
4,00E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	4,00E+05	0,00E+00	
3,85E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	2,03E+06	1,81E+06	
7,98E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	7,98E+05	
2,95E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	4,93E+05	0,00E+00	1,26E+06	1,20E+06	
4,88E+06	0,00E+00	4,63E+06	0,00E+00	0,00E+00	1,35E+05	0,00E+00	0,00E+00	0,00E+00	1,12E+05	
1,40E+08	8,94E+06	7,26E+06	4,45E+06	3,06E+06	6,09E+06	0,00E+00	6,09E+07	0,00E+00	4,96E+07	
1,11E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,31E+05	3,43E+05	2,75E+05	1,66E+05	
1,40E+06	6,99E+05	7,01E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,51E+06	7,74E+05	7,39E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
8,36E+06	1,24E+06	1,03E+06	5,78E+05	5,52E+05	6,20E+05	1,57E+06	1,16E+06	7,09E+05	8,97E+05	

3,14E+05	0,00E+00	3,14E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,52E+07	1,83E+06	1,60E+06	1,21E+06	8,55E+05	1,61E+06	2,63E+06	2,11E+06	1,87E+06	1,51E+06	
2,63E+06	0,00E+00	0,00E+00	3,43E+05	0,00E+00	7,66E+05	8,33E+05	3,15E+05	0,00E+00	3,74E+05	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
2,46E+06	2,94E+05	4,06E+05	1,92E+05	2,35E+05	2,27E+05	2,95E+05	3,19E+05	2,46E+05	2,43E+05	
6,77E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,98E+05	3,60E+05	1,20E+05	0,00E+00	
2,91E+06	2,38E+05	2,74E+05	4,37E+05	1,88E+05	2,19E+05	3,80E+05	4,60E+05	3,29E+05	3,83E+05	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,28E+08	1,25E+07	1,02E+07	1,43E+07	9,97E+06	1,34E+07	2,29E+07	1,68E+07	1,36E+07	1,46E+07	
1,27E+08	2,11E+07	1,50E+07	1,95E+06	2,19E+07	1,19E+07	1,66E+07	1,27E+07	1,41E+07	1,19E+07	
1,39E+07	1,79E+06	1,99E+06	7,91E+05	8,10E+05	1,69E+06	1,91E+06	1,95E+06	1,57E+06	1,45E+06	
3,26E+07	4,26E+06	4,94E+06	2,81E+06	3,18E+06	2,88E+06	3,30E+06	3,18E+06	3,77E+06	4,33E+06	
1,89E+06	1,42E+05	0,00E+00	7,84E+04	8,66E+04	1,35E+05	4,07E+05	3,89E+05	3,44E+05	3,11E+05	
3,97E+06	4,84E+05	4,62E+05	4,21E+05	1,66E+05	5,41E+05	5,84E+05	5,80E+05	3,08E+05	4,20E+05	
5,25E+05	2,99E+05	2,26E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,42E+07	1,19E+06	1,09E+06	1,37E+06	3,10E+06	2,34E+06	2,15E+06	0,00E+00	1,57E+06	1,36E+06	
4,98E+07	6,87E+06	5,82E+06	3,75E+06	3,94E+06	3,03E+06	7,73E+06	6,74E+06	6,21E+06	5,67E+06	
1,27E+08	2,17E+07	1,54E+07	8,18E+06	2,07E+07	1,44E+07	1,35E+07	1,14E+07	1,13E+07	1,08E+07	
4,48E+07	3,11E+06	2,85E+06	3,95E+06	4,96E+06	5,21E+06	8,82E+06	7,58E+06	4,40E+06	3,96E+06	
3,54E+07	2,32E+06	2,34E+06	1,35E+06	9,37E+05	1,36E+06	7,68E+06	6,27E+06	7,07E+06	6,11E+06	
6,33E+06	6,95E+05	6,77E+05	6,60E+05	0,00E+00	9,62E+05	0,00E+00	1,66E+06	8,98E+05	7,79E+05	
3,12E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,12E+05	
2,63E+07	0,00E+00	0,00E+00	1,16E+06	1,03E+06	9,20E+05	5,61E+06	4,15E+06	8,20E+06	5,22E+06	
2,40E+06	0,00E+00	0,00E+00	0,00E+00	1,03E+05	0,00E+00	5,79E+05	0,00E+00	8,77E+05	8,43E+05	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
6,72E+06	0,00E+00	2,49E+05	2,63E+05	6,39E+04	2,30E+05	1,87E+06	1,47E+06	1,33E+06	1,24E+06	
1,53E+06	0,00E+00	1,65E+05	1,24E+05	1,04E+05	1,64E+05	4,77E+05	4,98E+05	0,00E+00	0,00E+00	
3,41E+05	3,41E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,22E+06	0,00E+00	0,00E+00	1,48E+05	2,05E+05	2,32E+05	0,00E+00	2,75E+05	0,00E+00	3,55E+05	
2,99E+06	1,55E+06	1,44E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,36E+06	5,09E+05	5,16E+05	0,00E+00	0,00E+00	0,00E+00	1,78E+05	0,00E+00	1,54E+05	0,00E+00	
2,32E+07	1,32E+06	1,43E+06	9,62E+05	8,62E+05	1,00E+06	4,91E+06	3,57E+06	4,90E+06	4,29E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
8,22E+06	0,00E+00	0,00E+00	5,75E+05	0,00E+00	6,61E+05	1,42E+06	1,49E+06	1,42E+06	2,66E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
3,88E+06	2,01E+06	1,71E+06	9,13E+04	6,14E+04	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
5,94E+06	3,09E+06	2,78E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,91E+04	3,63E+04	
8,92E+05	4,09E+05	4,82E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
8,62E+06	6,82E+05	6,07E+05	7,02E+05	6,83E+05	1,00E+06	1,26E+06	7,30E+05	1,52E+06	1,44E+06	
3,66E+07	3,37E+06	3,86E+06	4,72E+05	1,33E+06	2,78E+06	5,55E+06	4,09E+06	8,76E+06	6,37E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,40E+06	6,87E+05	6,38E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	7,96E+04	0,00E+00	0,00E+00	
1,98E+06	4,39E+05	3,19E+05	0,00E+00	0,00E+00	1,51E+05	0,00E+00	4,03E+05	3,89E+05	2,83E+05	
9,86E+06	6,33E+05	5,04E+05	4,07E+05	6,01E+05	4,60E+05	2,09E+06	1,82E+06	1,74E+06	1,60E+06	

3,81E+06	1,02E+06	9,99E+05	1,78E+05	7,76E+04	1,73E+05	0,00E+00	3,24E+05	5,63E+05	4,73E+05
9,68E+07	6,69E+06	6,70E+06	7,72E+06	8,23E+06	1,01E+07	1,56E+07	1,59E+07	1,44E+07	1,14E+07
1,99E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,69E+05	4,36E+05	4,13E+05	3,69E+05	4,03E+05
1,03E+07	5,20E+05	5,92E+05	9,57E+05	7,82E+05	8,36E+05	1,27E+06	1,38E+06	2,03E+06	1,90E+06
2,92E+07	2,30E+06	1,77E+06	2,17E+06	6,09E+06	3,81E+06	4,74E+06	3,62E+06	2,44E+06	2,25E+06
9,68E+06	0,00E+00	0,00E+00	1,47E+05	1,17E+05	1,56E+05	4,82E+06	1,59E+06	1,57E+06	1,29E+06
3,80E+06	3,33E+05	2,01E+05	5,90E+05	4,72E+05	4,72E+05	3,73E+05	4,19E+05	5,03E+05	4,35E+05
2,06E+06	1,01E+06	9,39E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	5,12E+04	6,11E+04	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5,36E+06	2,53E+06	2,37E+06	6,35E+04	9,66E+04	8,89E+04	8,98E+04	7,13E+04	5,15E+04	0,00E+00
5,49E+05	2,92E+05	2,57E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,80E+07	9,94E+05	1,12E+06	1,27E+06	1,54E+06	1,44E+06	2,71E+06	3,21E+06	3,33E+06	2,35E+06
3,85E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,98E+05	0,00E+00	0,00E+00	1,87E+05
1,14E+07	6,37E+05	5,58E+05	3,63E+05	3,10E+05	3,56E+05	2,59E+06	1,92E+06	2,34E+06	2,37E+06
3,69E+06	3,15E+05	2,80E+05	2,38E+05	3,42E+05	2,02E+05	6,86E+05	6,72E+05	4,49E+05	5,09E+05
6,04E+06	0,00E+00	1,49E+05	0,00E+00	0,00E+00	0,00E+00	1,60E+06	1,34E+06	1,53E+06	1,41E+06
8,75E+07	3,78E+06	3,94E+06	2,20E+06	1,48E+06	2,72E+06	2,05E+07	1,74E+07	1,75E+07	1,79E+07
2,29E+07	5,49E+05	6,48E+05	5,63E+05	3,03E+05	5,35E+05	7,41E+06	4,73E+06	4,43E+06	3,73E+06
2,22E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	6,42E+04	0,00E+00	8,64E+05	6,78E+05	6,13E+05
1,15E+07	5,80E+06	5,54E+06	0,00E+00	0,00E+00	0,00E+00	1,30E+05	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,51E+06	7,39E+05	7,71E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,13E+07	1,23E+06	1,16E+06	7,05E+05	4,99E+05	7,20E+05	4,59E+06	3,83E+06	4,23E+06	4,31E+06
4,97E+06	3,68E+05	3,38E+05	0,00E+00	1,25E+05	1,93E+05	9,97E+05	1,01E+06	9,16E+05	1,02E+06
5,58E+05	2,90E+05	2,68E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,60E+06	1,84E+06	1,76E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,90E+06	4,12E+05	4,21E+05	0,00E+00	5,15E+05	0,00E+00	7,72E+05	6,32E+05	5,85E+05	5,63E+05
3,07E+06	1,19E+05	9,96E+04	9,43E+04	0,00E+00	4,83E+04	5,57E+05	4,38E+05	9,52E+05	7,58E+05
5,81E+07	3,86E+06	3,80E+06	7,03E+06	3,90E+06	6,90E+06	1,03E+07	7,80E+06	7,52E+06	7,03E+06
1,04E+07	5,69E+05	5,76E+05	7,88E+05	5,45E+05	8,92E+05	1,35E+06	1,15E+06	2,38E+06	2,16E+06
7,52E+07	7,25E+06	5,78E+06	7,61E+06	5,23E+06	5,91E+06	1,04E+07	9,22E+06	1,28E+07	1,10E+07
1,73E+07	1,85E+06	2,05E+06	1,88E+06	1,67E+06	1,70E+06	2,06E+06	2,08E+06	2,11E+06	1,95E+06
8,59E+06	1,02E+06	9,06E+05	7,53E+05	4,95E+05	8,94E+05	9,61E+05	9,77E+05	1,50E+06	1,08E+06
1,11E+06	3,76E+05	0,00E+00	3,27E+05	0,00E+00	4,10E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,94E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	6,45E+05	4,02E+05	5,03E+05	3,89E+05
1,11E+07	6,04E+05	3,16E+05	8,63E+04	0,00E+00	0,00E+00	3,12E+06	2,08E+06	2,91E+06	1,96E+06
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
8,03E+05	3,90E+05	4,13E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,72E+06	4,70E+05	4,88E+05	0,00E+00	0,00E+00	0,00E+00	3,52E+05	4,05E+05	0,00E+00	0,00E+00
1,28E+08	3,57E+07	3,42E+07	4,25E+06	1,60E+06	4,21E+06	1,57E+07	1,59E+07	8,57E+06	8,33E+06
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
8,14E+06	3,90E+06	4,24E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,71E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	6,94E+05	4,71E+05	5,43E+05	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,46E+06	1,18E+06	1,11E+06	3,95E+05	0,00E+00	0,00E+00	1,16E+06	6,14E+05	0,00E+00	0,00E+00
4,18E+06	1,84E+05	1,89E+05	1,19E+05	0,00E+00	1,13E+05	1,14E+06	9,39E+05	7,97E+05	7,00E+05
2,94E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	6,70E+05	6,77E+05	7,34E+05	8,58E+05

1,33E+06	0,00E+00	0,00E+00	0,00E+00	1,24E+05	0,00E+00	0,00E+00	2,40E+05	4,56E+05	5,12E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,16E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	2,35E+05	1,91E+05	3,79E+05	3,59E+05
7,92E+07	6,87E+06	6,55E+06	6,47E+06	2,11E+06	5,65E+06	1,54E+07	1,38E+07	1,18E+07	1,06E+07
1,02E+06	1,10E+05	1,19E+05	8,45E+04	8,15E+04	1,40E+05	1,13E+05	1,18E+05	1,24E+05	1,34E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
8,50E+05	0,00E+00	8,50E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,03E+07	3,81E+06	3,20E+06	0,00E+00	1,66E+05	2,93E+05	1,20E+06	1,36E+06	2,79E+05	0,00E+00
3,19E+07	1,15E+07	1,07E+07	6,23E+05	3,58E+05	5,84E+05	3,92E+06	2,66E+06	7,64E+05	7,75E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,76E+07	9,19E+06	8,45E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,25E+06	1,07E+05	0,00E+00	1,41E+05	1,57E+05	1,84E+05	1,77E+05	1,14E+05	1,85E+05	1,82E+05
6,88E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	9,05E+04	1,46E+05	0,00E+00	2,50E+05	2,02E+05
6,00E+05	6,00E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5,15E+06	5,06E+05	5,87E+05	2,97E+05	3,31E+05	4,20E+05	8,52E+05	8,10E+05	7,83E+05	5,59E+05
1,72E+06	0,00E+00	0,00E+00	1,60E+05	0,00E+00	0,00E+00	4,74E+05	2,93E+05	4,33E+05	3,59E+05
2,45E+07	0,00E+00	0,00E+00	1,06E+07	0,00E+00	1,12E+07	0,00E+00	0,00E+00	2,72E+06	0,00E+00
5,02E+06	6,54E+05	6,80E+05	6,70E+05	4,72E+05	6,64E+05	0,00E+00	1,88E+06	0,00E+00	0,00E+00
2,76E+06	3,55E+05	3,26E+05	4,49E+05	3,01E+05	3,54E+05	4,98E+05	4,79E+05	0,00E+00	0,00E+00
4,19E+06	5,17E+05	5,48E+05	4,03E+05	0,00E+00	5,15E+05	8,22E+05	6,62E+05	7,22E+05	0,00E+00
7,48E+06	4,14E+05	5,04E+05	4,79E+05	2,61E+05	4,90E+05	0,00E+00	1,51E+06	1,88E+06	1,94E+06
4,42E+06	0,00E+00	0,00E+00	5,36E+05	5,01E+05	7,07E+05	9,96E+05	1,32E+06	1,85E+05	1,75E+05
3,23E+08	2,66E+07	2,47E+07	3,72E+07	1,76E+07	3,63E+07	5,83E+07	5,46E+07	3,57E+07	3,19E+07
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,40E+06	1,81E+05	1,70E+05	2,69E+05	9,28E+04	0,00E+00	0,00E+00	2,53E+05	1,97E+05	2,34E+05
1,85E+07	2,34E+06	1,83E+06	1,73E+06	1,60E+06	2,07E+06	2,73E+06	2,59E+06	1,80E+06	1,84E+06
1,27E+07	6,51E+05	6,37E+05	5,53E+05	1,66E+05	6,30E+05	3,15E+06	2,69E+06	1,62E+06	2,63E+06
4,77E+06	3,38E+05	2,54E+05	4,09E+05	1,85E+05	4,41E+05	9,06E+05	7,38E+05	8,50E+05	6,45E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,24E+07	1,45E+06	1,07E+06	8,62E+05	3,37E+05	9,42E+05	7,64E+06	0,00E+00	5,33E+06	4,81E+06
4,51E+06	0,00E+00	0,00E+00	0,00E+00	2,90E+05	4,59E+05	9,61E+05	1,01E+06	8,35E+05	9,56E+05
4,08E+06	0,00E+00	0,00E+00	1,09E+05	5,82E+04	0,00E+00	8,06E+05	7,11E+05	1,18E+06	1,22E+06
1,64E+06	7,52E+05	8,89E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,91E+07	1,30E+06	1,22E+06	1,38E+06	1,15E+06	1,46E+06	8,54E+06	7,54E+06	8,44E+06	8,05E+06
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,22E+07	3,14E+06	3,73E+06	4,75E+05	8,06E+05	3,96E+05	6,74E+05	6,82E+05	1,18E+06	1,15E+06
2,32E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	8,67E+05	5,52E+05	5,19E+05	3,80E+05
4,59E+06	3,73E+05	1,73E+05	3,38E+05	8,58E+04	1,37E+05	1,04E+06	6,95E+05	1,03E+06	7,14E+05
8,15E+05	2,76E+05	0,00E+00	0,00E+00	1,22E+05	2,05E+05	0,00E+00	0,00E+00	0,00E+00	2,12E+05
2,13E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	6,14E+05	8,52E+05	6,64E+05	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,42E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	2,42E+05	0,00E+00	0,00E+00
3,60E+07	0,00E+00	0,00E+00	0,00E+00	6,63E+06	0,00E+00	2,94E+07	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,87E+07	4,39E+05	4,65E+05	6,73E+05	5,32E+05	8,41E+05	3,87E+06	3,93E+06	3,75E+06	4,20E+06
9,28E+06	1,35E+06	1,15E+06	0,00E+00	3,62E+05	7,37E+05	1,45E+06	1,12E+06	9,83E+05	2,12E+06

1,51E+06	5,85E+05	9,29E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
8,50E+06	3,32E+05	5,20E+05	0,00E+00	1,38E+05	0,00E+00	7,52E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00
6,87E+05	0,00E+00	0,00E+00	0,00E+00	4,84E+05	0,00E+00	2,04E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,05E+06	6,30E+05	4,22E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5,32E+05	5,32E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,37E+07	2,06E+06	2,19E+06	7,05E+05	4,58E+05	9,09E+05	2,09E+06	1,94E+06	1,72E+06	1,63E+06	1,63E+06
5,99E+06	7,68E+05	7,97E+05	2,79E+05	2,96E+05	2,79E+05	1,22E+06	1,11E+06	6,55E+05	5,81E+05	5,81E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,04E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,06E+05	3,39E+05	3,91E+05	3,91E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,77E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	4,71E+05	3,92E+05	5,59E+05	3,51E+05	3,51E+05
6,53E+07	2,43E+06	2,32E+06	1,72E+06	1,20E+06	2,13E+06	1,67E+07	1,50E+07	1,25E+07	1,13E+07	1,13E+07
2,04E+07	0,00E+00	6,70E+05	5,48E+05	0,00E+00	9,75E+05	5,24E+06	4,68E+06	4,34E+06	3,91E+06	3,91E+06
1,52E+07	4,31E+05	4,52E+05	4,69E+05	4,36E+05	6,50E+05	3,76E+06	3,43E+06	3,12E+06	2,41E+06	2,41E+06
2,03E+06	3,12E+05	3,44E+05	0,00E+00	1,16E+05	2,22E+05	0,00E+00	0,00E+00	0,00E+00	1,04E+06	1,04E+06
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,60E+06	0,00E+00	0,00E+00	4,86E+05	1,67E+05	3,72E+05	1,06E+06	9,89E+05	7,84E+05	7,35E+05	7,35E+05
5,18E+06	2,58E+06	2,60E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,28E+07	4,13E+06	4,15E+06	1,51E+06	8,07E+05	1,34E+06	6,23E+06	4,08E+06	5,50E+06	5,06E+06	5,06E+06
4,50E+06	3,13E+05	3,81E+05	4,82E+05	3,25E+05	4,46E+05	1,25E+06	3,93E+05	4,59E+05	4,53E+05	4,53E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,80E+07	0,00E+00	0,00E+00	6,66E+05	5,03E+05	1,16E+06	5,79E+06	0,00E+00	4,86E+06	5,01E+06	5,01E+06
2,28E+08	1,32E+07	1,43E+07	3,12E+07	1,16E+07	3,11E+07	4,17E+07	4,14E+07	2,14E+07	2,20E+07	2,20E+07
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,81E+06	4,77E+05	5,22E+05	5,48E+05	3,58E+05	7,00E+05	0,00E+00	6,76E+05	8,41E+05	6,86E+05	6,86E+05
2,10E+06	4,00E+05	3,66E+05	0,00E+00	0,00E+00	0,00E+00	4,61E+05	6,13E+05	2,54E+05	0,00E+00	0,00E+00
2,94E+06	8,17E+05	7,78E+05	1,37E+05	1,19E+05	1,91E+05	0,00E+00	1,30E+05	3,34E+05	4,34E+05	4,34E+05
3,24E+07	3,42E+06	3,82E+06	2,94E+06	1,29E+06	3,08E+06	5,06E+06	4,87E+06	4,35E+06	3,55E+06	3,55E+06
1,28E+06	6,32E+05	6,50E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
7,45E+06	1,55E+06	1,38E+06	4,47E+05	1,99E+05	4,24E+05	8,52E+05	8,12E+05	1,02E+06	7,63E+05	7,63E+05
2,21E+07	5,60E+05	6,75E+05	4,94E+05	2,77E+05	3,43E+05	6,01E+06	4,69E+06	4,96E+06	4,12E+06	4,12E+06
1,47E+07	5,82E+05	0,00E+00	4,79E+05	3,01E+05	7,42E+05	3,23E+06	2,81E+06	3,23E+06	3,35E+06	3,35E+06
6,42E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	2,76E+05	3,66E+05	0,00E+00	0,00E+00
2,28E+06	1,04E+06	1,24E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
7,53E+06	5,60E+05	4,73E+05	8,97E+05	5,17E+05	5,56E+05	1,26E+06	9,79E+05	1,33E+06	9,56E+05	9,56E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,65E+06	2,93E+05	0,00E+00	3,45E+05	4,80E+05	4,65E+05	2,56E+05	2,92E+05	2,86E+05	2,33E+05	2,33E+05
3,17E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	8,22E+05	7,63E+05	8,13E+05	7,73E+05	7,73E+05
2,37E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	7,13E+05	6,19E+05	4,71E+05	5,66E+05	5,66E+05
1,24E+06	0,00E+00	8,04E+04	3,02E+05	2,27E+05	2,97E+05	3,32E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,96E+07	4,69E+05	5,14E+05	1,01E+06	2,12E+05	8,52E+05	7,87E+05	6,91E+06	9,16E+06	9,68E+06	9,68E+06

0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,62E+07	1,44E+06	9,81E+05	1,57E+06	5,78E+05	1,02E+06	3,53E+06	2,59E+06	2,72E+06	1,74E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,49E+06	2,27E+05	2,17E+05	1,75E+05	0,00E+00	1,92E+05	8,71E+05	9,18E+05	1,08E+06	8,03E+05	
1,24E+07	3,47E+05	8,31E+05	4,55E+05	2,34E+05	2,01E+05	1,85E+06	3,40E+06	2,66E+06	2,46E+06	
1,17E+06	5,24E+05	6,45E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,25E+06	1,13E+06	0,00E+00	1,16E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,32E+07	9,04E+05	8,88E+05	1,15E+06	1,31E+06	7,99E+05	6,85E+06	6,83E+06	7,93E+06	6,58E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,56E+06	6,28E+05	5,07E+05	9,69E+04	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,63E+05	1,61E+05	
2,21E+06	9,31E+05	1,28E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,54E+06	7,70E+05	7,74E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5,72E+07	3,12E+06	2,72E+06	1,08E+07	4,38E+06	6,78E+06	1,05E+07	8,40E+06	5,84E+06	4,66E+06	
9,74E+07	5,59E+06	4,71E+06	1,15E+07	4,76E+06	1,05E+07	2,15E+07	1,82E+07	1,09E+07	9,82E+06	
3,14E+06	0,00E+00	0,00E+00	6,82E+05	7,41E+05	6,24E+05	0,00E+00	6,68E+05	4,29E+05	0,00E+00	
2,13E+06	0,00E+00	0,00E+00	9,34E+05	3,72E+05	5,93E+05	0,00E+00	0,00E+00	2,33E+05	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,12E+06	1,19E+05	6,03E+04	0,00E+00	6,15E+04	7,71E+04	2,66E+05	1,79E+05	1,83E+05	1,75E+05	
2,43E+06	3,49E+05	2,31E+05	3,51E+05	1,42E+05	3,01E+05	0,00E+00	3,06E+05	3,55E+05	3,95E+05	
1,23E+07	4,63E+05	7,53E+05	1,01E+06	2,37E+06	7,23E+05	2,05E+06	0,00E+00	2,43E+06	2,49E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,68E+06	2,42E+06	2,25E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
6,26E+05	0,00E+00	1,45E+05	1,16E+05	0,00E+00	1,10E+05	1,40E+05	1,16E+05	0,00E+00	0,00E+00	0,00E+00
3,37E+05	3,37E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,16E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	8,51E+05	7,02E+05	8,28E+05	7,79E+05	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
9,62E+05	5,87E+05	3,75E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,31E+06	1,80E+06	1,51E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,08E+06	1,96E+05	0,00E+00	0,00E+00	5,29E+04	0,00E+00	3,85E+05	0,00E+00	2,07E+05	2,35E+05	
2,90E+06	1,20E+06	1,25E+06	0,00E+00	1,09E+05	0,00E+00	3,40E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,12E+06	1,09E+06	1,03E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,88E+06	1,65E+06	1,67E+06	2,97E+05	2,44E+05	2,75E+05	4,29E+05	3,15E+05	0,00E+00	0,00E+00	0,00E+00
2,64E+06	2,76E+05	2,03E+05	2,32E+05	1,93E+05	1,55E+05	3,70E+05	3,31E+05	5,02E+05	3,75E+05	

2,38E+06	1,36E+05	0,00E+00	0,00E+00	8,97E+04	0,00E+00	5,22E+05	4,72E+05	5,38E+05	6,18E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
9,89E+06	3,28E+05	3,18E+05	4,51E+05	0,00E+00	3,84E+05	3,26E+06	0,00E+00	2,86E+06	2,29E+06
1,83E+07	5,27E+06	4,71E+06	0,00E+00	3,08E+05	4,76E+05	2,07E+06	2,78E+06	1,60E+06	1,04E+06
2,93E+06	0,00E+00	0,00E+00	8,61E+04	0,00E+00	0,00E+00	9,83E+05	5,42E+05	6,43E+05	6,77E+05
3,46E+06	6,05E+05	5,07E+05	1,30E+05	6,98E+04	2,10E+05	5,48E+05	3,53E+05	5,45E+05	4,92E+05
1,59E+06	1,51E+05	8,46E+04	1,50E+05	0,00E+00	7,48E+04	2,86E+05	2,21E+05	3,29E+05	2,94E+05
3,80E+06	7,50E+05	8,85E+05	6,91E+05	4,08E+05	4,89E+04	0,00E+00	2,80E+05	4,08E+05	3,32E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,81E+07	1,25E+06	1,44E+06	2,13E+06	1,00E+06	2,47E+06	5,03E+06	4,97E+06	3,15E+06	6,70E+06
5,52E+06	4,83E+05	6,26E+05	6,54E+05	4,65E+05	8,18E+05	9,04E+05	8,81E+05	0,00E+00	6,90E+05
7,11E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	2,04E+06	1,86E+06	1,67E+06	1,53E+06
5,88E+07	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	8,84E+06	2,00E+07	1,61E+07	1,39E+07
8,02E+05	4,23E+05	3,79E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,96E+06	4,96E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
6,95E+06	6,29E+05	4,16E+05	8,96E+05	9,00E+05	1,12E+06	8,64E+05	7,53E+05	5,71E+05	8,01E+05
9,64E+05	4,88E+05	4,76E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5,19E+06	2,69E+06	2,49E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,15E+06	2,90E+05	2,96E+05	2,11E+05	1,37E+05	2,20E+05	3,32E+05	2,56E+05	1,59E+05	2,48E+05
1,82E+06	9,44E+05	8,74E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
7,22E+05	3,58E+05	3,63E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,85E+07	3,22E+06	3,01E+06	1,04E+06	7,29E+05	9,45E+05	2,96E+06	2,07E+06	2,37E+06	2,13E+06
4,83E+07	4,21E+06	3,89E+06	3,06E+06	2,02E+06	3,89E+06	9,39E+06	7,93E+06	7,32E+06	6,62E+06
1,27E+08	1,30E+07	1,32E+07	1,99E+07	1,76E+06	1,80E+07	3,20E+07	2,88E+07	3,61E+05	3,53E+05
4,22E+08	5,76E+05	4,81E+05	1,24E+05	1,50E+05	3,94E+05	1,43E+08	1,01E+08	9,43E+07	8,19E+07
2,00E+06	9,83E+04	0,00E+00	2,59E+05	1,51E+05	2,08E+05	4,31E+05	3,41E+05	0,00E+00	5,10E+05
5,15E+06	1,40E+06	1,42E+06	2,55E+05	2,13E+05	3,75E+05	2,84E+05	2,23E+05	5,24E+05	4,60E+05
5,73E+05	2,57E+05	3,15E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5,00E+06	1,20E+06	1,30E+06	4,23E+05	0,00E+00	4,97E+05	0,00E+00	9,38E+05	6,43E+05	0,00E+00
3,08E+06	9,82E+05	1,45E+06	1,95E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	4,51E+05
7,45E+06	2,07E+06	1,92E+06	0,00E+00	0,00E+00	3,29E+05	4,85E+05	3,54E+05	1,08E+06	1,20E+06
2,61E+07	3,50E+06	3,63E+06	2,12E+06	1,36E+06	2,67E+06	5,07E+06	4,08E+06	1,89E+06	1,77E+06
5,51E+06	3,79E+05	4,60E+05	4,80E+05	3,19E+05	4,97E+05	1,64E+06	6,97E+05	5,55E+05	4,82E+05
2,05E+08	3,35E+07	2,61E+07	1,24E+07	1,08E+07	1,37E+07	3,00E+07	2,28E+07	2,91E+07	2,70E+07
2,73E+06	0,00E+00	0,00E+00	0,00E+00	1,69E+05	0,00E+00	6,77E+05	0,00E+00	9,46E+05	9,34E+05
4,62E+06	3,94E+05	3,86E+05	3,47E+05	4,15E+05	4,94E+05	5,78E+05	5,25E+05	7,40E+05	7,45E+05
2,40E+06	1,32E+06	1,09E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,41E+07	6,58E+06	6,71E+06	0,00E+00	0,00E+00	3,42E+05	0,00E+00	2,81E+05	1,81E+05	0,00E+00
3,45E+06	1,49E+06	1,45E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	5,07E+05	0,00E+00	0,00E+00
2,05E+05	0,00E+00	2,05E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5,27E+06	0,00E+00	0,00E+00	1,89E+05	1,84E+05	0,00E+00	1,14E+06	1,16E+06	1,21E+06	1,38E+06
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,03E+07	1,47E+05	2,50E+06	6,66E+06	5,62E+06	6,12E+06	7,09E+06	4,67E+06	3,48E+06	3,96E+06
1,03E+06	0,00E+00	2,00E+05	2,04E+05	2,20E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	4,03E+05
2,14E+08	1,16E+07	2,41E+07	0,00E+00	2,28E+07	2,65E+07	4,44E+07	3,26E+07	3,55E+07	1,67E+07
1,30E+07	9,66E+05	2,71E+05	3,49E+06	2,35E+06	4,17E+06	0,00E+00	4,21E+05	6,83E+05	6,14E+05
1,54E+08	8,83E+06	8,01E+06	1,65E+07	1,33E+07	3,07E+07	2,64E+07	1,98E+07	1,62E+07	1,43E+07
8,79E+06	0,00E+00	0,00E+00	3,05E+06	1,71E+06	3,69E+06	0,00E+00	0,00E+00	0,00E+00	3,37E+05

0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,67E+06	3,96E+05	2,13E+05	2,31E+05	1,37E+05	1,97E+05	3,72E+05	4,42E+05	3,37E+05	3,43E+05	
1,67E+06	0,00E+00	0,00E+00	1,41E+05	0,00E+00	1,75E+05	3,32E+05	4,50E+05	3,05E+05	2,67E+05	
1,46E+06	7,34E+05	7,28E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,61E+07	1,09E+06	1,05E+06	1,50E+06	5,46E+05	1,38E+06	4,24E+06	0,00E+00	3,35E+06	2,96E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,90E+07	0,00E+00	0,00E+00	2,20E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,68E+07	
7,78E+07	4,09E+06	4,26E+06	6,85E+05	2,75E+06	3,90E+06	1,79E+07	1,72E+07	2,22E+07	4,88E+06	
1,65E+07	9,54E+05	8,85E+05	1,43E+06	7,22E+05	1,53E+06	2,89E+06	2,78E+06	2,87E+06	2,41E+06	
4,48E+09	5,55E+08	6,07E+08	4,17E+08	1,86E+08	5,49E+08	5,99E+08	5,41E+08	5,29E+08	5,00E+08	
1,06E+06	0,00E+00	0,00E+00	1,54E+05	3,63E+05	1,65E+05	0,00E+00	0,00E+00	2,08E+05	1,66E+05	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
6,12E+06	3,20E+06	2,92E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
4,34E+07	0,00E+00	2,90E+06	0,00E+00	6,41E+06	3,93E+06	8,90E+06	9,01E+06	6,00E+06	6,28E+06	
4,70E+06	2,44E+06	2,26E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
2,03E+07	1,19E+06	1,11E+06	1,19E+06	1,26E+06	1,31E+06	4,28E+06	3,21E+06	3,84E+06	2,91E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
3,66E+06	0,00E+00	0,00E+00	7,72E+05	7,98E+05	8,90E+05	6,49E+05	5,51E+05	0,00E+00	0,00E+00	
5,15E+06	8,37E+05	7,81E+05	3,50E+05	1,95E+05	3,55E+05	8,26E+05	6,11E+05	5,72E+05	6,21E+05	
2,34E+06	6,93E+05	5,98E+05	1,14E+05	7,25E+04	1,02E+05	2,22E+05	2,04E+05	1,62E+05	1,70E+05	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
2,25E+06	0,00E+00	0,00E+00	4,51E+05	6,99E+05	4,70E+05	0,00E+00	2,42E+05	3,93E+05	0,00E+00	
7,21E+06	3,58E+06	3,62E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,40E+07	7,47E+06	6,29E+06	1,44E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,35E+05	0,00E+00	
1,08E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	2,58E+05	3,09E+05	2,48E+05	2,69E+05	
2,84E+06	1,20E+06	1,23E+06	1,02E+05	1,27E+05	1,85E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
2,65E+06	1,28E+05	1,49E+05	2,02E+05	1,58E+05	2,00E+05	5,13E+05	4,18E+05	4,91E+05	3,95E+05	
1,07E+08	4,39E+06	4,16E+06	4,19E+06	3,36E+06	5,57E+06	2,90E+07	2,72E+07	1,85E+06	2,77E+07	
5,25E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,58E+06	1,28E+06	1,29E+06	1,10E+06	
8,55E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,75E+05	0,00E+00	6,80E+05	
5,93E+06	6,79E+05	6,21E+05	4,16E+05	0,00E+00	4,54E+05	1,20E+06	8,39E+05	9,57E+05	7,63E+05	
7,10E+05	3,78E+05	3,32E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
9,07E+06	3,82E+05	3,63E+05	3,47E+05	1,68E+05	3,37E+05	2,00E+06	1,97E+06	1,83E+06	1,69E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,90E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,96E+05	3,28E+05	5,78E+05	6,01E+05	
1,43E+06	7,37E+05	6,90E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
3,02E+06	0,00E+00	7,35E+04	0,00E+00	0,00E+00	0,00E+00	8,09E+05	6,40E+05	7,92E+05	7,05E+05	
4,19E+06	0,00E+00	0,00E+00	1,82E+05	0,00E+00	0,00E+00	1,50E+06	1,08E+06	6,83E+05	7,42E+05	
5,20E+06	2,25E+05	2,45E+05	2,62E+05	1,18E+05	3,27E+05	9,01E+05	1,16E+06	1,05E+06	9,09E+05	
2,02E+07	3,89E+06	3,96E+06	0,00E+00	7,45E+05	1,52E+06	2,54E+06	2,76E+06	2,35E+06	2,48E+06	
1,36E+08	1,16E+07	1,04E+07	1,43E+07	8,84E+06	1,70E+07	3,50E+07	0,00E+00	2,01E+07	1,88E+07	
5,69E+06	2,90E+05	3,01E+05	5,28E+05	5,79E+05	4,03E+05	9,65E+05	9,63E+05	9,36E+05	7,22E+05	
1,63E+06	8,27E+05	7,98E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,77E+06	1,21E+05	7,19E+04	0,00E+00	0,00E+00	0,00E+00	4,94E+05	4,59E+05	3,03E+05	3,26E+05	
1,25E+06	4,71E+05	4,59E+05	1,15E+05	1,08E+05	0,00E+00	0,00E+00	9,71E+04	0,00E+00	0,00E+00	

0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,44E+07	8,87E+05	6,51E+05	8,21E+05	0,00E+00	8,32E+05	6,02E+06	4,67E+06	5,49E+06	5,05E+06	
9,90E+06	5,34E+05	8,99E+05	9,59E+05	1,07E+06	4,19E+06	6,05E+05	8,86E+05	7,57E+05	0,00E+00	
1,84E+07	4,27E+06	4,41E+06	4,91E+05	3,28E+05	5,09E+05	3,21E+06	2,30E+06	1,53E+06	1,32E+06	
3,03E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	8,25E+05	7,86E+05	7,37E+05	6,80E+05	
4,16E+07	3,28E+06	2,67E+06	1,70E+06	6,48E+05	1,73E+06	9,26E+06	9,53E+06	4,18E+06	8,66E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,63E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	3,32E+05	4,01E+05	3,67E+05	5,31E+05	
6,05E+05	2,91E+05	3,15E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
5,83E+06	3,11E+06	2,72E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
9,70E+06	2,31E+06	2,36E+06	0,00E+00	5,05E+05	8,33E+05	1,01E+06	1,03E+06	1,03E+06	6,12E+05	
8,81E+06	4,55E+06	3,91E+06	0,00E+00	0,00E+00	1,04E+05	2,45E+05	0,00E+00	0,00E+00	0,00E+00	
4,36E+07	9,36E+05	9,25E+05	6,62E+05	0,00E+00	7,47E+05	9,89E+06	9,75E+06	1,02E+07	1,05E+07	
2,22E+06	1,11E+06	1,11E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
9,00E+06	0,00E+00	8,78E+06	8,67E+04	0,00E+00	1,35E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
9,01E+07	1,08E+07	7,91E+06	5,80E+06	3,27E+06	6,93E+06	1,96E+07	1,29E+06	1,85E+07	1,60E+07	
3,98E+06	0,00E+00	2,80E+05	8,02E+05	0,00E+00	5,00E+05	1,09E+06	4,25E+05	6,41E+05	2,43E+05	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
2,83E+06	1,48E+06	1,34E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
4,58E+05	0,00E+00	4,58E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,90E+06	9,52E+05	9,51E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
7,00E+05	4,00E+05	3,01E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
3,95E+06	4,53E+05	4,48E+05	3,18E+05	2,60E+05	3,07E+05	5,40E+05	5,64E+05	5,66E+05	4,89E+05	
4,89E+06	2,74E+06	2,16E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
1,21E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	2,61E+05	4,34E+05	2,63E+05	2,50E+05	
8,65E+05	3,59E+05	5,06E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
2,25E+07	6,04E+05	5,66E+05	6,24E+05	4,26E+05	8,09E+05	5,86E+06	5,02E+06	4,50E+06	4,10E+06	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
3,58E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,05E+06	9,94E+05	8,33E+05	6,99E+05	
1,46E+06	0,00E+00	0,00E+00	0,00E+00	1,80E+05	1,32E+05	2,55E+05	2,51E+05	3,71E+05	2,70E+05	
1,55E+06	0,00E+00	0,00E+00	0,00E+00	4,41E+04	0,00E+00	5,33E+05	3,60E+05	3,62E+05	2,54E+05	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
3,26E+06	9,85E+05	2,27E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
9,24E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	2,88E+05	2,72E+05	3,65E+05	
1,92E+06	1,03E+06	8,84E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
3,59E+06	2,42E+05	2,31E+05	1,12E+05	1,32E+05	0,00E+00	1,03E+06	7,66E+05	1,07E+06	0,00E+00	
1,80E+08	1,73E+07	1,69E+07	2,44E+07	0,00E+00	0,00E+00	3,22E+07	2,89E+07	2,81E+07	3,22E+07	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
9,07E+05	4,70E+05	4,37E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	
3,05E+07	4,31E+06	3,93E+06	0,00E+00	1,33E+06	3,13E+06	4,42E+06	4,45E+06	4,62E+06	4,33E+06	

2,32E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	6,34E+05	5,97E+05	5,18E+05	5,71E+05
2,87E+06	4,46E+05	4,52E+05	1,98E+05	4,06E+05	2,75E+05	3,58E+05	3,37E+05	2,01E+05	1,98E+05
2,69E+07	3,01E+06	2,47E+06	8,87E+05	2,27E+06	2,97E+06	5,07E+06	3,59E+06	3,63E+06	3,04E+06
4,08E+08	4,93E+07	4,30E+07	5,49E+07	2,49E+07	5,76E+07	0,00E+00	7,01E+07	5,71E+07	5,09E+07
4,91E+07	4,38E+06	3,90E+06	2,82E+06	2,79E+06	2,92E+06	1,56E+07	5,63E+06	5,97E+06	5,09E+06
2,38E+07	5,12E+06	5,83E+06	1,43E+06	8,15E+05	1,40E+06	2,13E+06	1,83E+06	2,44E+06	2,81E+06
1,33E+08	6,79E+06	7,61E+06	1,82E+07	1,10E+07	1,99E+07	2,23E+07	1,99E+07	1,36E+07	1,39E+07
5,77E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,49E+05	0,00E+00	1,96E+05	2,32E+05
5,30E+07	3,56E+06	3,77E+06	4,53E+06	3,13E+06	4,73E+06	1,19E+07	8,80E+06	6,68E+06	5,89E+06
7,00E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,90E+06	1,79E+06	1,45E+06	1,85E+06
1,52E+06	3,80E+05	0,00E+00	0,00E+00	4,39E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	6,97E+05
1,32E+07	5,42E+06	0,00E+00	7,30E+05	3,83E+05	6,20E+05	2,22E+06	1,98E+06	8,60E+05	9,53E+05
4,80E+06	4,90E+05	2,85E+05	3,79E+05	2,59E+05	3,81E+05	7,84E+05	9,05E+05	5,97E+05	7,20E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
7,32E+06	2,47E+05	2,14E+05	3,09E+05	5,43E+05	2,68E+05	1,01E+06	1,29E+06	1,85E+06	1,59E+06
1,74E+06	1,74E+05	1,65E+05	2,41E+05	1,70E+05	2,09E+05	2,07E+05	1,84E+05	2,22E+05	1,69E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
3,16E+05	0,00E+00	0,00E+00	0,00E+00	3,16E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
9,72E+07	8,60E+06	8,56E+06	0,00E+00	5,93E+06	1,42E+07	1,86E+07	1,90E+07	1,12E+07	1,11E+07
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
2,23E+06	4,80E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,75E+06
1,73E+07	7,62E+05	6,40E+05	7,12E+05	4,67E+05	6,35E+05	3,77E+06	3,09E+06	3,45E+06	3,81E+06
5,85E+06	0,00E+00	2,26E+05	1,59E+05	1,47E+05	2,12E+05	1,18E+06	1,16E+06	1,52E+06	1,25E+06
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,51E+06	0,00E+00	2,13E+05	4,37E+05	3,63E+05	5,06E+05	6,76E+05	8,38E+05	6,94E+05	7,86E+05
0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
1,01E+06	4,96E+05	5,18E+05	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00	0,00E+00
4,94E+06	3,50E+05	0,00E+00	1,88E+05	1,50E+05	2,08E+05	1,10E+06	9,78E+05	9,41E+05	1,03E+06
1,09E+07	9,09E+05	1,18E+06	1,02E+06	1,04E+06	1,40E+06	9,23E+05	1,12E+06	1,66E+06	1,68E+06
4,39E+06	0,00E+00	0,00E+00	0,00E+00	0,00E+00	1,76E+05	1,76E+06	8,88E+05	1,07E+06	4,99E+05

Reverse	Potential	cid	Protein gr	Mod. pept	Evidence I	MS/MS ID	Best MS/N	Oxidation	MS/MS Co
		0	124	0	0;1;2;3;4	0;1;2	1		3
		1	136	1	5;6	3;4;5;6;7	5		5
		2	66	2	7;8	8;9	9		2
		3	69	3	9;10;11;12	10;11;12;1	17		9
		4	69	4	18;19;20;21	19;20;21;2	19		10
		5	198	5	35;36;37;38	29;30	29		2
		6	101	6	40;41;42;43	31;32;33;3	40		9
		7	128	7	49;50;51;52	41;42;43	42	206	0
		8	150	8	57;58	44;45	45		2
		9	71;72	9	59;60;61;62	46;47;48;4	51		15
		10	98	10	68;69;70;71	61;62	62		2
		11	94	11	72;73;74;75	63;64;65;6	65		4
		12	69	12	78;79;80;81	67;68;69;7	72		4
		13	69	13	94;95;96;97	73;74;75	75		3
		14	152	14	103;104;105	76;77	76	245	0
		15	151	15	110;111;112	78;79;80;8	83	239	0
	+	16	12	16	117;118;119	85;86;87;8	90	28	0
	+	17	12	17	126;127;128	94;95;96	95	28	0
		18	59	18	132;133;134	97;98	98		2
		19	144	19	137;138;139	99	99		0
	+	20	2;7;18	20	142;143;144	100;101;10	101		5
	+	21	8	21	149;150;151	105;106;10	112		9
	+	22	8	22	158;159;160	114;115;11	114		2
	+	23	2;7;18;27	23	168;169;170	117;118;11	121		6
	+	24	6	24	177;178;179	123;124;12	124		4
		25	89	25	186;187;188	127;128;12	129		3
		26	174	26	190;191;192	130	130		1
	+	27	12	27	194;195;196	131;132;13	153		24
		28	51;121;120	28	211;212;213	155;156;15	158	83	0
		29	53	29	222;223;224	166;167;16	167	88	0
		30	79;60	30	231;232;233	170	170		1
	+	31	29	31	234;235;236	171	171		1
		32	103;118	32	239;240;241	172;173;17	182		13
		33	172	33	247;248	185;186	186		2
		34	172	34	249	187;188	187	267	0
		35	152	35	250;251;252	189	189		1
		36	69	36	257;258;259	190;191;19	202		16
		37	144;176	37	271;272;273	206;207;20	206		3
		38	71	38	274;275;276	209	209	128	0
		39	100	39	277;278;279	210;211;21	212		6
		40	100	40	285;286;287	216;217;21	231		17
		41	181	41	294;295;296	233;234	233	281	0
		42	105	42	299;300;301	235;236	236		2
		43	41	43	308;309	237	237		1
		44	69	44	310;311;312	238;239;24	238		4
	+	45	2;18	45	319;320;321	242;243;24	242		6
		46	66	46	328;329	248;249	249		2
		47	3;201;126;2	47	330;331;332	250;251;25	257	203	0
		48	167	48	345;346;347	262;263	263	262	0

	49	68;87	49	349;350;31264;265;20	265		4
	50	68;87	50	358;359	268	268	1
	51	216	51	360;361;31269;270	269		2
	52	41	52	363 271;272	272	72	0
	53	174	53	364;365;31273;274;21	274	270	0
+	54	10;1	54	368;369;31276;277;21	282		10
+	55	12	55	376;377;31286;287;21	294		9
	56	144	56	385;386;31295;296;21	299		6
	57	144	57	389;390;31301;302;30	303	227	0
	58	206	58	398;399	305	305	1
	59	35	59	400;401;41306;307;30	311	63	0
	60	128	60	405;406;41313;314;31	313	207	0
	61	171	61	414;415;41	326	326	1
	62	208	62	417;418	327	327	298
	63	2;203;212;1	63	419;420;41328;329;31	335	188	0
	64	158;201	64;65	427;428;41337;338;31	354	254	1
	65	126	66	437;438;41356;357;31	370		15
	66	145	67	446;447;41	371	371	1
+	67	2;7;18	68	453;454;41372;373;31	373	7;8	0
	68	142	69	456;457	375	375	1
	69	76	70	458;459;41376;377;31	379	138	0
	70	168	71	466;467;41381;382;31	381	263	0
	71	163	72	474;475;41	384	384	1
	72	234	73	482;483 385;386;31	387		3
	73	186	74	484;485;41	388	388	1
	74	78	75	489	389	389	1
	75	216	76	490;491	390	390	1
	76	216	77	492;493	391	391	1
	77	222	78	494;495;41392;393	392		2
	78	216	79	504	394	394	1
+	79	10	80	505;506;51395;396;31	396		8
+	80	1	81	514;515;51403;404;40	411		9
	81	92	82	524;525;51412;413	412		2
	82	90	83	533;534;51414;415;41	416		3
	83	78	84	538;539 417;418	418	141	0
	84	216	85	540;541 419;420	420		2
	85	66	86	542;543 421;422;41	423	101;102	0
	86	134	87	544;545;51425;426;41	430		8
+	87	13	88	553;554;51434;435;41	434		9
+	88	17;2;7;18	89	562;563;51443;444;41	447		8
	89	113	90	570;571	451	451	0
	90	50	91	572	452	452	1
	91	66	92	573;574	453	453	1
	92	68	93	575;576;51454;455;41	455		4
+	93	19	94	581;582;51	458	458	1
+	94	10;1	95	588;589;51459;460;40	460		3
+	95	10;1	96	597	462	462	1
	96	66	97	598;599 463;464;40	464	103	0
	97	202	98	600;601;61466;467;40	471	292	0
	98	210	99	609;610 475;476	475		2

	99	228	100	611;612;6477;478;4	478		5
+	100	7	101	618;619;6482	482		1
	101	160	102	625;626;6483;484;4	489		8
	102	159	103	634;635;6491;492;4	492		3
	103	207	104	643;644;6494;495;4	496		5
	104	51;121;120	105	652;653;6499;500;5	517	84	0
	105	129	106	667;668;6525;526;5	528		6
	106	103;118	107	674;675;6531;532;5	533		4
	107	103;118	108	679;680;6535;536;5	538		3
	108	120	109	688;689;6539;540;5	541		13
	109	51;121	110	702;703;7555;556;5	575		23
	110	144	111	717;718;7578;579	578		2
	111	66;216	112	720;721 580;581;5	580		3
	112	122;203	113	722;723;7583;584;5	592	189	0
+	113	5	114	731;732;7593;594;5	593	13	0
	114	168	115	738;739;7597	597		1
	115	119	116	743;744;7598;599;6	601		4
	116	216	117	752;753;7602;603;6	607		8
	117	199	118	756;757 610;611	610		2
	118	142	119	758 612	612	224;225	0
	119	34	120	759;760;7613	613	61;62	0
	120	148	121	766;767 614	614		1
	121	142	122	768;769;7615;616	616		2
	122	62	123	771;772;7617;618;6	620		7
	123	51;121;120	124	780;781;7624;625;6	624	85	0
	124	151	125	785;786;7630	630		1
+	125	6;5	126	788;789;7631;632;6	633		3
	126	160	127	794;795;7634;635;6	635		0
+	127	1;19	128	798;799;8637;638;6	637	1	0
	128	86	129	805;806;8642;643;6	642		4
	129	86	130	809;810;8646;647;6	648		6
+	130	12	131	817;818;8652;653;6	656		7
+	131	10	132	825;826;8659;660	660		2
+	132	6	133	832;833;8661;662;6	661		3
	133	50	134	838;839;8664	664		0
	134	113	135	847;848;8665;666;6	673		13
	135	132	136	856;857 678	678	216	0
	136	71	137	858;859;8679;680;6	685		9
	137	111	138	865;866;8688	688		1
+	138	5	139	870;871;8689;690	689		2
+	139	6	140	877;878;8691;692;6	691		4
+	140	6	141	884;885;8695	695		1
+	141	15	142	893;894;8696;697	697		2
	142	98	143	901;902;9698;699;7	703		6
	143	176	144	908;909 705;706;7	705		3
	144	172	145	910;911;9708;709	708		2
	145	228	146	915;916;9710;711;7	712	322	0
	146	152	147	924;925;9721	721		1
	147	89	148	927 722	722	152	0
+	148	16	149	928;929;9723;724;7	740		29

	149	37	150	946;947;952;753;754	752		3	
	150	66	151	951;952	755	755	1	
	151	77	152	953;954	756;757	757	2	
	152	216	153	955;956	758;759;760	759	3	
	153	65	154	957;958;959	761	761	0	
	154	144	155	962;963;964	762	762	1	
	155	216	156	965;966;967	763;764	763	2	
	156	86	157	968;969	765;766	766	2	
	157	130	158	970;971;972	767;768;769	769	3	
+	158	6	159	975	770	770	1	
	159	179	160	976;977;978	771	771	1	
	160	88	161	985;986	772;773;774	773	3	
	161	103;118;160	162	987;988;989	775;776;777	777	172	0
	162	66	163	995;996	782;783	782	2	
	163	103	164	997;998;999	784;785;786	798	173	0
	164	235	165	1012;1013	800;801;802	800	327	0
+	165	4	166	1014;1015	804;805;806	804	12	0
	166	162	167	1017;1018	807	807	1	
	167	111	168	1019;1020	808;809	808	2	
+	168	20	169	1028;1029	810	810	1	
	169	59	170	1030;1031	811;812	812	95;96;97	0
+	170	16	171	1036;1037	813;814;815	813	4	
+	171	10	172	1045;1046	817;818;819	817	23	0
	172	216	173	1054;1055	820	820	1	
	173	46	174	1056;1057	821	821	78	0
	174	103;118	175	1060;1061	822;823;824	830	10	
	175	103;118	176	1069;1070	832;833	833	2	
	176	222	177	1071;1072	834	834	0	
	177	216	178	1075;1076	835;836	835	2	
	178	48	179	1078;1079	837;838;839	844	9	
	179	151	180	1087;1088	846;847;848	851	7	
+	180	13;7;18;2	181	1095;1096	853;854;855	858	9	0
+	181	8	182	1104;1105	862;863;864	868	17	0
+	182	17	183	1113;1114	872;873;874	877	47	0
	183	162;43	184	1121;1122	880;881;882	880	3	
+	184	5	185	1123;1124	883;884;885	883	14	0
	185	222	186	1126;1127	886;887;888	886	316	0
	186	120	187	1134;1135	890;891;892	893	6	
	187	51;121	188	1142;1143	896;897;898	902	9	
	188	174	189	1151;1152	905	905	1	
+	189	8	190;191	1153;1154	906;907;908	911	18	1
+	190	17	192	1162;1163	915;916;917	922	48	0
	191	193	193	1171;1172	926;927;928	926	3	
	192	216	194	1173	929;930	929	2	
	193	151	195	1174;1175	931;932;933	933	4	
	194	138	196	1177;1178	935	935	0	
	195	189	197	1179;1180	936;937	936	2	
	196	129	198	1181;1182	938;939;940	942	5	
	197	51;121;120	199	1187;1188	943;944	944	2	
	198	51;121;120	200	1195;1196	945;946;947	949	86	0

	199	152	201	1204;1205	950	950	246	0
	200	161	202	1212;1213	951	951		1
+	201	16	203	1214;1215	952	952	39	0
	202	123	204	1217;1218	953	953		1
+	203	27	205	1220;1221	954	954		1
	204	172	206	1229;1230 955;956;957	955	955	267	0
	205	216	207	1231;1232	958	958		1
	206	156	208	1236;1237	959	959	250	0
	207	56;109	209	1238;1239 960;961;962	961	961		3
	208	178	210	1245;1246 963;964	964	964		2
	209	200	211	1254;1255 965;966	965	965		2
+	210	16	212	1257;1258 967;968;969	982	982		18
	211	51;121	213	1272;1273 986;987;988	990	990		6
+	212	17	214	1281;1282 992;993;994	993	993		3
	213	103;118	215	1287;1288 996;997;998	999	999	174	0
	214	187	216	1296;1297	1005	1005		1
	215	122;203	217	1304;1305 1006;1007	1010	1010		11
	216	135	218	1315;1316	1017	1017	218	0
	217	69	219	1324;1325 1018;1019	1018	1018		4
	218	144	220	1333;1334	1022	1022		1
	219	59	221	1338	1023	1023		1
	220	229	222	1339	1024	1024		1
+	221	20	223	1340;1341	1025	1025		1
	222	183	224	1344;1345	1026	1026		1
	223	131	225	1348;1349 1027;1028	1027	1027		2
+	224	12	226	1350;1351 1029;1030	1047	1047		24
	225	45	227	1373;1374	1054	1054		0
	226	149	228	1381;1382 1055;1056	1056	1056	238	0
	227	216	229	1389;1390 1060;1061	1060	1060	309;310	0
	228	66	230	1392;1393 1062;1063	1064	1064	104;105	0
	229	66	231	1394;1395 1065;1066	1066	1066	106	0
	230	41	232	1396;1397 1067;1068	1068	1068		2
	231	216	233	1398;1399	1069	1069		1
	232	94	234	1400	1070	1070		1
+	233	25	235	1401;1402	1071	1071		0
	234	221	236	1406	1072	1072		1
	235	66	237	1407;1408	1073	1073		1
+	236	31	238;239	1409;1410 1074;1075	1074	1074	59	1
	237	66	240	1416;1417 1078;1079	1080	1080		3
	238	216	241	1418;1419	1081	1081		1
	239	55	242	1420;1421 1082;1083	1083	1083		4
	240	66	243	1429;1430 1086;1087	1087	1087		2
	241	186	244	1431;1432 1088;1089	1090	1090		4
	242	129	245	1439;1440 1092;1093	1092	1092		6
+	243	10	246	1443;1444 1098;1099	1099	1099		8
+	244	1;19	247	1452;1453 1106;1107	1111	1111		8
	245	212	248	1460;1461 1114;1115	1118	1118	301	0
	246	2;158;201;202	249;250	1469;1470 1122;1123	1131	1131	190	4
	247	203	251	1487;1488 1139;1140	1145	1145	293	0
+	248	10	252	1495;1496 1148;1149	1148	1148		2

	249	185	253	1504	1150	1150		0
	250	172	254	1505;1506	1151;1152	1151	267	0
	251	66	255	1515;1516	1155	1155		1
+	252	13	256	1517;1518	1156;1157	1162	31	0
+	253	;7;18;27;13	257	1526;1527	1163;1164	1163	10	0
	254	90	258	1534;1535	1165;1166	1165		4
	255	172	259	1540;1541	1169;1170	1169		2
+	256	;18;27;25;:	260	1545;1546	1171;1172	1175		9
+	257	;18;27;25;:	261	1563;1564	1180;1181	1181		5
	258	116	262	1572;1573	1185;1186	1186		2
	259	51;121;120	263	1576;1577	1187;1188	1200		27
	260	51;121;120	264	1589;1590	1214;1215	1215	87	0
+	261	16	265	1597;1598	1218;1219	1219	40	0
	262	162	266	1606;1607	1227;1228	1227	258	0
	263	35	267	1608;1609	1229;1230	1232		0
+	264	17	268	1617;1618	1233;1234	1236		11
	265	43	269	1626;1627	1244;1245	1245		2
+	266	6	270	1628;1629	1246;1247	1246		4
+	267	;7;18;27;13	271	1637;1638	1251;1252	1252		2
+	268	21;22	272	1645;1646	1253;1254	1257		7
+	269	17;8;25	273	1654;1655	1260;1261	1261		17
+	270	8	274	1670;1671	1277;1278	1283		16
	271	168	275	1679;1680	1293	1293		1
	272	148	276	1685;1686	1294;1295	1294		2
	273	100	277	1687;1688	1296;1297	1297	161	0
	274	197	278	1695;1696	1298	1298		0
	275	!01;126;20:	279	1697;1698	1299;1300	1304		11
	276	216	280	1706;1707	1310	1310		1
	277	95	281	1708;1709	1311;1312	1312	155	0
	278	37	282	1715;1716	1313;1314	1317	65;66	0
+	279	5	283	1722;1723	1322;1323	1323		2
	280	216	284	1729;1730	1324;1325	1326		3
+	281	23	285	1731;1732	1327;1328	1328		6
+	282	8	286	1740;1741	1333;1334	1340		10
+	283	16	287	1749;1750	1343;1344	1344		5
	284	71	288	1755;1756	1348;1349	1353		8
	285	100	289	1762;1763	1356;1357	1358		4
	286	65	290	1769;1770	1360	1360		1
	287	50	291	1777;1778	1361;1362	1361		3
	288	212	292	1779	1364	1364		1
	289	158;201	293	1780;1781	1365;1366	1369		5
	290	126	294	1784	1370	1370		1
	291	122;203	295	1785;1786	1371;1372	1373		3
	292	216	296	1788;1789	1374;1375	1374		2
	293	70	297	1791;1792	1376;1377	1379		5
	294	204	298	1798;1799	1381	1381		1
	295	142	299	1802;1803	1382;1383	1383		2
	296	79;60	300	1804;1805	1384	1384	99	0
	297	172	301	1812;1813	1385	1385		1
	298	141	302	1814;1815	1386;1387	1389		7

	299	161	303	1823	1393	1393		1
	300	101;232	304	1824;1825	1394;1395	1400		10
	301	65	305	1833;1834	1404;1405	1405		5
	302	235	306	1838;1839	1409;1410	1409	328	0
	303	184	307	1842;1843	1411;1412	1418		12
	304	35	308	1851;1852	1423	1423		1
	305	44	309	1854;1855	1424	1424		1
	306	225	310	1863	1425	1425		1
+	307	17	311	1864;1865	1426;1427	1432		9
+	308	8	312	1875;1876	1435;1436	1444		20
	309	44	313	1892;1893	1455;1456	1459		5
+	310	16	314	1901;1902	1460;1461	1485		28
	311	213	315	1919;1920	1488;1489	1490		3
	312	44	316	1927;1928	1491;1492	1493		6
	313	138	317	1936;1937	1497	1497		1
+	314	17	318	1938;1939	1498;1499	1504		9
+	315	16	319	1946;1947	1507;1508	1519		19
+	316	16	320	1964;1965	1526;1527	1538		18
+	317	17	321	1982;1983	1544;1545	1551		9
	318	69	322	1991;1992	1553;1554	1559		9
+	319	17	323	2000;2001	1562;1563	1562		2
	320	89	324	2007	1564	1564		1
	321	3;201;126;2	325	2008;2009	1565;1566	1581		30
	322	3;201;126;2	326	2022;2023	1595;1596	1597		5
	323	210	327	2026	1600	1600		0
	324	164	328	2027;2028	1601;1602	1602	260	0
	325	129	329	2032;2033	1604	1604		1
	326	85	330	2040;2041	1605	1605		1
	327	224	331	2046	1606	1606		1
	328	115	332	2047;2048	1607	1607		1
	329	172	333	2052;2053	1608	1608		1
	330	185	334	2054	1609	1609		1
	331	208	335	2055;2056	1610	1610		1
	332	102	336	2059;2060	1611;1612	1615		7
	333	94;98	337	2068;2069	1618;1619	1618	154	0
+	334	2	338	2077;2078	1626;1627	1629	11	0
	335	129	339	2084;2085	1630;1631	1634	210	0
	336	71;72	340	2091;2092	1638;1639	1644		6
	337	159	341	2098;2099	1645	1645		0
	338	142	342	2103;2104	1646	1646		1
	339	146	343	2107;2108	1647;1648	1648		2
	340	131	344	2111;2112	1649	1649		1
+	341	26	345	2113;2114	1650;1651	1650		2
+	342	26	346	2128;2129	1653;1654	1655		17
+	343	10	347	2150;2151	1670;1671	1671	24	0
+	344	1	348	2158;2159	1679;1680	1690	2	0
+	345	19	349	2167;2168	1691;1692	1691	52	0
	346	133	350	2175;2176	1696	1696		1
+	347	10;1	351	2178;2179	1697	1697		1
	348	80	352	2184;2185	1698;1699	1703		7

	+	349	2;7;18	353	2193;2194	1705;1706	1706		0
	+	350	12	354	2201;2202	1707;1708	1720		14
		351	37	355	2210;2211	1721;1722	1723		5
	+	352	12	356	2215;2216	1726;1727	1748		25
	+	353	17	357	2231;2232	1751;1752	1754		10
		354	180	358	2240;2241	1761;1762	1762		4
		355	130	359	2247;2248	1765;1766	1770		10
		356	230	360	2256;2257	1775;1776	1775		2
		357	84	361	2260	1777	1777		1
		358	180	362	2261;2262	1778;1779	1779	278	0
		359	216	363	2267;2268	1781	1781		1
		360	58	364	2275;2276	1782	1782		1
		361	.51;152;17	365	2277;2278	1783;1784	1789		12
		362	99	366	2290;2291	1795	1795		1
		363	71	367	2292;2293	1796;1797	1800		7
		364	59	368	2310;2311	1803;1804	1804		10
		365	129	369	2319;2320	1813;1814	1814		3
		366	103	370	2324;2325	1816;1817	1822		8
		367	129	371	2333;2334	1824;1825	1833		11
		368	189	372	2342;2343	1835;1836	1836		2
		369	88	373	2346;2347	1837;1838	1837		2
		370	144	374	2349;2350	1839;1840	1840	228	0
		371	132	375	2353;2354	1841	1841		1
		372	69	376	2355;2356	1842;1843	1845		7
		373	69	377	2364;2365	1849;1850	1849		4
		374	42	378	2372;2373	1853	1853		1
		375	162;43	379	2374;2375	1854;1855	1855		4
	+	376	17	380	2378;2379	1858;1859	1858		3
		377	144	381	2385;2386	1861;1862	1861		2
	+	378	17	382	2393;2394	1863;1864	1870		16
	+	379	26	383	2411;2412	1879;1880	1886		11
	+	380	16	384	2420;2421	1890;1891	1891		19
	+	381	16	385	2438;2439	1909;1910	1909		10
	+	382	3	386	2447;2448	1919;1920	1921		3
		383	217	387	2456;2457	1922	1922		1
		384	59	388	2459;2460	1923	1923		1
		385	185	389	2463;2464	1924;1925	1927		4
		386	142	390	2470;2471	1928;1929	1929	226	0
		387	230	391	2474;2475	1930	1930	323	0
		388	132	392	2476;2477	1931;1932	1932		2
		389	131	393	2478;2479	1933	1933		0
		390	91	394	2480;2481	1934	1934		1
	+	391	6	395	2484;2485	1935;1936	1946		13
		392	66	396	2501;2502	1948;1949	1949	107;108	0
		393	66	397	2505;2506	1950;1951	1951		2
		394	235	398	2507;2508	1952;1953	1954		4
		395	128	399	2511;2512	1956;1957	1957	208	0
	+	396	6	400	2520;2521	1960;1961	1961		2
		397	235	401	2525;2526	1962	1962		1
		398	170	402	2533;2534	1963;1964	1963		4

	399	3	403	2537;2538	1967	1967		1
+	400	.03;118;16	404;405	2541;2542	1968;1969	1971	175;176	0
	401	144	406	2552;2553	1972	1972		1
	402	48	407	2556;2557	1973;1974	1975		3
+	403	14	408	2571;2572	1977	1977		1
	404	216	409	2580;2581	1978	1978	311	0
	405	66	410	2582	1979	1979		1
+	406	11	411	2583;2584	1980;1981	1982		5
+	407	11	412	2592;2593	1986;1987	1990		8
	408	224	413	2601;2602	1994	1994	319	0
	409	88;223	414	2605;2606	1995;1996	1995	148	0
	410	77	415	2611;2612	1999	1999	139	0
	411	172	416	2613;2614	2000;2001	2003		4
	412	50	417	2617;2618	2004	2004		1
	413	205	418	2625;2626	2005	2005		1
	414	66	419	2629	2006	2006		1
	415	64	420	2630;2631	2007;2008	2010		7
	416	176	421	2639;2640	2014;2015	2017		4
	417	169	422	2644;2645	2018	2018		1
	418	151	423	2647;2648	2019;2020	2021		5
	419	137	424	2653;2654	2025	2025		1
	420	44	425	2660;2661	2026;2027	2031		8
	421	71	426	2668;2669	2034	2034		1
	422	226	427	2676;2677	2035;2036	2038		4
+	423	17;8	428	2683;2684	2039;2040	2045		9
	424	165	429	2692;2693	2048;2049	2052	261	0
	425	190	430	2701;2702	2056	2056		1
	426	137	431	2708;2709	2057;2058	2061		13
	427	71	432	2717;2718	2070;2071	2074		12
	428	76	433	2734;2735	2082;2083	2090		9
	429	49	434	2743;2744	2091;2092	2093	82	0
	430	56;109	435	2748;2749	2094;2095	2099		7
	431	100	436	2756;2757	2101	2101		1
	432	144	437	2762;2763	2102;2103	2105		4
	433	229	438	2768;2769	2106;2107	2109		4
	434	51;121;120	439	2770;2771	2110;2111	2134		32
	435	172	440	2788;2789	2142	2142		0
	436	117	441	2790;2791	2143	2143	186	0
+	437	10	442	2792;2793	2144;2145	2145		23
	438	86	443	2808;2809	2168;2169	2168		2
	439	76	444	2812;2813	2170;2171	2172		3
	440	113	445	2827;2828	2173	2173		1
	441	113	446	2831;2832	2174;2175	2174		2
+	442	0	447	2834;2835	2176;2177	2191	0	0
+	443	0	448	2850	2196	2196	0	0
	444	107	449	2851	2197	2197		1
+	445	12	450	2852;2853	2198	2198		1
+	446	16	451	2854;2855	2199;2200	2206	40	0
	447	129	452	2870;2871	2212;2213	2225		14
	448	139	453	2881;2882	2226;2227	2226		2

	449	41	454	2889;2890	2228;2229	2229		2
+	450	32	455	2891;2892	2230	2230		1
	451	168	456	2896;2897	2231	2231		1
	452	104	457	2898;2899	2232;2233	2234	179	0
+	453	10	458	2903;2904	2237;2238	2237	23;25	0
	454	234	459	2911;2912	2241;2242	2241		3
+	455	19	460	2913;2914	2244;2245	2247		5
+	456	1	461	2916;2917	2249;2250	2269		34
	457	84	462	2932;2933	2283;2284	2284		12
	458	73	463	2941;2942	2295;2296	2296	137	0
	459	143	464	2943;2944	2297;2298	2297		4
	460	100	465	2947;2948	2301;2302	2310	162	0
	461	176	466	2956;2957	2312	2312	274;275	0
	462	58;201;18	467	2958;2959	2313;2314	2319	255;256	0
	463	2;126;203;2	468	2965;2966	2321;2322	2323	191	0
	464	100	469	2975;2976	2333;2334	2334	163	0
	465	221	470	2983;2984	2340;2341	2340		2
	466	158	471	2987;2988	2342;2343	2346		8
	467	122	472	2996;2997	2350;2351	2355		6
	468	203	473	3003;3004	2356;2357	2370		17
	469	201	474	3018;3019	2373	2373		1
	470	132	475	3023;3024	2374;2375	2374	217	0
	471	238	476	3025;3026	2376;2377	2377	330;331	0
	472	100	477	3028;3029	2378;2379	2384	164;165	0
	473	100	478	3040;3041	2385	2385		1
	474	197	479	3047;3048	2386	2386		1
+	475	16	480	3049;3050	2387;2388	2390		6
	476	53	481	3058;3059	2393;2394	2396		4
	477	97	482	3067;3068	2397;2398	2397	157;158	0
	478	180	483	3074;3075	2401;2402	2402		4
+	479	12	484	3080;3081	2405;2406	2405		16
	480	3;201;126;2	485	3098;3099	2421;2422	2426	192	0
	481	38	486	3106;3107	2428;2429	2432		7
	482	111	487	3115;3116	2435;2436	2436		2
+	483	2;7;18	488	3120;3121	2437;2438	2440		5
+	484	13	489	3128;3129	2442;2443	2446		5
	485	229	490	3137;3138	2447;2448	2447		2
+	486	10;1	491	3139;3140	2449;2450	2449		7
	487	212	492	3148;3149	2456;2457	2458		9
	488	126	493	3161;3162	2465;2466	2467		4
	489	60	494	3169;3170	2469	2469		1
	490	66	495	3171;3172	2470;2471	2472		5
	491	144	496	3173;3174	2475;2476	2477	229	0
	492	37	497	3175;3176	2478;2479	2479		5
	493	37	498	3190;3191	2483	2483	67	0
	494	168	499	3195;3196	2484;2485	2485		2
	495	40	500	3203;3204	2486;2487	2488		4
	496	70	501	3207;3208	2490;2491	2492		6
	497	192	502	3211;3212	2496;2497	2496		2
	498	103;118	503	3216;3217	2498;2499	2511		16

	499	124	504	3230;3231 2514;2515	2514		4
	500	235	505	3234;3235 2518	2518	329	0
	501	99	506	3241;3242 2519;2520	2520		6
	502	151	507	3247;3248 2525;2526	2529	239	0
	503	142	508	3255;3256 2531;2532	2532		2
	504	69	509	3261;3262 2533;2534	2536		7
	505	68	510	3270;3271 2540;2541	2541		3
+	506	12	511	3274;3275 2543;2544	2549		9
	507	139	512	3283;3284 2552	2552		1
	508	103	513	3289;3290 2553;2554	2557	173	0
+	509	8	514;515	3298;3299 2560;2561	2563	17	1
+	510	17	516	3307;3308 2565;2566	2568	47	0
	511	144	517	3315;3316 2571	2571		1
	512	229	518	3320;3321 2572;2573	2573		2
	513	225	519	3322;3323 2574;2575	2574		3
	514	234	520	3324;3325 2577	2577		1
	515	101;126;201	521	3326;3327 2578;2579	2585	193	0
	516	66	522	3342;3343 2587;2588	2587		2
+	517	3;7;18;27;101	523	3344;3345 2589;2590	2591		5
	518	88;223	524	3353;3354 2594	2594	149	0
	519	86	525	3355;3356 2595;2596	2605		12
+	520	10	526	3358;3359 2607;2608	2608	26	0
	521	225	527	3366;3367 2609	2609		0
	522	41	528	3368;3369 2610;2611	2610		2
+	523	8	529	3372;3373 2612;2613	2615		4
+	524	6	530	3381;3382 2616;2617	2617		6
+	525	5	531	3390;3391 2622	2622		1
	526	101	532	3397;3398 2623;2624	2623	170	0
	527	88	533	3404;3405 2625;2626	2625		2
	528	87	534	3406;3407 2627	2627		1
	529	144	535	3408;3409 2628	2628		0
	530	71	536	3411;3412 2629	2629		1
	531	71	537	3417;3418 2630;2631	2630		4
+	532	6;5	538	3422;3423 2634;2635	2645		20
+	533	17	539	3440;3441 2654;2655	2668		17
	534	152	540	3471;3472 2671	2671		1
+	535	13	541	3480;3481 2672;2673	2674		8
	536	92	542	3489;3490 2680	2680		1
	537	234	543	3495;3496 2681	2681		1
+	538	8	544	3497;3498 2682;2683	2688		11
+	539	;13;7;18;27	545	3506;3507 2693;2694	2694		7
+	540	;13;7;18;27	546	3513;3514 2700;2701	2701		4
	541	72	547	3521;3522 2704;2705	2704	133;134	0
	542	71	548	3524;3525 2706;2707	2710	129;130	0
	543	110	549	3530;3531 2715;2716	2715		2
+	544	14	550	3532;3533 2717	2717		1
	545	86	551	3536;3537 2718;2719	2726	143;144	0
+	546	16	552	3542;3543 2727;2728	2741		20
+	547	.2;10;1;19;101	553	3559;3560 2747;2748	2750		6
	548	212	554	3567;3568 2753;2754	2753	302	0

	549	93	555	3572;3573	2759	2759		0
	550	130	556	3576;3577	2760;2761	2764		8
	551	101;126;20	557	3585;3586	2768;2769	2779	193	0
+	552	6	558	3594;3595	2782;2783	2782		2
	553	103	559	3596;3597	2784;2785	2785	177	0
	554	69	560	3603;3604	2792;2793	2794		3
	555	51;121;120	561	3609;3610	2795;2796	2806	87	0
	556	110	562	3625;3626	2808	2808		1
	557	99	563	3627;3628	2809	2809		0
	558	113	564	3632	2810	2810		0
	559	97	565	3633	2811	2811	159;160	0
	560	216	566	3634;3635	2812;2813	2812	312	0
	561	216	567	3636;3637	2814;2815	2814	312	0
	562	69	568	3640;3641	2817;2818	2821	120	0
+	563	8	569	3645;3646	2823;2824	2832	19;20	0
	564	172	570	3662;3663	2838;2839	2838		2
	565	172	571	3665;3666	2840;2841	2840		3
	566	61	572	3667;3668	2843;2844	2844	100	0
	567	70	573	3675;3676	2846	2846		0
	568	129	574	3682;3683	2847	2847		1
	569	69	575	3691;3692	2848;2849	2850		6
	570	66	576	3695;3696	2854;2855	2856	109	0
+	571	12	577	3697;3698	2857;2858	2863		10
	572	168	578	3706;3707	2867;2868	2868		4
+	573	10;1;19;9	579	3715;3716	2871;2872	2871		11
	574	130	580	3724;3725	2882;2883	2884	213	0
	575	168	581	3735;3736	2893;2894	2895	264;265	0
	576	144	582	3742;3743	2896;2897	2898	230;231	0
	577	136	583	3747;3748	2900;2901	2905		6
	578	184	584	3750;3751	2906;2907	2906		9
	579	44	585	3758;3759	2915;2916	2924		14
+	580	6	586	3767;3768	2929;2930	2932		5
	581	72	587	3773;3774	2934	2934		1
	582	88	588	3778;3779	2935;2936	2936		2
+	583	0	589	3780;3781	2937;2938	2969		35
	584	237	590	3809;3810	2974;2975	2974		3
+	585	6	591	3818;3819	2977;2978	2978		11
	586	130	592	3827	2988	2988	214	0
	587	75	593	3828;3829	2989;2990	2989		2
	588	216	594	3836;3837	2991;2992	2991		2
	589	172	595	3839;3840	2993;2994	2994		2
	590	212;187	596	3844;3845	2995;2996	2999	284	0
	591	58;201;120	597	3850;3851	3002;3003	3013	194	0
	592	102	598	3863;3864	3020;3021	3021		4
	593	51;152;17	599	3872;3873	3024	3024		1
	594	121	600	3882;3883	3025;3026	3033		14
	595	51;152;17	601	3890;3891	3039;3040	3043		5
	596	51;120	602	3898;3899	3044;3045	3047		6
	597	70	603	3905;3906	3050;3051	3056		12
+	598	6	604	3918	3062	3062		1

	599	132	605	3919;3920 3063;3064	3063		2
	600	66	606	3921;3922 3065;3066	3065		4
	601	101	607	3926;3927 3069;3070	3071		3
+	602	12	608	3935;3936 3072;3073	3075		12
	603	238	609	3952;3953 3085;3086	3086		3
	604	35	610	3956;3957 3088;3089	3091		4
+	605	10	611	3964;3965 3092;3093	3093		2
+	606	1	612	3972;3973 3094;3095	3094		2
+	607	;7;18;27;13	613	3981;3982 3096;3097	3100		9
+	608	21	614	3990;3991 3105;3106	3106		2
	609	41	615	3999;4000 3107;3108	3107	73	0
	610	130	616	4001;4002 3109;3110	3119	215	0
	611	81	617	4009;4010 3122;3123	3122		2
	612	76	618	4014;4015 3124;3125	3129		6
	613	94;98	619	4023;4024 3130;3131	3138		9
	614	128	620	4035;4036 3139;3140	3141		4
	615	128	621	4042;4043 3143	3143		1
+	616	8	622	4048;4049 3144;3145	3148	18	0
+	617	17	623	4066;4067 3150;3151	3152	48	0
	618	238	624	4072;4073 3153;3154	3155		4
	619	43	625	4076;4077 3157;3158	3158	76	0
	620	71	626	4078;4079 3159;3160	3159	131;132	0
	621	233	627	4086;4087 3163;3164	3164	325;326	0
	622	157	628	4095;4096 3169;3170	3172	252;253	0
+	623	8	629	4103;4104 3175;3176	3181		10
+	624	8	630	4112;4113 3185;3186	3185		2
+	625	17	631	4118;4119 3188;3189	3194		10
	626	177	632	4127;4128 3199;3200	3199		3
	627	151;152	633	4135;4136 3202;3203	3208		9
	628	56;109	634	4144;4145 3211;3212	3213		5
	629	41	635	4153;4154 3216;3217	3216		0
	630	180	636	4155;4156 3218;3219	3221	279	0
	631	227	637	4160;4161 3222;3223	3226		6
+	632	17	638	4169;4170 3228;3229	3231		7
	633	82	639	4183;4184 3235;3236	3237		4
	634	208	640	4187;4188 3239	3239		1
	635	188	641	4194;4195 3240	3240		1
	636	57	642	4196;4197 3241;3242	3245	93	0
+	637	13	643	4205;4206 3246;3247	3250		7
+	638	2;7;18	644	4214;4215 3253;3254	3253		2
+	639	8	645	4222;4223 3255	3255		1
+	640	8	646	4231;4232 3256;3257	3269		18
	641	90	647	4253;4254 3274	3274		1
	642	69	648	4257;4258 3275;3276	3279		7
+	643	15	649	4264;4265 3282;3283	3282		3
	644	66	650	4268;4269 3285;3286	3285	110	0
	645	224;220	651	4270;4271 3287	3287		0
	646	229	652	4275;4276 3288;3289	3289		2
+	647	6	653	4277;4278 3290	3290		0
	648	216	654	4286;4287 3291	3291		1

	649	0	655	4288;4289	3292;3293	3297		3
	650	161	656	4297;4298	3302	3302		1
	651	70	657	4299;4300	3303;3304	3303	121	0
	652	53	658	4303;4304	3306;3307	3307		4
+	653	9	659	4309;4310	3310;3311	3310	22	0
	654	58;201;121	660	4312;4313	3312;3313	3314	195	0
	655	88	661	4317;4318	3318;3319	3319		2
+	656	15	662	4319	3320	3320		1
	657	70	663	4320;4321	3321;3322	3321		5
	658	100	664	4327;4328	3327;3328	3331		10
	659	194	665	4345;4346	3337;3338	3337	287	0
+	660	6	666	4353;4354	3340;3341	3341		6
+	661	5	667	4362;4363	3346;3347	3346		5
	662	188	668	4368;4369	3351	3351		1
+	663	6	669	4370;4371	3352	3352		1
	664	168	670	4374;4375	3353;3354	3358	266	0
	665	168	671	4381;4382	3360	3360	266	0
	666	203	672	4385;4386	3361	3361	294	0
	667	213	673	4389;4390	3362;3363	3364	306	0
	668	187	674	4396;4397	3366;3367	3367		2
	669	147	675	4398;4399	3368;3369	3369	237	0
	670	126	676	4404;4405	3371;3372	3372	204	0
	671	33	677	4411	3373	3373	60	0
	672	37	678	4412;4413	3374;3375	3374	68	0
	673	109	679	4421;4422	3376;3377	3378	181	0
	674	56	680	4427;4428	3379;3380	3379	91	0
	675	88;223	681	4436;4437	3383;3384	3383	149	0
	676	144	682	4440;4441	3385	3385	232	0
	677	39	683	4442;4443	3386	3386	71	0
+	678	25	684	4444;4445	3387	3387		0
	679	89	685	4448	3388	3388	153	0
	680	208	686	4449;4450	3389;3390	3389	299	0
	681	221	687	4453;4454	3391	3391	315	0
+	682	13	688	4456;4457	3392;3393	3393	32;33;34	0
	683	137	689	4462;4463	3396;3397	3400	220	0
	684	66	690	4470	3401	3401	109;111	0
	685	86	691;692	4471;4472	3402;3403	3412	145	8
	686	53	693	4498;4499	3421;3422	3424	89	0
	687	182	694	4503	3425	3425	283	0
	688	225	695	4504;4505	3426	3426	320	0
	689	215	696	4506;4507	3427;3428	3428	308	0
	690	172	697	4513;4514	3429	3429		0
	691	195	698	4515;4516	3430;3431	3430	288	0
+	692	6	699	4517;4518	3432;3433	3438	15	0
	693	124	700	4526;4527	3445	3445		0
	694	173	701	4529;4530	3446	3446	269	0
	695	86	702;703;704	4536;4537	3447;3448	3465	146;147	4
	696	152	705	4559;4560	3472;3473	3474	247	0
	697	151	706	4566;4567	3480;3481	3487	240	0
	698	187	707	4572;4573	3490;3491	3490	285	0

	699	122;203	708	4574;4575	3492;3493	3496	196	0
	700	.22;158;20	709	4582;4583	3500;3501	3500	197	0
	701	163	710	4585;4586	3503;3504	3508	259	0
	702	112	711	4593;4594	3511;3512	3516	183	0
+	703	17	712	4602;4603	3517;3518	3535	49	0
+	704	8	713	4618;4619	3539;3540	3541	21	0
	705	66	714	4627;4628	3548;3549	3548	112	0
	706	212	715	4631;4632	3550;3551	3550	101;303;30	0
	707	2;158;201;:	716	4640;4641	3553;3554	3558	.90;198;19	0
	708	203	717	4649;4650	3562;3563	3562	193;295;29	0
	709	212	718;719	4657;4658	3566;3567	3588	305	15
+	710	1;9	720	4677;4678	3593	3593		0
	711	146	721	4686;4687	3594;3595	3599	235	0
+	712	16	722;723	4688;4689	3600;3601	3602	41	2
	713	72	724	4703;4704	3610;3611	3616	135;136	0
	714	37	725	4712;4713	3620;3621	3622	69	0
	715	69	726	4719;4720	3623;3624	3623		0
	716	36	727	4722;4723	3626;3627	3626	64	0
	717	102	728	4730;4731	3630;3631	3641	171	0
	718	180	729	4739;4740	3644;3645	3647	280	0
	719	73	730	4745;4746	3649;3650	3649		2
	720	192	731	4751;4752	3651	3651		1
	721	86	732	4758;4759	3652;3653	3654		5
	722	156	733	4761;4762	3657;3658	3658		2
	723	128	734	4763;4764	3659	3659		1
	724	218	735	4766	3660	3660	313	0
	725	39	736	4767;4768	3661;3662	3661		2
	726	179	737	4769	3663	3663		1
	727	89	738	4770;4771	3664;3665	3666		3
+	728	10	739	4775;4776	3667;3668	3668	26	0
+	729	1;19	740	4781;4782	3670;3671	3672	3	0
+	730	16	741	4795;4796	3679;3680	3679	39	0
	731	136	742	4798;4799	3682;3683	3682	219	0
	732	104	743	4800;4801	3685	3685		1
	733	110	744	4803;4804	3686	3686		1
+	734	2;7;18	745	4805;4806	3687;3688	3687		4
+	735	8	746	4813;4814	3691;3692	3704		18
+	736	8	747	4831;4832	3709;3710	3711		11
+	737	17	748	4839;4840	3720;3721	3735		17
+	738	8;2;13;7;18	749	4857;4858	3737	3737		1
+	739	8;2;13;7;18	750	4866;4867	3738;3739	3747		17
	740	157	751	4884;4885	3755;3756	3758		4
	741	233	752	4890;4891	3759;3760	3766		10
	742	51;121;120	753	4899;4900	3770;3771	3774		5
+	743	.7;2;13;7;1	754	4911;4912	3775;3776	3780		10
	744	.51;152;17	755	4918;4919	3786	3786		0
	745	37	756	4922;4923	3787;3788	3787		2
	746	79	757	4930;4931	3789	3789		0
	747	183	758	4937;4938	3790;3791	3792		3
	748	144	759	4942;4943	3793;3794	3794	233	0

	749	85	760	4945;4946	3795;3796	3795	142	0
	750	41	761	4951;4952	3799;3800	3799	74	0
	751	44	762	4953;4954	3802;3803	3806	77	0
	752	!01;126;20	763	4969;4970	3812;3813	3815	200;201	0
+	753	13	764	4978;4979	3818;3819	3822	35	0
+	754	8	765;766	4985;4986	3824;3825	3840	19;20	0
	755	.51;152;17	767	5006;5007	3843;3844	3849	241	0
+	756	12	768	5015;5016	3852;3853	3880		36
	757	113	769	5033;5034	3888;3889	3888	184	0
	758	69	770	5043;5044	3898;3899	3899		4
	759	69	771	5051;5052	3902;3903	3910		10
	760	216	772	5068;5069	3912	3912		1
	761	196	773	5070;5071	3913	3913	289;290	0
	762	113	774	5076;5077	3914;3915	3915	185	0
	763	142	775	5085;5086	3918	3918		1
	764	!01;126;20	776	5087;5088	3919;3920	3931		17
	765	.51;152;17	777	5099;5100	3936;3937	3937	242	0
	766	47	778	5102;5103	3938;3939	3938	79	0
	767	176	779	5105;5106	3941;3942	3941	276	0
	768	144	780	5109;5110	3943;3944	3946	234	0
+	769	2;7;18	781	5114;5115	3947	3947		1
	770	88	782	5119;5120	3948;3949	3952		5
	771	66	783	5123;5124	3953;3954	3954		2
	772	208	784	5125;5126	3955;3956	3955	300	0
	773	238	785	5127;5128	3957;3958	3960	332	0
	774	129	786	5130;5131	3961;3962	3963	211	0
+	775	12	787	5137;5138	3968;3969	3988		32
+	776	17	788	5155;5156	4000;4001	4007		15
+	777	17	789	5172;5173	4015	4015		0
+	778	17	790	5177;5178	4016;4017	4016		3
+	779	12	791	5181;5182	4019;4020	4028	29;30	0
	780	205	792	5201;5202	4051	4051		1
	781	108	793	5209;5210	4052	4052		1
+	782	16	794	5217;5218	4053;4054	4057		9
	783	66	795	5227	4063	4063		1
	784	172	796	5228;5229	4064	4064		1
	785	44	797	5230;5231	4065	4065		1
	786	66	798	5235	4066	4066		1
	787	238	799	5236;5237	4067;4068	4067		4
+	788	28	800	5240;5241	4071	4071	57	0
	789	.51;152;17	801	5250;5251	4072;4073	4079	243	0
	790	218	802	5261;5262	4083	4083		1
	791	172	803	5263;5264	4084;4085	4085		5
+	792	13	804	5265;5266	4089	4089		1
+	793	11	805	5270;5271	4090;4091	4090		2
	794	141	806	5274;5275	4092;4093	4097	223	0
	795	218	807	5280;5281	4098	4098		1
	796	104	808	5282;5283	4099;4100	4101	180	0
+	797	2;7;18	809	5286;5287	4104	4104		1
+	798	16	810	5293;5294	4105;4106	4110		10

	799	140	811	5302;5303	4115;4116	4115	222	0
	800	172	812	5311;5312	4120;4121	4121		2
	801	103	813	5313;5314	4122;4123	4132		11
+	802	16	814	5324;5325	4133;4134	4139		7
+	803	16	815	5332;5333	4140;4141	4142		4
	804	.51;152;17	816	5341;5342	4144;4145	4151		11
	805	.51;152;17	817	5350;5351	4155;4156	4155		2
+	806	16	818	5358;5359	4157;4158	4164		10
	807	94	819	5367;5368	4167;4168	4168		3
	808	37	820	5375;5376	4170;4171	4175		6
	809	180	821	5384;5385	4176;4177	4177		0
	810	196	822	5389;5390	4178;4179	4179	291	0
+	811	8	823	5393;5394	4180;4181	4193		19
+	812	8	824	5411;5412	4199	4199		1
+	813	8	825	5419	4200	4200		1
	814	229	826	5420;5421	4201;4202	4201		2
	815	154	827	5422;5423	4203	4203		1
+	816	2;13;7;18	828	5425;5426	4204;4205	4206		3
	817	144	829	5440;5441	4207;4208	4208		2
	818	51;121;120	830	5447;5448	4209;4210	4211		17
	819	51;121;120	831	5464;5465	4226;4227	4237		19
	820	149	832	5482;5483	4246;4247	4247		2
	821	144	833	5488	4248	4248		1
	822	67	834	5489;5490	4249;4250	4250	118;119	0
+	823	6	835	5496;5497	4251	4251		1
+	824	2;13;7;18	836	5505;5506	4252;4253	4254		3
	825	125	837	5511;5512	4255;4256	4255	202	0
	826	224	838	5515;5516	4258	4258		1
+	827	1	839	5518;5519	4259;4260	4265		7
+	828	10	840	5527;5528	4266;4267	4267		2
+	829	12	841	5536;5537	4268;4269	4274		9
	830	45	842	5544;5545	4277;4278	4278		2
	831	232	843	5549;5550	4279;4280	4279		8
	832	238	844	5560;5561	4287;4288	4287	333;334	0
	833	238	845	5564;5565	4292;4293	4292	333;334	0
+	834	12	846	5568;5569	4296;4297	4302		12
+	835	12	847	5577;5578	4308;4309	4308		6
	836	149	848	5585;5586	4314	4314		1
+	837	10	849	5593	4315	4315		1
+	838	25	850	5594;5595	4316;4317	4318	55	0
	839	225	851	5601;5602	4321;4322	4321	321	0
	840	144	852	5603;5604	4323;4324	4324		4
+	841	16	853	5609;5610	4327;4328	4331	42	0
	842	36	854	5618;5619	4336;4337	4337		2
	843	66	855	5622;5623	4338	4338		1
	844	216	856	5624;5625	4339;4340	4340		2
	845	195	857	5630;5631	4341	4341		1
+	846	6	858	5632;5633	4342;4343	4351		16
	847	238	859	5647;5648	4358;4359	4358	330;331	0
	848	3;201;126;7	860	5651;5652	4360;4361	4361	192	0

	849	69	861	5654;5655	4362;4363	4364		4
	850	191	862	5660;5661	4366	4366	286	0
	851	51;121;120	863	5664;5665	4367;4368	4369		3
+	852	6	864	5671;5672	4370;4371	4374		6
	853	69	865	5686;5687	4376	4376		1
+	854	2;13;7;18	866	5691;5692	4377;4378	4377		2
	855	159	867	5700;5701	4379;4380	4380		1
+	856	8	868	5708;5709	4381	4381		1
	857	70	869	5716;5717	4382;4383	4383	122;123	0
+	858	12	870	5721;5722	4387;4388	4388		8
	859	37	871	5730;5731	4395;4396	4400		6
	860	86	872	5738;5739	4401;4402	4404		6
	861	86	873	5742;5743	4407;4408	4411		5
	862	210	874	5749;5750	4412;4413	4413		2
	863	210	875	5751	4414	4414		1
	864	186	876	5752;5753	4415	4415		1
	865	166	877	5761;5762	4416;4417	4416		2
	866	66	878	5763;5764	4418;4419	4419		2
+	867	16	879	5765;5766	4420;4421	4454	43;44	0
+	868	16	880	5781;5782	4456;4457	4464	43;44	0
	869	184	881	5787;5788	4465	4465		1
	870	66	882	5796;5797	4466;4467	4470		5
	871	148	883	5798;5799	4471	4471		1
+	872	1;19	884	5800;5801	4472;4473	4475		5
+	873	12	885	5809;5810	4477;4478	4478		2
+	874	12	886	5818;5819	4479;4480	4482		4
	875	86	887	5833;5834	4483;4484	4489		9
+	876	26	888	5849;5850	4492	4492		1
+	877	10	889	5856;5857	4493	4493		1
	878	150	890	5865;5866	4494	4494		1
+	879	13	891	5867;5868	4495;4496	4498		6
+	880	7;18	892	5874;5875	4501;4502	4501		2
+	881	2	893	5878;5879	4503;4504	4504		3
+	882	8	894	5885;5886	4506;4507	4520		16
+	883	12	895	5900;5901	4522;4523	4527		9
+	884	16	896	5909;5910	4531;4532	4531		9
	885	58;201;120	897	5918;5919	4540;4541	4544		7
+	886	23	898	5922;5923	4547	4547		1
	887	68;87	899	5931;5932	4548	4548		1
	888	68;87	900	5933;5934	4549;4550	4550		2
+	889	6	901	5938;5939	4551;4552	4552		2
	890	216	902	5941;5942	4553;4554	4553		2
	891	51;120	903	5943;5944	4555;4556	4559		5
	892	181	904	5949;5950	4560;4561	4561	282	0
+	893	17	905	5957;5958	4563;4564	4577		21
	894	37	906	5975;5976	4584	4584		0
+	895	8	907	5979;5980	4585;4586	4589		13
+	896	8	908	5993;5994	4598;4599	4601		8
+	897	17	909	6005;6006	4606;4607	4625		26
+	898	17	910	6032;6033	4632;4633	4635		4

	899	83	911	6037;6038	4636;4637	4637		2
+	900	12	912	6045;6046	4638;4639	4644		9
	901	48	913	6060;6061	4650;4651	4655	81	0
	902	224	914	6068;6069	4658	4658		1
+	903	8;27	915	6071;6072	4659;4660	4664		7
+	904	6	916	6075;6076	4666;4667	4667		9
+	905	5	917	6083;6084	4675	4675		1
+	906	12	918	6090;6091	4676;4677	4680		9
+	907	8	919	6099;6100	4685;4686	4692		8
+	908	8	920	6106;6107	4693;4694	4700		12
	909	168	921	6124;6125	4706	4706		1
+	910	17	922	6129;6130	4707;4708	4713		9
+	911	8	923	6138;6139	4716;4717	4720		8
+	912	8	924	6146;6147	4724;4725	4740		19
+	913	13	925	6161	4743	4743		1
+	914	25	926	6162;6163	4744;4745	4747	56	0
	915	74	927	6169;6170	4750;4751	4752		3
	916	152	928	6178;6179	4753	4753		0
	917	66	929	6181;6182	4754;4755	4754		4
	918	66	930	6183;6184	4758;4759	4758		2
	919	216	931	6185;6186	4760;4761	4760		3
	920	66	932	6188	4763	4763	113	0
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+	922	12	934	6198;6199	4770;4771	4771		13
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+	924	2;7;18;27	936	6233;6234	4793	4793		1
+	925	13	937	6240;6241	4794	4794		1
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	927	165	939	6258;6259	4796;4797	4799		5
	928	216	940	6267;6268	4801;4802	4801		2
	929	211	941	6269;6270	4803	4803		1
	930	66	942	6271;6272	4804;4805	4804	114;115	0
	931	216	943	6273;6274	4806;4807	4806		3
	932	85	944	6278;6279	4809;4810	4809		3
	933	66	945	6285;6286	4812;4813	4813		2
	934	113	946	6287;6288	4814;4815	4816		4
	935	93	947	6296;6297	4818	4818		1
	936	228	948	6300;6301	4819	4819		1
	937	66	949	6309;6310	4820	4820		0
	938	66	950	6311;6312	4821;4822	4821		3
+	939	16	951;952	6315;6316	4824;4825	4829	45	8
	940	216	953	6328;6329	4842	4842		1
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	942	56;109	955	6336;6337	4844;4845	4845		2
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	952	.03;118;16	965	6392;6393	4876;4877	4889		15
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	961	.58;201;12	974	6481;6482	4934	4934		1
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	969	142	982	6537;6538	4965	4965		1
	970	95	983	6543;6544	4966	4966		0
	971	123	984	6552;6553	4967;4968	4967		2
	972	129	985	6555;6556	4969;4970	4974		12
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	1006	52	1019	6815;6816 5225;5226	5226		2
	1007	84	1020	6823;6824 5227	5227		1
	1008	138	1021	6828;6829 5228;5229	5228		2
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	1010	66	1023	6832;6833 5232;5233	5233		2
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	1021	100	1034	6904;6905 5276	5276	167	0
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	1059	53	1072	7181;7182 5501	5501		1
+	1060	13	1073	7186;7187 5502;5503	5506	37;38	0
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	1117	223	1130	7532;7533 5781	5781		1
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	1146	216	1160	7710;7711 5923	5923		1
	1147	175	1161	7712;77135924;5925	5925	272;273	0
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	1179	89	1193	7952;7953	6100;6101	6102		4
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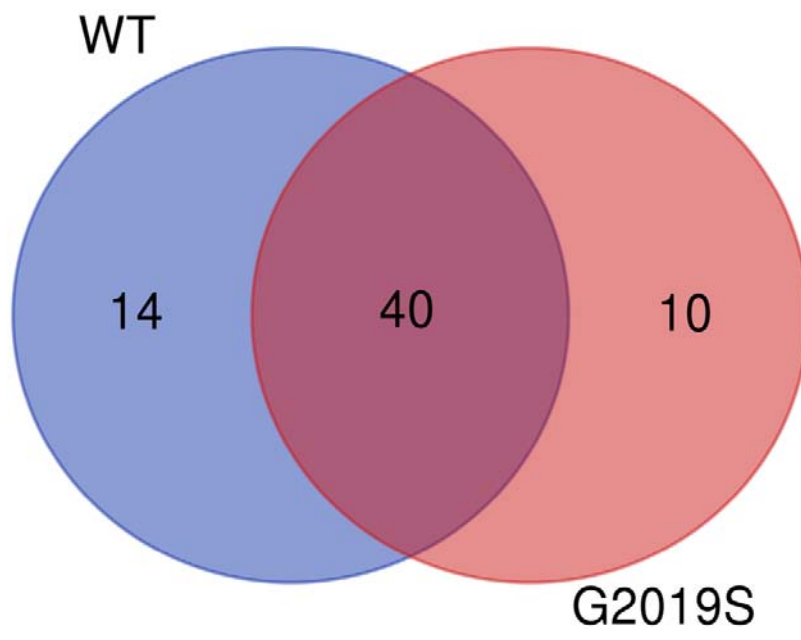
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>sp P1887 P18872		9,15E+05	6,41E+05	3,15E+06	2,72E+06	2,39E-33	3,8
>sp P1685 P16858		1,06E+07	9,15E+06	1,83E+07	7,90E+07	1,51E-03	3,9
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>sp P6813 P68134		9,17E+06	8,35E+06	4,25E+07	3,48E+07	3,07E-118	4,4
>tr A2AKV A2AKV1		1,06E+06	7,86E+05	4,81E+06	3,40E+06	6,98E-30	4,4
>sp P6326 P63260		1,98E+07	1,93E+07	9,54E+07	7,95E+07	2,77E-174	4,5
>tr A0A0N A0A0N4SU		7,15E+05	5,87E+05	3,21E+06	2,77E+06	1,49E-103	4,6
>sp Q99KI Q99KI0			8,04E+04	6,43E+05	2,31E+05	2,19E-03	4,8
>sp P1149 P11499		8,05E+05	5,65E+05	4,09E+06	2,56E+06	1,92E-20	4,8
>sp P1718 P17182		2,66E+06	2,84E+06	1,29E+07	1,38E+07	0,00E+00	4,8
>sp P1876 P18760		2,50E+05		1,34E+06	1,12E+06	1,07E-70	4,9
>sp P1012 P10126		2,22E+06	2,54E+06	1,72E+07	7,92E+06	2,10E-12	4,9
>sp P5648 P56480		1,71E+06	1,15E+06	6,93E+06	7,71E+06	1,96E-45	5,2
>sp Q8BFZ Q8BFZ3		1,71E+06	1,58E+06	1,01E+07	8,23E+06	8,72E-158	5,5
>tr Q29ZC Q29ZQ5		3,82E+05	3,63E+05	2,37E+06	2,20E+06	0,00E+00	6,1
>sp P0521 P05213		2,20E+07	2,08E+07	1,58E+08	1,13E+08	9,91E-76	6,3
>sp P6836 P68369		2,21E+07	2,08E+07	1,59E+08	1,13E+08	9,45E-76	6,3
>tr A0A0J A0A0J9YUI		1,21E+05	3,70E+05	1,41E+06	1,30E+06	1,03E-08	6,4
>sp P6836 P68368		1,30E+07	1,27E+07	9,89E+07	8,44E+07	0,00E+00	7,1
>sp P5188 P51881		2,51E+06	2,45E+06	2,09E+07	2,07E+07	0,00E+00	8,4
>sp Q7TM Q7TMM9		4,61E+06	3,84E+06	3,79E+07	3,31E+07	1,16E-230	8,4
>tr Q91VA Q91VA7		1,84E+05	1,89E+05	1,83E+06	1,41E+06	7,67E-176	8,6
>sp Q032f Q03265		4,52E+06	4,30E+06	4,34E+07	3,58E+07	0,00E+00	8,9
>sp Q9CW Q9CWF2		2,49E+06	1,86E+06	2,12E+07	1,81E+07	1,84E-116	9,1
>sp Q9D6l Q9D6F9		3,10E+06	2,61E+06	2,76E+07	2,45E+07	7,30E-289	9,1
>sp P4896 P48962		2,75E+06	2,32E+06	2,22E+07	2,44E+07	0,00E+00	9,2
>sp P4646 P46460		5,75E+05	2,45E+05	3,53E+06	3,51E+06	1,20E-19	9,4
>sp P9902 P99024		3,46E+06	2,53E+06	3,01E+07	2,58E+07	1,75E-109	9,4
>sp Q643z Q64332		2,25E+05	1,06E+05	1,56E+06	1,36E+06	4,89E-24	9,4
>sp Q9ERI Q9ERD7		2,26E+06	2,42E+06	2,70E+07	2,34E+07	0,00E+00	10,8
>sp P6837 P68372		2,67E+06	2,83E+06	3,53E+07	2,99E+07	0,00E+00	11,8
>sp Q922f Q922F4		1,79E+06	1,74E+06	2,37E+07	1,94E+07	0,00E+00	12,1
>sp Q6187 Q61879		3,40E+05	3,63E+05	4,69E+06	4,03E+06	0,00E+00	12,4
>tr Q7M6' Q7M6W1		8,38E+04		1,14E+06	1,14E+06	0,00E+00	13,6
>sp P4300 P43006		6,31E+05	4,81E+05	2,73E+08	2,27E+08	0,00E+00	452,4
>sp P4796 P47963				4,59E+05	3,59E+05	#N/D	#DIV/0!
>tr A0A1L A0A1L1SU37				1,98E+05	3,87E+05	#N/D	#DIV/0!
>tr A0A33 A0A338P6R8				4,71E+05	3,92E+05	#N/D	#DIV/0!
>tr Q8C04 Q8C048				4,21E+05	3,92E+05	#N/D	#DIV/0!
>sp Q8VD Q8VDD5				8,69E+05	6,21E+05	#N/D	#DIV/0!

>sp P9780 P97807	1,09E+06	9,09E+05	#N/D	#DIV/0!
>tr Q3U4F Q3U4F0	9,60E+05	9,73E+05	#N/D	#DIV/0!
>sp O8893 O88935	1,06E+06	1,05E+06	#N/D	#DIV/0!
>tr Q8BRC Q8BRQ9	3,65E+05	1,14E+06	#N/D	#DIV/0!
>sp Q8VEI Q8VEM8	1,06E+07	1,59E+06	#N/D	#DIV/0!
>sp P4666 P46660	2,28E+06	1,82E+06	#N/D	#DIV/0!
>tr A0A0R A0A0R4J107	2,19E+06	2,12E+06	#N/D	#DIV/0!
>tr Q9Z1A Q9Z1A1	5,53E+06	4,32E+06	#N/D	#DIV/0!

G2019S

Fasta head	UniProt ID	Intensity Q	Intensity Q	Intensity Q	Intensity Q	p value	FC
>sp O889E O88935		2,69E+05	1,75E+05	1,01E+06	7,91E+05	2,86E-23	4,1
>tr H3BKN H3BKM0		7,86E+04	9,05E+04	4,46E+05	2,91E+05	5,87E-29	4,3
>sp P6836 P68368		1,80E+07	2,03E+07	6,88E+07	9,77E+07	3,29E-42	4,3
>sp P6280 P62806		1,56E+05	1,92E+05	7,91E+05	7,26E+05	1,33E-116	4,4
>sp P1718 P17182		3,24E+06	3,60E+06	1,48E+07	1,65E+07	6,63E-252	4,6
>tr Q29ZC Q29ZQ5		4,58E+05	4,09E+05	2,16E+06	2,00E+06	0,00E+00	4,8
>sp P0521 P05213		2,64E+07	2,73E+07	1,19E+08	1,45E+08	1,83E-170	4,9
>sp P1685 P16858		5,68E+06	7,45E+06	1,48E+07	7,00E+07	4,58E-04	4,9
>sp P6836 P68369		2,63E+07	2,74E+07	1,22E+08	1,45E+08	2,52E-227	5,0
>sp P1633 P16330		8,43E+06	8,30E+06	4,26E+07	4,46E+07	0,00E+00	5,2
>sp Q8VEI Q8VEM8		8,13E+05	1,32E+06	6,43E+06	6,29E+06	1,59E-38	6,1
>sp P6263 P62631		1,58E+06	1,78E+06	1,17E+07	1,01E+07	2,43E-258	6,5
>sp P4646 P46460		4,50E+05	5,35E+05	3,11E+06	3,27E+06	3,20E-286	6,5
>sp Q032E Q03265		4,80E+06	5,46E+06	3,68E+07	3,03E+07	1,15E-170	6,5
>sp P1012 P10126		1,58E+06	1,96E+06	1,28E+07	1,06E+07	1,26E-118	6,6
>sp P9902 P99024		4,69E+06	4,58E+06	3,28E+07	2,90E+07	0,00E+00	6,7
>sp Q922F Q922F4		3,51E+06	3,42E+06	2,52E+07	2,17E+07	0,00E+00	6,7
>sp Q9DD Q9DD18		2,92E+05	3,31E+05	2,18E+06	2,19E+06	0,00E+00	7,0
>sp Q9ERI Q9ERD7		3,80E+06	3,46E+06	2,98E+07	2,34E+07	4,98E-157	7,3
>sp Q7TM Q7TMM9		4,86E+06	5,03E+06	3,89E+07	3,43E+07	0,00E+00	7,4
>sp P6837 P68372		4,56E+06	4,66E+06	3,71E+07	3,18E+07	0,00E+00	7,5
>sp P6326 P63260		1,21E+07	1,53E+07	1,15E+08	9,19E+07	1,69E-101	7,6
>sp Q9D6I Q9D6F9		3,32E+06	3,42E+06	2,68E+07	2,43E+07	0,00E+00	7,6
>sp P6813 P68134		7,59E+06	7,04E+06	5,69E+07	5,40E+07	0,00E+00	7,6
>sp Q8BFZ Q8BFZ3		3,79E+06	1,40E+06	1,21E+07	2,75E+07	2,61E-08	7,9
>sp Q9CW Q9CWF2		3,15E+06	3,12E+06	2,64E+07	2,40E+07	0,00E+00	8,0
>tr Q91VA Q91VA7		1,19E+05	1,13E+05	1,34E+06	7,00E+05	1,74E-29	8,3
>sp P4666 P46660			1,55E+05	1,44E+06	1,23E+06	1,03E-167	8,5
>sp P1876 P18760		1,38E+05	1,43E+05	1,18E+06	1,23E+06	0,00E+00	8,6
>tr Q8BRC Q8BRQ9			6,42E+04	6,78E+05	6,13E+05	0,00E+00	10,0
>sp P5188 P51881		1,80E+06	8,68E+05	1,19E+07	1,80E+07	5,67E-24	11,7
>sp P4896 P48962		1,96E+06	8,68E+05	1,26E+07	2,00E+07	2,56E-20	12,2
>tr Q7M6' Q7M6W1		6,64E+04	7,86E+04	1,20E+06	1,25E+06	0,00E+00	17,0
>tr A2AKV A2AKV1		1,98E+05	1,14E+05	4,88E+06	2,62E+06	1,49E-39	23,8
>sp Q6187 Q61879		2,80E+05	4,83E+04	7,26E+06	8,98E+06	1,13E-16	69,3
>sp P4300 P43006		1,24E+05	5,91E+05	1,94E+08	1,84E+08	6,05E-48	696,6
>tr Q9DAY Q9DAY9				3,91E+04	3,63E+04	#N/D	#DIV/0!
>sp O5477 O54774				6,13E+05	6,65E+04	#N/D	#DIV/0!
>sp P1742 P17427				2,03E+05	1,53E+05	#N/D	#DIV/0!
>sp Q8BSI Q8BSL7				1,70E+05	2,56E+05	#N/D	#DIV/0!
>tr Q8C04 Q8C048				4,34E+05	2,71E+05	#N/D	#DIV/0!
>sp P4796 P47963				3,46E+05	3,16E+05	#N/D	#DIV/0!
>tr A0A33 A0A338P6R8				9,42E+05	3,51E+05	#N/D	#DIV/0!
>sp Q8QZ Q8QZT1				2,71E+05	3,81E+05	#N/D	#DIV/0!
>tr Q5SVI Q5SVI9				4,70E+05	4,11E+05	#N/D	#DIV/0!
>sp P1179 P11798				8,36E+05	4,11E+05	#N/D	#DIV/0!

>tr Q3U4F Q3U4F0		7,60E+05	6,89E+05	#N/D	#DIV/0!
>sp P9780 P97807		9,78E+05	7,70E+05	#N/D	#DIV/0!
>tr A0A0R A0A0R4J107		1,53E+06	1,37E+06	#N/D	#DIV/0!
>tr Q9Z1A Q9Z1A1		5,19E+06	5,43E+06	#N/D	#DIV/0!



WT

E9PZW0
A0A1L1SU37
Q8VDD5
D3YYN7
A0A0N4SUX5
P11499
A0A0J9YUE9
Q99KIO
P56480
Q8VDN2
P18872
Q64332
P60202
H7BXC3

G2019S

P62806
O54774
Q9DD18
Q8BSL7
H3BKMO
Q8QZT1
P11798
Q9DAY9
Q5SVI9
P17427

COMUNI

P17182
Q8BFZ3
P46660
Q7M6W1
P16858
Q9D6F9
Q9Z1A1
Q7TMM9
P99024
Q8VEM8
A0A0R4J107
P48962
P46460
P63260
P43006
A0A338P6R8
P18760
P68134
P62631
Q9ERD7
P68368
P47963
P16330
P68372
Q8BRQ9
P51881
Q8C048
Q922F4
Q91VA7
Q3U4F0
P10126
Q9CWF2
O88935
P05213
A2AKV1
Q61879
P97807
Q03265
P68369
Q29ZQ5