	Gene Name	Gelgi or Veskular	Transcript ¹ Allgoment Expression	Genomic Alignment Expression	Transcript Alignment Sold	Genomic Alignment
		Transport Annotation	-leg10 p valu	e -log10 p velu	Fold e Change	Fold Change
N832-1 90083A2	MCI transcription factor released, locus 3 [Evasaghila] secretopideles, family 35, member 2 chromosome 10 open reading frame 116 transcriptiones and immunosipidatini domain containing 1	No No	4.40 3.23	0.74 0.44	Logo ² logo	3.20 0.71
10orf136 DMSD1	thromosome 10 open reading frame 136 transpersionee and immunoglobulin demain containing 1	No No	3.21 0.95	6.87 3.34	Logo Logo	0.49
FAMISSA NRSHA	torcerombone and immunoglobulin domain containing 1 family with sequence similarity 55, member A nuclear receptor subfamily 1, group H, member 4	No	217	1.76	Logo	0.12 0.07 -0.10
MOTO		No No	4.76	0.27 0.33	logo logo	absent ³
ALZ MMECRI	SL2 tonsoription foctor, UM/homeodomain AMVE Complex, gene 1	No No	3.60 2.97	0.37 2.35	8.80 5.80	8.07 0.63
MIGCS2 EHDC1	AAMZ Complex, gene 1 3 Hydroxy 3 restinglishing Consignme A synthose 2 onlockwood feld ledd domain combining 1 interphotoeocopoor manis proteinglycon 2	No No	3.84	0.74 0.87	3.72 3.60	0.53
LHDC1 MPG2 (14or/168	interphotoreceptor matrix proteoglycon 2	No No	2.94 1.30 1.20	0.97 4.67 0.71	3.00 3.21 2.82	0.03
600	shapshirike 2	No	3.17	1.28	2.56	0.42
.DC400986 93766	protein immuno-reactive with anti-PTH polydonal antibodies learnin 60*	No No	1.26 4.76	2.96 8.13	2.32 2.65	0.90 -0.61
MANTA2 LOC649841	mannesidase, alpha, class 1A, member 2 similar to nomeio immunousmina salth and PTM polarizonal sorthodise	No No	3.54 3.47	3.34 absent	2.00 1.88	1.25 absent
IFI SAENGO	RAP1 interacting factor homolog calcium channel voltage-dependent gamma subunit 2	No No	103 105	2.05	1.80	0.67
56orf204	chromosome 6 open reading frame 204 similar to Zinc finger posein 85 (Zinc finger posein HPF4) (HTF1)	No	3.27	1.77	1.41	0.29
.DC644734 DITC3	transmembrane and tetratricopeptide repeat containing 3	No No	3.00 3.30	1.03	1.30	0.13
9809A76 9AA1212	small nucleolar RNA, HUNEA box 76 KNA1212	No No	4.50 3.56	626 3.21	1.22	0.45
NIG10	assertation linked observatation 10 homolog	No	2.35	1.46 1.26	1.05	1.62
18H64P5 10C731295	Rho GPase activating protein 5 similar to microsubule associated serine/thropeline kinase 2	No.	2.83 1.64	almont	1.61 1.80	0.69 absent
.0C729937 DNF148	similar to microtubule associated serine/threonine kinase 2 sinc finger protein 146	No No	3.18 2.95	1.20	0.99	1,42
TOPHIL DUBORE	t-complex 10 (mouse)-like C-type loctin domain family A, member E	No No	414 3.59	1.37	0.93	0.28
.0(157499	similar to SDA1 domain containing 1	No	3.36	3.57	0.90	0.86
EAT PANCI	early endocome antigen 1, 162 kD	Yes No	1.09 2.95	1.04 0.60	0.86	-0.01 -0.28
SISCS BOOKS	pepayayyone aptu-arkating menosoggenise COUP-terminal interactor bacslorini IAP repeat containing 3 Rho-associated, colled-coll containing passeri kinase 1	No	3.08	0.44	0.86	0.30
900KI .0C728222 MH09A	Rhe-associated, collect-cell containing passeln kinase 1 hypothetical protein LOC735222 myosin BIA	Yes No	295 299 320	2.50 0.19	0.85 0.81 0.81	0.60 0.04 0.53
WYOOA VYSM1	myosin DA mshilip: NAPM and MPM changin; 1	No No	3.20 2.95	0.19 1.87 2.21	0.81	0.53
20881 981	myb-like, SWRM and MPN domains 1 sinc finger CCHC-type and BNA binding most 1 retinoblestome 1 including outerstrooms!	No No	3.32 3.35	2.31 3.39	0.77	0.59
.00732360	similar to GT mismatch specific thymine DNA glycosylase membrane associated ring linger (CHC4 7	No.	102	alssort	0.71	absent
WARCH? SLC35A3		No Yes	1.58	182	0.09	0.43
MDRKT EIGALTI	IIID report domain 67 UDP-GalberaGcNAc bets 1,3-galactosyltransfersos, polypeptide 1	No No	1.85	3.95 3.30	0.68	0.23 0.77
90M128	RNA binding motif protein 128	No	4.15 1.75	4.19	0.67	0.50
LMEREN ZNFS34	UMBIT domain containing 1 ainc finger protein SM	No No	3.54	4.46 1.19	0.65	0.32 0.25
NAALAD2 BAKT	N-acetylated alpha linked acidic dipoptidase 2 slucine N-cholos/tons/ease	No No	2.11 3.20	3.90 0.91	0.65 0.65	0.99
752	fibroblast growth factor receptor substrate 2	No No	3.20	1.82	0.64	0.40
UAX1 L0C129522	AP2 associated kinase 1 similar to Balk-binding protein 1	Yes No	3.36 3.48	2.09 2.65	0.64	0.34
TCF4 DWF195	transolption factor 4 ainc finger protein 195	No No	2.97 2.97	2.02 2.20	0.59	0.57
WY		No	3.06	0.69	0.57	0.55
WE212 (PS15	neclear factor (orphresid-derived 2) like 2 secondar protein corting 15 homolog gamma-aminolosystic acid A receptor, alpha 1	No Yes	3.12 2.96	1.27 1.96	0.57 0.52	0.45
SABRAT GAACOSO	gammo-ominobutyvic acid A receptor, alpho 1 ISANO256 gene product	No No	319 103	3.25 1.04	0.52	0.46
SQLE	KSA40256 gene product squalenc epoxidase	No No	3.11	2.67	0.51	0.39
.0C736549 .0C728315	similar to 605 ribosomal protein L7s similar to 605 ribosomal protein L7s	No No	3.03	absent 0.40	0.50	absent 0.11
RIP11 AMSA1	thyroid homone receptor interactor 11 Smile with sensings similarly & recenter 61	Yes No	1.22 3.58	2.72 4.10	0.48	0.23
ATTA	WAVING family, member 4	No No	1.09	0.33	0.45	-0.03
0.00.0423 LDC205636	NAANA23 hypothetical protein LOC385635	No No	3.06 3.50	192 130	0.45	0.34 0.38
96951 98962	evicayotic translation initiation factor 3, subunit 1 alpha, 35 kDa SIRS protein kinase 2	No No	3.04 2.97	2.50 2.42	0.43 0.42	0.25 0.28
HHF14	PHD finger protein 14	No	3.61	2.27	0.43	0.41
.00547969 .598	PHD Singer process 14 similar to basic transcription factor 3 ubliquidin specific peptidase 8	No No	3.20 3.10	almont. 2.46	0.39	absent 0.42
DC163131		No.	2.20	129	0.39	0.54
DEMND4A	T9C1 donain family, member 12 DBNNMADD domain containing 4A	No No	1.43	1.69	0.39	0.35
	chromosome 8 open reading frame 53 BAN binding protein 5	No No	3.81 4.00	1.29 1.88	0.37 0.37	0.30 0.28
17012 60P	ST7 overlapping transcript 2 (antiverse RNA)	No Yes	3.18 3.53	139	0.37	0.28
3A290	voicle docking protein p115 IAAA4	Yes	2.49	3.19	0.35	0.23
069E .0C203523	dacylglycerol kinase, epolon 64 kDe similar to telomeric repeat binding factor 1 isoform 2	No No	2.11 1.20	3.47 145	0.35	0.97
NOMEN.	similar to elements repeat binding factor 1 keform 2 99A binding most protein 41 misochandrial translational release factor 1-like	No No	2.22	3.24 2.75	032	0.61
0066	component of objorneric galgi complex 6	Yes	2.40	3.50	0.90	0.37
QAA0095 QAA132NL	RAAGUS protein RAALSUHIKE	No No	314	1.73	0.30	0.31
SOLGAT	golgi autoveligen, golgin subfamily a, 1 ainc finger protein 658	Yes	4.33	1.84	0.28	0.14
ZNF658 .A550	DIGT homolog, counside synthase 6 ESF seasonipoles factor 8	No No	2.99 2.59	2.03 4.55	0.28	0.12
E2F8 MFA73	ESF transcription factor 8 microfibrillar-associated protein 3	No No	1.09 2.91	3.61 3.16	0.27	0.11
AMPI	WW domain containing E3 ubiquitin protein ligase 1	No	2.55	3.54	0.26	0.24
201830 PLC84	zinc finger and BTD domain containing 36 phospholipase C beta 4	No No	1.55	3.13 4.65	025	0.21
STG1	B-cill translocation gene 1, anti-proliferative	No No	109	2.30	0.34	0.14
3MERQ LOCSHISTS	Soull translocation gene 1, anti-proliferative SMEX homolog 2, suppressor of mekt (Dictyostellum) hypothetical LOCSH1915	No No	3.14	2.78 2.45	0.21 0.21	0.22
WP1L3 NT2	nucleosome assembly protein 1-like 3 Busilian without CAAX 2	No No	3.08 0.85	122	0.20 0.20	0.11 0.76
KTG10	ATG10 autophagy related 10 homolog checkpoint suppressor 1	No No	0.71	3.65	0.19	-0.29
DHEST LOCK2345		No	263 3.04	1.45 0.72	0.19	0.16
V5783	methionine sulforoide reductave 83 Integrin alpha FG GAP repeat containing 1 Naryophetin alpha 1 Importin alpha 50	No	0.86	3.17	0.79	0.20
OPERT DOSSESSE	karyopherin alpha 1 limportin alpha 5)	No	2.15	145	0.18	0.16
SRT1	similar to HLA class I, A-11 alpha chain precursor sistain bilant mating type information regulation 2 homologi	No No	3.98	absort 2.76	0.16 0.16	0.13
DASSE	connector enhancer of kinase suppressor of Ras 1 similar to hypothetical protein	No No	3.39	2.41 Waters	0.16 0.15	0.06 absent
NPS	neuropeptide II	No	3.13	2.20	0.15	0.18
NAHGEF7 CRIAT	Rho guarnine mucleotide exchange factor 7 X-oy radiation resistance associated 1 Sonilly with sequence similarity 21, mention C	No No	3.27 0.33	2.82 1.30	0.14	0.16
FAM21C WAP18		No No	3.18	2.45	0.13	0.08
DIMSE2	transmentirane 9 superfamily member 2	No.	3.46	2.48	0.12	0.14
TEXTA METTIOD	tests expressed sequence 14 methyltransfesse t0 dismain containing	No No	3.20 3.17	0.67 0.54	0.11 0.11	0.03
.0C544150 .0C731250	MAS-WAS, interacting protein family, member 3 hypothetical protein LOC/31290	No No	1.09 3.44	1.60 absent	0.11 0.10	-0.03 absent
57913 CBORRG2	spindin femily, member 3 Cliedf02 protein	No No	4.86 3.51	2.02	0.10	0.07
POT	Importin 7	No	2.96	1.99 4.74	0.09	0.06
DASC4 LOC391845	cancer succeptibility candidate 4 similar to 405 ribosomal protein 515	No No	403 3.45	1.99	0.09	0.29
.0C991845 (AT1 MGC16169	similar to 405 ribosomal protein S15 synaptesignin i hepothetical protein MGC16392	Yes No	3.45 4.00 1.69	2.59 1.52 3.45	0.09 0.08 0.08	0.19 0.15 0.49
PHC2	hypothetical protein MICC16399 sphingorine kinser 2 HCCA2 protein	No	166	1.16	0.08	0.00
HDDA2 DYCS	HCCAZ protein cytochrome c, sometic	No No	260 130	5.21 6.05	0.07	0.01 -4.02
89M2 AF2	cysochome c, sonusic seino/arginine repetitive matrix 2 CAP, adenylune cyclasa-associated protein, 2	No No	3.82 0.72	0.73 1.83	0.07	-0.02 0.12
17813	amploid beta (A4) precursor protein binding, family A, member 3	No No	1.85	3.68	0.07	0.04
(MD)	adaptor-related protein complex I, gamma 1 subunit outlands	Yes No	1.50	3.64	0.06 0.06	-0.13 -0.02
NET1 DKF2P434A0131	neurosphelial cell transforming gene 1 D6FZp6360131 pretein	No No	140	194	0.06	0.00
3	citrate surchase	No	3.35	2.47	0.05	0.01
ASK AFGEF2	calcium/calmodulin-dependent seine passein kinase ADF-ribosylation factor guarino naciontide-exchange factor 2	No Yes	4.05 3.47	3.42 0.87	0.04	0.38
Tior90	chromosome 11 open reading frame 30	No.	3.06	2.25	0.02	0.21
HRCZ AJPSO	phosphorylass kinase, gamma 2 nudeoponin 90 kiba	No No	1.50 3.43	1.83	0.02 0.02	-0.09 0.01
YA3 (14cef172	eyes absent homolog 5 chromosome 14 open reading frame 172	No No	3.44 3.10	1.51 3.17	-0.04 -0.04	0.27 -0.10
10CK3 1F9N2	dedicator of cytolerosis 5 glycoprosein, symptic 2	No Yes	1.58	3.83 4.61	-0.06 -0.06	0.12 -0.05
PBA2	amploid beta precursor protein-binding, family A, member 2	No	2.79	3.25	-0.09	-0.10
AGUN3 TRF	tunsgeln 1	No No	1.27 3.08	436 136	-0.09 -0.09	-0.16 -0.17
	polymerase I and transcript release factor			3.10	-0.10 -0.10 -0.10	-0.10
ISPOP1 PL3	polymense I and transcript release factor hsp/39-interacting protein	No No	2.15	3,45	A19	
PL3 FHS3	polymense: I and Stenoroist release factor hsp35-interacting protein ribosomal protein L3 D94 receptor B3	No No	2.96 1.59	3.45 3.09	-0.10	-0.14 -0.16
PL3 PHE3 LRFFP1 MEQIP	polymensor i and tenerolis release factor hapDil-instancting protein riscornal protein 13 Ethi socquez (3) ADH	No No Yes No	2.96 3.59 3.12 1.30	2.26 2.34	-0.10 -0.11	-0.12 -0.15
PLS PHISS URFRP1 MESSP SLTSSO1	polymonor I and bareoptic release factor hap32-incoming presents ribocomal pratich I.S. DRH seopper BS. ADP-Hoopstipon factor related protein 1.	No No Yes	2.36 3.59 3.12	2.26	-0.10	-0.12
PL3 PHS3 URFRP1 W628P SLT2501 HFZ	polymouse I and horsonys release factor hapility executing years EMP (application) EMP	No No Yes No No No	2.36 1.59 3.12 1.30 1.50 0.42 2.62	1.34 1.30 1.57 1.58	-0.10 -0.11 -0.11 -0.11 -0.12	-0.12 -0.15 -0.20 -0.25 -0.15
PU3 PHIS INFOP1 WIGOP SCTSO1 HHF2 CTHOS	polyments and transport cleans factors (high-Streamfort groups) (Appl-Streamfort groups) (Appl-S	No No Yes No No	2.30 3.59 3.12 1.30 1.50 0.42	1.26 1.34 1.30 1.57	-0.10 -0.11 -0.11 -0.11	-0.12 -0.15 -0.20 -0.25
PU3 PHIS3 LREEPI MISSIP SLT2501 THIFE ST LINES SPHICE SHIMES KERN	polymonic and for transcript shows face food for security present DRI respect ES CAP - Polymonic Total cardial protect 1 DRI respect present processing process	Mo Mo Yes Mo Mo Mo Mo No	2.96 1.99 3.12 1.90 1.90 0.42 2.62 0.09 2.22 3.51	236 134 130 157 158 130 121 122	-0.10 -0.11 -0.11 -0.11 -0.12 -0.12 -0.12	-0.12 -0.15 -0.20 -0.25 -0.15 -0.11 -0.16 -0.17
PU3 PHS3 URRP1 WRSP SUTSO1 HHZ URRS URRS KEN DC711086	polymonia and harmonia shared faces (Facebook general) (File support St. All Andropolymonia (Facebook general) (File support St. Andropolymonia (File Supp	No N	2.96 1.99 3.12 1.30 1.50 0.42 2.62 0.70 2.22 3.51 3.11	2.36 1.34 1.30 1.57 1.58 5.26 1.22 3.22 absert	-0.10 -0.11 -0.11 -0.11 -0.12 -0.12 -0.12 -0.12 -0.12	-0.12 -0.15 -0.20 -0.25 -0.15 -0.11 -0.16 -0.17
PL3 FPRIS LREFP1 MAGIP LTTS01 FPRIS STS01 FPRIS STS01 FRIF2 STS01 SSC0 SSC0 SSC0 SSC0 SSC0 SSC0 SSC0 S	Legislater and and transcript shows flavor (Salah Stemaning James) Difference and transcript	No N	2.96 1.99 3.12 1.30 1.50 4.42 2.62 0.00 2.22 3.51 3.11 3.35 2.77 3.66	2.36 1.34 1.30 1.57 2.56 5.20 2.22 3.22 3.22 3.22 3.22 3.22 3.22 3	-0.10 -0.11 -0.11 -0.11 -0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.13 -0.12 -0.13	-0.12 -0.25 -0.25 -0.15 -0.11 -0.16 -0.17 absent -0.19 -0.18
PL3 PH93 IARSPH NNGSP IATSSOT PH92 IATSSOT PH92 IATSSOT IATSC IATS	Legionesis and substancia debar face face face face face face face face	No N	2.96 1.99 3.12 1.30 1.90 0.40 2.62 0.00 2.22 3.51 1.11 3.35 2.77 3.66 4.51	2.56 1.34 1.30 1.57 2.58 3.26 3.25 3.22 absort 2.65 2.21 2.70 1.36	-010 -011 -011 -011 -012 -012 -012 -012	-0.12 -0.15 -0.20 -0.25 -0.15 -0.16 -0.17 -0.19 -0.18 -0.10
PL3 SPHS3 SHSPH SHSPH MAGSP AT1SO1 HH2 SHH02 SPHD2 SHD02 SHC05 SHC06 SHC	Legionesis and substancia debar face face face face face face face face	Mo M	2.29 3.19 3.12 1.30 3.42 1.50 0.40 2.22 3.51 3.11 3.33 2.77 3.65 4.51 1.86 3.14	2.00 1.34 1.30 1.57 2.58 1.20 1.22 3.22 absect 2.05 1.21 2.70 1.36 3.30 1.21 2.70 1.36 3.30 3.30 3.30 3.30 3.30 3.30 3.30 3	-010 -011 -011 -011 -012 -012 -012 -012	-0.12 -0.15 -0.20 -0.25 -0.15 -0.11 -0.16 -0.17 absert -0.19 -0.18 -0.10 -0.10 -0.17
PU3 PHISS SAFEPH	polymous and manurum debute face (File register B)	Mo M	2.29 3.19 3.12 1.30 3.12 1.30 9.42 2.22 3.31 3.33 2.27 3.45 3.45 3.16 3.14 1.27 3.06	2.00 1.34 1.30 1.57 1.52 1.30 1.22 3.22 3.22 3.00 1.21 2.70 1.36 3.79 2.46 3.70 2.00	-0.10 -0.11 -0.11 -0.11 -0.12 -0.12 -0.12 -0.12 -0.12 -0.13 -0.13 -0.13 -0.13 -0.13 -0.13 -0.14 -0.14	-0.12 -0.12 -0.25 -0.25 -0.15 -0.17 -0.16 -0.19 -0.17 -0.18 -0.10 -0.17 -0.21 -0.21
PL3 PH93 LRF9P1 LRF9P1 LRF9P1 LRF9P1 HF2 LFT1SD1 HF2 COPHO2 LRF8C	polymous and manurum debute face (File register B)	Mo M	2.29 3.19 3.12 1.30 3.12 1.30 9.42 2.22 3.31 3.33 2.27 3.45 3.45 3.16 3.14 1.27 3.06	2.00 1.34 1.30 1.37 1.56 1.30 1.37 1.56 1.32 1.32 1.31 1.30 1.37 1.30 1.37 1.30 1.30 1.30 1.30 1.30 1.30 1.30 1.30	-0.10 -0.11 -0.11 -0.11 -0.12 -0.12 -0.12 -0.12 -0.12 -0.13 -0.13 -0.13 -0.13 -0.13 -0.13 -0.14 -0.14	-0.12 -0.12 -0.25 -0.25 -0.15 -0.11 -0.16 -0.17 absert -0.19 -0.17 -0.18 -0.19 -0.19 -0.19 -0.19 -0.19
PLS 3 PMB 3	spicerous and instructive should have feedered uplants 1. (Per required in the control of the	May	2.99 1.99 1.19 1.10 1.10 1.10 1.10 1.10 1	2.26 1.34 1.30 1.357 1.26 1.20 1.22 1.22 1.20 1.22 1.20 1.21 2.70 1.36 3.79 1.46 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06 3.70 2.06	-0.10 -0.11 -0.11 -0.11 -0.12 -0.12 -0.12 -0.12 -0.12 -0.13 -0.13 -0.13 -0.13 -0.14 -0.14 -0.14 -0.15	-0.12 -0.12 -0.13 -0.25 -0.15 -0.15 -0.17 -0.16 -0.17 -0.18 -0.17 -0.18 -0.19 -0.19 -0.19 -0.19
PL J PERSON	Legislation of an Internative debute flavor Christopher St. (1997) and Chr	Mo. Mo. Mo. Pres Mo. Mo. Mo. Mo. Mo. Pre. Pre. Pre. Pre. Pre. Pre. Pre. Pre	2.50 3.19 3.12 3.20 3.12 3.20 3.24 3.24 3.22 3.51 3.53 3.27 3.45 3.16 3.14 1.27 3.00 2.00 2.10 2.10 2.10 2.10 2.10 2.10 2	2.06 1.54 1.50 1.57 1.58 1.59 1.59 1.50 1.50 1.50 1.50 1.50 1.50 1.50 1.50	-0.10 -0.11 -0.11 -0.11 -0.11 -0.11 -0.12 -0.12 -0.12 -0.12 -0.12 -0.13 -0.14 -0.14 -0.14 -0.14 -0.15 -0.15 -0.16 -0.16 -0.16 -0.17 -0.17 -0.17 -0.18	-0.12 -0.12 -0.13 -0.23 -0.23 -0.11 -0.16 -0.17 -0.18 -0.19 -0.17 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.16 -0.19 -0.16 -0.19 -0.16 -0.19 -0.16 -0.19 -0.19 -0.16 -0.19 -0.19 -0.16 -0.19 -0.19
PL J PERSON	spicycosci and for transport shows favor (Fire required prints)	May	2.96 3.12 1.30 3.12 1.30 0.42 2.62 0.76 2.22 3.31 3.11 3.35 3.45 4.51 1.66 3.14 1.12 2.08 2.09 2.09 2.00 2.00 2.00 2.00 2.00 2.00	2.06 1.34 1.30 1.57 1.56 1.22 3.22 3.22 3.22 3.22 3.22 2.05 1.27 1.36 3.70 2.00 1.36 3.70 2.00 2.00 1.36 3.70 2.00 2.00 2.00 2.00 2.00 2.00 2.00 2	-0.10 -0.11 -0.11 -0.11 -0.12 -0.12 -0.12 -0.12 -0.12 -0.13 -0.13 -0.13 -0.14 -0.14 -0.14 -0.15 -0.15	-0.12 -0.12 -0.15 -0.25 -0.15 -0.11 -0.16 -0.17 -0.19 -0.18 -0.10 -0.17 -0.16 -0.17 -0.18 -0.10 -0.17 -0.18 -0.19
PFL3 WESTERS WESTER	Legislation of an Internative debute flavor Filter Sequential Control (1997) Filter Sequential Control (19	Mo. Mo. Mo. Pres Mo. Mo. Mo. Mo. Mo. Pre. Pre. Pre. Pre. Pre. Pre. Pre. Pre	2.56 3.19 3.12 3.10 5.50 5.50 6.42 2.62 0.070 2.22 3.53 3.11 3.53 2.27 3.65 1.16 1.20 2.09 3.78 2.00 2.00 2.00 2.00 2.00 2.00 2.00 2.0	2.06 1.54 1.50 1.57 1.58 1.59 1.59 1.50 1.50 1.50 1.50 1.50 1.50 1.50 1.50	-018 -011 -011 -011 -011 -011 -010 -010	-0.12 -0.12 -0.13 -0.23 -0.23 -0.11 -0.16 -0.17 -0.18 -0.19 -0.17 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.16 -0.19 -0.16 -0.19 -0.16 -0.19 -0.16 -0.19 -0.19 -0.16 -0.19 -0.19 -0.16 -0.19 -0.19
PE-3 STREETS S	Legionesco de la formación debur fazor Circinardo planto L. Tidiri imperior de la composición del la co	Mo-	2.56 3.19 3.12 3.10 5.50 5.50 5.50 5.50 5.50 5.50 5.50 5	2.05 3.07 3.07 3.08 3.07 3.08 3.02 3.02 3.02 3.02 3.03 3.09 3.09 3.00 3.00 3.00 3.00 3.00	-010 -011 -011 -011 -011 -011 -010 -010	-0.12 -0.15 -0.20 -0.25 -0.11 -0.16 -0.17 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19 -0.19
PE-3 STREAM STRE	Legislation and Internative debute flavor Controlled prints 1. This requires the controlled prints 1. This requires the control	Mo No	2.56 1.59 3.12 1.50 1.50 1.50 1.50 1.50 2.62 2.63 2.77 2.73 2.73 2.73 2.72 2.72 2.72 2.7	2.06 1.34 1.00 1.57 1.69 1.69 1.20 1.20 1.20 1.20 1.20 1.20 1.20 1.20	-016 -011 -011 -011 -011 -012 -012 -012 -012	-0.12 -0.15 -0.20 -0.25 -0.15 -0.11 -0.17 -0.19
PELS SEPTINGS AND	Legionesco I and Transport debute face General plants I. J. This import this This	Mo No	2.56 1.59 3.12 1.50 3.12 1.50 5.42 2.63 0.75 3.22 3.33 3.13 3.13 3.13 3.13 3.13 3.13	2.06 1.34 1.00 1.57 1.52 1.52 1.52 1.52 1.52 1.52 1.52 1.52	-0.00 -0.01 -0.01 -0.01 -0.01 -0.01 -0.01 -0.02 -0.02 -0.02 -0.02 -0.02 -0.03 -0.03 -0.03 -0.03 -0.03 -0.03 -0.04 -0.04 -0.04 -0.04 -0.05	-0.12 -0.15 -0.20 -0.25 -0.11 -0.15 -0.11 -0.17 -0.19 -0.21 -0.19 -0.21 -0.21 -0.21 -0.21 -0.22 -0.23 -0.23 -0.23 -0.23 -0.23 -0.23
PELS SEPTINGS AND	pulserous of an informative debut favo (Control of State 1) (Con	No.	2.56 1.59 3.12 1.50 3.12 1.50 0.42 2.63 0.75 3.22 3.33 3.13 3.13 3.13 3.13 3.13 3.13	2.00 1.04 1.00 1.07 1.08 1.09 1.09 1.09 1.09 1.09 1.09 1.09 1.09	-016 -017 -017 -017 -017 -017 -017 -017 -017	-0.12 -0.15 -0.25 -0.15 -0.15 -0.15 -0.11 -0.11 -0.11 -0.19
PES 3 PEPS 3 PEP	Legislation of an Internative debut face Control (1997) 1. The Co	Mo No	2.56 1.59 1.12 1.12 1.10 1.10 1.10 1.10 1.10 1.10	2.00 1.34 1.30 1.37 1.39 1.30 1.30 1.30 1.30 1.30 1.30 1.30 1.30	-016 -017 -017 -017 -017 -017 -017 -017 -017	-0.12 -0.15 -0.20 -0.25 -0.15 -0.15 -0.15 -0.16 -0.17 -0.18 -0.19 -0.22 -0.19 -0.23
PES 3 PEPS 3 PEP	Legislation and Transport debut favor Centered plants 1. Centere	500 - 500 -	2.96 3.12 3.12 3.12 3.12 3.12 3.12 3.13 3.13	2.00 1.05 1.05 1.05 1.05 1.05 1.05 1.05 1	-010 -011 -011 -011 -011 -012 -013 -013 -013 -013 -013 -013 -013 -013	-0.12 -0.15 -0.20 -0.15 -0.15 -0.115 -0.116 -0.17 -0.16 -0.17 -0.18 -0.19
PES 3 PEPERS 3 PERS 3 PEPERS 3 PERS 3 PEPERS 3 P	Legislation of an Internative elevant flavor First Inspection Fi	Mac Nation 1 Mac N	2.50 1.59 1.12 1.12 1.130 1.130 1.130 1.130 1.130 1.130 1.130 1.130 1.131 1.131 1.131 1.131 1.131 1.131 1.131 1.131 1.131 1.14	2.00 1.34 1.37 1.32 1.32 1.32 1.32 1.32 1.32 1.32 1.32	-010 -011 -011 -011 -011 -011 -011 -012 -012	-0.12 -0.15 -0.25 -0.15 -0.115 -0.115 -0.117 -0.117 -0.117 -0.118 -0.119 -0.129 -0.139 -0.139 -0.140 -0.18 -0.18 -0.19 -
99.3 99.3	Legislation and Transport debut favor Celected plants 1, 1 Celec	500 - 500 -	2.00 3.12 3.12 3.13 3.13 3.13 3.13 3.13 3.13	2.00 1.34 1.37 1.37 1.37 1.37 1.37 1.37 1.37 1.37	-010 -011 -011 -011 -011 -012 -012 -012	-0.12 -0.15
95.3 (1975) 197	Legislation of an Internative debute flavor File General (2010) 1. File Gene	Mac Nation 1 Mac N	2.00 1.00 1.10 1.10 1.10 1.10 1.10 1.10	2.00 1.34 1.37 1.32 1.32 1.32 1.32 1.32 1.32 1.32 1.32	-010 -011 -011 -011 -011 -012 -012 -012	-0.12 -0.15 -0.25 -0.15 -0.15 -0.11 -0.16 -0.17 -0.19 -0.19 -0.17 -0.19
WEST STATES OF THE STATES OF T	Legislation of an Internative debut favor Chicken and points 1. This impacts this Chicken and this impacts and this Chicken and this impacts and this Chicken and this impacts and this Chicken and this Ch	Socio	2.00 1.00 1.12 1.12 1.10 1.10 1.10 1.10	2.00 3.00 3.00 3.00 3.00 3.00 3.00 3.00	-010 -011 -011 -011 -011 -011 -012 -012 -012 -012 -013 -013 -013 -013 -013 -014 -0	-0.12 -0.13
WEST STATES AND A	Legislation of the Control of the Co	Mar.	2.00 1.09 1.10 1.10 1.10 1.10 1.10 1.10 1	2.00 (1.00 m) (1.00 m	-010 -011 -0	-812 -415 -415 -416 -417 -417 -417 -417 -417 -417 -417 -417
	Legislation of an Internative debut favor Christopher St. Christopher St	March Marc	2.00 3.09 3.10 3.10 3.10 3.10 3.10 3.10 3.10 3.11 3.11	2.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00	-010 -011 -011 -011 -011 -011 -011 -011	-0.12 -0.03
WEST 3	Legislation of an Internative elevant flavor First Internative III First Internative III First Internative III First Internative III First Internative III Fir	Mar.	2.00 1.09 1.10 1.10 1.10 1.10 1.10 1.10 1	2.00 (1.00 to 1.00 to	-010 -011 -0	-812 -813 -814 -8
PLA STATE OF THE PLAN OF THE P	Legislation of an Internative elevant flavor Filinding and the Control of the Co	March Marc	2.00 3.09 3.10 3.10 3.10 3.10 3.10 3.10 3.10 3.11 3.11	2.00 (1.00 to 1.00 to	-018 (1911) -011 (1911) -011 (1911) -012 (1911) -013 (1911) -014 (1911) -015 (1911) -016 (1911) -017 (1911) -018 (1911) -019 (-0.12 -0.03
WEST STATES OF THE STATES OF T	Legislation and Instructive desire favor Centered plants 1. This impacts	500 - 500 -	226 103 103 103 104 105 105 105 105 105 105 105 105 105 105	200 120 120 120 120 120 120 120 120 120	-010 (101 (101 (101 (101 (101 (101 (101	-0.12 -0.03
NO. WILLIAM STATE OF THE STATE	species of an information debug flow First required in the control of the contro		226 103 103 103 104 105 105 105 105 105 105 105 105 105 105	120 120		-0.12 -0.02 -0.03
NO. TO SERVICE AND ADMINISTRATION OF THE	Legislation of the Control of the Co		230 130 130 130 130 130 130 130 130 130 1	120 120		-0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.12 -0.13
75.1 75.2 75.2 75.2 75.2 75.2 75.2 75.2 75.2	Legislation of an Internative debut flavor Filter Sequestic St.		236 326 327 327 328 328 328 328 328 328 328 328 328 328	2.00 (1.00 m) (1.00 m		-412 - 425 -
TO J. M. S.	speciment and instructive desire favor Centered prints 1. This impacts 1		230 320 320 320 320 320 320 320 320 320	120 120		-112 -123 -124 -124 -125 -1
NO. WILLIAM STATE OF THE STATE	Legislation of an Internative debut flavor Filter Sequestic St.		236 326 327 327 328 328 328 328 328 328 328 328 328 328	120 120		-412 - 425 -