#### **Supplementary Methods**

#### a) Study design

This study was designed as an investigator-initiated clinical study to investigate the molecular signatures of AD and psoriasis. Procedures were conducted according to the Declaration of Helsinki principles. Informed written consent was obtained from human subjects under a protocol approved by the local ethics board at the University Hospital Schleswig-Holstein, Campus Kiel, Germany (reference: A100/12). Adult patients with a history of AD or psoriasis for at least 3 years attending the dermatology department as well as adult volunteers without personal or familial history of atopic and chronic-inflammatory diseases of German ethnicity were invited to participate. Inclusion criteria for patients were a dermatologist-confirmed diagnosis of active chronic plaque-type psoriasis or AD. Exclusion criteria were presence of any other chronic skin disease, systemic treatment with immune-efficient medication ever, and topical treatment within one week prior to material sampling. AD or psoriasis was diagnosed on the basis of a skin examination by experienced dermatologists according to standard criteria (for AD, the American Academy of Dermatology Consensus Criteria were used) (Boehncke and Schon, 2015, Weidinger and Novak, 2015). From all participants, 9 ml of blood (collected into EDTA) as well as 5mm skin punch biopsies from the upper extremities (under local anesthesia) were obtained. From control individuals, a single biopsy was taken, while pairs of biopsies were taken and from adjacent (at least 50 mm from active lesions) clinically normal (i.e. no signs of erythema, edema, crusting, thickening, scaling or scratch marks) skin in psoriatic or AD patients. Skin tissue specimen were stored in PaxGene tissue containers (PreAnalytiX, Hombrechtikon, Switzerland) at -80°C according to the manufacturer's manual until further processing. A detailed cohort description can be found in **Supplementary Table 1**.

#### b) Filaggrin gene genotyping

Genomic DNA was isolated from peripheral EDTA blood with the automated chemagic Star workstation protocol (Hamilton Company, Reno, NV) and used to determine the *filaggrin* gene (FLG) status of AD patients and healthy controls. The four most common European mutations R501X, 2282del4, R2447X and S3247X were analyzed with the TaqMan allelic discrimination

method (Applied Biosystems, Carlsbad, CA) following the standard procedures based on the manufacturer's reagents. Probe detection was performed with the Applied Biosystems 7900HT Fast Real-Time PCR System. Results are presented in **Supplementary Table 1**.

#### c) Sample processing

Total RNA was isolated from PAXgene® fixed tissue samples using the AllPrep DNA/RNA Mini Kit (Qiagen, Hilden, Germany) following the manufacturers specifications. Samples of cases and controls were randomly distributed across the plates and pools before sequencing to minimize batch effects; in total we used 3 runs to obtain RNA-seq data. Preceding RNA isolation all samples were disrupted using innuSPEED Lysis Tubes W (1,4 - 1,6 mm steel beads & 3,5 mm ceramic beads) (Analytik Jena, Jena, Germany) in a SpeedMill Plus (3x 1min intervals) (Analytik Jena) together with 600µl of RLT-Plus-Buffer (Qiagen) including ß-Mercaptoethanol and additionally homogenized with QIAshredder spin-columns (Qiagen). In order to assure sufficient concentration, integrity and purity of isolated RNA all samples were measured with the Qubit 2.0 Fluorometer (Qubit RNA HS Assay) (LifeTechnologies, Carlsbad, CA) and the 2200 Tape Station (R6K ScreenTape Assay) (Agilent, Santa Clara, CA) following the manufacturer's instructions. Only samples with a concentration of >50ng/µl, an OD260/280 ≥1.8 and a RNA integrity number (RIN) >7 were included in subsequent library preparation and sequencing.

#### d) RNA library preparation and sequencing

RNA samples were prepared for sequencing using the Illumina Truseq® Stranded total RNA Protocol in combination with the RiboZero rRNA removal Kit, and sequenced on the HiSeq2500 in pools of 10 samples with 2x125bp, producing paired-end reads according to the manufacturer's protocol (Illumina, San Diego, CA). The case and control samples were randomly distributed across the plates and pools before sequencing to minimize batch effects. We sequenced libraries prepared from total RNA extracted from 147 skin biopsies (38 control;

27 psoriasis non-lesional (NL); 28 psoriasis lesional (LL); 27 AD NL; 27 AD LL) donated by 93 individuals.

#### e) RNA-seq data processing

Low quality reads were filtered from the data using the Illumina CASAVA FASTQ filter. Illumina standard primers were trimmed, and the quality of the data was assessed using FastQC (vs 0.11.3) (Andrews, 2010). Paired reads were mapped to the human reference genome (b37) using STAR (Dobin et al., 2013), only uniquely mapped read pairs were retained Number of reads for each gene was counted using HTSeq (Anders et al., 2015), only genes with on average ≥1 read/sample were used in our analysis. TMM was used to normalize the RNA-seq data (Robinson and Oshlack, 2010), and we applied voom transformation to model the mean-variance relationship of the expression data (Law C. W. et al., 2014).

#### f) Statistical and bioinformatics analysis

We conducted differential expression analysis between different conditions using empirical Bayes linear model as implemented in the limma package (Ritchie et al., 2015), controlling for individual specific effect (for nonlesional vs. lesional skin comparison) and gender effect (for normal vs. nonlesional/lesional skin comparison); False discovery rate (FDR) ≤5% and |log2 Fold Change (FC)| ≥1 were used to declare significance. Functional enrichment analysis was performed using the hypergeometric test for pathways/functions compiled from Gene Ontology (Ashburner et al., 2000), KEGG (Kanehisa et al., 2012), and Biocarta (Nishimura, 2001), and only those with ≥10 and ≤300 annotated genes were examined; FDR≤10% and Observed/Expected ratio ≥2 were declared significant. By using the current criteria (i.e. FDR<=5% and with more than 2 fold change between two groups) and assuming >10% of genes truly differentially expressed (with on average>500 read counts/sample, estimated from our cohort)

from the 31,364 genes we examined, retrospective power calculation estimates >75% of statistical power (Guo et al., 2014).

For illustration purposes, we grouped similar functions and presented the groupings in a piechart using ClueGO (Bindea et al., 2009). To identify genes that are close to T-cell specific chromatin marks, we first retrieved T-cell H3K27ac peak signals from a previous study (Farh et al., 2015), and, for each cell type, we computed the cell-type specific ratio of each peak's by comparing the signal in the cell type with the average of the remaining cell types. The 10,000 peaks with the highest ratios for each cell type were screened for cell-specific genes within a 5k bp interval. We performed the classification task (e.g. psoriatic vs AD lesional skin) using the Random Forest classifier in the MLR package (Bischl et al., 2016), and the top features were selected according to backward selection with permutation importance; the final Area under Receiver Operating Characteristic (AUROC) was estimated (using the selected features) from three-fold cross validation with 100-repetitions.

We compiled the expert-curated chemical/drug -- gene interactions from the Comparative Toxicogenomics Database (CTD) (Davis et al., 2016), DrugBank (Law V. et al., 2014) and PharmGKB (Hewett et al., 2002), and the chemical/drug -- disease associations from CTD and National Drug File-Reference Terminology (NDF-RT) (Carter et al., 2002). Although these resources also include chemicals, we apply a lexicon to only include associations/interactions involving three types of drugs (antibiotics, clinical drugs and pharmacologic active substances). All the resources use customized identifiers for drugs and diseases, thus recognizing duplicates across the resources is challenging. We therefore replaced the drug identifiers with customized identifiers from our previous work (Raja et al., 2017), plus the diseases' concept identifier (CUI) from UMLS Metathesaurus.

#### g) Cytokine stimulation in keratinocytes

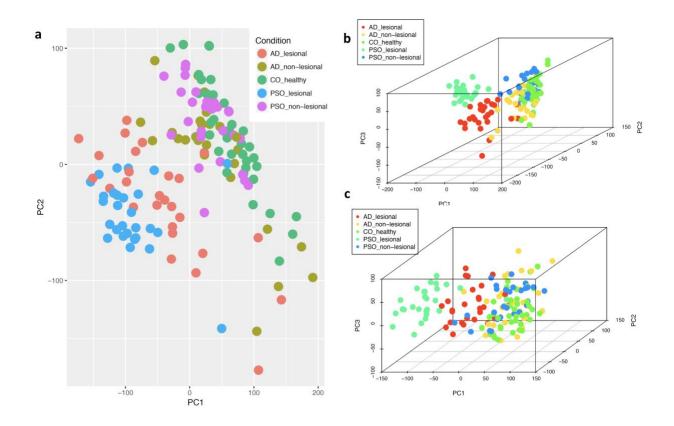
We determined whether the DEGs identified in our experiments were regulated by stimulations with various cytokines in keratinocytes. We obtained 50 normal human keratinocytes from 50 different healthy adults. Keratinocytes were grown in 12 well plate in 154 CF medium (Thermo Fisher #M154CF500) with human keratinocyte growth supplement (Thermo Fisher #S0015). Keratinocytes were grown to confluency at which time the complete medium (with supplements) was replaced by basal 154 CF medium (without supplements). Cells were then stimulated with cytokines (IL-4, IL-13, IFN-α, IFN-γ, TNF-α, IL-17A, IL-36α, IL-36β, IL-36γ, R&D Systems) individually at 10 ng/ml concentration. After 8 hrs cells were harvested and RNA was isolated using RNeasy Plus Mini kit (Qiagen # 74136). RNA was analyzed by RNA Nano Chips (Agilent Technologies) and sequenced (Sarkar et al., 2018).

#### h) Immunohistology

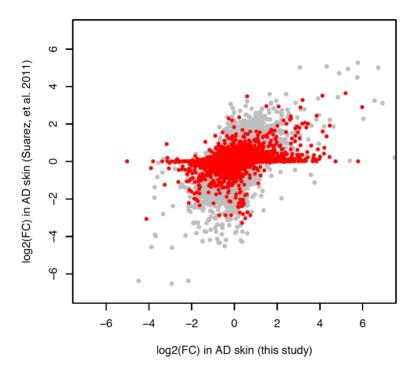
Sections were taken from formalin-fixed, paraffin-embedded biopsies. Tissue slides underwent thorough manual quality control check for the following parameters: dermis and epidermis present on the slide, tissue is well aligned on the glass without loss of large parts of the biopsy material, staining intensity is visible and present in the expected cell component. If any of the criteria were not met, reevaluation on freshly cut material from the identical biopsy was performed. If the second evaluation did not show concordance with the criteria, the slide was excluded from further processing for the digital image analysis. Tissue slides, stained with CD8, were digitally scanned at x20 magnification using a Hamamatsu Nanozoomer in brightfield mode. Quantitative image analysis was performed by on whole slide scanned images using Definiens Tissue Studio® software. A customized algorithm was developed per marker in Tissue Studio® using a subset of the study images. The customized algorithm was developed to accurately detect the whole tissue or if required, segment the specified regions of interest (ROI)

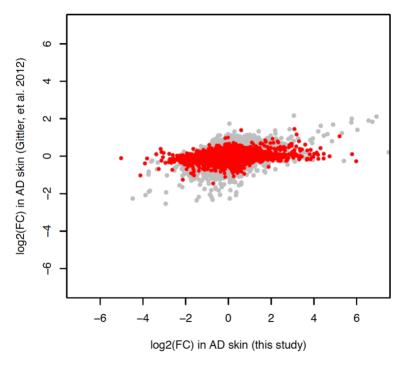
within the whole tissue section. Cellular analysis thresholds were then optimized per algorithm to specifically detect positive cells for the immunohistochemistry markers within the tissue ROI. The algorithms were then applied objectively to each section to quantify the required parameters. Evaluation was performed for total cell count (sum of epidermal and dermal cell counts) on the CD8 stains. The analyzed area was measured in mm2 and based on the absolute cell counts calculation of cells per mm2 was performed.

## **Supplementary Figures**

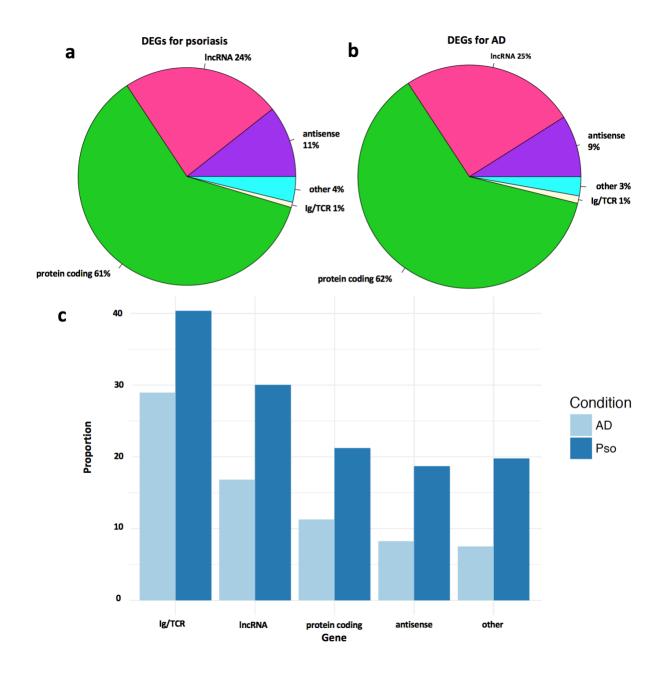


Supplementary Figure 1. a) top two principal components computed using the transcriptomes of the samples; b) the top three principal components using the transcriptome of the samples; c) the top three principal components after adjusting the batch variable estimated by the SVA algorithm.

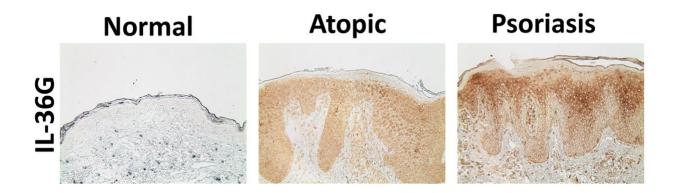




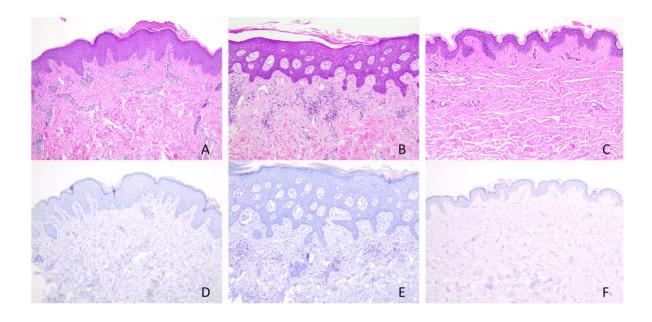
Supplementary Figure 2. Comparing the magnitude of dysregulation (Fold Change in logarithmic scale) in AD skin measured in this study (x-axis) versus previous microarray studies. Each point represents a gene that is common in both platforms; red color represents genes expressing in the lower 25% of the transcriptome.



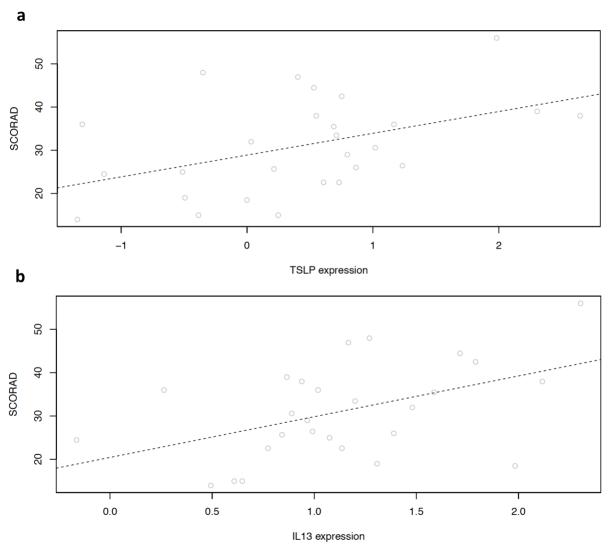
Supplementary Figure 3. The proportion of different gene categories in the DEGs for psoriasis (a) and atopic dermatitis (b). (c). For each category, the proportion of DEGs.



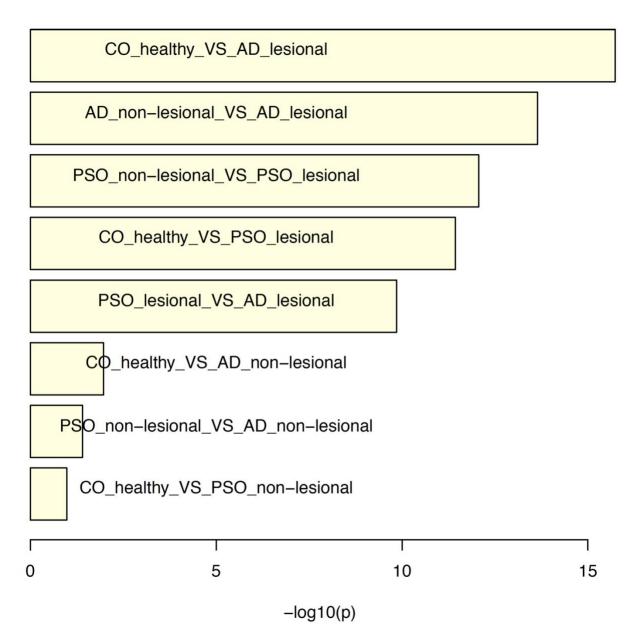
Supplementary Figure 4. Immunohistochemistry illustrates the detection of IL-36G in the skin of atopic dermatitis and psoriasis, concordant with the expression data.



Supplementary Figure 5. Lesional AD skin (A) with acanthotic thickening of the epidermis and parakeratosis. Perivascular infiltration of lymphomononuclear cells mainly in the dermis and focal epidermotropic lymphocytes. The lesional psoriatic skin (B) shows an acanthotic epidermis with parakeratosis and hypogranulosis and perivascular lymphomononuclear infiltrates in the upper dermis. The healthy control skin (C) displays a thin epidermis with regular structure and scarce perivascular lymphomononuclear infiltrates. CD8 is expressed in lymphocytic cells in the dermal compartment in lesional AD (D), lesional psoriasis (E) and control skin (F), accounting approximately for a quarter of all lymphocytes in each sample. In relation to the amount of lymphocytic infiltrates, the absolute count of CD8 positive cells is higher in D and E. Original magnification x100 in A-F.



Supplementary Figure 6. Correlation between SCORAD with normalized expression of TSLP (a) and IL13 (b) of AD lesional skin samples  $\frac{1}{2}$ 



Supplementary Figure 7. The enrichment analysis for AD drug targets among the genes dysregulated in different differential expression analysis.

### **Supplementary Tables**

**Supplementary Table 1. Cohort description:** Continuous traits as mean and standard deviation for atopic dermatitis patients (AD), psoriasis patients (Pso) and healthy control individuals (Healthy). Filaggrin (FLG) status (R501X, 2282del4, R2447X, S3247X) determined in AD and healthy control individuals only.

	AD	Pso	Healthy
Number of individuals (male/female)	27 (17/10)	28 (14/14)	38 (16/22)
Age	34.07+/-10.96	41.89+/-15.74	32.63+/-11.64
Objective Scorad / PASI	31.11+/-10.96	9.54+/-3.49	-
BMI	25.07+/-5.1	28.65+/-5.69	24.16+/-4.22
Age onset <6	80.77	7.14	-
FLG mutation carriers N (%)	7 (25.93)	NA	1 (2.63)
Asthma/Rhinitis (%)	48.15/62.96	-/-	0/0
Dennie-Morgan lines: weak/moderate/strong (%)	37.04/11.11/0	-/-/-	0/0/0
Herthoge's sign: weak/moderate/strong (%)	14.81/0/0	5.26/0/0	-/-/-
Palmar hyperlinearity: weak/moderate/strong (%)	37.04 /22.22/3.7	-/-/-	5.26/0/0
Sebostasis weak/moderate/strong (%)	29.63/44.44/22. 22	-/-/-	2.63/0/0
Keratosis pilaris weak/moderate/strong	37.04/11.11/0	-/-/-	7.89/5.26/0
PsA: questionable/yes (%)	-/-	28.57/14.29	-/-

# Supplementary Table 2. Sample description. Clinical and molecular features collected for each samples used in the RNA-seq analysis.

ID.pheno	Trait	Sex	Age	FLG Mutation	Severity (ScorAD/PASI)	Rhinitis	Asthma	PsA	biopsy site non- lesional	biopsy site lesional	Dennie	Hertoghe	Palmar hy- perlinearity	Xerosis	Keratosis pilaris
AD_004	AD	female	48	no	35.5	yes	yes	1 0/1	upper arm flexural	upper arm flexural left	moderate	no	weak	moderate	no
AD_005	AD	male	43	no	44.5	yes	yes		upper arm flexural left	upper arm flexural right	no	no	moderate	moderate	weak
AD_006	AD	male	25	2282del4	25	no	no		upper arm flexural left	upper arm flexural right	weak	weak	moderate	moderate	weak
AD_007	AD	male	33	R244X	15	yes	no		upper arm flexural left	antecubital fossa left	no	no	moderate	weak	weak
AD_009	AD	male	45	2282del4	32	yes	yes		upper arm flexural left	antecubital fossa left	no	no	moderate	moderate	weak
AD_011	AD	male	45	no	36	yes	yes		upper arm flexural left	upper arm flexural left	no	no	weak	weak	moderate
AD_014	AD	male	37	no	48	yes	no		upper arm flexural	upper arm flexural left	no	no	weak	moderate	no
AD_016	AD	female	25	no	18.5	no	no		upper arm flexural	upper arm flexural left	no	no	weak	moderate	moderate
AD_017	AD	female	42	no	38	yes	yes		upper arm flexural	upper arm flexural left	weak	no	moderate	strong	weak
AD_019	AD	female	22	no	24.5	no	no		upper arm flexural	antecubital fossa left	no	no	no	moderate	weak
AD_020	AD	female	43	no	42.5	yes	yes		upper arm flexural	antecubital fossa	weak	no	weak	strong	weak
AD_021	AD	female	29	no	15	no	no		upper arm flexural	antecubital fossa left	weak	no	no	weak	no
AD_023	AD	male	47	R244X/2282del	47	yes	yes		upper arm flexural left	upper arm flexural left	weak	weak	strong	strong	weak
AD_024	AD	female	45	no	22.6	no	yes		upper arm flexural	upper arm flexural right	no	no	weak	strong	weak
AD_025	AD	female	22	no	22.6	no	no		upper arm flexural	antecubital fossa left	weak	no	no	moderate	no
AD_026	AD	male	19	no	33.5	yes	yes		upper arm flexural	antecubital fossa left	no	no	weak	weak	no
AD_027	AD	female	22	no	14	yes	yes		upper arm flexural	upper upper arm flexural	no	weak	no	moderate	no
AD_028	AD	male	31	no	19	yes	yes		upper arm flexural	upper arm flexural right	weak	no	weak	moderate	no
AD_029	AD	male	21	no	25.7	yes	no		upper arm flexural	upper arm flexural left	moderate	no	weak	no	no
AD_030	AD	female	23	no	26.5	no	no		upper arm flexural	antecubital fossa right	no	no	no	weak	no
AD_031	AD	male	24	no	30.6	no	no		upper arm flexural	upper arm flexural left	weak	no	no	moderate	moderate
AD_032	AD	male	53	2282del4	29	no	no		upper arm flexural	antecubital fossa right	no	no	moderate	moderate	weak
AD_033	AD	male	48	no	39	yes	yes		upper leg flexural	upper leg flexural right	moderate	no	no	strong	no
AD_034	AD	male	30	R501X	38	yes	yes		upper arm flexural	upper arm flexural right	no	no	moderate	moderate	no
AD_035	AD	male	19	no R501X/2282del	26	yes	no		upper arm flexural left	lower arm left	weak	no	no	weak	no
AD_036	AD	male	45	A K3017/22620ei	56	yes	no		upper arm flexural left	upper arm flexural left	no	no	moderate	strong	no
AD_037	AD	male	34	no	36	no	no		upper arm flexural left	upper arm flexural left	weak	weak	no	weak	no
PSO_001	PSO	female	28		3.3			yes	upper arm extensor upper arm flexural	ellbow left					
PSO_002	PSO	male	50		5			no	loff	upper arm flexural left					
PSO_003	PSO	female	50		6.2			yes	upper leg flexural left lower leg flexural	upper leg flexural left					
PSO_005	PSO	female	33		4.3			no	right	lower leg flexural right					

					Severity (ScorAD/P								Palmar hy-		Keratosis
ID.pheno	Trait	Sex	Age	FLG Mutation	ASI)	Rhinitis	Asthma	PsA	biopsy site non-lesional	biopsy site lesional	Dennie	Hertoghe	perlinearity	Xerosis	pilaris
PSO_006	PSO	female	50		7			no	lower leg flexural left	lower leg flexural left					
PSO_007	PSO	female	68		3.8			unknown	upper arm extensor right	upper arm extensor right					
PSO_008	PSO	female	35		5			no	upper arm flexural left	ellbow left					
PSO_009	PSO	male	71		6.2			yes	lower leg flexural left	lower arm flexural left					
PSO_011	PSO	male	53		8.3			yes	lower leg extensor left	lower leg extensor left					
PSO_012	PSO	female	46		5.8			unknown	lower leg extensor left	lower leg extensor left					
PSO_014	PSO	male	22		6.8			no	upper arm extensor left	upper arm extensor left					
PSO_015	PSO	male	49		22.4			unknown	upper arm extensor left	upper arm extensor left					
PSO_016	PSO	male	23		5.4			no	upper arm extensor left	upper arm extensor left					
PSO_017	PSO	male	30		6.6			no	lower arm extensor left	lower arm extensor left					
PSO_018	PSO	female	38		1.8			no	upper arm extensor left	upper arm extensor left					
PSO_020	PSO	female	21		2.7			unknown	upper leg flexural left	upper leg flexural left					
PSO_023	PSO	female	36		1.2			unknown	upper arm extensor left	ellbow left					
PSO_024	PSO	male	69		2.9			no	upper arm extensor right	ellbow right					
PSO_027	PSO	male	46		3.6			no	upper arm flexural left	ellbow left					
PSO_028	PSO	male	41		9.7			no	upper arm extensor left	upper arm extensor left					
PSO_029	PSO	female	70		2			unknown	upper arm extensor right	ellbow right					
PSO_030	PSO	male	52		6.8			no	upper arm extensor right	ellbow right					
PSO_031	PSO	male	40		11.4			no	upper arm extensor right	ellbow right					
PSO_033	PSO	female	28		4.5			no	upper arm extensor right	upper arm extensor right					
PSO_034	PSO	male	28		4			unknown	upper arm flexural left	upper arm flexural left					
PSO_035	PSO	male	24		1.3			no	upper arm flexural left	upper arm flexural left					
PSO_036	PSO	female	18		3.5			no	upper arm extensor left	upper arm extensor left					
PSO_037	PSO	female	54		10.5			unknown	upper arm extensor right	upper arm extensor right					
CTRL_002	CTRL	female	42	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_003	CTRL	female	25	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_004	CTRL	female	28	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_006	CTRL	female	24	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_008	CTRL	male	28	no		no	no		upper arm flexural right		no	no	no	no	weak
CTRL_009	CTRL	female	33	no		no	no		upper arm flexural left		no	no	no	no	weak
CTRL_010	CTRL	female	27	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_011	CTRL	male	26	no		no	no		upper arm flexural left		no	no	no	no	moderate
CTRL_013	CTRL	male	42	no		no	no		upper arm extensor right		no	no	no	no	no

					Severity (ScorAD/PAS								Palmar hy-		Keratosis
ID.pheno	Trait	Sex	Age	FLG Mutation	I)	Rhinitis	Asthma	PsA	biopsy site non-lesional	biopsy site lesional	Dennie	Hertoghe	perlinearity	Xerosis	pilaris
CTRL_014	CTRL	male	24	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_015	CTRL	female	28	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_016	CTRL	female	32	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_017	CTRL	male	30	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_018	CTRL	male	23	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_019	CTRL	female	40	no		no	no		upper arm extensor left		no	no	weak	no	moderate
CTRL_020	CTRL	male	26	no		no	no		upper arm flexural left		no	no	no	weak	no
CTRL_022	CTRL	male	47	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_024	CTRL	female	47	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_025	CTRL	female	25	no		no	no		upper arm flexural left		no	weak	no	no	no
CTRL_026	CTRL	female	31	no		no	no		upper arm flexural left		no	weak	no	no	no
CTRL_029	CTRL	male	40	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_030	CTRL	male	40	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_031	CTRL	male	54	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_032	CTRL	male	37	no		no	no		upper arm flexural right		no	no	no	no	no
CTRL_033	CTRL	female	52	no		no	no		upper arm extensor left		no	no	no	no	no
CTRL_034	CTRL	male	61	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_035	CTRL	female	29	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_036	CTRL	female	25	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_037	CTRL	male	22	no		no	no		upper arm flexural left		no	no	no	no	weak
CTRL_038	CTRL	female	20	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_039	CTRL	female	19	no		no	no		upper arm extensor left		no	no	weak	no	no
CTRL_040	CTRL	female	20	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_041	CTRL	female	57	no		no	no		upper arm extensor right		no	no	no	no	no
CTRL_042	CTRL	female	20	2282del4		no	no		upper arm flexural left		no	no	no	no	no
CTRL_043	CTRL	female	24	no		no	no		upper arm flexural left		no	no	no	no	no
CTRL_044	CTRL	male	18	no		no	no		upper arm flexural right		no	no	no	no	no
CTRL_045	CTRL	female	25	no		no	no		upper arm flexural right		no	no	no	no	no
CTRL_046	CTRL	male	49	no		no	no		upper arm flexural left		no	no	no	no	no

**Supplementary Table 3. Transcriptomic studies conducted for AD/Eczema.** Only show the number of samples that have been profiled for transcriptome, remained after quality control, and presented in the paper (if the number cannot be determined in the paper, the number of samples deposited in the corresponding GEO was used). ^same control individuals; \*same patients; \*the study used skin tape strip for profiling the transcriptome.

Study	Platform	Study treatment	Control	Pso	Pso	AD/Eczema	AD/Eczema
		response		uninvolved	lesional	uninvolved	lesional
Nomura I, et al. 2003. JACI	Microarray	NA	NA	NA	6	NA	7
Guttman-Yassky E et al. 2009. <i>JACI</i>	Microarray	NA	9^	NA	15	NA	9
Suarez-Farinas Mayte, et al. 2011. <i>JACI</i>	Microarray	NA	8	NA	NA	12	13
Tintle S, et al. 2011. JACI	Microarray	UVB phototherapy	NA	NA	NA	12	12
Choy DF et al. 2012. JACI	Microarray	NA	5	NA	14	NA	12
Gittler JK et al. 2012. JACI			15^	NA	NA	8	8 chronic/8 acute
Cole C et al. 2014. JACI	RNA-Seq	NA	10	NA	NA	26	NA
Quaranta M et al. 2014. Sci Trans Med	Microarray	NA	NA	NA	psoriatic patients also with eczema	NA	24 eczema patients also with psoriasis
Rodriguez E, et al. 2014. JID	Microarray	NA	14 epidermal	NA	NA	7 epidermal	12 epidermal
Khattri S, et al. 2014. JACI	Microarray	Cyclosporine	NA	NA	NA	19*	19*
Beck LA, et al. 2014. NEJM	microarray	dupilumab	NA	NA	NA	7	16
Suarez-Farinas M, et al. 2015. <i>JACI</i>	Microarray & RNA-seq	NA	NA	NA	NA	18*	18*
Brunner, PM, et al. 2016. JACI	Microarray	Topical glucocorticosteroids	NA	NA	NA	9	14
Malik K. et al. 2017. Clin Exp Allergy	Microarray	House dust mite atopy patch test	14	NA	NA	8	8
Dyjack N, et al. 2018. JACI#	RNA-seq	NA	13	NA	NA	18	12
This study	RNA-seq	NA	38	27	28	27	27

# Supplementary Table 4. Number of differentially expressed genes in each of the comparisons.

	Number of Genes							
DE analysis	DEGs	Up-regulated	Down-regulated					
Healthy vs Pso non-lesional	246	82	164					
Healthy vs Pso lesional	6763	2502	4261					
Pso non-lesional vs Pso lesional	5156	2232	2924					
Healthy vs AD non-lesional	180	98	82					
Healthy vs AD lesional	3450	1529	1921					
AD non-lesional vs AD lesional	1785	919	866					
Pso non-lesional vs AD non-lesional	185	117	68					
Pso lesional vs AD lesional	2030	1259	771					

Supplementary Table 5. Functional enrichment results for lesional DEGs In Excel Table

**Supplementary Table 6. Functional enrichment results for uninvolved DEGs In Excel Table** 

Supplementary Table 7. Read counts obtained for IL4 and IL13 for all samples

Supplementary Table 8. Cell type enrichment analysis for different differential expression analysis

Supplementary Table 9. Proportion of CD8 cells obtained from the quantitative immunochemistry results.

Supplementary Table 10. Table for top features in classification.

	Ranking of selected	Selected
	features	features
Normal vs uninvolved		
AD	1	IL13
	2	EBI3
	3	1L26
	4	IL20
	5	IL5
	6	IL36A
	7	IL36G
Normal vs uninvolved		
Pso	1	IL36G
	2	IL19
	3	IL18
	4	IL36A
	5	EBI3
	6	IL13

Supplementary Table 11. Spearman correlation and significance level between gene expression and severity score in psoriatic lesional (PASI) and AD lesional (SCORAD) skin.

Supplementary Table 12. Current AD drugs (from the drug databases used in this study) whose targets are differentially expressed in AD lesioanl skin.

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Significant in Numburgener CYTORINE_CYTORINE_RECEPTOR_IMITERACTION DEGL_PRO_B_AD 229 CYTORINE_CYTORINE_RECEPTOR_IMITERACTION DEGL_AD_only 229	DEGC_both_Pio_AO_x	10 AD FOR DEGLISH, Foo AD FC DEGLISH, Foo AD J DEGLISH 18 2.0 OCC12; 120; CC11; CC 1 18 3.0 OCC12; 120; CC11; CC 1 18 3.0 OCC12; 120; CC11; CC 1 18 3.0 OCC12; 120; CC11; CC 1 19 3.00 OCC12; 120; CC11; CC11	Ny Piso x 0664 cen'y Piso y 0664 cen'y Piso F0R 7 7.696-01 9.806-01 7 7.696-01 9.806-01 7 7.696-01 9.806-01	0561_only_Poz_FC 0561_only 0561_on 0.84	hly DEGLORY AD D DEGLORY AD FOR DEG 7 5.105-08 2.035-04 7 5.105-08 2.035-04 7 5.105-08 2.035-04	5(_only_Ab_FC	**************************************	Pag_AD_FOR DEGC_Pag 716-00 2.30 716-00 2.30	28.   F   605, Fay, Pag. parent
Company   Comp	57 6356-19 1.896- 57 6356-19 1.896-	-15 3.62 AREG, BMPS; BMPS; C 1 -15 3.62 AREG, BMPS; BMPS; C 1 -15 3.62 AREG, BMPS; BMPS; C 1	1 8.515-01 9.805-01 1 8.515-01 9.805-01 1 8.515-01 9.805-01	0.74 C1QTNF4;1 1 0.74 C1QTNF4;1 1 0.74 C1QTNF4;1 1	1 2,325-05 2,955-02 1 2,325-05 2,955-02 1 2,325-05 2,955-02	4.85 E229A2; C 4.28 CCL22; CDI 4.28 CCL22; CDI 4.28 CCL22; CDI	27 3.305-05 3 26 3.325-06 7 26 3.325-06 7 26 3.325-06 7	1999	0 CLIS; EDN4; CDX; CDX; CLIS; PNG; LIS; ENG; CDX; ELIS; LIC; ELIX; LIS; LIS; LIS; LIS; LIS; LIS; LIS; LIS
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BASHDAL_TU_VRIDA	57 7.656-54 6.066- 67 8.156-54 6.066	-11 2.87 OCC12; OSCR1; HON 2 -11 2.87 OCC12; OSCR1; HON 2 -11 2.87 OCC12; OSCR1; HON 3	7 0.515-01 9.685-01 9 2.185-01 7.585-01 6 6.685-01 9.505-01 1 2.935-01 8.685-01 1 2.935-01 8.586-01 2.045-01 7.585-01	112 OXONG RB 6	1 1046-01 7366-01 1 1046-0	1.41 MARDE, NO 1.50 MARDE, NO 1.50 CAC, CD27, G.G. FNAG2, OI 1.55 GPR4, 195H 1.55 GPR4, 195H 1.55 GPR4, 195H 1.55 FDD2, GPR9 1.54 CD22 GPR 1.55 GPR 1	27 8.06E-06 1 27 8.06E-06 1 27 8.06E-06 1 33 3.12E-06 7	08-00 1.11 285-00 2.65 285-00 2.65 355-06 2.35	P READ, CHARTY, CHARTY, CANA, CHAPT, BYTS, DWG, LEAN, DWGS, PARK, THARTY, THEORY, THAR PRODUCT, CHART, CANA,
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CYTORINE RECEPTOR BINDING         DEGL. Pro. B. AD         192           CYTORINE RECEPTOR BINDING         DEGL. Plo. D. AD         192           CYTORINE RECEPTOR BINDING         DEG. Plo. V. AD         192           CYTORINE RECEPTOR BINDING         DEG. Plo. V. AD         192	66 1756-90 4216- 66 1756-90 4216- 66 1756-90 4216- 39 1881-90 4216-	-08 2.69 CCL17; CCL18; CCL18; 1 0 -08 2.69 CCL17; CCL18; CL18; 1 1 -08 2.69 CCL17; CCL18; CL18; 1 1 -08 2.67 BM; CMSD1; CCL19;	0 9.50E-01 9.96E-01 0 9.50E-01 9.96E-01 0 9.50E-01 9.96E-01 8.80E-01 9.80E-01 1 5.80E-01 9.30E-01	0.62 CC24; PG 1 0.62 CC24; PG 1 0.62 CC24; PG 1 0.73 8C2; ICO5	2 1.425-05 2.825-02 2 1.425-05 2.825-02 2 1.425-05 2.825-02	4 31 BAMB; CC 4 31 BAMB; CC 4 31 BAMB; CC 1 40 C0209; TG	5 4.251-06 8 5 4.251-06 8 5 4.251-06 8 9 2.251-01 6	955-04 2.65 955-04 2.65 955-04 2.65	B COLL; COLLE; COLLE; COLLE; CORLE; CORC, CLOTE; CHOLLE; CHOLLE; GATAX; HANG, LLE; HLTF B COLL; COLLE; COLLE; COLLE; CORLE; CORC, CHOS; CHOLLE; CHOLS; GATAX; HANG, LLE; HLTF B COLL; COLLE; COLLE; COLLE; COLLE; CORC, CLOTE; CHOLLE; CHOLLE; GATAX; HANG, LLE; HLTF B MANN, CLOTE; CHESC, COLLE; COLLE; CHOLLE; CHOLLE; CHOLLE; CHOLLE; B MANN, CLOTE; FSF10; HANG, LLE; HLTR, HLTR; HLTR; B MANN, CLOTE; FSF10; HANG, LLE; HLTR; HLTR; HLTR; HLTR; B MANN, CLOTE; CHOLLE; HLTR; HLTR; HLTR; HLTR; B MANN, CLOTE; HLTR; HLTR
Manufactor   Section   S	39 1,855-90 4,315- 22 2,035-90 4,696- 50 2,045-90 4,696- 39 2,246-90 4,855-	200	8.00E-01 9.80E-01 5.87E-01 9.30E-01 3 9.00E-01 9.85E-01 9.86EE-01 9.80E-01	Section   Sect	2.65E-01 8.52E-01 1 3.76E-01 8.52E-01 7.07E-02 6.86E-01 1 19E-01 6.96E-01	4.31 BANES; CC 4.31 BANES; CC 1.60 CD09; TG 1.36 MCB 1.89 CD27; GBA 1.85 CD29; CS 1.35 NCS1, TMS 0.00 0.75 AMS1C2 1.09 FOWN, CC1 1.09 FOWN, CC1 1.09 DUCKS; FF	9 2,335-05 6 3 3,905-05 7 21 1,725-09 4 9 2,645-05 6	865-01 1.25 925-01 1.13 405-02 1.97 955-04 1.39	Seminar (COT): 1-60'00 (Marc, CLE, SEL CLEAN, CLEAN
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PEPTIDE LIGAND, BRONNE, SECEPTIONS DEGL., Pro. B., AD 120 PEPTIDE LIGAND, BRONNE, SECEPTIONS DEGL., Pro. J., AD 120 CYTOWINE, MEDIATIO, SIGNALIMG PATHWAY DEGL., Pro. B., AD 258	25 2,726-00 6,946- 25 2,726-00 6,946- 57 4,006-00 7,216-	-08 3.11 OXC11; CON; CON; C 10 -08 3.11 OXC11; CON; CON; C 10 -08 2.36 AM2; CC12; CC5; CC8 10	2 2.16E-01 7.91E-01 2 2.16E-01 7.91E-01 8 8.58E-01 9.80E-01	0.52 CST6 0.13 ABCA12 1.23 CKD6; E09 1.23 CKD6; E09 1.24 CKD6; E09 0.79 BBCS; E69 0.77 AP2S; APC 0.78 BCC; GST9 0.46 CD47; CIGS 0.46 CD47; CIGS	6.165-01 8.526-01 6.165-01 8.526-01 8.4606-01 8.526-01	0.75 AARSCS 1.09 PDYN; CCL: 1.09 PDYN; CCL: 1.01 DUCKE; FF	15 8.196-04 2 15 8.196-04 2 34 2.666-03 5	976-02 2.44 976-02 2.44 566-02 1.81	6 CERS; CORR; ENRO; FREZ; CECKE; MESSR; NTS; COTTR; BLANZ; CCCLE;; CRECE; CECLEZ; TACKE; GERS; CECLEZ; TACKE; TACKE; GERS; CORR; CORR; CACCE; CECLEZ; CECLEZ; TACKE; ADMINOZ; CAMACIA; CAMACIA; CORR; CORR; CORR; CORR; CERC; CERC; CERCE; CE
### ##################################	69 4.521-20 7.925- 29 5.641-20 9.565- 48 8.881-20 1.385- 39 8.731-20 1.605-	-08 2.56 AMAZ, PCIZ; PCIS; CCS 125 AMAZ, PCIZ; PCIS; CCS 126 AMAZ, PCIZ; PCIS; CCS 126 AMAZ, PCIZ; PCIZ; CCS 126 AMAZ, PCIZ; P	8 88E-01 9.86C-01 0 7.89E-01 9.86C-01 1 9.96E-01 1.00E-00 9.94E-01 1.00E+00	0.78 BCL2; GSTP 0.45 CD47; CHC1 12 CD47; CD57 CD57; CD	6.00-01 8.00-01 1.58-01 7.02-01 1.27-01 6.88-01 7.286-02 6.97-01 1.22-01 6.96-01 6.26-01 8.52-01 6.55-01 8.52-01	1.59 CD4016, D 1.80 CD2019, CS 2.25 CAMER, CC 1.78 GBAP2, B2 0.64 AMS1C3 1.02 CD4016, N 1.02 CD4016, N	18 1.66F-02 1 9 2.69E-01 6 15 7.91E-02 3 13 2.91E-02 2	905-01 1.21 655-01 1.86 115-01 1.72	\$\text{\titt{\text{\titt{\text{\ti}\text{\
ERCEMBAL CELL DEFERENTATION DEGL. PIO. BLAD 102 POSITIVE, REGULATION, OF, CYTOKINE, PRODUCTION DEGL. PIO. DL. ALD 102 POSITIVE, REGULATION, OF, CYTOKINE, PRODUCTION DEGL. PIO., VII. AD 102	08 R.88-32 1.66- 29 R.73C-32 1.66- 21 116C-09 1.78C- 66 117C-09 1.78C- 66 117C-09 1.78C- 66 117C-09 1.78C- 66 117C-09 1.78C-	G7 3.26 ONFN; EPHA2; FA2H; F G7 2.55 ADAMB; ADCHAP1; AG 1 G7 2.55 ADAMB; ADCHAP1; AG 1	9.946-01 1.004-00 9.946-01 1.004-00 9.976-01 1.004-00 0 9.686-01 1.004-00 0 9.686-01 1.004-00	0.39 CD47; ICOS 6 0.22 ABCA12; H 1 0.59 CD34; DDX 0.59 CD34; DDX	6.296-01 8.526-01 8.526-01 8.526-01 8.4526-01 8.526-01	1.25 CAMEG CE 1.78 GRAP2; H2 0.64 AM31C3 1.02 CDM1G; N 1.02 CDM1G; N	13 2.915-02 2 8 1.165-05 4 23 9.185-05 7 23 9.185-05 7	485-01 1.53 805-03 2.33 805-03 2.33	2 CTA; (556); FORE; FORE; FORE; SUZ; SETZ; SERAR AMPIGO; FZIG; GATA; PROS; SEM; ELIZ; ELIZ; ELIZ; ELIZ; ELIZ; ELIZ; AMPIGO; FZIG; GATA; PROS; SEM; ELIZ; ELIZ; ELIZ; ELIZ; ELIZ; ELIZA; ELZA; ELZA; ELZA; ELZA; ELZA; ELZA; ELZA; ELZA; ELZA; ELZA; ELZA; ELZA; ELZ
BESFORES, TO, INTERFERON, CAMMA POSITIVE, REQUIATION, OF, IMPROCYTE, ACTIVATION DEGL. Pro. S., AD 102 CRUINER, RESPONSE TO, MOLECUE, OF SACTERIAL, ONC. DEGL. Pro. S., AD 103 CRUINER, RESPONSE TO, MOLECUE, OF SACTERIAL, ONC. DEGL. Pro. S., AD 104	36 3165-09 4.605- 27 2336-09 4.695- 65 4.366-09 6.215- 28 5.125-09 7.065- 23 5.375-09 7.266-	-07 2.95 APOBECSA, APOBECSA (2016) CES, CEP, CES, CES, CES, CES, CES, CES, CES, CES	2 3.66E-01 9.06E-01 3.96E-01 9.08E-01 2 9.03E-01 9.86E-01 7.66E-01 9.80E-01 9.08E-01 9.80E-01	1.11 ABCC0; API 0 1.08 ACP4; 8575 1 0.70 AXI; 90.2; 6 0.75 AXI; CVP17 1	9.25E-01 9.60E-01 5.68E-01 8.5E-01 5.28E-02 6.70E-01 5.8E-01 8.5E-01	0.00 0.78 VCAM1 2.03 C027; GRA 0.72 TGGB1 1.01 VCAM1 0.76 TGGB1	7 3.715-05 7. 7 1.035-05 4. 17 1.585-02 1. 8 6.935-02 2. 4 3.355-05 7.	236-06 1.63 556-06 1.73 426-06 1.71	ADDROG, PDIC, GAPAG, HANG, SHOCK, ELE, ELINE, ELINE, SILE, ELINE, E
POSITIVE SEGULATION OF Y, CELL PROCESSIATION DEED, No. 8, AD 65 CELLULA SESPONSE TO LEPPOCYSTACOMEND DEED, NO. 8, AD 66 ESCULATION OF LYMPHOCYTE CHEMOTROS DEED, No. 8, AD 12 ESCULATION OF LYMPHOCYTE CHEMOTROS DEED, No. 8, AD 12	22 5.716-09 7.266 22 5.776-09 7.478 10 5.786-09 7.478 45 6.186-09 7.826 45 6.186-09 7.826	47 3.35 CCL2; CCL3; CCL5; CCR	9.58E-01 9.86E-01 7.13E-01 9.80E-01 9.80E-01 9.80E-01	0.75 AKE; CVP17 1 0.35 ICOSIG; PV 1 0.79 AKE; CVP17 1 0.00 ICOSIG; PV 1	1000   1000	0.76 TGFR1 0.00	4 3.355-01 7. 7 1.135-01 4 0 7.485-01 1. 18 8.575-00 1	426-06 1.20 296-06 1.56 206+00 0.00	O INNG, ELEY, ELZAY, ELZAY O ANGE, ENGÉ, ELEY ELRET, NRIDE, RASA, STATI O TEMPORAL MENON CONTRACTOR CONTRA
LEUROCYTE MEGRATION OF INFLAMMATORY RESPONSE DEGLIND , B, AD 66 POSITIVE SEGULATION OF LEUROCYTE PROLIFERATION DEGLIND , B, AD 68	65 6.186-00 7.826- 22 7.546-00 9.006- 20 7.576-00 9.006- 20 7.576-00 9.006-	207 3.46 ASSAME, MARCHA (CCL) 407 3.46 ASSAME, MARCHA (CCL) 407 3.51 ASSAME, MARCHA (CCL) 407 3.51 BANC, MARCHA (CCL) 408 3.51 BANC, MARCHA (CCL) 408 ASSAME, MARCHA (CCL) 409 ASSAME, MARCHA (CCL)	5 7,03E-01 9,76E-01 7,03E-01 9,76E-01 8,90E-01 9,86E-01 7,08E-01 9,80E-01	0.87 ARTN; ATP 1 0.87 ARTN; ATP 1 0.52 CCL24; CD4 0 0.81 BCL2; ICO5 0 0.23 ICO5LG; PV 3	2 2.8E-05 2.9E-02 0 8.20E-01 8.80E-01 2.17E-01 8.52E-01	\$0.00 C1.13, 000 c1.13, 000 c1.13, 000 c1.13, 000 c1.14, 000 c1.15, 000 c1.15	18 8.576-03 1 8 1.286-02 1 7 1.846-01 5	115-01 1.80 155-01 2.30 875-01 1.30	PHYSIC PRINC COLL SCIED, CHES. DR. CATAL CREEK PAY, LIE, ROAM, RGS AFFELD, PRINC COLL CREEK, CHES. DRIVE, CHES. DRIVE, LIE, ROAM, RGS AFFELD, PRINC COLL CREEK, CHES, DRIVE, DRIVE, CHES, DRIVE, AFFELD, ROAM, RGS AFFELD, RGS
REGULATION OF T. CELL PROLIFERATION DEGE, Pro. B. AD 98 T. CELL ACTIVATION REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, Pro. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOSIS. DECOMPASSING MUTURAL DEGE, PRO. B. AD 30 REGULATION OF SYMMOS	29 7.576-09 9.006- 41 1.046-08 1.216- 12 1.456-08 1.636- 21 1.476.09 1.636-	-07 3.55 BLM; CARD11; CC.19; -06 2.54 BATE; BCL2; BLM; CARD -06 6.60 CAMP; CDS; HS2STS; -06 3.65 BLM; CO.19; CO.2-10;	7.085-01 9.805-01 9.865-01 1.005-00 9.865-01 1.005-00 9.865-01 9.865-01 1.005-01 9.305-01 9.285-01 9.865-01 6.765-01 9.865-01 4.725-01 9.165-01	023 ICOSEG: PV 3 059 BCI2; EOM 8 057 BST2 C	1.2%-01 6.886-01 2.186-02 2.086-01 6.386-01 8.526-01 4.005-01 8.556-01	2.00 CD209;TG 3.04 DDCK2; HZ 0.00	8 1286-02 1 7 1865-05 5 5 4.805-05 8 9 4.575-01 8 1 4.675-01 8 4 2.675-01 5 7 1.655-01 5 4 5.806-01 5 7 1.795-04 5	876-06 0.96 656-06 1.02 656-06 0.97 905-06 1.34	9 88694; 596; 1118; 1234; 1238 2 021; Crofiliz; 5994; 5205; GATAZ; 5905; 11234; 175444; TEX21 1905 64747 19724 19724 19729 18894
POSITIVE_REGULATION_OF_LYMPHOCYTE_PROLIFERATION_DEGL_PIO_B_AD 96 POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_PROLIFE DEGL_PIO_B_AD 96 POSITIVE_REGULATION_OF_MONONUCLEAR_CELL_PROLIFE DEGL_PIO_B_AD 96	41 104-08 1245- 12 1455-08 1.636- 21 1475-08 1.636- 28 1485-08 1.636- 27 1.735-08 1.876- 28 1.937-08 2.036-	06 2.54 8EM; CARDIE; CCL19; 06 3.20 AM2; BATF; CCL19; CC 06 3.11 8EM; CARDIE; CCL19;	6.766-01 9.666-01 4.726-01 9.116-01 6.876-01 9.306-01	0.57 8572 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.	5.96-01 8.52-01 5.76-01 8.52-01 2.06-01 8.52-01	0.00 1.13 H2F1 0.69 VCAM1 0.73 CAM64 1.36 CSF1,VCAH 1.54 MSN,VCGS 0.64 FROC	7 1.655-00 5 4 5.895-00 9 7 1.715-00 5	456-00 1.64 996-00 0.87 696-00 1.43	7 ING  4 GATAR, ELZAC, ELZOR, BARA  4 GLOS, PÓSICO, PINC, ELZO, ELZOR, E
REQUIATION OF LEUROCYTE MERATION DEGL. Pro. R. AD 85 CELLULAR RESPONSE TO BIOTIC STITUSUUS DEGL. Pro. R. AD 102 SERINE, TYPE SINDOPPTIBASE ACTIVITY DEGL. Pro. R. AD 120	26 1996-08 20% 29 2066-08 2116- 22 2266-08 22%	06 3.56 ADMAR APOD, BMPS, 06 3.09 CCL2; CCL3; CCL5; CCR 06 2.44 GR; GP; CTS; CLANE 1	4.07E-01 9.00E-01 7.47E-01 9.00E-01 4 1.38E-01 7.57E-01	107 C108P; CA 2 078 AXI, CYP27 1 132 APRI; C1R; 1	2 .586-01 8.526-01 6 2.586-01 8.526-01 6 .576-01 8.526-01 0 6.606-01 8.526-01 0 2.666-01 8.526-01 8 .506-02 6.586-01	1.54 MSN; VEGI 0.64 TGFR1 0.54 PROC	7 1.08E-01 4 8 1.16E-01 4 9 1.26E-01 4	276-01 1.66 686-01 1.51 676-01 1.66	O CICLEZ EDNO, EDA, EJAS, SUTZ, THESS, THESS AGE, ESDS, FANG, LIES, ENANC, SHOTI, SHAPA, STATI OPPO, CAMPA, HTRAT, KLESS, PARKE, PCSK2, TMPRESSIF, TMPRESS; TPSDS
CELL RELEGION MODELLES CAMES DEGLE PLOS AND 105 EGGL PLOS ADDESSES DEGLE PLOS AD	12 2.5%-08 2.2%- 12 1.5%-08 1.9%- 15 4.04C-08 1.9%- 29 4.26C-08 4.0%- 26 4.44C-08 4.16C-	-06 5.54 BCL2; CD274; CD81; FC -06 4.85 AUE; ADDL2; CAMP; CL -06 2.94 CDH2; CDH4; CDH4; CD -06 3.35 CD19; CD26; CD26; C	1.884-01 7.34-01 2.786-01 8.586-01 6.886-01 9.706-01 0 3.856-01 9.086-01 9.726-01 1.006-00	132 APAR CIR; 1 136 C036; PRO 069 PROXI; RM 108 CIDN7; VO 039 HPX; PVCAI	2.45E-01 R.53E-01 8.50E-02 6.58E-01 8.57E-01 R.53E-01	1.98 NCF1 2.49 ITGR2; SEU 0.74 TGFR1	2 2.52E-01 6 1 6.68E-01 1 9 6.66E-02 3 9 2.54E-02 1	206+00 0.56 276-01 1.67 996-01 1.96	2 GOD; (Spid); mice, 431; MR; 1931; CUBP GOD; (Spid); mice, 431; MR; 1931; Mice) GOD; (Spid); mice, 431; MI; Mice) GOD; (Spid); mice, 432; MI; MI; MI; MI; MI; MI; MI; MI; MI; GOD; (Spid); mice, 432; MI; MI; MI; MI; MI; MI; MI; MI; MI; GOD; (Spid); mice, 432; MI; MI; MI; MI; MI; MI; MI; MI; MI; MI
CYTORINE SECEPTOR ACTIVITY DEG. Pro. B. AD 72 CYTORINE SECEPTOR, ACTIVITY GEULLAR SESPONSE 70, INTERFERON_GAMMA DEG. Pro. B. AD 67 CEULLAR SESPONSE 70, INTERFERON_GAMMA DEG. Pro. B. AD 67	23 4955-08 4605- 22 4955-08 4605- 22 5,366-08 4936-	66 3.41 CCR1; CCR2; CCR4; CCI 66 3.41 CCR1; CCR2; CCR4; CCI 66 3.50 CC2; CC1; CC1; CCR5; CF4	6.96E-01 9.36E-01 6.96E-01 9.36E-01 4.61E-01 9.11E-01	0.79 CXCRG IFN 2 0.79 CXCRG IFN 2 1.01 AGP4; FCG 1	6.125-02 6.865-01 6.125-02 6.865-01 4.565-01 8.525-01	2.72 IFNAR2; E1 2.72 IFNAR2; E1 0.98 VCAM1	12 1.716-04 1 12 1.716-04 1 6 9.196-02 4	226-02 3.25 226-02 3.25 026-06 1.75	GERI, CORE, COSE, COSEZ, GERZE, SERZE, LEZRE, LE
IN STATE SEGNATION OF APPROXIMATION OF A	12 6.326-08 5.715- 22 6.475-08 5.746- 17 6.936-08 5.976- 17 6.936-08 5.976-	-06 5.81 ADMAR, APOD; CCL2; 1 -06 2.73 IRFR; L3c; CATER; CSC -06 4.21 IRM; CCL19; CCD; CD -06 4.21 ADMAR, AURIS; CCL11	6.48E-01 9.08E-01 9.79E-01 1.00E-00 1 9.42E-01 9.86E-01 8.24E-01 9.80E-01	103 GCSAM; PV 1 0.45 SPR2; FN 5 0.26 IFNS 1 0.53 AN; ISS2 0	1 1.665-01 7.415-01 2.785-02 5.225-01 3.135-01 8.526-01 7.435-01 8.565-01	2.97 MSN 2.61 E22RA2; PI 1.52 HZF1 0.00	0 8.68E-0s 1. 11 4.17E-02 2 3 2.79E-0s 7 3 2.79E-0s 7	626-01 1.71 026-01 1.36 026-01 1.36	1 CSH, M28R, CLEF1; FMG; MR; ML18RA; ML1; ML18RA2; LIFR; M23RA; STAT1 6 M23R; M23R; RAMA 6 M8C7; MRMPC; CMC12
POSITIVE, SEGULATION OF LEUROCYTE MISSANTON DE SEGU-PIO, SLAD 61 POSITIVE, SEGULATION OF SESPONSES, TO, EXTERNAL, STH. DEGG. PIO, SLAD 165 POSITIVE, SEGULATION OF SESPONSES TO, EXTERNAL, STH. DEGG. PIO, VI, AD 145	27 6.07-08 5.76- 17 6.08-08 5.97- 17 6.08-08 5.97- 21 7.86-08 6.06- 26 8.71-08 6.88- 26 8.71-08 6.88- 20 8.78-08 7.26- 10 1.28-07 1.06-	106	4.03E-01 9.08E-01 2 5.77E-01 9.30E-01 2 5.77E-01 9.30E-01	0.53 ANURS2 0 108 C1Q8P, CA 1 0.94 ARTN; C1Q 3 0.94 ARTN; C1Q 3 1.07 C034; F2R; 0 0.71 PYCARD 0	1 6.365-01 8.525-01 5.185-01 8.525-01 5.185-01 8.525-01	0.00 1.04 VEGFA 0.90 TGFR1; VEC 0.90 TGFR1; VEC 0.00 0.00	5 1.635-01 5 17 8.635-01 3 17 8.636-01 3	615-01 1.55 005-02 2.26 005-02 2.26	1 CORP. (EAST), COST, SHAN, SHE SHAN, RET, KERRAZ, LIFK KERRAZ, STATE  EIRA, KERRAZ  E
POSITIVE_REGULATION_OF_EMMPHOCYTE_MIGRATION DEGL_PIO_B_AD 16 PRFTDS_CROOS_ENVENIO DEGL_PIO_B_AD 27 PRFTDS_CROOS_ENVENIO DEGL_PIO_B_AD 27	22 8.786-08 7.256- 10 1.286-07 1.086- 13 1.266-07 1.086- 13 1.266-07 1.086-	140   CORP. CORP	4.054-01 9.086-01 1.054-01 9.306-01 1.566-01 9.226-01 1.566-01 9.226-01 1.866-01 9.326-01 1.866-01 9.866-01 1.866-01 9.866-01 1.866-01 9.866-01 1.866-01 9.866-01	0.71 PYCARD 0 0.84 MANDC2; 0 0.84 MANDC2; 0 0.70 C108P; CC 4	1 3.15C 01 8.15C 02 7.316C 01 8.15C 02 7.316C 01 8.15C 03 7.316C 01 8.15C 03 8.15C	0.00 0.00 0.00	8 2.436-02 1 0 7.856-01 1 5 6.586-00 9 5 6.586-00 9	006+00 0.00 436-02 3.61 436-02 3.61	CTTA; FEBAL; PAIS; 5900H; THRES:  CTTA; FEBAL; PAIS; 5900H; THRES:  CERB; CCCL; CCLS; CCLS; CCCLS; CCCLS; CNCLS; CNCLS; MBAP2; NDP; 57891; W CERS;  CERS;
G PROTEIN, COUPLED, SECEPTOR, BINDING BEG. Pro. B. AD 161 CC, CHEMORIUM, RECEPTOR, BINDING MCGULLETION, OF GROWTH, OF SYMBEON T, INNOVVED, IN DEG. Pro. B. AD 12 MCGULLETION, OF GROWTH, OF SYMBEON T, INNOVVED, IN DEG. Pro. B. AD 12	12 1.06-07 1.06- 13 1.06-07 1.06- 27 1.46-07 1.07- 9 1.46-07 1.07- 9 1.46-07 1.07- 9 1.46-07 1.07-		0 8.916-01 9.816-01 0 8.506-01 9.806-01 0 8.506-01 9.806-01	0.70 C1Q8P; CC 6 0.00 1 0.00 0	1 1.675-01 7.665-01 1 9.905-02 6.865-01 5.915-01 8.515-01	0.00 0.00 1.62 BAMB; CC 5.03 CC123 0.00	5 6.585-00 9 5 6.585-00 9 14 2.815-00 2 1 3.186-00 7 1 3.186-00 7	076-06 1.66 236-06 1.50 236-06 1.50	9 CDEBR, CCL1; CCL26; CCL26; CCL21; CDE2; CUCG; CNCL12; CNCL5; MRAP2; NDP; SFRP1; W CCL22 0 FRG
NEGATIVE RESOLUTION OF GROWTH OF SYMBONT IN DEGL PIO. 8, AD 13 SEGULATION OF GROWTH OF SYMBONT IN HOST DEGL PIO. 8, AD 13 CELLULAR DIVELENT MORGANIC CATION HOMBOTASIS DEGL PIO. 8, AD 213	9 1.46-07 1.076- 9 1.46-07 1.076- 44 2406-07 2.035	-05 7.88 CAMP, COME, RICH, R.I. 1 -05 2.20 ADCEMP (2 AMP, AGTR 2 -05 2.51 CRIC (2 CMM) (3 CMM) (	9 8.56-01 9.80-01 8.56-01 9.80-01 4 1.07-01 7.56-01 2 5.16-01 9.17-01 7 8.46-02 7.06-01 5.16-01 9.17-01	000 000 128 ADRAIA; B	5.91E-01 8.52E-01 5.91E-01 8.52E-01 5.28E-01 8.52E-01	0.00 0.00 0.00	1 3.16-01 7 1 3.16-01 7 1 3.16-01 7 18 1.96-02 1 16 1.61-03 3 9 2.31-01 6 16 1.61-03 3	236-0s 1.50 236-0s 1.50 736-0s 1.60	O BING O BING O MING S ANG, ATP282; CCKBR, CCL1; CCL12; CCR2; CSR2; CSHR1; CHCL12; CHCR2; DR01; EDN2; GNI
MEASTING SEGLECTION OF GEORGIES OF SYMMOTORY BY SEGLECTION, B, AD 11 MICHAEL PROVINCE OF THE PARTY OF THE PAR	28 2.834-07 2.025- 28 2.834-07 2.025- 22 2.834-07 2.025- 22 2.006-07 2.126-	06 2.53 OX.11; IBHN; IBMN; IBM	2 5.16E-01 9.77E-01 7 8.66E-02 7.06E-01 2 5.16E-01 9.77E-01 1 9.95E-01 1.00E-00	128 ADRATA B 0.98 CXCR6; RB 6 129 APSH; C1R; 0.98 CXCR6; RB 6 0.16 IFPKS	1.18-01 6.86-01 6.98-01 8.56-01 1.18-01 6.86-01 6.28-02 6.86-01	1.88 GNG10; PO 0.94 DPP6; PRO 1.88 GNG10; PO 2.69 CAM66; RG	16 1.415-03 3 9 2.315-01 6 16 1.415-03 3 7 5.655-02 3	966-02 2.24 966-05 1.26 966-02 2.24	6 MINCE ATTRODE; COCKE, COLE; COLE; COCKE; CORRE; CORRE; COCKE; COCKE
DEVALENT_NOBERANC_CATION_PROMISOTASS DESC_PLO_E_AD 228 DESCENSE_DESC_DENALING_PATHERY DESC_PLO_E_AD 172 CALCUM_JON_HOMOGRAPS DESC_PLO_E_AD 226  CALCUM_JON_HOMOGRAPS	86 1176-07 2285- 38 1366-07 2385-	-05 2.15 ADCHAPI, ADM, AGTR 2 -05 2.34 BASGREY, CML12; CD -05 2.17 ADCHAPI, ADM, AGTR 2	7 S.86E-02 6.28E-01 8 9.8E-01 1.00E+00 6 5.29E-02 6.08E-01	134 ADRAIA; B 052 CKCRG; TIA 136 ADRAIA; B	8 5.725-01 8.525-01 6 3.375-02 5.676-01 8 5.386-01 8.526-01	0.86 CCL23; HRI 2.27 DOCK2; PB	19 1.985-02 1 16 4.725-02 2 19 1.175-02 1	736-01 1.63 866-01 1.53 326-01 1.71	8 ADDCT; PEGGGG, COCTE; CCCE; CCCCE; CCCCE
### SECURATION, 07 1, CELL, particularithmon ### SECL, Puc. 8, Ab 97 21 CELL, particularithmon ### SECL, Puc. 8, Ab 97 21 CELL, particularithmon ### SECL, Puc. 8, Ab 97 21 CELL, particularithmon, particularith	28 4.276-07 2.896- 18 4.466-07 2.986- 46 4.306-07 2.916-	-05 3.05 CCL10; CCR2; CD226; C -05 3.62 CD96; ULR82; CD236; I -05 2.12 CSCR3; H6H2; CH8M 1	9.865-01 1.005-00 7.795-01 9.805-01 2.665-01 8.305-01	028 HPX; TAP1 1 064 LERB2; KLR 6	5 236-01 8:35-01 5 236-01 8:35-01 6 396-02 3:23-01 6 396-02 3:23-01 5 215-01 8:15-02	0.92 TGF81 4.99 ITGR2; MIC 1.41 CHRNE; GR 1.41 CHRNE; GR 0.92 DP9C; PRO 0.97 CC122; HRI	9 1.43E-02 1 3 4.02E-01 8 27 3.86E-05 4	665-01 2.15 055-01 1.10 025-09 2.28	9 CLOTS; 1996; CLESA; KLESA; KLESA; KLESA; KLESA; TRICE: CECONOMIC; CLESA; KLESA; KLESA; CLESA; CLESA; TRICE: CHEMIS; CENET; ADRACE; ADRACE; CROCS; CENEZ; FREC; GARREC; GARRE
MATTER SERVICE AND ADMITTANT SERVICE AND ADM	66 4705-07 2,105- 22 4,805-07 2,126- 42 4,885-07 2,165- 22 6,955-07 4,86-	-05 2.12 CYSUTRI; HONG; CHOM 2 -05 2.68 GFR; GFD; CTSC; SLANS 1 -05 2.21 ADCHAPT; ADM; AGTR 2 -06 2.99 ADAMR; AMICAT; CCI:	2 2.66E-01 8.30E-01 7 9.92E-02 7.36E-01 8 1.07E-01 7.56E-01 8 2.68E-01 9.06E-01	113 ADCHAPIR 136 APRIC (18: 128 ADRAIA; B 111 CLL24; EDB 0.77 HBBCOX; HB	2.125-01 8.136-01 2.125-01 8.136-01 2.066-01 8.526-01 8.496-01 8.526-01 9.276-04 2.146-01	0.92 DPPG PRD 0.97 CCL23; HRI 4.78 CCL23; HRI	27 1866-05 4 27 1866-05 4 11 8.765-02 1 18 1276-02 1 8 4.165-02 2	856-01 1.51 356-01 1.77 626-01 1.90	### CHARGE CARREST, EMBASE CARREST, EMBASE CARREST, CARRE
	23 £55£07 £55£ 26 7.20£07 £55£ 9 £66£07 £36£ 15 £66£07 £36£	2	3.68E-01 9.08E-01 7.84E-01 9.80E-01 9.75E-01 9.80E-01 7.88E-01 9.80E-01	100 COM-100 CO	1,000   1,00	0.60 CL122; H80 0.62 TG811 4.59 IFG81; MC 1.61 CS9N; G8 1.62 CS9N; G8 0.00 CL122; H80 0.00 CL122; H80 0.00 CL122; H80 0.00 CS9 1.63 CD8066	8 4.165-02 2 9 2.545-02 1 1 3.625-01 7 7 2.345-03 5	995-01 1.96 645-01 1.30 325-02 3.41	9 CLOTS; GBSR1; FMG; B1R; B224; B236; B2794; B1R1; TBR21 B234 1 FMG; B224; B236; BARD; SS; MEDP; TMSS1
HEALTON, G., MITHERINE, I.J., PROGETTON SCI., Ju., J., 40.0 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	15 8.664-07 126: 15 8.664-07 126: 26 1.141-06 8.106: 42 1.561-06 9.670: 46 1.861-06 1.161- 18 2.001-06 1.206:	-05 4.00 ADMR AGTR; AMC 1 -05 2.00 ADMR AGTR; AMC 1 -05 2.00 ADMR AGTR; AMC 1 -06 2.00 AC CUP; DHSO; DHS 1 -06 3.31 CL19; CC12; CC12; CC	7.895-01 9.805-01 7.896-02 9.805-01 2 1.896-02 7.715-01 5 8.596-02 9.806-01 2 9.886-01 1.005-00 4.986-03 9.176-01	0.57 C1Q8P, RS1 1 0.57 C1Q8P, RS1 1 1.32 ARRIGITIE, 0 0.78 C(32P, CD) 0 0.56 ARCA12, D) 0 0.88 C1Q8P, CA	1 2.98-01 8.03-01 1 2.98-01 8.03-01 2.98-01 8.03-01 3.03-01 8.03-01 1.28-01 8.35-01 4.97-01 8.83-01	1.63 CDM16 1.63 CDM16 2.81 CC122; Hib 1.19 ITG82; MA 1.62 AMR3C2; FJ 1.13 VSGFA	7 2.86540 5 7 2.86540 5 9 6.06542 3 15 1.28541 4 10 3.86542 2 6 5.26542 2	221-02 2.41 176-06 1.70 726-06 1.33 236-06 1.53	0 IEJAA   IBAQ IEJA, IEJAR (BAKE; IGLI; MIPP; THIGGI   IBAQ IEJA, IEJAR (IBAC), IEJAR (IBAC), IBAQ IEJAR (IB
BEGULATION, OF LIUROCYTE, CHEMOTAKE DEGC, Pro, B., AD SI BEGULATION, OF JAPHA, BETA, T. CELL, PROLIFERATION DEGL, Pro, B., AD 21 CYTORINE, SIGNALINE, N., RAMAINE, SYSTEM DEGL, Pro, B., AD 215	18 2.045-06 1.205- 10 2.146-06 1.266- 42 2.366-06 1.306- 18 2.666-06 1.536-	-06 3.31 CCL10; CCL2; CCL3; CC -06 5.33 BLA; CCR2; CD2; CD3 -06 2.08 BF9; FTMG; USP10; G	4.985-01 9.1%-01 9.215-01 9.886-01 7 6.785-01 9.625-01 5.135-01 9.1%-01	0.98 C1Q8P; CA 1 0.00 (F190; FCGF 0.96 85T2; HMC 0.	4.076-01 8.536-01 0 6.286-01 8.536-01 0 7.486-01 8.566-01 1 2.716-02 5.876-01	1.13 VSSFA 0.00 0.61 SNAR2; VC 3.32 CDMMG; TI 3.32 CDMMG; TI	6 5.205-02 2 1 4.695-01 8 11 4.865-01 8 9 1.865-03 4	995-06 2.03 656-06 0.97 926-06 1.00	2 CHCL12; EDN2; ILZNA; SLITZ; THRES; THRES 1 ILZNA 1 I
BEQUIATION OF PRODUCTION OF MOLECULAR MEDIAT DESC, Pro, B, Ab 59 BEQUIATION OF PRODUCTION OF MOLECULAR MEDIAT DESC, Pro, V, Ab 59 BEQUIATION OF COL, POSITIVE _ALPHA, BETA_T_CELL_M DESC_Pro, B, Ab 29 BENOCHTS MEDIATED IMMUNITY  DESC PRO B. Ab 210  DESCONTE MEDIATED IMMUNITY  DESC PRO B. Ab 210  DESCONTE MEDIATED IMMUNITY  DESC PRO B. Ab 210  DESCRIPTION AND PROPERTY DES	18 2,665-06 1,536- 12 2,865-06 1,636- 20 7,000,00 1,000	-04 2.31 CLIS (CLIS, CCI, CCI, CCI, CCI, CCI, CCI, CCI, C	5.13E-01 9.17E-01 5.13E-01 9.17E-01 0 9.66E-01 1.00E-00 1 4.32E-01 9.08E-01 9.66E-01 1.00E-00	0.96 8572; HMC 3 0.96 8572; HMC 3 0.00 0 1.04 C1QR; C1Q 5 0.23 ITPKB 3	8 2.71E-02 5.87E-01 8 2.71E-02 5.87E-01 0 6.80E-01 8.53E-01 5 2.27E-02 4.86E-01 1.06E-01 6.88E-01	3.32 CDM01G; TI 0.00	9 1.865-03 4 9 1.865-03 4 4 3.705-02 2 1 9.935-01 1.	586-02 2.97 586-02 2.97 626-05 2.66 306+00 0.16	THE CONTROL THAN THE CONTROL T
POSITIVE REGULATION OF T_CELL_DIFFERENTIATION DEGL_PIO_B_AD 49 NGATINE REGULATION OF LEUROCYTE_APOPTOTIC_PRO DEGL_PIO_B_AD 25 CYTOSCUE_CALCIJUM_JON_MONEOSTASS DEGL_PIO_B_AD 124 CYTOSCUE_CALCIJUM_JON_MONEOSTASS DEGL_PIO_B_AD 124 CYTOSCUE_CALCIJUM_JON_MONEOSTASS DEGL_PIO_W_AD 124	16 1316-06 1346- 11 1486-06 1386- 30 1446-06 1386- 30 1446-06 1386-	-06 2.48 ADAME; CCL19; CD80; -06 6.69 AURE; CCL19; CCL5; C -06 2.39 ADCHP1; ADM; AGTR 1	9.64E-01 1.00E+00 5.21E-01 9.17E-01 3 3.48E-01 9.07E-01	022 IFF09 2 091 ANI; IRS2 0 110 ADRAIA; C 1 110 ADRAIA; C 1	1.06E-01 6.86E-01 0 6.60E-01 8.53E-01 1 7.48E-01 8.54E-01	2.72 CD27; CD8 2.67 8/2F1; TESF 0.00 0.69 H9H1 0.69 H9H1	6 2516-02 1 2 2526-01 6 14 6286-03 9	975-06 2.36 865-06 1.56 835-02 2.06	9 GATAR, GLD; 1L234; 1L238; RARA; VINNI 6 BAMM; CNCL12 6 ATTROX, COORD; CORD; CORD; CHORD; CNCR2; DADD; EDW2; GALAR2; JPH2; CNCTR; PTGERR; SLC
REARMIN, RECURSING OF, LICEOCHYL, ADDITION, WIS DEEL, PAG, B, AD 25 CYTOSCUC, CALCIANI, DAN, HORMOSTARIS CYTOSCUC, CALCIANI, DAN, HORMOSTARIS ELIMATION, DC, CYTOSCUC, CALCIANI, DAN, CONCENTRATY, DEEL, PAG, B, AD 21 ELIMATION, DC, CYTOSCUC, CALCIANI, DAN, CONCENTRATY, DEEL, PAG, B, AD 21 ELIMATION, DC, CYTOSCUC, CALCIANI, DAN, CONCENTRATY, DEEL, PAG, B, AD 21 ELIMATION, DC, CYTOSCUC, CALCIANI, DAN, CONCENTRATY, DEEL, PAG, MA, DC, CALCIANI, DAN, CANCENTRATY, DEEL, PAG, MA, DC, CANCENTRATY, DEEL, PAG, PAG, PAG, PAG, PAG, PAG, PAG, PAG	28 1556-06 1926-	08 8.99 AUDRECCUSS CCSS C 08 2.99 ADCHREST, ADMS, AGTR 1 08 2.29 ADCHREST, ADMS, AGTR 1 08 2.47 ADCHREST, ADMS, AGTR 1 08 2.47 ADCHREST, ADMS, AGTR 1 08 2.47 ADCHREST, ADMS, AGTR 1 08 2.48 ACC 105 CCC12 CCL12 CC	1   1   1   1   1   1   1   1   1   1	110 ADRAIA; C 1 094 ADRAIA; C 1 094 ADRAIA; C 1 113 C1Q8P; CA 1	7.68-01 8.58-01 1 7.68-01 8.58-01 7.68-01 8.58-01 1 3.58-01 8.58-01	0.69 H6H1 0.54 H6H1 0.54 H6H1 1.31 V6G6A	14 6.285-03 9 13 6.405-03 9 13 6.405-03 9 5 7.695-02 3	496-02 2.06 496-02 2.06 496-02 2.06 576-06 1.96	
CHOOSE, DELEVAÇÃO, CARRANDA MARIO, CONCENTRATOR ME SER, PLA, VA, M. E. I.	16 4.474-66 2.365- 18 4.574-66 2.465- 18 4.574-66 2.465- 24 4.574-66 2.465- 25 4.574-66 2.465- 15 4.575-66 2.465- 15 4.575-66 2.465- 15 4.575-66 2.465- 15 4.575-66 2.465-	-06 2.15 8CL2; CCR2; CCR	7.17E-01 9.80E-01 7.17E-01 9.80E-01 9.86E-01 1.00E+00	0.74 AXI; CLQBI G 0.74 AXI; CLQBI G 0.35 AXI; ITPKR, 4	1 7011-01 R.S.H-01 2.SSE-01 R.S.H-02 0 R.OSE-01 R.FE-02 0 R.OSE-01 R.FE-02 0 7.OSE-01 R.SEE-03 0 7.OSE-01 R.SEE-03 0 7.OSE-01 R.SEE-03 0 7.OSE-01 R.SEE-04	0.54 H0H1 0.54 H0H1 1.31 V0GFA 0.00 0.00 0.70 CAMK4; CE 0.00 0.00	13 6.085-06 1 13 6.085-06 1 9 4.385-02 2	105-09 6.15 105-09 6.15 715-01 1.81	5 F205; GATAS; K10; K10K1; K20A; K20A; K200; K270V; K30; GS1; K10K1; PG5K0P4; RABA; T087 F205; GATAS; K10; K10K1; K20A; K20A; K20A; K20A; K10; K51; K10A; K51; K10A; I BAD4; GATAS; K20A; K20A; K20A; K20A; K50A; K50A; K10A; I BAD4; GATAS; K20A; K20A; K20A; K20A; K50A; K50A; K10A;
CONTRACTOR   CARRELET OF THE PARTY   CARRELT OF THE PARTY	15 455.06 2.465.16 15 455.06 2.465.16 15 455.06 2.465.16 15 455.06 2.465.17 13 4551.06 2.465.17 13 4551.06 2.465.17 13 4551.06 2.465.17 13 4551.06 2.465.17 13 4551.06 2.465.17 13 4551.06 2.465.17 13 4551.06 2.465.17 13 4551.06 2.465.17 13 4551.06 2.4651.06	48   10	7.175-01 9.805-01 9.855-01 1.005-00 1 8.465-01 9.805-01 4.685-01 9.115-01 4.685-01 9.115-01	074 ARI, (COS) C	7.50E-01 8.50E-01 7.50E-01 8.50E-01 7.50E-01 8.50E-01	0.00 0.00 0.00	4 1.396-01 4 4 1.396-01 4 4 1.396-01 4	965-00 1.77 965-00 1.77 965-00 1.77 365-00 2.77	6 COLUZI, ERNO, 1234, THOSE, THOSE  5 COLUZI, ERNO, 1244, THOSE, THOSE  5 COLUZI, ERNO, 1244, THOSE, COLUZI, COLUZI, COLU, BRICE, TRECOPE, BARA, THO  100 COLUZI, COLU
### MEADORNEY, STATE, LANSON MICE, PAR, A, M. B. 12  ***EMACHINE, STATE, LANSON MICE, PAR, A, M. B. 12  ***EMACHINE, STATE, LANSON MICE, PAR, A, M. B. 12  **EMACHINE, STATE, LANSON MICE, PAR, A, M. B. 12  **EMACHINE, STATE, LANSON MICE, PAR, A, M. B. 13  **EMACHINE, D. S. MINISTER, MICE, PAR, A, M. B. 13  **EMACHINE, D. S. MINISTER, MICE, PAR, A, M. B. 13  **EMACHINE, D. S. MINISTER, MICE, PAR, A, M. B. 13  **EMACHINE, D. S. MINISTER, MICE, PAR, A, M. B. 13  **EMACHINE, D. S. MINISTER, MICH, MICE, PAR, A, M. B. 13  **EMACHINE, D. S. MINISTER, MINISTE	13 481-06 24N- 13 481-06 24N- 1 552-06 281- 9 644-06 226- 12 655-06 236- 12 827-06 408- 12 827-06 408-	-08 3.55 C223c; CRTAN; FCRN; 1-08 3.56 C223c; CRTAN; FCRN; 1-08 5.36 C223c; CRTAN; FCRN; 1-08 5.33 AMA; C210; CC12; CC 1-08 2.21 AMA; C210; CC12; CC 1-08 2.21 ACAND; CASST; CC1; CC1 1-08 2.27 ACCADI; ASCADI; CC1 1-08 2.27 ACCADI; ASCADI; ASCADI; CC1 1-08 2.27 ACCADI; ASCADI; ASCADI; CC1 1-08 2.27 ACCADI; ASCADI; ASCADI; CC1 1-08 2.27 ACCADI; ASCADI; AS	4.91F-01 9.17F-01 5.80F-02 9.17F-01 1 1.88F-02 9.17F-01 1 9.50F-01 9.50F-01 4 7.98F-01 9.80F-01 7.98F-01 9.80F-01	0.81 PYCARD 0 1.89 NLSP2; PAY 0 0.57 AXL; ILS; IT 5	7.094-01 8.534-01 5.397-01 8.534-01 0 6.314-01 8.534-01 6.654-02 6.864-01 8.664-01 8.534-01 8.664-01 8.534-01	0.00 0.00 2.06 CAMER, CC 1.00 ARRICK; CI 1.00 ARRICK; CI 2.47 PRORK; ID 1.09 CAI; GGTT 1.09 CAI; GGTT	4 6.785-02 3 0 7.695-05 1. 1 4.265-05 8 16 5.515-08 8 22 3.265-06 1 22 3.265-06 1	006+00 0.00 265-05 1.06 785-02 1.96	0 8 IFNG  6 ADMONG BAMPY, CA2; GATAX; GLI2; IFNG; ELTA; ELZA; ELZR; ERRCET; PGLYRRY; RARA; SFR
CELLULAR, MESPONSE, TO, LIPID DEGE, Pro, JE, AD 106 CELLULAR, SESPONSE, TO, LIPID DEGE, Pro, JE, AD 106 MATURAL, SOLIER, CELL, MEDIANED_CYTOTOMOCITY DEGE, Pro, JE, AD 112 ANYWINDED, TO INSMREASEE  100  100  100  100  100  100  100	38 8.275-06 4.035- 38 8.275-06 4.035- 26 8.486-06 4.105- 27 8.086-06 4.255- 27 8.086-06 4.255-	-06 2.07 ADCHAP1; APGI; CCL2 1 -06 2.07 ADCHAP1; APGI; CCL2 1 -06 2.45 CL5C24; EL872; RAFT1 -04 2.40 ADER: CD1272 CD1275	4 7,94E-01 9,80E-01 4 7,94E-01 9,80E-01 6 7,33E-01 9,80E-01 7 7,44E-01 7,94E-01	0.81 ACP4; ASC; 3 0.81 ACP4; ASC; 3 0.80 PROX1; RM 6	8 4.66-01 8.53-01 8 4.66-01 8.53-01 4.78-03 3.32-01	2.06 CAMER; CE 1.00 ARRICE; CI 1.00 ARRICE; CI 2.47 PRORE; EP 1.00 CAMER GGTS	22 3.265-06 1 22 3.265-06 1 6 4.835-01 8 18 2.515-05 3	856-02 2.15 856-02 2.15 866-05 1.03 1150-00 7.03	BRIGE SHOPE CASE GASTER, GAST, PRICE LETT,
ANCHORED TO MEMBERNE DEG. Fr. V. A.O. 120 CYTORNE, BRIDING CHORNOR, OF SPACE STRUCKATED, GEASS DEG. Fr. J. A.O. 12 BEQUIATION, OF SPACE STRUCKATED, GEASS DEG. Fr. J. A.O. 12 BEQUIATION, OF SERVICE MEDIATED, CYTOTOCKETTY DEG. Fr. J. A.O. 12 BEQUIATION, OF SERVICE TOTAL MEDIATED, MAMMINITY DEG. Fr. J. A.O. 20 20 20 20 20 20 20 20 20 20 20 20 20 2	27 9.086-06 4.265- 18 9.586-06 4.555- 12 9.726-06 4.565- 12 9.726-06 4.565-	2.00   2.00   3.00	1 7,941-01 9,800-01 1 7,941-01 9,800-01 2 2,946-01 7,946-01 2 2,946-01 9,906-01 1 4,946-01 9,906-01 4,946-01 9,906-01	1.23 BST2; CEAC 2 1.06 CHRD; FMC 3 1.42 IF30; FCG9 1	6 4.765-03 2.325-01 6.166-01 8.035-01 6.166-01 8.035-01 8.035-01 8.035-01 8.415-01 6.935-01 8.415-01	1.07 PROBE; IP 1.09 CAI; GGTS 1.09 CAI; GGTS 2.06 IFNAR2; ILI 2.04 VOAM1	18 2.516-05 3 8 1.05-02 1 4 5.08-02 2 3 1.526-06 5	115-03 2.93 285-04 2.64 875-04 2.64	2 ACHE, CERCANE, CNTHE; FCGREE, FCKR1; GFRK2; GFCE; LVPG2; MDGA2; MFG2, MTM CER2; COSE; CNCR2; ELTF; ELER1; E226; E218A; THES1 GGREE; GGREE, CCCR2; GGREE; GGREE
HEGULATION OF LEUROCYTE MEDIATED CYTOTOCKTYT DEG FAC, B, AD 22 HEGULATION OF SYMPHOCYTE MEDIATED JAMMUNITY DEG FAC, B, AD 70 GEVCOSAMMOGETCAN, EMDING DEG FAC, B, AD 155 HOCKMANOGETCAN, BINDING DEG FAC, B, AD 155 HOCKMANOGETCAN, BINDING DEG FAC, B, AD 155 HOCKMANOGETCAN, BINDING DEG FAC, B, AD 155 HOCKMAN GEOLATION, OF CYTOCHN SECRETION DEG FAC, B, AD 52  HOCKMAN GEOLATION, DE CYTOCHN SECRETION	19 9:925-06 4.615- 32 1.045-05 4.776- 33 1.045-05 4.776-	-06 6.00 CD236; CRTAN; ICAM1 -06 2.89 CD236; CD37; CRTAN; -06 2.20 APOE; BGN; CC12; CC1 -06 2.20 APOE; BGN; CC12; CC1 -07 APOE; BGN; CC12; CC1 -08 2.20 APOE; BGN; CC12; CC1 -09 APOE; CC12; CC1 -09	1 8.285-01 9.085-01 8.165-01 9.005-01 2 7.005-03 2.205-01 2 7.005-03 2.205-01	106 LAG?, NCR 0 0.65 HPY, LMG?, 1 1.68 ANG, C1Q8 5 1.68 ANG, C1Q8 5 1.28 C036; F2R; 0	0 6.96E-01 8.52E-01 1 6.76E-01 8.52E-01 6.09E-02 6.96E-01 6.09E-02 6.96E-01	0.00 TGFB1 2.11 AGAN; CCL 2.11 AGAN; CCL	3 1.526-01 5 8 1.796-02 1 25 2.066-07 2 25 2.066-07 2	225-05 1.83 655-05 2.23 035-06 2.16	2 ILZDA; ILZDR; ELBER  2 CLCSS; IRRG; LER; ILZDA; ILZDR; ILZDRA; ELBER; TRICES  4 ABSSEP, ADMATTIS; BANNE; CHY, COPICE, FRENCY; FGE SE; FGET; FGERS; FMS; MAPENS; TGAM  5 CLCSTRE; CLCCS; GAND, FRENC; ELBER; LESS; TGE SE; FGET; FGERS; FMS; MAPENS; TGAM  6 CLCSTRE; CLCCS; GAND, FRENC; ELBER; LESS; TGET; FGET; FGET; FGES; FMS; MAPENS; TGAM  7 CLCSTRE; CLCCS; GAND, FRENC; ELBER; LESS; TGET; FGES  7 CLCSTRE; CLCCS; GAND, FRENC; ELBER; LESS; TGET; FGES  7 CLCSTRE; CLCCS; GAND, FRENC; ELBER; LESS; TGET; FGES  7 CLCSTRE; CLCCS; GAND, FRENC; ELBER; LESS; TGET; FGES  7 CLCSTRE; TGENS  7 CLCSTRE  7
POSITIVE SEGULATION OF CYTORNE SECRETION DEGL. PLO. B. AD ST  DENNISTIT. CELL. CHEMOTIANS DEGL. PLO. B. AD ST  POSITIVE SEGULATION OF COLL POSITIVE ALPHA SETA DEGL. PLO. B. AD 43  POSITIVE SEGULATION OF ADAPTIVE INMULISE SESPONS DEGL. PLO. B. AD 43	8 1126-06 5.0% 9 1176-06 5.266	-06 3.22 AM2; CCL19; CCL2; CC -06 5.69 CCL19; CCL2; CCR1; CC -06 5.05 CCL19; CD80; CD81; FC	2.54E-01 8.30E-01 8.76E-01 9.80E-01 9.14E-01 9.85E-01	128 CD34; F2R; C 000 000	7.766-01 8.666-01 0 6.036-01 8.536-01 0 6.276-01 8.536-01	0.00	7 1.165-02 1 1 3.625-01 7 1 4.665-01 8	225-06 2.57 645-06 1.36 645-06 1.03	7 CIQTNFI; CICCE; GATAL; IFNC; ILERI; E32; TWISTI CICIE 2 SARA
POSITIVE REQUIATION OF ADAPTIVE INMUSER RESPONS DEGL. PAO. 8, AD. 43 REQUIATION, OF MUSTI, COMMISSIN, PROCESS DEGL. PAO. 8, AD. 207 LYMPHOCYTE, MEDIATIO, IMMUNITY DEGL. PAO. 8, AD. 40 REGAINIVE, REQUIATION OF LYMRAL GENOME, REPULATION DEGL. PAO. 8, AD. 22	15 1196-05 5.226- 29 1296-05 5746- 22 1306-05 5.726- 12 1481-05 6.106-	- ON 2.05 AM2; AP152; AP086C 1 - ON 2.55 BATF; BCL2; CE; C7; C0	7.155-01 9.805-01 4 8.535-01 9.805-01 4 8.065-01 9.805-01	0.71 HPX; PVCAI 0 0.77 AP251; APC 1 106 C1QR; C1Q 1 109 AP066C3G 0	7.535-01 8.605-01 8.506-01 8.535-01 8.1.245-01 6.865-01 7.006-01 8.535-01	0.00 0.95 CD180; DO 2.06 CD27; CD8 0.00	4 1,655-01 5 8 7,905-01 1, 1 9,776-01 1, 2 3,756-01 7,	456-01 1.63 306+00 0.75 306+00 0.20	
Section Section Conference Confer	12 1.416-05 6.106- 34 1.526-05 6.576- 34 1.526-05 6.576-	-06 3.88 APGECA; CCC; MAN -06 2.11 APGC BGN; CCL2; CCL -06 2.11 APGC BGN; CCL2; CCL	0 4.08E-01 9.08E-01 6 4.68E-01 9.08E-01 6 4.68E-01 9.08E-01 4 1.27E-02 4.56E-01 6 1.27E-02 4.56E-01	1.03 APOSSCIG C 1.58 ANG; C1Q8 6 1.58 ANG; C1Q8 6	3 226-02 5.676-01 5 2.26-02 5.676-01	0.00 2.28 AGAN; CCL 2.28 AGAN; CCL	2 3.755-01 7 28 3.315-08 1 28 3.315-08 1	815-06 1.16 975-06 2.17 975-06 2.17	B BITTS (APP)  BITTS (APP)  BERBEY, ADMANTSE, ADRICOD, BIMPRI, CRIV, CPYELT; FEELD; FGFD; FGFD; FGFR1; FRE; HAPLIN  ABISBEY, ADMANTSE, ADRICOD, BIMPRI, CRIV, CPYELT; FEELD; FGFD; FGFT; FGFR1; FRE; HAPLIN  ABISBEY, ADMANTSE, ADRICOD, BIMPRI, CRIV, CPYELT; FEELD; FGFD; FGFT; FGFR1; FRE; HAPLIN
ISLINDOCYTE, MIDINATED, CYTOTOCOCITY DEGG, Pio. JE, AD 24 PD, 1, SSIGNALIMO POSITIVE, REGULATION; GF, HUMODAN, HAMBURE, RESPON DEGG, Pio. JE, AD 12 POSITIVE, REGULATION; GF, YOU MODERAL HUMODAN, PROPERTY DEGG, Pio. JE, AD 12 POSITIVE SEGULATION; GF, YOU MEGRATION. POSITIVE SEGULATION; GF, YOU MEGRATION. POSITIVE SEGULATION; GF, YOU MEGRATION.	10 1.65f-95 7.0 N- 7 1.74f-95 7.2 N- 26 1.93f-95 7.9 N-		1 4.95 cd 9.1% cd 0 8.35 cd 9.05 cd 1 4.76 cd 9.15 cd 1 4.76 cd 9.15 cd 1 4.76 cd 9.15 cd 0 5.36 cd 9.17 cd 0 5.36 cd 9.17 cd	0.94 PROX1; RN 1 0.00 0 0.94 HPX 0	1 1.81E-01 7.66E-01 5.86E-01 8.03E-01 0 5.86E-01 8.03E-01 0 5.86E-01 8.03E-01 5.86E-01 8.03E-01	0.00 1.28 AGAN; CCL 1.28 AGAN; CCL 2.72 NCF1 0.00 0.00 0.00 0.00 2.22 CDMMG; G	0 8.586-06 1. 0 7.366-06 1. 0 7.366-06 1. 0 7.366-06 1. 1 2.966-06 7. 12 1.276-02 1.	006-00 0.00 006-00 0.00 006-00 0.00 006-00 0.00 006-00 1.63 006-00 1.63 006-00 1.63 006-00 1.63 006-00 1.63 006-00 1.63 006-00 1.63 006-00 1.63 006-00 1.63	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
BESPONSE TO INTERFERON ESTA DEGLIPIO, B. AD 12 BEGULATION OF PROTEIN SECRETION DEGLIPIO, B. AD 118 BEGULATION OF INTERFERONS 1, SECRETION DEGLIPIO, B. AD 20	7 1745-05 7.225- 26 1935-05 7.935- 9 1965-05 8.055-	-06 6.22 ARIZ; IFTRE; IFTRE; -06 2.35 ADMR; ARIZ; CC19; 1 -08 6.80 ARIZ; CC19; CC12; CC -06 2.60 ARIS; BC12; CC; C7; CO	6.786-01 9.116-01 0 5.366-01 9.176-01 6.036-02 6.286-01	094 HPX 0 094 PYCARD 0 094 RST2 096 ANG CD36 2.27 NLRP 2 PAN 0	5.865-01 8.525-01 7.115-02 6.855-01 6.335-01 8.525-01	0.00 2.22 CD40LG; G :	1 2.965-01 7 12 1.275-02 1 1 4.635-01 8	096-0s 1.63 356-0s 1.96 656-0s 0.97	2 STATS 8 ACHS; CSQTNF3; CLECKS; FFARK; GATA3; IFNG; ELS; ELRLS; ELS; REPK; SRCINS; TWISTS 7 IFNG
HIMMORAL IMMOVE ESSPONSE DEGL. Fig. B. AD 16 PAR SIGNALING, PATHWAY DEGL. FIG. B. AD 17 CEL. SURFACE, INTERACTIONS, AT_THE_VASCULAR_WAL DEGL. Fig. B. AD 17 THE LI THARETES MINISTRUTINE THE CONTROL OF THE PARTICULAR_WAL DEGL. FIG. B. AD 17 THE LI THARETES MINISTRUTINE THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE CONTROL OF THE PARTICULAR_WALD DEGL. FIG. B. AD 17 THE PARTICULA	9 1962-05 2052- 21 2162-05 8262- 17 2176-05 9586- 21 2661-05 1066- 12 2861-05 1166- 16 2188-05 1166-	-06 2.50 ARS; BCL2; CS; C7; C0 1 -06 2.52 SORRES; CYPBE; FABI -03 2.57 MEETC; ScCANG; AMIC -03 3.55 OFS; GEOME; FAGE; BC -03 2.59 UGTZAZ; ADNER; ADN	9.705-01 1.005+00			0.00 0.00 1.76 ITGR2; GP6			
METABOLISM OF JEROBIOTICS, BY CYTOCHROME, PASO DEGL. Pro. B., AD 57 POSITIVE, REGULATION, OF ACUTE, INSLAMMATORY, PSSP DEGL. Pro. B., AD 21 POSITIVE, REGULATION, OF, INTERSEAUND, 3E PRODUCTION DEGL. Pro. B., AD 21	16 2,895-05 1146- 9 3,185-05 1246- 7 3,505-05 1246- 26 1586-05 1246-		6.53E-01 9.56E-01 9.28E-01 9.89E-01 5.10E-01 9.17E-01 7.02E-01 9.76E-01	0.97 PRF1; PTPN 0 0.80 CYP2A4; A1 3 0.00 0 0.87 CD34 0	6.451-03 2.585-01 7.586-01 8.535-01 8 2.386-02 5.576-01 0 6.385-01 8.535-01 5.916-01 8.535-01 6 8.286-01 8.536-01	1.75 (FIGAS, COV	4 2.515-01 6 3 5.516-02 3 1 3.166-01 7 9 1.166-01 4	003-64 1.70 SET-04	STATE OF THE STATE
POSTIVE SEGULATION, OF INTERELLION 18 PRODUCTION DEGL PIO, & AD 12 INTERFERON, SEGNALING DESASE DEGL PIO, & AD 12 AUTOMORIAN, THYROLO, DESASE DEGL PIO, & AD 17 DESABOURG, BINDONG DEGL DEGL PIO, & AD 17 DEMBEROURG, BINDONG DEGL PIO, & AD 17 DEMBEROURG, COLL MOGRATION DEGL PIO, & AD 17	8 1636-05 1356- 8 1636-05 1356-	-03 5.74 CDB2; FCERSC; B128; 608 2.27 BF9; FFIRM; ISP18; 6 609 5.02 CTLA; CDB2; GF8; FFIRM; ISP18; 6 609 5.02 CDB2; CDB2	7.025-01 9.796-01 1 3.185-01 9.806-01 0 8.065-01 9.805-01	0.87 CD34 0 0.84 IF30; FGS8 1 1.33 LS; PRF1 1	6 6.28E-01 8.52E-01 1 129E-01 6.88E-01 1 129E-01 6.88E-01 0 6.15E-01 8.53E-01	0.00 1.07 FNAR2; VC 3.85 CDI01G 3.85 ZFP36	9 1.365-01 4 0 7.965-01 1 3 3.155-02 2 1 4.065-01 8	88E-05 1.64 30E+00 0.00 23E-05 2.64	8 GBH; GBH; GBH; FFGT; FFT; FNG; STAT1; CAMICA; CAMICB 0 CBH; CDB; CIGR2 5 CBH2
NATURAL VILLER CELL MEDIATED IMMUNITY DEGL PIO & AD 17 POSITIVE REGULATION OF INTERESSION 1 BETA SECRET DEGL PIO & AD 17 CYTORING SECRETION 2 BETA SECRET DEGL PIO & AD 26	8 1631-65 1365- 8 1631-65 1365- 10 1321-65 1.605- 10 1321-65 1.605-	-03 5.02 CTL-Mc CEMBR, FASSO, 10-03 5.03 CTL-Mc CEMBR, FASSO, 10-03 5.03 CTL, COST,	9 8564-01 9.866-01 8.664-02 9.866-01 1 3.184-02 8.866-01 1 2214-01 7.566-01 7.664-02 9.806-01 5.664-02 9.376-01	000 133 PROSE; RM 1 200 MASP2; PM 0 044 MG6A2 054 MG7; PM 0 058 MG6A2 054 MG7; PM 0 058 MG7; PM 0 05	615E-01 R.52E-01 6.15E-01 R.52E-01 6.65E-01 R.52E-01	0.00 0.00 0.00	0 7.965-05 1 1 4.065-05 8 2 2.676-05 6 1 5.676-05 9	006+00 0.00 096-00 1.15 906-00 1.50	0 5 ISNG O GATAR VECNI
NATURAL WILLEY, CREL, ACTINATION  REQUIRED OF CHRONIC PRODUCTION INVOCATED IN DEGL. PIO. B. AD 36  INTERPROCYTE, DISFERENTIATION  MAIABAM  AND	12 3.88E-05 1.41E- 30 4.10E-05 1.47E-	-03 4.00 (D2; E12R; E21R; EER -03 3.55 (D3R; FCERDS; FORP2; -03 2.12 (D3R; ECC2; EER); CAR -03 3.18 (D3R); HBA1; HBA2; H	5.64E-01 9.1%-01 5.11E-01 9.1%-01 9.86E-01 9.86E-01 8.62E-01 9.80E-01	0.97 AXI; RAB23 1 0.94 8572; HMC 3 0.68 AXI; BAX1; 6 0.69 MC2; W291	0 6.555-01 8.555-00 6.555-01 8.555-01 6.555-01 8	2.51 9/271 3.63 TGF81; TGF 3.66 CD801G; D 6.96 ITGR2; TGF	1 5.635-01 9 2 4.196-01 8 5 8.436-01 1 6 2.086-02 1	756-05 0.75 265-05 1.05 266-00 0.65 765-00 2.65	0 mm.
POSITIVE_REGULATION; OF_MAX_STRIT_CASCADE DEGL_PIO_B_AD 47 POSITIVE_REGULATION; OF_MAX_STRIT_CASCADE REGEREN; REGULATION; OF_MANUEL SYSTEM_PROCESS DEGL_PIO_B_AD 166	16 4.114-05 1.476- 16 4.115-05 1.47X- 16 4.115-05 1.47X- 12 4.475-05 1.57X- 15 4.455-05 1.56X- 16 4.573-05 1.28X- 6 5.372-05 1.28X-	-03 3.88 COMP; HANC; HANC; H HANC; H HANC; H HANC; H HANC; H HANC; COCK; COT; ES HAS AGAP; COCK; COT; ES HANC; COCK; COCK; ES HANC; COCK; COCK	\$ 5,001-01 9,176-01 1 5,001-01 9,176-01 9,176-01 9,176-01 9,166-01 9,166-01 1 6,001-01 9,466-01 9,466-01 9,466-01 9,466-01 9,466-01 9,466-01 9,466-01	0.96 F2R; HPX; I 0 0.96 F2R; HPX; I 0 0.68 AXI; 8512; S	7.58E-01 8.58E-01 7.58E-01 8.58E-01 7.76E-02 6.85E-01	0.00 0.00 1.97 AMBP; MK	7 6.001-03 9 7 6.001-03 9 15 1.766-02 1 5 9.386-02 4 6 5.586-02 3 0 7.066-01 1.	236-02 2.90 236-02 2.90 656-06 1.70	0 CLCF1; 1996; 113; 1234; 1236; 12384; 1511 CLCF1; 1996; 113; 1234; 1236; 12384; 151 6 6896; 1971; 1834; 11374; 12384; 1334; 1344; 1910; PGLYSP4; 57894; 57891; 5172; 50911; Tr
POSITIVE, SEGULATION, OF, CYTOKINE, SEGNATIVETTE, PARE DEGL. PAL. SL. AD 53. POSITIVE, SEGULATION, OF, EXMININOTED SEGULAND, S.A. D 59. HEPARAN, SULFATE, SCREOTRANSFERASE, ACTIVITY DEGL., PAL., S., AD 50.	15 4.65-05 1.586- 16 4.636-05 1.626- 6 5.376-05 1.886-	-08 3.02 8CLR; CARD11; CCR2; I -08 2.89 ADAMR; CCL19; CDR0; -08 6.40 HSSST1; HSSST2; HSSS	6.03E-01 9.80E-01 8.00E-01 9.80E-01 9.80E-01	0.86 HM0X1; IC 0 0.58 AX1; ITPKR; 3 0.00 1 1.68 CA6; SLGA 1	7.796-01 8.666-01 8 3.716-02 5.876-01 1 7.686-02 6.866-01	0.00 3.32 C027; HZF 6.54 HG35T4 2.42 CM	5 9.385-02 4 6 5.585-02 3 0 7.056-06 1	02E-01 1.86 01E-01 1.96 00E+00 0.00	6 (RNG; (L1E); L0; THES; THE? G GATA; GEO; (L2A; (L2B; RABA; VIN1 0
BIGULATION OF COM POSITIVE_ALPHA_BETA_T_CELL_D_DEGL_PIO_E_AD 27 PRIMARY_MAILUNDEFICENCY DEGL_PIO_E_AD 32 BIGULATION OF BLOOD_COMBULATION DEGL_PIO_E_AD 54	10 \$665-65 1925- 10 \$665-65 1925- 11 \$665-65 1925- 15 \$675-65 1925-	-03 6.40 MSGTT1 MSGT2 MSG -02 3.65 CA12 CA22 CA22 CA22 -03 3.65 CL156 C000, C000, FC -03 2.66 MCC C006, C000, FC -04 2.66 MCC C006, F12 F12 F1 -04 2.66 MCC C006, F12 F12 F1 -05 C000, C000, C000, F12 F12 F1 -06 2.26 MCC C006, F12 F12 F1 -07 C000, C000	1.88E-01 7.71E-01 0.58E-01 9.88E-01 6.68E-01 9.88E-01 6.33E-01 9.08E-01	0.00 0.71 SLINC TAP1 1 1.05 CD36; F28; 2	2 2,035-01 8,015-01 0 6,706-01 8,516-01 4,926-02 6,516-01 1,256-01 6,886-01	0.00 4.09 RAG2; CD4 2.42 PDPN; PRO	4 2.985-02 2 4 2.985-02 2 0 9.085-05 1 3 4.145-05 8	115-05 2.85 305+00 0.00 215-05 1.08	9 OAZ PEDERIC SICIAN) SICON 9 GATAZ EZA EZA RASA 0 GATAZ EZA EZAS RASA 0 COMEZ HÁSI, THESI
BEGULATION OF JERNOSTASE BEGULATION OF JERNOSTASE BEGULATION OF COMBILITION BEGULATION OF BEGULATION OF BEGULATION BEGULATION OF BEG	11 5.68-05 1.92- 15 5.57-05 1.92- 15 5.57-05 1.92- 15 5.57-05 1.92- 16 5.78-05 1.94- 16 5.78-05 1.94- 9 6.662.65 1.94-		8.236-01 9.086-01 4.236-01 9.086-01 4.236-01 9.006-01 9.236-01 9.006-01 5.296-01 9.776-01	000 071 BLINC, TAP1 105 CD4; F2R; 105 CD4; F2R; 069 AN; HM00 094 CD4; F2R; 2.52 NL892; PM 129 ANG; CD8 129 ANG; CD8	6 1.251-01 6.385-01 1.251-01 6.385-01 1.251-01 6.385-01 2.1176-01 8.535-01 1.661-01 7.261-01 6.216-01 8.535-01 2.316-01 8.276-01	4.09 RAG2; CD8 2.42 PDPN; PRO 2.42 PDPN; PRO 1.23 MILR1; TGI 2.18 PDPN; PRO	1 4.165-00 8 3 4.165-00 8 6 3.135-00 7 3 4.865-00 8	295-00 1.08 235-00 1.15 925-00 0.97 245-00 1.08	C CHMS2; MMSC; THEGS  C MMS2; MMSC; THEGS  B MMM; EXIST, PECKEP 555P4; SDX11; VTCW1  C CMMS2; MMSC; THEGS  B MSC
March 1997   1	8 £06£-05 2.035- 19 £311-05 2.105- 19 £311-05 2.105- 7 £506-05 2.135- 22 £356-05 2.135-	-03 4.36 AMAZ, CCL19, CCL2, NS03 2.56 AMAMS, AMAZ, CCL19, -03 2.56 AMAMS, AMAZ, CCL19, -03 5.33 AMAMS, CCL2, CCL2, CC03 5.33 AMAMS, CCL2, CCL2, CC04 2.37 CCL19, CCL2, CCL2, CC05 CCL2, CCL2, CCL2, CC05 CCL2, CCL2, CCL2, CC06 CCL2, CCL2, CC07 CCL19, CCL2, CCL2, CC08 CCL2, CCL2, CC08 CCL2, CCL2, CCL2, CC08 CCL2, CCL2, CC08 CCL2, CCL2, CC08 CCL2,	426E-02 5.736-01 2.08E-01 7.90E-01 2.08E-01 7.90E-01 5.60E-03 9.376-01	### APPLIANCE OF THE PROPERTY	5 2.11-01 8.28-01 2.21-01 8.27-01 2.21-01 8.27-01 5.37-01 8.28-01 1.26-01 6.88-01	1	1 4.265-01 8 10 4.626-03 7 10 4.626-03 7 0 7.636-01 1	996-02 2.47 996-02 2.47 906-00 0.00	8 INSG 7 ACHS; CROTNES; CLECKS; GATAR; FING; ILIR; ILIRS; ILIR; RRPH; TWISTS 7 ACHS; CROTNES; CLECKS; GATAR; FING; ILIR; ILIRS; ILIR; RRPH; TWISTS 9 CREUZ; DECAM; EDINZ; FGF SP; ILIZA; NTF2; NTRIC; SEMADA; SUTZ; THRES; THRES
T COLL DEFENDATION OF COLL ACTIVATION DEGLINO, & AD 99 INGERTINE REGULATION OF COLL ACTIVATION DEGLINO, & AD 106 IMMUNOLOGICAL SYMPSES NACIONAL AN 107 IMMUNOLOGICAL SYMPSES NACIONAL AN	22 6.756-65 2.216- 22 6.756-65 2.216- 23 7.086-65 2.296- 9 7.257-65 2.486- 9 7.257-65 2.486-	-03 2.37 CCL19, CCL2; CCL2; CCL3; CC -03 2.37 BATS; BCL2; BLM; CAR -08 2.31 APOE; CCR2; CD276; C -09 4.37 CD81; CD61; CD84; G	8.11-01 9.80-01 6.645-01 9.56-01 9.80-01 9.56-01	081 SAA1 149 ARTN; CLQ 3 059 BCL2; EDM 086 ARE; HMCD 0	2.476-03 2.026-03 2.476-03 2.026-03 2.256-01 8.286-03 0.686-01 8.086-03	0.00 1.98 PTPRO; TG 3.96 DOCK2; HZ 1.22 MLR1; TGI 0.00	7 2615-06 1 1 1 8.605-09 1 4 6.675-01 1 2 6 3.825-01 7 0 8.515-01 1 2 2 2.225-01 6	2.17 306+00 0.76 816-01 1.10 306+00 0.76	7 CECLEZ, DECAM, CDM2, FGF-93; ILIZAN, NTFR; NTRICE; SEMARAN, SLITZ; THESE; THESE 9 FSDS, GRATAS, FROS, TRISE; SERVEI; STCN1; VTCN1 0 BMMH; ILZEN, FGC.YRPH; SERVEI; STCN1; VTCN1
POSITIVE REGULATION, OF INTERECUON 1, BETA PRODUCTION DEGLES NO. 8, AD 22 REGULATION, OF INTERECUON 1, BETA PRODUCTION DEGLES NO. 8, AD 23 REGULATION OF J. CELL, MEDIATION DIMMUNITY DEGLES NO. 8, AD 23 REGULATION OF J. CELL, MEDIATION DIMMUNITY DEGLES NO. 8, AD 23 REGULATION OF STREET, ADMINISTRATION OF	2 10000 200000 200000 200000 200000 200000 200000 200000 200000 200000 200000 200000 2000000	262   263   264	1	000 1.48 NLSP2; PAA 2.06 F34; CSTP1 0.48 F34; CSTP1 0.68 CLOSP; CS	\$ 2,075 00 1,005 00 6 \$ 1,016 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.06 01 5,015 01 \$ 0.07 01	0.00 0.00 0.00 2.33 H8H1	2 2.25-01 6 3 1.66-01 5 3 1.66-01 5 3 1.126-01 4	596-00 1.66 616-00 1.77 616-00 1.77	9
SEGULATION OF ACUTE INFLAMMATIONY SESSIONSE DEGLE PLO, B, AD 20 ANTIGEN BINDING DESCRIPTION OF ACUTE INFLAMMATIONY SESSIONSE DEGLE PLO, B, AD 50 ANTIGEN BINDING DESCRIPTION SECURITY SEGNATION PATHWAY DESCRIPTION SECURITY SEGNATION PATHWAY DESCRIPTION SECURITY SEGNATION PATHWAY DESCRIPTION SECURITY SEGNATION PATHWAY DESCRIPTION SECURITY SEGNATION SECURITY SECURI	9 9 2,366.65 2.46.65 11 1 10.00 12.0	4.81 ADREC CHRM1; CHRM -03 2.58 ADMAR, ADCVAP1; ALI -03 3.28 CDR; (SHA1; ISHA2); -03 4.69 CQ2-CVI-CVI-CVI-CVI-	5.88E-01 9.30E-01 7.42E-01 9.80E-01 1.90E-01 7.89E-01 6.68E-01 0.00E-01	0.81 ADRAIA; H 1 0.68 C108P; GS 0 1.45 IGHGR; LAC 1 0.60 XCR1	2.086-01 8.026-01 7.666-01 8.026-01 1 2.866-01 8.026-01 0 6.276-01 6.036.01	2.33 HRH1 0.00 1.68 CD209 0.00	4 1.886-01 5 1 7.306-01 1. 5 1.366-00 1	2.05 856-01 1.56 106+00 0.50 826-02 0.41	9 ADBADA, ADBADA, CARBAD 6 GIR, LIE PEGEST THE ST 11 GIR. CARBAD 12 GIR. CARBAD 1
REQUILITION, OF INFLAMMATORY RESPONSE TO ANTICE DEGL FIG. A. AD 19 CHEMONINE INSTINUTE SEGNATION PATHWAY DEGL FIG. V. AD 19 REQUILITION, OF CALCIUM INSTINUTED SEGNATING DEGL FIG. A. AD 34	8 9.765.05 2.965 8 9.765.05 2.965 11 1.065.04 2.265	03 4.69 ADCNOT; COZ; COZ; COZ; COZ; COZ; COZ; COZ; COZ	6.685-01 9.585-01 6.685-01 9.585-01 8.865-01 9.815-01	060 GP12 0 060 XCR1 0 033 SLA2 1	0 6.275-01 8.535-01 0 6.275-01 8.536-01 1 2.536-01 8.536-01	0.00 0.00 1.92 TRAT1 2.56 F202; GRM	4 1885-06 5 1 7.205-06 1. 5 1265-00 2. 0 8.165-06 1. 5 1265-00 2. 1 6.805-06 1.	006+00 0.00 826-02 5.13 906+00 0.57	0 CERC CORP. CORE.; CHICLE; GWELT O 0 CERC; CORE.; CORE.; CRICLE; GWELT O 1 LIGAM
PROGRAMMENT OF CYCLES PROCEDURES METABOLIC PROCED DEGLE PRO. BL. AD 102 DENDRITIC, CELL DEFERENTIATION DEGLE PRO. BL. AD 11 NGGETTING REGULATION, OF JUMILIUM, RESPONSE DEGLE PRO. BL. AD 51 POSITIVE, REGULATION, OF CELL INJUING REGIO RAY & AN 55	11 1066-04 2266- 22 1086-04 2366- 6 1106-04 3366- 14 1116-04 2366- 10 1126-04 2366- 10 1126-04 2366- 10 1126-04 2366- 10 1126-04 2366- 18 1186-04 2366-	-02 2.65 CC2; CC12; CD3; CC9 -03 2.50 ACMP4; ARM, ARM -03 58 ANTH; CC18; CC05; C -03 2.83 ANTH; CC18; CC05; C -03 2.84 CD22; CC19A; CC87; C -04 2.86 CD22; CC19A; CC87; C -05 2.86 CD22; CC19A; CC82 -05 2.86 CD2; CC22; CC88; L1: -05 2.86 SC2; CC22; CC88; L1: -06 2.86 SC2; CC22; CC88; L1: -07 2.87 AMBCA2; CC12; CC14 -08 2.51 AMBCA2; CC22; CC88; L1: -09 2.51 AMBCA2; CC22; CC88; L1: -09 2.51 AMBCA2; CC22; CC88; L1: -09 2.51 AMBCA2; CC24; CC44 -09 2.51 AMBCA2; CC24 -09 2.51 AMB	# #805 cd 9 806-cd 9 806-cd 1	100 ADCHAPIR 6 103 AXL 0 022 GPH2 3 117 LAG-MCH	2.531-01 8.531-01 8.571-02 8.58-01 8.578-01 8.531-02 9.580-01 8.531-03 6.660-01 8.531-03 6.660-01 8.531-03 6.660-01 8.531-03 6.660-01 8.531-03 6.660-01 8.531-03	2.56 F202; GRM : 0.00 3.85 AMBP; TGF 0.00	10 2.596-02 2 0 7.206-01 1 4 1.926-01 6 4 3.706-02 2	006+00 0.00 006+00 1.53 426-01 2.53	ADBREZ, CERREL, CUCKZ, DRD1; GARGRZ; MCSR; MRAP2; MTNRLA; NPRL; NTRK2  BERLS; NZ790; NZ2; ROAKS  BRAG (EZRA; NZ20; KRRL)
POSITIVE REGULATION OF INTESPERON CAMMANA PRODUC DESC. Pro., S., AD 29 POSITIVE REGULATION, OF INTESPERON, GAMMANA PRODUC DESC. Pro., VI, AD 29 REGATINE REGULATION, OF JESPECUCTIVE PRODUCTS  DESC., Pro., S., AD 76	10 1126-04 2,296- 10 1126-04 2,296- 18 1186-04 2,516-	-03 3.68 BCL2; CC92; CD3; ILL: -03 3.68 BCL2; CC92; CD3; ILL: -03 2.52 AP086C3A; CCL1; CCU	8.355-01 9.805-01 8.355-01 9.805-01 5.915-01 9.305-01	117 LAG2, NCK 0 0.39 PYCARD 0 0.39 PYCARD 0 0.89 APOSSC3G 2	6.805-01 8.535-01 6.805-01 8.535-01 2.185-01 8.145-01	0.00 0.00 1.72 GPR149; H	4 1.02-01 b 4 3.705-02 2 7 3.005-04 1 7 3.025-04 1 5 2.795-01 6	735-02 6.70 735-02 6.70 905-01 1.29	0 5205; E18; 1224; E278; E2784; S61; KLRET 5205; E18; 1224; E278; E278; E178; S61; KLRET 8 8894; E775; S19; S195; S195; S195;
HIPTORIAL JAMESTICS (CENTRY )  HIPTORIAL JAMESTICS (CENTRY )  HIBERATORIS (F. STOTOMS, HOOMSTATE, PROCESS  LIMINGOUTH, HOOMSTATE, PROCESS  LIMINGOUTH, HOOMSTATE, PROCESS  HIBERATORIS (F. STOTOMS, HOOMSTATE,	27 128-04 2655- 27 128-04 2655- 19 128-04 2765- 25 1465-04 428-	-02 2.09 BRCS; CST7; CST8; OV 1 -02 2.09 BRCS; CST7; CST8; OV 1 -03 2.44 BCL3; CARD11; CSR2; I -03 1.87 ADCNAP1; APG; ARC; 1	6 1296-01 7.586-01 7 5296-01 9.376-01 8 6.666-01 9.086-01	131 8572; COL2 5 131 8572; COL2 5 0.96 HMCOX1; IC 1 1.02 ADRAIA; C 6	6 4.025-02 6.015-01 4.025-02 6.015-01 5 5.436-01 8.526-01 8 2.766-01 8.526-01	1.72 GPR169; H 2.27 AMBP; CDI 2.27 AMBP; CDI 0.79 RNF128 1.31 GRM3; HR	16 1305-03 3 16 1305-03 3 8 4.685-02 2 21 9.815-06 3	926-02 2.36 926-02 2.36 796-05 1.86 176-02 2.06	LEREL_LIPMS, CER. BOOD
OHMORONE, RECEPTOR, ACTIVITY DEGL., Pro., R., Ab 20 G. PROTEIN, COUPLED, CHEMOATTRACTANT, RECEPTOR, At DEGL., Pro., R., Ab 20 LYMPPINCTTE, MEGATION DEGL., Pro., R., Ab 20	27 128-04 265-5 10 138-04 276-5 25 1465-04 426-5 8 1505-04 426-5 8 1505-04 426-5 8 1505-04 426-5 8 1505-04 426-5 8 1505-04 426-5	-02 1.87 ADCHOP1; APG; ARC; 10-03 4.26 CDR; CDR; CDR; CDR; CDR; CDR; CDR; CDR;	2,975-01 9,085-01 2,975-01 9,085-01 2,975-01 9,086-01	102 ADBATA; C 1 113 CXCRG; XCS C 113 CXCRG; XCS C 113 ARTN; SAA 057 SEMARA	1	0.00 0.00 0.00	# 446-02 J 11 986-04 4 5 1,03-03 4 5 1,03-03 4 2 4,03-02 2 0 8,36-64 1 5 1,03-03 4 5 1,03-03 4 5 1,03-03 4 5 1,03-03 4	215-02 6.87 215-02 6.87 875-01 2.92	7 CERG CORR: CORR.; CHICA; GREAT 7 CERG; CORR.; CHICA; CHICA; CHICA; GREAT 2 GETTA; ERT; TRACE
FORTHER, DISEIDATING OF CYTHORN PRODUCTION, NYTE DRIGE, NO. 8, NO. 20 SEGULATION, OF J. MEMPEY, LYVE, IMMUNE, SESSONES DRIGE, NO. 8, NO. 20 CHEMORIUS, SECEPTOR, ACTIVITY  G. PROTEIN, COUNCED, CHEMORITEM/CENT, SECEPTOR, M. DEG, July, NO. 20 SEGULATION, OF J. MEMPEY, LYVE, IMMUNE, SESPONES DRIGE, No. 10, NO. 20 SEGULATION, OF J. MEMPEY, LYVE, IMMUNE, SESPONES DRIGE, No. 10, NO. 20 SEGULATION, OF J. MEMPEY, LYVE, IMMUNE, SESPONES DRIGE, NO. 10, NO. 20 SEGULATION, OF J. MEMPEY, LYVE, IMMUNE, SESPONES DRIGE, NO. 10, NO. 20 SEGULATION, OF J. MEMPEY, LYVE, IMMUNE, SESPONES DRIGE, NO. 10, NO. 20 SEGULATION, OF J. MEMPEY, LYVE, IMMUNE, SESPONES DRIGE, NO. 10, NO. 20 SEGULATION, OF J. MEMPEY, SESPONES DRIVE, NO. 20 SEGULATION, OF J. MEMPEY, SESPONES, SESPONES DRIVE, NO. 20 SEGULATION, OF J. MEMPEY, SESPONES DRIVE, NO. 20 SEGULATION, OF J. MEMPEY, SESPONES,	8 1505-04 4285- 8 1505-04 4285- 8 1506-04 4285- 8 1506-04 4285- 9 1506-04 4285-	-03 4.36 AMAMB, CCL2; CCL2; C -03 4.36 CDB, CCL19; CCB, CDB, CDB, CDB, CDB, CDB, CDB, CDB,	9.216-01 9.886-01 9.216-01 9.886-01 1.076-01 9.086-01 1.076-01 9.886-01 9.216-01 9.886-01	000 000 000 000 000 000 000 000 000 00	0 6.36-01 8.52-01 0 6.36-01 8.52-01 0 6.36-01 8.52-01	0.00	0 826-00 1 5 1626-00 4 5 1626-00 4 5 1626-00 4	216-02 6.87 216-02 6.87 216-02 6.87 216-02 6.87	7 KURLE (KIDA), KIDAN, KIDAN, KIDA 7 CORR, CORR, CORR, CHRIZ, GRRIT 7 CORR, CORR, CORR, CHRIZ, GRRIT 7 KURLE, KIDAN, KIDAN, KIDAN, KIDAN
REQUILATION OF T. MELFER, 1, TYPE, IMMUNE, RESPONSE DEGE, Pro. V., AD 20 MATTY, ACID, BINDING POSITIVE, DEGLETON, OF, INTERLEURIN, 1, PRODUCTION, DEGL., Pro. B., AD 25 POSITIVE, REGULATION, OF, INTERLEURIN, 1, PRODUCTION, DEGL., Pro. B., AD 25	8 1505-04 4.285- 9 1626-04 4.565- 9 1626-04 4.565-	-03 4.36 CCL19; CCR2; CDR0; IL1 -03 3.86 ALR; ALDXSAP; APOC1 -03 3.86 AMA; CCL18; CCL2; ER	9.215-01 9.885-01 7.815-01 9.805-01 1.186-01 7.586-01	0.00 0.45 SNCA 0 1.81 NLRP2; PAN 0	6.33E-01 8.53E-01 6.66E-01 8.53E-01 6.66E-01 8.53E-01	0.00 0.00 0.00	5 1.636-00 4 1 5.536-01 9 2 2.526-01 6	215-02 6.87 576-06 0.79 866-06 1.56	7 (1861) (1204) (1206) (1206) (120 9 (1804) (121 6 (1804) (121
CELL SECONDITION  BEGULATION OF JAM, STAT_CASCADA  BEGULATION, OF JAM, STAT_CASCADA  BEGULATION, OF _TUMOR_SECROIS_FACTOR_PRODUCTION  DESCRIPTOR_SEA  GRADO SECRIPTOR_ACTIVITY  DESCRIPTOR_ACTIVITY  D	9 102-04 456- 9 102-04 456- 16 102-04 456- 16 102-04 456- 16 102-04 456- 15 121-04 478-	-08 0.36 CLTING COLD CERRO (1) 1-00-0 3.86 Mails NUCLEAR, MOCE 1-00-0 3.86 Mails CLTING COLD, 60-0 -00-0 2.62 CLTING COLD, 60-0 -00-0 2.62 MAPPLY COLD, CONSTR. 1-00-0 2.62 MAPPLY COLD, CONSTR. 1-00-0 2.62 MAPPLY COLD, CONSTR. 1-00-0 2.62 MAPPLY COLD, COLD, 60-0 MAPPLY COLD, 60-0 MA	1 7.81 - 01 9.80 - 01 1 1.95 - 01 7.86 - 01 9.80 - 02 7.65 - 01 1 7.64 - 01 9.80 - 01 4.26 - 01 9.80 - 01 6.95 - 01 9.80 - 01 6.95 - 01 9.80 - 01	0.05 SNCA C 1.81 NARP2; PAN C 1.57 CIGN; DSC 2 0.70 F2R; HPC; 1 1.05 AN; CD34; 0.77 SNDOU; EN C	1 8.86-01 8.526-01 1 8.86-01 8.526-01 0 7.966-01 8.76-01	2.01 CD209; DO 1.01 E229A2 1.01 2FP36 0.00	1 5.525-01 9 2 2.526-01 6 5 1.786-01 5 7 3.296-02 2 8 1.176-02 1 3 4.766-01 8	711-01 1.50 271-01 2.10 321-01 2.40 861-01 0.96	7
DRUG_METABOLISMCYTOCHROME_PHS0 DSGL_Pko_8_AD 50 BON_DON_BRIDDES BON_DON_BRIDDES BON_DON_BRIDDES DSGL_Pko_vc_AD 141	15 1.711-04 4.746- 15 1.711-04 4.726- 27 1.716-04 4.926- 27 1.716-04 4.926-	03 2.71 UGTZAS; ADHIB; ADH 03 2.64 ACPS; CHQSH; CYPIAS 3 03 2.64 ACPS; CHQSH; CYPIAS 3	2.06E-01 7.90E-01 0 1.75E-02 4.53E-01 0 1.75E-02 4.53E-01	134 CYPAR CO 1 161 AGMO AO 1 161 AGMO AO 1 071 PYCARD 1 142 CPCR; RT 1	7,98-01 8,78-01 8 2,71-02 5,97-01 8 2,685-01 8,525-01 9 2,685-01 8,525-01 0 6,096-01 8,525-01 1,215-01 6,986-01	3.32 CH2CH; CI 1.39 CH2CH; CI 1.39 CH2CH; CI	2 4.765-01 8 2 4.765-01 8 18 2.165-04 1 18 2.165-04 1 2 1.655-02 2 0 7.855-04 1 2 1.215-04 4	965-05 0.96 405-02 2.46 405-02 2.46	CHICAGO, CHICAGO, CONTRACTOR
MAST_CEL_ACTINATION OF JOHNSON MASTINE MANUAL JASON DOGS, Pop. 8, AD 16 MASTINE REQUIRITION OF JOHNSON MANUAL JASON DOGS, Pop. 8, AD 16 POSITIVE JASQUATION, OF JURICIOTE APOPTOTIC, PROC. DOGS, Pop. 8, AD 14	15 1.71-04 4.76- 15 1.71-04 4.76- 27 1.76-04 4.92- 7 1.76-04 5.02- 7 1.77-04 5.02- 7 1.77-04 5.02- 7 1.77-04 5.02- 7 1.77-04 5.02- 7 1.77-04 5.02-		2.915-01 8.585-01 2.915-01 8.585-01 8.865-01 9.815-01 8.865-01 9.815-01	1.42 CPDQ; EIT 1 0.00 0.00	0 6.08-01 8.53-01 1 1.215-01 6.86-01 0 6.08-01 8.53-01 0 6.08-01 8.53-01	0.00 4.09 MLRI 0.00 0.00	3 2.676-02 2 0 7.866-06 1. 2 1.216-06 4 0 7.866-06 1.	2.65 205+00 0.00 565-01 2.66 205+00 p.or	5 8234; 8236; MM07 6 8284; 823 0
REGULATION OF INTERESION 1 PRODUCTION DEGLINO, A AD 36 C.C. CHEMOISINE INVENTS DEGLINO, A AD 12 DEFENDE, RESPONSE TO PROTOZOAN DEGLINO, A AD 12	7 1374-04 5.002- 11 1305-04 5.002- 6 2205-04 5.365- 6 2205-04 5.365-	43 3.26 ACPS; AIM2; CCL19; CC 43 5.33 CCR1; CCR2; CCR4; CCI	2.86E-03 5.34E-01 8.85E-01 9.80E-01 9.83EE-01 9.80E-01	220 F2R; GSTP1 0 000 1	0 0.004-01 8.53-01 0 7.18-01 8.53-01 1 9.16-02 6.86-01 0 5.86-01 8.53-01 0 5.86-01 8.53-01 0 5.86-01 8.53-01	0.00 5.45 25P36 0.00	0 7864-01 1. 3 1966-01 6 2 7.226-02 3 2 7.226-02 3	096-01 1.63 426-01 3.25 426-01 3.25	2 (RNG; (SLE; NSFV) 5 (CKR; CORB 5 (AUT; ENG) 7 (RAKE; MSFV; THRES
MIGRITHY RESOLUTION OF INTERCEMENT 12 PRODUCTS DESIGNOUS AND 12 NEGATING RESOLUTION OF LEMBORTHY MEDIATIDS, NAM. DESIGNOUS AS AD 12 NEGATING RESOLUTION OF LYMPHOCYTE MEDIATIDS IN DESIGNOUS AS AD 12 PROSTREY REQUILITION, OF PROTEIN PROCESSING. DESIGNOUS AS AD 12 NEGATING RESOLUTION, OF PROTEIN PROCESSING.	1   1   1   1   1   1   1   1   1   1	-04 5.44 MINTS BLECK LELLOW, II -02 5.33 ADPS LILLS MAKE MOD -03 5.33 FORDPS, ILTS; LERBE, IN -03 5.33 FORDPS, ILTS; LERBE, IN -04 5.33 ADMAN, CS; CECCE; C -05 5.34 ADMAN, CS; CECCE; C -06 2.36 CD2N; CORNA, CTA07 2.36 CD2N; CORNA, CTA08 3.44 CD220; CODE, FCERIE; -09 3.44 CD220; CODE, FCERIE;	6.78E-01 9.11E-01 9.15E-01 9.80E-01 9.82E-01 9.80E-01 1.85E-01 7.78E-04	0.94 C1Q8P 0 0.00 0 0.00 0 1.89 KUR1; PLG 0	5.86-01 8.53-01 5.86-01 8.53-01 5.86-01 8.53-01 5.86-01 6.53-01	0.00 0.00 0.00	3 1.176-02 1 0 7.366-06 1 0 7.366-06 1 1 2.966-06 7	000+00 0.00 000+00 0.00 000+00 0.00	o enedd(BBFY; IHBS 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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PROTEIN, SECRETION DEGLE PIO, A, AD SI T, CRLL, COSTMULATION DEGLE PIO, A, AD SI INTERFERON, GAMMA, MEDIATED, SEGNALING, PATHWAY, DEGLE, PIO, A, AD 43 MONDOLARIONYLE, ACID, BRIVING.	14 2.37.64 6.45.65 6.45 6.4	1	9.12E-01 9.85E-01 9.12E-01 9.85E-01 5.11E-01 9.15E-01 7.15E-01	0.42 MG4A2, ST 1 0.42 ICONG, TR 1 0.94 FCGRIA; G 1	2.411-01 8.774-01 2.886-01 8.556-01 2.886-01 8.556-01 2.886-01 8.556-01 2.886-01 8.556-01 2.886-01 8.556-01 0.7.656-01 8.656-01 0.7.656-01 8.656-01 0.7.656-01 8.656-01 0.7.656-01 8.556-01 0.7.666-01 8.556-01 0.7.666-01 8.556-01	121 CDM1G 121 GM92 136 VOM1	1 2.966-ds 7 5 5 6.666-ds 7 7 4 4.606-ds 2 2 6.516-ds 1 8 6 2.266-ds 1 3 4.466-ds 2 5 5.806-ds 1 5 6.266-ds 1 5 6.266-ds 1 5 6.266-ds 1 5 6.266-ds 1 6 7 4.466-ds 4 6 7 4.466-ds 4 7 4.466-ds 4 7 4.466-ds 4 7 4.466-ds 1	006+00 0.72 216-01 1.06 856-01 2.46 426-01	BEAR SEGIONS SERVE, SCHILL, VITONA BEAR SEGIONS SERVE, SCHILL, VITONA SERVE, SALE, SALE SERVE, SALE SE
BEGULATION_OF_VIRIAL_GENOME_REPLICATION DEGL_PIO_B_AD 48 BEGULATION_OF_WORKD_HALMING DEGL_PIO_B_AD 72 POSITIVE_REGULATION_OF_PEPTID'NI_TYROSINE_PROSPH; DEGL_PIO_B_AD 116	12 2.17-04 5.65- 12 2.17-04 5.65- 13 2.17-04 5.65- 12 2.17-04 5.65- 17 2.26-04 5.65- 22 2.25-04 5.66- 22 2.25-04 5.66-	-08 2.96 CAMPUTE (CLTR) (CLDR) -03 2.99 KE, MICHES (PR) (RF) -03 2.99 KE, MICHES (PR) (RF) -03 2.99 KE, MICHES (PR) -04 2.98 MOSECUL (CLTS, CD) -04 2.98 MOSECUL (CLTS, CD) -05 2.98 MOSECUL (CLTS, CD) -06 2.98 MOSECUL (CLTS, CD) -07 MOSECUL (CLTS, CD) -08 2.95 MAPPLIC, COC) (CLTS, CD) -08 2.95 MAPPLIC, COC) (CLTS, CD) -09 2.95 MAPPLIC, COC) (CLT	\$135-01 \$176-01 \$235-01 \$100-01 \$235-01 \$100-01 \$556-01 \$115-01 \$155-01 \$155-01 \$155-01 \$155-01	0.94 FCGRIA-G 0.71 CV93681;5 1.18 APORCAG 0.93 C034;F2R; 0.60 HGC;HPI; 0.60 HGC;HPI;	7.626-01 8.666-01 8 6.326-02 6.866-01 1 6.766-01 8.526-01	0.00 0.00 2.69 HOPE; POP 0.57 VGGFA	2 5,926-01 9 3 6,266-01 1. 17 4,606-05 4	915-01 0.81 305+00 0.81 155-03 2.91	1 (871); (324) (7.042); (495); (7.465) 1 ASPOQ; (400A)Q; (CLCF); (CSPG4; FGF30; FGF7; (FMG; 8.12; (1.234; (1.236; 1.1384; 52.1; (FG8)
PENTIVE REQUIATION OF PEPTIDIN, TYROSINE PROSPHE DEGL PLO, M, AD 114 POSITIVE REQUIATION OF LIDINGCYTE, MEDIATIO, CYTOT DEGL PAO, B, AD 36 REGULATION OF A, CELL, ACTIVATION POSITIVE REQUIATION OF LIPINGCYTE DISCRESSIVATION  THE STATE OF TH	18 2,376-04 5,846-	-03 3.69 CD226; CRTAM; IL128; -03 2.60 CARD11; CD28; CD38;	9.15E-01 9.85E-01 2.99E-01 9.66E-01 7.489E-01 9.17E-01 7.24E-01 9.80E-01	050 HGF; HFY; 1 131 LAGR; NCH 0 099 BCI2; LS; 1 078 AN: 107	6.765-01 8.526-01 0 6.655-01 8.526-01 2.265-01 8.366-01	0.00 1.63 C027; TGR 3.01 C027; CSR	17 4.605-05 4 2 9.425-02 4 6 1.725-01 5 11 3.205-03 6	136-03 2.91 026-04 2.25 636-04 1.66 236-02	1 ADMPCOS ADMADIS CLOSS; COPPOS ROSSIS ROSS; INVOS BLES BLESA (BLESA (BRESA (BRESA (BLESA (BLESA (BRESA (BR
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PERITIVE_REGULATION_OF_CHEMOTRANS DEGL_PILE_VL_AD 74 BEGULATION_OF_B_CEU_MEDIATED_IMMUNITY DEGL_PILE_B_AD 22 BEFUREN_BENEENG DEGL_PILE_B_AD 116 BEFUREN_BENEENG DEGL_PILE_B_AD 117	17 2.636-04 6.396- 10 2.886-04 6.986- 22 2.946-04 7.046-	08 2.65 CC119; CC12; CC1; CC 09 3.38 C0226; C030; FCER10; 08 2.11 APOE; CC12; CC2; CC1 08 2.11 APOE; CC12; CC2; CC2; CC2	1.586-01 7.716-01 8.686-01 9.806-01 8 9.506-03 2.596-01 8 9.506-03 2.596-01	138 ARTN; C1Q 2 035 MPX 1 176 ANG; CCDC 6 176 ANG; CCDC 6	2 2.096-01 8.086-01 1 2.386-01 8.416-01 6.766-02 6.866-01 6.766-02 6.866-01	1.77 TGFR1; VEC 2.04 TGFR1 2.25 CC122; CSC 2.25 CC122; CSC 3.85 CHRNE 0.00	10 2.865-03 5 4 5.086-02 2 20 1.086-06 4 20 1.086-06 4	861-02 2.63 876-04 2.64 726-04 3.36 726-04 5.50	CHCL12; DICAN; SDN2; RGF10; H234; NTF2; NTRK1; SLIT2; THBS1; THBS4     CLCFS; IRNG; H2794; TB021     MBBBP; ADMINTS; BMP4; CRF; FBLN7; RGF10; FGF7; FGF81; FM1; ITGAN; LAMC2; PCDLCS2     ABBBP; ADMINTS; BMP4; CRF; FBLN7; FGF10; FGF7; FGF81; FM1; ITGAN; LAMC2; PCDLCS2
SEGUATION CF #, ECEL WIGHTE , MANUFACT   SOC, PAS, A, AD   23	7 2.965-04 7.045- 7 2.965-04 7.045-	439 ORM1; DRM2; DR9 439 CCL19; CD80; CD82; FC	8,965-01 9,865-01 8,965-01 9,865-01 6,211-01 9,455-01	000 1 000 0 067 TAP1 0	1 136-01 6.86-01 0 6.55-01 8.55-01 0 6.55-01 8.55-01 5.826-02 6.86-01		1 4.06-01 8 1 4.06-01 8 2 1.366-01 4 04 C665.00 3	055-01 1.15 055-01 1.15 855-01 2.25	5 C 1990A 1990A 9 E 1300C #04ACTC BARDY CD 1990
Mental publication  Ministry (March 1997)  Mi	7 2.864-50 7.065- 28 2.864-50 7.256- 9 2.184-50 7.256- 8 2.277-60 7.256- 8 2.277-60 7.256- 8 2.277-60 7.256- 12 2.376-60 7.256- 6 2.376-60 7.256- 6 2.376-60 7.256- 6 2.386-60 8.866- 6 2.386-60 8.866- 6 2.386-60 8.866- 6 2.386-60 8.866- 6 2.386-60 8.866- 6 2.386-60 8.866-60	03 2.33 CDD2(CDD2(CDD2(CDD2(CDD2(CDD2(CDD2(CDD2	100   100	600 M.	1	0.00 2.14 CCL29; CSC : 2.42 H6941 8.91 CDM04G; TI 0.00 2.97 TRAT1 2.97 CDM04G 1.49 STMAR2 0.00	1 A.DMOT A 2 1.365-06 4 30 5.965-07 3 4 2.915-02 2 2 2.007-06 6 1 5.005-06 9 4 1.435-02 1	1.00	H.ZZAC, H.ZZBC     H.ZZAC, H.ZZBC     H.ZZAC, H.ZZBC     H.ZZAC, H.ZZBC, H.ZZBC, FRILITY, FGF 10; FGF7; FGFR1; FN1; GALZETE; GFC1;     GRAND, JARANUR; ASRB2; CRED     H.ZZBC, H.ZZBC, H.ZZBC, FRILITY, FGF 10; FGF7; FGFR1; FN1; GALZETE; GFC1;     GRAND, JARANUR; ASRB2; CRED     GETA, A.ZBC, GETA, GETA
POSITIVE REGULATION OF CALCIUM MEDIATIC SIGNAL DEGL PIO, B. AD 22 POSITIVE REGULATION OF INTERECLION 12 PRODUCTION DEGL PIO, B. AD 22 MA, STAT CARCADE DEGL PIO, B. AD 44 POSITIVE REGULATION OF B 2011	8 1276-04 7.596- 8 1276-04 7.596- 8 1276-04 7.596- 12 1286-04 7.846- 6 3.000.00 9.906-	-00 3.88 ALCIGENCE, GST 100, G	9.35E-01 9.9E-01 9.35E-01 9.9E-01 6.55E-01 9.56E-01 5.9E-01 9.17E-01 5.10E-01 9.17E-01	0.00 1 0.00 1 0.77 F2R; (RS1; ) 1	1.66E-01 7.41E-01 1.66E-01 7.41E-01 1.16E-01 8.52E-01 0.59E-01 8.52E-01 0.59E-01 8.52E-01	2.97 TRAT1 2.97 CDM0LG 1.69 IFNAR2	1 5.005-01 9 4 1.635-02 1 4 1.355-01 4	065-01 0.86 665-01 3.54 815-01 1.77	9 LICAM 9 LICAM 1000, (1234; 1237; 10.1 7 CSH; (1051; 12384; 57A7)
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MEDP; PLASGDA; PDESR2; PDESS; TLRP; TIMES 11

MEDV; PLASGDA; PDESR2; PDESS; TLRP; TIMES 11

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