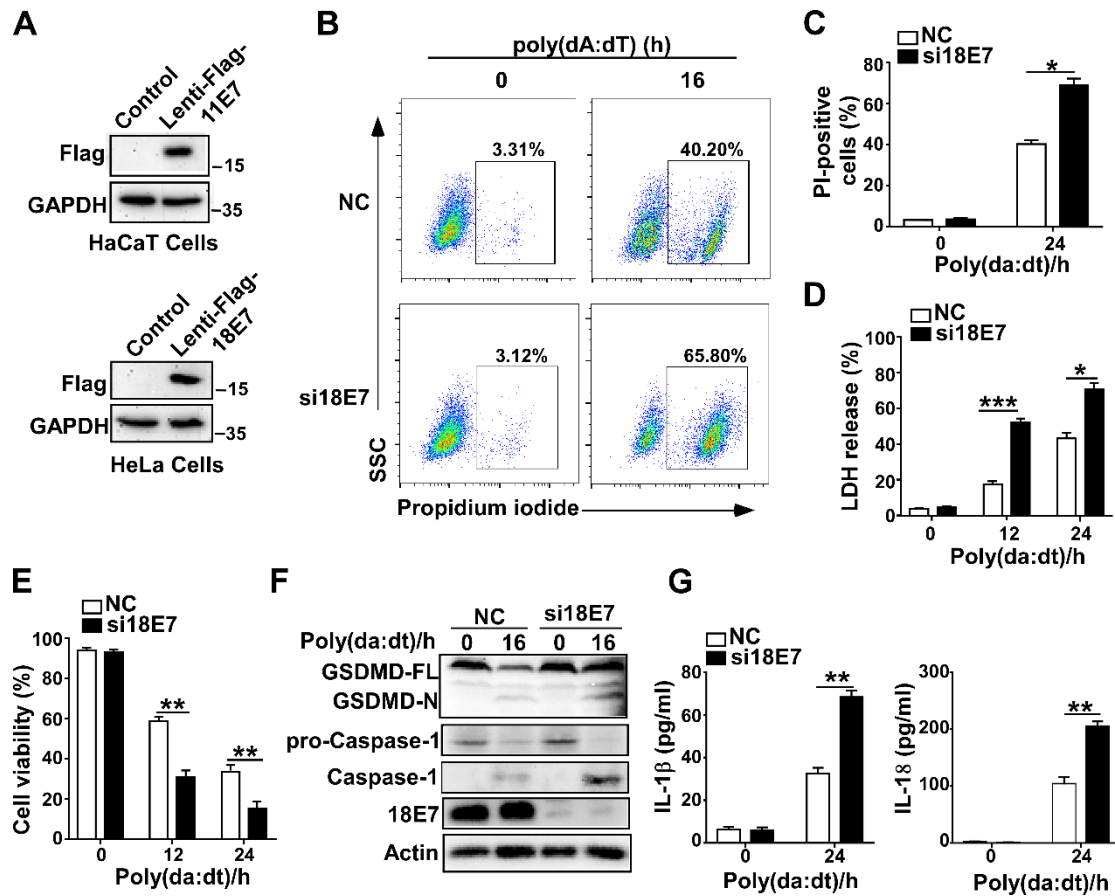


1 **Supplementary information:**

2 **Supplementary figure 1**

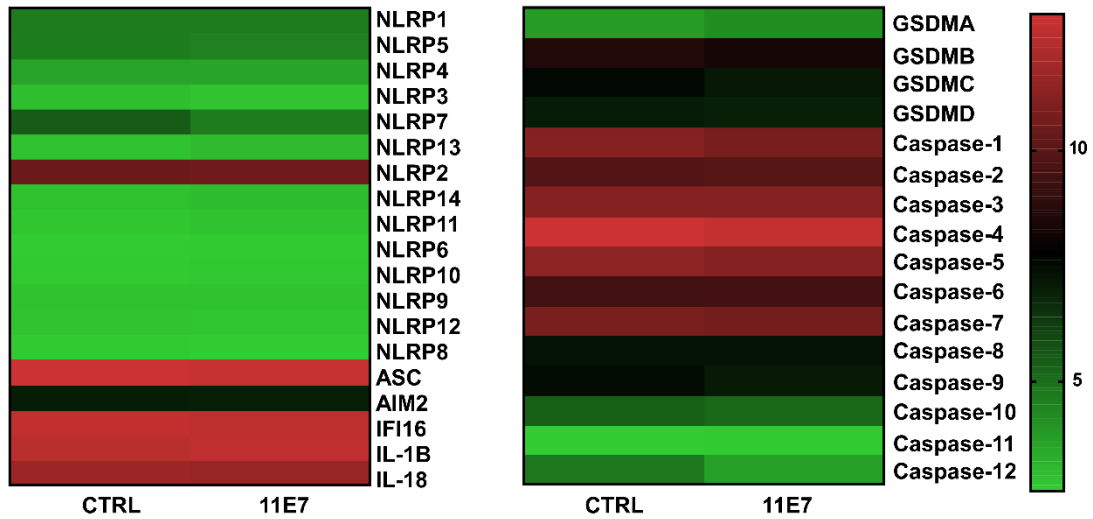


3  
 4 **Figure S1. HPV E7 inhibits pyroptosis induced by intracellular dsDNA.** (A) Immunoblot  
 5 analysis of HPV E7 in HaCaT cells stably expressing HPV11E7 or HeLa cells stably  
 6 expressing HPV 18E7. (B-C) Flow cytometry analysis (B) and statistical analysis (C) of  
 7 propidium iodide-positive control or HPV 18E7 silenced HeLa cells after transfection with  
 8 poly(da:dt) for the indicate times. (D-E) LDH assay (D) and Cell viability assay (E) to  
 9 detect dead control or HPV 18E7 silenced HeLa cells after transfection with poly(da:dt) for  
 10 the indicate times. (F) Immunoblot analysis of GSDMD and caspase-1 in the lysates of  
 11 control or HPV 18E7 silenced HeLa cells transfected with poly(da:dt) for 16 hr. (G) ELISA  
 12 analysis of IL-18 and IL-1 $\beta$  in control or HPV 18E7 silenced HeLa cells transfected with  
 13 poly(da:dt) for 24 hr. Data are presented as mean  $\pm$  SD of duplicate samples and are  
 14 representative of at least three independent experiments. P values are determined by  
 15 two-tailed Student's *t* test. \**p* < 0.05, \*\**p* < 0.01, \*\*\**p* < 0.001.

16

17 **Supplementary figure 2**

**A**



18

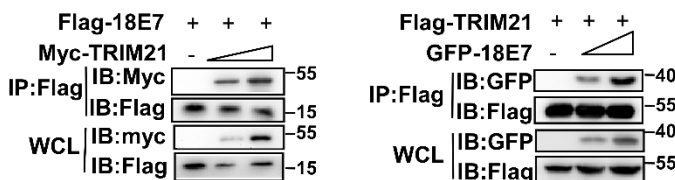
19 **Figure S2. HPV E7 does not affect the mRNA level of genes associated with pyroptosis.**

20 (A) RNA-seq analysis of HaCaT cells stably expressing HPV 11E7. Data are representative of  
21 at two independent experiments.

22

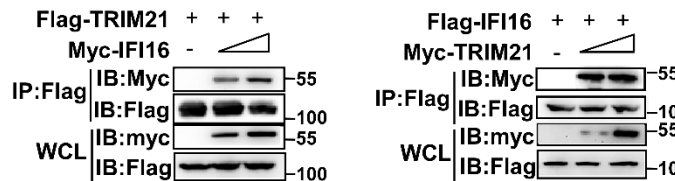
23 **Supplementary figure 3**

**A**

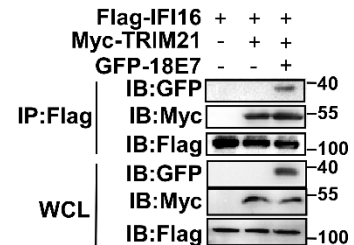


24

**B**



**C**



25 **Figure S3. HPV E7 interacts with IFI16 and the E3 ligase TRIM21.** (A)

26 Coimmunoprecipitation and immunoblot analysis of 293T cells cotransfected for 36 h with

27 Flag-18E7 and Myc-TRIM21 or Flag-TRIM21 and GFP-18E7, followed by

28 immunoprecipitation with anti-FlagM2 beads. (B) Coimmunoprecipitation and immunoblot

29 analysis of 293T cells cotransfected for 36h with Flag-TRIM21 and Myc-IFI16 or Flag-IFI16

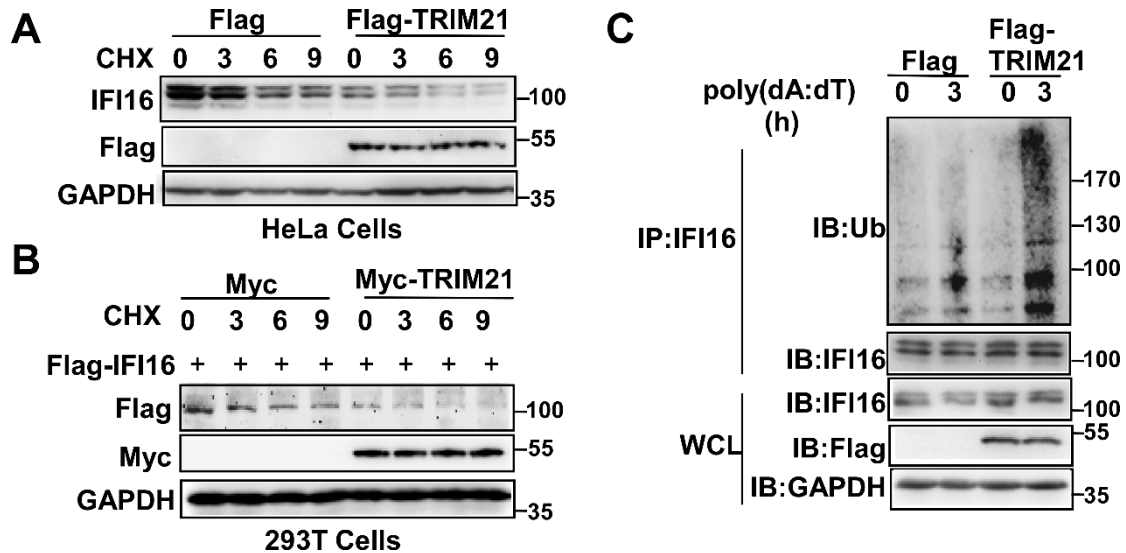
30 and Myc-TRIM21, followed by immunoprecipitation with anti-FlagM2 beads. (C)

31 Coimmunoprecipitation and immunoblot analysis of 293T cells cotransfected for 36 h with

32 Flag-IFI16 and Myc-TRIM21 or GFP-18E7, followed by immunoprecipitation with  
 33 anti-FlagM2 beads. Data are representative of at least three independent experiments.

34

35 **Supplementary figure 4**



36

37 **Figure S4. HPV E7 interacts with IFI16 and the E3 ligase TRIM21.** (A) Immunoblot  
 38 analysis of control HeLa cells or TRIM21-overexpressing HeLa cells transfected with  
 39 poly(dA:dT) for the indicated times. (B) Immunoblot analysis of control HeLa cells or  
 40 TRIM21-overexpressing HeLa cells treated with CHX (40  $\mu$ g/ml) for the indicated times after  
 41 transfection with poly(dA:dT) for 1 hr. (C) Immunoblot analysis of ubiquitinated IFI16 in  
 42 control HeLa cells or TRIM21-overexpressing HeLa cells transfected with poly(dA:dT) for  
 43 the indicated times and treated with MG132 for 6 hours before cell harvest. Data are  
 44 representative of at least three independent experiments.

45

46 **Supplementary table 1. The information of HPV 11E7 interacted proteins in stable**  
 47 **expression of HPV 11E7 HaCaT cells.**

Accession	Description	Score	Coverage
B4DTN0	cDNA FLJ51085, highly similar to Retinoblastoma-associated protein OS=Homo sapiens PE=2 SV=1 - [B4DTN0_HUMAN]	111.86	15.10
P28749	Retinoblastoma-like protein 1 OS=Homo sapiens GN=RBL1 PE=1 SV=3 - [RBL1_HUMAN]	95.77	17.42
Q9Y2W1	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2 - [TR150_HUMAN]	92.02	11.73

P19474	E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=1 SV=1 - [RO52_HUMAN]	91.99	10.11
Q86V81	THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3 - [THOC4_HUMAN]	71.23	17.12
Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	67.15	5.14
X5D2J9	General transcription factor Ii isoform D (Fragment) OS=Homo sapiens GN=GTF2I PE=2 SV=1 - [X5D2J9_HUMAN]	58.09	13.27
Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	55.18	4.41
Q96DI9	POLDIP3 protein (Fragment) OS=Homo sapiens GN=POLDIP3 PE=2 SV=2 - [Q96DI9_HUMAN]	53.69	19.66
A0A024RAR0	Proline-rich protein HaeIII subfamily 1, isoform CRA_a OS=Homo sapiens GN=PRH1 PE=4 SV=1 - [A0A024RAR0_HUMAN]	49.31	45.78
Q8TB01	Similar to cytoskeleton-associated protein 4 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TB01_HUMAN]	41.41	15.71
Q96RE1	Translation elongation factor 1 alpha 1-like 14 OS=Homo sapiens GN=EEF1A1L14 PE=2 SV=1 - [Q96RE1_HUMAN]	41.32	14.82
K7EK45	Polypyrimidine tract-binding protein 1 (Fragment) OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [K7EK45_HUMAN]	40.41	23.05
B7Z3V1	Sodium/potassium-transporting ATPase subunit alpha (Fragment) OS=Homo sapiens PE=2 SV=1 - [B7Z3V1_HUMAN]	40.36	8.04
B4DSZ9	E3 ubiquitin-protein ligase TTC3 OS=Homo sapiens GN=TTC3 PE=1 SV=1 - [B4DSZ9_HUMAN]	37.11	2.61
A0A024R1X8	Junction plakoglobin, isoform CRA_a OS=Homo sapiens GN=JUP PE=4 SV=1 - [A0A024R1X8_HUMAN]	36.17	8.59
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	36.00	28.48
F6IB50	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=4 SV=1 - [F6IB50_HUMAN]	35.30	14.13
E5RI99	60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=1 SV=1 - [E5RI99_HUMAN]	32.33	24.56
B2RAM6	Kinesin-like protein OS=Homo sapiens PE=2 SV=1 - [B2RAM6_HUMAN]	29.65	6.25
Q2VPJ6	HSP90AA1 protein (Fragment) OS=Homo sapiens	29.17	9.91

	GN=HSP90AA1 PE=1 SV=1 - [Q2VPJ6_HUMAN]		
Q15208	Serine/threonine-protein kinase 38 OS=Homo sapiens GN=STK38 PE=1 SV=1 - [STK38_HUMAN]	28.74	17.42
Q8IYY2	KCTD2 protein (Fragment) OS=Homo sapiens GN=KCTD2 PE=2 SV=1 - [Q8IYY2_HUMAN]	28.05	11.43
A0A0J9YXZ5	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [A0A0J9YXZ5_HUMAN]	27.22	5.12
Q96BG6	ACTN4 protein (Fragment) OS=Homo sapiens GN=ACTN4 PE=2 SV=2 - [Q96BG6_HUMAN]	27.14	8.20
E9PPJ5	Midkine (Fragment) OS=Homo sapiens GN=MDK PE=1 SV=1 - [E9PPJ5_HUMAN]	25.50	19.85
D3DUZ3	Interferon, gamma-inducible protein 16, isoform CRA_a OS=Homo sapiens GN=IFI16 PE=4 SV=1 - [D3DUZ3_HUMAN]	25.46	7.37
Q5JYR4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (Fragment) OS=Homo sapiens GN=RPN2 PE=1 SV=7 - [Q5JYR4_HUMAN]	25.38	23.95
Q59FC6	Tumor rejection antigen (Gp96) 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FC6_HUMAN]	25.28	10.24
Q96HX3	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96HX3_HUMAN]	24.96	9.15
F8VSC5	SCY1-like protein 2 (Fragment) OS=Homo sapiens GN=SCYL2 PE=1 SV=1 - [F8VSC5_HUMAN]	24.16	6.02
Q96PK6	RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 - [RBM14_HUMAN]	24.13	5.98
Q96BS4	FBL protein (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=2 - [Q96BS4_HUMAN]	21.82	14.62
F5H837	Retinoblastoma-like protein 2 (Fragment) OS=Homo sapiens GN=RBL2 PE=1 SV=2 - [F5H837_HUMAN]	19.58	2.50
Q96AF9	ZYX protein (Fragment) OS=Homo sapiens GN=ZYX PE=2 SV=2 - [Q96AF9_HUMAN]	19.51	8.58
Q9H0A0	RNA cytidine acetyltransferase OS=Homo sapiens GN=NAT10 PE=1 SV=2 - [NAT10_HUMAN]	18.59	4.78
Q7Z759	CCT8 protein OS=Homo sapiens GN=CCT8 PE=2 SV=1 - [Q7Z759_HUMAN]	17.68	6.64
A0A087WXU5	Nucleolar protein of 40 kDa OS=Homo sapiens GN=ZCCHC17 PE=1 SV=1 - [A0A087WXU5_HUMAN]	17.55	18.49
Q9BQA1	Methylosome protein 50 OS=Homo sapiens	17.45	8.48

	GN=WDR77 PE=1 SV=1 - [MEP50_HUMAN]		
A8K6H6	cDNA FLJ76875, highly similar to Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6H6_HUMAN]	16.70	2.36
Q504U8	EGFR protein OS=Homo sapiens GN=EGFR PE=1 SV=1 - [Q504U8_HUMAN]	15.87	2.66
A0A0S2Z415	Heat shock 60kDa protein 1 isoform 4 OS=Homo sapiens GN=HSPD1 PE=2 SV=1 - [A0A0S2Z415_HUMAN]	15.71	14.79
F5H2D2	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=1 - [F5H2D2_HUMAN]	15.69	34.48
X6R700	Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=1 - [X6R700_HUMAN]	15.65	18.83
Q59H46	Integrin beta (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59H46_HUMAN]	15.52	3.50
G3V1B3	60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=1 - [G3V1B3_HUMAN]	15.30	17.24
B3KU66	cDNA FLJ39263 fis, clone OCBBF2009571, highly similar to ATP-dependent RNA helicase A (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KU66_HUMAN]	14.64	2.91
Q7Z5X3	EIF3L protein OS=Homo sapiens GN=EIF3L PE=2 SV=2 - [Q7Z5X3_HUMAN]	13.60	8.51
B3KUD7	DNA helicase OS=Homo sapiens PE=2 SV=1 - [B3KUD7_HUMAN]	13.60	7.19
Q9BUZ4	TNF receptor-associated factor 4 OS=Homo sapiens GN=TRAF4 PE=1 SV=1 - [TRAF4_HUMAN]	13.44	16.17
F8WAM2	T-complex protein 1 subunit eta (Fragment) OS=Homo sapiens GN=CCT7 PE=1 SV=1 - [F8WAM2_HUMAN]	13.36	22.45
Q5JSD2	Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=7 - [Q5JSD2_HUMAN]	13.34	6.67
A0A0D9SFE5	Lamin B1, isoform CRA_a OS=Homo sapiens GN=LMNB1 PE=1 SV=1 - [A0A0D9SFE5_HUMAN]	12.81	10.94
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	12.80	21.79
H0YF10	Histone-binding protein RBBP4 (Fragment) OS=Homo sapiens GN=RBBP4 PE=1 SV=1 - [H0YF10_HUMAN]	12.51	6.28
A8K6A2	cDNA FLJ77317, highly similar to Homo sapiens	12.51	3.06

	retinoblastoma binding protein 7 (RBBP7), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6A2_HUMAN]		
A8KA74	cDNA FLJ76065 OS=Homo sapiens PE=2 SV=1 - [A8KA74_HUMAN]	12.24	4.90
B4DN87	cDNA FLJ52569, highly similar to Collagen-binding protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DN87_HUMAN]	11.32	6.80
E5RGH4	Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 - [E5RGH4_HUMAN]	11.22	33.00
B3KMA6	cDNA FLJ10609 fis, clone NT2RP2005276, highly similar to Long-chain-fatty-acid--CoA ligase 3 (EC 6.2.1.3) OS=Homo sapiens PE=2 SV=1 - [B3KMA6_HUMAN]	10.23	6.02
Q14011	Cold-inducible RNA-binding protein OS=Homo sapiens GN=CIRBP PE=1 SV=1 - [CIRBP_HUMAN]	10.20	26.74
A0A0C4DGS1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=1 - [A0A0C4DGS1_HUMAN]	9.96	2.51
H0YE40	CD44 antigen (Fragment) OS=Homo sapiens GN=CD44 PE=1 SV=1 - [H0YE40_HUMAN]	9.78	15.85
D6RAN4	60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=1 SV=7 - [D6RAN4_HUMAN]	9.69	19.78
Q9BS10	Similar to ribosomal protein S8 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9BS10_HUMAN]	9.66	16.25
D6R991	Matrin-3 (Fragment) OS=Homo sapiens GN=MATR3 PE=1 SV=1 - [D6R991_HUMAN]	9.46	7.39
Q6J1T2	Intersectin 1 isoform 7 (Fragment) OS=Homo sapiens GN=ITSN1 PE=2 SV=1 - [Q6J1T2_HUMAN]	9.36	5.70
A0A0J9YVQ7	ATP-dependent RNA helicase DDX3X (Fragment) OS=Homo sapiens GN=DDX3X PE=1 SV=1 - [A0A0J9YVQ7_HUMAN]	9.34	7.32
A0A024QYX7	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3S8 PE=3 SV=1 - [A0A024QYX7_HUMAN]	9.22	2.68
Q9BU76	Multiple myeloma tumor-associated protein 2 OS=Homo sapiens GN=MMTAG2 PE=1 SV=1 - [MMTA2_HUMAN]	9.21	4.94
A4FS09	Minichromosome maintenance protein 4 (Fragment)	9.04	15.29

	OS=Homo sapiens GN=MCM4 PE=2 SV=1 - [A4FS09_HUMAN]		
D3DWL9	Cleavage and polyadenylation specific factor 1, 160kDa, isoform CRA_a OS=Homo sapiens GN=CPSF1 PE=4 SV=1 - [D3DWL9_HUMAN]	9.02	1.25
F2Z388	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=1 - [F2Z388_HUMAN]	8.96	10.42
B4DFE6	cDNA FLJ59861, highly similar to ATP synthase gamma chain, mitochondrial (EC 3.6.3.14) OS=Homo sapiens PE=2 SV=1 - [B4DFE6_HUMAN]	8.80	8.39
H0YNQ3	Aldehyde dehydrogenase family 1 member A3 OS=Homo sapiens GN=ALDH1A3 PE=1 SV=1 - [H0YNQ3_HUMAN]	8.77	7.80
B4E190	cDNA FLJ57770, moderately similar to ADP-ribosylation factor 3 OS=Homo sapiens PE=2 SV=1 - [B4E190_HUMAN]	8.68	6.94
B4DM30	DEAH (Asp-Glu-Ala-His) box polypeptide 38, isoform CRA_d OS=Homo sapiens GN=DHX38 PE=2 SV=1 - [B4DM30_HUMAN]	8.63	2.56
F5GZQ3	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=1 - [F5GZQ3_HUMAN]	8.61	4.79
A8K9J7	Histone H2B OS=Homo sapiens PE=2 SV=1 - [A8K9J7_HUMAN]	7.84	11.90
D3DV75	Adenosine deaminase, RNA-specific, isoform CRA_b OS=Homo sapiens GN=ADAR PE=4 SV=1 - [D3DV75_HUMAN]	7.80	2.03
O43290	U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 - [SNUT1_HUMAN]	7.57	5.38
B4DRA2	cDNA FLJ57828, highly similar to Treacle protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DRA2_HUMAN]	7.44	2.71
M1XJE8	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-C PE=3 SV=1 - [M1XJE8_HUMAN]	7.44	8.05
M0R2L9	40S ribosomal protein S19 (Fragment) OS=Homo sapiens GN=RPS19 PE=1 SV=1 - [M0R2L9_HUMAN]	7.31	15.49
A0A075B6R9	Protein IGKV2D-24 (Fragment) OS=Homo sapiens GN=IGKV2D-24 PE=4 SV=1 - [A0A075B6R9_HUMAN]	7.06	10.83
H3BVI7	Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=1 - [H3BVI7_HUMAN]	7.03	3.38



E4W6B6	RPL27/NME2 fusion protein (Fragment) OS=Homo sapiens GN=RPL27 PE=2 SV=1 - [E4W6B6_HUMAN]	6.88	16.67
B4DDH8	cDNA FLJ55184, highly similar to Homo sapiens leukocyte receptor cluster (LRC) member 4 (LENG4), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DDH8_HUMAN]	6.56	2.64
Q3SYB5	SERPINB12 protein OS=Homo sapiens GN=SERPINB12 PE=2 SV=1 - [Q3SYB5_HUMAN]	6.55	8.74
Q14692	Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1 - [BMS1_HUMAN]	6.50	1.09
H0YIZ0	Serine hydroxymethyltransferase (Fragment) OS=Homo sapiens GN=SHMT2 PE=1 SV=1 - [H0YIZ0_HUMAN]	6.06	4.17
Q15800	Methylsterol monooxygenase 1 OS=Homo sapiens GN=MSMO1 PE=1 SV=1 - [MSMO1_HUMAN]	6.02	4.78
M0R0Y6	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=1 - [M0R0Y6_HUMAN]	5.97	11.11
Q9BSE8	ZNF607 protein OS=Homo sapiens GN=ZNF607 PE=2 SV=1 - [Q9BSE8_HUMAN]	5.91	6.41
Q8TA90	Similar to Elongation factor 2b (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TA90_HUMAN]	5.82	4.64
Q6DCA8	BCLAF1 protein (Fragment) OS=Homo sapiens GN=BCLAF1 PE=2 SV=1 - [Q6DCA8_HUMAN]	5.79	3.97
Q9BTC0	Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5 - [DIDO1_HUMAN]	5.75	0.76
B4DZB4	cDNA FLJ51707, highly similar to Heat-shock protein 105 kDa OS=Homo sapiens PE=2 SV=1 - [B4DZB4_HUMAN]	5.73	2.03
J3KTD9	Fatty aldehyde dehydrogenase (Fragment) OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [J3KTD9_HUMAN]	5.71	19.35
Q2M243	Coiled-coil domain-containing protein 27 OS=Homo sapiens GN=CCDC27 PE=2 SV=2 - [CCD27_HUMAN]	5.56	2.29
B4DYP6	cDNA FLJ57094, highly similar to Probable ATP-dependent RNA helicase DDX47 (EC3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DYP6_HUMAN]	5.50	9.85
F2Z2I2	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatas	5.49	2.86

	e 3 OS=Homo sapiens GN=PFKFB3 PE=1 SV=1 - [F2Z2I2_HUMAN]		
G3V119	Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=1 - [G3V119_HUMAN]	5.22	5.52
B4DIW2	cDNA FLJ54035, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1 - [B4DIW2_HUMAN]	4.63	2.53
H3BNP9	Sulfide:quinone oxidoreductase, mitochondrial (Fragment) OS=Homo sapiens GN=SQRDL PE=1 SV=1 - [H3BNP9_HUMAN]	4.18	11.29
Q8TA86	Retinitis pigmentosa 9 protein OS=Homo sapiens GN=RP9 PE=1 SV=2 - [RP9_HUMAN]	3.98	4.98
F5GZQ4	L-lactate dehydrogenase A chain (Fragment) OS=Homo sapiens GN=LDHA PE=1 SV=1 - [F5GZQ4_HUMAN]	3.92	20.83
Q5VVC9	60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=1 SV=1 - [Q5VVC9_HUMAN]	3.91	10.69
B3KN82	cDNA FLJ13913 fis, clone Y79AA1000231, highly similar to Nucleolar protein NOP5 OS=Homo sapiens PE=2 SV=1 - [B3KN82_HUMAN]	3.90	2.79
P01275	Glucagon OS=Homo sapiens GN=GCG PE=1 SV=3 - [GLUC_HUMAN]	3.82	11.11
A1L1B8	FSIP2 protein (Fragment) OS=Homo sapiens GN=FSIP2 PE=2 SV=1 - [A1L1B8_HUMAN]	3.79	13.85
B3KY11	cDNA FLJ46571 fis, clone THYMU3041428, highly similar to Probable ATP-dependent RNA helicase DDX23 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KY11_HUMAN]	3.70	2.00
F5H7Y1	T-complex protein 1 subunit alpha (Fragment) OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [F5H7Y1_HUMAN]	3.68	25.42
Q5H9P4	Putative uncharacterized protein DKFZp686M19106 (Fragment) OS=Homo sapiens GN=DKFZp686M19106 PE=4 SV=1 - [Q5H9P4_HUMAN]	3.67	1.41
Q1LZN2	NOMO3 protein (Fragment) OS=Homo sapiens GN=NOMO3 PE=2 SV=1 - [Q1LZN2_HUMAN]	3.64	1.36
P11766	Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4 - [ADHX_HUMAN]	3.61	4.28
E0WBQ9	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-C PE=3 SV=1 - [E0WBQ9_HUMAN]	3.60	11.05
Q59FN3	Acyl-Coenzyme A dehydrogenase family, member 9	3.58	5.47

	variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59FN3_HUMAN]		
A0A0U1RQV5	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1 - [A0A0U1RQV5_HUMAN]	3.56	21.82
P02814	Submaxillary gland androgen-regulated protein 3B OS=Homo sapiens GN=SMR3B PE=1 SV=2 - [SMR3B_HUMAN]	3.55	26.58
A0A0C4DH52	Constitutive coactivator of PPAR-gamma-like protein 1 (Fragment) OS=Homo sapiens GN=FAM120A PE=1 SV=1 - [A0A0C4DH52_HUMAN]	3.53	3.43
A0A024R326	Ribosomal protein L29, isoform CRA_a OS=Homo sapiens GN=RPL29 PE=4 SV=1 - [A0A024R326_HUMAN]	3.51	9.55
M0QXM4	Amino acid transporter OS=Homo sapiens GN=SLC1A5 PE=1 SV=1 - [M0QXM4_HUMAN]	3.51	5.48
P0C0S5	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2 - [H2AZ_HUMAN]	3.48	10.94
E5RFH5	Set1/Ash2 histone methyltransferase complex subunit ASH2 (Fragment) OS=Homo sapiens GN=ASH2L PE=1 SV=1 - [E5RFH5_HUMAN]	3.47	12.94
S4R456	40S ribosomal protein S15 (Fragment) OS=Homo sapiens GN=RPS15 PE=1 SV=1 - [S4R456_HUMAN]	3.43	27.94
B4DKX6	cDNA FLJ53584, highly similar to Desmoplakin (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DKX6_HUMAN]	3.43	2.20
H0Y8X1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (Fragment) OS=Homo sapiens GN=SDHA PE=1 SV=1 - [H0Y8X1_HUMAN]	3.43	11.11
Q6AZY7	Scavenger receptor class A member 3 OS=Homo sapiens GN=SCARA3 PE=1 SV=1 - [SCAR3_HUMAN]	3.40	4.46
A0A0S2Z4X1	RNA binding motif protein 10 isoform 1 (Fragment) OS=Homo sapiens GN=RBM10 PE=2 SV=1 - [A0A0S2Z4X1_HUMAN]	3.38	1.88
P01833	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4 - [PIGR_HUMAN]	3.36	2.62
O60762	Dolichol-phosphate mannosyltransferase subunit 1 OS=Homo sapiens GN=DPM1 PE=1 SV=1 - [DPM1_HUMAN]	3.36	6.15
Q9UG16	Putative uncharacterized protein DKFZp564P0562 (Fragment) OS=Homo sapiens GN=DKFZp564P0562 PE=2 SV=1 - [Q9UG16_HUMAN]	3.35	0.91

E9PLX0	Calpain-1 catalytic subunit (Fragment) OS=Homo sapiens GN=CAPN1 PE=1 SV=1 - [E9PLX0_HUMAN]	3.34	14.75
A0A075BTL2	Endoplasmic reticulum aminopeptidase 1 delta-Exon-11 isoform OS=Homo sapiens GN=ERAP1 PE=2 SV=1 - [A0A075BTL2_HUMAN]	3.21	2.37
Q9HAP1	Valosin-containing protein (Fragment) OS=Homo sapiens GN=VCP PE=2 SV=1 - [Q9HAP1_HUMAN]	3.19	5.54
Q86WX3	Active regulator of SIRT1 OS=Homo sapiens GN=RPS19BP1 PE=1 SV=1 - [AROS_HUMAN]	3.16	9.56
J3KTL8	Structural maintenance of chromosomes flexible hinge domain-containing protein 1 (Fragment) OS=Homo sapiens GN=SMCHD1 PE=1 SV=1 - [J3KTL8_HUMAN]	3.16	1.08
A1XP52	Catecholamine-regulated protein 40 OS=Homo sapiens PE=2 SV=1 - [A1XP52_HUMAN]	3.10	3.43
A0A0S2Z4Q6	Hydroxysteroid dehydrogenase 4 isoform 4 OS=Homo sapiens GN=HSD17B4 PE=2 SV=1 - [A0A0S2Z4Q6_HUMAN]	3.08	16.47
Q1RMG2	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=2 SV=1 - [Q1RMG2_HUMAN]	3.06	3.92
H7C1I9	Microtubule-associated serine/threonine-protein kinase 4 (Fragment) OS=Homo sapiens GN=MAST4 PE=1 SV=1 - [H7C1I9_HUMAN]	3.05	0.95
K7EJT5	60S ribosomal protein L22 (Fragment) OS=Homo sapiens GN=RPL22 PE=1 SV=1 - [K7EJT5_HUMAN]	3.04	23.40
Q9BVI4	Nucleolar complex protein 4 homolog OS=Homo sapiens GN=NOC4L PE=1 SV=1 - [NOC4L_HUMAN]	3.01	1.74
H7C5W9	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (Fragment) OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 - [H7C5W9_HUMAN]	3.00	1.39
A0A0A0MRQ5	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 - [A0A0A0MRQ5_HUMAN]	3.00	11.34
H0Y8L8	Probable ATP-dependent RNA helicase DDX41 (Fragment) OS=Homo sapiens GN=DDX41 PE=1 SV=1 - [H0Y8L8_HUMAN]	3.00	6.36
E9PMJ3	Ribonuclease inhibitor (Fragment) OS=Homo sapiens GN=RNH1 PE=1 SV=1 - [E9PMJ3_HUMAN]	2.99	7.94
F8VV32	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 - [F8VV32_HUMAN]	2.98	11.54

B4DN27	cDNA FLJ57057, highly similar to Small subunit processome component 20 homolog OS=Homo sapiens PE=2 SV=1 - [B4DN27_HUMAN]	2.97	2.40
Q03252	Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=4 - [LMNB2_HUMAN]	2.97	1.61
B3KNN7	cDNA FLJ30049 fis, clone ADRGL1000033, highly similar to 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens PE=2 SV=1 - [B3KNN7_HUMAN]	2.96	3.01
B4DNS2	cDNA FLJ51602, highly similar to Interferon-induced guanylate-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DNS2_HUMAN]	2.92	3.36
Q6P0M4	IARS protein OS=Homo sapiens GN=IARS PE=2 SV=1 - [Q6P0M4_HUMAN]	2.92	0.95
B4DZH8	cDNA FLJ50311, highly similar to Tumor necrosis factor, alpha-induced protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DZH8_HUMAN]	2.92	3.41
B4E0F7	cDNA FLJ61512 OS=Homo sapiens PE=2 SV=1 - [B4E0F7_HUMAN]	2.91	4.58
M0QZK8	Uncharacterized protein OS=Homo sapiens PE=4 SV=1 - [M0QZK8_HUMAN]	2.91	9.71
A0A0A0MQZ6	Ribosome biogenesis protein NSA2 homolog OS=Homo sapiens GN=NSA2 PE=1 SV=1 - [A0A0A0MQZ6_HUMAN]	2.89	6.88
A0A024QZT8	Serpin peptidase inhibitor, clade B (Ovalbumin), member 6, isoform CRA_b OS=Homo sapiens GN=SERPINB6 PE=3 SV=1 - [A0A024QZT8_HUMAN]	2.86	7.51
B4DFQ0	cDNA FLJ60239, highly similar to Proto-oncogene tyrosine-protein kinase MER (EC 2.7.10.1) OS=Homo sapiens PE=2 SV=1 - [B4DFQ0_HUMAN]	2.86	4.52
P62861	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1 - [RS30_HUMAN]	2.84	18.64
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	2.84	3.65
A0A0C4DGH5	Cullin-associated NEDD8-dissociated protein 1 (Fragment) OS=Homo sapiens GN=CAND1 PE=1 SV=1 - [A0A0C4DGH5_HUMAN]	2.83	1.43
Q4JFL9	Protein S100 (Fragment) OS=Homo sapiens GN=FLG PE=2 SV=1 - [Q4JFL9_HUMAN]	2.81	10.87
B4DWX8	cDNA FLJ52669, highly similar to Regulator of G-protein signaling 9 OS=Homo sapiens PE=2 SV=1	2.81	2.40

	- [B4DWX8_HUMAN]		
A7E2T1	Uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [A7E2T1_HUMAN]	2.80	13.39
Q49AJ9	RPL3 protein OS=Homo sapiens GN=RPL3 PE=2 SV=1 - [Q49AJ9_HUMAN]	2.79	4.78
A0A087X2D0	Serine/arginine-rich-splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1 - [A0A087X2D0_HUMAN]	2.78	14.74
B3KSC3	cDNA FLJ35987 fis, clone TESTI2014269, highly similar to D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) OS=Homo sapiens PE=2 SV=1 - [B3KSC3_HUMAN]	2.78	3.01
D3DPU8	Collagen, type IX, alpha 2, isoform CRA_a OS=Homo sapiens GN=COL9A2 PE=4 SV=1 - [D3DPU8_HUMAN]	2.78	2.35
B4E1D4	cDNA FLJ54399, highly similar to Golgin subfamily A member 5 OS=Homo sapiens PE=2 SV=1 - [B4E1D4_HUMAN]	2.77	3.13
Q4ZG72	Putative uncharacterized protein DDX18 (Fragment) OS=Homo sapiens GN=DDX18 PE=3 SV=1 - [Q4ZG72_HUMAN]	2.76	1.83
D6RHJ3	Calnexin (Fragment) OS=Homo sapiens GN=CANX PE=1 SV=7 - [D6RHJ3_HUMAN]	2.76	20.25
H3BUH7	Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens GN=ALDOA PE=1 SV=1 - [H3BUH7_HUMAN]	2.76	9.03
Q9Y657	Spindlin-1 OS=Homo sapiens GN=SPIN1 PE=1 SV=3 - [SPIN1_HUMAN]	2.76	3.82
P15515	Histatin-1 OS=Homo sapiens GN=HTN1 PE=1 SV=2 - [HIS1_HUMAN]	2.75	28.07
F8W0G4	Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens GN=PCBP2 PE=1 SV=1 - [F8W0G4_HUMAN]	2.75	8.23
H0Y920	Mastermind-like protein 3 (Fragment) OS=Homo sapiens GN=MAML3 PE=1 SV=1 - [H0Y920_HUMAN]	2.75	8.06
H0YFC6	GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 - [H0YFC6_HUMAN]	2.75	10.68
O15327	Type II inositol 3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4B PE=2 SV=4 - [INP4B_HUMAN]	2.72	1.41
B3KQH1	cDNA FLJ90452 fis, clone NT2RP3001475, highly similar to Splicing factor 3B subunit 3 OS=Homo	2.71	1.56

	sapiens PE=2 SV=1 - [B3KQH1_HUMAN]		
F6UXX1	Heterogeneous nuclear ribonucleoprotein Q (Fragment) OS=Homo sapiens GN=SYNCRIP PE=1 SV=1 - [F6UXX1_HUMAN]	2.71	7.03
P0C1S8	Wee1-like protein kinase 2 OS=Homo sapiens GN=WEE2 PE=2 SV=2 - [WEE2_HUMAN]	2.70	3.17
B4DT32	cDNA FLJ54383, highly similar to Valyl-tRNA synthetase (EC 6.1.1.9) OS=Homo sapiens PE=2 SV=1 - [B4DT32_HUMAN]	2.70	1.78
Q7KZP0	Catechol-O-methyltransferase OS=Homo sapiens PE=2 SV=1 - [Q7KZP0_HUMAN]	2.68	30.95
B4DSR0	cDNA FLJ60080, highly similar to 130 kDa leucine-rich protein (LRP 130) (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DSR0_HUMAN]	2.68	1.01
B4DTH5	cDNA FLJ55592, weakly similar to Sel-1 homolog OS=Homo sapiens PE=2 SV=1 - [B4DTH5_HUMAN]	2.67	3.53

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50 **Supplementary table 2. The information of HPV 11E7 interacted proteins in stable**  
51 **expression of HPV 11E7 HaCaT cells after transfection with poly(dA:dT).**

Accession	Description	Score	Coverage
P06400	Retinoblastoma-associated protein OS=Homo sapiens GN=RB1 PE=1 SV=2 - [RB_HUMAN]	297.41	27.48
P28749	Retinoblastoma-like protein 1 OS=Homo sapiens GN=RBL1 PE=1 SV=3 - [RBL1_HUMAN]	234.59	19.01
B7ZMG8	Uncharacterized protein OS=Homo sapiens PE=2 SV=1 - [B7ZMG8_HUMAN]	204.79	15.66
P19474	E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=1 SV=1 - [RO52_HUMAN]	201.07	18.53
C9JIR6	Protein phosphatase 1B (Fragment) OS=Homo sapiens GN=PPM1B PE=1 SV=1 - [C9JIR6_HUMAN]	123.36	16.40

Q8WUW7	Pyruvate kinase (Fragment) OS=Homo sapiens GN=PKM2 PE=2 SV=2 - [Q8WUW7_HUMAN]	78.43	21.28
B0QYK0	RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1 - [B0QYK0_HUMAN]	71.82	9.39
B7Z3V1	Sodium/potassium-transporting ATPase subunit alpha (Fragment) OS=Homo sapiens PE=2 SV=1 - [B7Z3V1_HUMAN]	58.31	9.22
B3KML9	cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain OS=Homo sapiens PE=2 SV=1 - [B3KML9_HUMAN]	56.57	19.14
B4DW52	cDNA FLJ55253, highly similar to Actin, cytoplasmic 1 OS=Homo sapiens PE=2 SV=1 - [B4DW52_HUMAN]	55.52	22.19
Q96RE1	Translation elongation factor 1 alpha 1-like 14 OS=Homo sapiens GN=EEF1A1L14 PE=2 SV=1 - [Q96RE1_HUMAN]	53.70	14.82
Q0QET7	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Homo sapiens GN=GAPDH PE=2 SV=1 - [Q0QET7_HUMAN]	52.15	26.09
V9HWC6	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=HEL-S-39 PE=2 SV=1 - [V9HWC6_HUMAN]	51.14	12.50
B2RDD7	Protein arginine N-methyltransferase 5 OS=Homo sapiens PE=2 SV=1 - [B2RDD7_HUMAN]	48.59	12.24
Q9NXV2	BTB/POZ domain-containing protein KCTD5 OS=Homo sapiens GN=KCTD5 PE=1 SV=1 - [KCTD5_HUMAN]	47.96	26.50
Q9BV28	TUBB3 protein (Fragment) OS=Homo sapiens GN=TUBB3 PE=2 SV=2 - [Q9BV28_HUMAN]	47.75	12.81



A8K6H6	cDNA FLJ76875, highly similar to Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6H6_HUMAN]	40.18	7.58
Q6P1L8	39S ribosomal protein L14, mitochondrial OS=Homo sapiens GN=MRPL14 PE=1 SV=1 - [RM14_HUMAN]	39.09	20.00
Q8WUT1	POLDIP3 protein OS=Homo sapiens GN=POLDIP3 PE=1 SV=1 - [Q8WUT1_HUMAN]	38.89	15.72
P27816	Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 - [MAP4_HUMAN]	36.11	3.91
E9PKE3	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [E9PKE3_HUMAN]	34.10	10.69
A0A0U1RQF0	Fatty acid synthase OS=Homo sapiens GN=FASN PE=4 SV=1 - [A0A0U1RQF0_HUMAN]	33.87	0.96
B3KU16	cDNA FLJ39066 fis, clone NT2RP7014743, highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K OS=Homo sapiens PE=2 SV=1 - [B3KU16_HUMAN]	33.76	18.83
F8VSC5	SCY1-like protein 2 (Fragment) OS=Homo sapiens GN=SCYL2 PE=1 SV=1 - [F8VSC5_HUMAN]	29.76	8.22
Q969I0	KRT8 protein (Fragment) OS=Homo sapiens GN=KRT8 PE=2 SV=2 - [Q969I0_HUMAN]	28.98	17.26
B4DSZ9	E3 ubiquitin-protein ligase TTC3 OS=Homo sapiens GN=TTC3 PE=1 SV=1 - [B4DSZ9_HUMAN]	28.88	2.61
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	28.12	19.39

Q99714	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3 - [HCD2_HUMAN]	27.92	19.92
E7EN95	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=1 - [E7EN95_HUMAN]	27.51	2.16
Q5JYR4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (Fragment) OS=Homo sapiens GN=RPN2 PE=1 SV=7 - [Q5JYR4_HUMAN]	26.82	17.37
A8K9J7	Histone H2B OS=Homo sapiens PE=2 SV=1 - [A8K9J7_HUMAN]	26.77	11.90
F2Z2S8	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=1 - [F2Z2S8_HUMAN]	26.43	29.06
C9JLM5	Serpin B5 (Fragment) OS=Homo sapiens GN=SERPINB5 PE=1 SV=1 - [C9JLM5_HUMAN]	26.09	11.63
Q13707	ACTA2 protein (Fragment) OS=Homo sapiens GN=ACTA2 PE=3 SV=1 - [Q13707_HUMAN]	24.16	9.70
Q96P47	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3 OS=Homo sapiens GN=AGAP3 PE=1 SV=2 - [AGAP3_HUMAN]	23.44	4.69
F5H837	Retinoblastoma-like protein 2 (Fragment) OS=Homo sapiens GN=RBL2 PE=1 SV=2 - [F5H837_HUMAN]	23.20	4.38
Q2VPJ6	HSP90AA1 protein (Fragment) OS=Homo sapiens GN=HSP90AA1 PE=1 SV=1 - [Q2VPJ6_HUMAN]	23.15	8.21
A0A024R599	Solute carrier family 3 (Activators of dibasic and neutral amino acid transport), member 2, isoform	22.94	7.29

	CRA_e OS=Homo sapiens GN=SLC3A2 PE=4 SV=1 - [A0A024R599_HUMAN]		
B4DUP0	cDNA FLJ59433, highly similar to Elongation factor 1-gamma OS=Homo sapiens PE=2 SV=1 - [B4DUP0_HUMAN]	22.42	6.80
Q9UHS8	PRO1975 OS=Homo sapiens PE=2 SV=1 - [Q9UHS8_HUMAN]	22.03	7.12
Q9Y2W1	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2 - [TR150_HUMAN]	20.27	4.08
Q86V81	THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3 - [THOC4_HUMAN]	18.38	7.00
Q8IYY2	KCTD2 protein (Fragment) OS=Homo sapiens GN=KCTD2 PE=2 SV=1 - [Q8IYY2_HUMAN]	18.02	11.43
Q02413	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2 - [DSG1_HUMAN]	17.34	1.53
B4DN39	cDNA FLJ53065, highly similar to T-complex protein 1 subunit zeta OS=Homo sapiens PE=2 SV=1 - [B4DN39_HUMAN]	16.60	4.11
F6IB50	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=4 SV=1 - [F6IB50_HUMAN]	16.25	14.13
O15327	Type II inositol 3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4B PE=2 SV=4 - [INP4B_HUMAN]	16.12	1.41
B4DH39	cDNA FLJ57028, highly similar to Long-chain-fatty-acid--CoA ligase 4 (EC 6.2.1.3) OS=Homo sapiens PE=2 SV=1 - [B4DH39_HUMAN]	15.42	5.08
Q6J1T2	Intersectin 1 isoform 7 (Fragment) OS=Homo	15.09	5.70

	sapiens GN=ITSN1 PE=2 SV=1 - [Q6J1T2_HUMAN]		
B4DWX8	cDNA FLJ52669, highly similar to Regulator of G-protein signaling 9 OS=Homo sapiens PE=2 SV=1 - [B4DWX8_HUMAN]	14.99	2.40
F8W0P7	ATP synthase subunit beta, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5B PE=1 SV=2 - [F8W0P7_HUMAN]	13.50	5.19
F8VV32	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 - [F8VV32_HUMAN]	13.35	11.54
B4DRH6	cDNA FLJ54509, highly similar to Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B4DRH6_HUMAN]	12.94	5.02
Q9BS10	Similar to ribosomal protein S8 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9BS10_HUMAN]	12.91	16.25
B4DHT9	cDNA FLJ58812, highly similar to Endoplasmic (Heat shock protein 90kDa beta member 1) OS=Homo sapiens PE=2 SV=1 - [B4DHT9_HUMAN]	12.05	2.99
B3KM90	cDNA FLJ10529 fis, clone NT2RP2000965, highly similar to Targeting protein for Xklp2 OS=Homo sapiens PE=2 SV=1 - [B3KM90_HUMAN]	12.05	4.13
Q9UNW1	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1 - [MINP1_HUMAN]	11.88	4.52
J3KTD9	Fatty aldehyde dehydrogenase (Fragment) OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [J3KTD9_HUMAN]	11.78	19.35

Q9P172	PRO2281 OS=Homo sapiens PE=2 SV=1 - [Q9P172_HUMAN]	11.47	9.73
H0Y9R4	60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=1 SV=1 - [H0Y9R4_HUMAN]	10.37	29.67
A0A087WWP1	Ras GTPase-activating-like protein IQGAP1 (Fragment) OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [A0A087WWP1_HUMAN]	9.74	14.95
Q5JSD2	Voltage-dependent anion-selective channel protein 2 (Fragment) OS=Homo sapiens GN=VDAC2 PE=1 SV=7 - [Q5JSD2_HUMAN]	9.74	6.67
Q7Z5X3	EIF3L protein OS=Homo sapiens GN=EIF3L PE=2 SV=2 - [Q7Z5X3_HUMAN]	9.27	8.51
P62081	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [RS7_HUMAN]	8.98	11.86
P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	8.63	8.48
Q68GS6	Epidermal growth factor receptor (Fragment) OS=Homo sapiens GN=EGFR PE=2 SV=1 - [Q68GS6_HUMAN]	8.60	3.57
B4DRA2	cDNA FLJ57828, highly similar to Treacle protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [B4DRA2_HUMAN]	8.38	1.08
Q86UM1	Putative uncharacterized protein EIF3S9 (Fragment) OS=Homo sapiens GN=EIF3S9 PE=4 SV=1 - [Q86UM1_HUMAN]	7.61	15.06
Q86Y46	Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1 - [K2C73_HUMAN]	7.54	4.44
H0YE40	CD44 antigen (Fragment) OS=Homo sapiens	7.33	35.37

	GN=CD44 PE=1 SV=1 - [H0YE40_HUMAN]		
J3QL15	Ribosomal protein L19 (Fragment) OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [J3QL15_HUMAN]	7.21	13.28
A0A075B6R9	Protein IGKV2D-24 (Fragment) OS=Homo sapiens GN=IGKV2D-24 PE=4 SV=1 - [A0A075B6R9_HUMAN]	6.66	10.83
A0A024R409	Microtubule-associated protein OS=Homo sapiens GN=MAP2 PE=4 SV=1 - [A0A024R409_HUMAN]	6.54	5.10
B2RAM6	Kinesin-like protein OS=Homo sapiens PE=2 SV=1 - [B2RAM6_HUMAN]	5.90	2.27
B4DVK5	cDNA FLJ54759, highly similar to DNA replication licensing factor MCM5 OS=Homo sapiens PE=2 SV=1 - [B4DVK5_HUMAN]	5.76	3.16
F8W0G4	Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens GN=PCBP2 PE=1 SV=1 - [F8W0G4_HUMAN]	5.73	8.23
Q96J17	NOLC1 protein OS=Homo sapiens GN=NOLC1 PE=2 SV=1 - [Q96J17_HUMAN]	5.69	2.63
A8K525	cDNA FLJ76817, highly similar to Homo sapiens non-POU domain containing, octamer-binding (NONO), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K525_HUMAN]	4.83	4.67
F5H2D2	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=1 - [F5H2D2_HUMAN]	4.46	19.54
B4DJP0	cDNA FLJ60601, highly similar to Methylosome protein 50 OS=Homo sapiens PE=2 SV=1 - [B4DJP0_HUMAN]	4.44	13.39

A0A0S2Z415	Heat shock 60kDa protein 1 isoform 4 OS=Homo sapiens GN=HSPD1 PE=2 SV=1 - [A0A0S2Z415_HUMAN]	4.37	14.79
A0A024QYX7	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3S8 PE=3 SV=1 - [A0A024QYX7_HUMAN]	4.35	2.68
Q86W20	Protease serine 1 (Fragment) OS=Homo sapiens GN=PRSS1 PE=3 SV=1 - [Q86W20_HUMAN]	4.34	23.81
Q53GM6	U5 snRNP-specific protein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GM6_HUMAN]	4.25	3.52
E9PQI8	U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 - [E9PQI8_HUMAN]	3.80	12.20
A0A087WXU5	Nucleolar protein of 40 kDa OS=Homo sapiens GN=ZCCHC17 PE=1 SV=1 - [A0A087WXU5_HUMAN]	3.72	9.59
Q6ZNL4	FLJ00279 protein (Fragment) OS=Homo sapiens GN=FLJ00279 PE=2 SV=1 - [Q6ZNL4_HUMAN]	3.67	2.31
B3KUD7	DNA helicase OS=Homo sapiens PE=2 SV=1 - [B3KUD7_HUMAN]	3.54	2.12
H0Y8X1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (Fragment) OS=Homo sapiens GN=SDHA PE=1 SV=1 - [H0Y8X1_HUMAN]	3.37	11.11
E9PKC4	Plakophilin-3 (Fragment) OS=Homo sapiens GN=PKP3 PE=1 SV=1 - [E9PKC4_HUMAN]	3.36	7.61
H0YMU6	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial (Fragment) OS=Homo sapiens	3.31	14.95

	GN=PCK2 PE=1 SV=1 - [H0YMU6_HUMAN]		
A0A0S2Z4X1	RNA binding motif protein 10 isoform 1 (Fragment) OS=Homo sapiens GN=RBM10 PE=2 SV=1 - [A0A0S2Z4X1_HUMAN]	3.28	1.88
S4R3N9	Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=1 SV=1 - [S4R3N9_HUMAN]	3.26	7.34
B4DNS2	cDNA FLJ51602, highly similar to Interferon-induced guanylate-binding protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DNS2_HUMAN]	3.23	3.36
Q53T09	Putative uncharacterized protein XRCC5 (Fragment) OS=Homo sapiens GN=XRCC5 PE=4 SV=1 - [Q53T09_HUMAN]	3.22	2.11
B5MD38	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=1 - [B5MD38_HUMAN]	3.19	3.70
R4GN64	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=1 - [R4GN64_HUMAN]	3.11	17.81
F2Z2I2	6-phosphofructo-2-kinase/fructose-2,6-bisphosphata se 3 OS=Homo sapiens GN=PFKFB3 PE=1 SV=1 - [F2Z2I2_HUMAN]	3.08	2.86
Q5T8R3	Monocarboxylate transporter 1 (Fragment) OS=Homo sapiens GN=SLC16A1 PE=1 SV=1 - [Q5T8R3_HUMAN]	3.08	4.05
Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1 - [FILA2_HUMAN]	3.05	0.50
Q68DE0	Putative uncharacterized protein DKFZp781D2217 OS=Homo sapiens GN=DKFZp781D2217 PE=2	3.04	4.70



	SV=1 - [Q68DE0_HUMAN]		
H0Y4T6	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (Fragment) OS=Homo sapiens GN=PIN4 PE=1 SV=1 - [H0Y4T6_HUMAN]	3.04	13.19
Q7Z5Y0	EIF4B protein (Fragment) OS=Homo sapiens GN=EIF4B PE=2 SV=1 - [Q7Z5Y0_HUMAN]	3.02	4.58
G3XAN0	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [G3XAN0_HUMAN]	3.01	18.75
H0YEP8	Serpin H1 (Fragment) OS=Homo sapiens GN=SERPINH1 PE=1 SV=1 - [H0YEP8_HUMAN]	3.01	21.43
Q75L23	Putative uncharacterized protein PSMC2 (Fragment) OS=Homo sapiens GN=PSMC2 PE=3 SV=1 - [Q75L23_HUMAN]	3.00	3.18
Q9NV86	cDNA FLJ10873 fis, clone NT2RP4001730, weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE (EC 2.4.1.-) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q9NV86_HUMAN]	2.97	1.10
D3DWL0	Plectin 1, intermediate filament binding protein 500kDa, isoform CRA_b OS=Homo sapiens GN=PLEC1 PE=4 SV=1 - [D3DWL0_HUMAN]	2.96	0.76
H7C1I9	Microtubule-associated serine/threonine-protein kinase 4 (Fragment) OS=Homo sapiens GN=MAST4 PE=1 SV=1 - [H7C1I9_HUMAN]	2.96	0.95
A0A0A0MSD 6	Teneurin-3 OS=Homo sapiens GN=TENM3 PE=1 SV=1 - [A0A0A0MSD6_HUMAN]	2.95	0.83
Q9BTC0	Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5 - [DIDO1_HUMAN]	2.94	0.76

E5RJH3	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=1 - [E5RJH3_HUMAN]	2.93	21.43
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	2.92	3.65
H0YD14	Myoferlin (Fragment) OS=Homo sapiens GN=MYOF PE=1 SV=1 - [H0YD14_HUMAN]	2.91	0.85
P62861	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1 - [RS30_HUMAN]	2.88	18.64
Q6ZQN2	cDNA FLJ46846 fis, clone UTERU3004635, moderately similar to Neuroblast differentiation associated protein AHNAK (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q6ZQN2_HUMAN]	2.85	0.82
B3KU66	cDNA FLJ39263 fis, clone OCBBF2009571, highly similar to ATP-dependent RNA helicase A (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1 - [B3KU66_HUMAN]	2.85	2.91
Q9BSE8	ZNF607 protein OS=Homo sapiens GN=ZNF607 PE=2 SV=1 - [Q9BSE8_HUMAN]	2.83	6.41
Q9H369	PRO1633 OS=Homo sapiens PE=2 SV=1 - [Q9H369_HUMAN]	2.83	6.56
A8MV73	Activating transcription factor 7-interacting protein 1 (Fragment) OS=Homo sapiens GN=ATF7IP PE=1 SV=2 - [A8MV73_HUMAN]	2.82	5.24
B4DW08	cDNA FLJ50886, highly similar to Aconitate hydratase, mitochondrial(EC 4.2.1.3) OS=Homo sapiens PE=2 SV=1 - [B4DW08_HUMAN]	2.82	2.65
Q7Z6E9	E3 ubiquitin-protein ligase RBBP6 OS=Homo sapiens GN=RBBP6 PE=1 SV=1 - [RBBP6_HUMAN]	2.82	0.84

P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2 - [DCD_HUMAN]	2.80	10.00
M0QXI6	RuvB-like 2 (Fragment) OS=Homo sapiens GN=RUVBL2 PE=1 SV=1 - [M0QXI6_HUMAN]	2.80	11.01
Q5T4L4	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=1 - [Q5T4L4_HUMAN]	2.80	19.70
A0A024R9T5	HCG20693, isoform CRA_a OS=Homo sapiens GN=hCG_20693 PE=3 SV=1 - [A0A024R9T5_HUMAN]	2.78	9.46
B7Z1C9	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a OS=Homo sapiens GN=CCT7 PE=2 SV=1 - [B7Z1C9_HUMAN]	2.77	3.86
Q6ZU52	Uncharacterized protein KIAA0408 OS=Homo sapiens GN=KIAA0408 PE=1 SV=1 - [K0408_HUMAN]	2.75	2.59
B5LY67	Uridine monophosphate synthetase isoform E OS=Homo sapiens GN=UMPS PE=2 SV=1 - [B5LY67_HUMAN]	2.75	2.92
G3V4V5	E3 ubiquitin-protein ligase HECTD1 (Fragment) OS=Homo sapiens GN=HECTD1 PE=1 SV=1 - [G3V4V5_HUMAN]	2.75	1.62