DNA Repair Interest Group Webinar

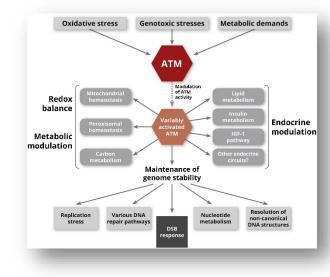
Yossi Shiloh

May 19, 2020



DNA Repair Interest Group at NIH

What has ATM taught us so far about ataxia-telangiectasia (A-T)?



May 19, 2020

Yossi Shiloh

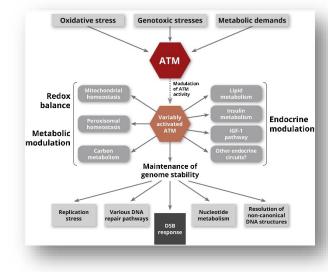






DNA Repair Interest Group at NIH

...and what are we still learning from A-T about ATM?



May 19, 2020

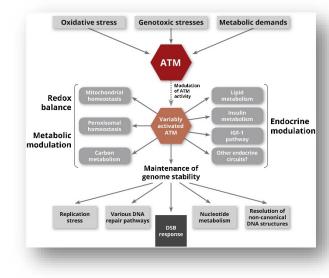
Yossi Shiloh







DNA Repair Interest Group at NIH



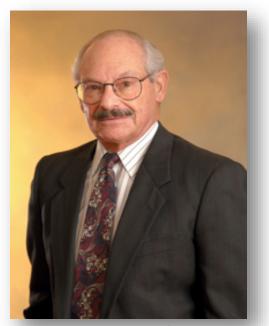
May 19, 2020

Yossi Shiloh







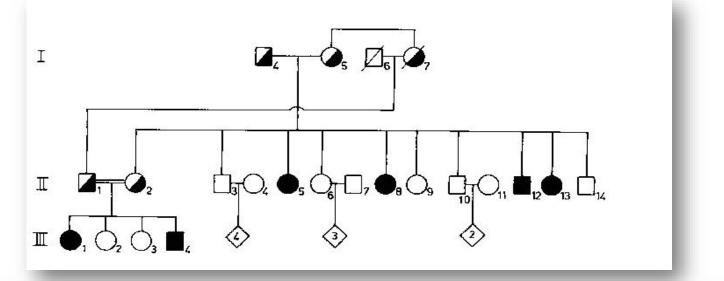


Maimon M. Cohen 1935 - 2007

Dr.



Family Y. (Moroccan-Jewish)



Interview



2019

The A-T gene hunt

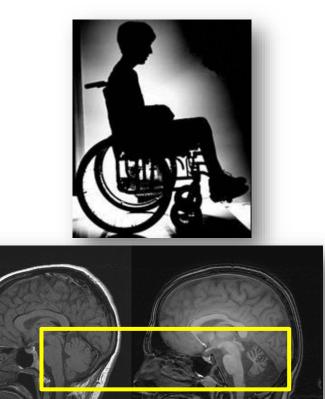
An interview with Yossi Shiloh on decision making, the discovery of the ATM gene and the lessons from genetics

Esther Schnapp & Holger Breithaupt

Ataxia-Telangiectasia (A-T)

- Autosomal recessive
 - □ 1:40,000 1:100,000
- Ataxia
 - Cerebellar atrophy (begins with loss of Purkinje cells), leading to severe neuromotor dysfunction
- > Telangiectasia
- Chronic lung disease
- Immunodeficiency; recurrent infections
- Cancer predisposition
- > Thymic and gonadal atrophy
- Growth retardation
- Endocrine abnormalities
- Genome instability (chromosomal breakage)
- Acute sensitivity to ionizing radiation
- Broad variability of the A-T phenotype

Telangiectasia Immune defects Cancer Sterility Cancer McKinnon, 2004

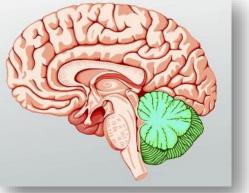




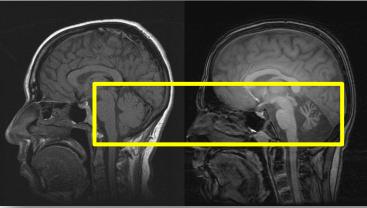
Differential sensitivity of tissues/cells to the A-T mutation

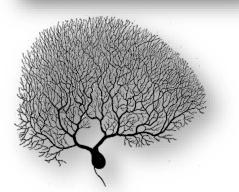
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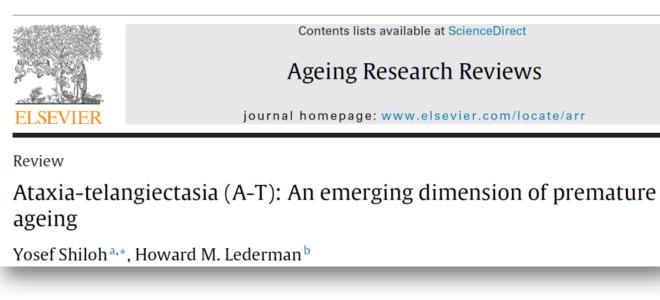
Differential sensitivity of tissues/cells to the A-T mutation

Symptoms Developing in Young Adults with A-T

- > Liver inflammation and cirrhosis
- > Metabolic syndrome
 - Type 2 diabetes mellitusHyperlipidemia
- > Incapacitating fatigue
- > Osteoporosis
- > Different spectrum of cancers:

Fewer lymphomas and leukemias
 compared to younger children with A-T

Higher proportion of solid tumors



Ageing Research Reviews 33 (2017) 76-88

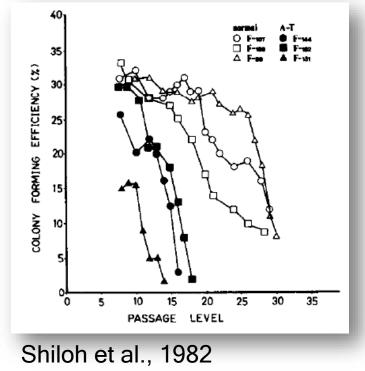


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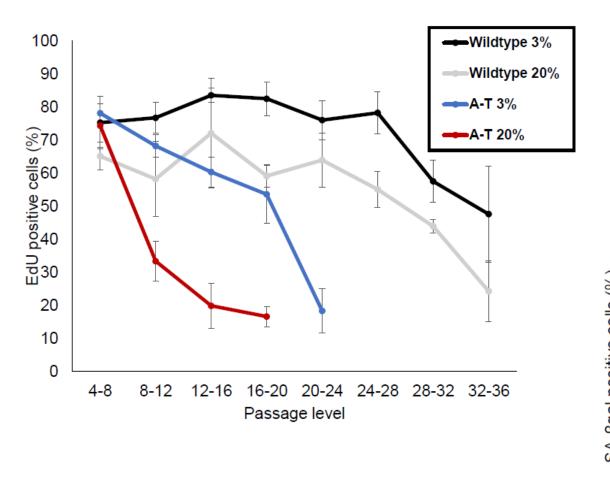


Premature senescence of primary A-T fibroblasts

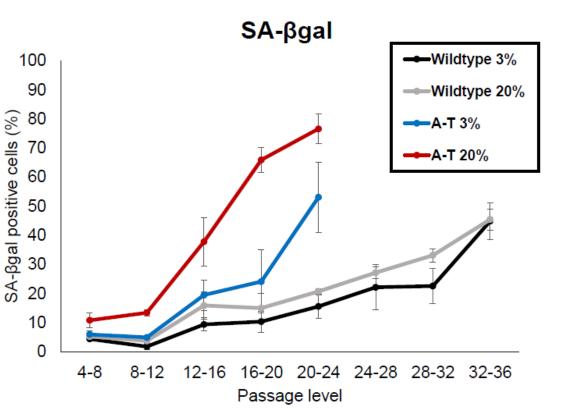


Premature Senescence of Primary A-T Fibroblasts

Proliferation Rate



 Majd Haj

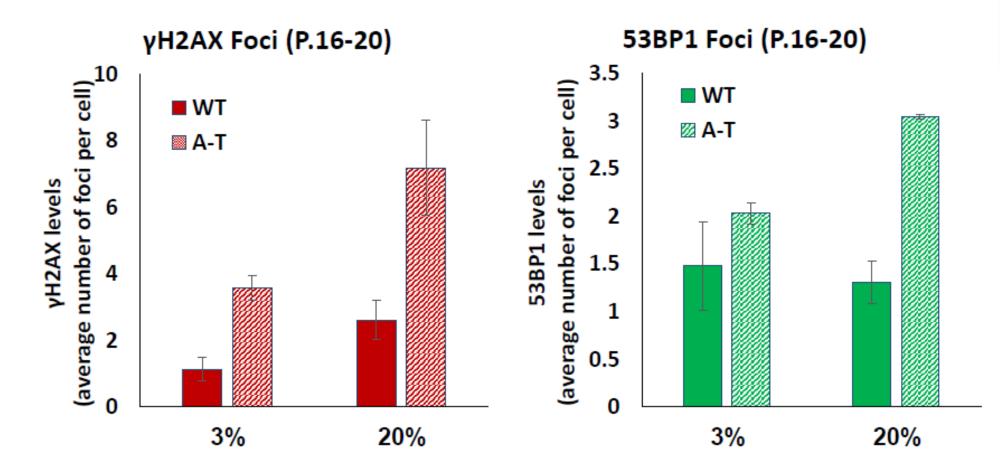


Majd Haj, unpublished

Premature Senescence of Primary A-T Fibroblasts

Accumulation of endogenous DNA damage

Majd Haj



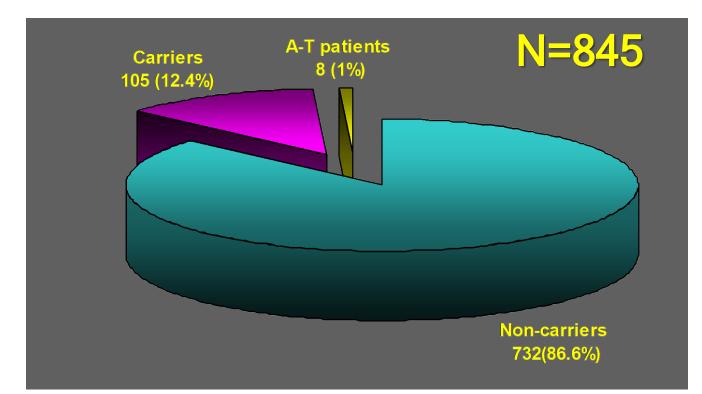
Majd Haj, unpublished

A-T Carriers

- > 1% -2% in various populations
- Cancer predisposition?
 An ongoing controversy...

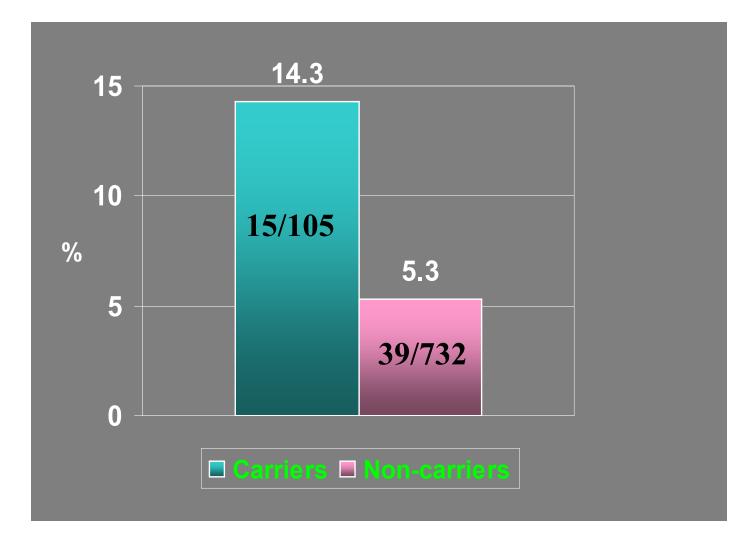


- > Carrier screening carried out in two communities, each with a single A-T mutation
 - □ Cohorts visited twice in 7 years and subsequently followed through the National Cancer Registry.



Siegal Sadetsky Angela Chetrit Relly Forrer

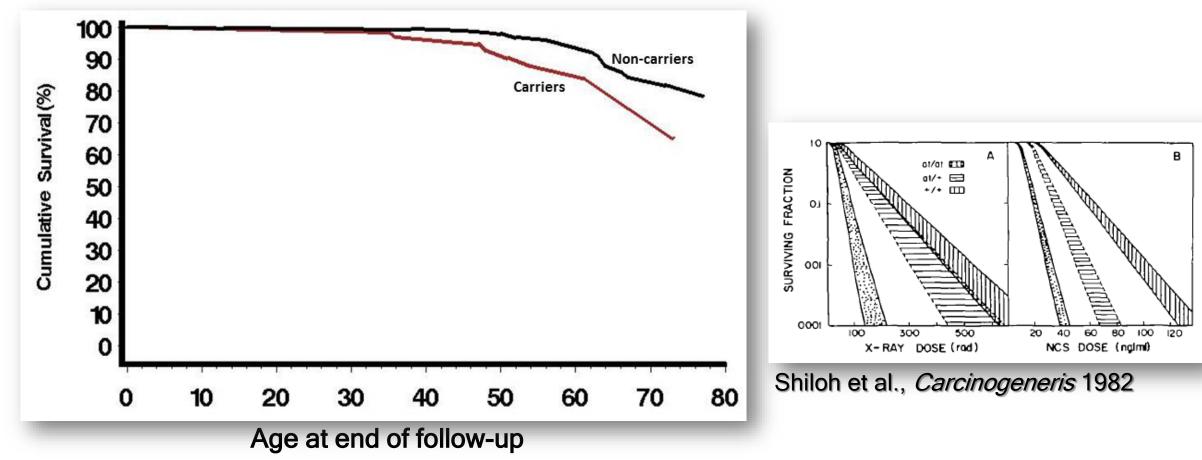
Cardiovascular Diseases among A-T Carriers



HR=1.91 95%CI=0.93-3.91

Multivariate analysis adjusted for age, gender and smoking habits

Cancer in A-T Carriers

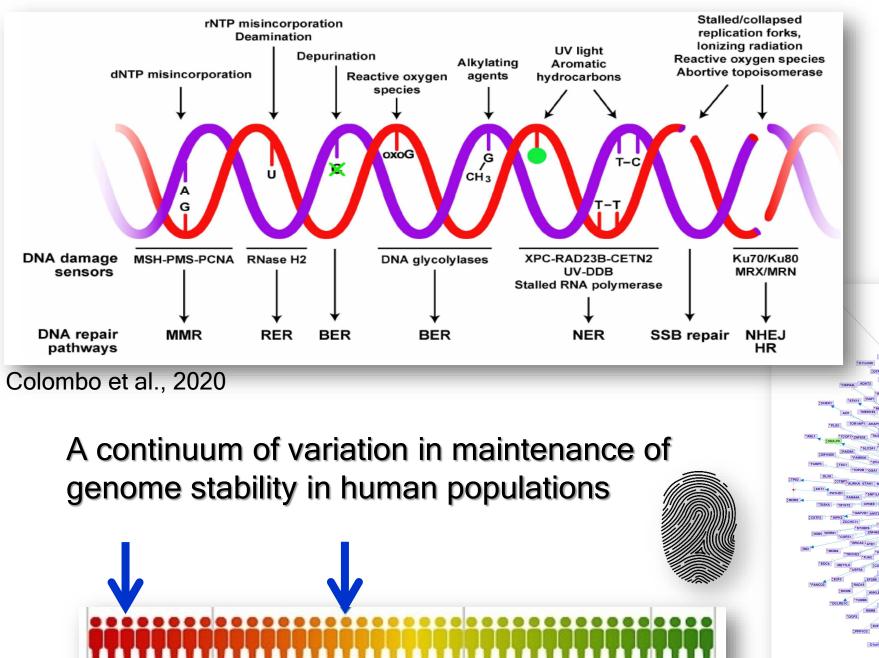


Controlled for gender, age and smoking. Hazard ratio: 2.03; 95%CI: 0.91-4.57 p=0.085.

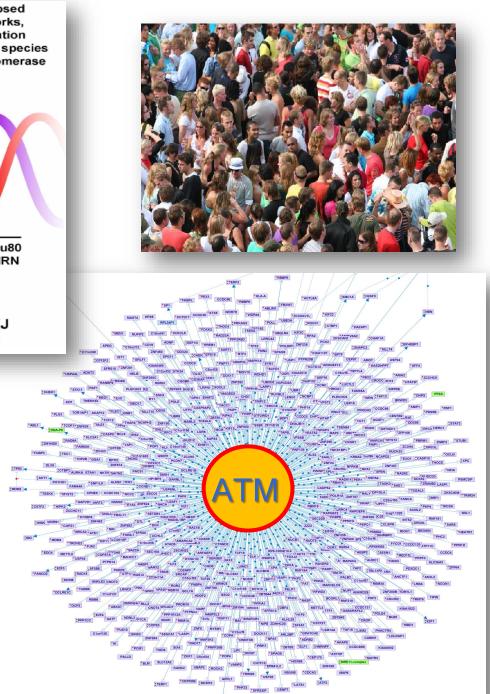
Significance particularly strong for participants below 50 yr of age at diagnosis

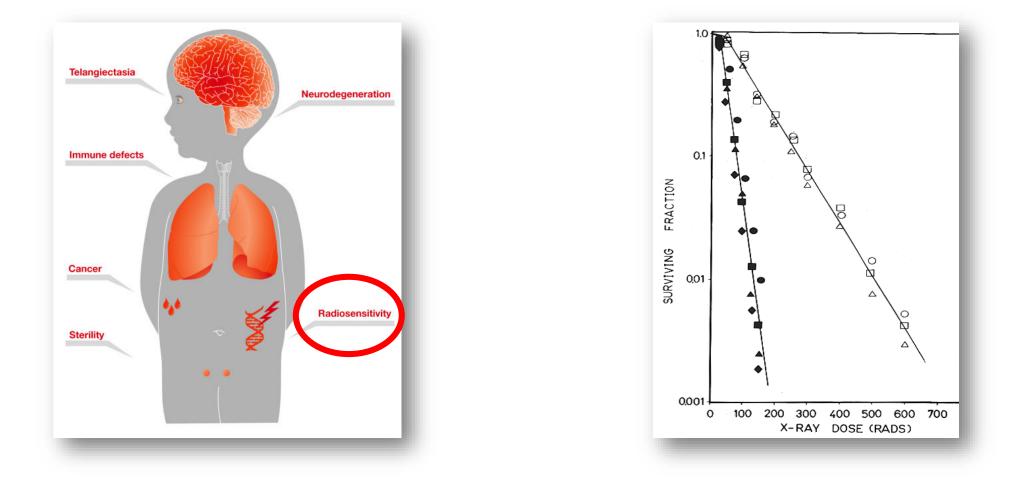
<u>Cancer types</u>: breast, lung, bladder, brain, lymphomas, melanoma (in situ), thyroid, hypopharynx, pancreas, kidney, stomach, hepatic flexure of colon, cervix uteri.

Slight premature aging in A-T carriers



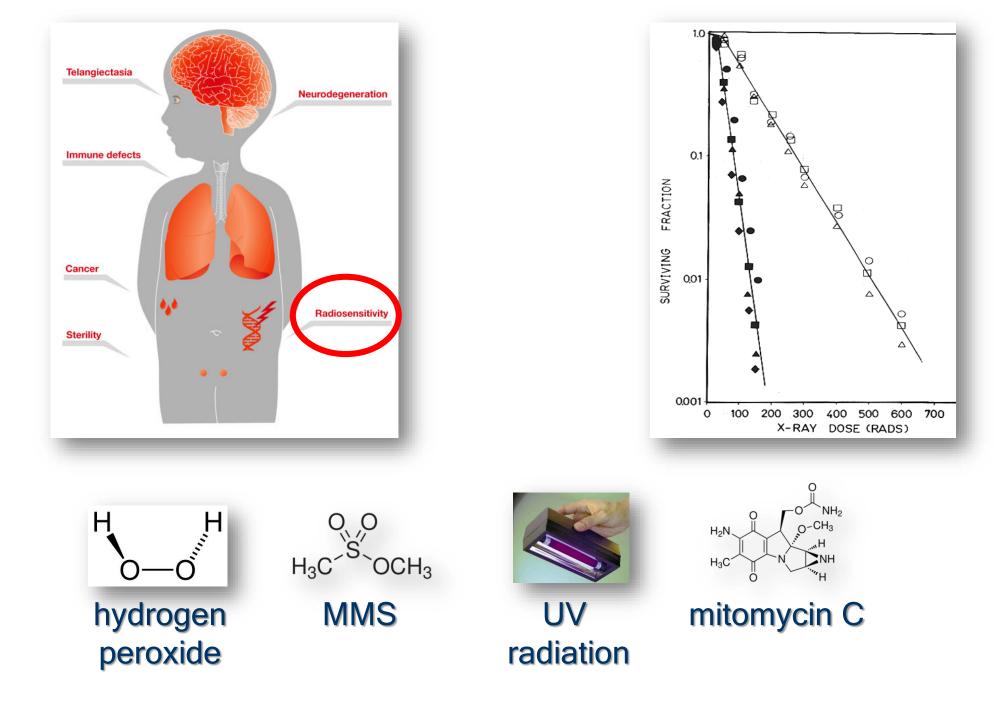
Genome Stability Index





Defective response to double-strand breaks in the DNA



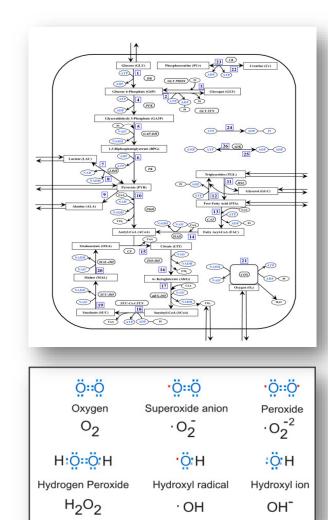


Endogenous DNA Damage in Mammalian Cells

Lesion	Events/cell/da
Single-strand break	55,200
Depurination	12,000
	13,920
Depyrimidination	600
	696
06-methylguanine	3,120
Cytosine deamination	192
Glucose-6-phosphate adduc	et 2.7
Thymine glycol	270
Thymidine glycol	70
Hydroxymethyluracil	620
8-oxo-G	178
Interstrand cross-link	8
Double-strand break	8

day Reference

Tice and Setlow, 1985 Lindahl, 1977 Tice and Setlow, 1985 Lindahl, 1977 Tice and Setlow, 1985 Tice and Setlow, 1985 Tice and Setlow, 1985 Bucala, et al, 1985 Saul et al, 1987 Saul et al, 1987 Saul et al. 1987 Shigenaga et al 1989 Bernstein and Bernstein, 1991 Bernstein and Bernstein, 1991



Erling Seeberg

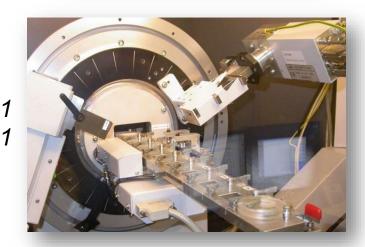
Endogenous DNA Damage in Mammalian Cells

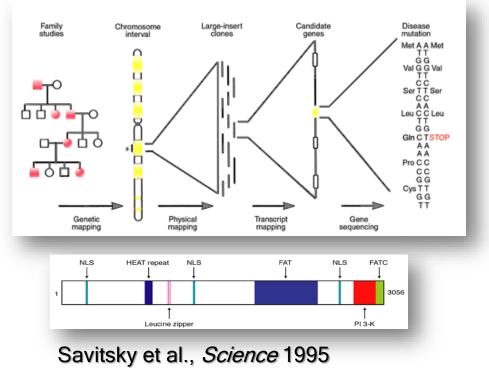
Lesion	Events/cell/day
Single-strand break	55,200
Depurination	12,000
	13,920
Depyrimidination	600
	696
06-methylguanine	3,120
Cytosine deamination	192
Glucose-6-phosphate adduc	xt 2.7
Thymine glycol	270
Thymidine glycol	70
Hydroxymethyluracil	620
8-oxo-G	178
Interstrand cross-link	8
Double-strand break	8

Reference

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The DSB response network is highly structured and streamlined in space and time

Importance of checks and balances

NLS

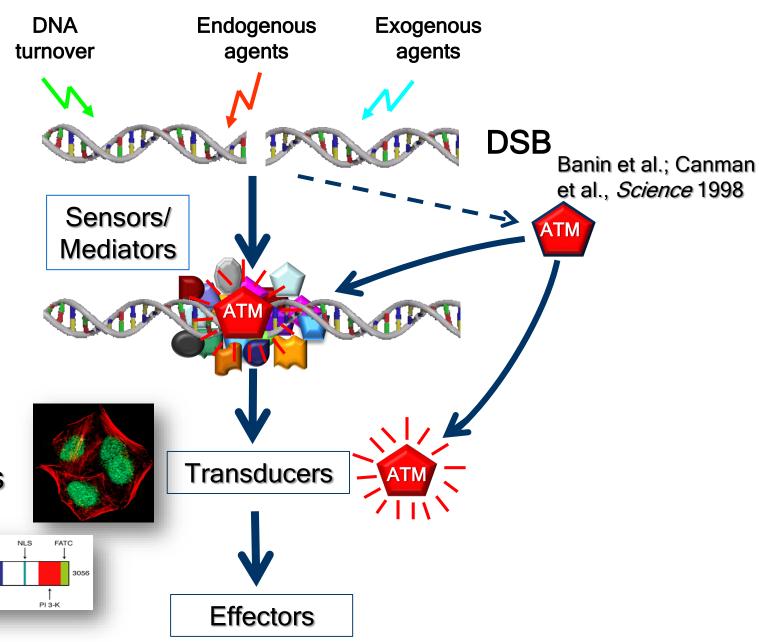
HEAT repeat

Leucine zipper

NLS

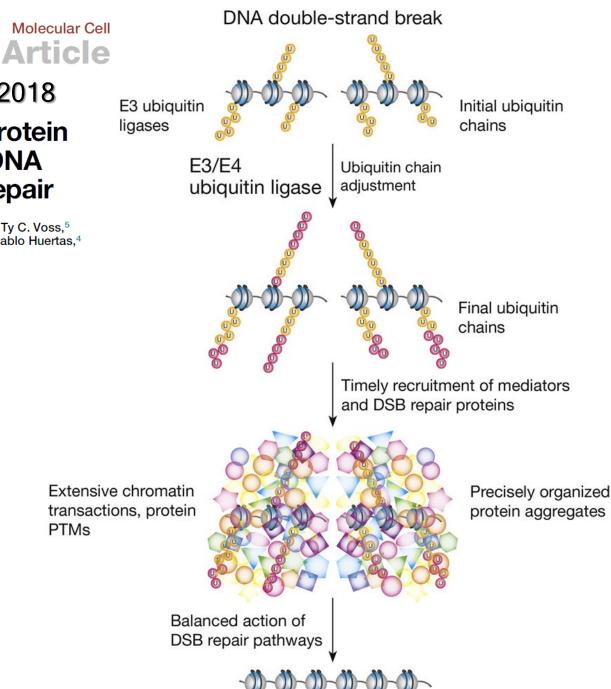
FAT

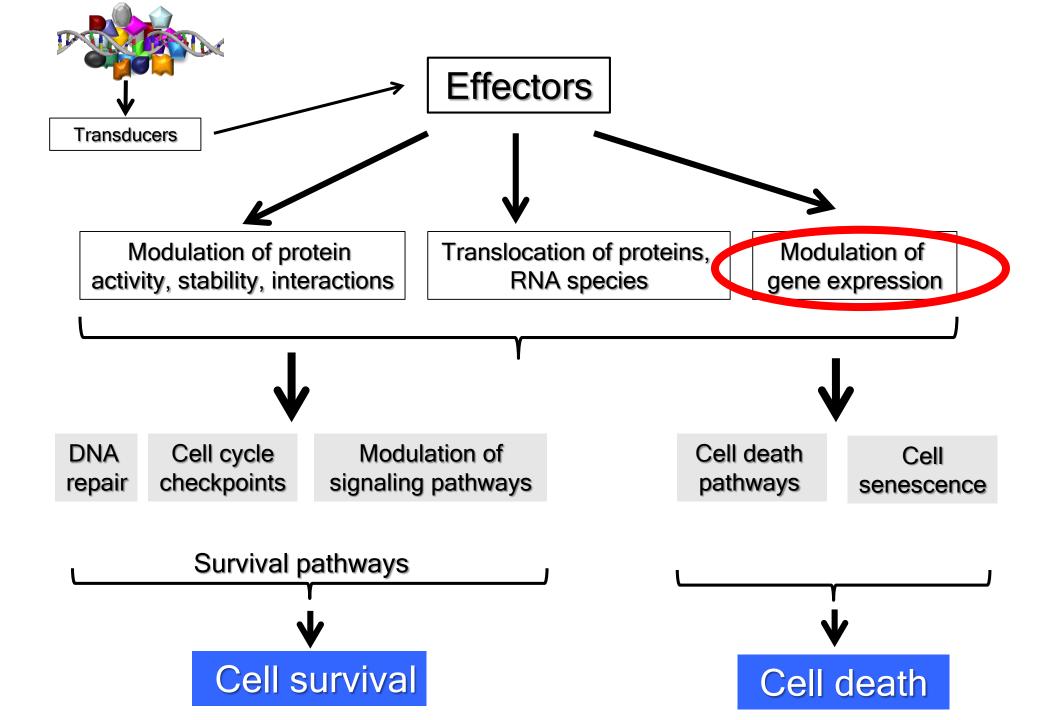
The DSB Response

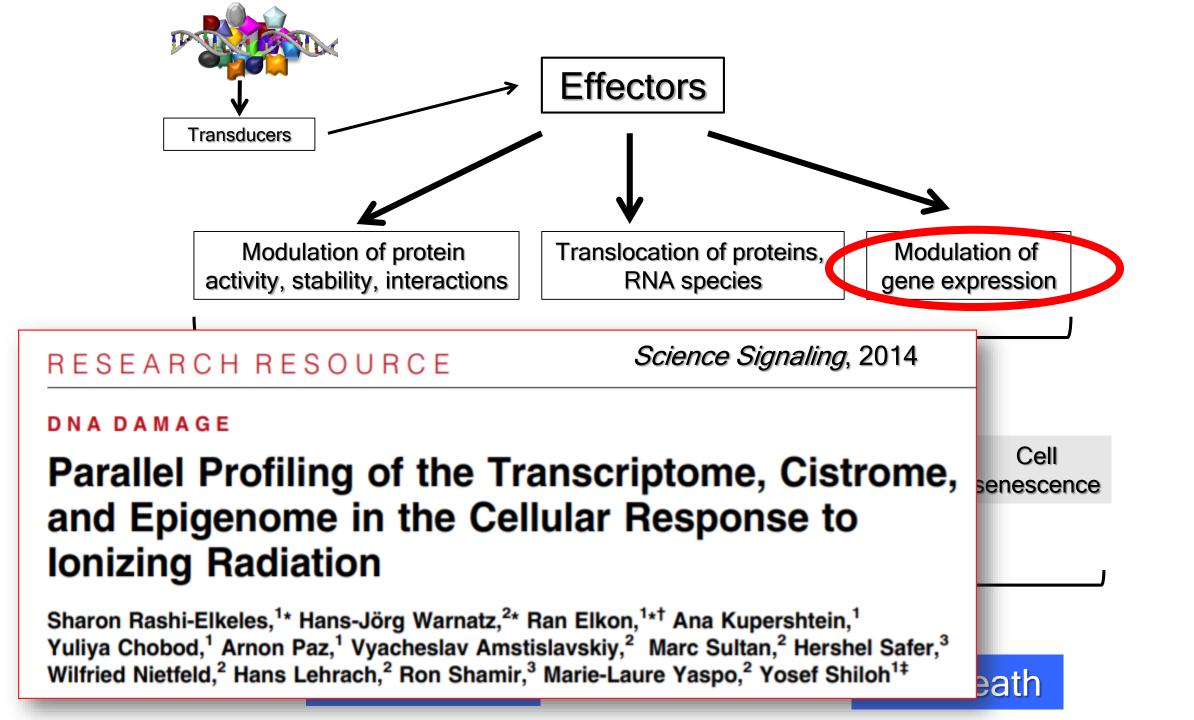


2018 The Ubiquitin E3/E4 Ligase UBE4A Adjusts Protein Ubiquitylation and Accumulation at Sites of DNA Damage, Facilitating Double-Strand Break Repair

Keren Baranes-Bachar,¹ Adva Levy-Barda,¹ Judith Oehler,² Dylan A. Reid,³ Isabel Soria-Bretones,⁴ Ty C. Voss,⁵ Dudley Chung,⁶ Yoon Park,⁷ Chao Liu,⁸ Jong-Bok Yoon,⁷ Wei Li,⁸ Graham Dellaire,⁶ Tom Misteli,⁵ Pablo Huertas,⁴ Eli Rothenberg,³ Kristijan Ramadan,² Yael Ziv,¹ and Yosef Shiloh^{1,9,*}







TERF2 *FKBPL CCDC98 *RBBP6 "HLA-A H2AFX ACTL6A ABLIMI *SP1 *KCTD17 CCDC35 WDR79 WDR44 *KIF22 MAST4 HPS5 *ZC3HAV1L FOXK2 POLL UBE3A RPL34P1 ROCK1 CTBP1 ISOLA TSEN2 TSE *MEN1 NUFIP2 C19orf41 *CDC2L5
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 NUFir2
 ADNP
 *EEF1G
 *RREB1
 *TPX2
 *POLDIP2
 *Nr 200

 SPEG
 *C10orff2
 *CD19
 *DX24
 *SAR11
 *BTF3
 *FIN2
 *SAG9
 *KIAA1107
 *BPTF

 ZNF460
 *DX24
 *POLEX
 *BTF3
 *FIN2
 *SAG9
 *KIAA1107
 *BPTF
 RAD23A CHAF1A EIF4EBP1 SNAPC3 MLLT4 C11orf48 CCDC9 PNPT1 UBAP2L MAPH14 SVN1 USP1 PTPN208 CEP97 AMOT U CCDC9 CEP97 AMOT UBAP2L MAPH14 SVN1 CEP97 AMOT U 24 CEP97 CEP97 AMOT CEP97 AMOT U GTF2F2 KIAA0460
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 CCDC8
 PMPT1
 STN1
 *KCTD12*ARHGEF12
 *AA

 C12or32
 STK24
 CGor/25
 *DX17
 *OGFI
 KIAA2018
 C19orf6
 *TSPYL4

 280C
 CGGBF
 *CGBAF
 *DX17
 *OGFI
 KIAA2018
 C19orf6
 *PBX2

 RIMS3
 CGGBF
 *CD3EAF
 *X01
 *UBXD2
 *NUP107
 *UC7L2
 *C
 SFRS18 ZNF281 C12orf32 STK24 *DLG7 HELB ZNF280C *HSPA4L ADAT3 ARIH2

 *RANBP9 *ID4B
 RIMS3
 COGOBF *CUSEAP
 ZNP292
 *UBX02 H3PX02A
 *NUP107
 *DEX2
 CROCC 3H13
 *HATIP

 *STK11
 *RAFT
 PLEKHGT R21
 *ZBTB33 KNTB
 *LARP1
 *SOL2
 *PPP1R*LARP1
 *UBR1
 *GOL2
 *MOD107
 *UUC7L2
 CROCC 3H13
 *HATIP

 AZH
 *MED1
 *EVH
 RY1
 *OP51
 *MAGE02
 *GOL7
 *UUR1
 *INCP17
 *UBR1
 *MAGA
 INPP56

 AZH
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 *EVH
 RP17
 *OL6
 *TRP12
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 *USR1
 *INCP17
 VURN *TAFIC
 BRW03
 *INP56

 AZH
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 *OL6
 *TRP12
 *GOL7
 *USR1
 PPP1R*LARP1
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 VURN *TAFIC
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 AZH
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 *TRC112
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 *USR1
 ERC6
 *UNR *TAFIC
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 *INP1
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 *INP56
 *INP1
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 *INP1
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 *ZFHX3
 GTF2B

 *TOP2B
 *GGA1
 RPTN

 *TOP2B
 *GGA1
 RPTN

 CTBPP
 AURKA
 ETAA1

 NKTR
 MATN2
 PACS1

 *MS1
 FGTF3C1

 *MS1
 FGTF3C1
 ZC3H4 ORC3L *RNF138 TNKS1BP1 *ALS2 *SALI1 KRBA2 10/155 NCAPD2 *EX01 CASP10 *OCLN *FUBP3 TSC1 *ZNF24 *ZNF24 *ZNF24 *ZNF24 *ZNF24 *ZNF26 PWWP: XPC, CBORRB, NFRKB RPA1 *SPEN *RAD61/:PER1 *RAD61/:PER1 *AD651/:PER1 TP53 PHYHD1 FAM44A MDM2 *TSSK4 - MYST2 - CPNE8 CCDC104 *RCC2 ZF ESC01 PHF6 CSTF2 HIPK2 GAPVD1 ART3 NSMAF EYA3 ZNF624 NACA CIZ1

 Ennage
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 Rapger a
 Revuers
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 * MAD2L18P
 * SEC229
 * FKBP5
 ZINF830
 C26
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 * SA

 ATE1
 * NIN
 * SETDB1
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 * MAD2L18P
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 * C25
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 * SA

 ATE1
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 ZINF808
 * PSMD4
 * RIOK1
 BEGAIN

 * KIF11
 * CIBort25
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CREB1



 *STK11
 *NAT
 PLEKH01
 ?23
 ?23
 PART
 *SGOL2
 PPPP1R'sARP1
 *GROU
 *UBR1
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 *HAP1
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 *AURKA
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 NKTR
 MATN2
 PACS1
 SMG1

 PHYHD1
 *SNF1LK
 ALMS1
 TFR1
 FORMET
 GARNL1
 *ALS2 *SAAL1 KRBA2 10/755 NCAPD2 *EX01 :CASP10 *OCLN THOCS *ZNF24 PWWP XPC, Coords NFRK8 RPA1 *SPEN *RAD52 *RAD51 *PER1 *SPEN *RAD52 *RAD51 *PER1 *HSPA4 *CADP52 *ZRAN52 LASP1 CADP52 *ZRAN52 LASP1 •NFIA AKT1 PHYHD1 SNF1LK ALMS1 TFR1 CCNE1 SUSPEND PSMC3IP

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 ESCOI
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 ZCADP2
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 TOLADY
 TOLALY
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 FM S
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 "DBF4
 METTL3
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 "HIF0
 CCDC131

 *AATE
 NDM2.*PICA
 MUM1
 "RBM14
 "SVL
 "RUFY1
 "BA* SMARCB1
 "HIF0
 ZBTB40
 "CROP

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SF3A1
CSTF2T COP33 ZNFB MYSM1 C12orf5 DOCK11 ARI20P GPATCH8 CABINI CABINI *SSSCA1 *LASP1 F264
*COPA C1orf135 GINS2 LDLRAP1 CABIN1 ZNF264 *DNMT3B ADRB2 *AKAP9
 "WNK1
 "ZETB2
 "ELF1
 "HNRNPF

 "PRPF38B
 LIPI
 "MCM7
 "SPAG5
 "AT
 RAD17 TIGD4 SIX4 CCDC90B KIAA0802 PCM1 *CEP170 ZHX1 C5orf24 POP4 PALLD MATR3 41 VAMP2 CHTP18 EPB41L2 HOXB6 ZI *TRIM28 USP28 CDCA3 BLM SLC12A2 MRE11-complex ZNF420 KANK2 UBAP2 ROCK2 MAP9

CNTROB MCM10 ATF2 TERF1 LATS1 *PHF23 *SFRS2IP CENPT CREB1

TERF2

TSEN2

CCDC8 PNPT1 UBAP21 MAPK14 SYN1

*HLA-A

*ABLIM1

UBQLN4 KIF2C

ACTL6A

ROCK1

*KCTD12 ARHGE

*SEPT6

CCNC

ZC3HAV1L

*KIF22

*FKBPL *PEX1 CCDC98 *RBBP6

MAST4 HPS5

GTF2F2 ISY1 •GRLF1

*STXBP4 * DNAJ*FBXL11 * *SETDB1

SFRS18 ZNF281

RANBP9 RID4B

C11orf48

HSPA4L ADAT3

ZCCHC11

*MDM4 *TROVE2 *PJA2

MCM6 DCLRE1C

DCP2

*COPZ1 ZNF462

*ABL1

*FUBP3 TSC1

DLX6

IKBK WDR91

*EDC4 METTL8

*FANCD2

TP53

MDM2

*STK11

MEN1 NUFIP2 C19orf41 CDC2L5

RPL34P1

*KCTD17 CCDC35 STX6 WDR79 *WDR44

 SPEG
 *C10orf12
 *CD19
 ADNP
 TEEF10
 *REB1
 *TP22
 *POLDP/
 ZNF450
 PCK2

 ISY1
 *GRLF1
 \$P011
 *CHEK *EPS16
 *BTF3
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PLEKHGI R2I *ZBTB33 jKN1B *LRFN1 SGOL2 *PPPP1R1=

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 *OGF KIAA2018

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 *OGF KIAA2018

 B
 RIMS3
 CGG6P*C05EAP 2X01
 ZNF282
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 *NUP107



*ZFP106 *MARCKS*MYST3 *PBRM1 ZNRF2 *STUB1 CLNS1 OXSR1 FNIP1 ZC3H4 ORC3L *RNF138 TNKS1BP1 NUCKS1 *ALS2 SAAL1 KRBA2 10rf55 NCAPD2 *EX01 CASP10 *ZNF24 THOC5
 *ZNF24
 THOCS

 *ZNF24
 C9orfbs

 PWWP:XPCJ
 *NFRKB

 *RAD614*PER1
 *NSPA1

 *RAD614*PER1
 *TAD63

 *RAD614*PER1
 *TAD64*PER1

 *RAD614*PER1
 *TAD64*PER1

 *RAD614*PER1
 *TAD64*PER1

 *RAD614*PER1
 *TAD64*PER1

 *SC0228
 *FAD64*PER1

 *SC028 THOCS *ZNF24

*HEATR1 PPM1D

*ZFP64 NIPE ZDHHC20 SF3A1

ARL28P C12orf5 DOCK11 COPA LDLRAP1 CABIN1 *DNMT3B ADRB2 *ZBTB2 *ELF1 *HNRNPF CCCDC90B KIAA0802 *WNK1 LIPI MCM7 *CEP170 POP4 MATR3 HOXB6 MRE11-C *VAMP2 CHTF18 EPB41L2 ZNF420

*TRIM28 *USP28 NSUN5 CDCA3 MAP9 ATF2 LATS1 *PHF23 SFRS2IP CENPT

TERF2

*FOXK2 THOC4 74117192

"HLA-A

ABLIM1

POLL UBE3A

TPX2 POLDIPS ZNF238

IT STRI

UBQLN4 KIF2C

ACTL6A

ROCK1

PCK2

*KIAA1107

ZC3HAV1L

*FKBPL PEX1 CCDC98 RBBP6

*KCTD17 CCDC35 STX6 WDR79 WDR44

*RAD23A

*SP1

RPL34P1

TERF1

CREB1

MAST4 HPS5

MEN1 NUFIP2 C19orf41 CDC2L5

 SPEG
 •C10orf12
 •CD19
 ADNP
 EEF1G
 •RREB1
 •SPR2

 ISP1
 ZNF480
 •DDX24
 •CHEK*EPS16
 •TPX2
 •POLDIP

 ISV1
 •GRLF1
 SPG11
 •CHEK*EPS16
 •TTX2
 •SPAG9
 GTF2F2 ISY1 •GRLF1 CCDC8 KIAA0460 C12orf32 STK24 C5orf25 SFRS18 ZNF281
 NP.201
 C12orf32
 STK24
 C5orf25
 *MOV10
 *SCF01
 *CGFI

 HELB
 *ZNF280C
 *OGEF
 *OGEF
 *OGEF
 *OGEF
 *IOX17

 B
 RIMS3
 CGGEF
 *ODEAP
 XO1
 ZNF292
 *UBXD2
 H3PXD2A
 *NUP10
 *HSPA4L ADAT3
 *HSPA4L
 ADA13
 **Exercite
 CGGB#
 CGGB#</t CHEK1 *PLS3 TOR1AIP1 AKAP12 *PLEC1 ONB1 *MLLT10 DDX6 UBR5 *ABL1 SLC2A1 CASP8 BCL9 IRS2 CXort26 JMJD1C SAPS3 *FAM60A *ZFHX3 :GTP2B *YAP1 *POP1 /KLI Claurias *EMMT
 *ZMYND8
 *FAM60A
 *ZFHX3
 GGTP2B

 *FUBP3
 *TOP2B
 *GGA1
 RPTN
 MMM2
 *GTF2G1

 *DLX6
 ZNF574
 *CTF2G1
 POLRE1B

 X6
 ZNF574
 DCLRE1B

 *CTBP*AURKA ETAA1 NKTR MATN2
 PACS1
 SMG1

 HP1BP3
 GARNL1
 TP53 AKT1 PHYHD1 SNF1LK ALMS1 TFR1 CCNE1 USP6NL MDM2 *TSSK4 MYST2 CPNE8 CCDC104 RCC2 ZF ESC01 PHF6 CSTF2 HIPK2 GAPVD1 ART3 NSMAF EYA3 ZNF624 NACA CIZ1
 *BRCA2 *ATE1
 *NIN
 *FIGNL1
 *SETDB1

 *BRCA2 *ATE1
 *NIN
 *FIGNL1
 *GRCA2

 *BRCA2 *ATE1
 *NIN
 *FIGNL1
 *GRCA2

 *BRCA2 *ATE1
 *FIGNL1
 *GRCA2
 *GRCA2

 *KIF11
 LC4A1AB
 *UCHL3
 *BARCA2

 *FIGNL1
 *GRCA2
 *GRCA2
 *GRCA2

 *FIGNL1
 *GRCA2
 *GRCA2
 *GRCA2

 *FIGNL1
 *GRCA2
 *GRCA2
 *GRCA2

 *GRCA2
 *GRCA2
 *GRCA2
 *GRCA2
 ZCCHC11 *IKBK WDR91 ZNF462 *MDM4 *TROVE2 *PJA2 *EDC4 METTL8 USP34 FANCD2

MCM6 TOARME YOUR COUNT

RAD18

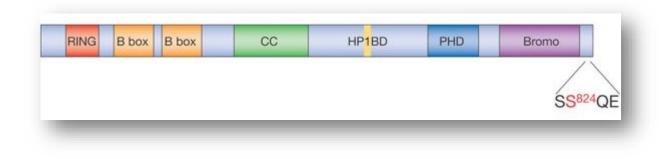
C11orf48

Physical and Functional Dynamics of DDR Factors



Chromatin relaxation in response to DNA double-strand breaks is modulated by a novel ATM- and KAP-1 dependent pathway

Yael Ziv^{1,5}, Dana Bielopolski¹, Yaron Galanty¹, Claudia Lukas², Yoichi Taya³, David C. Schultz⁴, Jiri Lukas², Simon Bekker-Jensen², Jiri Bartek² and Yosef Shiloh^{1,5}





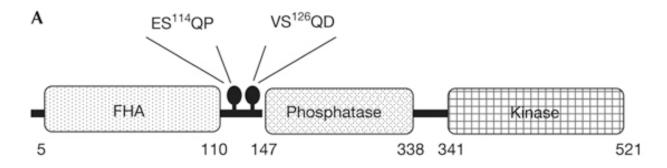


2011



ATM-mediated phosphorylation of polynucleotide kinase/phosphatase is required for effective DNA double-strand break repair

Hava Segal-Raz¹, Gilad Mass¹, Keren Baranes-Bachar¹, Yaniv Lerenthal¹, Shih-Ya Wang², Young Min Chung³, Shelly Ziv-Lehrman¹, Cecilia E. Ström⁴, Thomas Helleday^{4,5}, Mickey C.-T. Hu³, David J. Chen² & Yosef Shiloh¹⁺



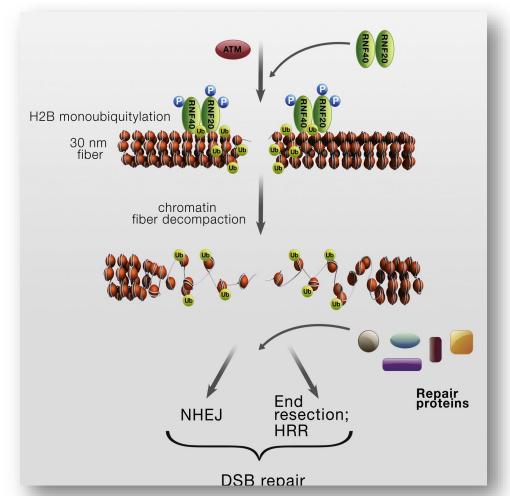






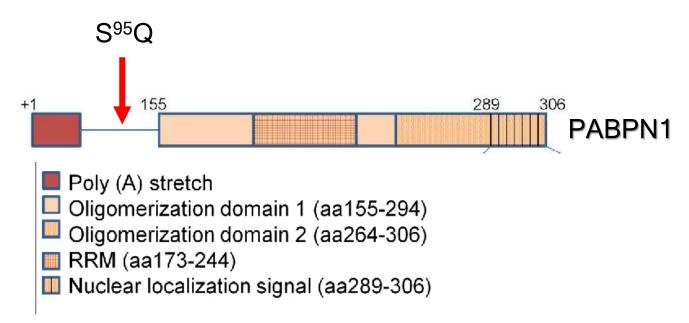
Requirement of ATM-Dependent Monoubiquitylation of Histone H2B for Timely Repair of DNA Double-Strand Breaks

Lilach Moyal,^{1,11} Yaniv Lerenthal,^{1,11} Mali Gana-Weisz,¹ Gilad Mass,¹ Sairei So,² Shih-Ya Wang,² Berina Eppink,³ Young Min Chung,⁴ Gil Shalev,¹ Efrat Shema,⁶ Dganit Shkedy,¹ Nechama I. Smorodinsky,⁶ Nicole van Vliet,³ Bemhard Kuster,⁷ Matthias Mann,⁸ Aaron Ciechanover,⁹ Jochen Dahm-Daphi,¹⁰ Roland Kanaar,³ Mickey C.-T. Hu,⁴ David J. Chen,² Moshe Oren,⁶ and Yosef Shiloh^{1,*}



Nuclear poly(A)-binding protein 1 is an ATM target and essential for DNA double-strand break repair

Michal Gavish-Izakson¹, Bhagya Bhavana Velpula¹, Ran Elkon¹, Rosario Prados-Carvajal², Georgina D. Barnabas¹, Alejandro Pineiro Ugalde³, Reuven Agami³, Tamar Geiger¹, Pablo Huertas², Yael Ziv^{1,*} and Yosef Shiloh^{1,*}



Please cite this article in press as: Jachimowicz et al., UBQLN4 Represses Homologous Recombination and Is Overexpressed in Aggressive Tumors, Cell (2019), https://doi.org/10.1016/j.cell.2018.11.024

2019 Article

Cell

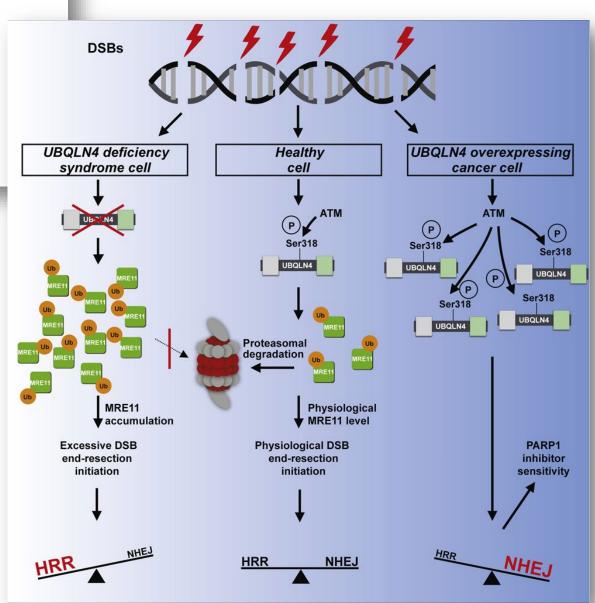
UBQLN4 Represses Homologous Recombination and Is Overexpressed in Aggressive Tumors

Ron D. Jachimowicz,^{1,2,3,*} Filippo Beleggia,^{3,5,18} Jörg Isensee,^{6,18} Bhagya Bhavana Velpula,^{1,2,18} Jonas Goergens,³ Matias A. Bustos,⁷ Markus A. Doll,^{4,8} Anjana Shenoy,² Cintia Checa-Rodriguez,⁹ Janica Lea Wiederstein,⁴ Keren Baranes-Bachar,^{1,2} Christoph Bartenhagen,^{10,11} Falk Hertwig,^{12,13,14} Nizan Teper,^{1,2} Tomohiko Nishi,⁷ Anna Schmitt,³ Felix Distelmaier,¹⁵ Hermann-Josef Lüdecke,^{5,16} Beate Albrecht,¹⁶ Marcus Krüger,^{4,11} Björn Schumacher,^{4,8} Tamar Geiger,² Dave S.B. Hoon,⁷ Pablo Huertas,⁹ Matthias Fischer,^{10,11} Tim Hucho,⁶ Martin Peifer, 11,17 Yael Ziv, 1,2,19,* H. Christian Reinhardt, 3,4,11,19,20,* Dagmar Wieczorek, 5,16,19,* and Yosef Shiloh 1,2,19,*



Yael Ziv

Christian Reinhardt



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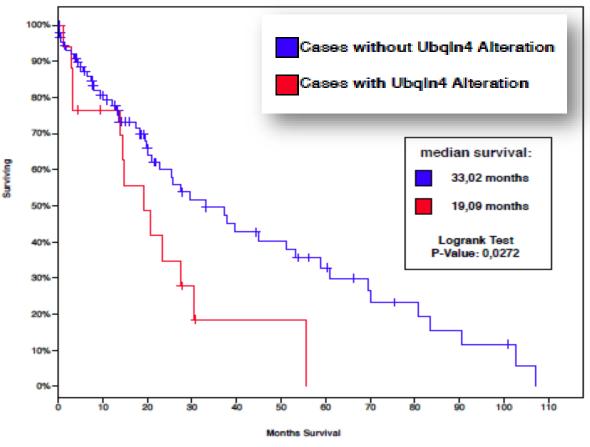
Article 2019

Cell

UBQLN4 Represses Homologous Recombination and Is Overexpressed in Aggressive Tumors

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DR. RON JACHIMOWICZ RECEIVES THE THEODOR-FRERICHS-PRICE FROM THE GERMAN SOCIETY FOR INTERNAL MEDICINE

Ron Jachimowicz Bhavana Velpula Yael Ziv

Christian Reinhardt

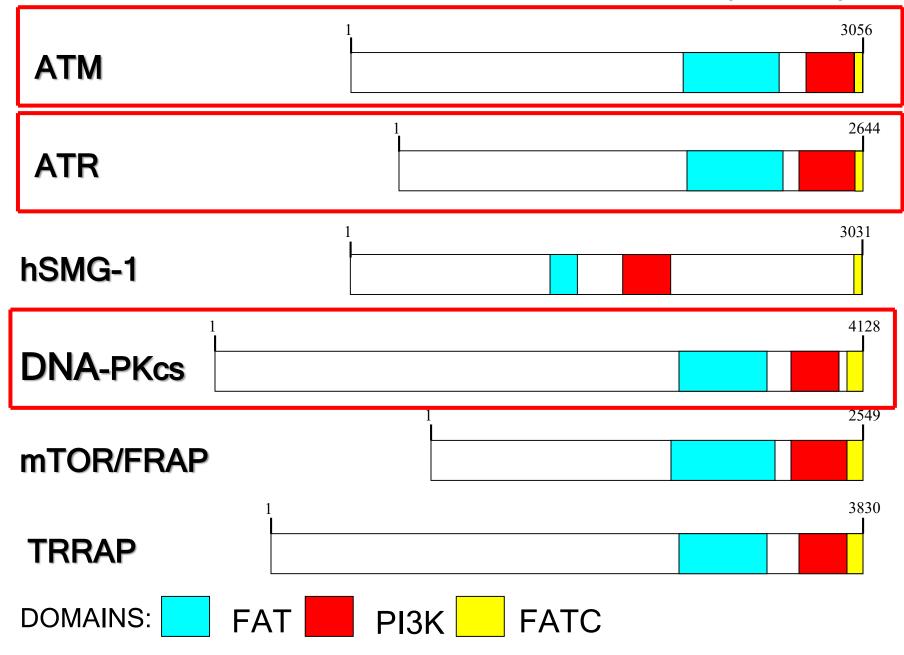
07/05/2020



Dr. Jachimowicz. ©MedizinFotoKöln

Our genetic material is damaged every day. When deciding how to repair serious damage to DNA, cells have to choose between an error-prone and an error-free repair route. The choice is important because the decision to repair the damage in a fault-prone way can lead to further DNA damage and contribute to the development of cancer. Dr. Ron Jachimowicz, physician and scientist at Clinic I for Internal Medicine of the University Hospital of Cologne, recently discovered that the protein

PI3-Kinase-Related Protein Kinases (PIKKs)

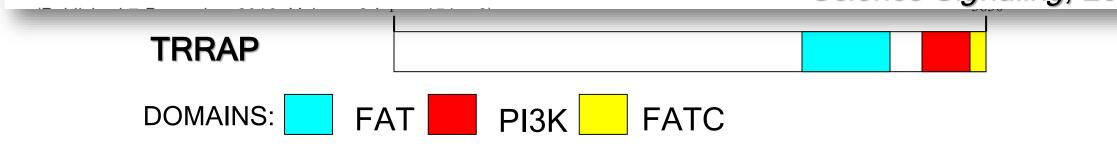


PI3-Kinase-Related Protein Kinases (PIKKs)

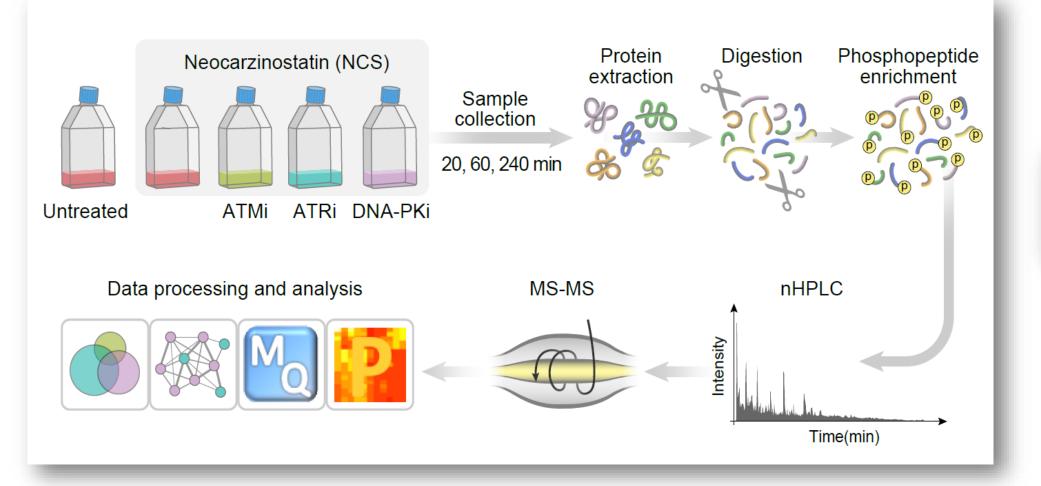


ATM-Dependent and -Independent Dynamics of the Nuclear Phosphoproteome After DNA Damage

Ariel Bensimon,^{1*†} Alexander Schmidt,^{2,3}* Yael Ziv,¹ Ran Elkon,⁴ Shih-Ya Wang,⁵ David J. Chen,⁵ Ruedi Aebersold,^{2,6,7‡} Yosef Shiloh^{1‡} *Science Signaling*, 2010



Phosphoproteomics reveals novel modes of function and inter-relationships among PIKKs in response to genotoxic stress





Ruedi Aebersold Ariel Bensimon



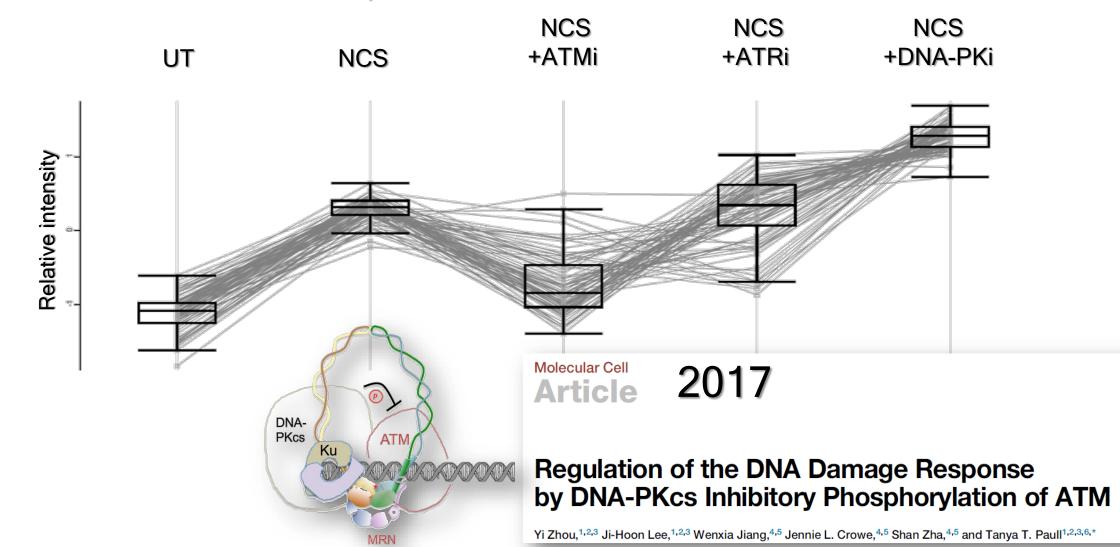
Phosphoproteomics reveals novel modes of function and inter-relationships among PIKKs in response to genotoxic stress

- Stringent criteria for defining hits
- Special attention to dephosphorylations
- Validation of scores of new phosphorylation targets using selection reaction monitoring (SRM)
- PIKKs remain the main players in genotoxic stress-induced phosphorylations, but motifs of additional protein kinases are present (e.g., CK-1)
- Close relationships among PIKKs
- Matching hits with our DDR meta-analysis database

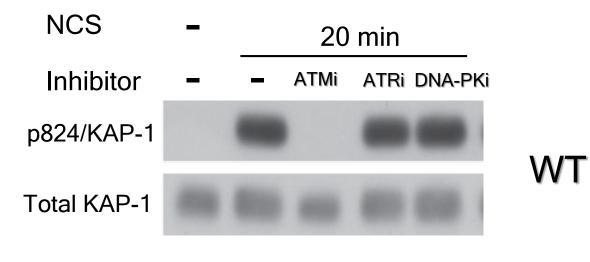


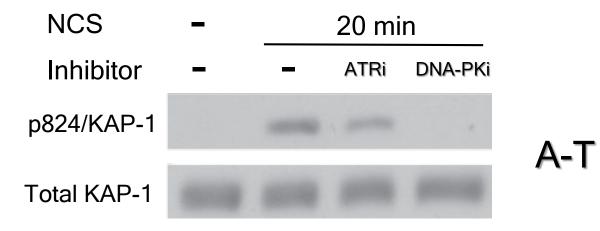
Distinct Patterns of NCS-Induced Phosphorylation Dynamics and PIKK-Dependence

NCS-treated WT cells, 4 hr, 71 p-sites

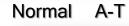


What happens to ATM substrates in A-T cells?







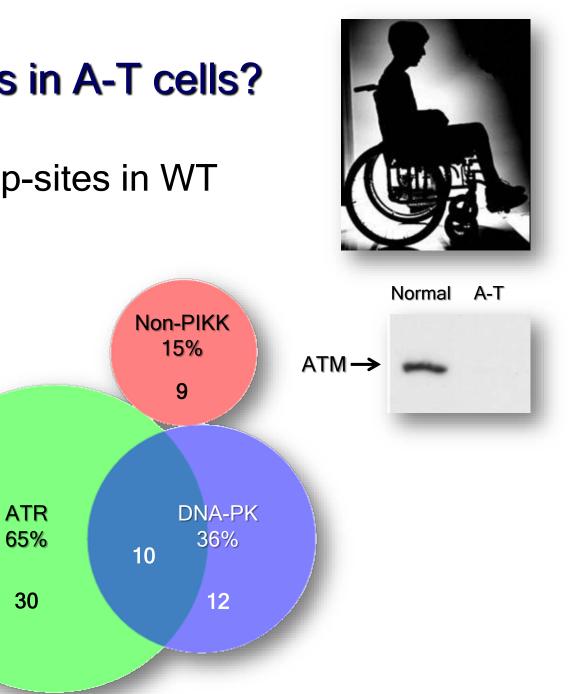


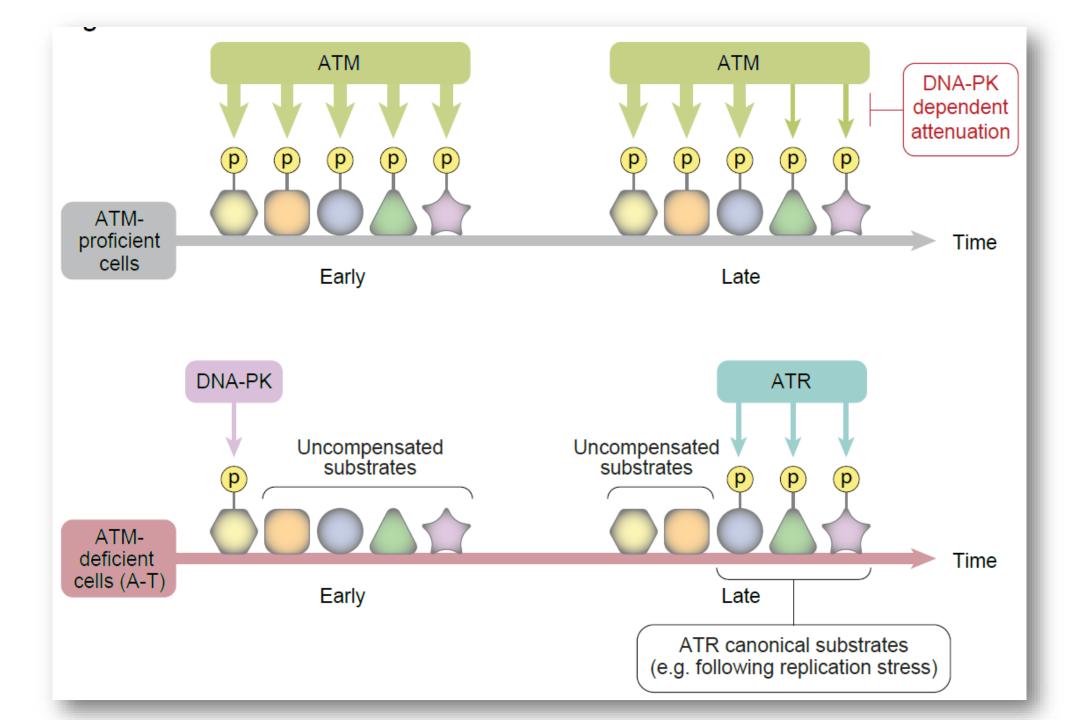




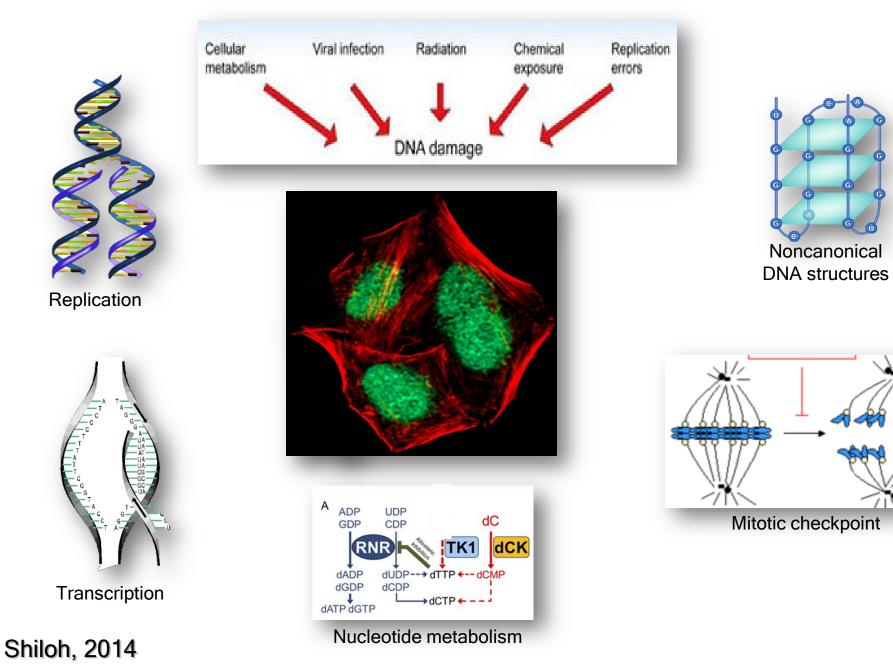
What happens to ATM substrates in A-T cells?

- Most of the strictly ATM-dependent p-sites in WT cells did not respond in A-T cells.
- > 61 sites did respond in A-T cells.
- The early phosphorylations were DNA-PK-dependent and the late ones - ATR-dependent.

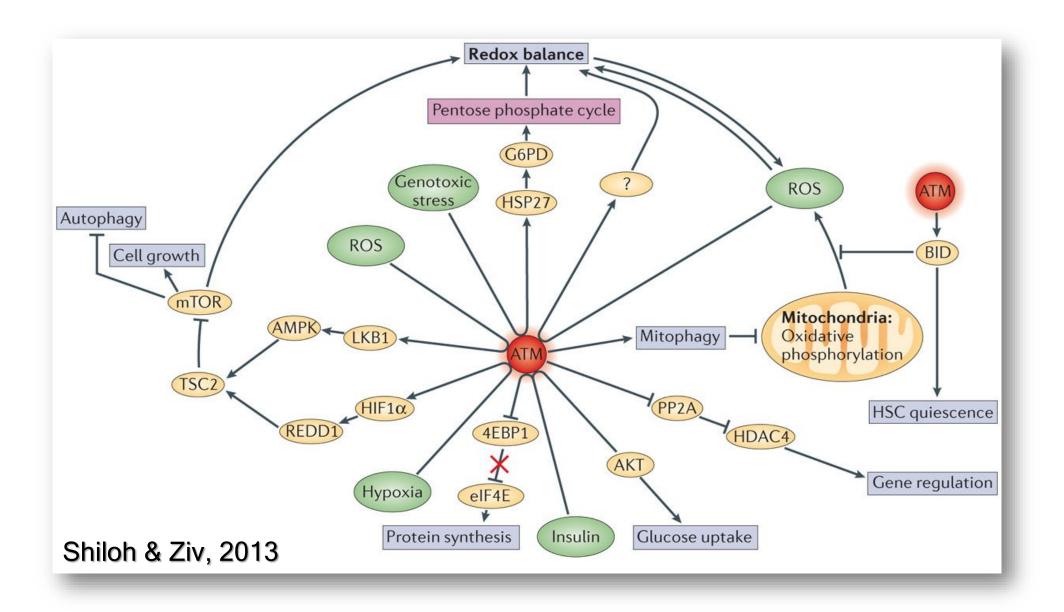


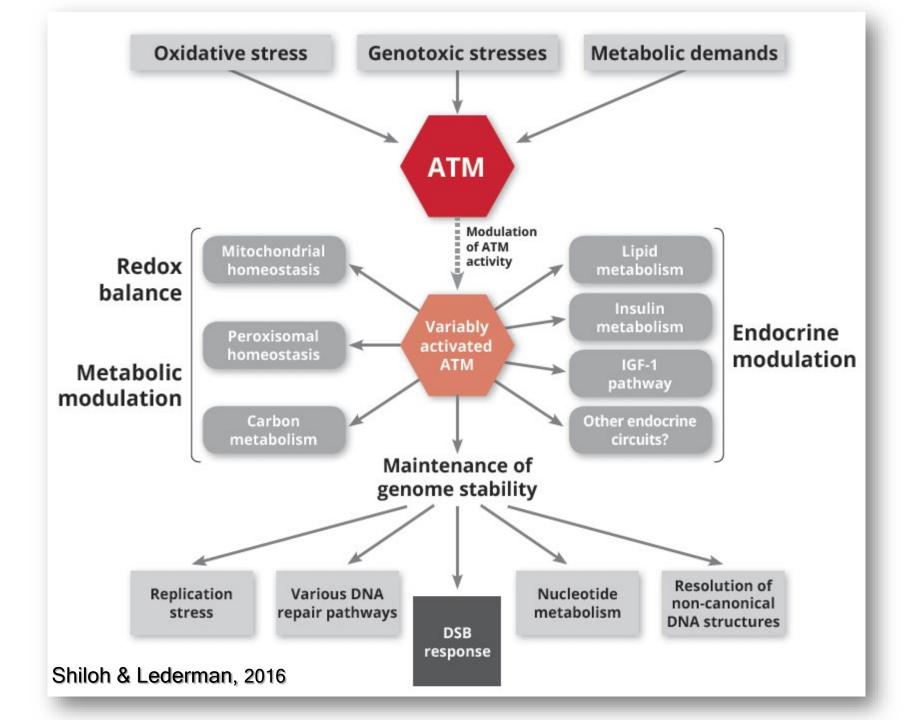


A General Role for ATM in Maintaining Genomic Stability

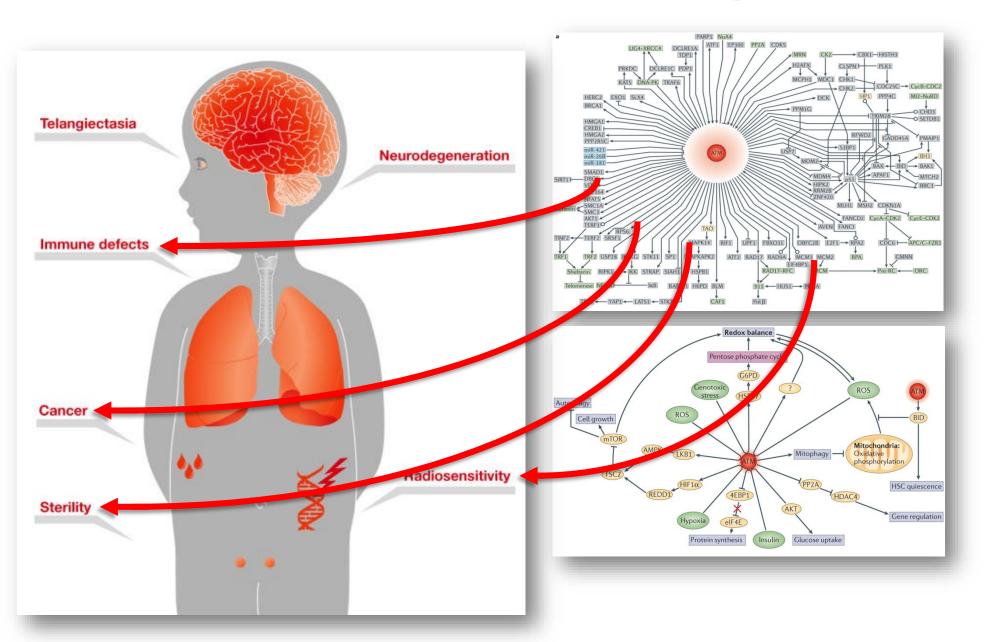


ATM is a Homeostatic Protein Kinase

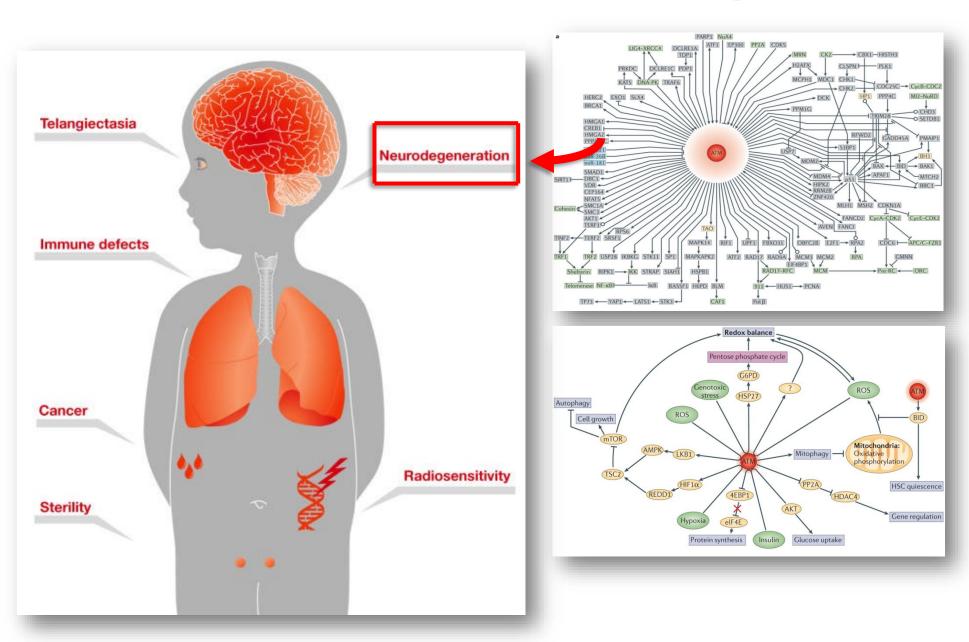


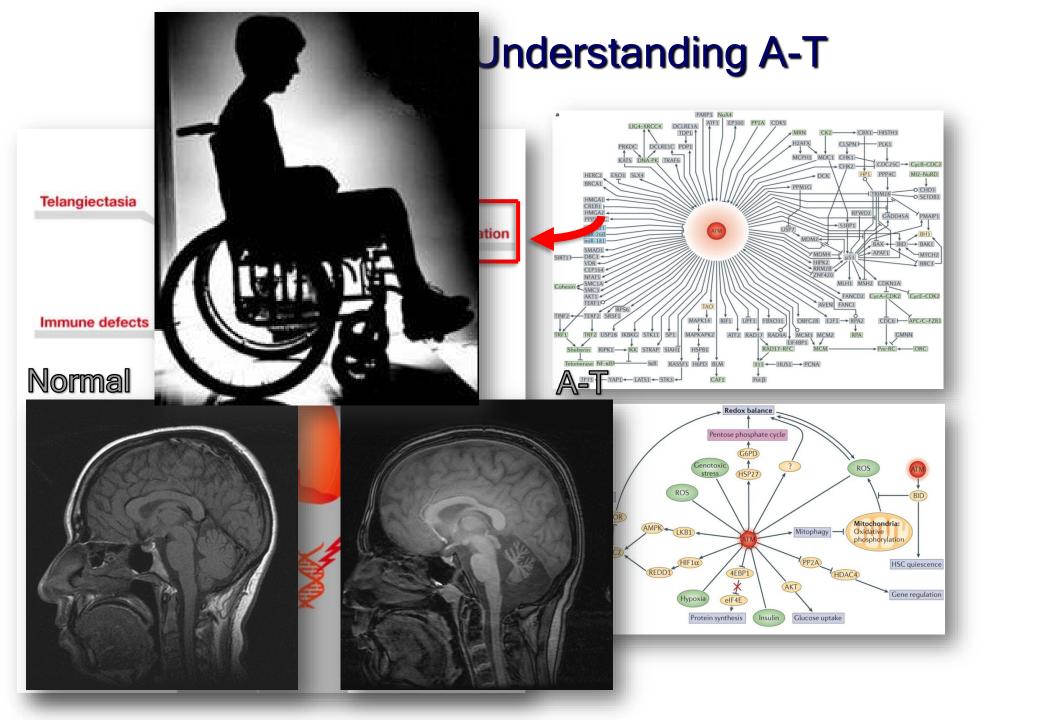


Understanding A-T

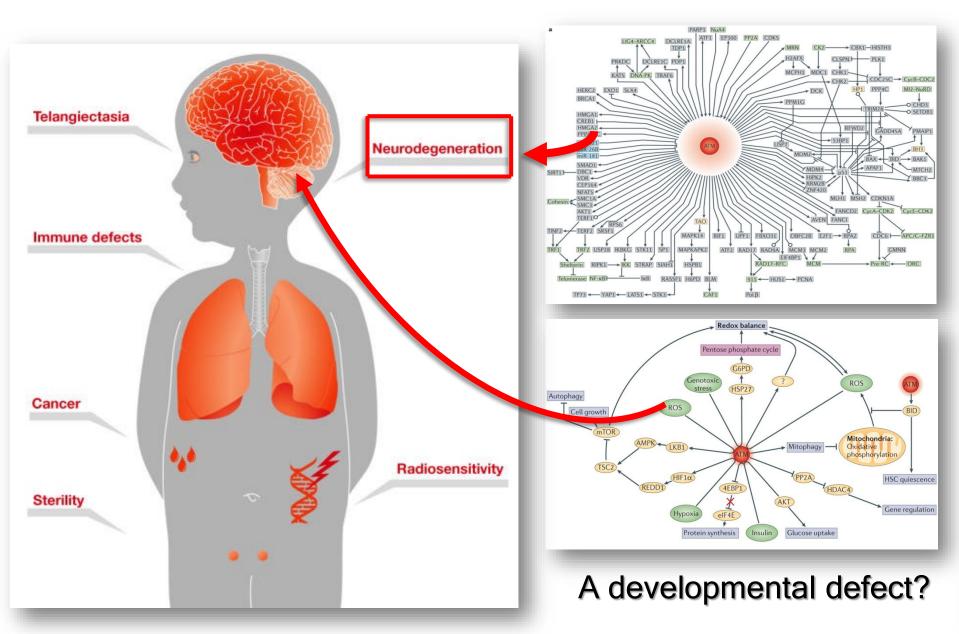


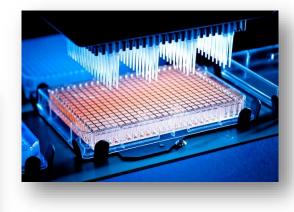
Understanding A-T





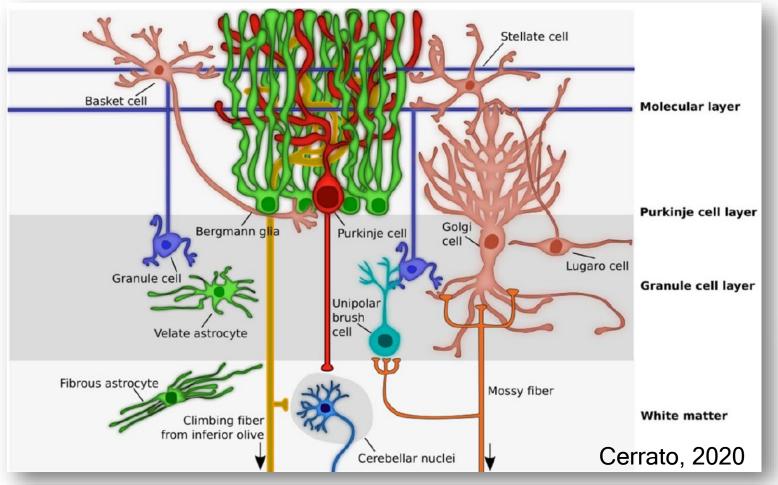
Understanding A-T



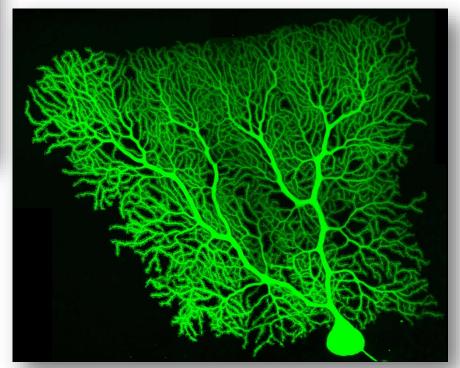


Comparison of WT to ATM-deficient tissues/cells using 'omics' profiling usually shows marked differences.

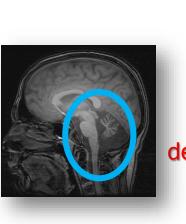




The cerebellar degeneration in A-T: a case for genome instability



Autosomal Recessive Cerebellar Ataxias Resulting from DNA Repair Deficiencies



A-T ATM deficiency

Healthy control



Spinocerebellar ataxia with axonal neuropathy (SCAN1) TDP1 deficiency



Ataxia with ocular motor apraxia 5 (AOA5) XRCC1 partial deficiency



Ataxia with ocular motor apraxia 1 (AOA1) Aprataxin (APTX) deficiency



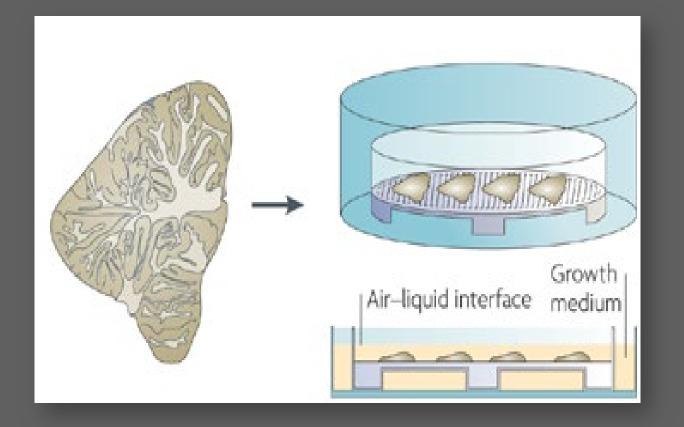


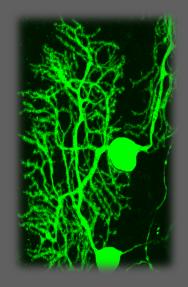
Ataxia with ocular motor apraxia 2 (AOA2) Senataxin (SETX) deficiency

Microcephaly with seizures (AOA4) PNKP deficiency



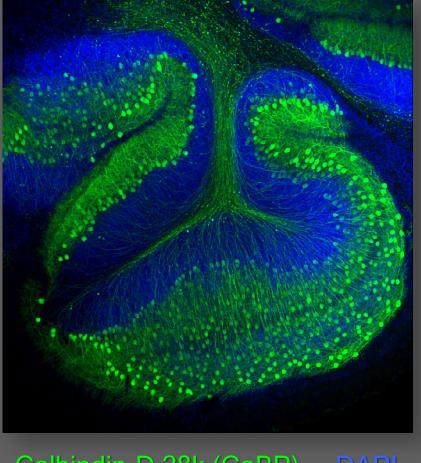
Cerebellar Organotypic Cultures





Tzur-Gilat et al., *Mech. Age. Dev.* 2014 Tal & Shiloh, *Methods in Mol. Biol.* 2016 Tal et al., *DNA Repair* 2018

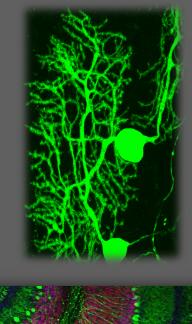
Cerebellar Organotypic Cultures

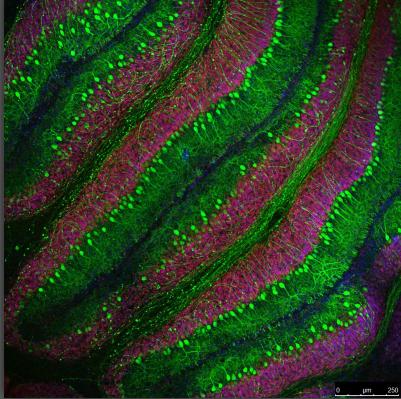


Calbindin-D 28k (CaBP) DAF

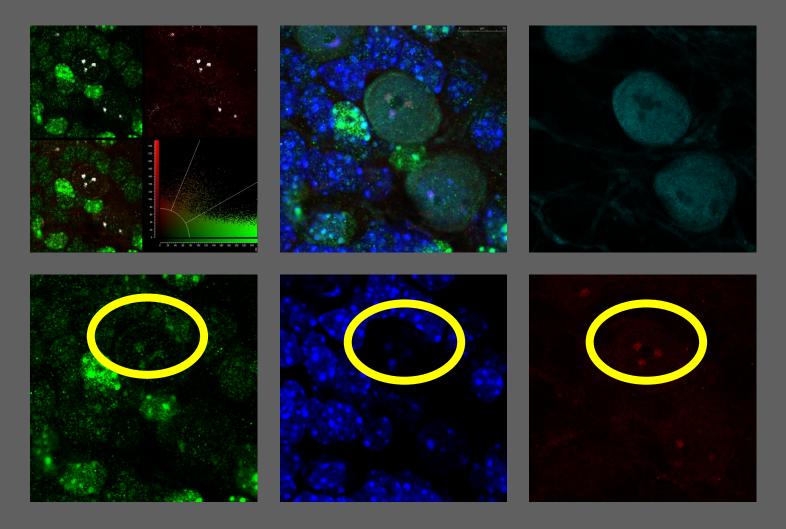
Tzur-Gilat et al., *Mech. Age. Dev.* 2014 Tal & Shiloh, *Methods in Mol. Biol.* 2016 Tal et al., *DNA Repair* 2018







Purkinje Cells Chromatin: Mostly Euchromatic



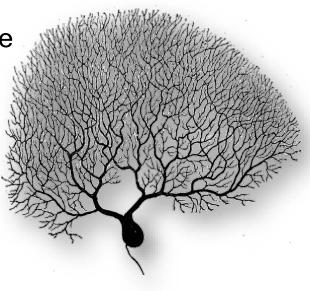
Calbindin-d28k/H3K9me3/HP1a/DAPI



Why are Purkinje Cells Sensitive to ATM Loss More than Other Types of Neurons?

- > A <u>combination</u> of factors creating a particularly unfortunate background for ATM loss:
 - No regeneration, long life
 - High metabolic rate and oxidative stress
 - Open chromatin: DNA exposed and vulnerable to ROS attack
 - very high transcriptional activity
 - Presumed formation of abnormal mRNAs resulting from genotoxic stress
 - Special importance for ATM's roles in responding to ongoing DNA damage and regulation of redox balance
- Random loss of transcripts, eventually including some that are essential for Purkinje cells function and/or survival
- Process is stochastic and slow
- Malfunctioning Purkinje cells might be more harmful than cell loss





Using Laboratory Mouse Models to Study A-T

- Atm-knockout mice: some phenotypic features are similar in A-T patients and the mouse model, some are augmented in the animals, and others are diminished (background-dependent).
- Atm-/- on a C57BL/6J background: Up to the age of 20 months - normal cerebellar histology and a slight, but distinct behavioral phenotype.
- Marked differences between WT and Atm-/- cerebellar tissues are observed using 'omics' methods.
- Strategies for boosting the cerebellar phenotype...





Megy Cemel



Kenneth Hollander



Bhavana Velpula



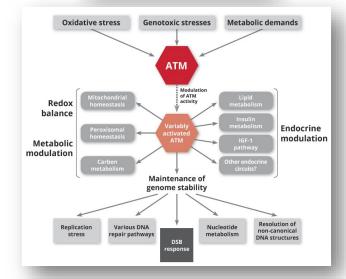






Marina Alfo





Sharone Naor



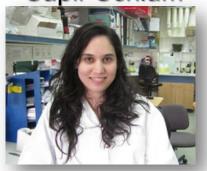
Yael Ziv



Ayelet Klartag



Sapir Schlam







Renate Klein 1981 - 2016

A-T is first and foremost like a very exclusive club. I like to think of it as a country club because the entrance fee is so high. The club keeps growing because A-T kids are being diagnosed sooner and we adults are living longer because of treatments...

We are born into this club that spans the entire globe. No one really wants to be a member, but we all do the best we can with the bodies we are given.