H2A1 MAGR - GKT		TSRSSKAGLQFPVGRI					ARFLKAGKY-AERV	GAGAPVYLAAVLEYLAAE-		- V L E L A G N A A R D N	KKTRIV		RHIQLAVRNDEELS			GDVT I ANGGVMPN I HNLL PKKA	G A S K P Q E D
112/12										- V L E L A G N A A N D N	N N						
2A.10 MAGR - GKT		TTRSSKAGLQFPVGRI					ARFLKKGKY - AERV	GAGAPVYLAAVLEYLAAE-		-VLELAGNAARDN	KKTR V		RHIQLAVRNDEELS			GDVT (ANGGVMPN (HNLLPKKT	G A S K P S A E D D
2A.13 MAGR - GKT	T LGSGVAKKST	TSRSSKAGLQFPVGRI					ARFLKNGKY-ATRV	GAGAPVYLAAVLEYLAAE-		- V L E L A G N A A R D N	KKTRIV		RHIQLAVRNDEELS			GDVT I ANGGVMPN I HSLLLPKKA	G A S K P S A D E D
H2A2 MAGR - GKQ		TSRSSKAGLQFPVGRI					ARFLKAGKY-AERV	GAGAPVYLAAVLEYLAAE-		-VLELAGNAARDN	KKTRIV		RHIQLAVRNDEELS			GDVT (ANGGVMPN (HNLLLPKKA	· G S S K P T E E D
4W.12 <mark>m d</mark> s g - t k v	VKKGAAGRRSGGGPKKKPV	VSRSVKSGLQFPVGRI					GRYLKKGRY-SKRV	· G T G A P V Y L A A V L E Y L A A E N	SCGFCSVASLTIYRCRMSS-SDF	RVLELAGNAARDN	K K N R 🛛 🖟		RHVLLAVRNDEELG		·	KGVT [AHGGVLPN]NP]LLPKKS	· EKAASTTK TPKSPSKATKSPKKS
2000 6 ME ST - GRV	VKKAFGGRKPPGAPKTKSV	WSKS MKAG DO F PMGP II					TRFLKKGRY-AQRL	GGGAPVYMAAVLEYLAAE-		- V L E L A G N A A R D N	K K S R [] []	PR	RHLLLAIRNDEELG			SGVTIAHGGVLPNINSVLLPKKS	ATKPAEEKATKSPVKSPKKA
2AW.7 MESSQAT - TKP	PTRGAGGR KGGDRKKSV	VSKSVKAGLQFPVGRI					ARYLKKGRY-ALRY	· G S G A P V Y L A A V L E Y L A A E -		- V L E L A G N A A R D N	KKNR N		RH			HGVT [ASGGVLPN]NPVLLPKKS	· TASSSQAEKASATKSPKKA
I2ΔX3 MSSGAGS - GTT	T KGG RGKPKATKSV	VSRSSKAGLOFPVGRII					ARFLKAGKY-AERV	GAGAPVYLSAVLEYLAAE-		-VLELAGNAARDN	KKTR V	PR	RHIQLAVRNDEELS			GSVT [ANGGVLPN]HQTLLPSKV	G K N K G D [] G S A S Q E F
2AX.5 M S T G A G S - G T T	T KGG RGKPKATKSV	VSRSSKAGLQFPVGRI					ARFLKSGKY - AERV	GAGAPVYLSAVLEYLAAE-		- V L E L A G N A A R D N	K K T R I V		RHIQLAVRNDEELS		<u> </u>	GSVT [ANGGVLPN]HQTLLPSKV	G K N K G D I G S A S Q E F
AZ.11 MAGKGGKGLVA	A A K T M A A N K D K D K D K K K P I	ISRSARAGIQFPVGRI					HRQLKTRVSAHGRV	GATAAVYTASILEYLTAE-		-VLELAGNASKDL	KVKR T		RHLQLAIRGDEELD			KG-TIAGGGVIPHIHKSLINKTT	KE
ZAZ.8 MAGKGGKGLLA	AAKTTAAAANKDSVKKKS []	I SRSSKAGIQFPVGRII					HRQLKQRVSAHGRV	GATAAVYTASILEYLTAE-		-VLELAGNASKDL	KVKR [] T		RHLQLAIRGDEELD			KG-TIAGGGVIPHIHKSLVNKVT	- KD
2AZ.9 <mark>M E</mark>	<mark>T</mark> K P N P	PRRPSNTVLPYQTPRLRDHYLLGK	KKLGQGQFGTTYLCTEKSTSANYACKSIPKRKLVCR	REDYEDVWRE [] Q [] MHHL SEHPNVVR [] KGTYEDSVFV	VH VM E V C E G G E L F D R V S K G H F S E R E A V K L K T L	GVVEACHS L GVMHRD L KPENF L FDSPKDDAK L KATDFG	SVFYKPGQYLYDVVGSPYYVAPEVL	KKCYGPE [DVWSAGV] LY [LSG	VPPFWAETESGIFRQILQGKLDF	KSDPWPT[SEAAKDL]YKMLE	RSPKKRISAHEALCHPWIVDE	E Q A A P D K P L D P A V L S R L K Q F S Q M N K I K K M A L R	RV	KM [] D T D N S G T [] T F E E L KAG L KR V G S E L M E S E [] K S L M D A A D [] D N S G T [] D Y G E F L A A T L H M N K M E R E E N L V A	AFSYFDKDGSGY I T I DE LQSACTEFGLCDTPLDDM	KE IDLDNDGK IDFSEFTAMMRKGDGVGRSRTMMKNLNF	NIADAFGVDGEKSDD
	P [V T [[N G S R S [S P]						HKQLKNRVSAHSSV	GATDVVYMTSILEYLTTE-		- V L Q L A E N T S K D L			RHLQLAIRGDEELD			KG-T00GSV0PH0H	
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1 2 2 4 5 5 6 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	15 15 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18	333 344 355 366 377 377 378 378 378 378 378 378 378 378	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	1125 126 127 128 130 130 130 130 130 130 130 130 130 130	161 163 164 165 165 165 165 165 165 165 165	200 201 202 203 204 204 205 205 206 207 207 208 208 208 208 208 208 208 208 208 208	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	248 250 250 251 251 251 251 251 251 251 251 251 251	27 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2997 2997 2997 2997 3907 3908 3908 310 310	8 1 2 2 3 3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	7	$\begin{smallmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 &$	4 4 3 4 4 3 3 4 3 3 4 3 3 4 3 3 4 3 3 4 3 3 4 3 3 4 3 3 4 3 3 4 3 3 4 3 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 6 9 9 9 9 9 9 9 9 9 9 9 9	50, 5008 5008 5008 5008 5008 5008 5008 5