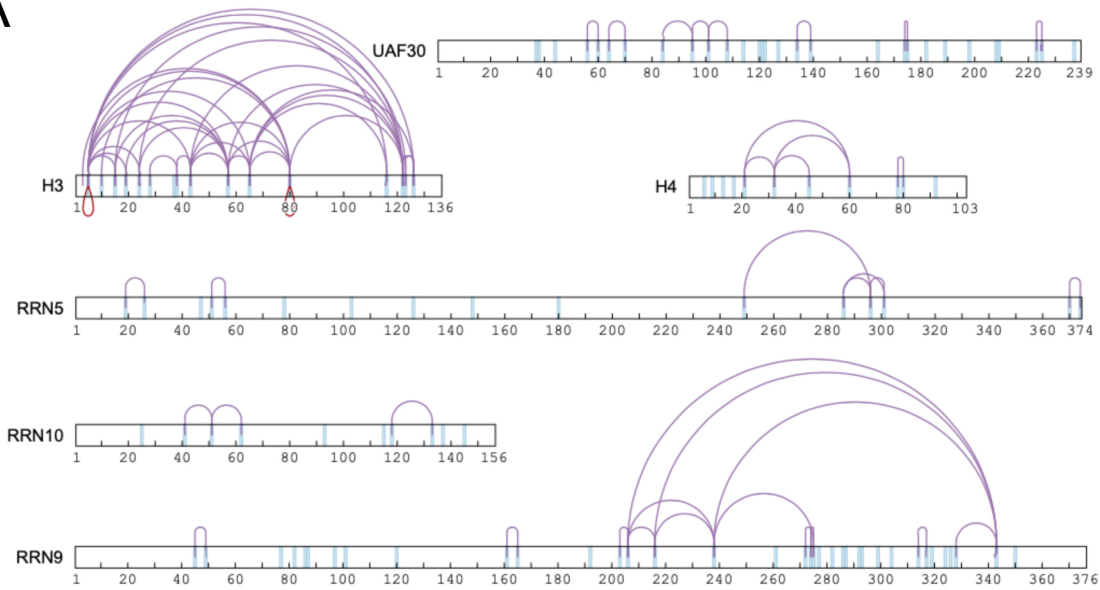


Figure S1

A



B

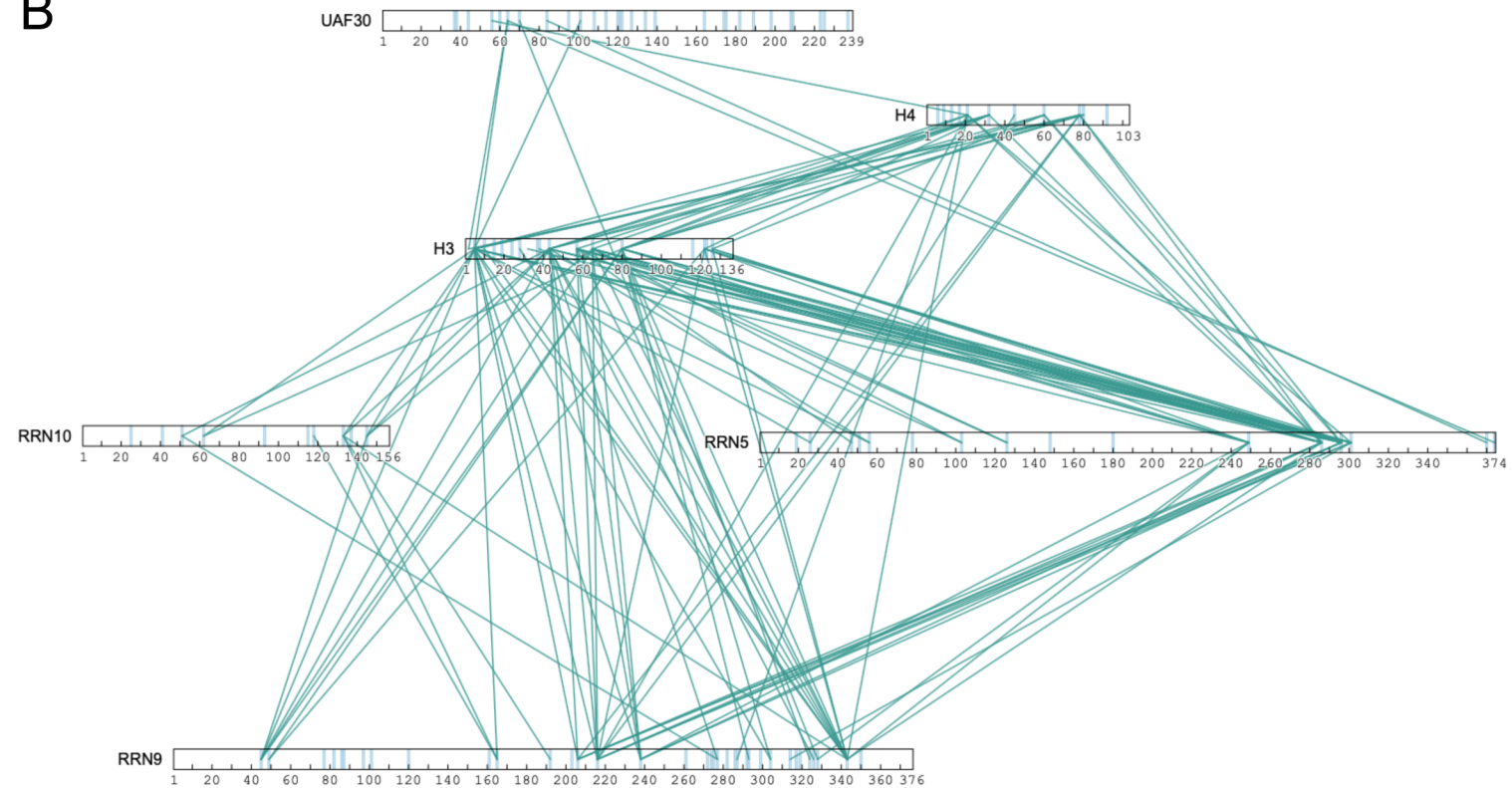


Figure S1. Position of lysine residues in the UAF linkage map. A. Intramolecular crosslinking within the UAF subunits. **B.** Intermolecular crosslinking between UAF subunits. The positions of the lysine residues are colored in light blue vertical lines. Intra- and Intermolecular crosslinks are depicted as purple loops and teal lines respectively. Red loops denote intra-molecular crosslinks where the same lysine in the same or similar peptides crosslink to each other.

Figure S2

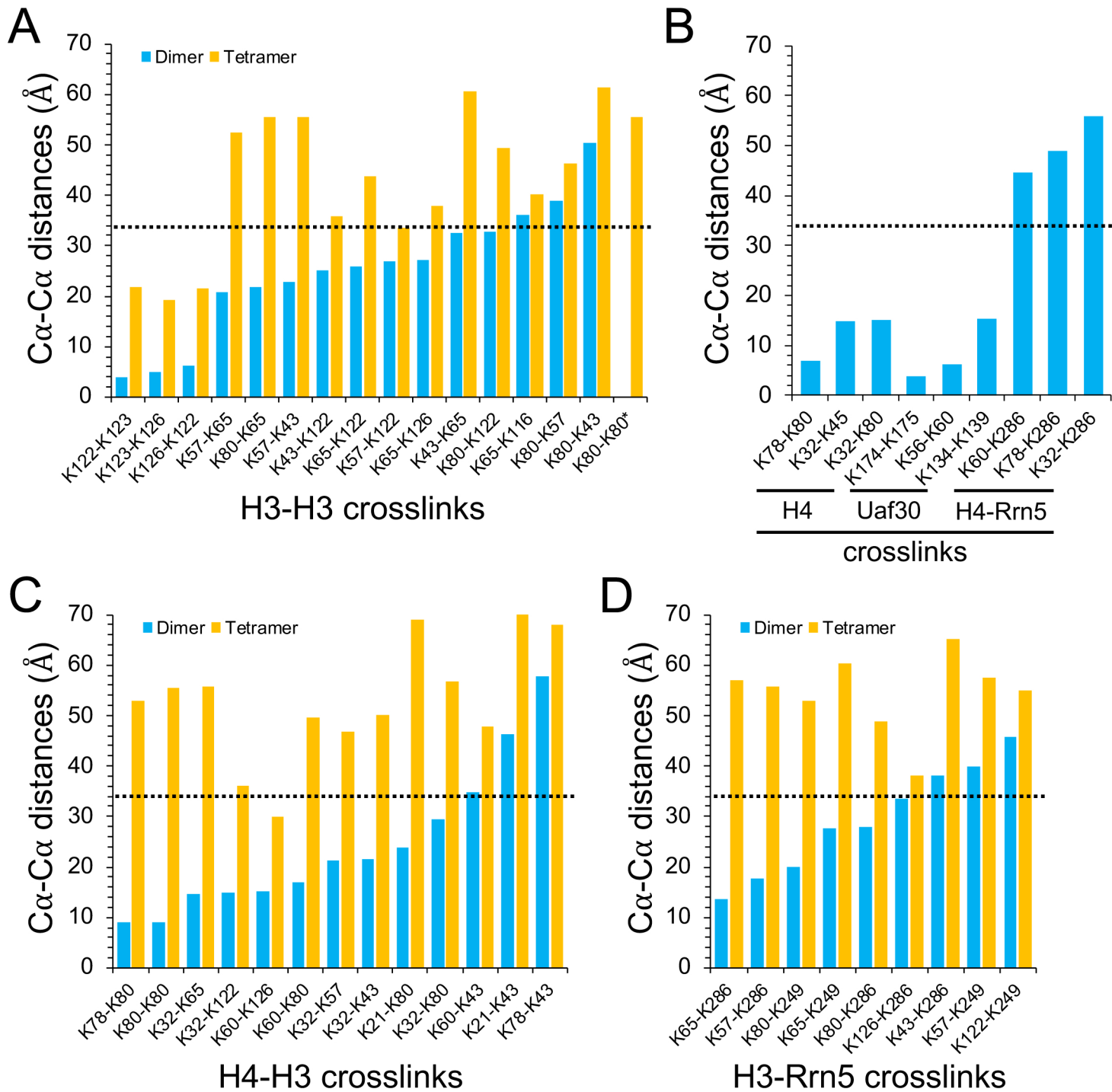


Figure S2. Intramolecular crosslinking within and between predicted UAF structural models. A-C. Calculated C α -C α distances between crosslinked lysines pairs with the dimer and tetrameric orientations for **(A)** H3-H4, **(B)** H3-H3, and **(C)** H3-Rrn5. **D.** Calculated C α -C α distances between crosslinked lysines pairs within H4, Uaf30 and between H4-Rrn5. The dashed line denotes the theoretical maximum crosslinking distance for BS3 of 34 Å.

Supplementary Table S1. UAF constructs used in this study

Construct	Description
pRS425-PGK-Myc-RRN5-WT	Wildtype RRN5 gene inserted into pRS425 PGK promoter yeast expression vector.
pRS425-PGK-Myc-RRN5-D1	Removed RRN5 DNA sequence encoding a.a. residues 5-45.
pRS425-PGK-Myc-RRN5-D2	Removed RRN5 DNA sequence encoding a.a. residues 59-112.
pRS425-PGK-Myc-RRN5-D3	Removed RRN5 DNA sequence encoding a.a. residues 123-177.
pRS425-PGK-Myc-RRN5-D4	Removed RRN5 DNA sequence encoding a.a. residues 332-355.
pRS425-PGK-Myc-RRN5-D5	Removed RRN5 DNA sequence encoding a.a. residues 236-300.
pRS425-PGK-Myc-RRN5-D6	Removed RRN5 DNA sequence encoding a.a. residues 194-261.
pRS425-PGK-Myc-RRN5-D2,6	Removed RRN5 DNA sequence encoding a.a. residues 59-112 & 194-261.
pRS425-PGK-Myc-RRN9-WT	Wildtype RRN9 gene inserted into pRS425 PGK promoter yeast expression vector.
pRS425-PGK-Myc-RRN9-D1	Removed RRN9 DNA sequence encoding a.a. residues 31-78.
pRS425-PGK-Myc-RRN9-D2	Removed RRN9 DNA sequence encoding a.a. residues 128-157.
pRS425-PGK-Myc-RRN9-D3	Removed RRN9 DNA sequence encoding a.a. residues 170-214.
pRS425-PGK-Myc-RRN9-D4	Removed RRN9 DNA sequence encoding a.a. residues 128-214.
pRS425-PGK-Myc-RRN9-D5	Removed RRN9 DNA sequence encoding a.a. residues 284-341.
pRS425-PGK-Myc-RRN9-D6	Removed RRN9 DNA sequence encoding a.a. residues 241-279.
pRS425-PGK-Myc-RRN9-D7	Removed RRN9 DNA sequence encoding a.a. residues 215-241.
pRS425-PGK-Myc-RRN10-WT	Wildtype RRN10 gene inserted into pRS425 PGK promoter yeast expression vector.
pRS425-PGK-Myc-RRN10-D1	Removed RRN10 DNA sequence encoding a.a. residues 5-14.
pRS425-PGK-Myc-RRN10-D2	Removed RRN10 DNA sequence encoding a.a. residues 5-33.
pRS425-PGK-Myc-RRN10-D3	Removed RRN10 DNA sequence encoding a.a. residues 95-109.
pRS425-PGK-Myc-RRN10-D4	Removed RRN10 DNA sequence encoding a.a. residues 128-135.
pRS425-PGK-Myc-RRN10-D5	Removed RRN10 DNA sequence encoding a.a. residues 37-87.
pRS425-PGK-Myc-UAF30-WT	Wildtype UAF30 gene inserted into pRS425 PGK promoter yeast expression vector.
pRS425-PGK-Myc-UAF30-D1	Removed UAF30 DNA sequence encoding a.a. residues 5-64.
pRS425-PGK-Myc-UAF30-D2	Removed UAF30 DNA sequence encoding a.a. residues 20-64.
pRS425-PGK-Myc-UAF30-D3	Removed UAF30 DNA sequence encoding a.a. residues 71-111.
pRS425-PGK-Myc-UAF30-D4	Removed UAF30 DNA sequence encoding a.a. residues 120-200.
pRS425-PGK-Myc-UAF30-D5	Removed UAF30 DNA sequence encoding a.a. residues 201-220.
pET-6his-Rrn9-WT	Wildtype RRN9 gene inserted into pET-Duet bacteria expression vector.
pET-6his-Rrn9-D1	Removed RRN9 DNA sequence encoding a.a. residues 31-78.
pET-6his-Rrn9-D2	Removed RRN9 DNA sequence encoding a.a. residues 128-157.
pET-6his-Rrn9-D3	Removed RRN9 DNA sequence encoding a.a. residues 170-214.
pET-6his-Rrn9-D4	Removed RRN9 DNA sequence encoding a.a. residues 128-214.
pET-6his-Rrn9-D5	Removed RRN9 DNA sequence encoding a.a. residues 284-341.
pET-6his-Rrn9-D6	Removed RRN9 DNA sequence encoding a.a. residues 241-279.
pET-6his-Rrn9-D7	Removed RRN9 DNA sequence encoding a.a. residues 215-241.
pET-6his-Rrn5-WT	Wildtype RRN5 gene inserted into pET-Duet bacteria expression vector.
pET-6his-Rrn5-D1	Removed RRN5 DNA sequence encoding a.a. residues 5-45.
pET-6his-Rrn5-D2	Removed RRN5 DNA sequence encoding a.a. residues 59-112.
pET-6his-Rrn5-D5	Removed RRN5 DNA sequence encoding a.a. residues 236-300.
pET-6his-Rrn5-D6	Removed RRN5 DNA sequence encoding a.a. residues 194-261.
pET-6his-Rrn5-D2,6	Removed RRN5 DNA sequence encoding a.a. residues 59-112 & 194-261.
pET-6his-Uaf30-WT	Wildtype UAF30 gene inserted into pET-Duet bacteria expression vector.
pET-6his-Uaf30-D1	Removed UAF30 DNA sequence encoding a.a. residues 5-64.
pET-6his-Uaf30-D2	Removed UAF30 DNA sequence encoding a.a. residues 20-64.
pET-6his-Uaf30-D3	Removed UAF30 DNA sequence encoding a.a. residues 71-111.
pET-6his-Uaf30-D4	Removed UAF30 DNA sequence encoding a.a. residues 120-200.
pET-6his-Uaf30-D5	Removed UAF30 DNA sequence encoding a.a. residues 201-220.
pCDF-H3-H4-RRN5	H3, H4, and RRN5 genes inserted into the pCDF-Duet bacteria expression vector.
pCDF-H3-H4-RRN10	H3, H4, and RRN10 genes inserted into the pCDF-Duet bacteria expression vector.
pACYC-RRN9-UAF30-Flag	RRN9 and UAF30 genes inserted into the pCDF-Duet bacteria expression vector.
pACYC-RRN5-UAF30-Flag	RRN5 and UAF30 genes inserted into the pCDF-Duet bacteria expression vector.

Supplementary Table S2. UAF intramolecular crosslinks and looplinks

Protein 1	Protein 2	Link Position 1	Link Position 2	Type	Peptide 1	Peptide 2
RRN9	RRN9	206	216	Intralink	IAK*ENEFDVDR	QDK*HSNNIR
RRN9	RRN9	238	206	Intralink	IK*YTYHDLVSR	IAK*ENEFDVDR
RRN9	RRN9	238	216	Intralink	QDK*HSNNIR	IK*YTYHDLVSR
RRN9	RRN9	343	238	Intralink	IK*YTYHDLVSR	LNREETEDALNK*R
RRN9	RRN9	343	328	Intralink	LNREETEDALNK*R	SK*LQR
RRN9	RRN9	343	206	Intralink	LNREETEDALNK*R	IAK*ENEFDVDR
RRN9	RRN9	238	275	Intralink	RIK*YTYHDLVSR	YKK*R
RRN9	RRN9	45	49	Looplink	GSELT TTTADK*ETLK*SANELLDLSLEHSHR	N/A
RRN9	RRN9	161	165	Looplink	VELDAQWQK*FLSK*SALDHDVTLVDDELNIPNEISR	N/A
RRN9	RRN9	274	275	Looplink	SLELYNDIPEKYK*K*R	N/A
RRN9	RRN9	203	206	Looplink	LDSLFEGLHDK*IAK*ENEFDVDR	N/A
RRN9	RRN9	272	274	Looplink	SLELYNDIPEK*YK*KR	N/A
RRN9	RRN9	314	317	Looplink	EDFIPVEK*LLK*DK	N/A
RRN9	RRN9	216	343	Intralink	QDK*HSNNIR	LNREETEDALNK*R
UAF30	UAF30	108	101	Intralink	SSGEEK*NDSETK	EITVSK*R
UAF30	UAF30	174	175	Looplink	AHNLQNPNNK*K*EILCDEK	N/A
UAF30	UAF30	95	101	Looplink	SLEDLLKENATLAIELTK*EITVSK*R	N/A
UAF30	UAF30	223	225	Looplink	RK*EK*PIVSDSEQSDTK	N/A
UAF30	UAF30	56	60	Looplink	MALKEVY AIDVESQ GK*AINK*LIR	N/A
UAF30	UAF30	134	139	Looplink	K*VTLSK*SLASLLGEHELTR	N/A
UAF30	UAF30	84	95	Looplink	SLEDLLK*ENATLAIELTK*EITVSKR	N/A
UAF30	UAF30	64	70	Looplink	K*HLDLVK*ERPR	N/A
RRN5	RRN5	286	296	Intralink	K*WELDYPR	EGK*LFR
RRN5	RRN5	301	296	Intralink	EGK*LFR	TK*EMAHFLQSQLSR
RRN5	RRN5	301	286	Intralink	K*WELDYPR	TK*EMAHFLQSQLSR
RRN5	RRN5	249	296	Intralink	GHK*SLPTVVTR	EGK*LFR
RRN5	RRN5	370	374	Looplink	SALHENLLK*WLSK*	N/A
RRN5	RRN5	51	56	Looplink	VHVK*SIHEK*AGTANAGVEISSVGVWDWSEEK	N/A
RRN5	RRN5	19	26	Looplink	K*YVELYNK*EVVEEFYNGAASGR	N/A
RRN10	RRN10	62	51	Intralink	IDNAVPIPFK*TR	EEIDADVEK*DRNEGVFEGNIIPDIDL R
RRN10	RRN10	118	133	Intralink	WVK*DYLTSIQTEQGR	QSK*VIGK
RRN10	RRN10	41	51	Looplink	EFGTHVVSADVEVLAEK*IDNAVPIPFK*TR	N/A
H4	H4	60	32	Intralink	DNIQGITK*PAIR	AVLK*SFLESVIR
H4	H4	60	21	Intralink	AVLK*SFLESVIR	K*ILR
H4	H4	32	45	Intralink	DNIQGITK*PAIR	RGGVK*R(
H4	H4	32	21	Looplink	K*ILRDNIQGITK*PAIR	N/A
H4	H4	80	78	Intralink	K*TVTSLDVVYALK	DSVTTYTEHAK*R
H3	H3	5	5	Intralink	TK*QTAR	TK*QTAR
H3	H3	5	19	Intralink	TK*QTAR	K*QLASK
H3	H3	5	24	Intralink	TK*QTAR	QLASK*AAR
H3	H3	15	5	Intralink	STGGK*APR	TK*QTAR
H3	H3	19	57	Intralink	K*QLASKAAR	RFQK*STELLIR
H3	H3	24	122	Intralink	QLASK*AAR	VTIQK*K
H3	H3	28	38	Intralink	K*SAPSTGGVK	K*PHR
H3	H3	43	5	Intralink	YK*PGTVALR	TK*QTAR
H3	H3	43	38	Intralink	YK*PGTVALR	K*PHR
H3	H3	43	65	Intralink	YK*PGTVALR	K*LPFQR
H3	H3	43	122	Intralink	YK*PGTVALR	VTIQK*K
H3	H3	57	5	Intralink	FQK*STELLIR	TK*QTAR
H3	H3	57	24	Intralink	RFQK*STELLIR	KQLASK*AAR
H3	H3	57	15	Intralink	RFQK*STELLIR	KSTGGK*APR
H3	H3	57	43	Intralink	FQK*STELLIR	YK*PGTVALR
H3	H3	57	65	Intralink	FQK*STELLIR	K*LPFQR
H3	H3	57	122	Intralink	FQK*STELLIR	VTIQK*K
H3	H3	65	5	Intralink	K*LPFQR	TK*QTAR
H3	H3	65	126	Intralink	K*LPFQR	DIK*LAR
H3	H3	65	122	Intralink	K*LPFQR	VTIQK*K
H3	H3	65	116	Intralink	K*LPFQR	FQSSAIGALQESVEAYLVSLFEDTNLAAIHAK*R
H3	H3	80	57	Intralink	EIAQDFK*TDLR	RFQK*STELLIR
H3	H3	80	122	Intralink	EIAQDFK*TDLR	VTIQK*K
H3	H3	116	5	Intralink	FQSSAIGALQESVEAYLVSLFEDTNLAAIHAK*R	TK*QTAR
H3	H3	122	123	Looplink	VTIQK*K*DIKLAR	N/A
H3	H3	122	5	Intralink	RVTIQK*K	TK*QTAR
H3	H3	123	15	Intralink	VTIQKK*DIK	KSTGGK*APR
H3	H3	123	126	Looplink	VTIQKK*DIK*LAR	N/A
H3	H3	126	5	Intralink	DIK*LAR	TK*QTAR
H3	H3	126	122	Intralink	DIK*LAR	VTIQK*K
H3	H3	80	80	Intralink	EIAQDFK*TDLR	EIAQDFK*TDLR
H3	H3	80	65	Intralink	EIAQDFK*TDLR	K*LPFQR
H3	H3	80	10	Intralink	EIAQDFK*TDLR	K*STGGK
H3	H3	80	5	Intralink	EIAQDFK*TDLR	TK*QTAR
H3	H3	80	43	Intralink	EIAQDFK*TDLR	YK*PGTVALR

Supplementary Table S3. UAF intermolecular crosslinks

Protein 1	Protein 2	Link Position 1	Link Position 2	Peptide 1	Peptide 2
UAF30	H3	101		5 EITVSK'R	TK*QTAR
UAF30	H3	64		5 K*HLDLVK	TK*QTAR
UAF30	RRN9	70		328 HLDLVK'ER	SK*LQR
UAF30	H4	56		21 EYVAIDVESQGK'AINK	HRK*ILR
UAF30	RRN5	64		374 K*HLDLVK	WLSK*
UAF30	RRN5	84		370 SLEDLLK*ENATLAIELTK	SALHENQLLK*WLSK
RRN9	RRN10	165		133 FLSK*SALDHDVTLDVDELNIPNEISR	QSK*VIGK
RRN10	RRN9	145		45 GPCEFIISK*HIDYR	GSELTITTTADK*ETLK
RRN10	RRN9	51		277 IDNAVPIPFK*TR	RK*FR
RRN9	RRN10	343		133 LNREETEDALNK'R	QSK*VIGK
RRN9	RRN10	192		133 NILVK*LDLFLFGLHDK	QSK*VIGK
RRN9	RRN10	165		118 FLSK*SALDHDVTLDVDELNIPNEISR	WWK*DYLSIQTEQGR
RRN5	RRN9	249		328 GHK*SLPTVVTR	SK*LQR
RRN9	RRN5	238		296 IK*YTYHDLVSR	EGK*LFR
RRN9	RRN5	216		286 QDK*HSNNIR	K*WELDYPR
RRN5	RRN9	301		314 TK*EMAHFLFQSQLSR	EDIPIVEK*LLK
RRN5	RRN9	301		206 TK*EMAHFLFQSQLSR	IAK*ENEFDVR
RRN5	RRN9	301		216 TK*EMAHFLFQSQLSR	QDK*HSNNIR
RRN9	RRN5	206		296 IAK*ENEFDVR	EGK*LFR
RRN9	RRN5	206		286 IAK*ENEFDVR	K*WELDYPR
RRN9	RRN5	238		286 IK*YTYHDLVSR	K*WELDYPR
RRN9	RRN5	343		249 LNREETEDALNK'R	GHK*SLPTVVTR
RRN9	RRN5	343		286 LNREETEDALNK'R	K*WELDYPR
RRN9	RRN5	216		296 QDK*HSNNIR	EGK*LFR
RRN5	RRN9	249		238 GHK*SLPTVVTR	IK*YTYHDLVSR
H4	RRN5	60		286 AVLK'SFLESVIR	K*WELDYPR
H4	RRN5	78		296 DSVTYTEHAK'R	EGK*LFR
H4	RRN5	78		286 DSVTYTEHAK'R	K*WELDYPR
RRN5	H4	301		21 TK*EMAHFLFQSQLSR	K*ILR
H4	RRN5	60		296 AVLK'SFLESVIR	EGK*LFR
H4	RRN5	32		286 DNIQGITK*PAIR	K*WELDYPR
RRN5	H4	286		21 K*WELDYPR	K*ILR
H4	RRN5	45		26 RGGVK'R	YVELYNK*VEEFYNGAASGR
H4	RRN9	78		206 DSVTYTEHAK'R	K*WELDYPR
H4	RRN9	78		216 DSVTYTEHAK'R	QDK*HSNNIR
RRN9	H4	343		21 LNREETEDALNK'R	K*ILR
RRN9	H4	216		21 QDK*HSNNIR	K*ILR
H4	RRN9	21		287 RHRK*ILR	K*YHQPQ
RRN10	H3	145		65 GPCEFIISK*HIDYR	YK*PGTVALR
RRN10	H3	145		5 GPCEFIISK*HIDYR	TK*QTAR
RRN10	H3	145		43 GPCEFIISK*HIDYR	YK*PGTVALR
RRN10	H3	62		80 EEIADAVEK*DRNEGVEFEGNIIPDIDL	EIAQDFK*TDLR
RRN10	H3	62		5 TREEIADAVEK*DR	TK*QTAR
RRN10	H3	133		5 QSK*VIGK	TK*QTAR
H3	RRN10	43		133 YK*PGTVALR	QSK*VIGK
H3	RRN10	43		51 PHRYK*PGTVALR	IDNAVPIPFK*TR
H4	H3	60		80 AVLK'SFLESVIR	EIAQDFK*TDLR
H4	H3	32		65 DNIQGITK*PAIR	K*LPFOR
H4	H3	32		5 DNIQGITK*PAIR	TK*QTAR
H4	H3	32		122 DNIQGITK*PAIR	VTIQK*K
H4	H3	78		5 DSVTYTEHAK'R	TK*QTAR
H4	H3	78		43 DSVTYTEHAK'R	YK*PGTVALR
H4	H3	78		80 DSVTYTEHAK'R	K*TVTSLDVIYALK
H3	H4	80		21 EIAQDFK*TDLR	K*ILR
H4	H3	80		80 K*TVTSLDVIYALK	EIAQDFK*TDLR
H4	H3	80		5 K*TVTSLDVIYALK	TK*QTAR
H4	H3	32		57 DNIQGITK*PAIR	FOK*STELLIR
H4	H3	32		43 DNIQGITK*PAIR	YK*PGTVALR
H3	H4	80		32 EIAQDFK*TDLR	DNIQGITK*PAIR
H4	H3	43		21 YK*PGTVALR	K*ILR
H4	H3	60		128 AVLK'SFLESVIR	DIK*LAR
H3	RRN5	126		43 AVLK'SFLESVIR	YK*PGTVALR
H3	RRN5	126		286 DIK*LAR	K*WELDYPR
H3	RRN5	5		286 TK*QTAR	K*WELDYPR
H3	RRN5	65		103 K*LPFOR	K*SAMEILGYR
H3	RRN5	43		296 YK*PGTVALR	EGK*LFR
H3	RRN5	65		296 K*LPFOR	EGK*LFR
H3	RRN5	57		47 RFOK*STELLIR	VEEFYNGAASGRPAEFHPSK*VHVK
H3	RRN5	126		286 DIK*LARR	EGK*LFR*EMAHFLFQSQLSR
H3	RRN5	6		301 TK*QTAR	TK*EMAHFLFQSQLSR
H3	RRN5	122		301 VTIQK*K	TK*EMAHFLFQSQLSR
H3	RRN5	43		301 YK*PGTVALR	TK*EMAHFLFQSQLSR
H3	RRN5	5		249 TK*QTAR	GHK*SLPTVVTR
H3	RRN5	122		249 RVTIQK*K	GHK*SLPTVVTR
RRN5	H3	296		5 EGK*LFR	TK*QTAR
RRN5	H3	296		122 EGK*LFR	RVTIQK*K
H3	RRN5	80		249 EIAQDFK*TDLR	GHK*SLPTVVTR
H3	RRN5	57		296 FOK*STELLIR	EGK*LFR
H3	RRN5	80		286 K*WELDYPR	EIAQDFK*TDLR
RRN5	H3	126		57 K*AGDGDGAPIYEMSAEWVALETK	FOK*STELLIR
RRN5	H3	126		65 K*AGDGDGAPIYEMSAEWVALETK	K*LPFOR
RRN5	H3	103		K*SAMEILGYR	K*PHR
RRN5	H3	286		65 K*WELDYPR	K*LPFOR
RRN5	H3	286		43 K*WELDYPR	YK*PGTVALR
RRN5	H3	56		43 SIHEK*AGTANAGVEISSVGDWDSEEK	YK*PGTVALR
RRN5	H3	301		80 TK*EMAHFLFQSQLSR	EIAQDFK*TDLR
RRN5	H3	301		57 TK*EMAHFLFQSQLSR	FOK*STELLIR
RRN5	H3	301		65 TK*EMAHFLFQSQLSR	K*LPFOR
RRN5	H3	26		5 YVELYNK*VEEFYNGAASGR(7)	TK*QTAR
H3	RRN5	80		296 EIAQDFK*TDLR	EGK*LFR
H3	RRN5	57		249 FOK*STELLIR	GHK*SLPTVVTR
RRN5	H3	249		65 GHK*SLPTVVTR	K*LPFOR
H3	RRN5	57		286 FOK*STELLIR	K*WELDYPR
RRN5	H3	56		5 SIHEK*AGTANAGVEISSVGDWDSEEK	TK*QTAR
RRN9	H3	343		65 LNREETEDALNK'R	K*LPFOR
RRN9	H3	343		122 LNREETEDALNK'R	VTIQK*K
H3	RRN9	80		343 EIAQDFK*TDLR	LNREETEDALNK'R
H3	RRN9	80		293 EIAQDFK*TDLR	K*TSSYLK
RRN9	H3	304		5 ELLSK*TR	TK*QTAR
RRN9	H3	165		5 FLSK*SALDHDVTLDVDELNIPNEISR	TK*QTAR
H3	RRN9	57		216 FOK*STELLIR	QDK*HSNNIR
RRN9	H3	45		80 GSELTITTTADK*ETLK	EIAQDFK*TDLR
RRN9	H3	45		65 GSELTITTTADK*ETLK	K*LPFOR
RRN9	H3	45		5 GSELTITTTADK*ETLK	TK*QTAR
RRN9	H3	45		43 GSELTITTTADK*ETLK	YK*PGTVALR
RRN9	H3	206		5 IAK*ENEFDVR	TK*QTAR
RRN9	H3	206		43 IAK*ENEFDVR	YK*PGTVALR
RRN9	H3	238		57 IK*YTYHDLVSR	FOK*STELLIR
RRN9	H3	238		65 IK*YTYHDLVSR	K*LPFOR
RRN9	H3	238		43 IK*YTYHDLVSR	YK*PGTVALR
RRN9	H3	343		126 LNREETEDALNK'R	DIK*LAR
RRN9	H3	343		57 LNREETEDALNK'R	FOK*STELLIR
RRN9	H3	343		10 LNREETEDALNK'R	K*STGGK
H3	RRN9	43		277 PHRYK*PGTVALR	RK*FR
RRN9	H3	343		5 LNREETEDALNK'R	TK*QTAR
H3	RRN9	65		216 K*LPFOR	QDK*HSNNIR
RRN9	H3	216		5 QDK*HSNNIR	TK*QTAR
RRN9	H3	216		43 QDK*HSNNIR	YK*PGTVALR
H3	RRN9	80		304 EIAQDFK*TDLR	ELLSK*TR
H3	RRN9	5		343 TK*QTAR	EETEDALNK'R
RRN9	H3	49		122 ETLK*SANELLDLSLESHR	VTIQK*K
RRN9	H3	238		5 IK*YTYHDLVSR	TK*QTAR
H3	RRN9	28		343 K*SAPSTGGVK	LNREETEDALNK'R
H3	RRN9	80		49 EIAQDFK*TDLR	ETLK*SANELLDLSLESHR
H3	RRN9	43		326 PHRYK*PGTVALR	LTSKDK*SK
H3	RRN9	80		324 EIAQDFK*TDLR	LTSK*DK
RRN9	H3	216		122 QDK*HSNNIR	VTIQK*K
RRN9	H3	343		43 LNREETEDALNK'R	YK*PGTVALR