

A 3D surface model of a spliceosome complex, showing several subunits in different colors: purple, orange, yellow, green, blue, and pink. The model is set against a light gray background. The text is overlaid on the central part of the model.

Spliceosome:

The crucial role of Prp8

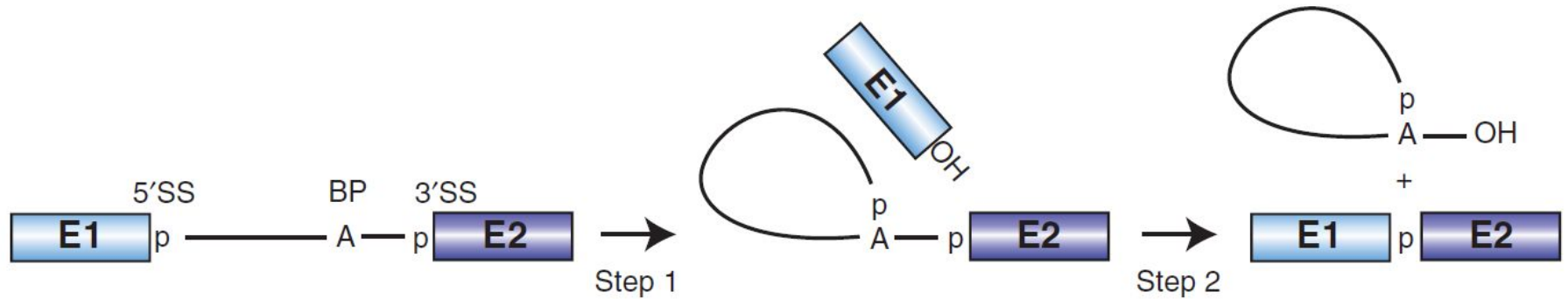
Structural Biology

Ariadna Martínez, Laura Sans, Marta Vilademunt and Mar Villa

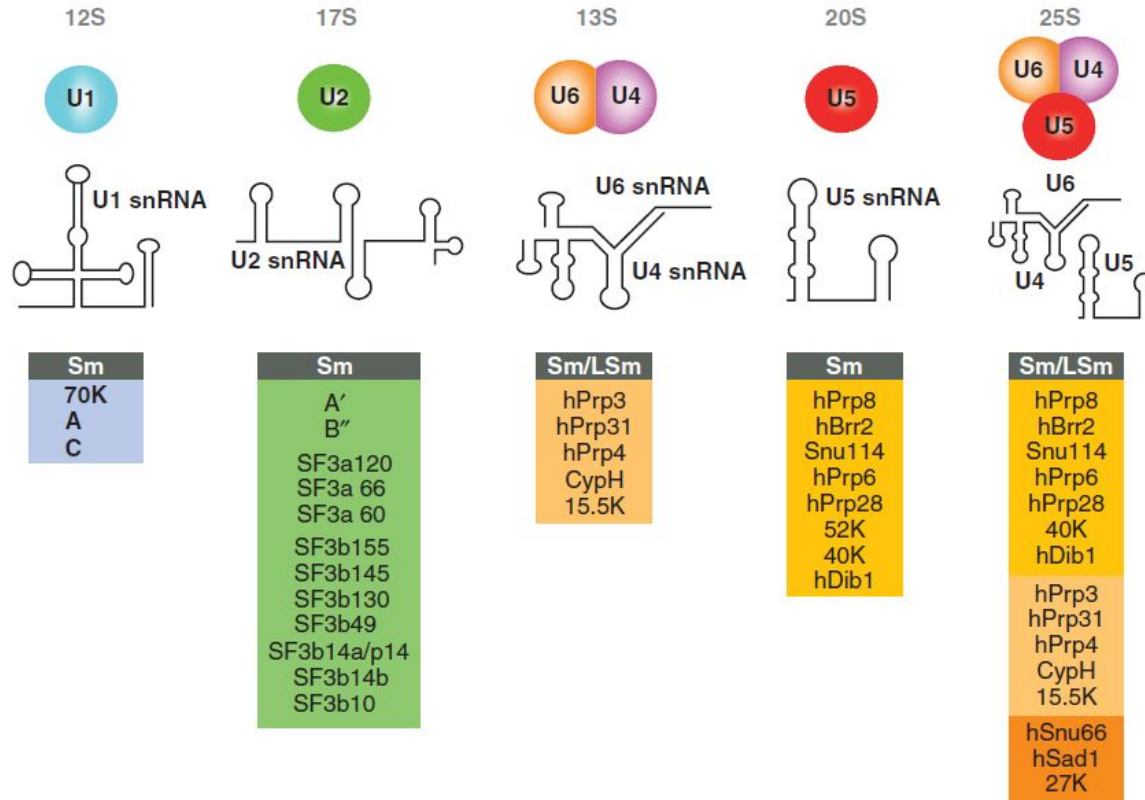
Index

1. **Spliceosome basics**
 - a. Introduction - Branching and exon ligation
 - b. Assembly and activation of spliceosome - Steps
 - c. Splicing active site
2. **Prp8 analysis**
 - a. N-terminal (N-domain)
 - b. Reverse transcriptase (RT) fingers/palm
 - c. Thumb/X
 - d. Linker
 - e. RNase H-like
 - f. Jab1/MPN
3. **Aar2**
4. **Transition Aar2-Brr2**
5. **Brr2**

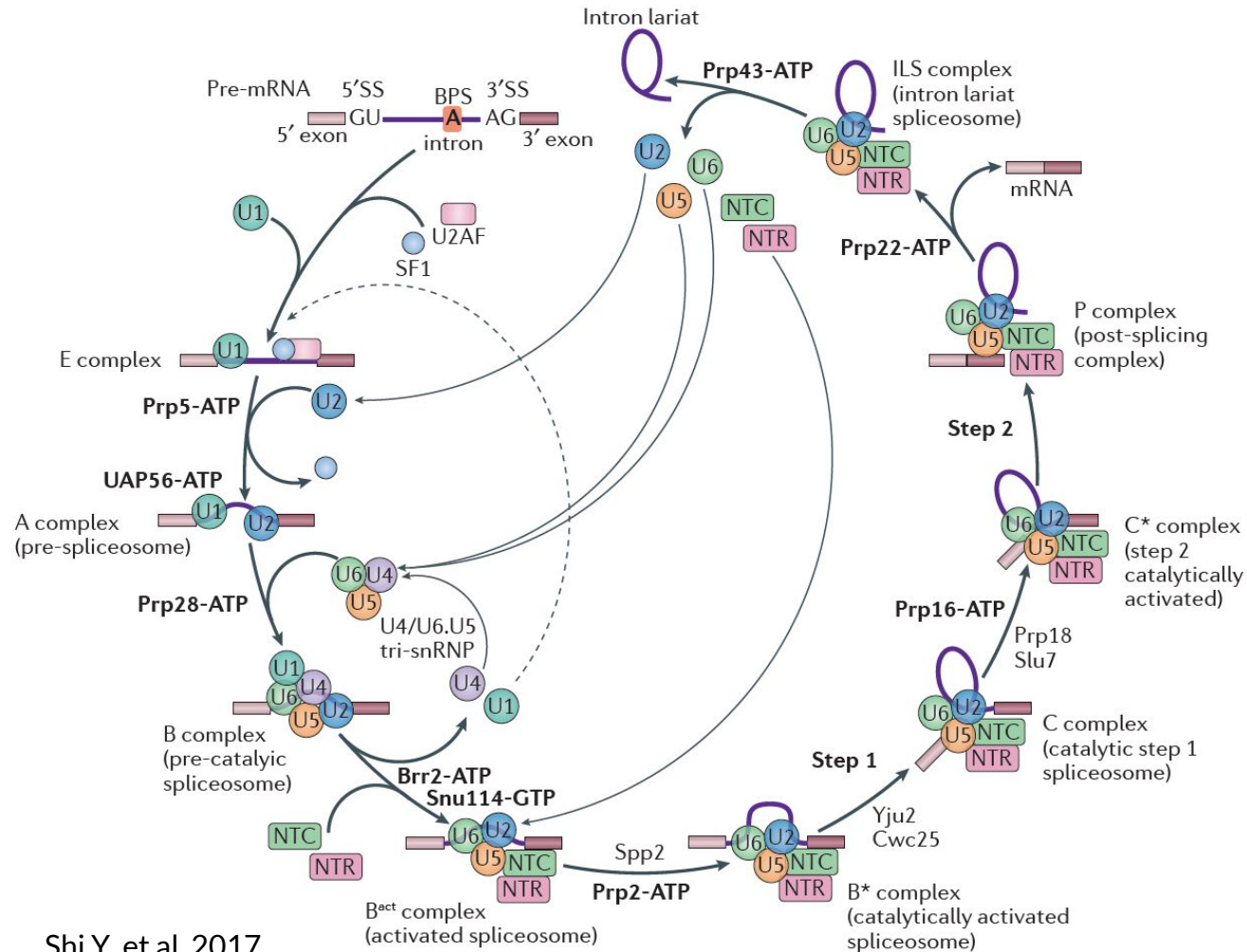
Spliceosome basics - Branching and exon ligation



Spliceosome basics - Branching and exon ligation

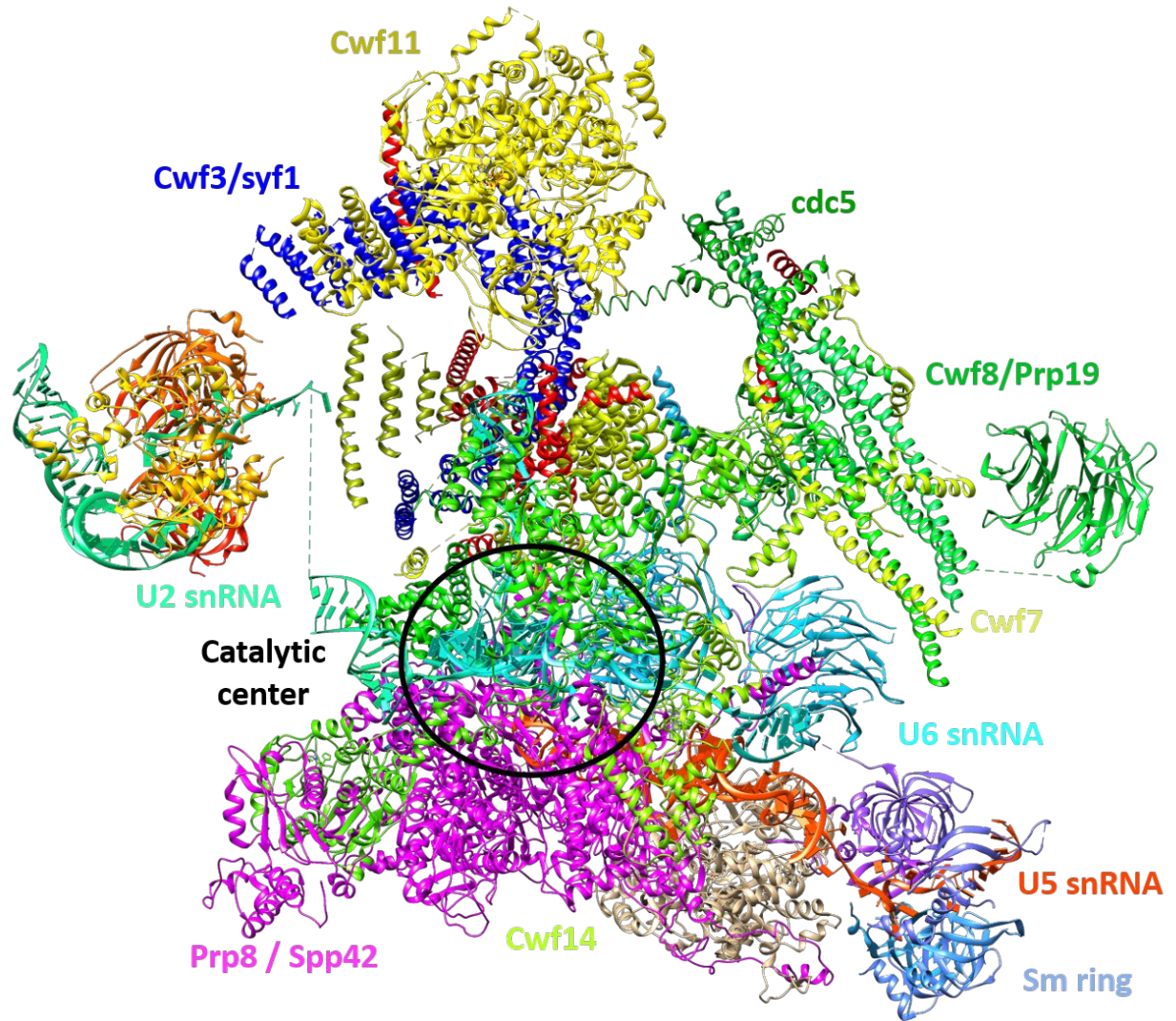


Spliceosome basics - STEPS



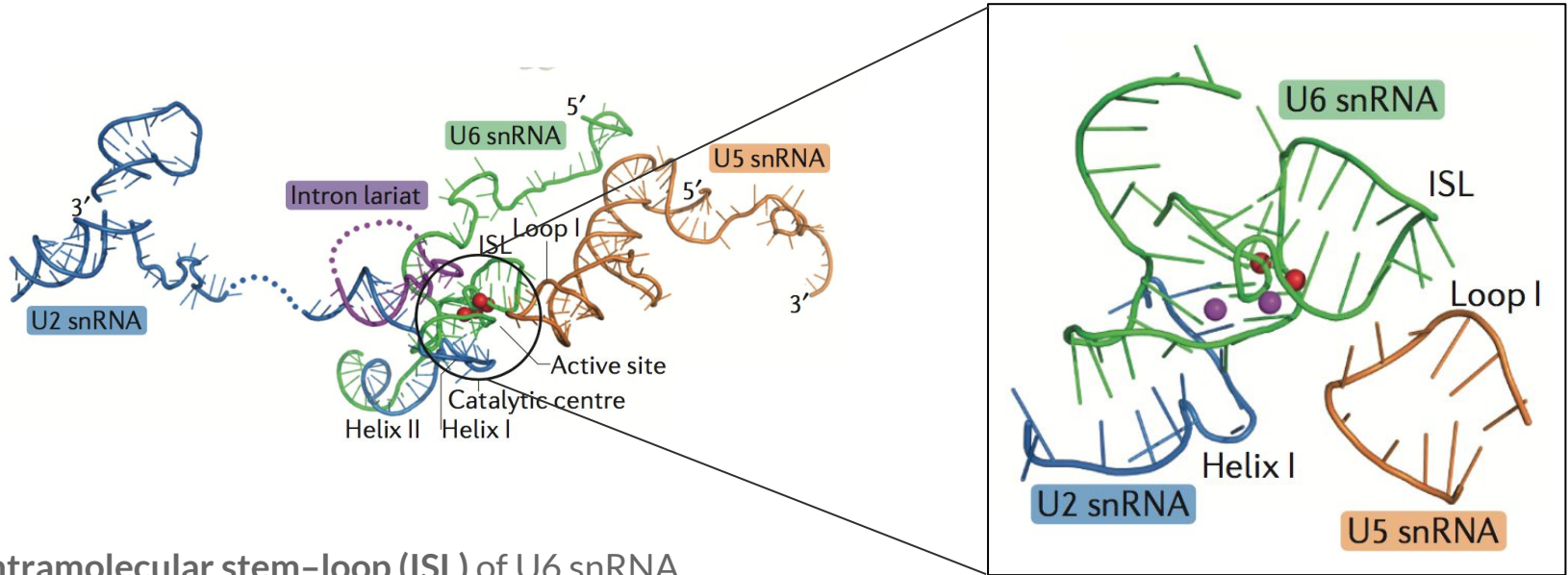
Shi Y, et al. 2017

Structure of yeast spliceosome



PDB code: 3JB9
Resolution: 3,6 Å

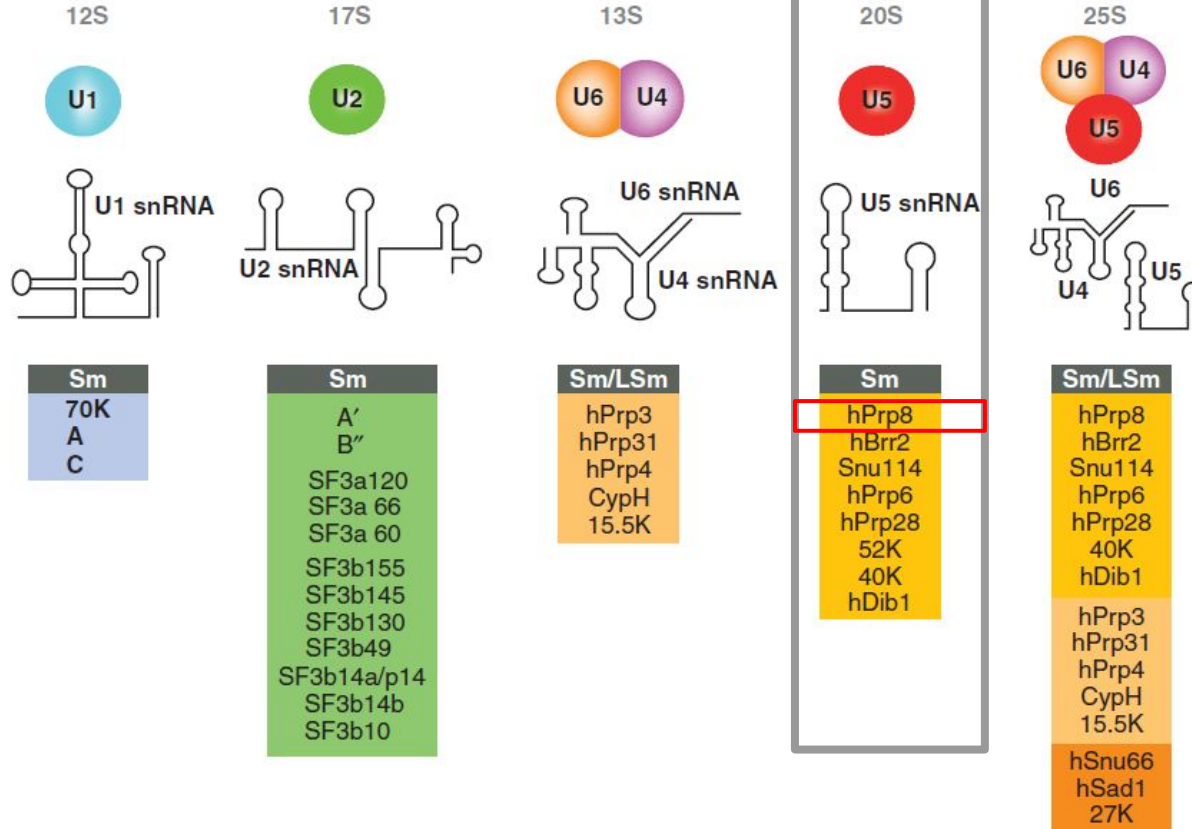
Catalytic core



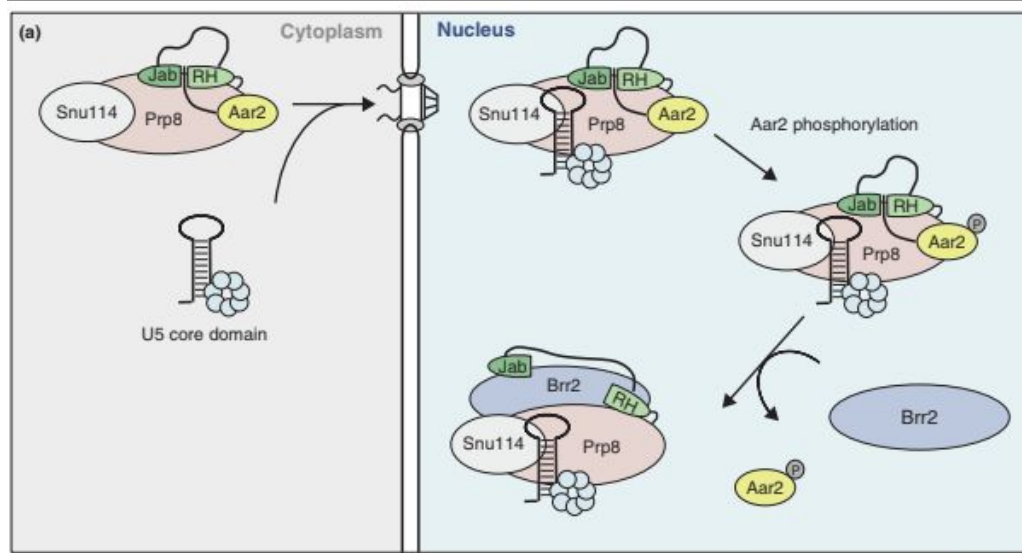
- Intramolecular stem-loop (ISL) of U6 snRNA
- helix I of the U2–U6 duplex
- Mg^{2+} ions
- loop I of U5 snRNA

Shi Y, et al. 2017

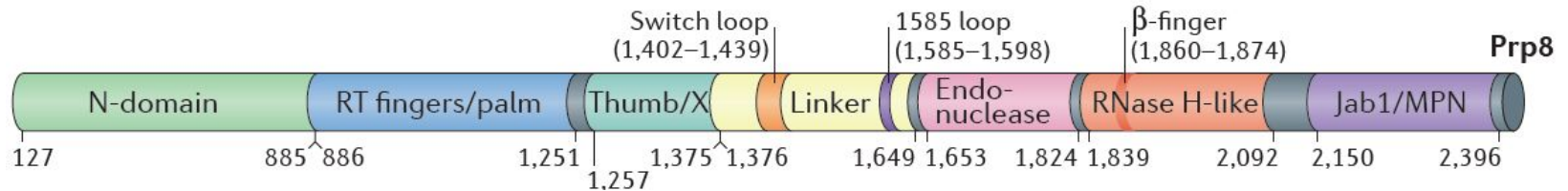
U5 snRNP



Prp8

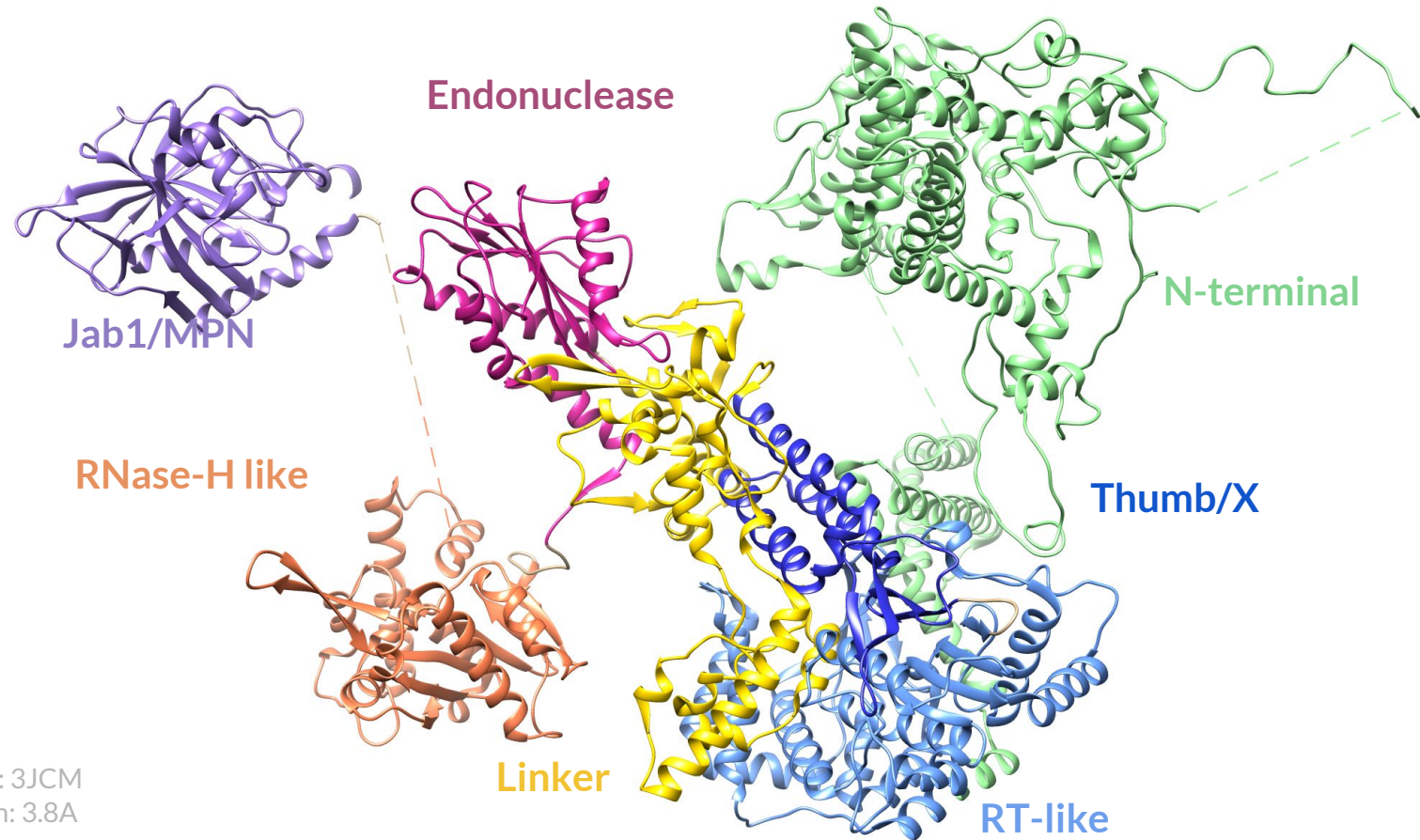


Galej, et al. 2014



Shi Y, et al. 2017

Prp8



PDB code: 3JCM
Resolution: 3.8Å

Prp8

Class
Fold
Superfamily
Family
Protein
Species

Alpha and beta proteins

Ribonuclease H-like motif

(3 layers: a/b/a; mixed beta-sheet of 5 strands, order 32145; strand 2 is antiparallel to the rest)

Ribonuclease H-like

Prp8 beta-finger domain-like

Pre-mRNA-splicing factor 8

Saccharomyces cerevisiae



Generated from scop database 1.75 with scopm 1.101 on Wed Jun 3 10:42:06 2009

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Prp8

HMMalign from PFAM (of each domain)

	1261				1320
H.sapiens	mcgfecrilp	krcrtsyeeft	HKDGVWNLQN	EVTKERTAQC	FLRVDDESMQ RFHNRVRQIL
M.mulatta	mcgfecrilp	krcrtsyeeft	HKDGVWNLQN	EVTKERTAQC	FLRVDDESMQ RFHNRVRQIL
C.lupus	mcgfecrilp	krcrtsyeeft	HKDGVWNLQN	EVTKERTAQC	FLRVDDESMQ RFHNRVRQIL
M.musculus	mcgfecrilp	krcrtsyeeft	HKDGVWNLQN	EVTKERTAQC	FLRVDDESMQ RFHNRVRQIL
G.gallus	mcgfecrilp	krcrtsyeeft	HKDGVWNLQN	EVTKERTAQC	FLRVDDESMQ RFHNRVRQIL
D.erio	mcgfecrilp	krcrtsyeeft	HKDGVWNLQN	EVTKERTAQC	FLRVDDESMQ RFHNRVRQIL
D.melanogaster	msgfecrilp	krcrtneeft	HRDGVWNLQN	EITKERTAQC	FLRVDDESLQ RFHNRVRQIL
C.elegans	msgfecrilp	krcrtaneefv	HRDGVWNLQN	EVTKERTAQC	FLRVDDESMQ RFHNRVRQIL
S.cerevisiae	smcgfevrilp	prqrmeevvs	NDEGVWDLVD	ERTKQRTAKA	YLKVSEEEIK KFDSTRIRGIL
S.pombe	mtgfevrilp	kirqneefsl	.KDGVWNLTD	NRTKQRTAQA	FIRVTEDGIN QFGNRIRQIL
N.crassa	cgfevrilp	irnqndefpv	.KDSVWSLVD	NTTKERTAHA	FLQVTEEDIQ KFNNRIRQIL
A.thaliana	cgfevrilp	irmgqeafss	TRDGVWNLQN	EQTKERTAQA	FLRADDEHMK VFENNRVRQIL
X.tropicalis	mcgfecrilp	krcrtsyeeft	HKDGVWNLQN	EVTKERTAQC	FLRVDDESMQ RFHNRVRQIL

	1321				1380
H.sapiens	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCNENKIQTR IKIGLNSKMP
M.mulatta	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCNENKIQTR IKIGLNSKMP
C.lupus	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCNENKIQTR IKIGLNSKMP
M.musculus	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCNENKIQTR IKIGLNSKMP
G.gallus	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCNENKIQTR IKIGLNSKMP
D.erio	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCNENKIQTR IKIGLNSKMP
D.melanogaster	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCNENKIQTR IKIGLNSKMP
C.elegans	MSSGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCNENKIQTR IKIGLNSKMP
S.cerevisiae	MASGSTTFTK	IAAKWNTSLI	SLFTTYFREAI	VATEPLLDIL	VKIGLNSKMP
S.pombe	MSSGSTTFTK	IAAKWNTALI	ALMTYFREAA	ISTPELLDIT	VKCESKIQTR VKIGLNSKMP
N.crassa	MSSGSTTFTK	IVNKWNTALI	ALFTTYFREAA	VSTVNLDDTI	VKICGLNSKMP
A.thaliana	MSSGSTTFTK	IVNKWNTALI	GLMTYFREAV	VHTQELLDLL	VKCNENKIQTR VKIGLNSKMP
X.tropicalis	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCNENKIQTR IKIGLNSKMP

	1381				1440
H.sapiens	SRFPVVVFY	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms heedqlipnl
M.mulatta	SRFPVVVFY	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms heedqlipnl
C.lupus	SRFPVVVFY	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms heedqlipnl
M.musculus	SRFPVVVFY	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms heedqlipnl
G.gallus	SRFPVVVFY	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms heedqlipnl
D.erio	SRFPVVVFY	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms heedqlipnl
D.melanogaster	SRFPVVVFY	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms heedqlipnl
C.elegans	SRFPVVVFY	PKELGGLGML	SMGHVLIPQS	DLRW.mqqte	aggvthfrsfg shdedqqlip
S.cerevisiae	TRFPPAVFY	PKELGGLGMI	SASHLLIPAS	DLWSkqtdt	githfrsagmt hedeeklipti
S.pombe	SRFPPAVFY	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdt	githfrsagmt tngheqlipnl
N.crassa	SRFPPAVFY	PKELGGLGMI	SGSHLLIPT	DKRWSkqtdl	gvthfrsagms hdeetlipnl
A.thaliana	SRFPVVVFY	PKELGGLGML	SMGHLLIPQS	DLRYSnqtdv	gvshfrsagms heedqlipnl
X.tropicalis	SRFPVVVFY	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms heedqlipnl

ConSurf Color Coded MSA

001 A.thaliana
002 S.pombe
003 C.lupus
004 X.tropicalis
005 D.xerio
006 M.musculus
007 D.melanogaster
008 S.cerevisiae
009 G.gallus
010 H.sapiens
011 N.crassa
012 C.elegans
013 M.mulatta

H	G	D	M	S	S	K	K	R	L	D	K	R	V	Y	L	G	A	L	K	F	V	P	H	A	V	F	K	L	E	N	M	P	M	P	W	E	Q	V	R	D	V	K	V	L	Y	H	I	
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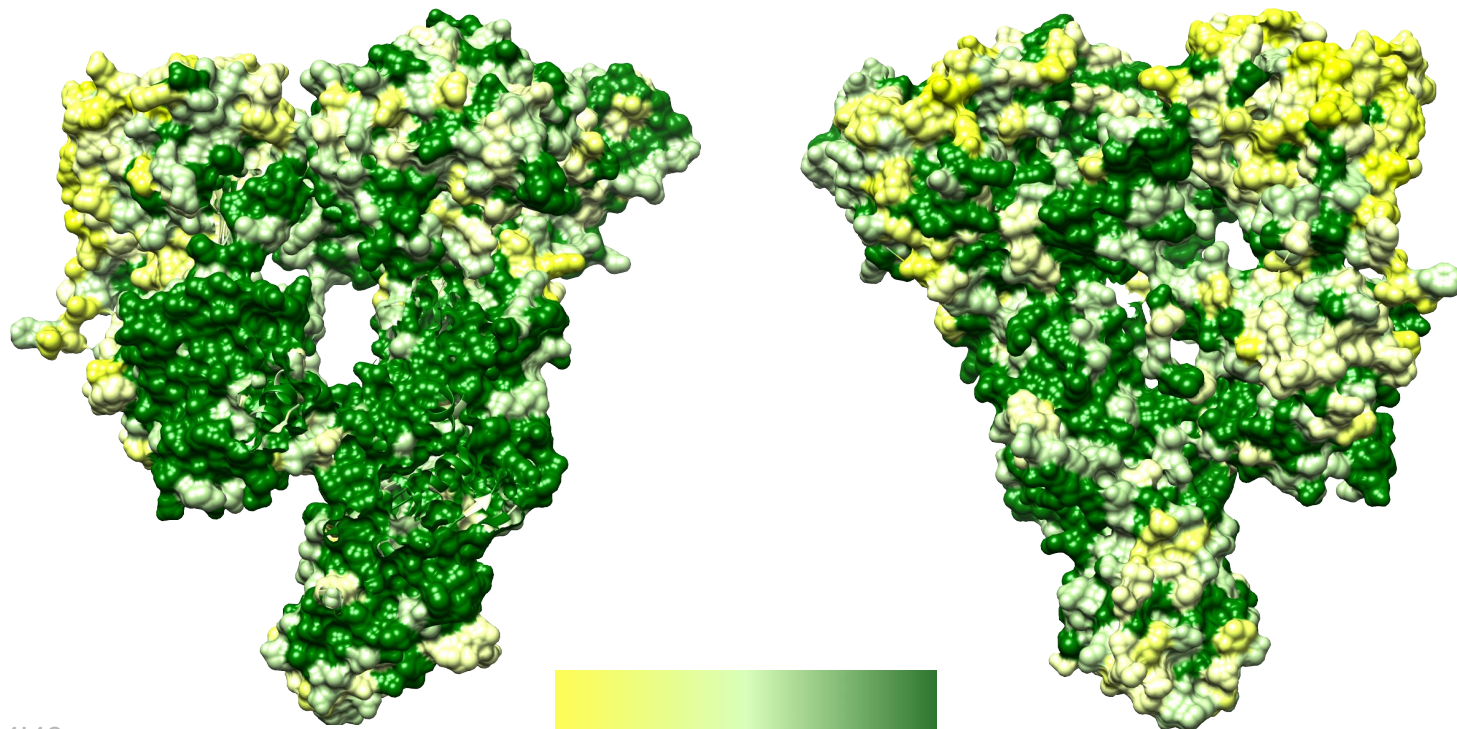
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011 N.crassa
012 C.elegans
013 M.mulatta

T	G	A	I	T	F	V	N	E	V	R	W	V	E	P	I	Y	M	A	Q	W	G	S	M	W	I	M	M	R	R	E	K	R	D	R	H	F	K	R	M	R	F	P	P	F	D	D	E		
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007 D.melanogaster
008 S.cerevisiae
009 G.gallus
010 H.sapiens
011 N.crassa
012 C.elegans
013 M.mulatta

E	P	P	L	D	Y	A	D	N	L	D	V	D	P	L	E	A	I	Q	L	E	L	D	E	E	D	S	A	V	Y	S	W	F	Y	D	H	K	P	L	V	K	T	-	K	M	I	N	G		
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Prp8

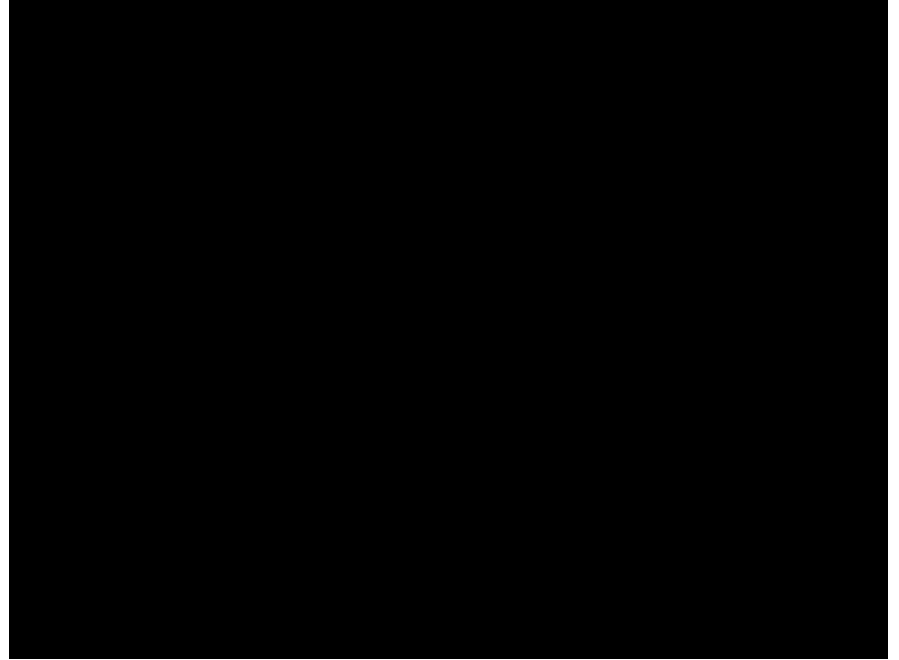
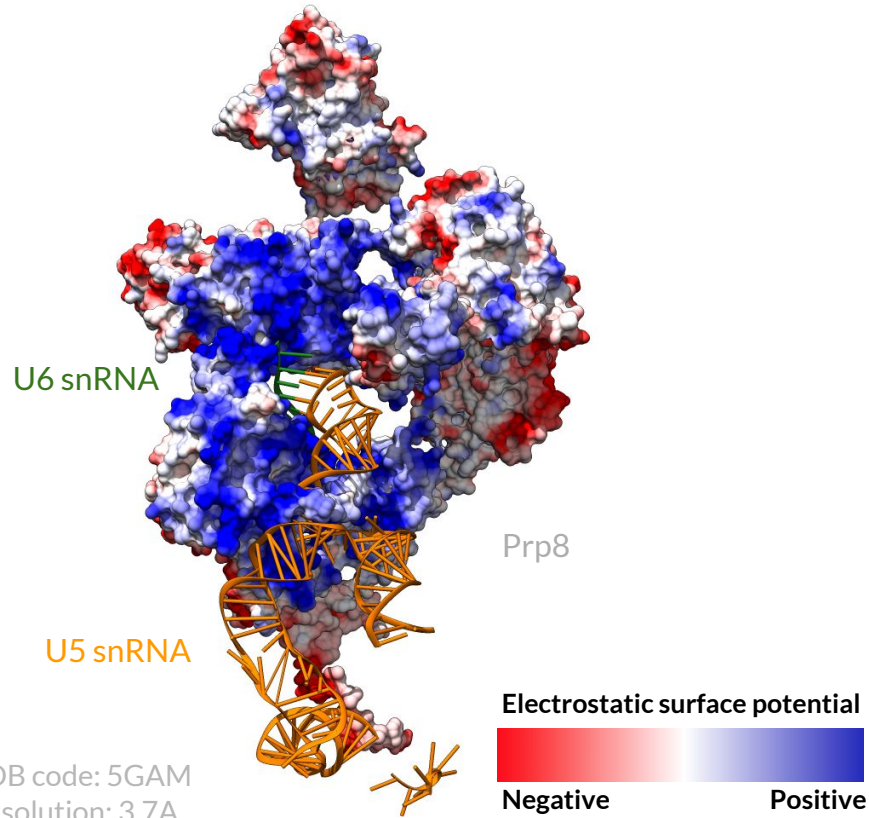


PDB code: 4I43
Resolution: 2Å

Variable

Conserved

Electrostatic surface potential in the cavity





A 3D ribbon diagram of a protein complex. The protein is composed of several subunits, each represented by a grey ribbon. One subunit, located on the right side of the complex, is highlighted in green. This green subunit is the N-terminal domain. The text "N-terminal domain" is overlaid on the image, centered horizontally and slightly below the middle vertically, in a bold black font. The background is white, and there is a light grey horizontal band behind the text.

N-terminal domain

N-domain

RT fingers/palm

Thumb/X

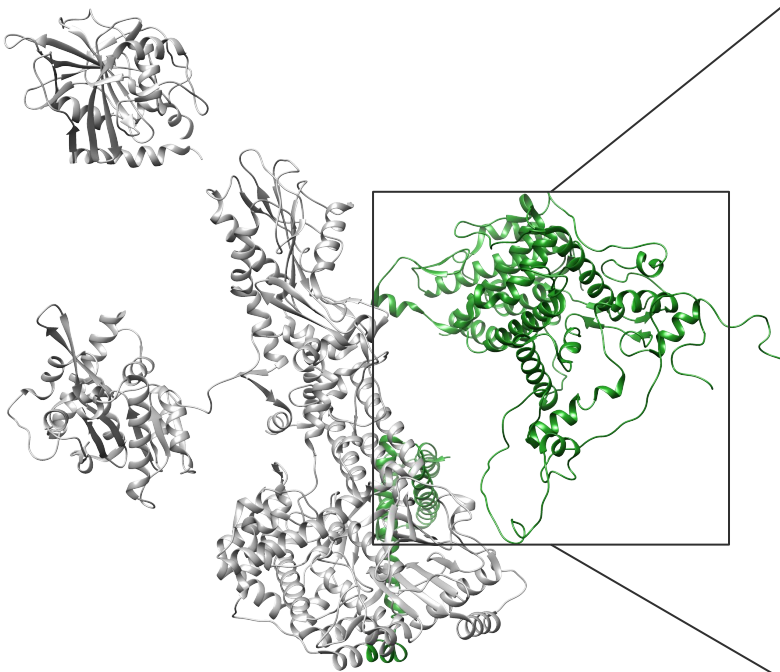
Linker

Endonuclease

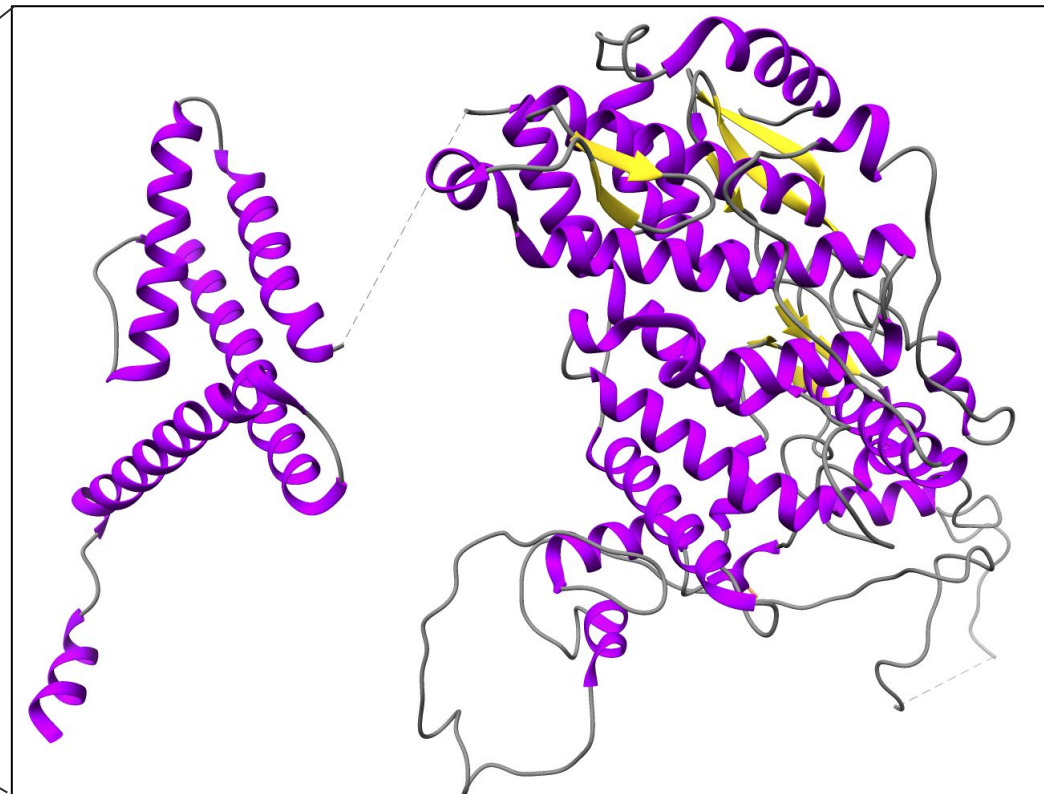
RNase H-like

Jab1/MPN

N-terminal



PDB code: 3JCM
Resolution: 3.8Å



N-domain

RT fingers/palm

Thumb/X

Linker

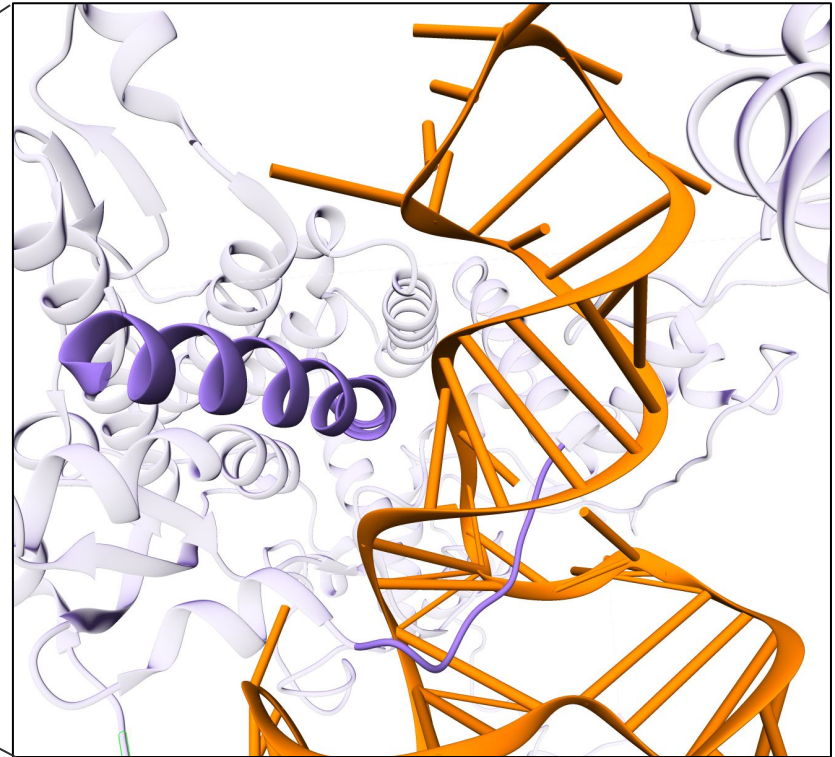
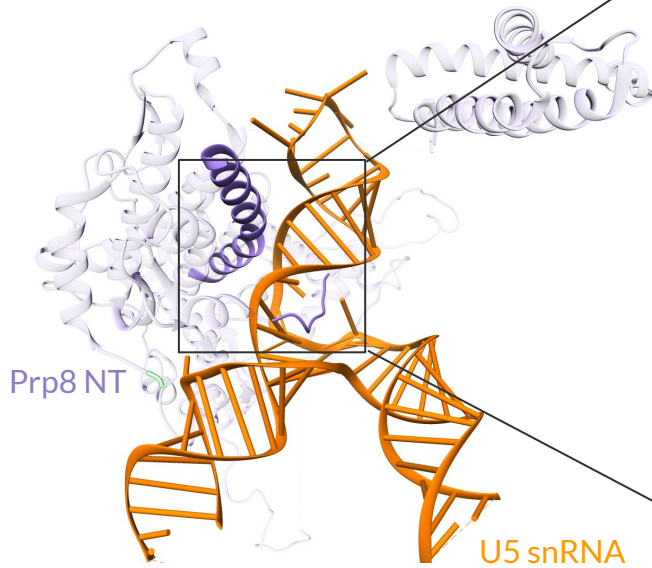
Endonuclease

RNase H-like

Jab1/MPN

N-terminal

The N-domain recognises the U5 snRNA...



PDB code: 3JCM
Resolution: 3.8Å

...and harnesses it with a polypeptide loop!

N-domain

RT fingers/palm

Thumb/X

Linker

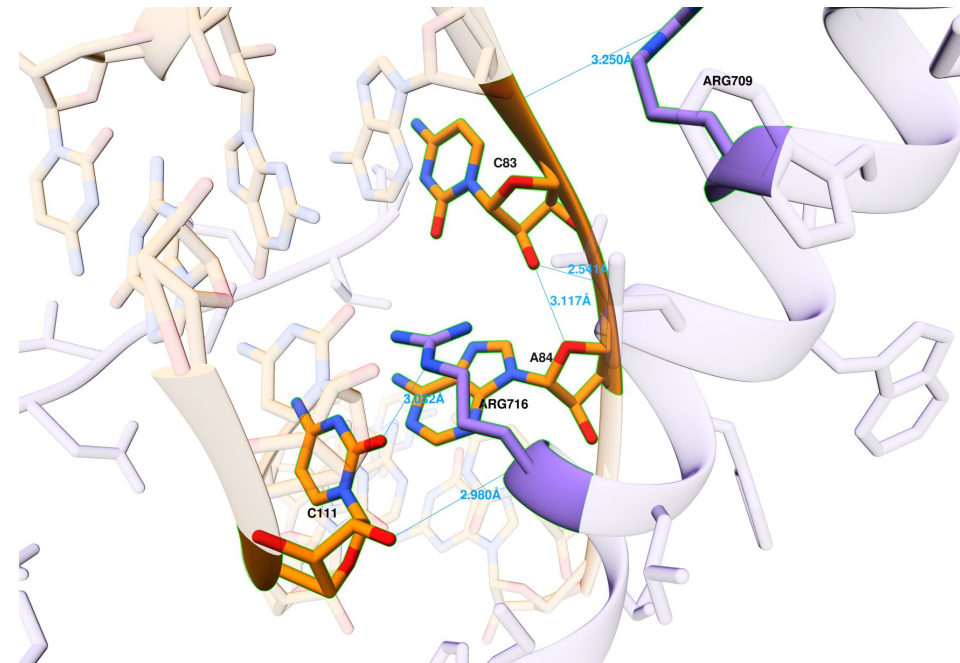
Endonuclease

RNase H-like

Jab1/MPN

N-terminal

Closed-up view of the hydrogen bonds between the α -helix and the minor groove



PDB code: 3JCM
Resolution: 3.8Å

N-domain

RT fingers/palm

Thumb/X





Linker

Endonuclease

RNase H-like

Jab1/MPN

N-terminal

-  Negatively charged
-  Positively charged
-  Non-polar
-  Polar

	661					720
H.sapiens	HVGQLTGMYP	YKYKLMRQIR	MCKDLKHLIY	YRFNTgPVGK	GP GCGFWAAG	WRVWLFFMRG
M.mulatta	HVGQLTGMYP	YKYKLMRQIR	MCKDLKHLIY	YRFNTgPVGK	GP GCGFWAAG	WRVWLFFMRG
C.lupus	HVGQLTGMYP	YKYKLMRQIR	MCKDLKHLIY	YRFNTgPVGK	GP GCGFWAAG	WRVWLFFMRG
M.musculus	HVGQLTGMYP	YKYKLMRQIR	MCKDLKHLIY	YRFNTgPVGK	GP GCGFWAAG	WRVWLFFMRG
G.gallus	HVGQLTGMYP	YKYKLMRQIR	MCKDLKHLIY	YRFNTgPVGK	GP GCGFWAPG	WRVWLFFMRG
D.rerio	HVGQLTGMYP	YKYKLMRQIR	MCKDLKHLIY	YRFNTgPVGK	GP GCGFWAPG	WRVWLFFMRG
D.melanogaster	HVGQLTGMYP	YKYKLMRQIR	MCKDLKHLIY	YRFNTgPVGK	GP GCGFWAPG	WRVWLFFMRG
C.elegans	HVGQLTGMYP	YKYKLMRQVR	MCKDLKHLIY	YRFNTgPVGK	GP GCGFWAPG	WRVWLFFLRG
S.cerevisiae	HIGQLTGIYP	YKYKVMHQIR	ACKDLKHIIY	YKFNK.NLgK	GP GCGFWQPA	WRVWLNF LRG
S.pombe	HVGQLTGMYP	YKYRLMRQIR	ACKDFKHIIY	YRFNTgPVGK	GP GCGFWAPS	WRVWLFFLRG
N.crassa	HVGQLTGMYP	YKYKLMHQIR	SCKDLKHLIY	YRFNagPVGK	GP GCGFWAPA	WRVWLFFMRG
A.thaliana	HVGQLTGMYP	YKYRLMRQIR	MCKDLKHLIY	YRFNTgPVGK	GP GCGFWAPM	WRVWLFFLRG
X.tropicalis	HVGQLTGMYP	YKYKLMRQIR	MCKDLKHLIY	YRFNTgPVGK	GP GCGFWAAG	WRVWLFFMRG
	721					780
H.sapiens	ITPLLERWLG	NLLARQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRAAVMHDI	LDMMPGIIKQ
M.mulatta	ITPLLERWLG	NLLARQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRAAVMHDI	LDMMPGIIKQ
C.lupus	ITPLLERWLG	NLLARQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRAAVMHDI	LDMMPGIIKQ
M.musculus	ITPLLERWLG	NLLARQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRAAVMHDI	LDMMPGIIKQ
G.gallus	ITPLLERWLG	NLLARQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRAAVMHDI	LDMMPGIIKQ
D.rerio	ITPLLERWLG	NLLARQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRAAVMHDI	LDMMPGIIKQ
D.melanogaster	ITPLLERWLG	NLLSRQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRASVMHDI	VDMMPGIIKQ
C.elegans	ITPLLERWLG	NLLSRQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRAAVMHDI	LDMMPDGIKQ
S.cerevisiae	TIPLLERYIG	NLITRQFEGR	.SNEIVKTTT	KQRDAYYDL	ELRNSVMDDI	LEMPESIRQ
S.pombe	IVPLLERWLG	NLLARQFEGR	HSTGVAKQIT	KQRVDSHQDL	ELRAAVMNDI	LDMIPEGIRQ
N.crassa	IIPLLERWLG	NLLSRQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRASVMADL	LDMMPGIIKQ
A.thaliana	IVPLLERWLG	NLLARQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRAAVMHDI	VDAMPEGIKQ
X.tropicalis	ITPLLERWLG	NLLARQFEGR	HSKGVAKTVT	KQRVESHFDL	ELRAAVMHDI	LDMMPGIIKQ

Sequence alignment based on PFAM domains

N-domain

RT fingers/palm

Thumb/X

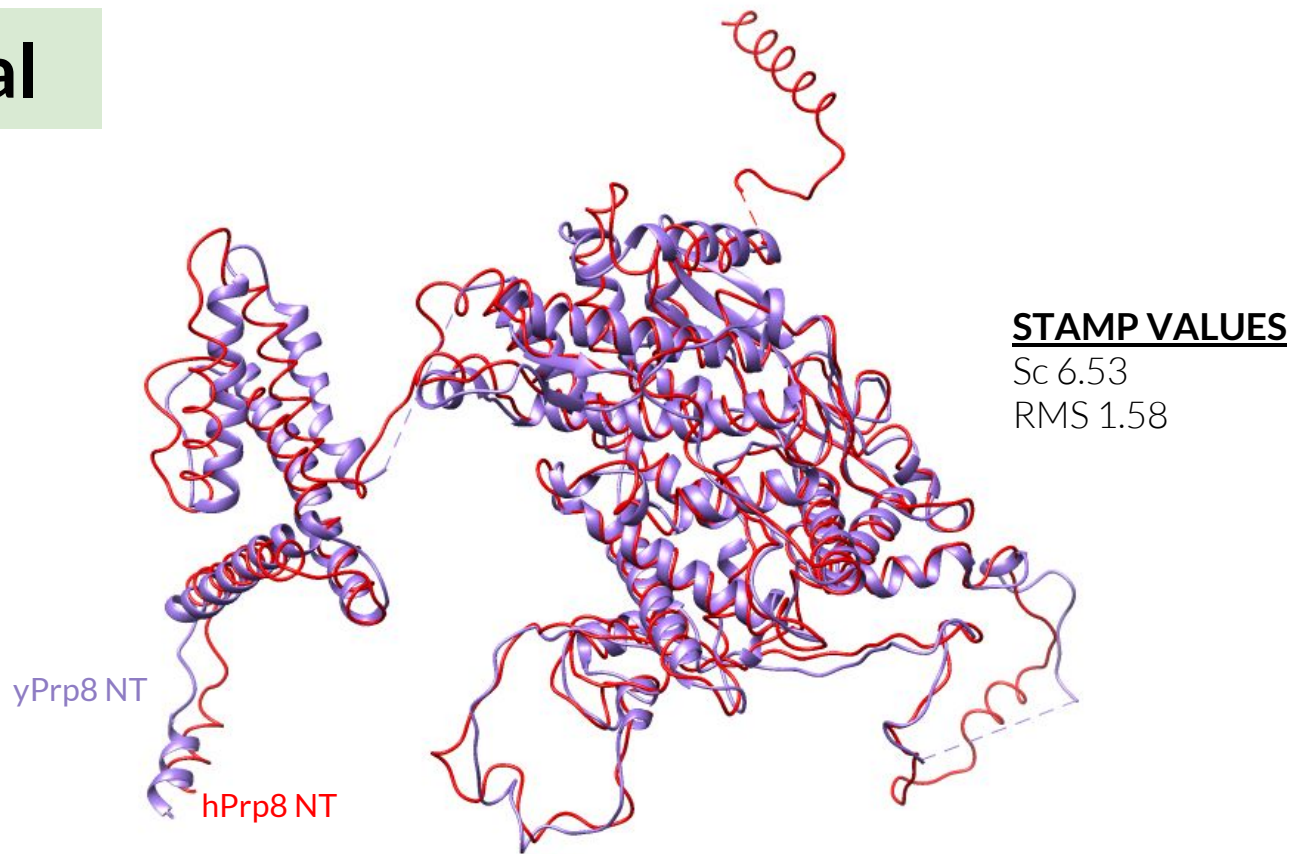
Linker

Endonuclease

RNase H-like

Jab1/MPN

N-terminal



PDB code: 3JCM
Resolution: 3.8Å

PDB code: 3JCR
Resolution: 7Å

N-domain

RT fingers/palm

Thumb/X

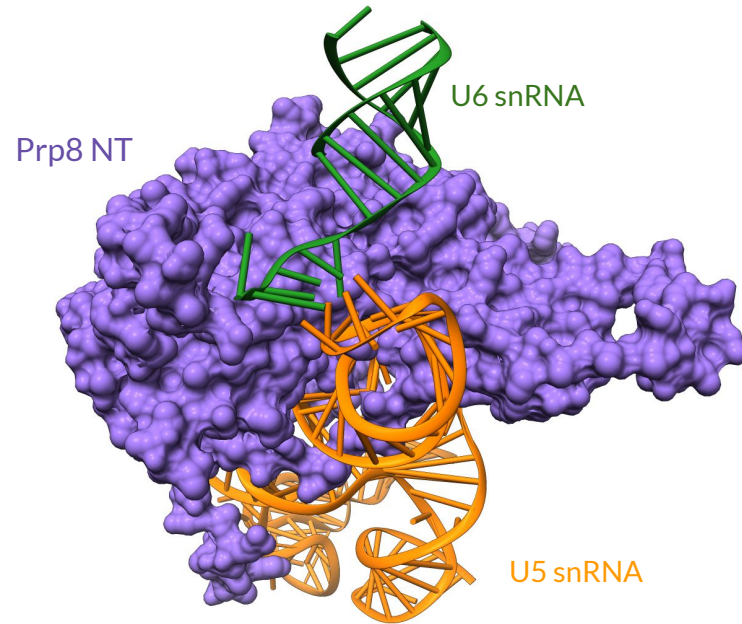
Linker

Endonuclease

RNase H-like

Jab1/MPN

N-terminal



PDB code: 5GAM
Resolution: 3.7Å

N-domain

RT fingers/palm

Thumb/X

Linker

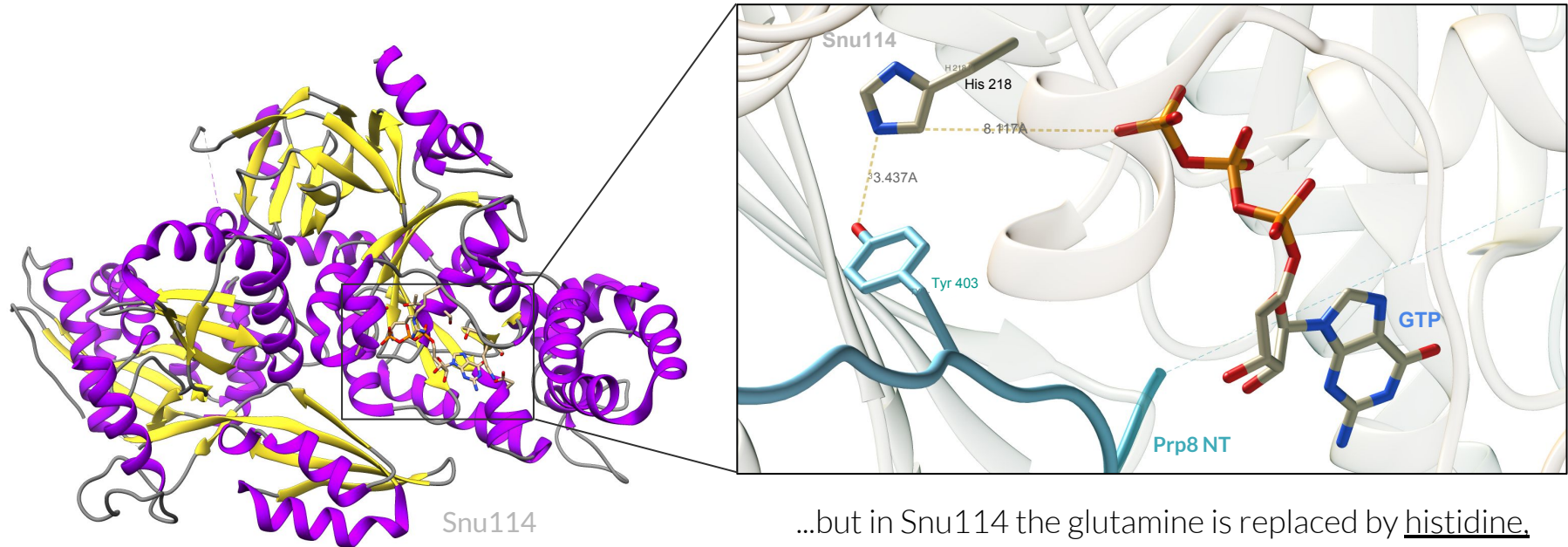
Endonuclease

RNase H-like

Jab1/MPN

Snu114

In most GTPases the glutamine residue hydrolyses the phosphate ester...



...but in Snu114 the glutamine is replaced by histidine, which is hydrogen bonded to tyrosine.

PDB code: 5GAM

Resolution: 3.7 Å

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

N-terminal

Tyr 403

	361					420
H.sapiens	VRDINLQDED	WNEFNDINKI	IIRQPIRTEY	KIAFPYLYNN	LP..HHVHLT	WYHTPNVVFI
C.lupus	VRDINLQDED	WNEFNDINKI	IIRQPIRTEY	KIAFPYLYNN	LP..HHVHLT	WYHTPNVVFI
M.musculus	VRDINLQDED	WNEFNDINKI	IIRQPIRTEY	KIAFPYLYNN	LP..HHVHLT	WYHTPNVVFI
M.mulatta	VRDINLQDED	WNEFNDINKI	IIRQPIRTEY	KIAFPYLYNN	LP..HHVHLT	WYHTPNVVFI
G.gallus	VRDINLQDED	WNEFNDINKI	IIRQPIRTEY	KIAFPYLYNN	LP..HHVHLT	WYHTPNVVFI
X.tropicalis	VRDINLQDED	WNEFNDINKI	IIRQPIRTEY	KIAFPYLYNN	LP..HHVHLT	WYHTPNVVFI
D.rerio	VRDINLQDED	WNEFNDINKI	IIRQPIRTEY	KIAFPYLYNN	LP..HHVHLT	WYHTPNVVFI
D.melanogaster	IKDHNVGDED	WNEFNDINKV	IIRQPIRTEY	RIAFPYLYNN	MP..HFVHLS	WYHTPNVVYI
C.elegans	VKDLHT.DED	WNEFNDINKV	IIRAPIRTEY	RIAFPYLYNN	LISSLPVQVS	WYHTPSVVFI
A.thaliana	HRDMEKGDED	WNEFNDINKL	IIRSPLRTEY	KVAFPHLYNN	RP..RKVKLC	VYHTPMVMYI
S.pombe	YKDEAPEMED	WNEFNDIYKL	IIRHPIKTEY	RIAFPYLYNS	RA..RSVALS	EYHQPSNVFV
N.crassa	YKDIDPNDED	FGEFNAMDRI	IFRNPIRTEC	RVAYPHLYNA	LP..RSVQLS	VHSYPQVVYT
S.cerevisiae	YP..REEEED	YNEFNSIDRV	IFRVPIRSEY	KVAFPHLYNS	RP..RSVRIP	WYNNPVSCII

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

N-domain

RT fingers/palm

Thumb/X

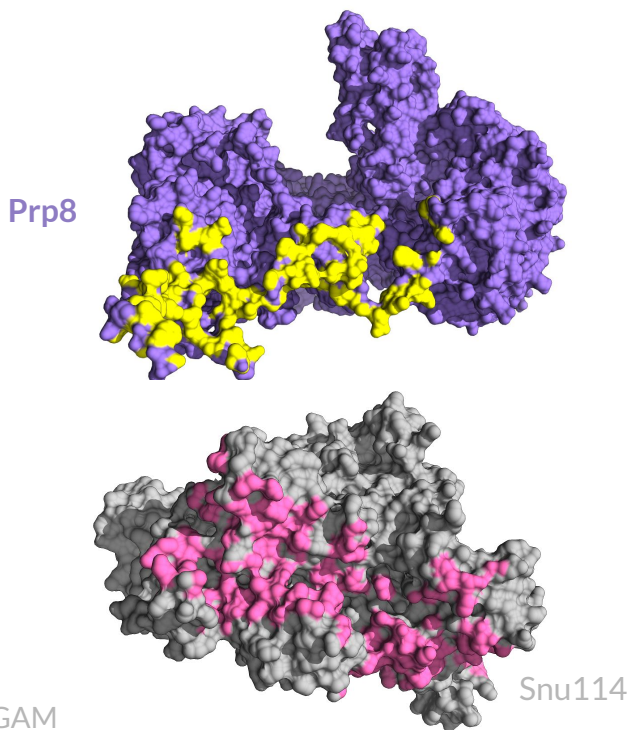
Linker

Endonuclease

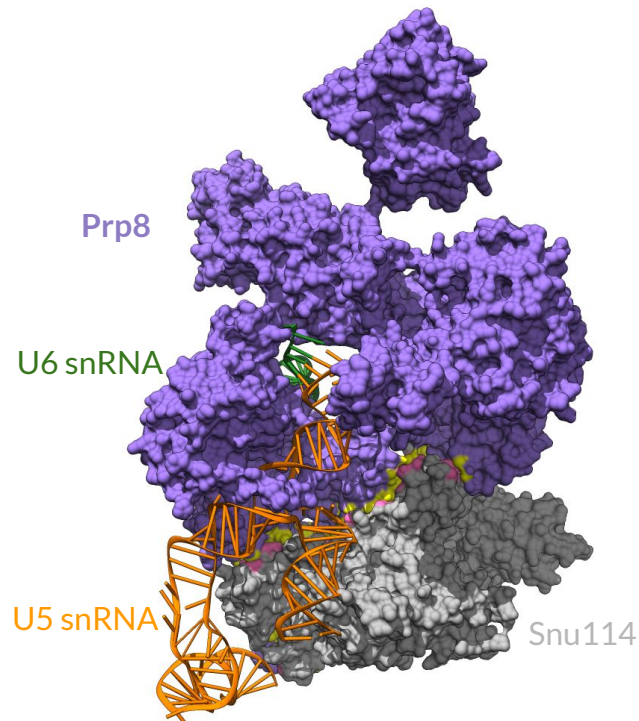
RNase H-like

Jab1/MPN

N-terminal - Snu114



PDB code: 5GAM
Resolution: 3.7Å





The image displays a 3D ribbon diagram of the Reverse Transcriptase (RT) protein structure. The protein is shown in a light gray color, with a prominent blue-colored subunit at the bottom. The structure is complex, featuring numerous alpha-helices and beta-sheets. A horizontal gray bar is positioned across the middle of the image, serving as a background for the text.

Reverse Transcriptase (RT)

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

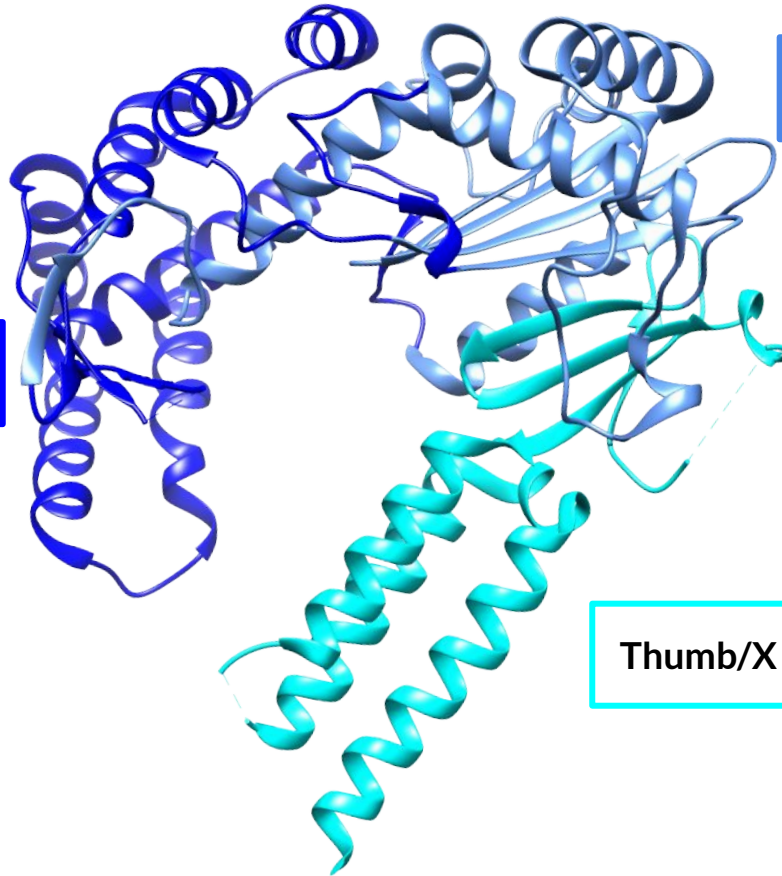
Reverse transcriptase (RT)

Finger

Palm

Thumb/X

PDB code: 4l43
Resolution: 2Å



N-domain

RT fingers/palm

Thumb/X

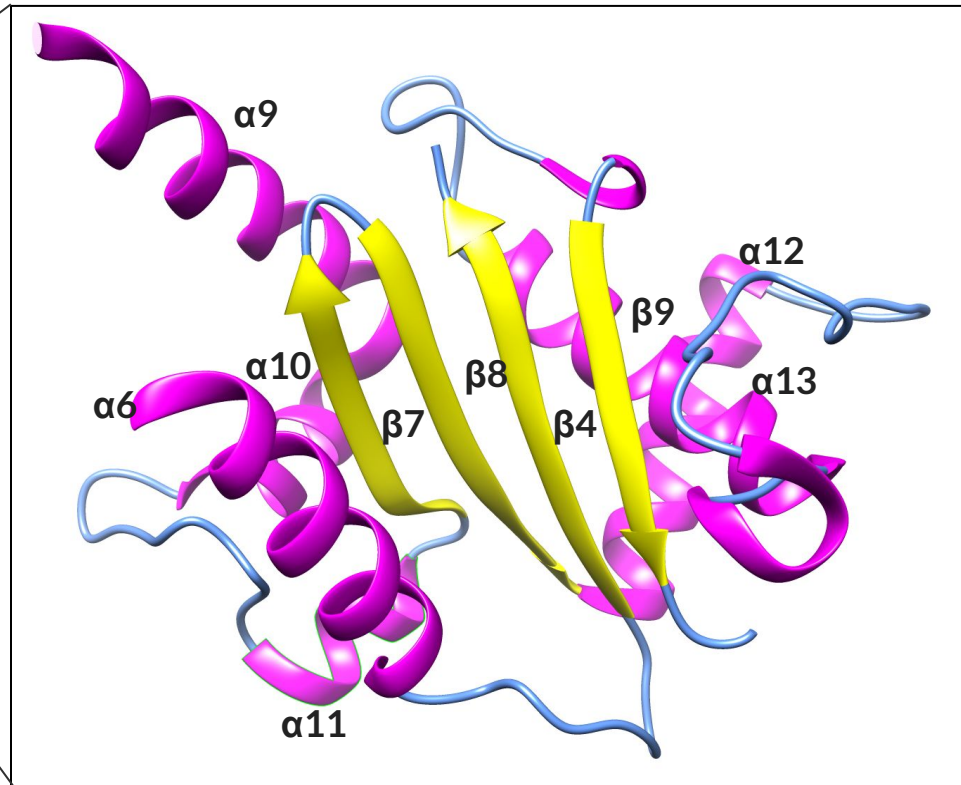
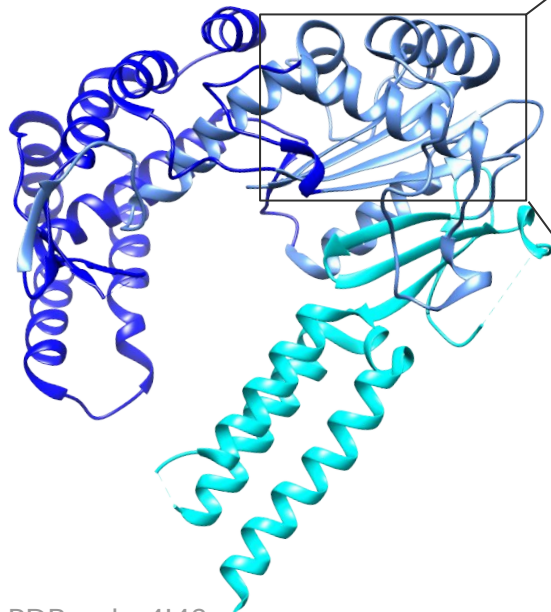
Linker

Endonuclease

RNase H-like

Jab1/MPN

RT palm



PDB code: 4l43

Resolution: 2Å

N-domain

RT fingers/palm

Thumb/X

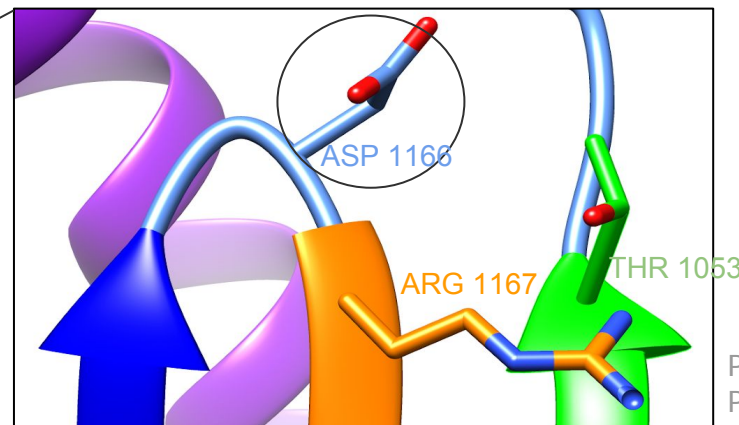
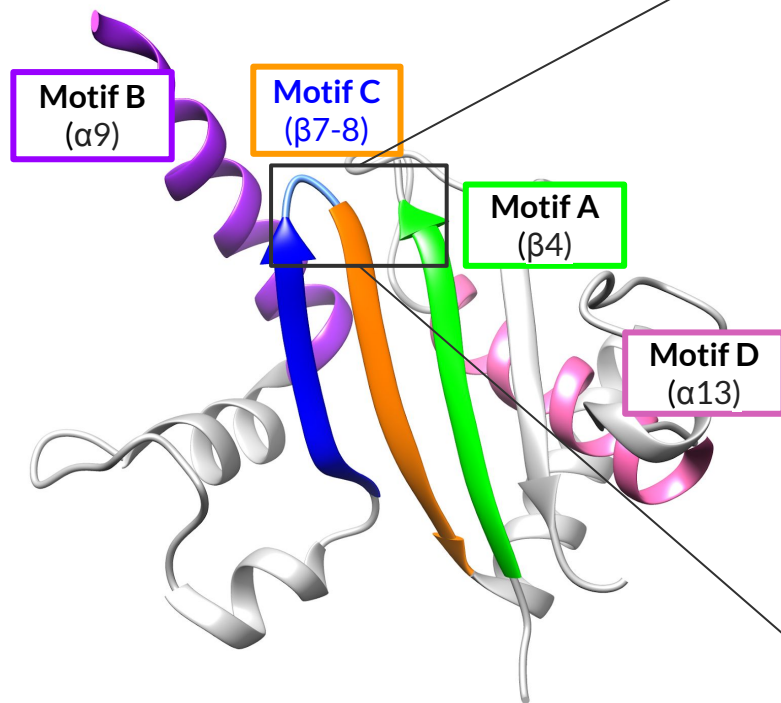
Linker

Endonuclease

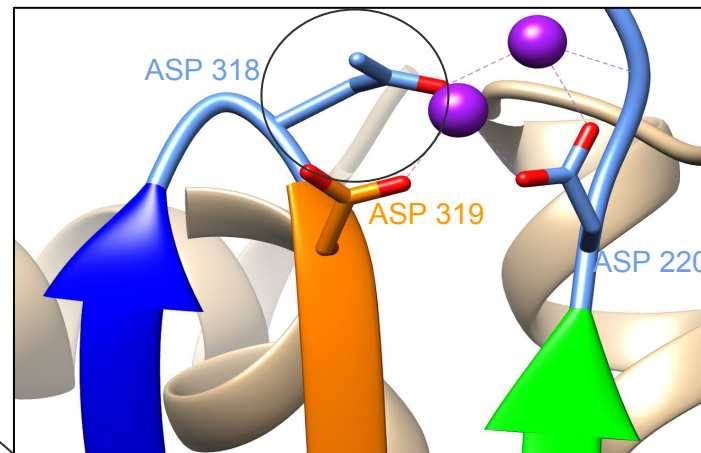
RNase H-like

Jab1/MPN

RT palm



Prp8
PDB code: 4I43



HCV
PDB code: 1NB6

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

RT palm

Thr 1053

Motif A

1021

1080

H.sapiens	LWYEADKRRL	FPPWIKPADT	EPPPLLVEYKW	CQGINNLQDV	WETSEGECEV	MLES ^S RFEKMY
C.lupus	LWYEADKRRL	FPPWIKPADT	EPPPLLVEYKW	CQGINNLQDV	WETSEGECEV	MLES ^S RFEKMY
M.musculus	LWYEADKRRL	FPPWIKPADT	EPPPLLVEYKW	CQGINNLQDV	WETSEGECEV	MLES ^S RFEKMY
M.mulatta	LWYEADKRRL	FPPWIKPADT	EPPPLLVEYKW	CQGINNLQDV	WETSEGECEV	MLES ^S RFEKMY
G.gallus	LWYEADKRRL	FPPWIKPADT	EPPPLLVEYKW	CQGINNLQDV	WETSEGECEV	MLES ^S RFEKMY
X.tropicalis	LWYEADKRRL	FPPWIKPADT	EPPPLLVEYKW	CQGINNLQDV	WDTTEGECEV	MLES ^S RFEKMY
D.rerio	LWYEADKRRL	FPPWIKPADT	EPPPLLVEYKW	CQGINNLQDV	WETAEGECEV	MLES ^S RYEKMY
D.melanogaster	LWYEADKRRL	FPPWIKPSDT	EPPPLLAYKW	CQGINNLQDV	WDVGEGECEV	LLES ^S RFEKLY
C.elegans	LWYEADKRRL	FPAWVKPGDT	EPPPLLTYKW	CQGLNNLQDV	WETSEGECEV	IMETKLEKIA
A.thaliana	LWYEGDKRHL	FPNWIKPADS	EPPPLLVEYKW	CQGINNLQGI	WDTSDGQCIV	MLQTKFEKLF
S.pombe	LWFEADRRHL	FPSWVKPSDS	EPPPLLVEYKW	CQGINNLTDV	WETSNGECEV	LMETRLSKVF
N.crassa	LWYQADQRHL	FPAWIKPSDS	EVPLLVEYKW	AQGINNLDRV	WETANGECEV	MIETQLSKVY
S.cerevisiae	LWYEADQRKL	FPNWIKPSDS	EIPPLLVEYKW	TQGINNLSEI	WDVSRGQSAV	LLETTLGEMA

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

RT palm

Asp 1166

Arg 1167

Motif C

1141

1200

H.sapiens	LVMDLLVLGL	HRASEMAGPP	QMPNDFLSFQ	DIATEAAHPI	RLFCRYIDRI	HIFFRFTADE
C.lupus	LVMDLLVLGL	HRASEMAGPP	QMPNDFLSFQ	DIATEAAHPI	RLFCRYIDRI	HIFFRFTADE
M.musculus	LVMDLLVLGL	HRASEMAGPP	QMPNDFLSFQ	DIATEAAHPI	RLFCRYIDRI	HIFFRFTADE
M.mulatta	LVMDLLVLGL	HRASEMAGPP	QMPNDFLSFQ	DIATEAAHPI	RLFCRYIDRI	HIFFRFTADE
G.gallus	LVMDLLVLGL	HRASEMAGPP	QMPNDFLSFQ	DIATEVAHPI	RLFCRYIDRI	HIFFRFTADE
X.tropicalis	LVMDLLVLGL	HRASEMAGPP	QMPNDFLSFQ	DVATESAHPI	RLFCRYIDRI	HIFFRFSADE
D.rerio	LVMDLLVLGL	HRASEMAGPP	QMPNDFLSFQ	DTATESAHPI	RLYCRYIDRI	HIFFRFSADE
D.melanogaster	LVLDLLVLGL	HRSEMAGPP	QMPNDFLTQF	DTVTETAHPI	RLYCRYVDRI	HLFFRFSAAE
C.elegans	LVLDLLVLGL	RRASEIAGPP	QCPNEFLQFQ	DVATEIGHPI	RLYCRYIDRV	WIMFRFSADE
A.thaliana	LVLDLLLLGL	TRASEIAGPP	QRPNEFMTYW	DTKVETRHP	RLYSRYIDKV	HIMFKFTHEE
S.pombe	LVLDLLILGL	QRATEIAGPA	DAPNDFLHFK	DQATETSHPI	RLYTRYIDKV	YIMFRFTDEE
N.crassa	LILDLLLLGP	QRASEIAGPP	HAPNDFLQFK	DRETETRHP	RLYTRYIDKI	WVFLRFTADE
S.cerevisiae	LVIDLLLLGQ	ERATDLAGPA	NNPNEFMQFK	SKEVEKAHPI	RLYTRYLDRI	YMLFHFEED

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

N-domain

RT fingers/palm

Thumb/X

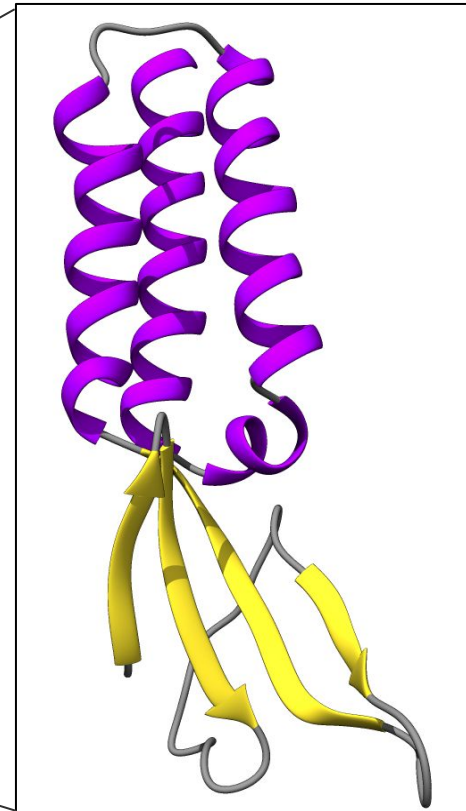
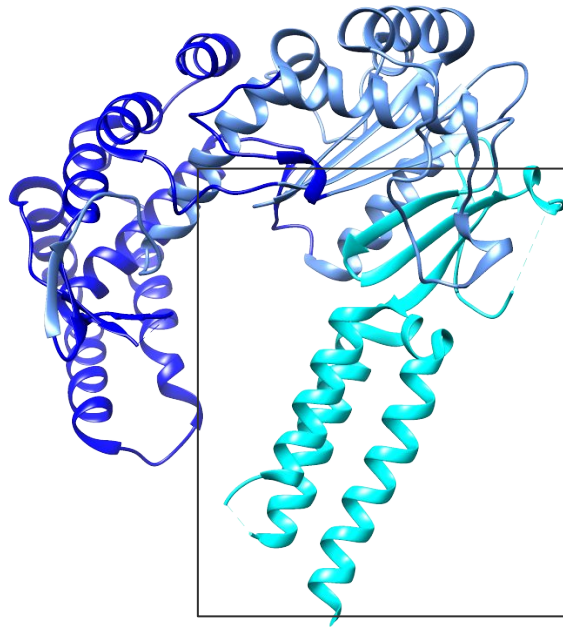
Linker

Endonuclease

RNase H-like

Jab1/MPN

Thumb/X



PDB code: 4l43
Resolution: 2Å

N-domain

RT fingers/palm

Thumb/X

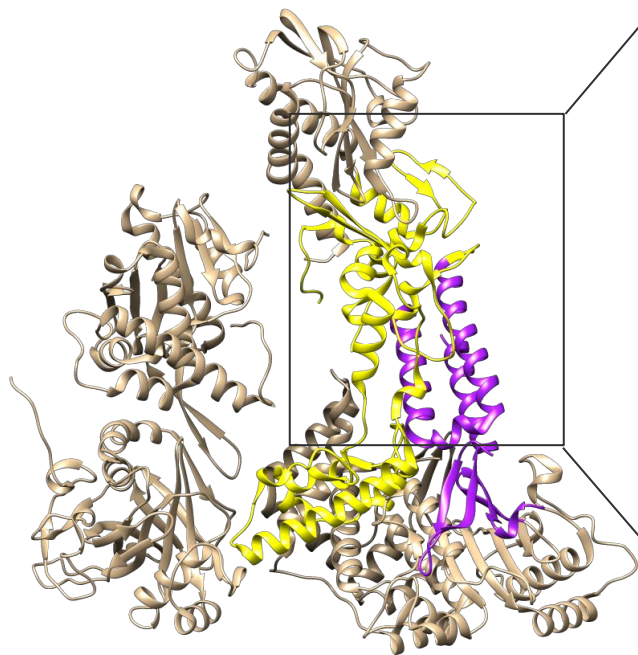
Linker

Endonuclease

RNase H-like

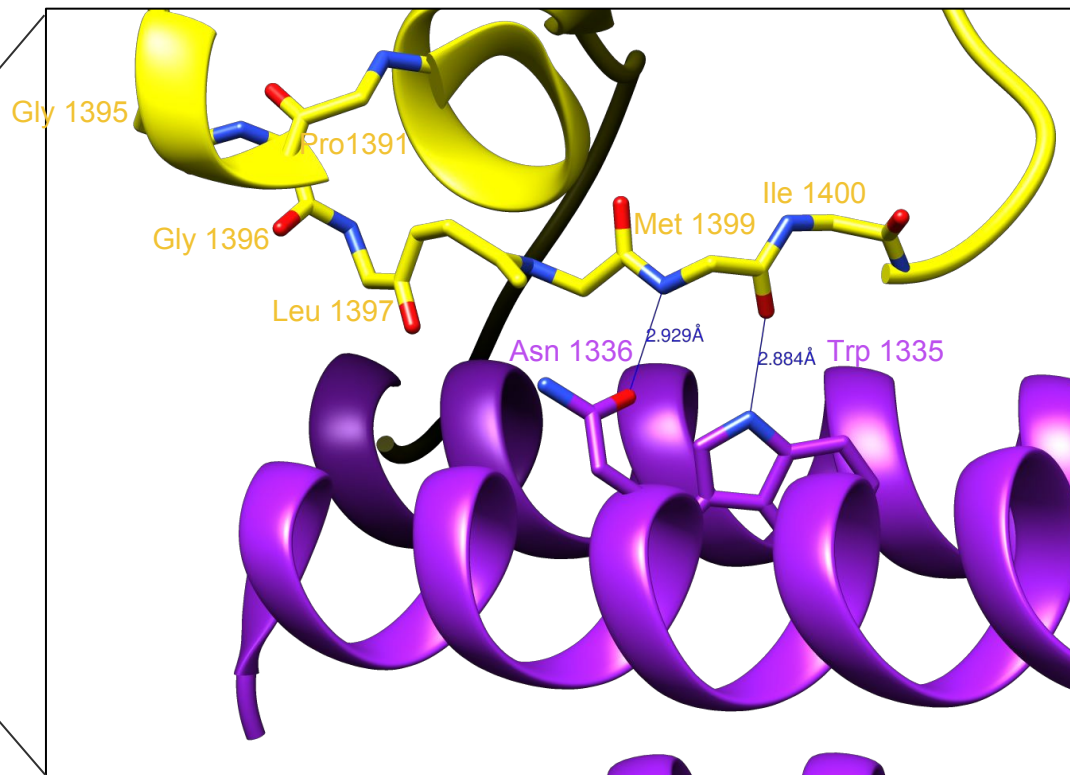
Jab1/MPN

Thumb/X - Linker



PDB code: 4I43

Resolution: 2Å



Linker

Thumb/X

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Thumb/X - Linker

Trp 1335

Asn 1336

Thumb region

	1321					1380
H.sapiens	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCENKIQTR	IKIGLNSKMP
M.mulatta	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCENKIQTR	IKIGLNSKMP
C.lupus	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCENKIQTR	IKIGLNSKMP
M.musculus	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCENKIQTR	IKIGLNSKMP
G.gallus	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCENKIQTR	IKIGLNSKMP
D.rerio	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCENKIQTR	IKIGLNSKMP
D.melanogaster	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCENKIQTR	IKIGLNSKMP
C.elegans	MSSGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCENKIQTR	IKIGLNSKMP
S.cerevisiae	MASGSTTFTK	VAAKWNTSLI	SLFTYFREAI	VATEPLLDIL	VKGETRIQNR	VKLGLNSKMP
S.pombe	MSSGSTTFTK	IANKWNTALI	ALMTYYREAA	ISTPELLDLL	VKCESKIQTR	VKISLNSKMP
N.crassa	MSSGSTTFTK	IANKWNTALI	ALFTYYREAA	VSTVNLLDTI	VKCETKIQTR	VKIGLNSKMP
A.thaliana	MSSGSTTFTK	IVNKWNTALI	GLMTYFREAT	VHTQELLDLL	VKCENKIQTR	VKIGLNSKMP
X.tropicalis	MASGSTTFTK	IVNKWNTALI	GLMTYFREAV	VNTQELLDLL	VKCENKIQTR	IKIGLNSKMP

Negatively charged

Non-polar

Positively charged

Polar

Sequence alignment based on PFAM domains

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Thumb/X - Linker

Gly 1395
Gly 1396
Leu 1397

Linker region

Sequence alignment based
on PFAM domains

	1381					1440
H.sapiens	SRFPPVVFYT	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms	heedqlipnl
M.mulatta	SRFPPVVFYT	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms	heedqlipnl
C.lupus	SRFPPVVFYT	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms	heedqlipnl
M.musculus	SRFPPVVFYT	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms	heedqlipnl
G.gallus	SRFPPVVFYT	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms	heedqlipnl
D.rerio	SRFPPVVFYT	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms	heedqlipnl
D.melanogaster	SRFPPVVFYT	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms	hdedqlipnl
C.elegans	SRFPPVVFYT	PKEIGGLGML	SMGHVLIPQS	DLRW.mqqte	aggvthfrsg	mshdedqlip
S.cerevisiae	TRFPPAVFYT	PKELGGLGMI	SASHILIPAS	DLSWSkqtdt	githfragmt	hedeklipti
S.pombe	SRFPPAVFYS	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdt	githfrsgmt	tngehlplnl
N.crassa	SRFPPAVFYT	PKELGGLGMI	SGSHILIPTS	DKRWSkqtdl	gvthyragms	hdeetlipni
A.thaliana	SRFPPVIFYT	PKEIGGLGML	SMGHILIPQS	DLRYSnqtdv	gvshfrsgms	heedqlipnl
X.tropicalis	SRFPPVVFYT	PKELGGLGML	SMGHVLIPQS	DLRWSkqtdv	githfrsgms	heedqlipnl

Pro 1384
Pro 1385
Pro 1391

Gly 1398
Met 1399
Leu/Ile 1400

Negatively charged Non-polar
Positively charged Polar

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

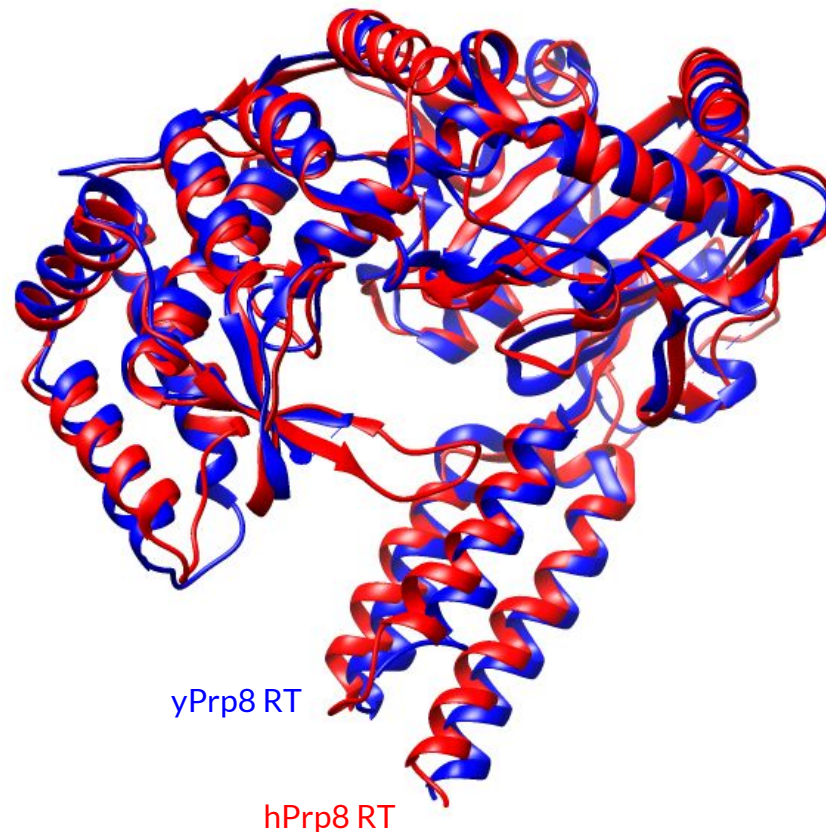
Jab1/MPN

Reverse transcriptase (RT)

STAMP VALUES

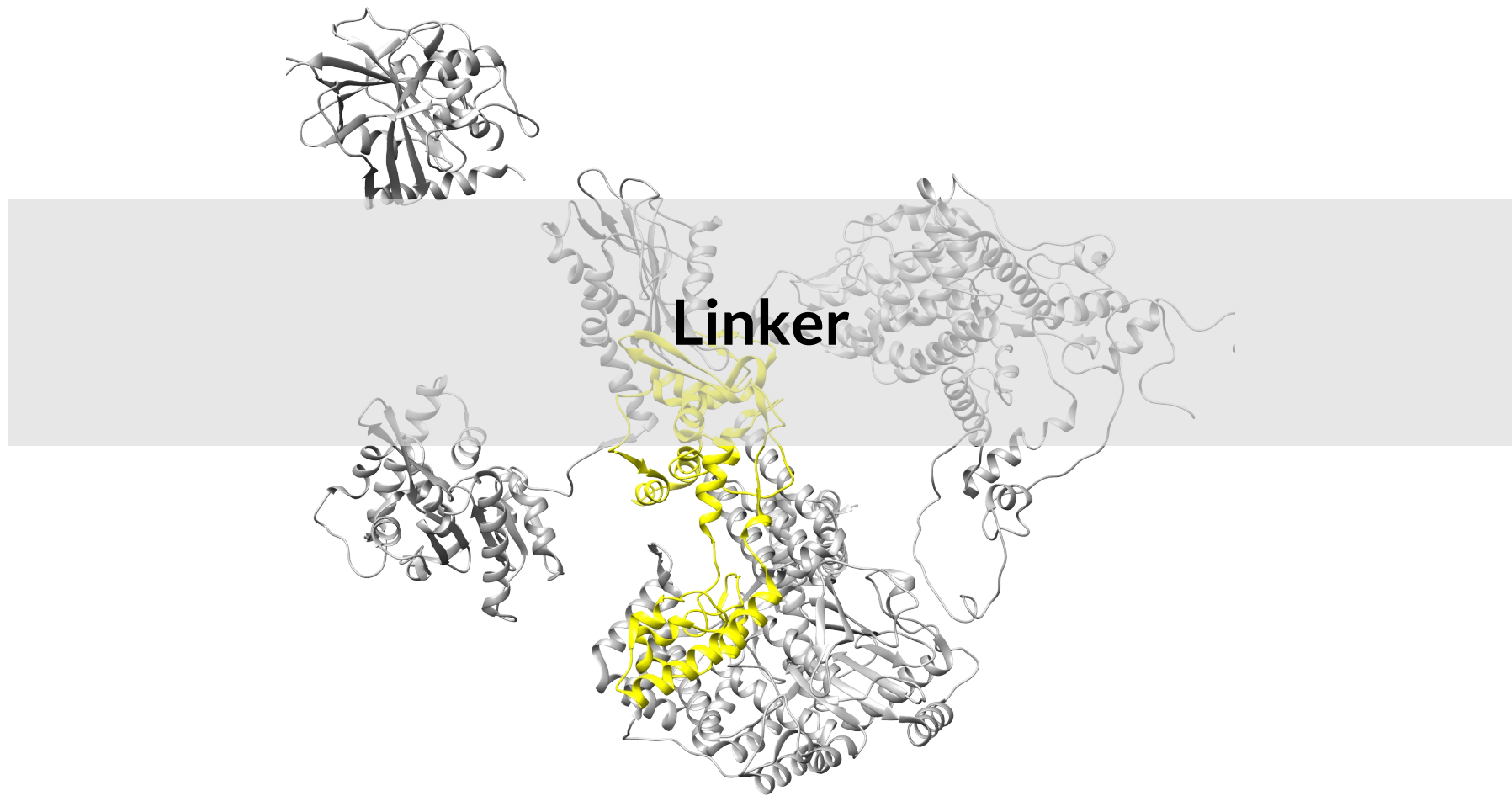
Sc 7.21

RMS 1.65



PDB code: 5MQF
Resolution: 5.9Å

PDB code: 4I43
Resolution: 2Å



Linker

N-domain

RT fingers/palm

Thumb/X

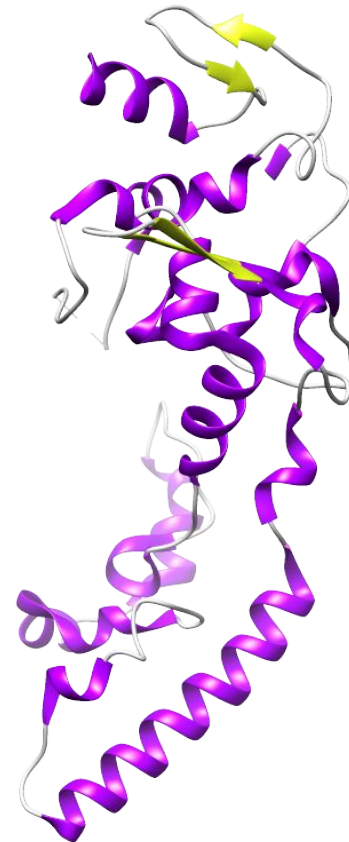
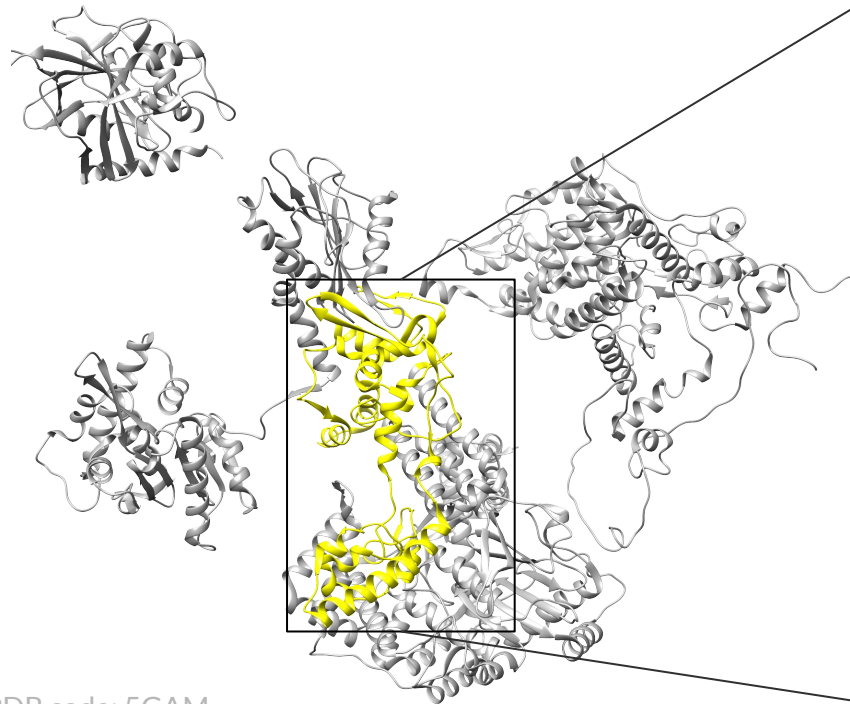
Linker

Endonuclease

RNase H-like

Jab1/MPN

Linker



PDB code: 5GAM
Resolution: 3.7Å

N-domain

RT fingers/palm

Thumb/X

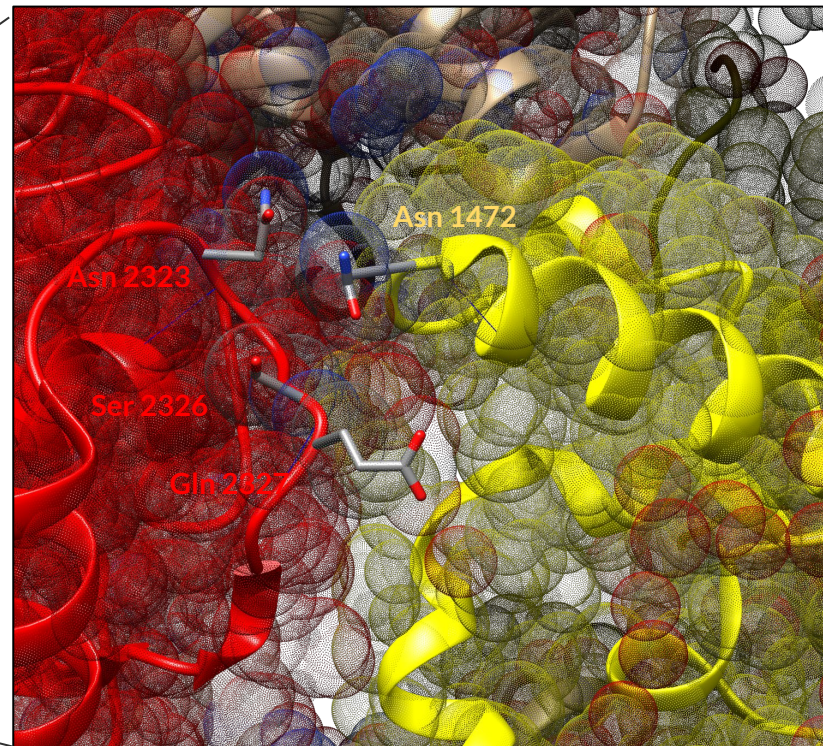
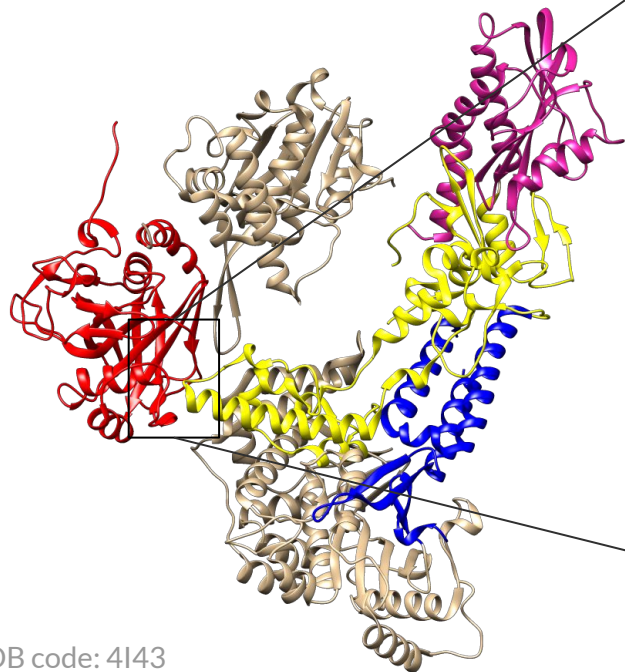
Linker

Endonuclease

RNase H-like

Jab1/MPN

Linker- Jab1/MPN



PDB code: 4I43

Resolution: 2Å

Linker

Thumb/X

Jab1/MPN

Endonuclease

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Linker- Jab1/MPN

Jab1/MPN region

						Asn 2323 Ser 2326	Glu 2327	
	2281							2340
H.sapiens	pswdgekTII	ITCSFTPGSC	TLTAYKLTPS	GYEWGRQNTD	.KGNNPKGYL	PSHYERVQML		
M.mulatta	pswdgekTII	ITCSFTPGSC	TLTAYKLTPS	GYEWGRQNTD	.KGNNPKGYL	PSHYERVQML		
C.lupus	pswdgekTII	ITCSFTPGSC	TLTAYKLTPS	GYEWGRQNTD	.KGNNPKGYL	PSHYERVQML		
M.musculus	pswdgekTII	ITCSFTPGSC	TLTAYKLTPS	GYEWGRQNTD	.KGNNPKGYL	PSHYERVQML		
G.gallus	pswdgekTII	ITCSFTPGSC	TLTAYKLTPS	GYEWGRQNTD	.KGNNPKGYL	PSHYERVQML		
D.rerio	pswdgekTII	ITCSFTPGSC	TLTAYKLTPS	GYEWGRQNTD	.KGNNPKGYL	PSHYERVQML		
D.melanogaster	snwdgekTIV	ITCSFTPGSC	SLTAYKLTPS	GFEWGSKNTD	.KGNNPKGYL	PSHYERVQML		
C.elegans	iswdgekTVM	ITCSFTPGSV	SLTAYKLTPS	GYEWGKANTD	.KGNNPKGYM	PTHYEKVQML		
S.cerevisiae	fadkkrdCID	ISIFSTPGSV	SLSAYNLTD	GYQWGEENKD	IMNVLSEGE	PTFSTHAQLL		
S.pombe	pewdtka.VT	LTVSYIPGSI	SLAAYTVSKE	GIEWGSKNMD	INSDEAIGYE	PSMAEKCQLL		
N.crassa	nwdkqnt.LT	VAVSFTPGSV	SLSAWALTPQ	GFKWGVENKD	IASDQPQGFT	TSMGEKRQLL		
A.thaliana	kqwdaeKCII	LTCSTFTPGSC	SLTSYKLTQA	GYEWGRLNKD	.TGSNPHGYL	PTHYEKVQML		
X.tropicalis	pawdgekTII	ITCSFTPGSC	TLTAYKLTPS	GYEWGRQNTD	.KGNNPKGYL	PSHYERVQML		

Negatively charged

Non-polar

Positively charged

Polar

Sequence alignment based on PFAM domains

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Linker- Jab1/MPN

Linker region

Asn 1472

	1441					1500
H.sapiens	SKQTDVG.IT	HFRSGMSHEE	DQLIPNLYRY	IQPWESEFID	SQRVWAEYAL	KRQEAIQAQNR
C.lupus	SKQTDVG.IT	HFRSGMSHEE	DQLIPNLYRY	IQPWESEFID	SQRVWAEYAL	KRQEAIQAQNR
M.musculus	SKQTDVG.IT	HFRSGMSHEE	DQLIPNLYRY	IQPWESEFID	SQRVWAEYAL	KRQEAIQAQNR
M.mulatta	SKQTDVG.IT	HFRSGMSHEE	DQLIPNLYRY	IQPWESEFID	SQRVWAEYAL	KRQEAIQAQNR
G.gallus	SKQTDVG.IT	HFRSGMSHEE	DQLIPNLYRY	IQPWESEFID	SQRVWAEYAL	KRQEAIQAQNR
X.tropicalis	SKQTDVG.IT	HFRSGMSHEE	DQLIPNLYRY	IQPWESEFID	SQRVWAEYAL	KRQEAIQAQNR
D.rerio	SKQTDVG.IT	HFRSGMSHEE	DQLIPNLYRY	IQPWESEFID	SQRVWAEYAL	KRQEAIQAQNR
D.melanogaster	SKQTDVG.IT	HFRSGMSHDE	DQLIPNLYRY	IQPWESEFID	SQRVWAEYAL	KRQEANAQNR
C.elegans	MQQTEAGGV	T HFRSGMSHDE	DQLIPNLYRY	IQPWEAEFVD	SVRVWAEYAL	KRQEANAQNR
A.thaliana	SNQTDVG.VS	HFRSGMSHEE	DQLIPNLYRY	IQPWESEFID	SQRVWAEYAL	KRQEQAQNR
S.pombe	SKQTDG.IT	HFRSGMTTNG	EHLIPNLYRY	IQPWESEFID	SQRVWAEYAM	KRQEALQQNR
N.crassa	SKQTDLG.VT	HYRAGMSHDE	ETLIPNIFRY	IIPWEAEFID	SQRVWTEYSQ	KRLEANQQNR
S.cerevisiae	SKQTDG.IT	HFRAGMTHED	EKLIPNIFRY	ITTWENEFLD	SQRVWAEYAT	KRQEAIQQNR

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Linker

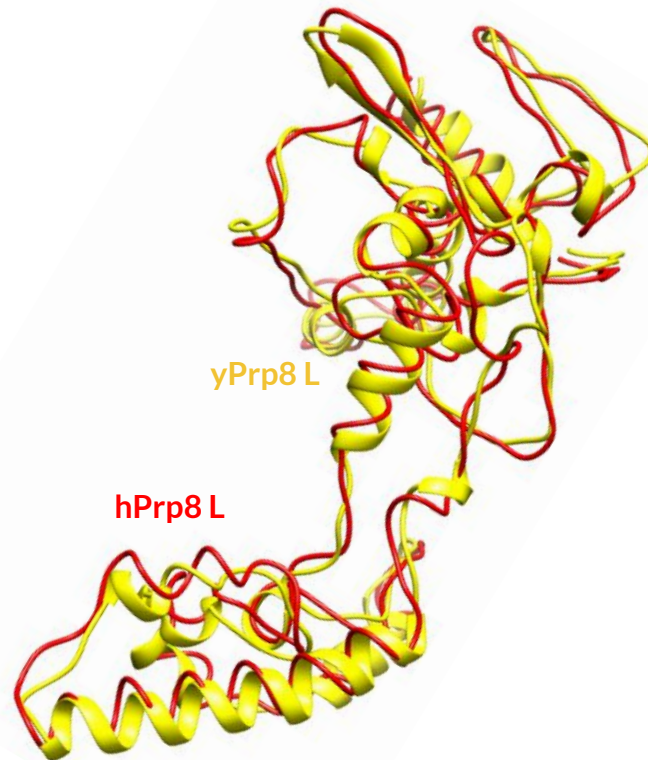
STAMP VALUES

Sc 8.43

RMS 1.42

PDB code: 3JCM
Resolution: 3.8Å

PDB code: 3JCR
Resolution: 7Å





The image displays a 3D ribbon diagram of a protein, identified as an endonuclease. The protein is shown in a light gray color, with its complex structure featuring numerous alpha-helices and beta-sheets. A specific region of the protein, likely the active site, is highlighted in a vibrant magenta color. This highlighted region is positioned centrally, overlapping a horizontal gray band. The word "Endonuclease" is written in a bold, black, sans-serif font across this gray band, directly beneath the magenta-highlighted area. The overall composition is clean and scientific, emphasizing the structural details of the enzyme.

Endonuclease

N-domain

RT fingers/palm

Thumb/X

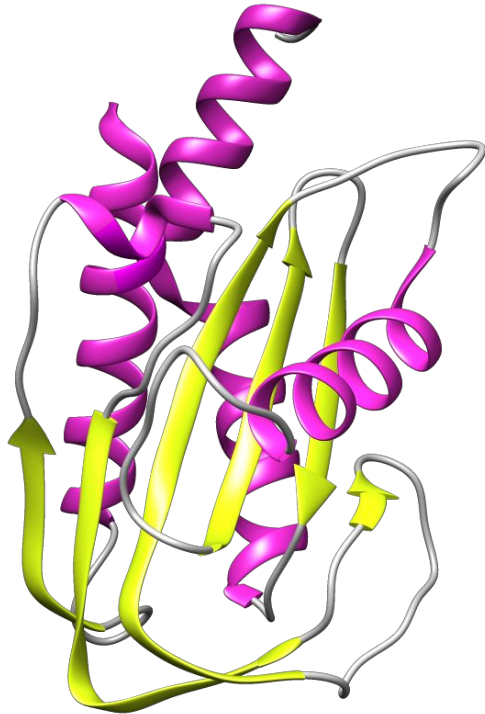
Linker

Endonuclease

RNase H-like

Jab1/MPN

Endonuclease



PDB code: 4I43
Resolution: 2Å

N-domain

RT fingers/palm

Thumb/X

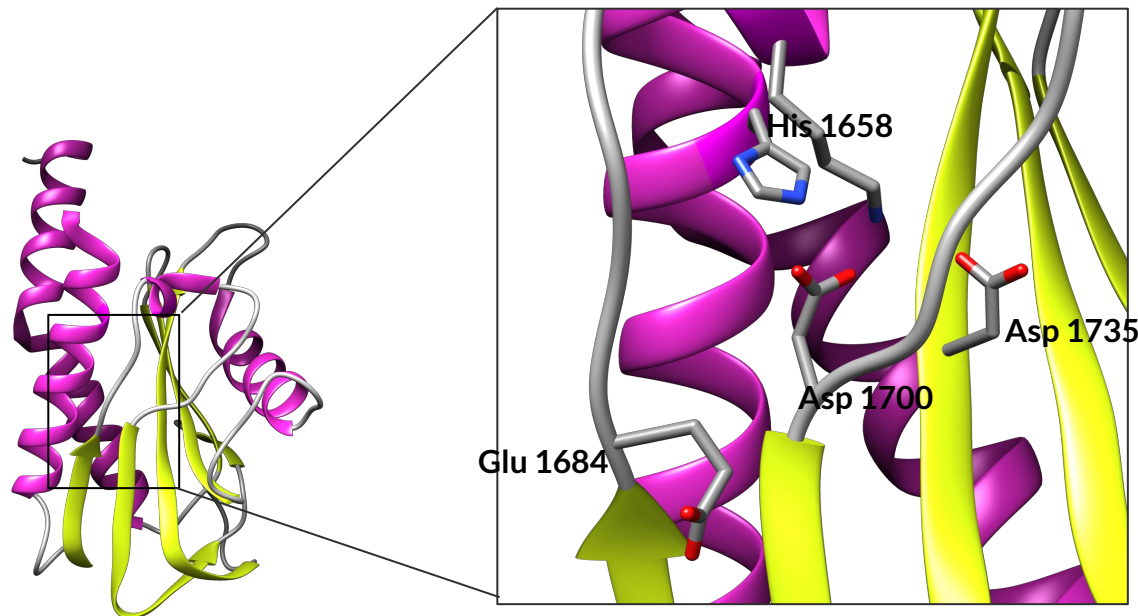
Linker

Endonuclease

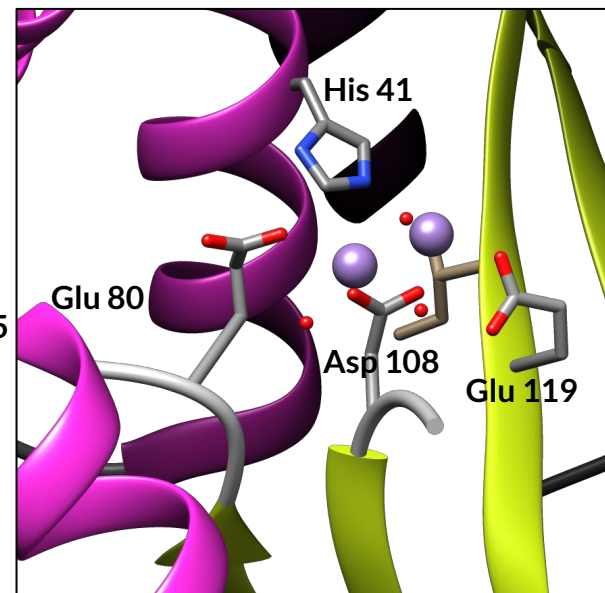
RNase H-like

Jab1/MPN

Endonuclease



Prp8
PDB code: 4I43



Influenza Virus
PDB code: 2W69

N-domain

RT fingers/palm

Thumb/X

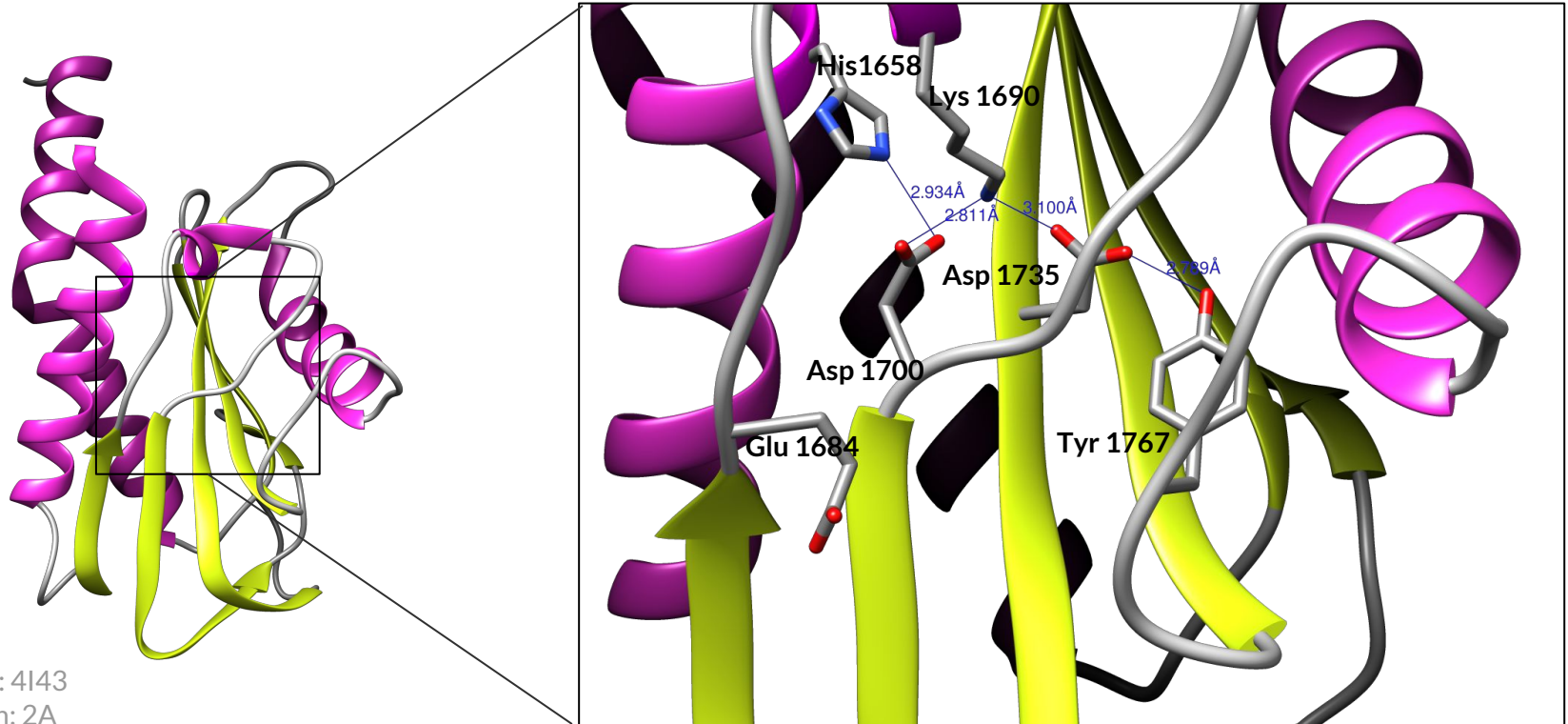
Linker

Endonuclease

RNase H-like

Jab1/MPN

Endonuclease



PDB code: 4I43
Resolution: 2Å

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Endonuclease

His 1658

1621

1680

H.sapiens	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKI	HES	IVMDLCQVFD	QELdaleiet
M.mulatta	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKI	HES	IVMDLCQVFD	QELdaleiet
C.lupus	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKI	HES	IVMDLCQVFD	QELdaleiet
M.musculus	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKI	HES	IVMDLCQVFD	QELdaleiet
G.gallus	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKI	HES	IVMDLCQVFD	QELdaleiet
D.rerio	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKI	HES	IVMDLCQVFD	QELdaleiet
D.melanogaster	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKI	HES	IVMDLCQVFD	QELdaleiet
C.elegans	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKI	HES	VVMDLCQVFD	QELdaleiqt
S.cerevisiae	VGFLVQLDLT	GIFLHGKIPT	LKISLIQIFR	AHLWQKI	HES	IVFDICQILD	GELdvlqies
S.pombe	VGFQVQLDLT	GIMMHGKIPT	LKISLIQIFR	SHLWQKI	HES	VVWDLQVLD	QELeslqiet
N.crassa	VGFQVQLDLT	GIFLHGKIPT	LKISLIQIFR	AHLWQKI	HES	VVMDLCQVFD	QELealsies
A.thaliana	VGFQVQLDLT	GIYMHGKIPT	LKISLIQIFR	AHLWQKI	HES	VVMDLCQVLD	QELepleiet
X.tropicalis	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKI	HES	IVMDLCQVFD	QELdaleiet

Negatively charged

Non-polar

Positively charged

Polar

Sequence alignment based on PFAM domains

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Endonuclease

Glu 1684

Lys 1690

Asp 1700

	1681					1740
H.sapiens	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
C.lupus	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
M.musculus	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
M.mulatta	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
G.gallus	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
X.tropicalis	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
D.rerio	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
D.melanogaster	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FPAYKWNVSR
C.elegans	WQKIHESVVM	DLCQVFDQEL	DALEIQT VQK	ETIHPRKSYK	MNSSCADVLL	FAQYKWNVSR
A.thaliana	WQKIHESVVM	DLCQVLDQEL	EPLIETVQK	ETIHPRKSYK	MNSSCADVLL	FAAHKWPM SK
S.pombe	WQKIHESVVM	DLCQVLDQEL	ESLQIETVQK	ETIHPRKSYK	MNSSCADILL	LAAYKWNVSR
N.crassa	WQKIHESVVM	DLCQVFDQEL	EALSIETVQK	ETIHPRKSYK	MNSSCADIQL	FASHKWNVTR
S.cerevisiae	WQKIHESIVF	DICQILDGEL	DVLQIESVTK	ETVHPRKSYK	MNSSAADITM	ESVHEWEVSK

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Endonuclease

Asp 1735

Tyr 1767

	1741					1800
H.sapiens	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
C.lupus	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
M.musculus	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
M.mulatta	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
G.gallus	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
X.tropicalis	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
D.rerio	PSLLADSKDV	MDSTTTQKFW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
D.melanogaster	PSLLADTKDT	MDNTTTQKYW	LDIQLRWGDY	DSHDVERYAR	AKFLDYTTDN	MSIYPSPTGV
C.elegans	PSLMADSKDV	MDNTTTQKYW	LDVQLRWGDY	DSHDVERYAR	AKFLDYTTDN	MSIYPSPTGV
A.thaliana	PSLIAESKDV	FDQKASNKYW	IDVQLRWGDY	DSHDIERYTK	AKFMDYTTDN	MSIYPSPTGV
S.pombe	PSLLNDNRDV	LDNTTTNKYW	IDVQLRFGDY	DSHDIERYTR	AKFLDYSTDA	QSMYPSPTGV
N.crassa	PSLLFDTKDV	IESTTTNKFW	IDVQLRYGDY	DSHDIERYVR	AKYLDYTTDS	MSLYPSPTGL
S.cerevisiae	PSLLHETNDS	FKGLITNKMW	FDVQLRYGDY	DSHDISRYVR	AKFLDYTTDN	VSMYPSPTGV

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

Endonuclease

	1681					1740
H.sapiens	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
C.lupus	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
M.musculus	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
M.mulatta	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
G.gallus	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
X.tropicalis	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
D.rerio	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FASYKWNVSR
D.melanogaster	WQKIHESIVM	DLCQVFDQEL	DALEIETVQK	ETIHPRKSYK	MNSSCADILL	FPAYKWNVSR
C.elegans	WQKIHESVVM	DLCQVFDQEL	DALEIQTVMQ	ETIHPRKSYK	MNSSCADVLL	FAQYKWNVSR
A.thaliana	WQKIHESVVM	DLCQVLDQEL	EPLIETVQK	ETIHPRKSYK	MNSSCADVLL	FAAHKWPMSK
S.pombe	WQKIHESVVM	DLCQVLDQEL	ESLQIETVQK	ETIHPRKSYK	MNSSCADILL	LAAYKWNVSR
N.crassa	WQKIHESVVM	DLCQVFDQEL	EALSIETVQK	ETIHPRKSYK	MNSSCADIDL	FASHKWNVTR
S.cerevisiae	WQKIHESIVF	DICQILDGEL	DVLQIESVTK	ETVHPRKSYK	MNSSAADITM	ESVHEWEVSK
	1741					1800
H.sapiens	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
C.lupus	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
M.musculus	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
M.mulatta	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
G.gallus	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
X.tropicalis	PSLLADSKDV	MDSTTTQKYW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
D.rerio	PSLLADSKDV	MDSTTTQKFW	IDIQLRWGDY	DSHDIERYAR	AKFLDYTTDN	MSIYPSPTGV
D.melanogaster	PSLLADTKDT	MDNTTTQKYW	LDIQLRWGDY	DSHDVERYAR	AKFLDYTTDN	MSIYPSPTGV
C.elegans	PSLMADSKDV	MDNTTTQKYW	LDVQLRWGDY	DSHDVERYAR	AKFLDYTTDN	MSIYPSPTGV
A.thaliana	PSLIAESKDV	FDQKASNKYW	IDVQLRWGDY	DSHDIERYTK	AKFMDYTTDN	MSIYPSPTGV
S.pombe	PSLLNDNRDV	LDNTTTNKYW	IDVQLRFGDY	DSHDIERYTR	AKFLDYSTD	QSMYPSPTGV
N.crassa	PSLLFDTKDV	IESTTTNKFV	IDVQLRYGDY	DSHDIERYVR	AKYLDYTTDS	MSLYPSPTGL
S.cerevisiae	PSLLHETNDS	FKGLITNKMW	FDVQLRYGDY	DSHDISRYVR	AKFLDYTTDN	VSMYPSPTGV

Loops sequence highly conserved:

- Residues 1685-1699
- Residues 1762-1771

Clustal Sequence alignment

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

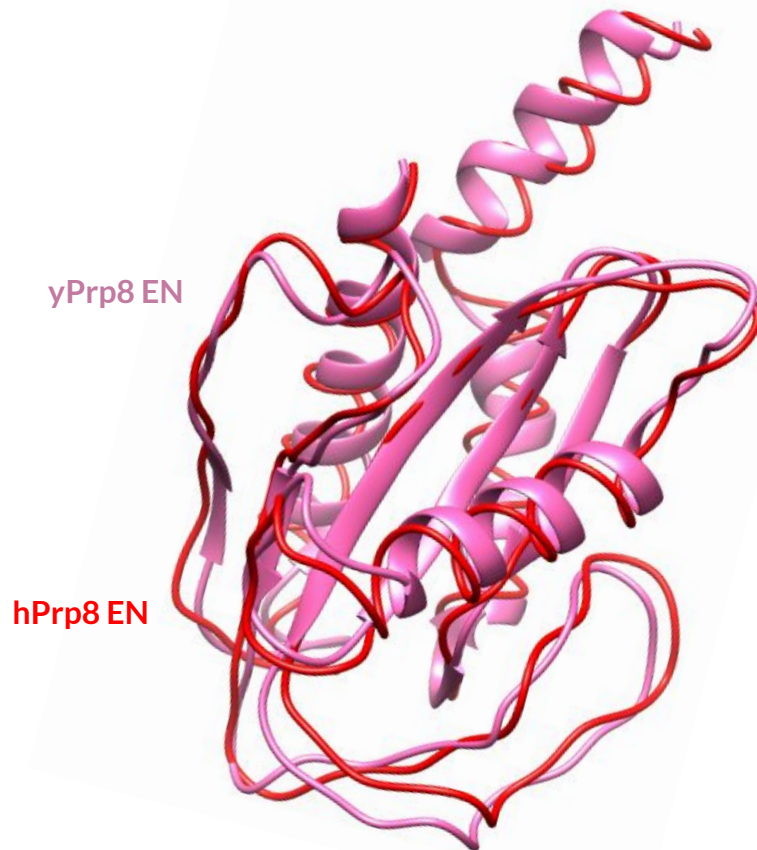
Endonuclease

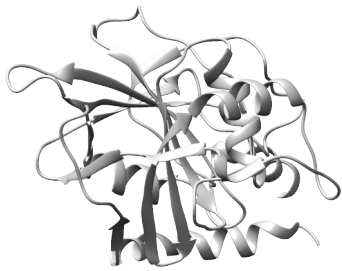
STAMP VALUES

- Sc 9.12
- RMS 1.19

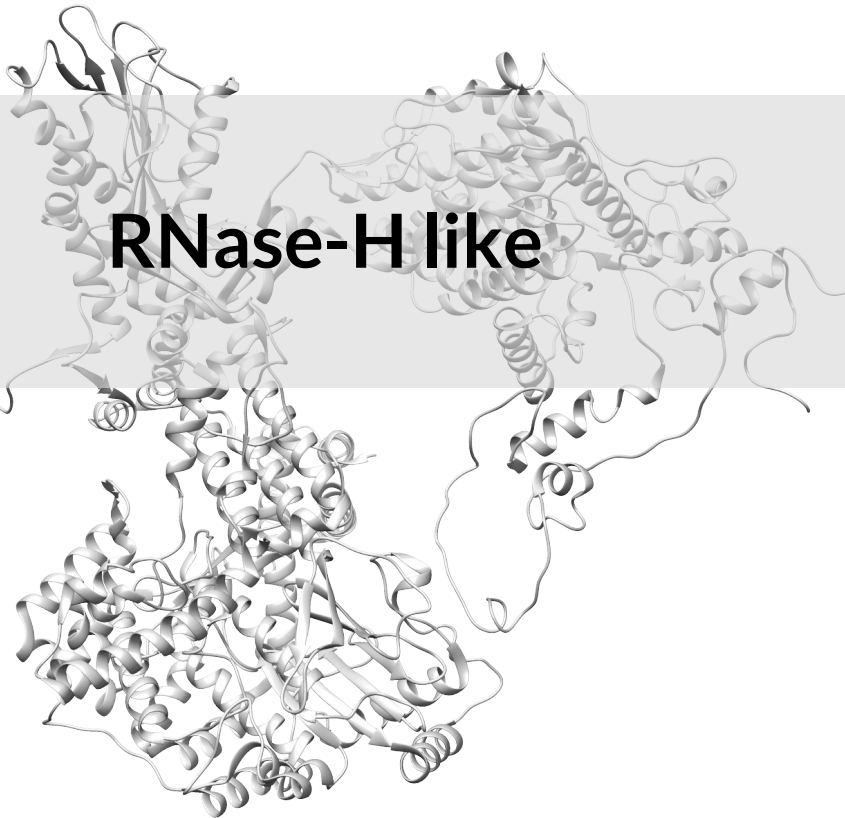
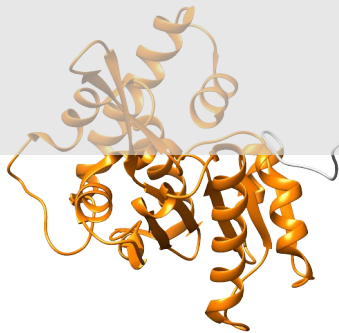
PDB code: 3JCM
Resolution: 3.8Å

PDB code: 3JCR
Resolution: 7Å





RNase-H like



N-domain

RT fingers/palm

Thumb/*X*

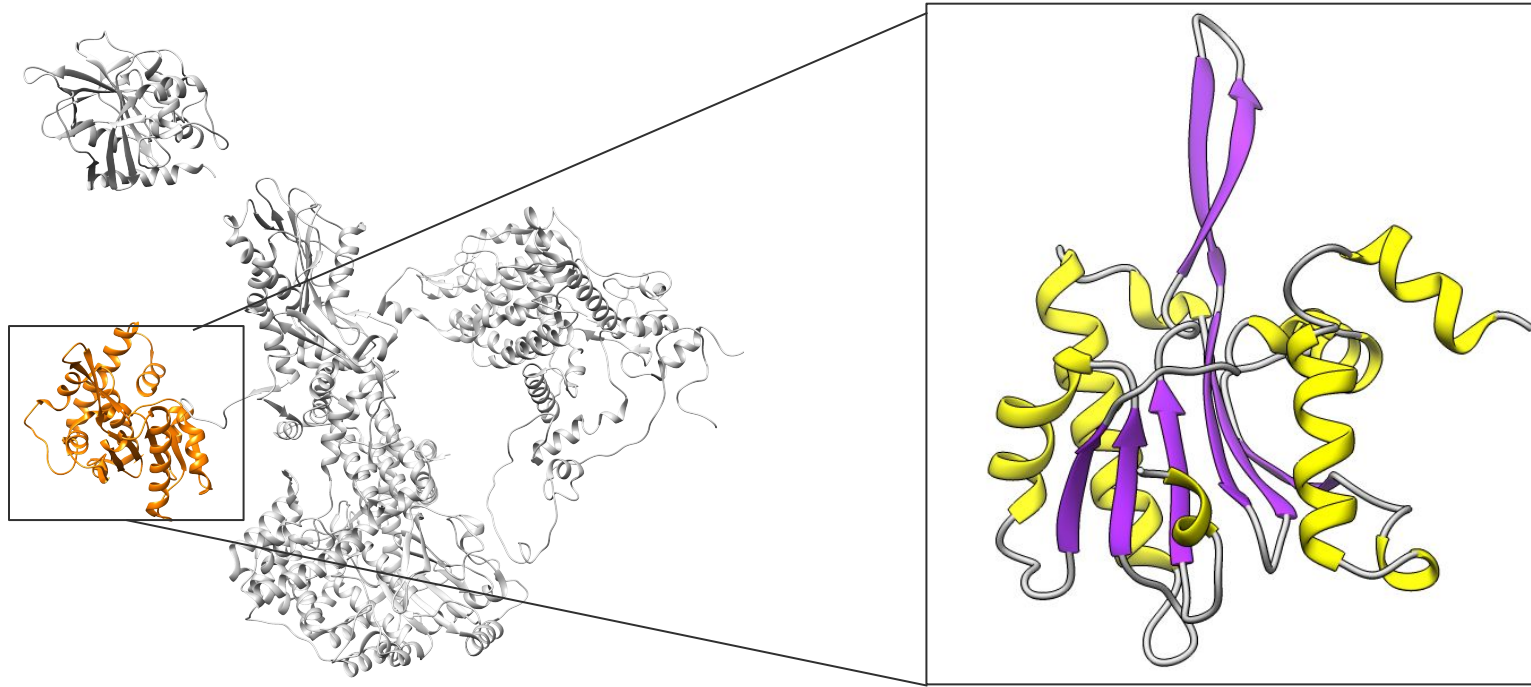
Linker

Endonuclease

***RNase H*-like**

Jab1/MPN

RNase H



PDB code: 4I43

Resolution: 2Å

N-domain

RT fingers/palm

Thumb/X

Linker

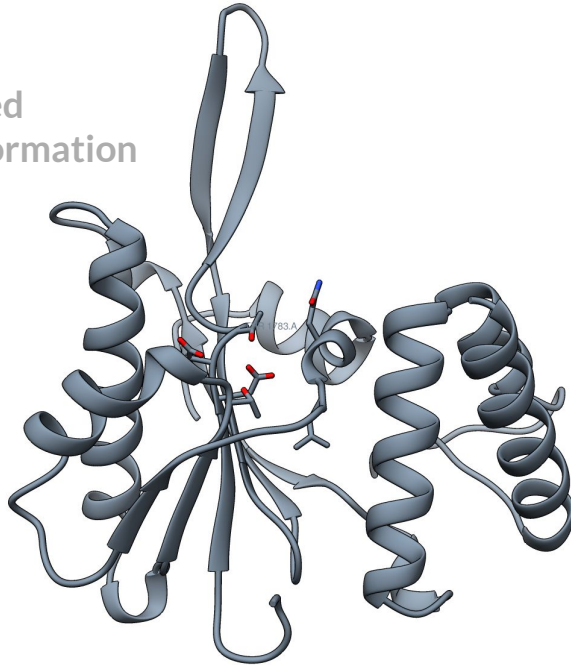
Endonuclease

RNase H-like

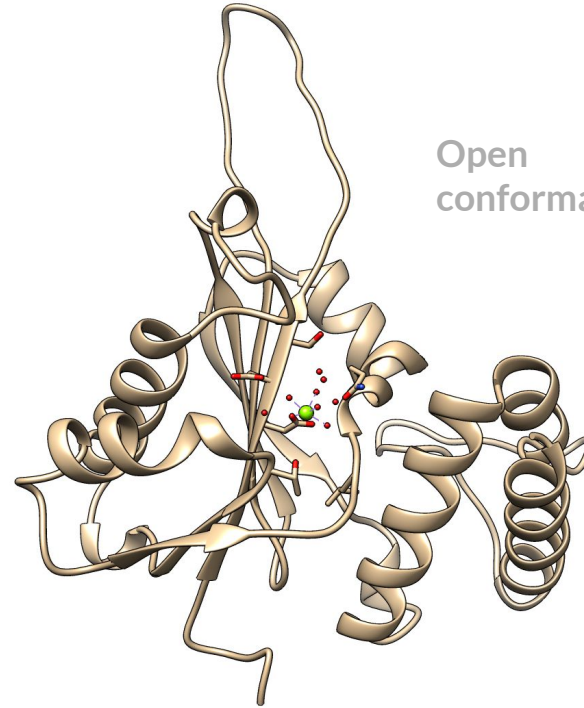
Jab1/MPN

RNase-H

Closed
conformation



Open
conformation



PDB code: 4JK7
Resolution: 1,4Å

N-domain

RT fingers/palm

Thumb/X

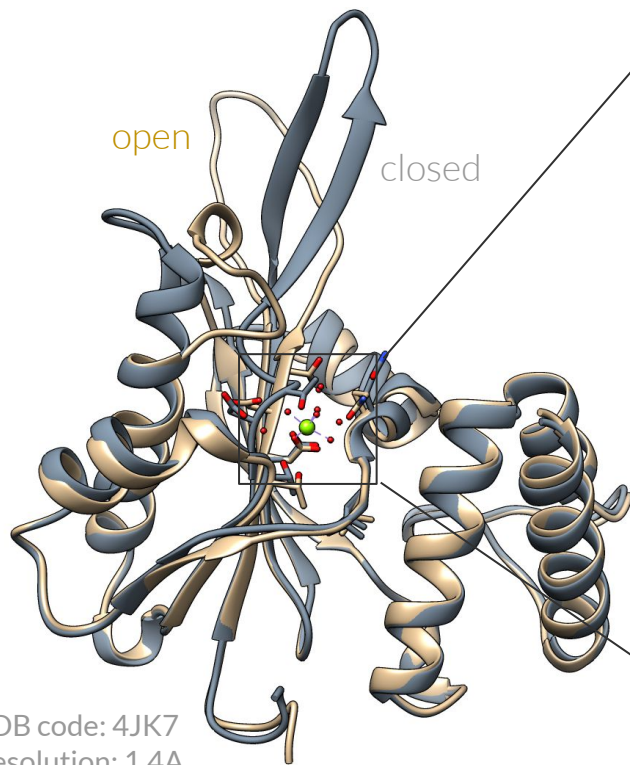
Linker

Endonuclease

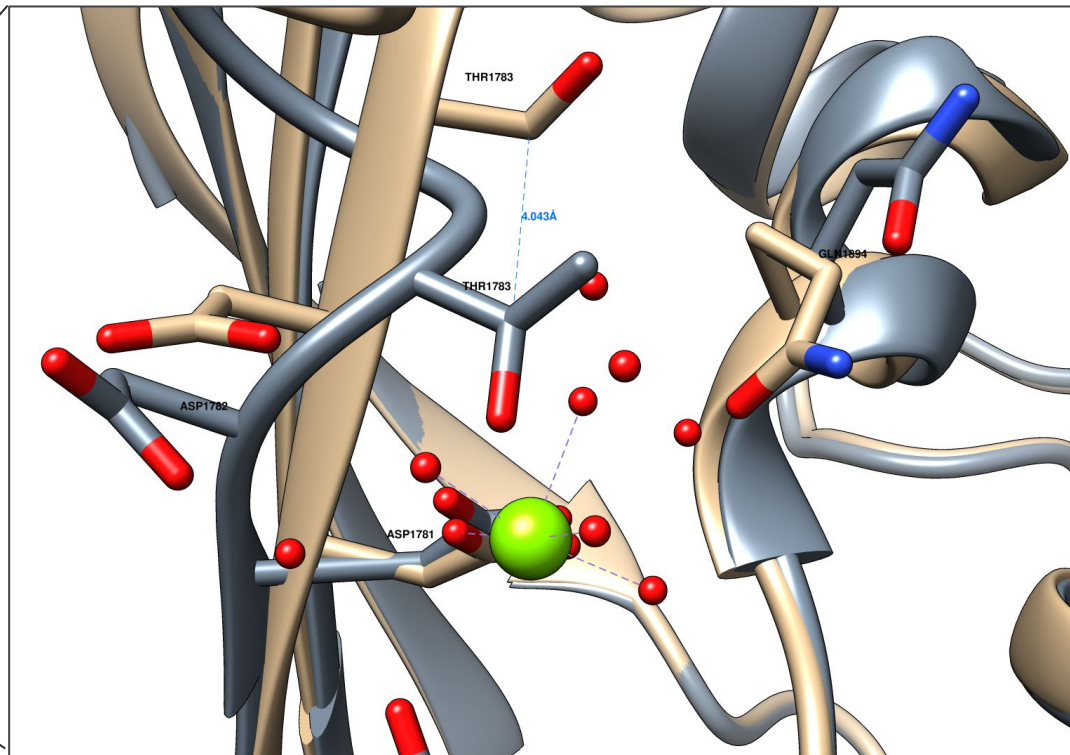
RNase H-like

Jab1/MPN

RNase-H



PDB code: 4JK7
Resolution: 1,4Å



STAMP VALUES Sc 7.40 RMS 0.93

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

RNase-H

		Asp 1781 Asp 1782	Tyr 1783			
	1861					1920
H.sapiens	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
C.lupus	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
M.musculus	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
M.mulatta	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
G.gallus	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
X.tropicalis	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
D.rerio	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
D.melanogaster	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
C.elegans	YLTSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
A.thaliana	YLSSQNYGEI	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGVIFIFN	PRTGQLFLKI
S.pombe	YLSSSNYAEL	FSNQIQLFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKV
N.crassa	FLNSQNYSEL	FSNQTQLFID	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
S.cerevisiae	FLNSSNYAEL	FNNDIKLFVD	DTNVYRVTVH	KTFEGNVATK	AINGCIFTLN	PKTGHLFLKI

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

RNase-H

yPrp8 RNase

hPrp8 RNase



STAMP VALUES

Sc 7.11

RMS 1.24

PDB code: 3JCM
Resolution: 3.8Å

PDB code: 3JCR
Resolution: 7Å

N-domain

RT fingers/palm

Thumb/X

Linker

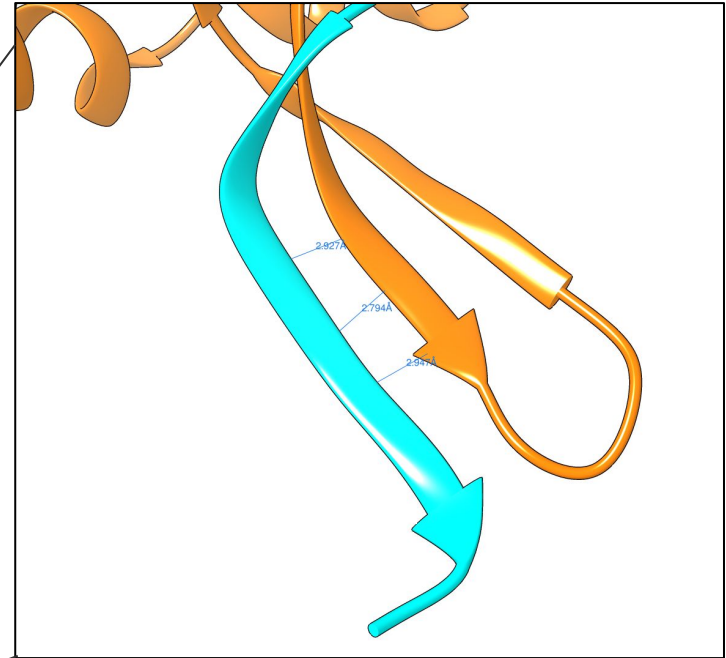
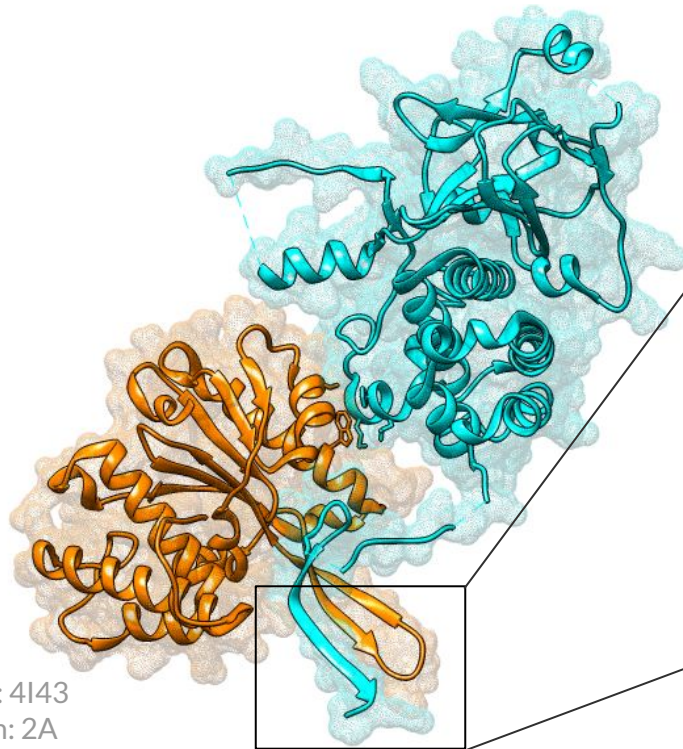
Endonuclease

RNase H-like

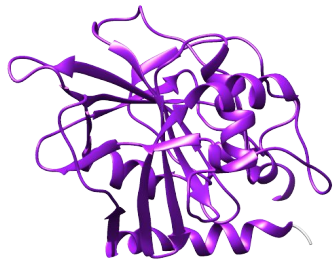
Jab1/MPN

RNase-H

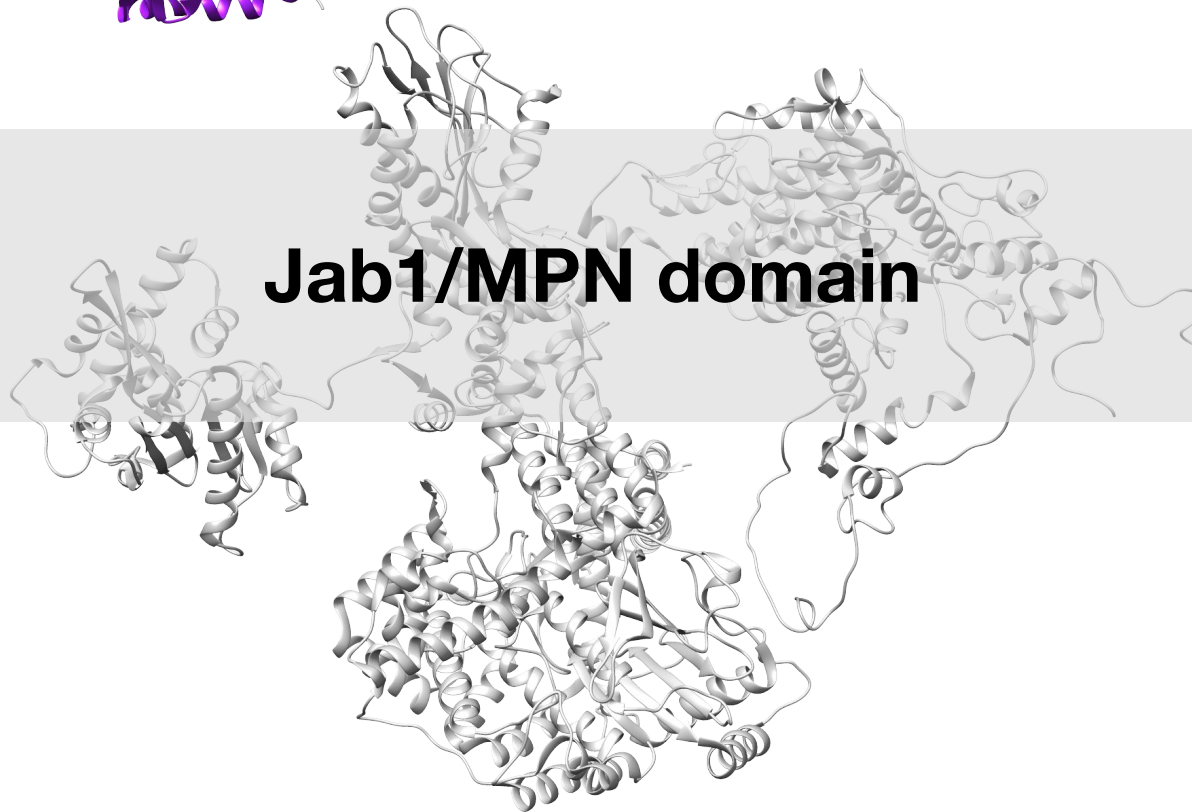
Aar2 stabilizes the β -hairpin...



...in order to make it stay in the
pre-catalytic conformation
(closed)



Jab1/MPN domain



N-domain

RT fingers/palm

Thumb/X

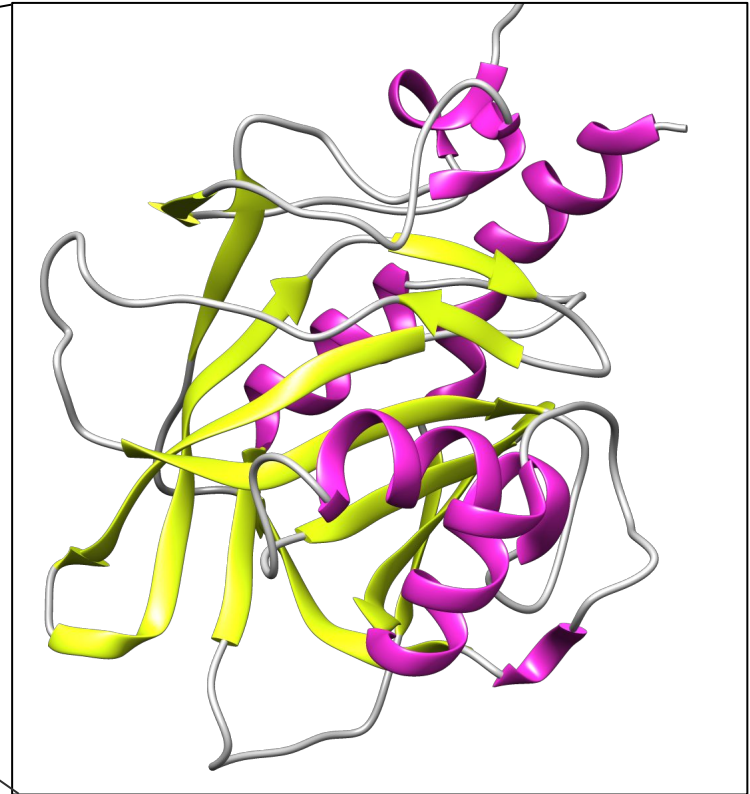
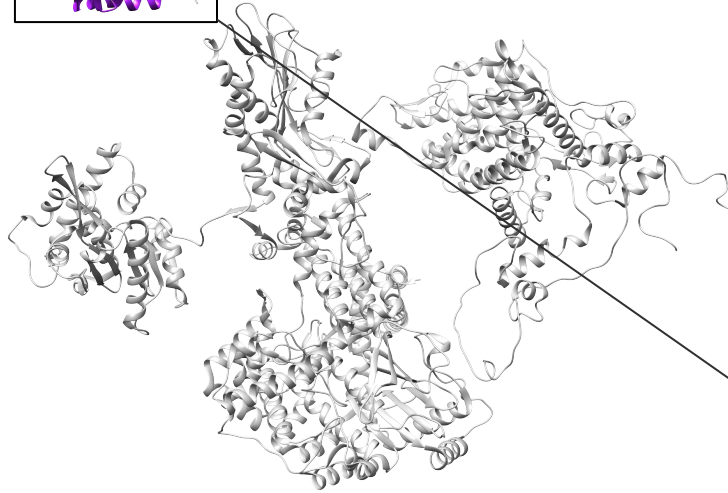
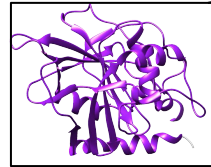
Linker

Endonuclease

RNase H-like

Jab1/MPN

Jab1/MPN



PDB code: 4I43
Resolution: 2Å

N-domain

RT fingers/palm

Thumb/X

Linker

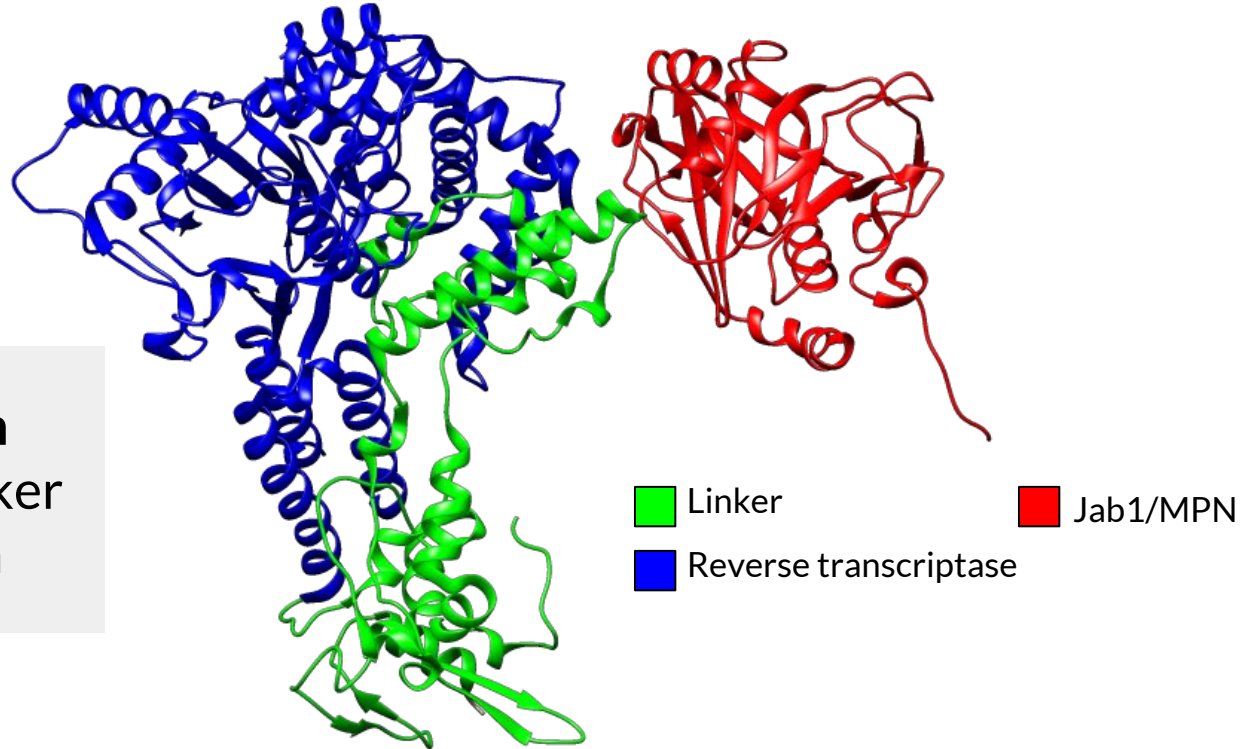
Endonuclease

RNase H-like

Jab1/MPN

Jab1/MPN

Jab1/MPN domain
interacts with the linker
and the RT domain



PDB code: 4I43

Resolution: 2Å

N-domain

RT fingers/palm

Thumb/X

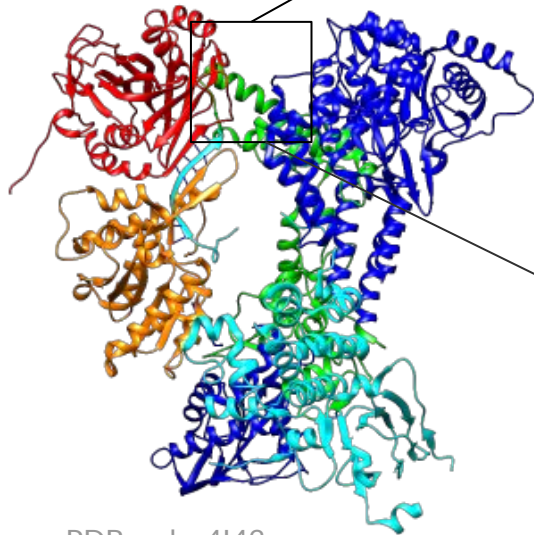
Linker

Endonuclease

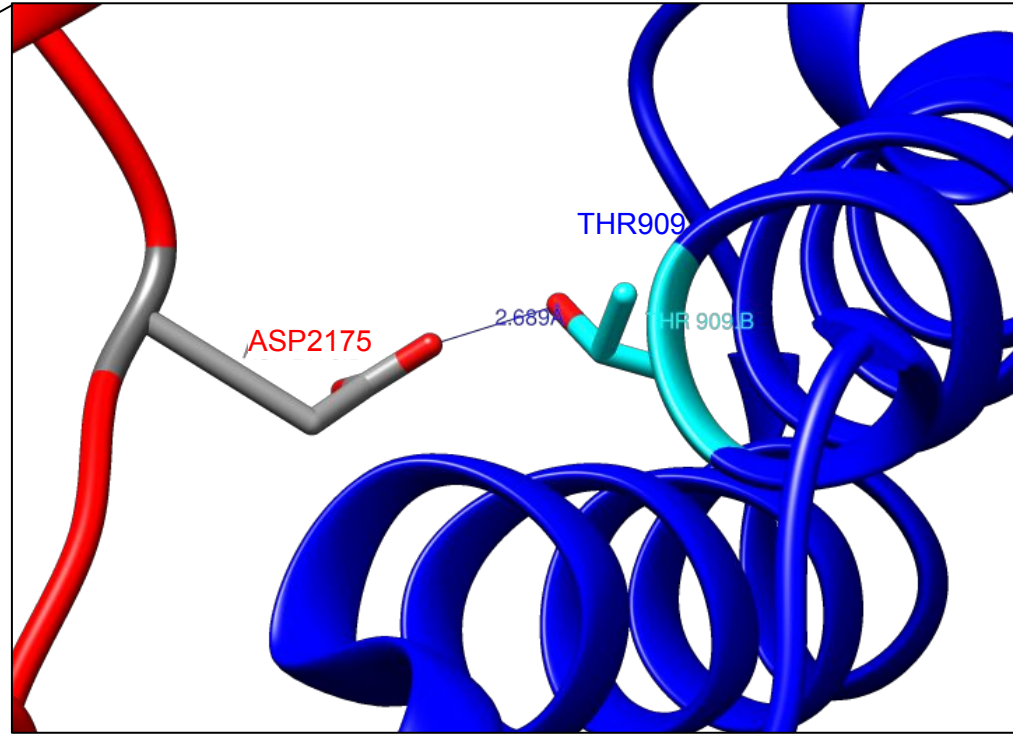
RNase H-like

Jab1/MPN

Jab1/MPN



PDB code: 4I43
Resolution: 2Å



■ Jab1/MPN

■ RT

N-domain

RT fingers/palm

Thumb/X

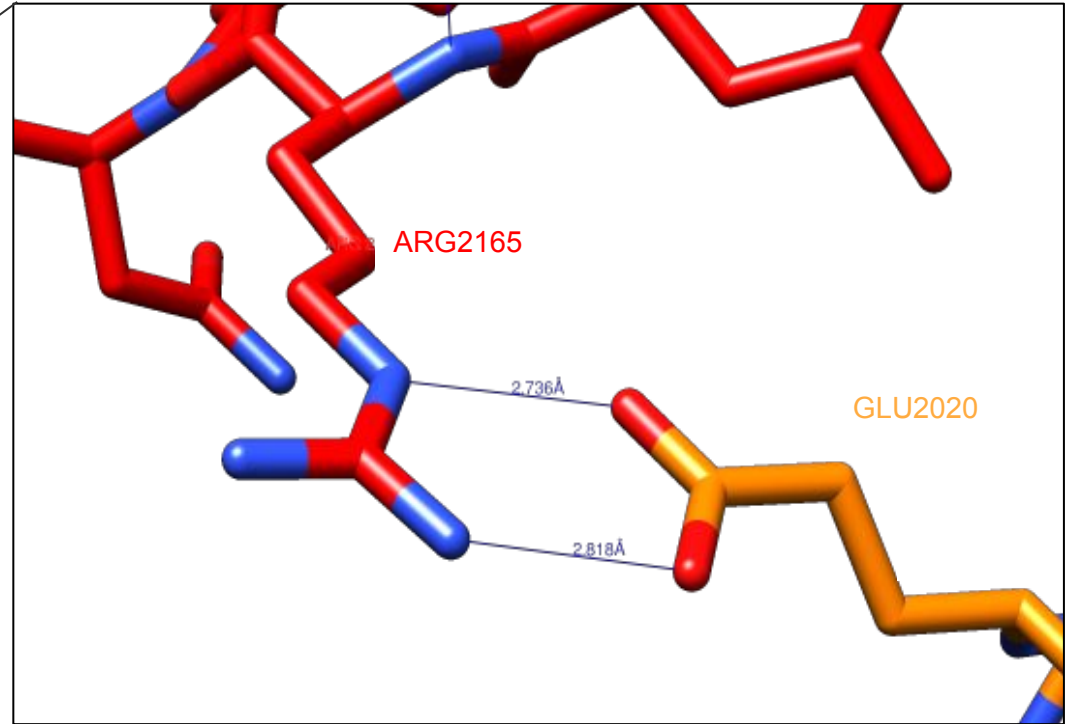
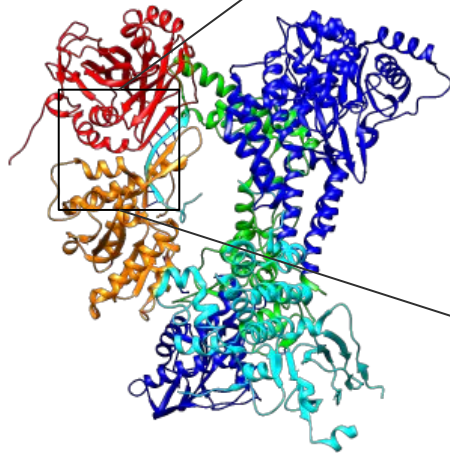
Linker


Endonuclease


RNase H-like

Jab1/MPN

Jab1/MPN



 Jab1/MPN

 RnaseH-like

PDB code: 4I43
Resolution: 2Å

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Jab1/MPN

RNaseH-like region

Glu 2020

1981

2040

H.sapiens	ATEPQMVLFN	LYDDWLKTIS	SYTAFSRLIL	ILRALHVNN	D	RAKVILKPKD	TTITEPHHIW
M.mulatta	ATEPQMVLFN	LYDDWLKTIS	SYTAFSRLIL	ILRALHVNN	D	RAKVILKPKD	TTITEPHHIW
C.lupus	ATEPQMVLFN	LYDDWLKTIS	SYTAFSRLIL	ILRALHVNN	D	RAKVILKPKD	TTITEPHHIW
M.musculus	ATEPQMVLFN	LYDDWLKTIS	SYTAFSRLIL	ILRALHVNN	D	RAKVILKPKD	TTVTEPHHIW
G.gallus	ATEPQMVLFN	LYDDWLKTIS	SYTAFSRLIL	ILRALHVNN	D	RAKVILKPKD	TTITEPHHIW
D.rerio	ATEPQMVLFN	LYDDWLKTIS	SYTAFSRLIL	ILRALHVNN	D	RAKVILKPKD	TTITEPHHIW
D.melanogaster	ATEPQMVLFN	LYDDWLKTIS	SYTAFSRLIL	ILRALHVNT	E	RTKIILKPKD	TTITEAHHIW
C.elegans	ATEPQMVLFN	LYDDWLKTIS	SYTAFSRVL	IMRGMHIN	P	KTKVILKPKD	TTITEPHHIW
S.cerevisiae	ATEPQMVLFN	IYDDWLDRIS	SYTAFSRLTL	LLRALKTNE	E	SAKMILLSDP	TITIKSYHLW
S.pombe	ATEPQMVLFN	LYDDWLQSVS	SYTAFSRLIL	ILRALNVNT	E	KTKLILRPDK	SIITKENHVV
N.crassa	ATEPQMVLFN	LYDEWLKSIS	SYTAFSRLIL	ILRALHVNQ	D	KTKLILRPDK	TVITQDHHIW
A.thaliana	ATEPQMALFN	IYDDWLMTVS	SYTAFQRLIL	ILRALHVNNE		KAKMLLKPD	SVVTEPNHIW
X.tropicalis	ATEPQMVLFN	LYDDWLKTIS	SYTAFSRLIL	ILRALHVNN	D	RAKVILKPKD	TTVTEPHHIW

Negatively charged

Non-polar

Positively charged

Polar

Sequence alignment based on PFAM domains

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Jab1/MPN

RT region

Thr 909

	901					960
H.sapiens	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
C.lupus	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
M.musculus	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
M.mulatta	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
G.gallus	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
X.tropicalis	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
D.rerio	AVAIYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
D.melanogaster	AVAIYTTTVH	WLESRRFAPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
C.elegans	AVAIYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKESYSVKNR	LNQSQREELA
A.thaliana	GIAIYSTTVN	WLESRKFSAI	PFPPLSYKHD	TKLLILALER	LKESYSAVK	LNQQQREELG
S.pombe	AVAIYTTTFVH	WLESRRFQPI	PFPPLSYKHD	TKLLVLALER	LKEAYSVKGR	LNQSQREELA
N.crassa	AVAIYTTTVH	WLESRKFSPI	PFPVSYSKHD	TKILILALER	LREAYSTKGR	LNQSQREELA
S.cerevisiae	ATTIFSVMVE	WLESRSFSPI	PFPPLTYKND	TKILVLALED	LKDVIASKVR	LNASEREELA

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

RNase H-like

Jab1/MPN

Jab1/MPN

Arg 2165

Asp 2175

Jab1/MPN region

	2161					2220
H.sapiens	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
C.lupus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
M.musculus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
M.mulatta	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
G.gallus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
X.tropicalis	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
D.rerio	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
D.melanogaster	ITSTTSNYET	QTFSSKTEWR	VRAISATNLH	LRTNHIYVSS	DDIKETG.YT	YILPKNILKK
C.elegans	ITATTSNYET	ASFASRTEWR	VRAISSTNLH	LRTQHIYVNS	DDVKDTG.YT	YILPKNILKK
A.thaliana	ISTTISPYEQ	SAFGSKTDWR	VRAISATNLY	LRVNHIYVNS	DDIKETG.YT	YIMPKNILKK
S.pombe	VVTTTSAYEN	EKFSSKTEWR	NRAISSISLP	LRTKNIYVNS	DNISETFPHYT	YILPQNLLRK
N.crassa	IVTTTSQFEQ	QTFASKTEWR	TRAIATSNLR	TRANMYVSP	VDSLDD.VT	YVMPKNILKR
S.cerevisiae	VVASADYES	QTFSSKNEW	KSAIANTLLY	LRLKNIYVSA	DDFVEEQ.NV	YVLPKNLLKK

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

N-domain

RT fingers/palm

Thumb/X

Linker

Endonuclease

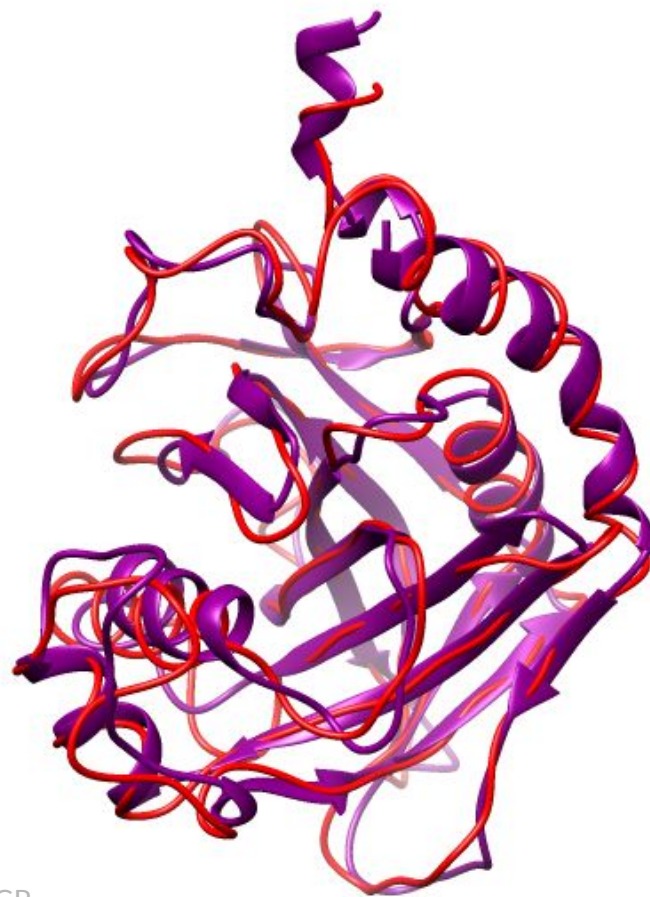
RNase H-like

Jab1/MPN

Jab1/MPN

yPrp8 Jab1

hPrp8 Jab1



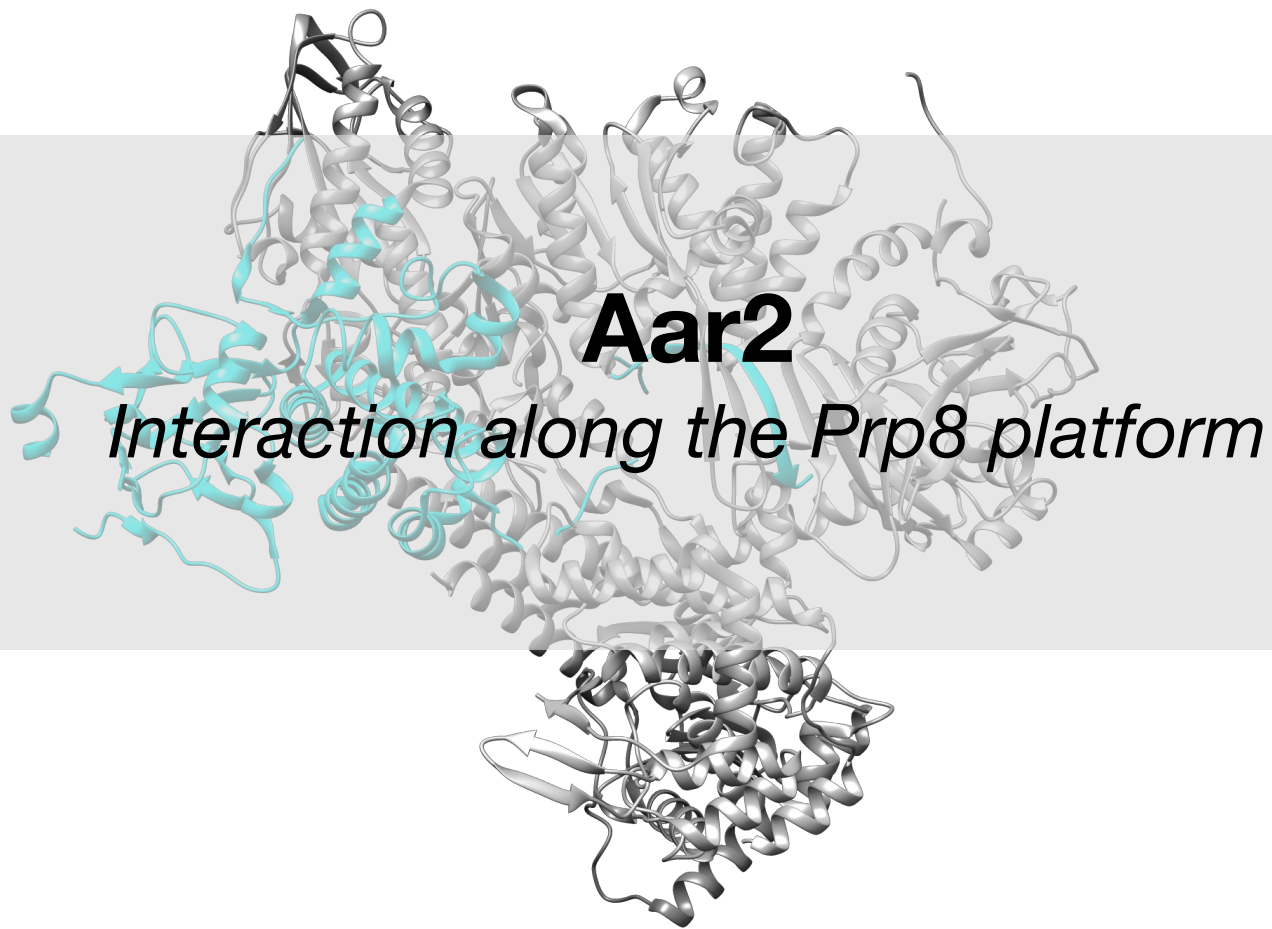
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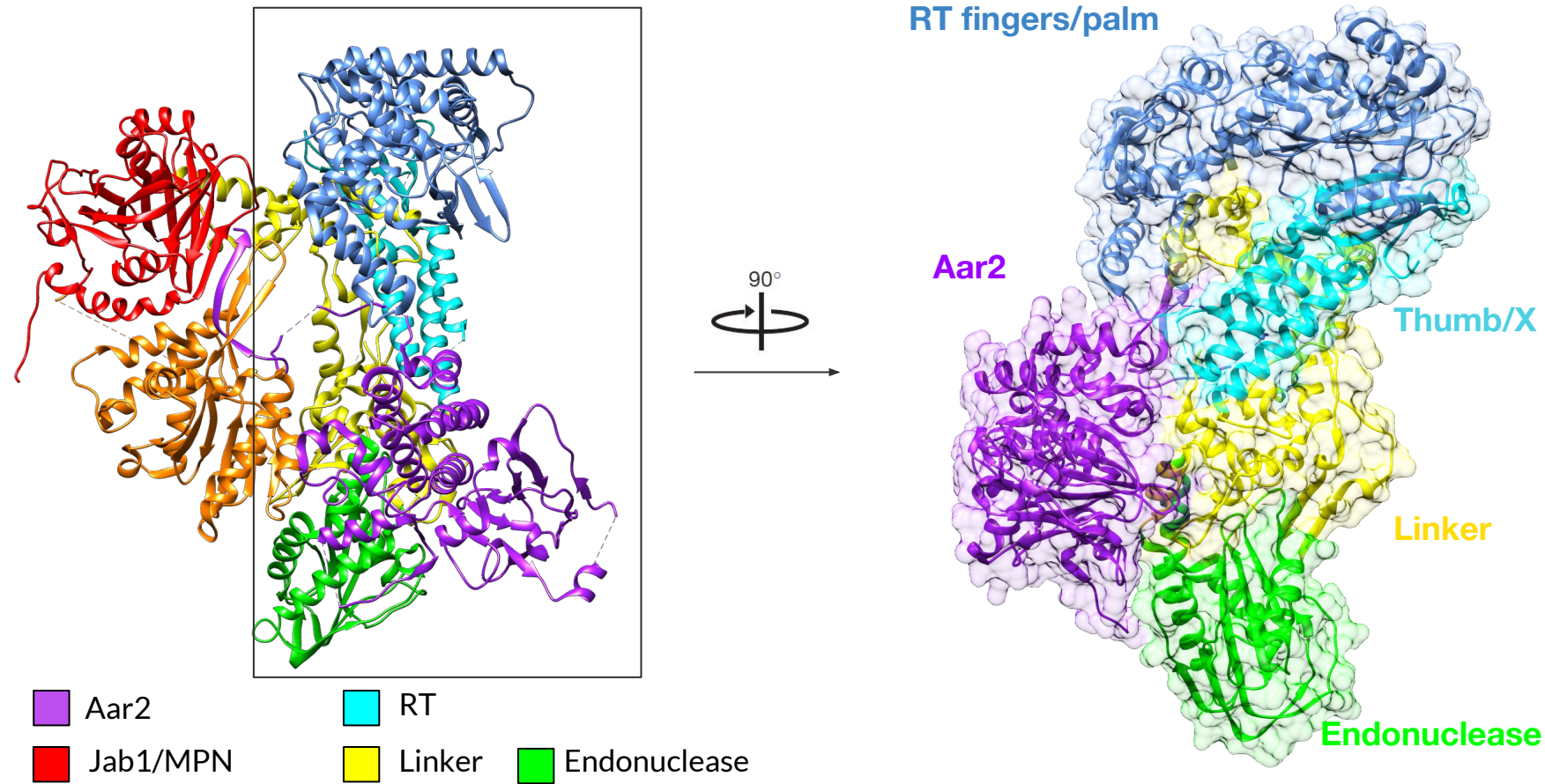
RMS 1.29

PDB code: 3JCM
Resolution: 3.8Å

PDB code: 3JCR
Resolution: 7Å

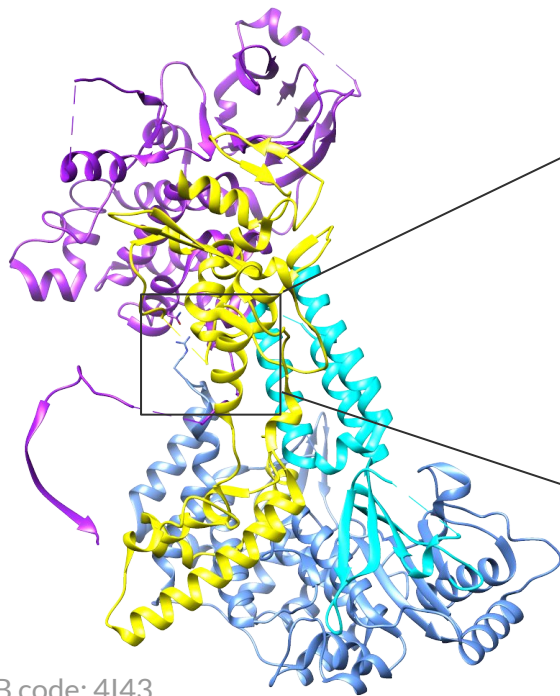


Aar2

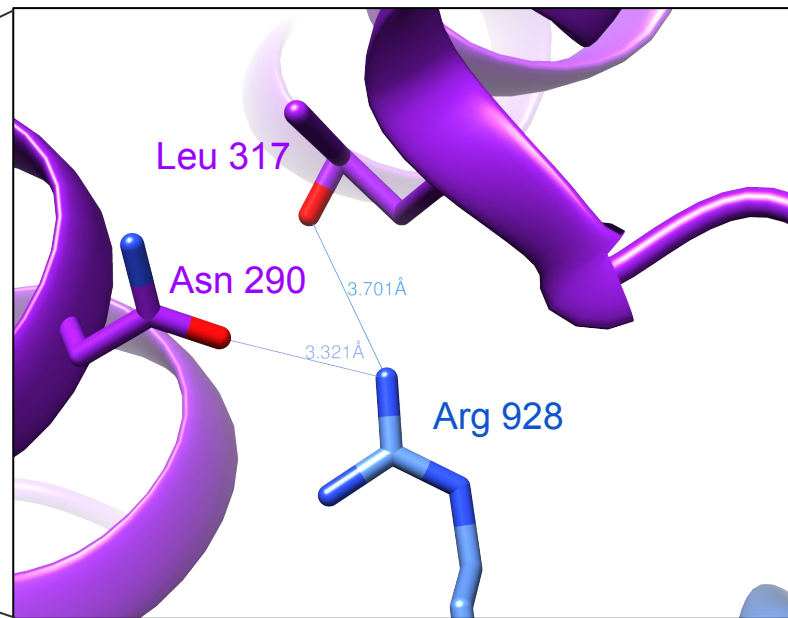


Aar2

Aar2 - RT



PDB code: 4I43
Resolution: 2Å



RT fingers/palm

Aar2

Aar2

Aar2 - RT

RT region

Arg 928

901

960

H.sapiens	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
C.lupus	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
M.musculus	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
M.mulatta	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
G.gallus	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
X.tropicalis	AVAVYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
D.rerio	AVAIYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
D.melanogaster	AVAIYTTTVH	WLESRRFAP	PFPPLSYKHD	TKLLILALER	LKEAYSVKSR	LNQSQREELG
C.elegans	AVAIYTTTVH	WLESRRFSPI	PFPPLSYKHD	TKLLILALER	LKESYSVKNR	LNQSQREELA
A.thaliana	GIAIYSTTVN	WLESRKFSAI	PFPPLSYKHD	TKLLILALER	LKESYSAVK	LNQQQREELG
S.pombe	AVAIYTTTFVH	WLESRRFQPI	PFPPLSYKHD	TKLLVLALER	LKEAYSVKGR	LNQSQREELA
N.crassa	AVAIYTTTVH	WLESRKFSPI	PFPVSVYKHD	TKILILALER	LREAYSTKGR	LNQSQREELA
S.cerevisiae	ATTIFSVMVE	WLESRSFSPI	PFPPLTYKND	TKILVLALED	LKDVYASKVR	LNASEREELA

Negatively charged

Non-polar

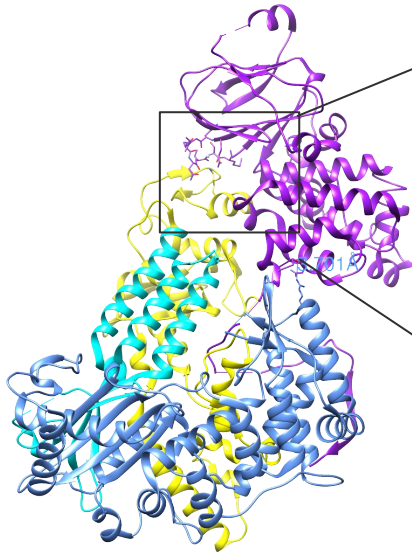
Positively charged

Polar

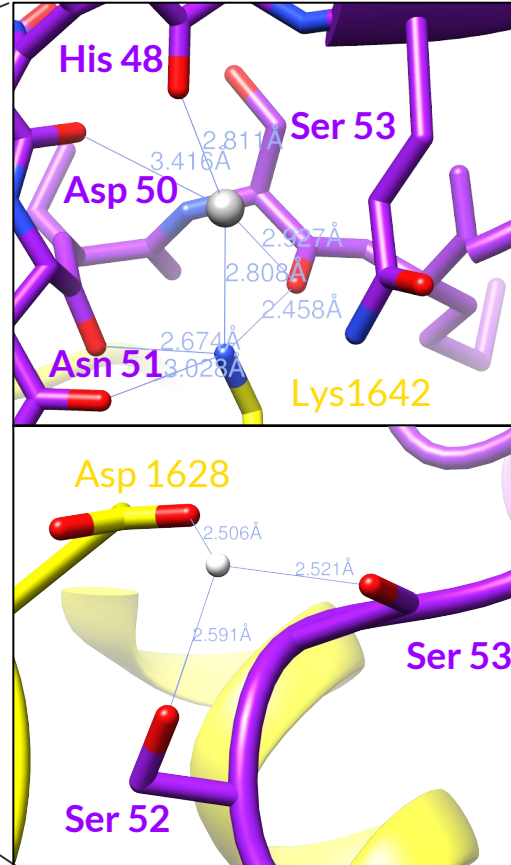
Clustal Sequence alignment



Aar2

Aar2 - Linker



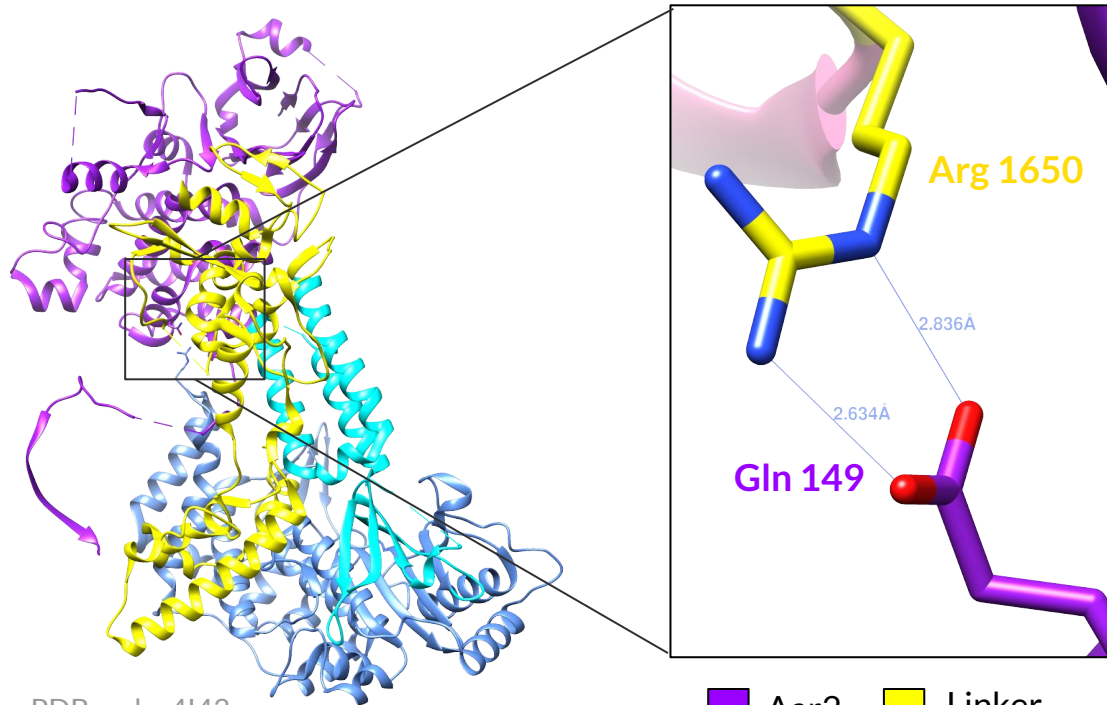
PDB code: 4I43
Resolution: 2Å



 Aar2
 Linker

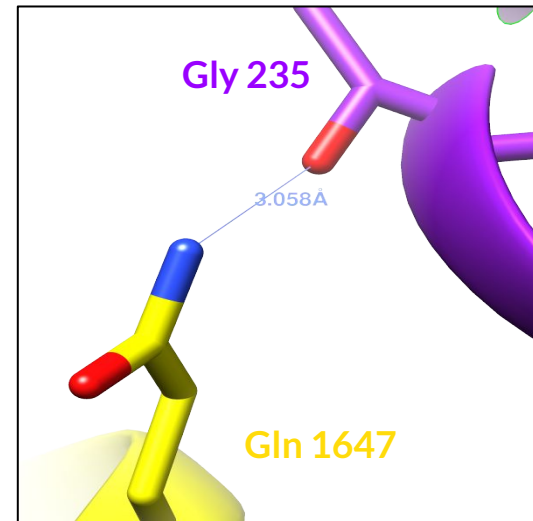
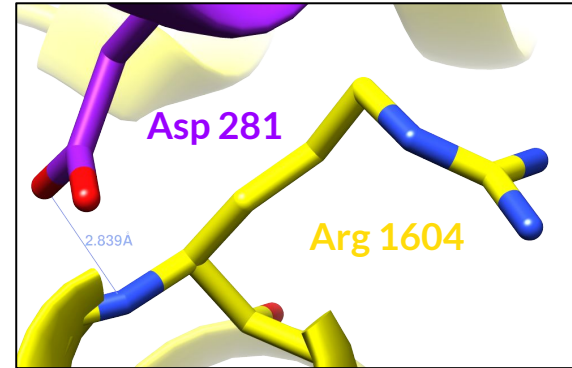
Aar2

Aar2 - Linker



PDB code: 4I43
Resolution: 2 Å

■ Aar2 ■ Linker



Aar2

Aar2 - Linker





Linker region

Arg 1604

1561

1620

H.sapiens	LFKGTYFPTW	EGLFWEKASG	FEESMKWKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
M.mulatta	LFKGTYFPTW	EGLFWEKASG	FEESMKWKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
C.lupus	LFKGTYFPTW	EGLFWEKASG	FEESMKWKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
M.musculus	LFKGTYFPTW	EGLFWEKASG	FEESMKWKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
G.gallus	LFKGTYFPTW	EGLFWEKASG	FEESMKWKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
D.rerio	LFKGTYFPTW	EGLFWEKASG	FEESMKWKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
D.melanogaster	LFKGTYFPTW	EGLFWEKASG	FEESMKYKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
C.elegans	LFRGTYFPTW	EGLFWERASG	FEESMKFKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
S.cerevisiae	LFKGTGFNSW	EGLFWEKASG	FEDSMQFKKL	THAQRSGLSQ	IPNRRFTLWW	SPTINRANVY
S.pombe	MFKATGFPSW	EGLFWEKASG	FEESMKFKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
N.crassa	LFKATGFPSW	EGLFWEKASG	FEESMKFKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
A.thaliana	LFKGTYFPTW	EGLFWEKASG	FEESMKYKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY
X.tropicalis	LFKGTYFPTW	EGLFWEKASG	FEESMKWKKL	TNAQRSGLNQ	IPNRRFTLWW	SPTINRANVY

 Negatively charged
  Non-polar
 Positively charged
  Polar

Sequence alignment based on PFAM domains

Aar2

Aar2 - Linker

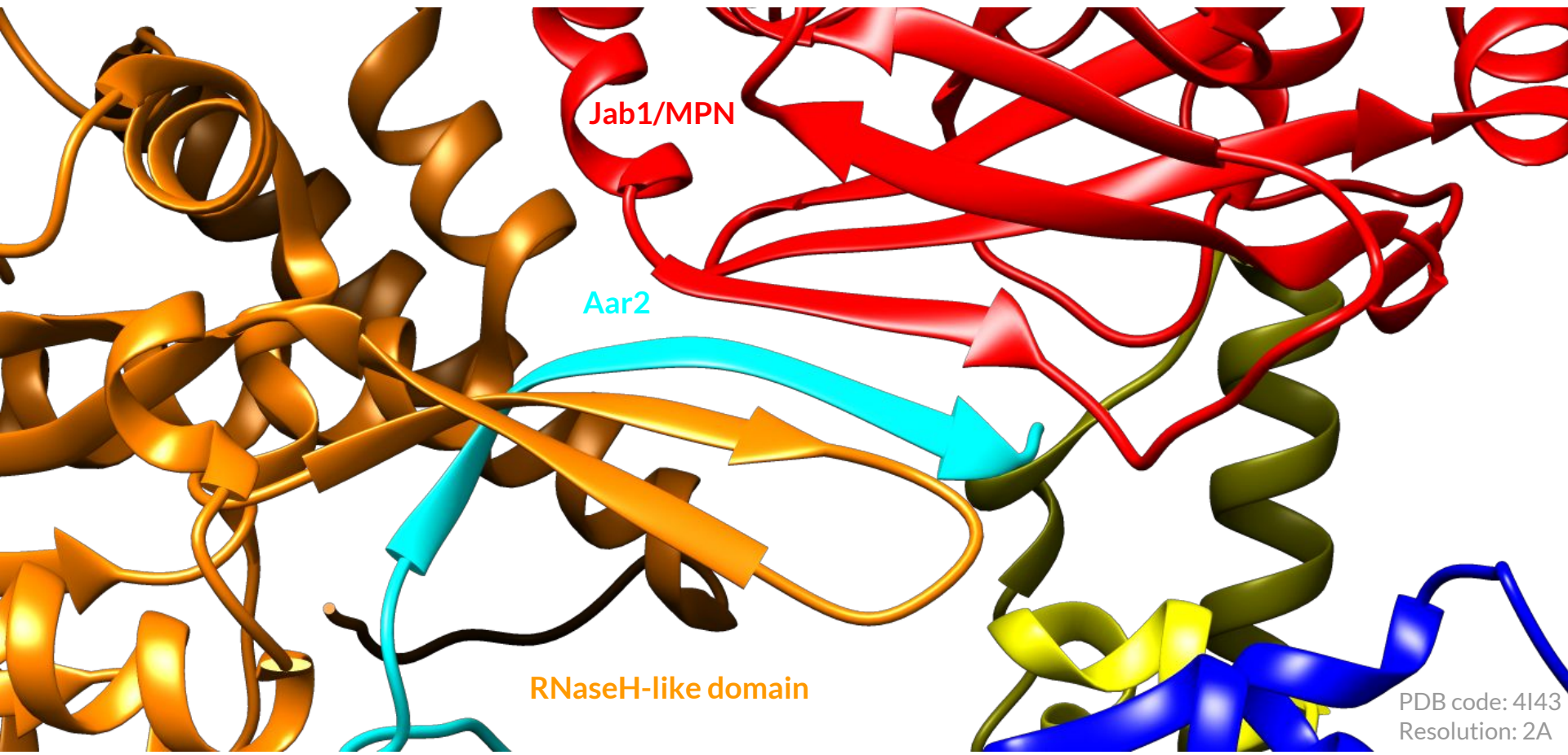
Linker region

	1621	Asp 1628	Lys 1690	Gln 1647	Arg 1650	1680
H.sapiens	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKIHES	IVMDLCQVFD	QELdaleiet
M.mulatta	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKIHES	IVMDLCQVFD	QELdaleiet
C.lupus	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKIHES	IVMDLCQVFD	QELdaleiet
M.musculus	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKIHES	IVMDLCQVFD	QELdaleiet
G.gallus	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKIHES	IVMDLCQVFD	QELdaleiet
D.rerio	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKIHES	IVMDLCQVFD	QELdaleiet
D.melanogaster	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKIHES	IVMDLCQVFD	QELdaleiet
C.elegans	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKIHES	VVMDLCQVFD	QELdaleiqt
S.cerevisiae	VGFLVQLDLT	GIFLHGKIPT	LKISLIQIFR	AHLWQKIHES	IVFDICQILD	GELdvlqies
S.pombe	VGFQVQLDLT	GIMMHGKIPT	LKISLIQIFR	SHLWQKIHES	VVWDLQVLD	QELeslqiet
N.crassa	VGFQVQLDLT	GIFLHGKIPT	LKISLIQIFR	AHLWQKIHES	VVMDLCQVFD	QELealsies
A.thaliana	VGFQVQLDLT	GIYMHGKIPT	LKISLIQIFR	AHLWQKIHES	VVMDLCQVLD	QELepleiet
X.tropicalis	VGFQVQLDLT	GIFMHGKIPT	LKISLIQIFR	AHLWQKIHES	IVMDLCQVFD	QELdaleiet

Negatively charged
 Non-polar
 Positively charged
 Polar

Sequence alignment based on PFAM domains

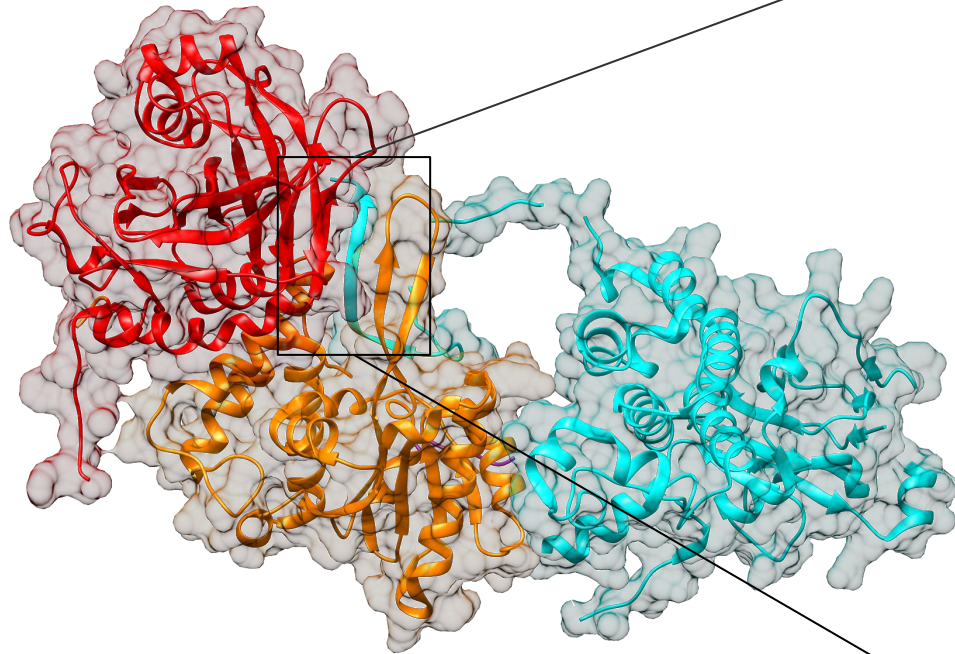
Aar2



PDB code: 4I43
Resolution: 2Å

Aar2

Aar2 - Jab1/RNase

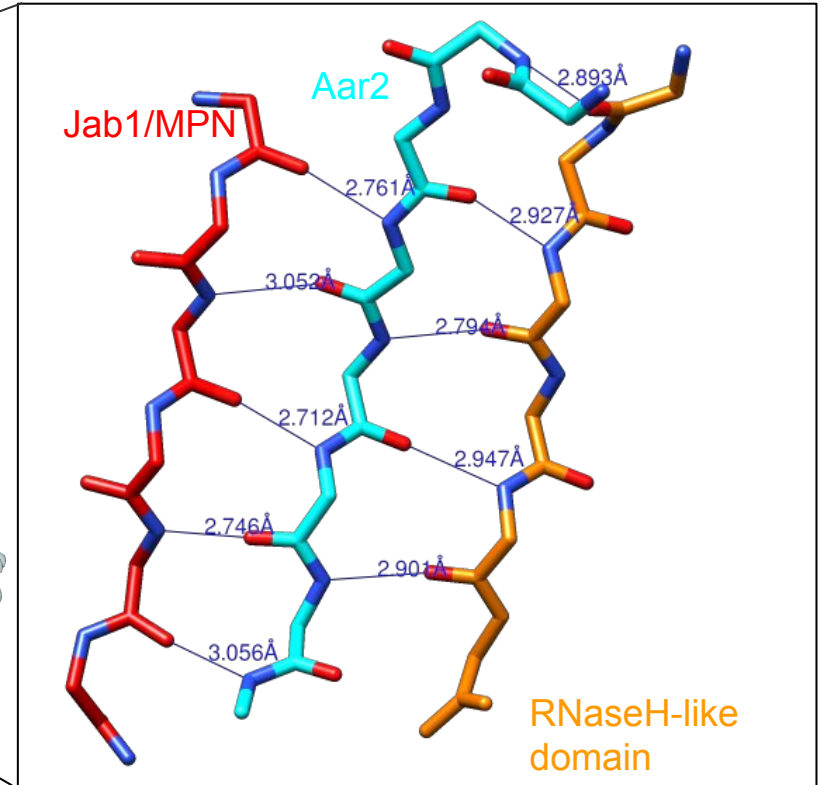


PDB code: 4I43
Resolution: 2Å

■ RNaseH-like

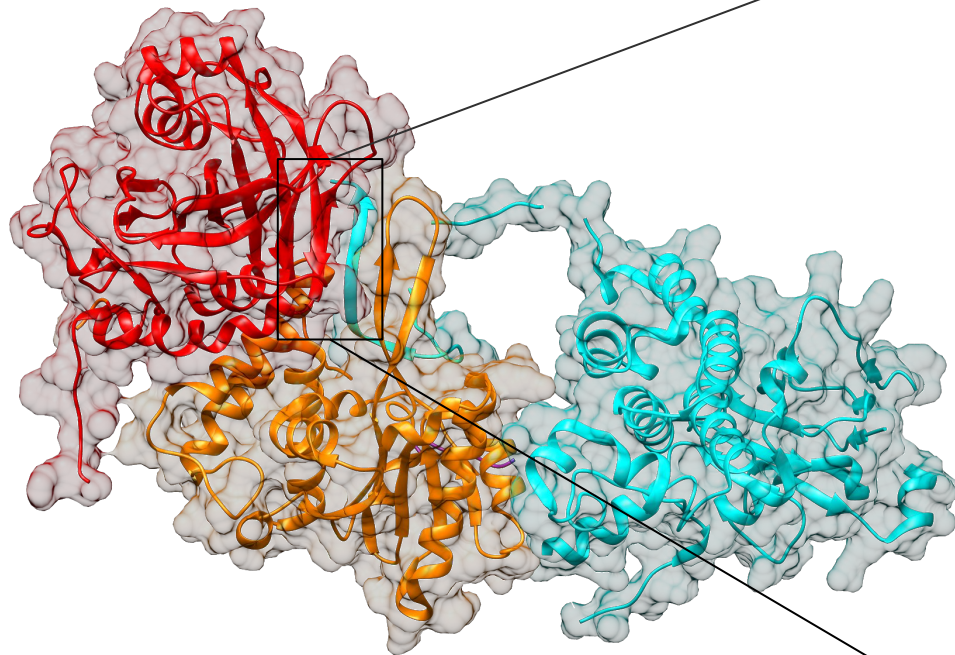
■ Jab1/MPN

■ Aar2





Aar2

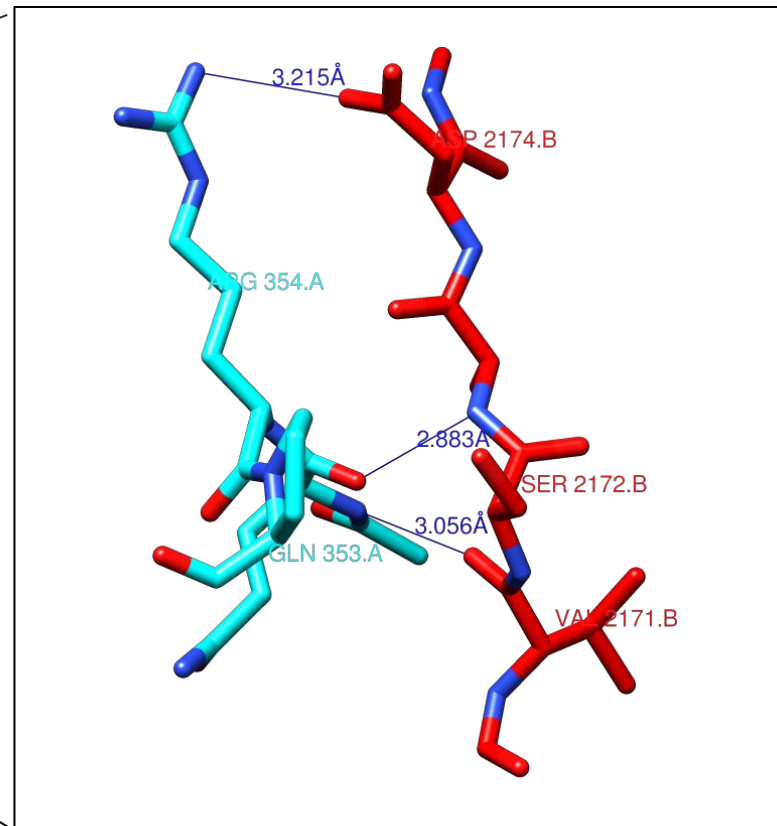
Aar2 - Jab1/RNase



PDB code: 4I43
Resolution: 2Å

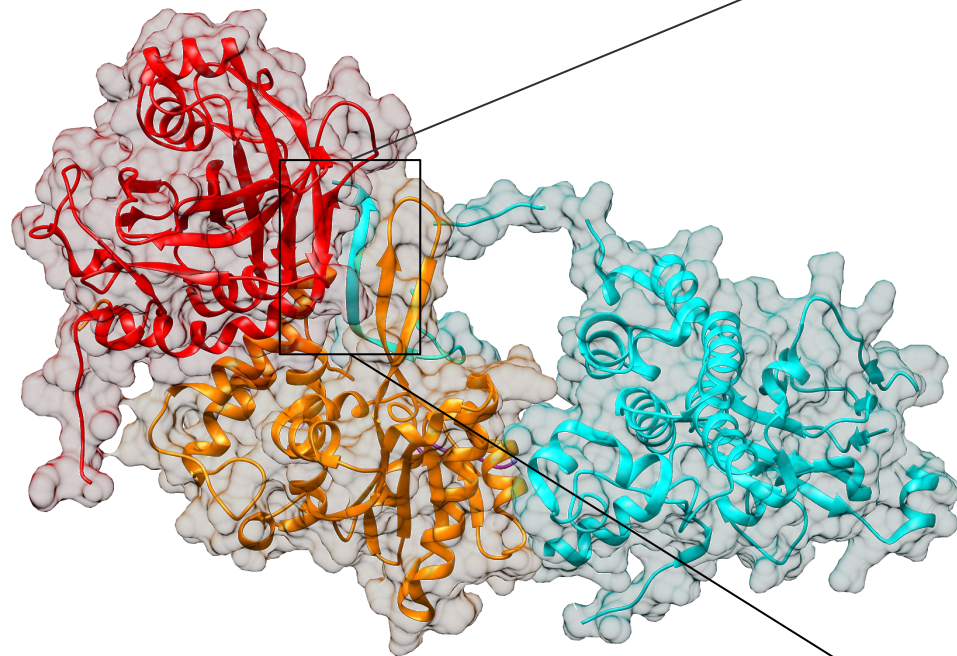
 RNaseH-like
 Jab1/MPN

 Aar2





Aar2

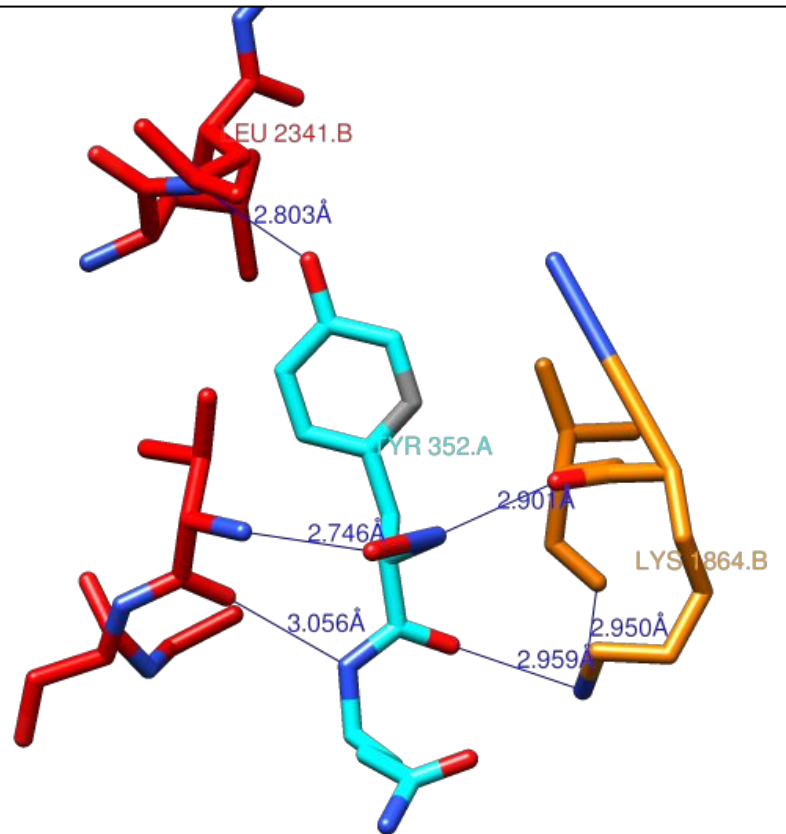
Aar2 - Jab1/RNase



PDB code: 4I43
Resolution: 2Å

 RNaseH-like
 Jab1/MPN

 Aar2



Aar2





Leu 2341

Jab1/MPN region

2341

2400

H.sapiens	LSDRFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHEVHR	PSHFLNFALL
M.mulatta	LSDRFLGFFM	VPAQSSWNYN	FMGK.....
C.lupus	LSDRFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHEVHR	PSHFLNFALL
M.musculus	LSDRFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHEVHR	PSHFLNFALL
G.gallus	LSDRFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHEVHR	PSHFLNFALL
D.rerio	LSDRFLGFFM	VPGQVSWNYN	FMGVRHD..P	NMKYDLQLAN	PKEFYHEVHR	PSHFLNFASL
D.melanogaster	LSNKFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHELHR	TSHFLLFSNL
C.elegans	LSDRFLGYFM	VPSNGVWNYN	FQGQRWS..P	AMKFDVCLSN	PKEYYHEDHR	PVHFHNFKAF
S.cerevisiae	LSDRITGNFI	IPSGNVWNYT	FMGTAFN..Q	EGDYNFKYGI	PLEFYNEMHR	PVHFLQFSEL
S.pombe	LSDRIQGFFL	VPEEGVWNYN	FNGASF..P	KMTYSLKLDV	PLPFFALEHR	PTHVISYTEL
N.crassa	LSEKFRGFFL	VPDGGKWNYN	FMGSAFGg1E	KKPVHVKLDT	PLPFYSQDHR	PIHFSSFNEL
A.thaliana	LSDRFFGFYM	VPENGPWNYN	FMGANHT..V	SINYSLTLTG	PKEYYHQVHR	PTHFLQFSKM
X.tropicalis	LSDRFLGFFM	VPAQASWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHEVHR	PSHFLNFALL

 Negatively charged
  Non-polar
 Positively charged
  Polar

Sequence alignment based on PFAM domains

Aar2

Jab1/MPN region

Val 2171

Ser 2172

	2161					2220
H.sapiens	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
C.lupus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
M.musculus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
M.mulatta	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
G.gallus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
X.tropicalis	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
D.rerio	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
D.melanogaster	ITSTTSNYET	QTFSSKTEWR	VRAISATNLH	LRTNHIYVSS	DDIKETG.YT	YILPKNILKK
C.elegans	ITATTSNYET	ASFASRTEWR	VRAISSTNLH	LRTQHIYVNS	DDVKDTG.YT	YILPKNILKK
A.thaliana	ISTTISPYEQ	SAFGSKTDWR	VRAISATNLY	LRVNHIYVNS	DDIKETG.YT	YIMPKNILKK
S.pombe	VVTTTSAYEN	EKFSSKTEWR	NRAISSISLP	LRTKNIYVNS	DNISETFPHYT	YILPQNLLRK
N.crassa	IVTTTSQFEQ	QTFASKTEWR	TRAIATSNLR	TRANMYVSP	VDSLDD.VT	YVMPKNILKR
S.cerevisiae	VVASADYES	QTFSSKNEW	KSAIANTLLY	LRLKNIYVSA	DDFVEEQ.NV	YVLPKNLLKK

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

Aar2

Lys 1864

Jab1/MPN region

	1861					1920
H.sapiens	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
C.lupus	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
M.musculus	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
M.mulatta	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
G.gallus	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
X.tropicalis	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
D.rerio	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
D.melanogaster	YLSSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
C.elegans	YLTSQNYGEL	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
A.thaliana	YLSSQNYGEI	FSNQIIWFVD	DTNVYRVTIH	KTFEGNLTTK	PINGVIFIFN	PRTGQLFLKI
S.pombe	YLSSSNYAEL	FSNQIQLFVD	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKV
N.crassa	FLNSQNYSEL	FSNQIQLFID	DTNVYRVTIH	KTFEGNLTTK	PINGAIFIFN	PRTGQLFLKI
S.cerevisiae	FLNSSNYAEL	FNNDIKLFVD	DTNVYRVTVH	KTFEGNVATK	AINGCIFTLN	PKTGHLFLKI
	1921					1980

Negatively charged

Non-polar

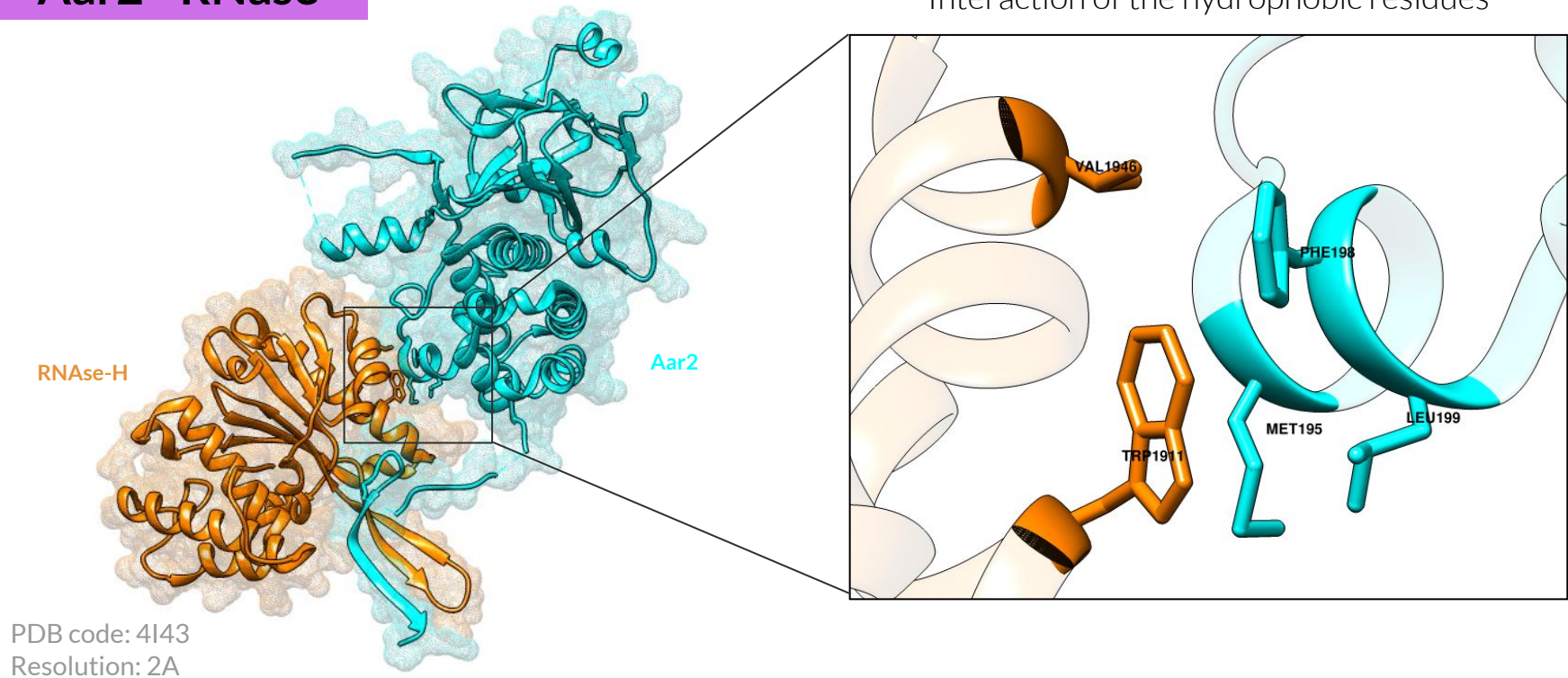
Positively charged

Polar

Clustal Sequence alignment

Aar2

Aar2 - RNase



Aar2

Trp1911

Val1946

RNaseH-like region

		1921				
H.sapiens	WKTAE EVAAL	IRSLPVEEQP	KQIIIVTRKGM	LDPLEVHLLD	FPNIVIKGSE	LQLPFQACLK
M.mulatta	WKTAE EVAAL	IRSLPVEEQP	KQIIIVTRKGM	LDPLEVHLLD	FPNIVIKGSE	LQLPFQACLK
C.lupus	WKTAE EVAAL	IRSLPVEEQP	KQIIIVTRKGM	LDPLEVHLLD	FPNIVIKGSE	LQLPFQACLK
M.musculus	WKTAE EVAAL	IRSLPVEEQP	KQIIIVTRKGM	LDPLEVHLLD	FPNIVIKGSE	LQLPFQACLK
G.gallus	WKTAE EVAAL	IRSLPVEEQP	KQIIIVTRKGM	LDPLEVHLLD	FPNIVIKGSE	LQLPFQACLK
D.rerio	WKTAE EVAAL	IRSLPVEEQP	KQIIIVTRKGM	LDPLEVHLLD	FPNIVIKGSE	LQLPFQACLK
D.melanogaster	WKTAE EVAAL	IRSLPVEEQP	KQIIIVTRKGM	LDPLEVHLLD	FPNIVIKGSE	LQLPFQACLK
C.elegans	WKTAE EVAAL	IRSLPVEEQP	RQIIIVTRKAM	LDPLEVHLLD	FPNIVIKGSE	LMLPFQAIMK
S.cerevisiae	WKTAE EVSAL	VRSLPKEEQP	KQIIIVTRKAM	LDPLEVHMLD	FPNIAIRPTE	LRLPFS AAMS
S.pombe	WKTAE EVAAL	IRSLPVEEQP	RQIIIVTRKGM	LDPLEVHLLD	FPNITIKGSE	LQLPFQAIK
N.crassa	WKTAE EVAAL	IRSLPVEEQP	KQLIVTRKGL	LDPLEVNLLD	FPNISIRASE	LQLPFQAAMK
A.thaliana	WKTAE EVAAL	VRSLPVEEQP	KQVIVTRKGM	LDPLEVHLLD	FPNIVIKGSE	LQLPFQACLK
X.tropicalis	WKTAE EVAAL	IRSLPVEEQP	KQIIIVTRKGM	LDPLEVHLLD	FPNIVIKGSE	LQLPFQACLK

Negatively charged

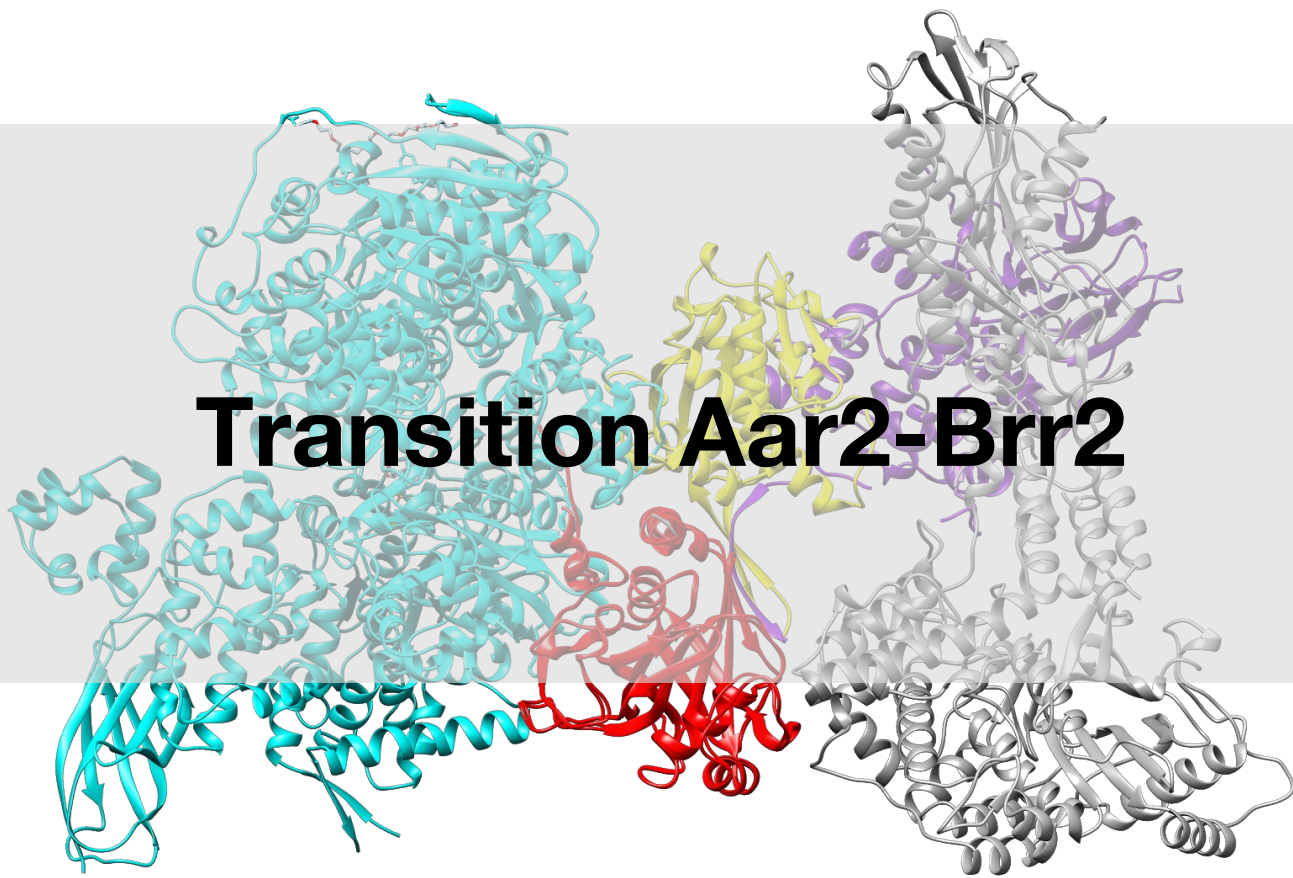
Non-polar

Positively charged

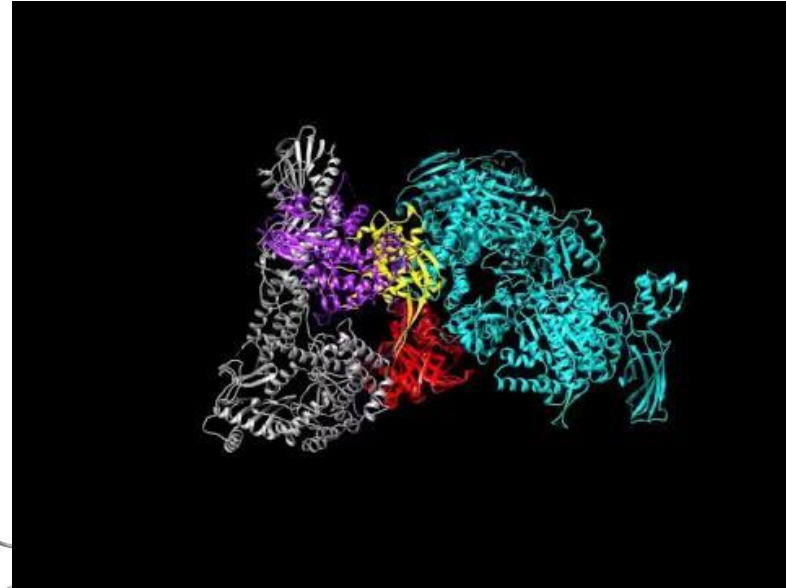
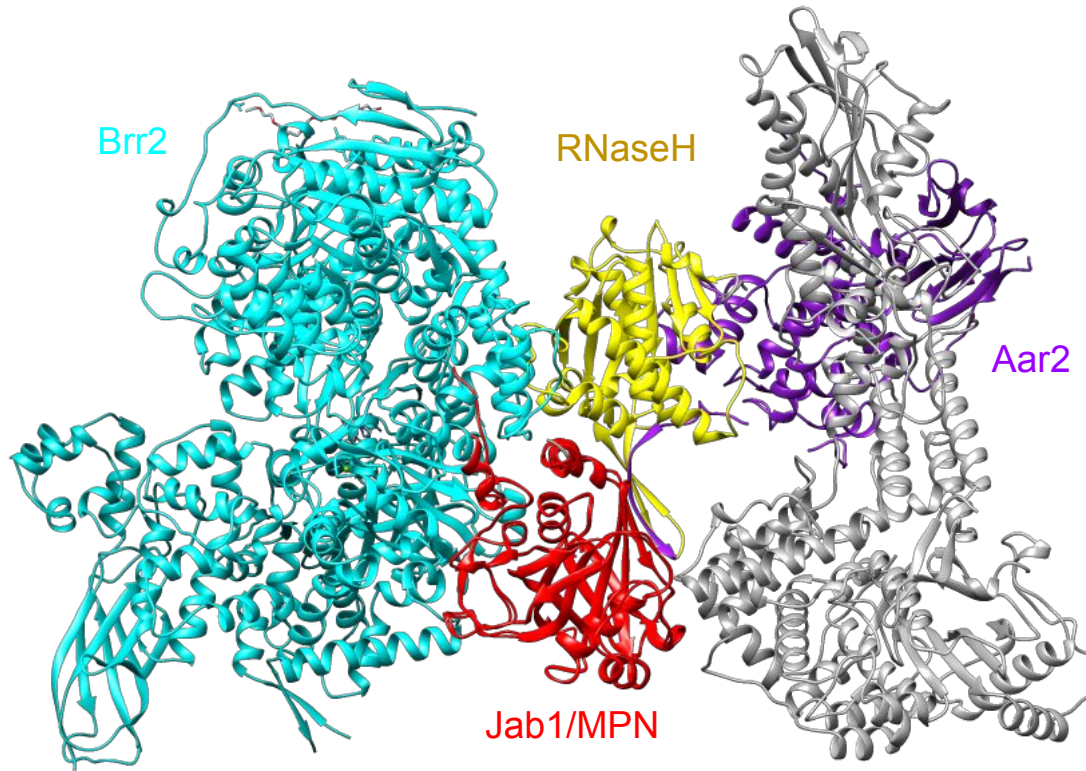
Polar

Sequence alignment based on PFAM domains

Transition Aar2-Brr2

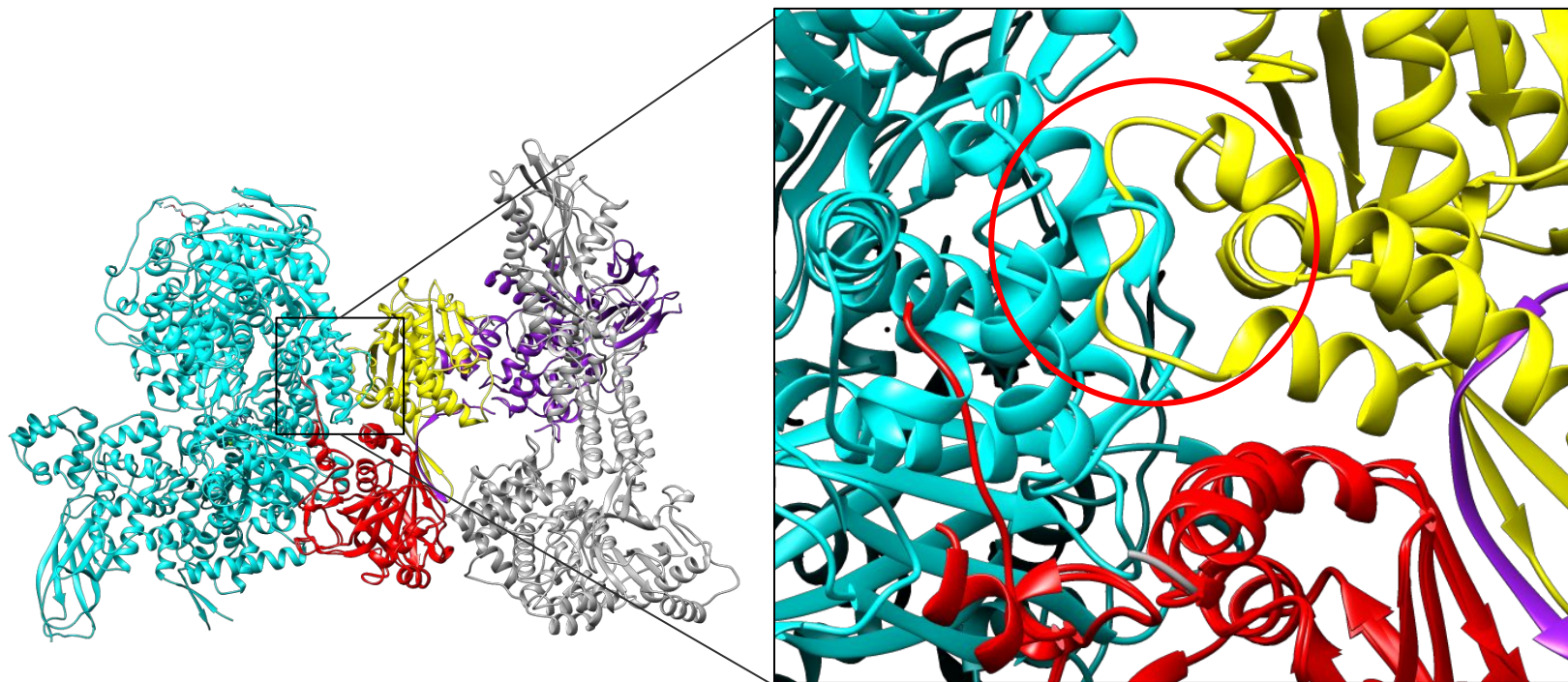


Transition Aar2-Brr2







PDB code: 4l43 and 4bdg
Resolution: 2Å and 2,38Å

Transition Aar2-Brr2

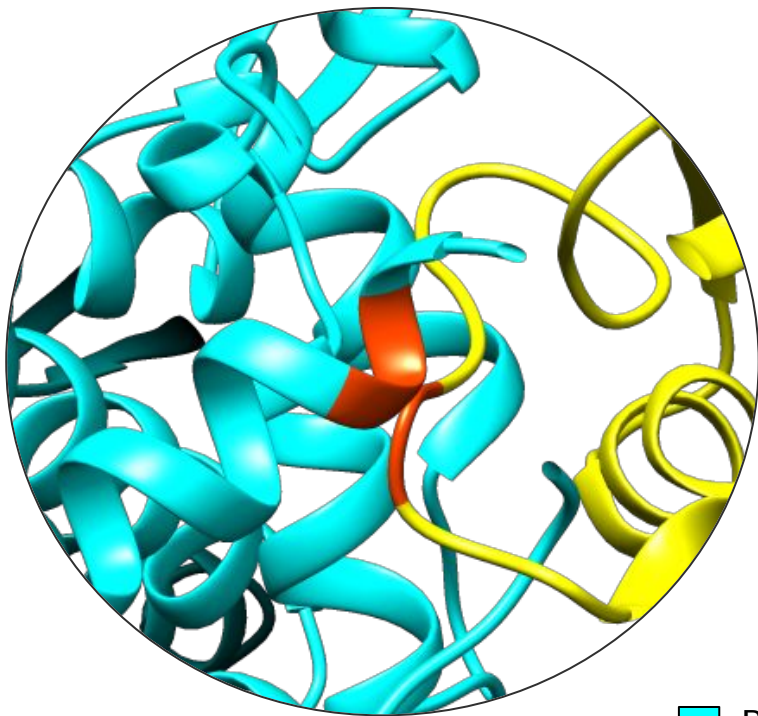


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Resolution: 2Å and 2,38Å

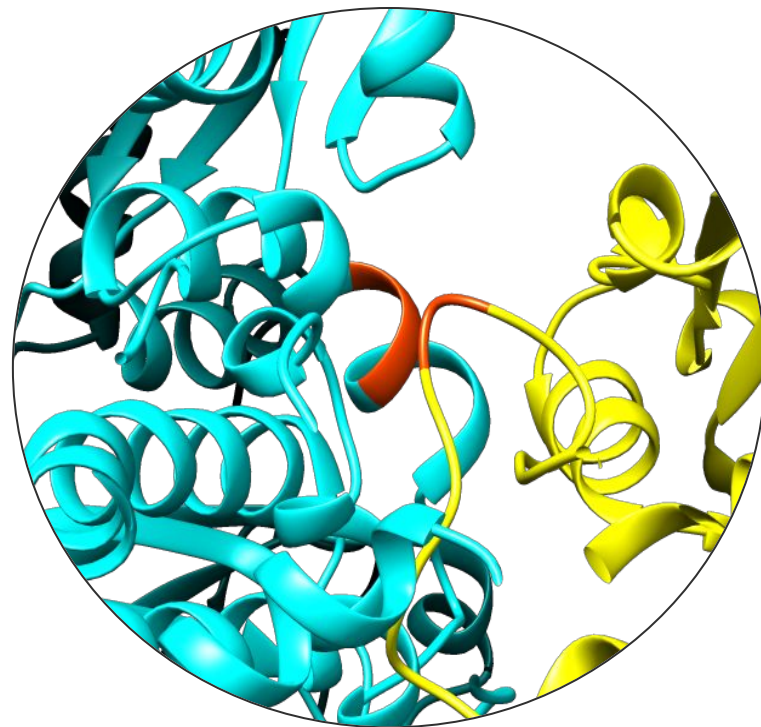
 Aar2
 Jab1/MPN



 Brr2
 RnaseH-like

Transition Aar2-Brr2



PDB code: 4l43 and 4bdg
Resolution: 2Å and 2,38Å



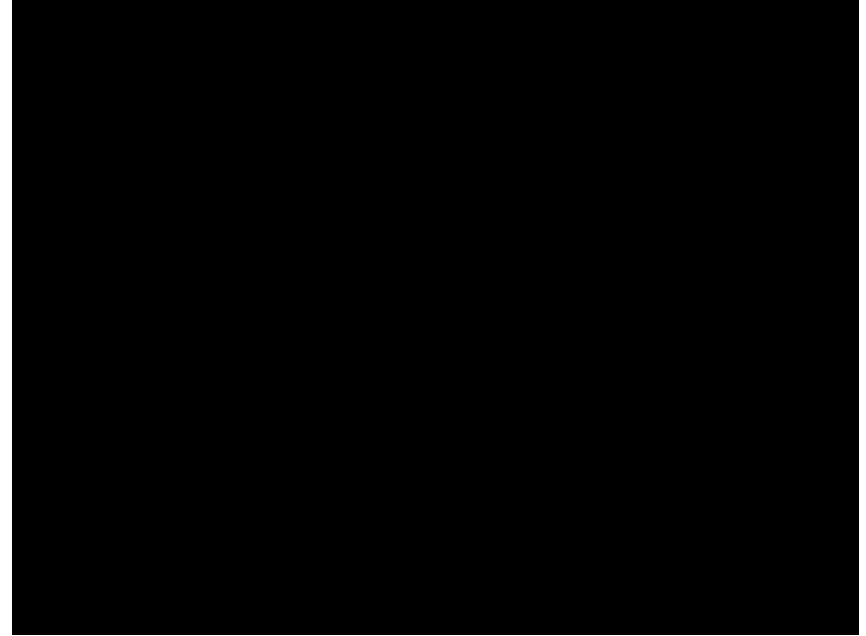
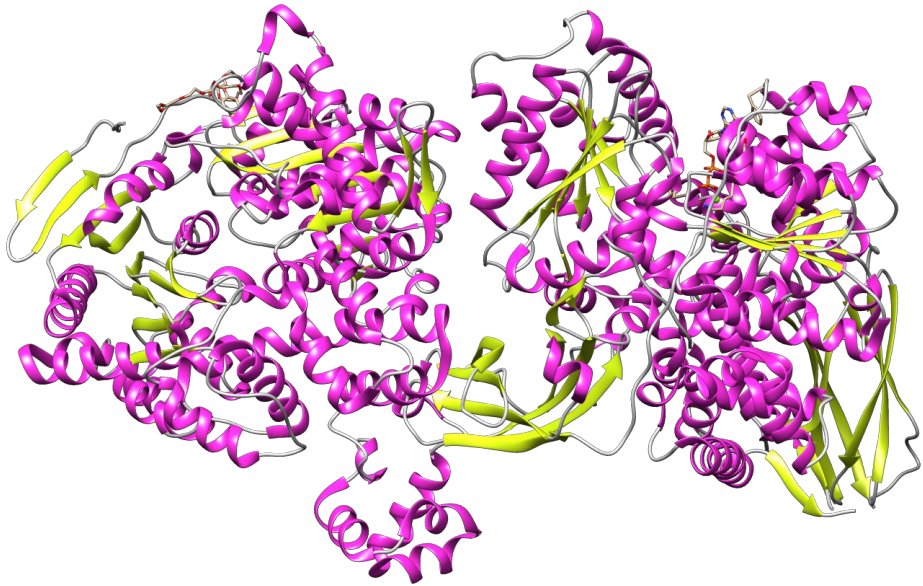
 Brr2
 RnaseH-like

A 3D ribbon diagram of the Brr2 protein structure. The protein is shown in a cyan color, with a red ribbon structure visible at the bottom left. The structure is complex, with many loops and helices. The text "Brr2" is overlaid in the center.

Brr2

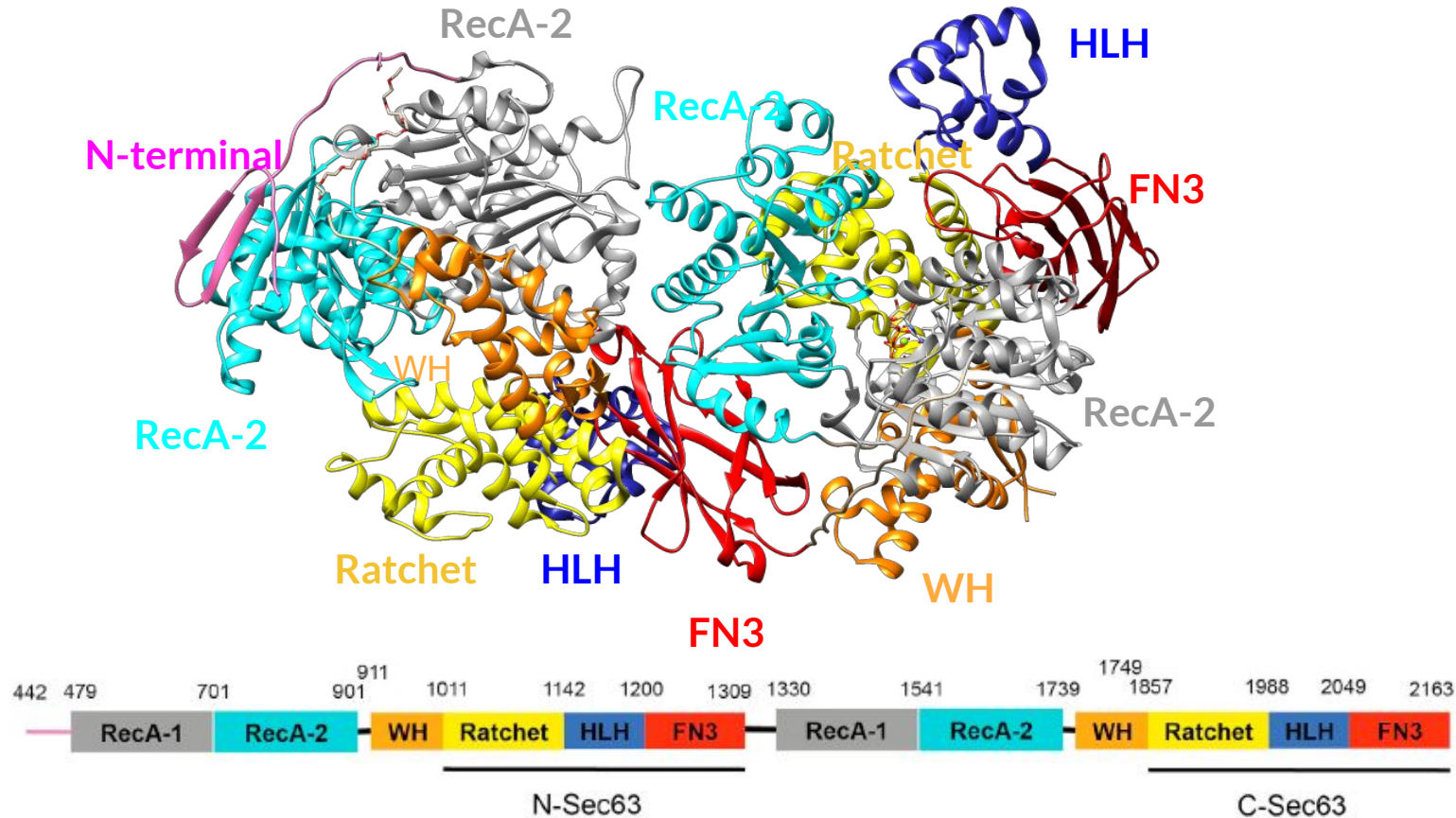
Interaction along the Prp8 platform

Brr2

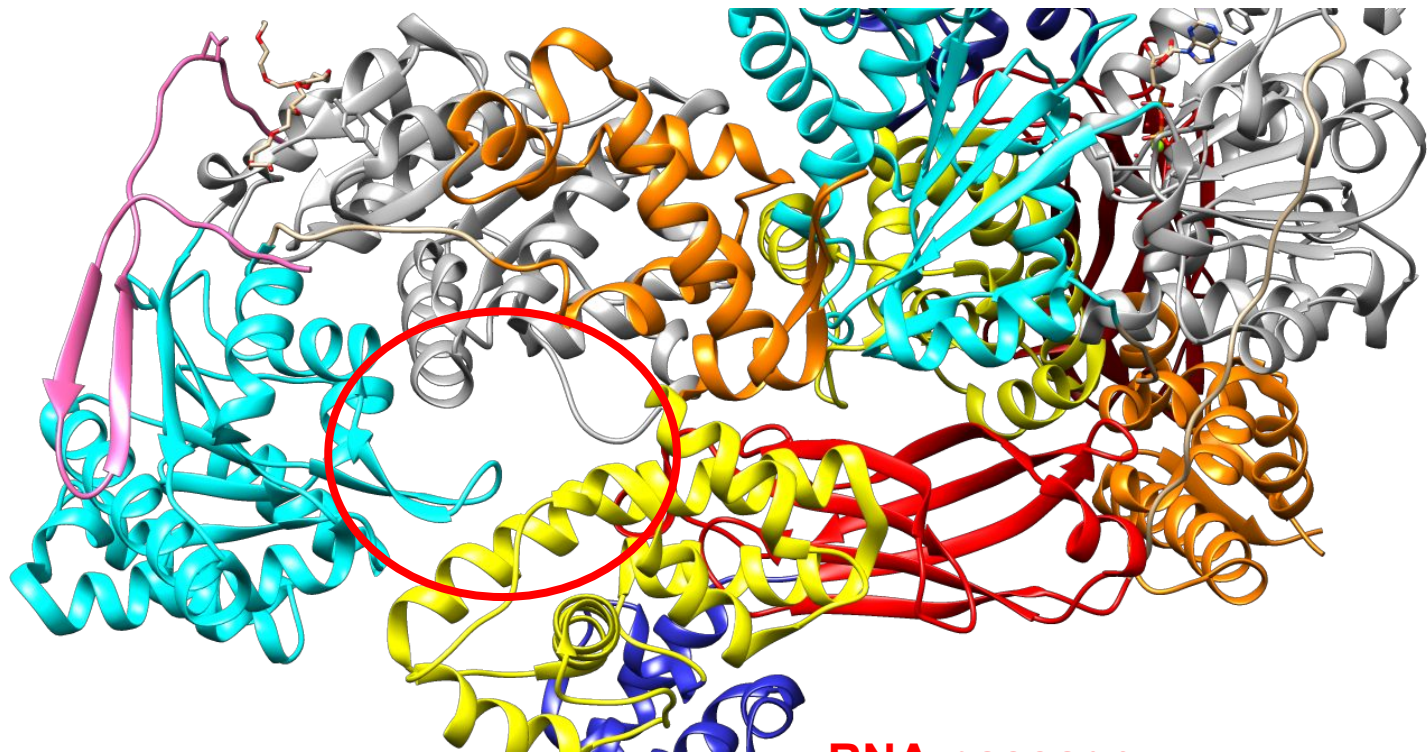


PDB code: 4BGD
Resolution: 2,84 Å

Brr2



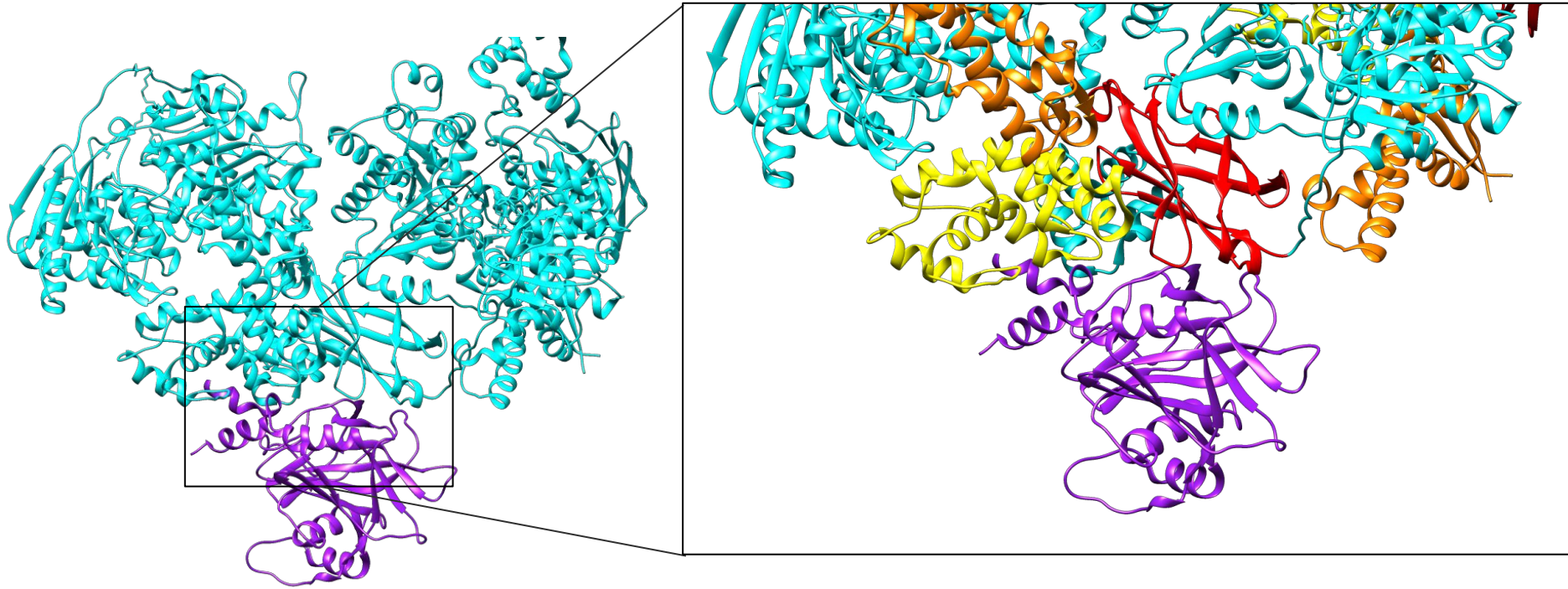
Brr2



RNA passage



PDB code: 4bgd
Resolution: 2,84Å

Brr2



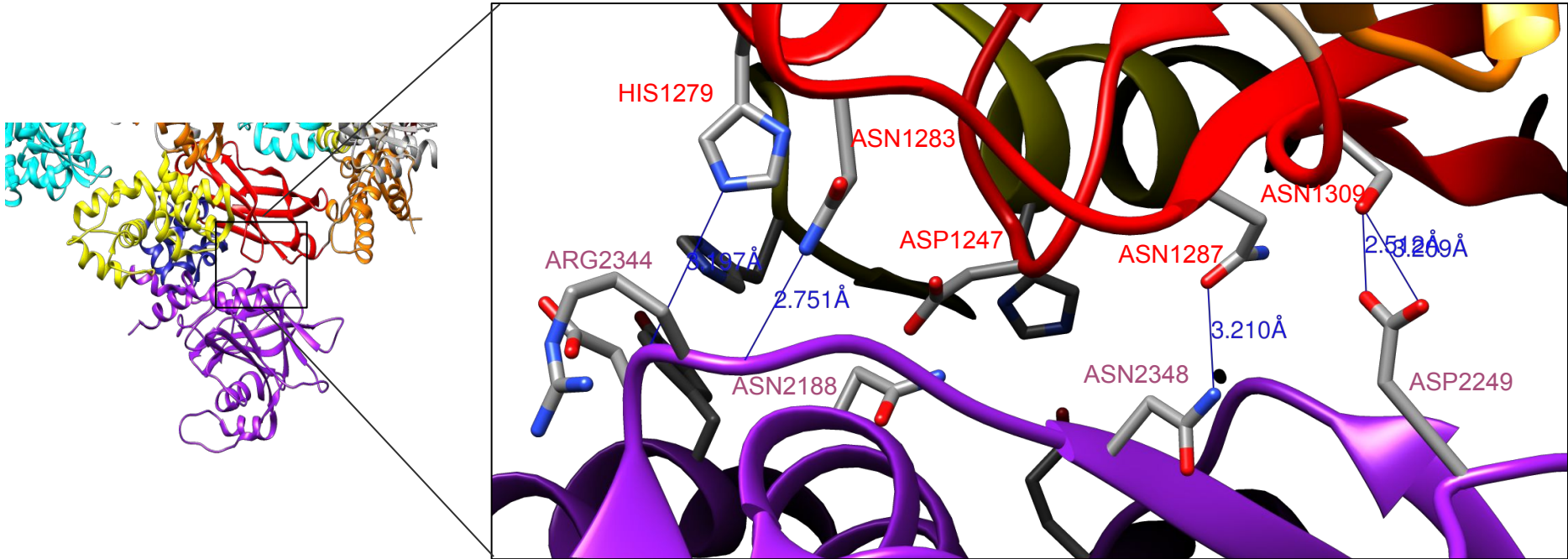
PDB code: 4bgd
Resolution: 2,84Å

 Brr2
 Ratchet

 FN3
 Jab1/MPN

Brr2

Interaction Between Prp8 and the FN3 domain



PDB code: 4bgd
Resolution: 2,84Å

Brr2

Asp 2343

Arg 2344

Jab1/MPN region

	2341					2400
H.sapiens	LS D RFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHEVHR	PSHFLNFALL
M.mulatta	LS D RFLGFFM	VPAQSSWNYN	FMGK.....
C.lupus	LS D RFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHEVHR	PSHFLNFALL
M.musculus	LS D RFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHEVHR	PSHFLNFALL
G.gallus	LS D RFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHEVHR	PSHFLNFALL
D.rerio	LS D RFLGFFM	VPGQVSWNYN	FMGVRHD..P	NMKYDLQLAN	PKEFYHEVHR	PSHFLNFASL
D.melanogaster	LS N KFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHELHR	TSHFLNFSNL
C.elegans	LS D RFLGYFM	VPSNGVWNYN	FQGQRWS..P	AMKFDVCLSN	PKEYYHEDHR	PVHFHNFKAF
S.cerevisiae	LS D RITGNFI	IPSGNVWNYT	FMGTAFN..Q	EGDYNFKYGI	PLEFYNEMHR	PVHFLQFSEL
S.pombe	LS D RIQGFFL	VPEEGVWNYN	FNGASF..P	KMTYSLKLDV	PLPFFALEHR	PTHVISYTEL
N.crassa	LS E KFRGFFL	VPDGGKWNYS	FMGSAFGgLE	KKPVHVKLDT	PLPFYSDQHR	PIHFSSFNEL
A.thaliana	LS D RFFGFYM	VPENGPNWNYN	FMGANHT..V	SINYSLTLTGT	PKEYYHQVHR	PTHFLQFSKM
X.tropicalis	LS D RFLGFFM	VPAQASWNYN	FMGVRHD..P	NMKYELQLAN	PKEFYHEVHR	PSHFLNFALL

Negatively charged

Non-polar

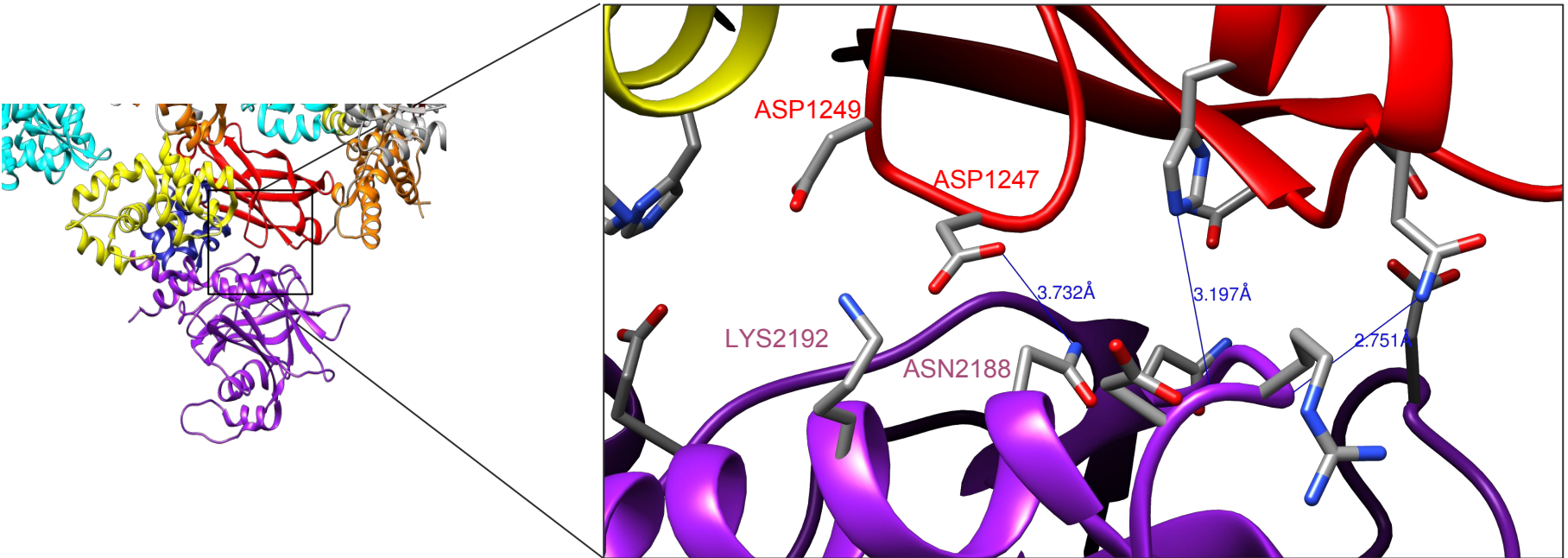
Positively charged

Polar

Sequence alignment based on PFAM domains

Brr2

Interaction Between Prp8 and the FN3 domain

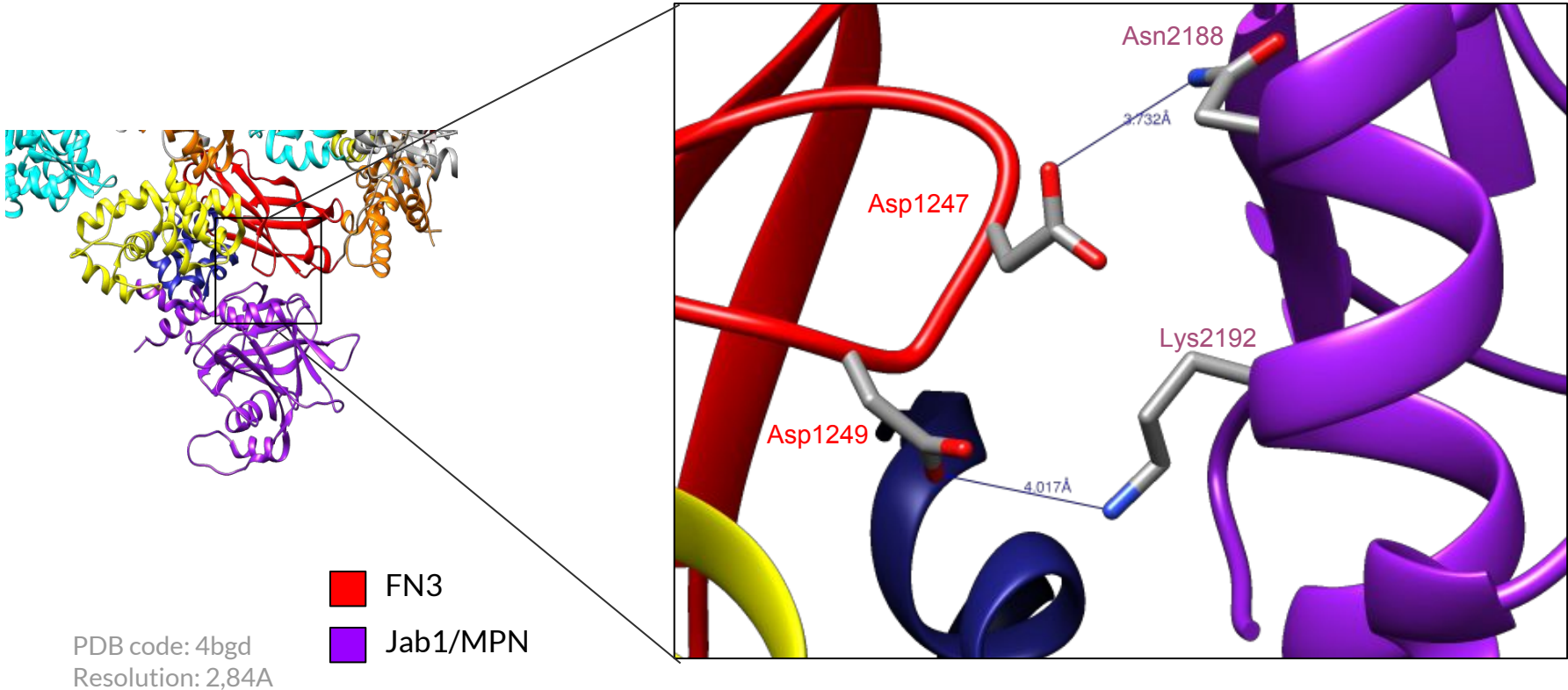


PDB code: 4bgd
Resolution: 2,84Å

■ FN3
■ Jab1/MPN

Brr2

Interaction Between Prp8 and the FN3 domain







Brr2

Jab1/MPN region

Asn 2188

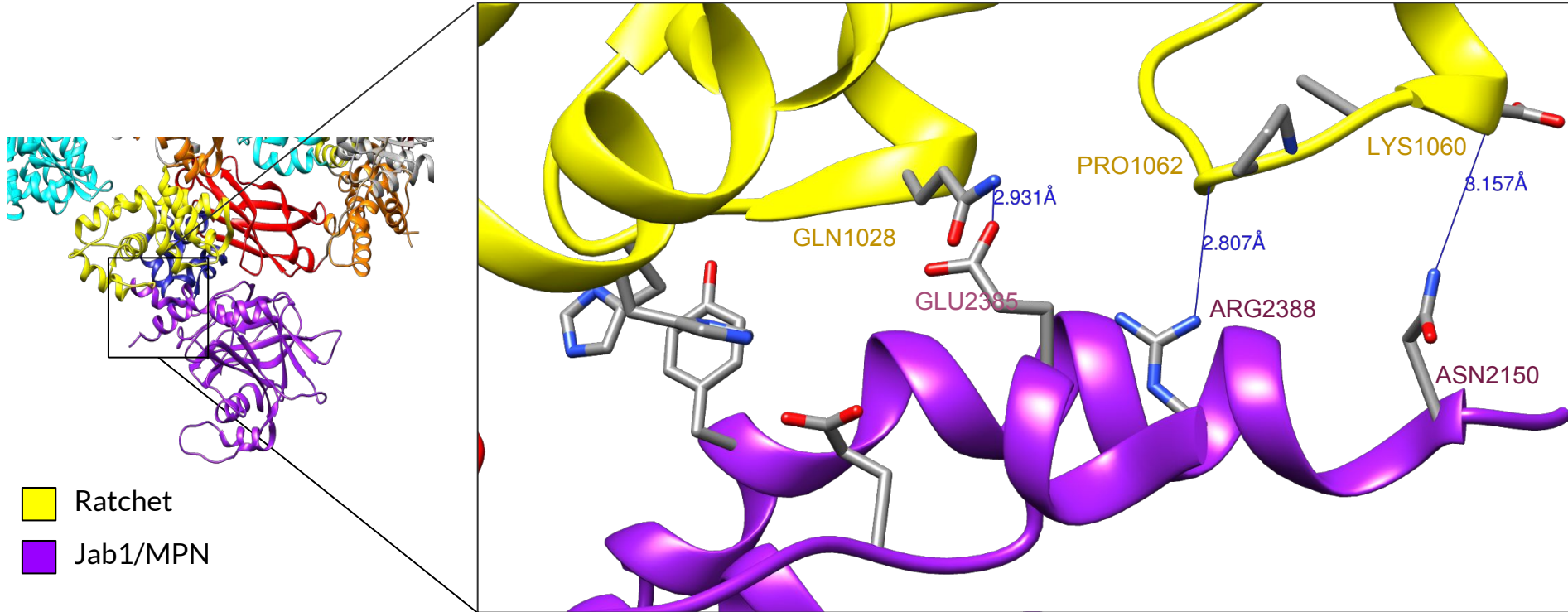
Lys 2192

	2161						2220
H.sapiens	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK	
C.lupus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK	
M.musculus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK	
M.mulatta	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK	
G.gallus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK	
X.tropicalis	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK	
D.rerio	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK	
D.melanogaster	ITSTTSNYET	QTFSSKTEWR	VRAISATNLH	LRTNHIYVSS	DDIKETG.YT	YILPKNILKK	
C.elegans	ITATTSNYET	ASFASRTEWR	VRAISSSTNLH	LRTQHIYVNS	DDVKDTG.YT	YILPKNILKK	
A.thaliana	ISTTISPYEQ	SAFGSKTDWR	VRAISATNLY	LRVNHIYVNS	DDIKETG.YT	YIMPKNILKK	
S.pombe	VTTTTSAYEN	EKFSSKTEWR	NRAISSISLP	LRTKNIYVNS	DNISETFPT	YILPQNLLRK	
N.crassa	IVTTTSQFEQ	QTFASKTEWR	TRAIATSNLR	TRANMYVSP	VDSLDD.VT	YVMPKNILKR	
S.cerevisiae	VVASADYES	QTFSSKNEW	KSAIANTLLY	LRLKNIYVSA	DDFVEEQ.NV	YVLPKNLLKK	

 Negatively charged
  Non-polar
  Positively charged
  Polar

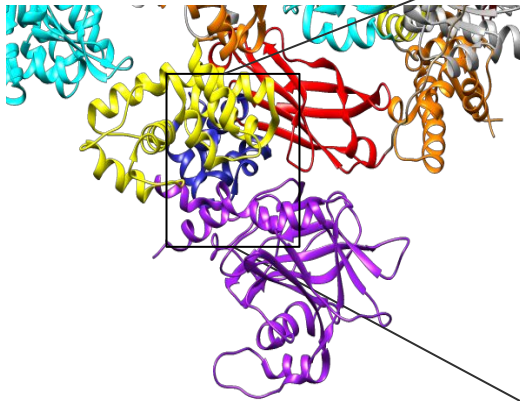
Clustal Sequence alignment



Brr2

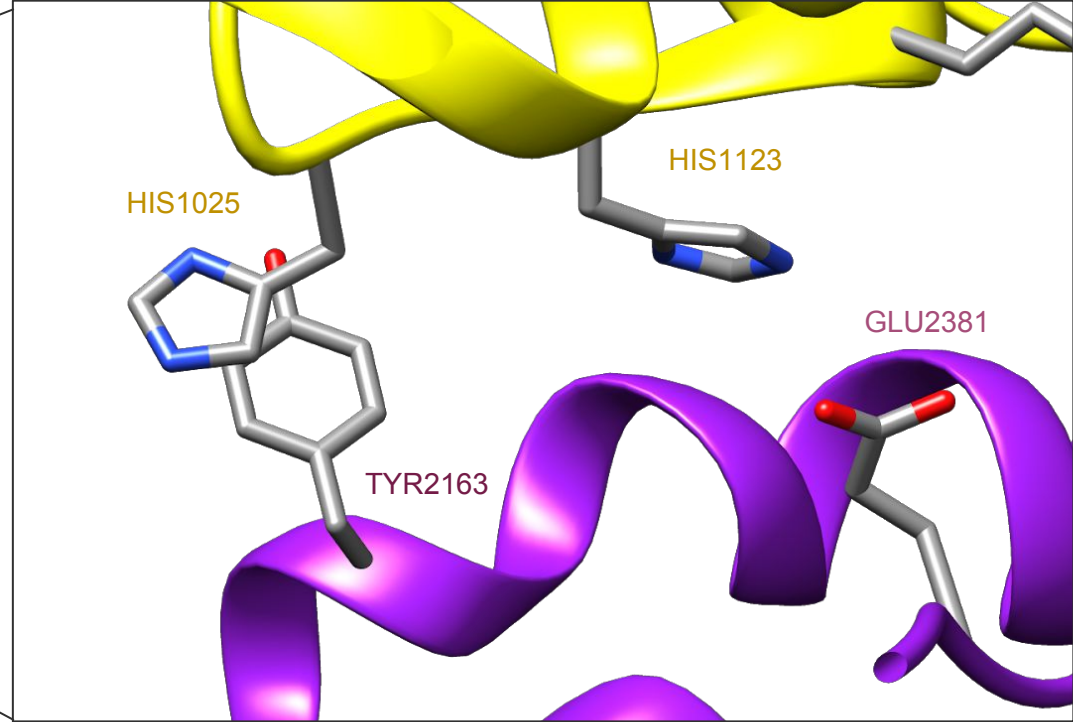


PDB code: 4bgd
Resolution: 2,84Å

Brr2

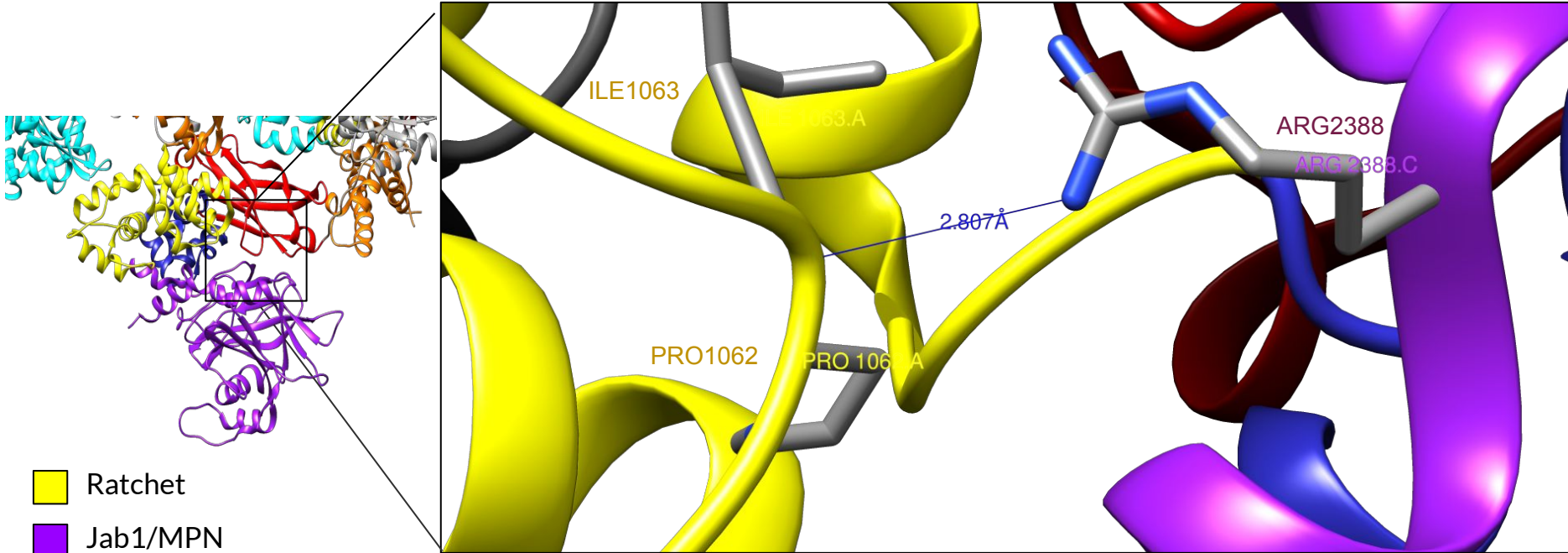


 Ratchet
 Jab1/MPN



PDB code: 4bgd
Resolution: 2,84Å

Brr2



PDB code: 4bgd
Resolution: 2,84Å

Brr2

Jab1/MPN region

Glu 2381
Glu 2385

Arg 2388

2341

2400

H.sapiens	LSDRFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PK	EFYHEVHR	PSHFLNFALL
M.mulatta	LSDRFLGFFM	VPAQSSWNYN	FMGK.....
C.lupus	LSDRFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PK	EFYHEVHR	PSHFLNFALL
M.musculus	LSDRFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PK	EFYHEVHR	PSHFLNFALL
G.gallus	LSDRFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PK	EFYHEVHR	PSHFLNFALL
D.rerio	LSDRFLGFFM	VPGQVSWNYN	FMGVRHD..P	NMKYDLQLAN	PK	EFYHEVHR	PSHFLNFASL
D.melanogaster	LSNKFLGFFM	VPAQSSWNYN	FMGVRHD..P	NMKYELQLAN	PK	EFYHELHR	TSHFLLFSNL
C.elegans	LSDRFLGYFM	VPSNGVWNYN	FQGQRWS..P	AMKFDVCLSN	PK	EYYHEDHR	PVHFHNFKAF
S.cerevisiae	LSDRITGNFI	IPSGNVWNYT	FMGTAFN..Q	EGDYNFKYGI	PL	EFYNEMHR	PVHFLQFSEL
S.pombe	LSDRIQGFFL	VPEEGVWNYN	FNGASF..P	KMTYSLKLDV	PL	PFFALEHR	PTHVISYTEL
N.crassa	LSEKFRGFFL	VPDGGKWNYS	FMGSAFGgLE	KKPVHVKLDT	PL	PFYSDQHR	PIHFSSFNEL
A.thaliana	LSDRFFGFYM	VPENGPWNYN	FMGANHT..V	SINYSLTLTGT	PK	EYYHQVHR	PTHFLQFSKM
X.tropicalis	LSDRFLGFFM	VPAQASWNYN	FMGVRHD..P	NMKYELQLAN	PK	EFYHEVHR	PSHFLNFALL

*

Negatively charged
 Non-polar
 *RP13

Positively charged
 Polar

Sequence alignment based on PFAM domains

Brr2

Asn 2150

Jab1/MPN region

	2161					2220
H.sapiens	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
C.lupus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
M.musculus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
M.mulatta	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
G.gallus	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
X.tropicalis	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
D.rerio	ITSTTSNYET	QTFSSKTEWR	VRAISAANLH	LRTNHIYVSS	DDIKETG.YT	YILPKNVLKK
D.melanogaster	ITSTTSNYET	QTFSSKTEWR	VRAISATNLH	LRTNHIYVSS	DDIKETG.YT	YILPKNILKK
C.elegans	ITATTSNYET	ASFASRTEWR	VRAISSTNLH	LRTQHIYVNS	DDVKDTG.YT	YILPKNILKK
A.thaliana	ISTTISPYEQ	SAFGSKTDWR	VRAISATNLY	LRVMHIYVNS	DDIKETG.YT	YIMPKNILKK
S.pombe	VVTTTSAYEN	EKFSSKTEWR	NRAISSISLP	LRTKNIIYVNS	DNISETFPHYT	YILPQNLLRK
N.crassa	IVTTTSQFEQ	QTFASKTEWR	TRAIATSNLR	TRANMIVVSP	VDSLDLDD.VT	YVMPKNILKR
S.cerevisiae	VVVASADYES	QTFSSKNEW	KSAIANTLLY	LRLKNIIYVSA	DDFVEEQ.NV	YVLPKNLLKK

Negatively charged

Non-polar

Positively charged

Polar

Clustal Sequence alignment

Conclusions

- Prp8 represents a **fundamental platform** for the splicing reactions. Its conservation through species is the first prove of its important role in cells.
- Nevertheless, further studies are needed to fully understand the **whole spliceosomal protein complex**.
- Although its complicated nature makes it proper difficult to understand.
- The **transition from Aar2 to Brr2** is crucial in order to finally form the catalytic complex.
- Interaction of Brr2 with Prp8 plays a key role in the formation of the **catalytic centre of the spliceosome**.

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- ❑ Nguyen, Thi Hoang Duong, et al. Structural basis of Brr2-Prp8 interactions and implications for U5 snRNP biogenesis and the spliceosome active site. *Structure* 2013 (21.6); 910-919.

Questions

1. The proteins Aar2 and Brr2 of the spliceosome:
 - a) **Are mutually exclusive**
 - b) Interact in the spliceosome
 - c) Doesn't exist
 - d) Are not important
 - e) All the others

2. Regarding Brr2 protein in the spliceosome, which of the following is wrong:
 - a) It only interacts with the Jab1/MPN domain
 - b) **Brr2 is disassembled when Prp8 gets inside the nucleus.**
 - c) It's the only ski2-like helicase in the spliceosome
 - d) It is a very large protein
 - e) Aar2 is not longer needed once the Prp8 complex goes inside the nucleus.

3. Regarding Prp8:
 - a) **It's one of the most conserved proteins in the spliceosome**
 - b) It is not important for the spliceosome
 - c) The last two ones
 - d) It only has one domain
 - e) All the others

4. Which one of the following domains is present in *S.cerevisiae* Prp8?

- a. N-terminal
- b. RNase-H like
- c. Thumb/X
- d. Jab1/MPN
- e. Tots els anteriors.

5. What type of residues interact better with RNA?

- a. Non-polar
- b. Negatively charged
- c. A and C
- d. Positively charged
- e. RNA doesn't interact with proteins.

6. Which of the following proteins contains a GTP ligand?

- 1. Snu114
- 2. Brr2
- 3. Aar2
- 4. U1 snRNA

7. Which of the following snRNP is the first to recognise the 5'-splice site (5'-SS)?

1. U1
2. U2
3. U3
4. U4

8. In U5 snRNA recognition, which of the following Prp8 domains is crucial?

1. N-terminal domain
2. Jab1/MPN
3. RNase H like
4. None of them

9. Regarding the RH domain of Prp8, which of the following is true:

- a. Suffers a conformational change so it offers a Mg^{2++} ion to the splicing active site.
- b. In the close conformation the RH domain forms a loose loop.
- c. Is in the close conformation when the RH domain can host a Mg^{2++} ion.
- d. RH doesn't suffer any conformational change at all, that's why it's called RH-like.
- e. None of them is true.

10. Which part of Aar2 allows the different domains of Prp8 to interact?

- a) The tail
- b) N-terminal
- c) Betta domain
- d) Zing domain
- e) The loops

A 3D surface model of a spliceosome complex, showing several subunits in different colors: purple, orange, yellow, green, blue, and pink. The model is set against a light gray background. The text is overlaid on the central part of the model.

Spliceosome:

The crucial role of Prp8

Structural Biology

Ariadna Martínez, Laura Sans, Marta Vilademunt and Mar Villa

STAMP Structural Alignment of Multiple Proteins

Version 4.4 (May 2010)

by Robert B. Russell & Geoffrey J. Barton

Please cite PROTEINS, v14, 309-323, 1992

Running roughfit.

Sc = STAMP score, RMS = RMS deviation, Align = alignment length

Len1, Len2 = length of domain, Nfit = residues fitted

Secs = no. equivalent sec. strucs. Eq = no. equivalent residues

%I = seq. identity, %S = sec. str. identity

P(m) = P value (p=1/10) calculated after Murzin (1993), JMB, 230, 689-694

(NC = P value not calculated - potential FP overflow)

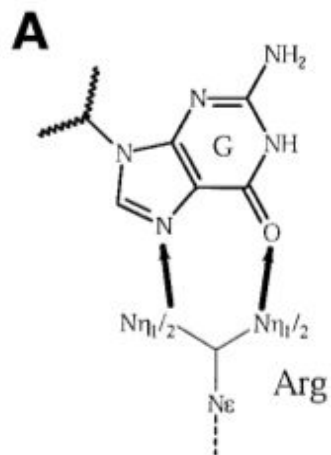
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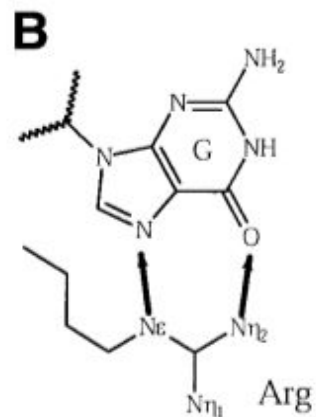
Doing cluster analysis...

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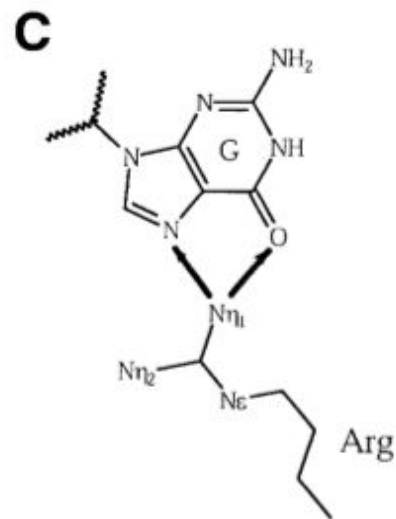
See file RNase.1 for the alignment and transformations



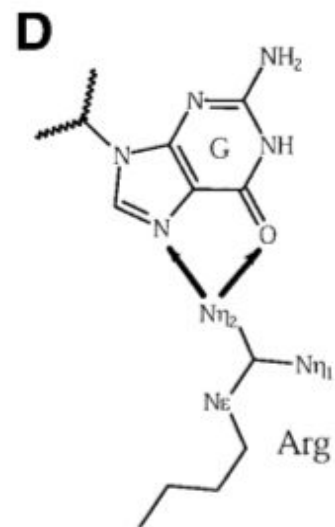
(21 examples, 47 bonds)



(2 examples, 4 bonds)



(2 examples, 4 bonds)



(4 examples, 8 bonds)

Prp8

STAMP Structural Alignment of Multiple Proteins

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Sc = STAMP score, RMS = RMS deviation, Align = alignment length
Len1, Len2 = length of domain, Nfit = residues fitted
Secs = no. equivalent sec. strucs. Eq = no. equivalent residues
%I = seq. identity, %S = sec. str. identity
P(m) = P value (p=1/10) calculated after Murzin (1993), JMB, 230, 689-694
(NC = P value not calculated - potential FP overflow)

Cluster: 1 (hENDO & yENDO) Sc 9.12 RMS 1.19 Len 172 nfit 172
See file templates_OK.1 for the alignment and transformations
Cluster: 2 (hLINKER & yLINKER) Sc 8.43 RMS 1.42 Len 278 nfit 264
See file templates_OK.2 for the alignment and transformations
Cluster: 3 (hJAB & yJAB) Sc 8.02 RMS 1.29 Len 248 nfit 228
See file templates_OK.3 for the alignment and transformations
Cluster: 4 (hRNase & yRNase) Sc 7.11 RMS 1.24 Len 192 nfit 190
See file templates_OK.4 for the alignment and transformations
Cluster: 5 (hRT & yRT) Sc 6.94 RMS 0.90 Len 367 nfit 364
See file templates_OK.5 for the alignment and transformations
Cluster: 6 (hNT & yNT) Sc 6.53 RMS 1.58 Len 779 nfit 590
See file templates_OK.6 for the alignment and transformations
Cluster: 7 (hENDO yENDO & hJAB yJAB) Sc 1.45 RMS 3.88 Len 267 nfit 56 LOW SCORE
See file templates_OK.7 for the alignment and transformations
Cluster: 8 (hENDO yENDO hJAB yJAB & hRNase yRNase) Sc 0.92 RMS 4.69 Len 400 nfit 30 LOW SCORE
See file templates_OK.8 for the alignment and transformations
Cluster: 9 (hLINKER yLINKER & hENDO yENDO hJAB yJAB hRNase yRNase) Sc 1.04 RMS 5.04 Len 540 nfit 21 LOW SCORE
See file templates_OK.9 for the alignment and transformations
Cluster: 10 (hLINKER yLINKER hENDO yENDO hJAB yJAB hRNase yRNase & hRT yRT) Sc 0.62 RMS 4.69 Len 746 nfit 18 LOW SCORE
See file templates_OK.10 for the alignment and transformations
Cluster: 11 (hLINKER yLINKER hENDO yENDO hJAB yJAB hRNase yRNase hRT yRT & hNT yNT) Sc 0.63 RMS 5.31 Len 1303 nfit 10 LOW SCORE
See file templates OK.11 for the alignment and transformations