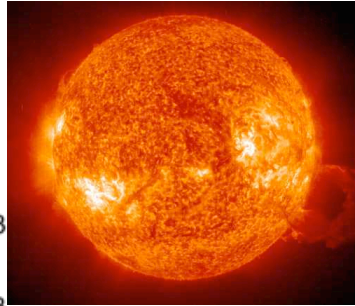
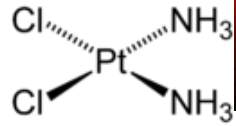
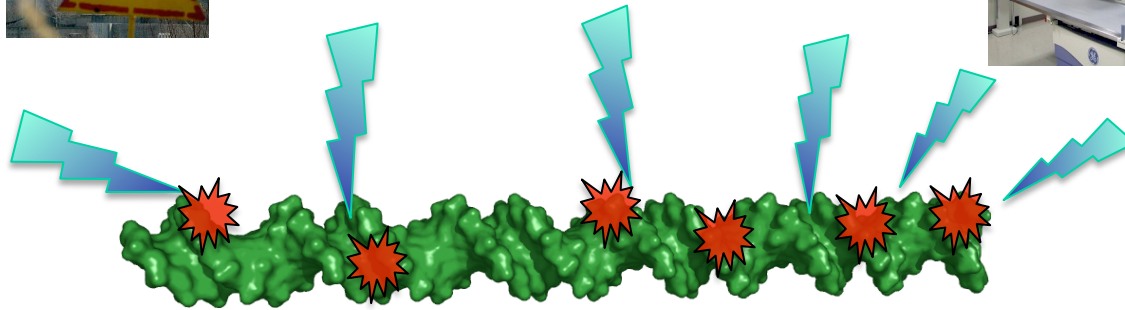


Structure and Function of BRCT Phosphoprotein Binding Domains in the DNA damage response





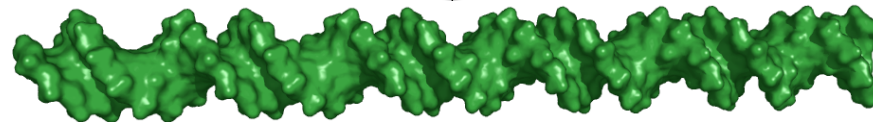
ROS



DNA repair

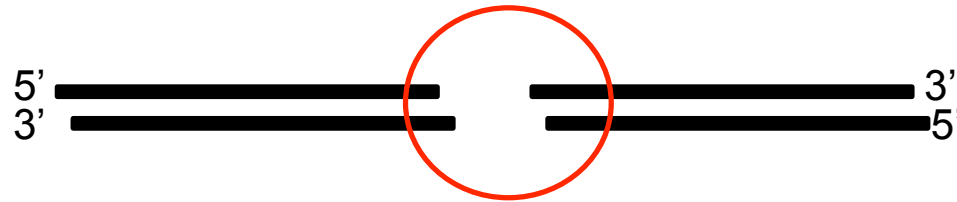


Mutations (Cancer,
neurodegenerative
diseases)

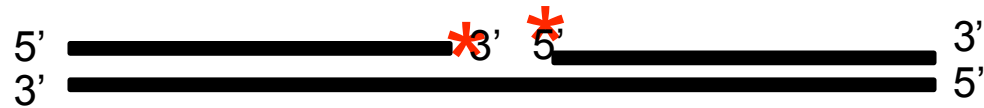


Genome Stability Structural Biology Group (LSB)

1. DNA double strand break repair (DSBR)



2. DNA end processing factors



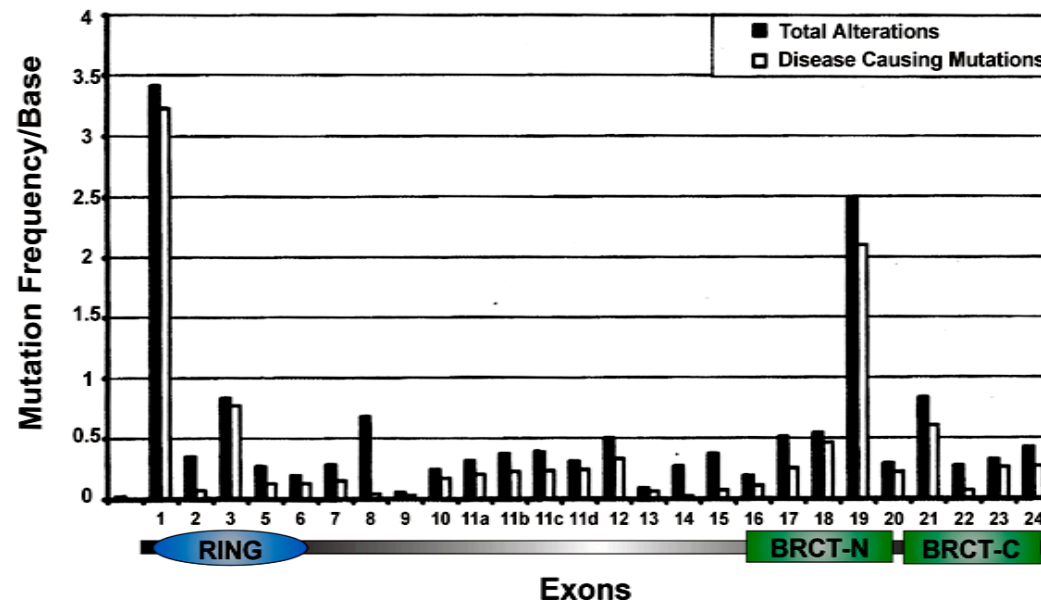
- Structural analysis (eg. X-ray crystallography, SAXS) of DNA repair
- Mechanisms of repair factor inactivation in human diseases
- Targeted inhibition DNA repair factors

Overview

Structure and function of BRCT phosphoprotein binding
Domains in the DNA damage response

1. Background on BRCT domains
2. BRCT domain integration into multi-protein complexes
 - Structure/function of Nbs1, a DNA damage response signaling adaptor
3. Molecular basis for BRCT phosphoprotein binding and specificity
 - Structure/function of a fission yeast phospho-H2A binding BRCT protein, Brc1

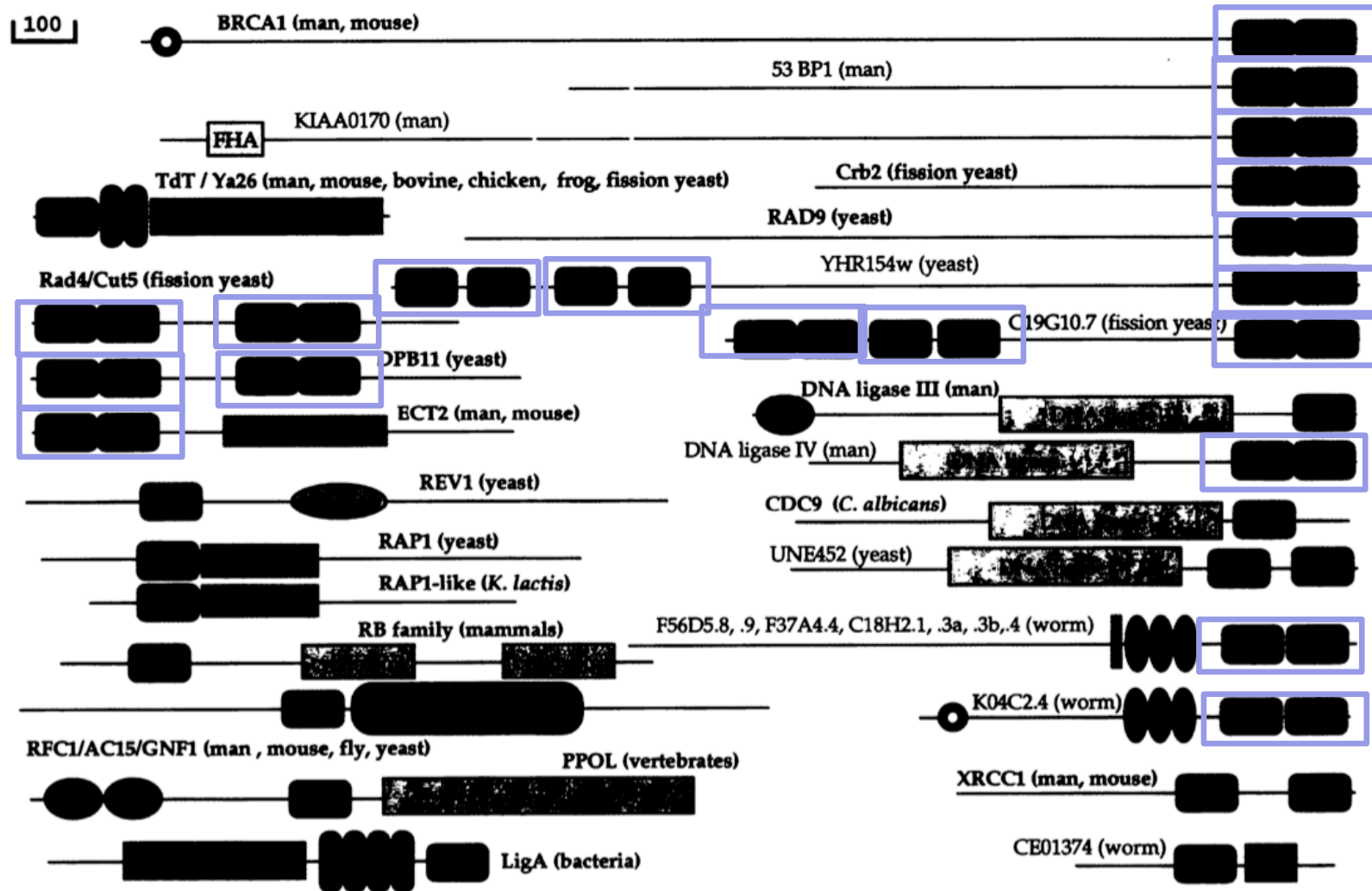
BRCA1 mutations



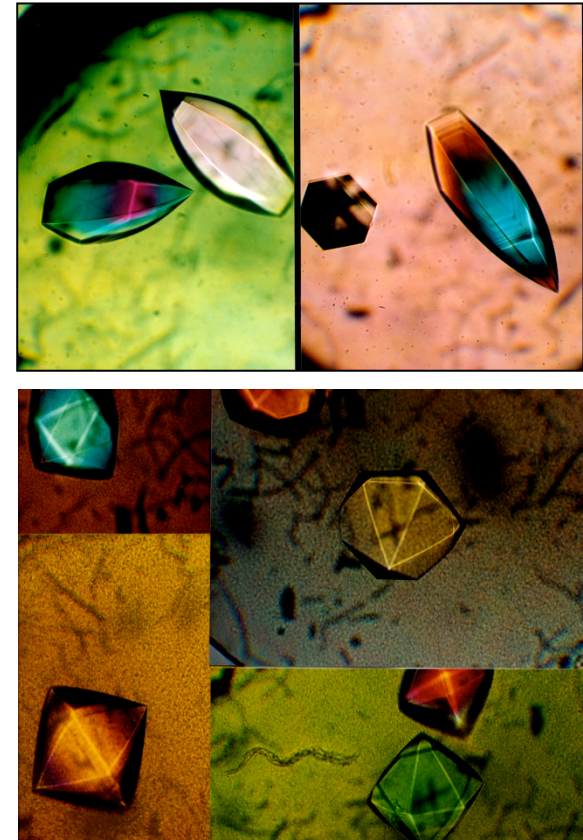
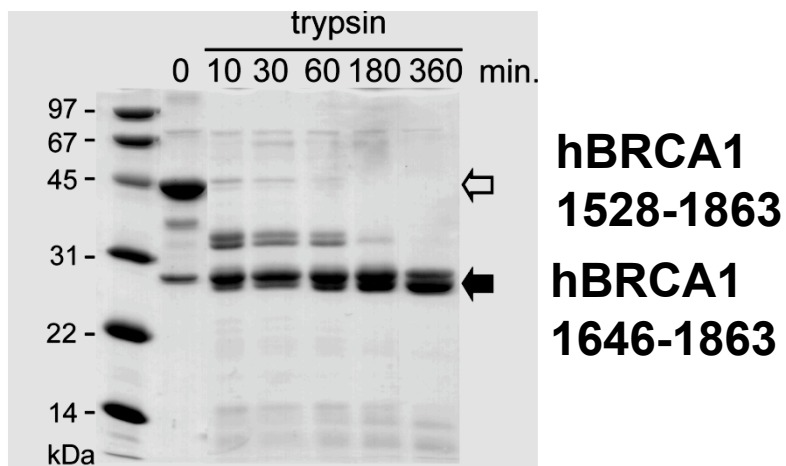
~80% of mutations lead to truncated protein products which delete all or > 25% of the BRCT repeat region

- All truncations are presumed to be cancer predisposing eg. 1853ter

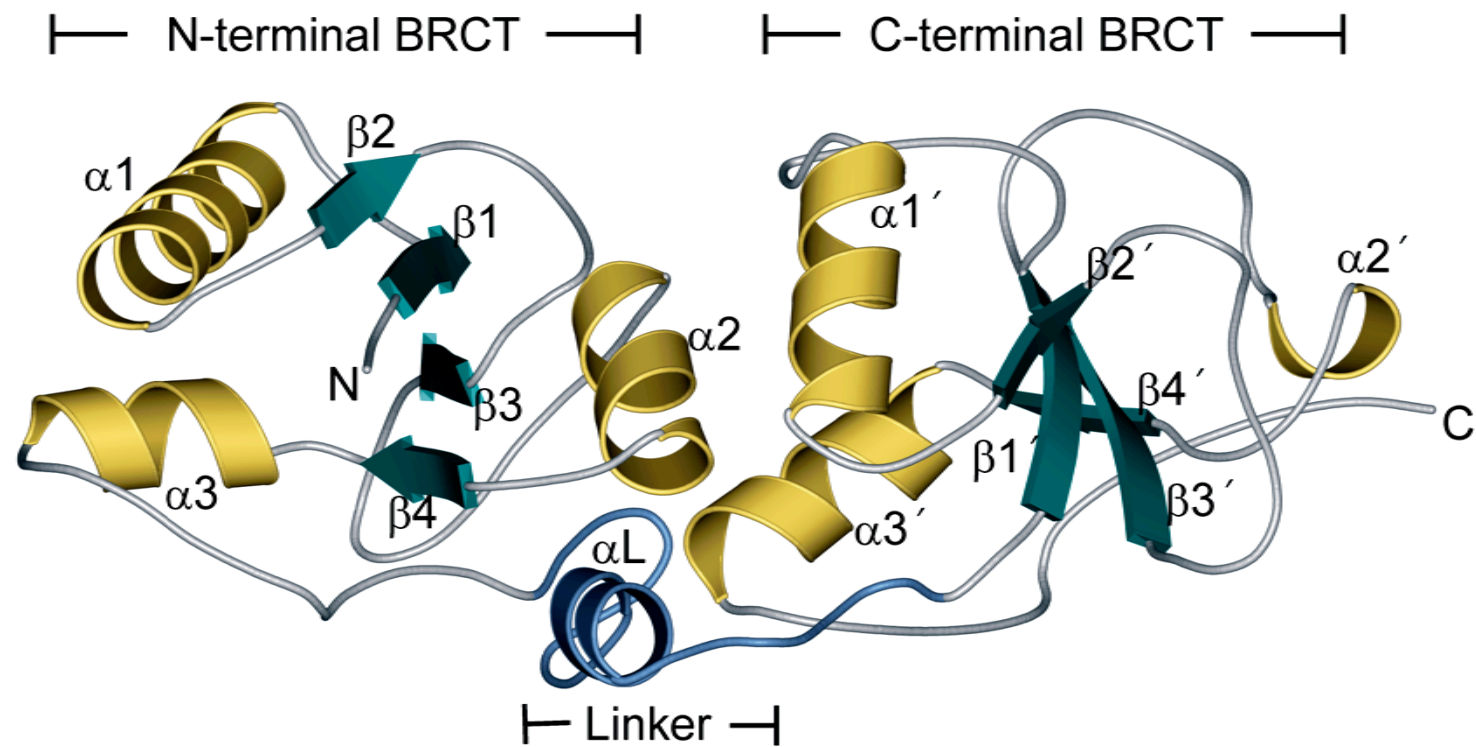
BRCA1 Carboxyl terminal (BRCT) Domains in DNA replication and repair proteins



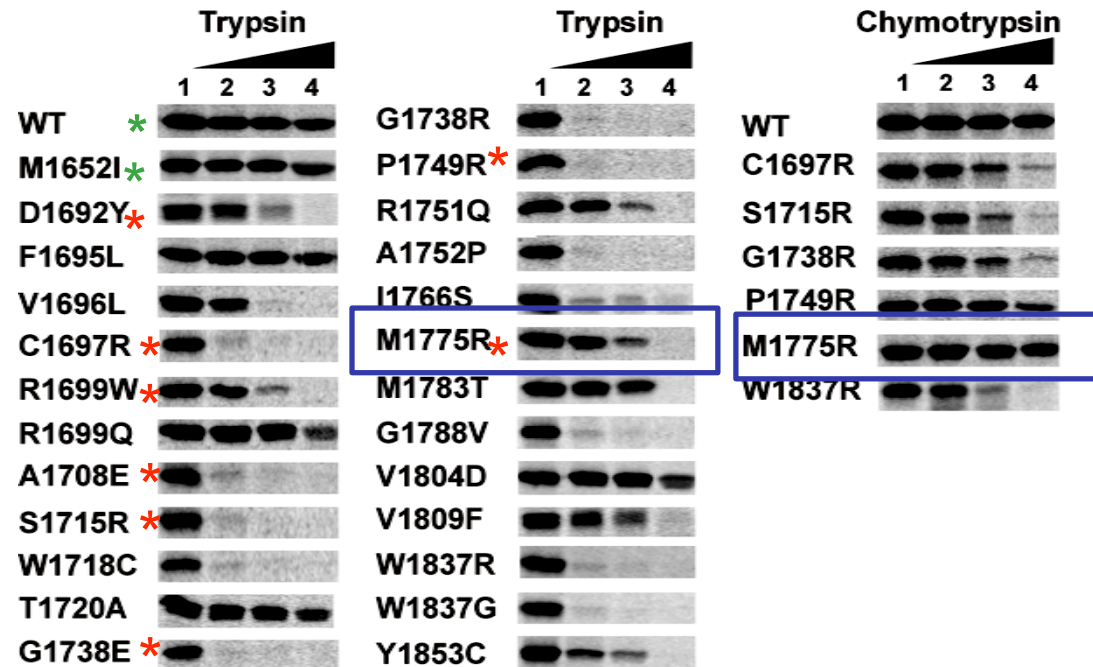
BRCT domains of hBRCA1 are an ordered tandem repeat



hBRCA1 tandem BRCT repeat Architecture



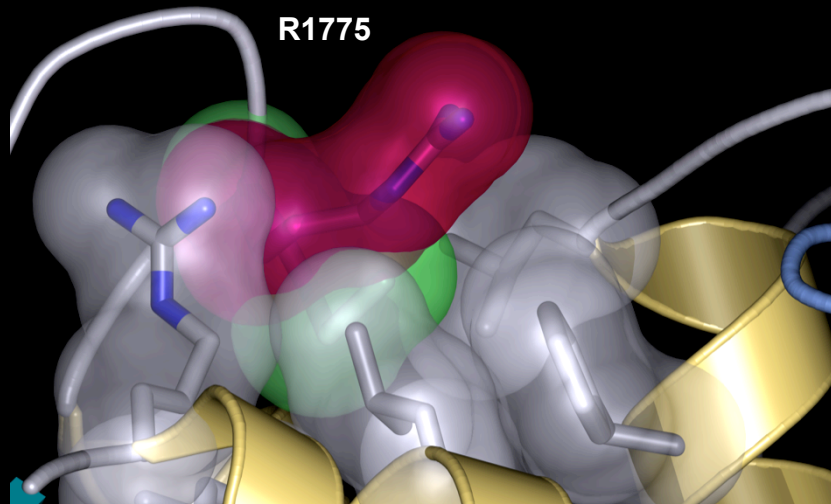
Most Patient BRCA1-BRCT mutations are destabilizing



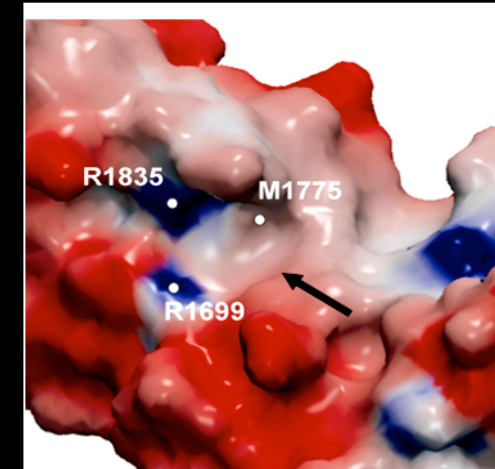
- * WT and Benign Polymorphisms are stable to proteolysis
- * Disease associated truncation and missense mutations destabilize the BRCT fold

BRCA1 Cancer associated mutant M1775R

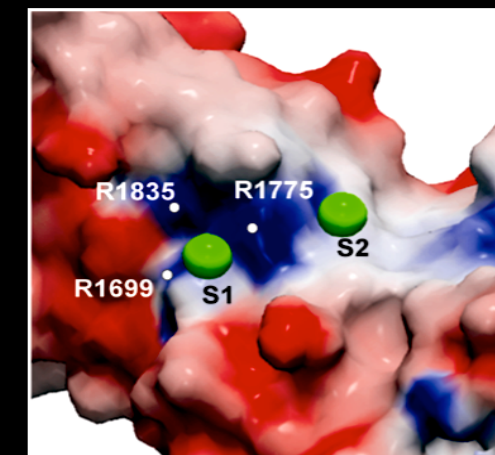
- Mutant BRCA1 allele encoding BRCA1-M1775R segregates with disease in families with breast and ovarian cancer (Futreal et al, 1994)
- Impaired kinetics of double strand DNA break repair
- Impaired protein binding to CtIP, histone deacetylase complexes and BACH1



WT



M1775R



Protein stability or protein-ligand binding defect??

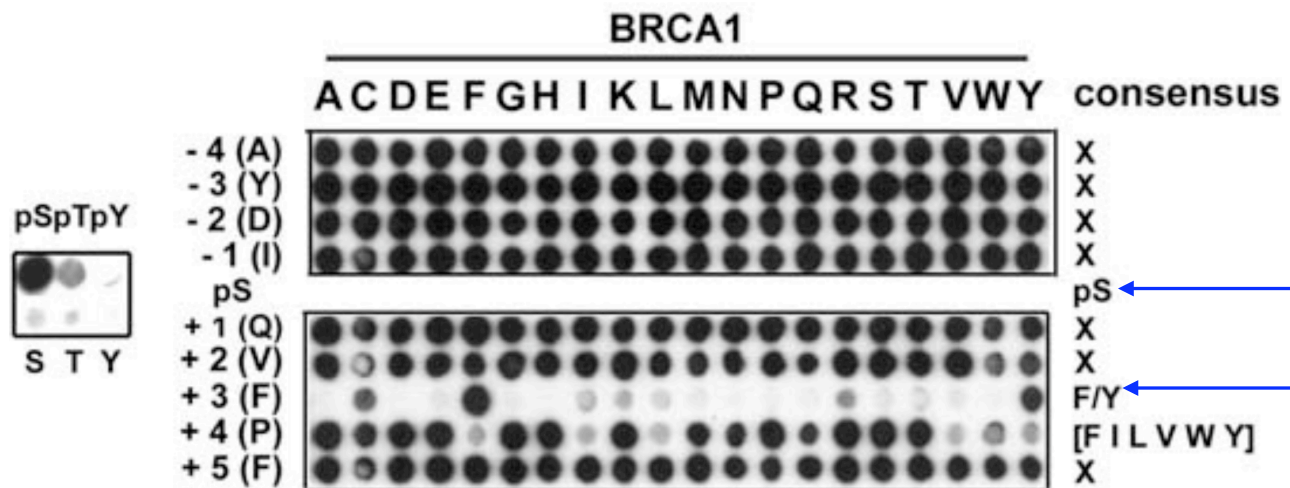
Tandem BRCT domains bind phosphoserine-modified proteins

In vitro optimized phosphopeptides:
ATM kinase pSQ targets

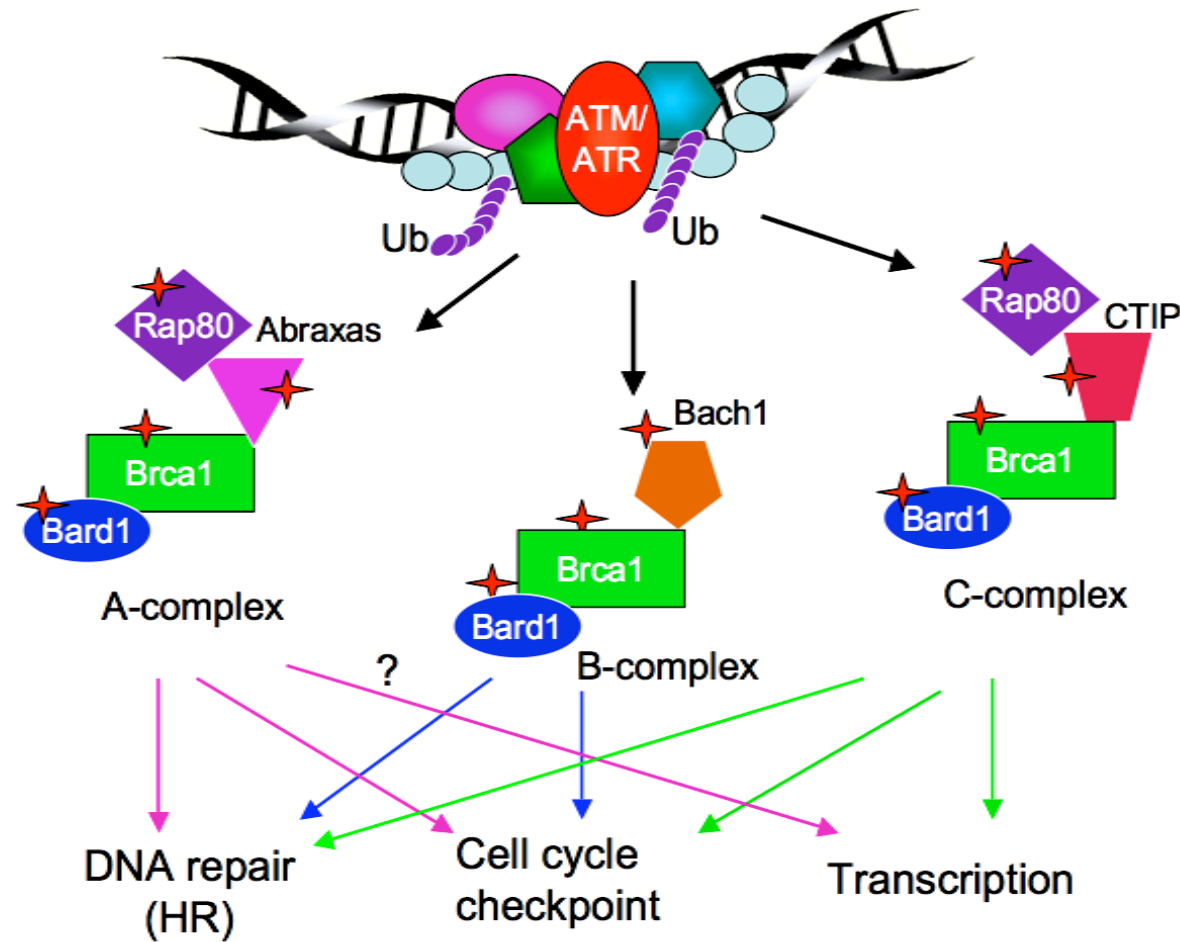
- BRCTtide: ...AYD

pS

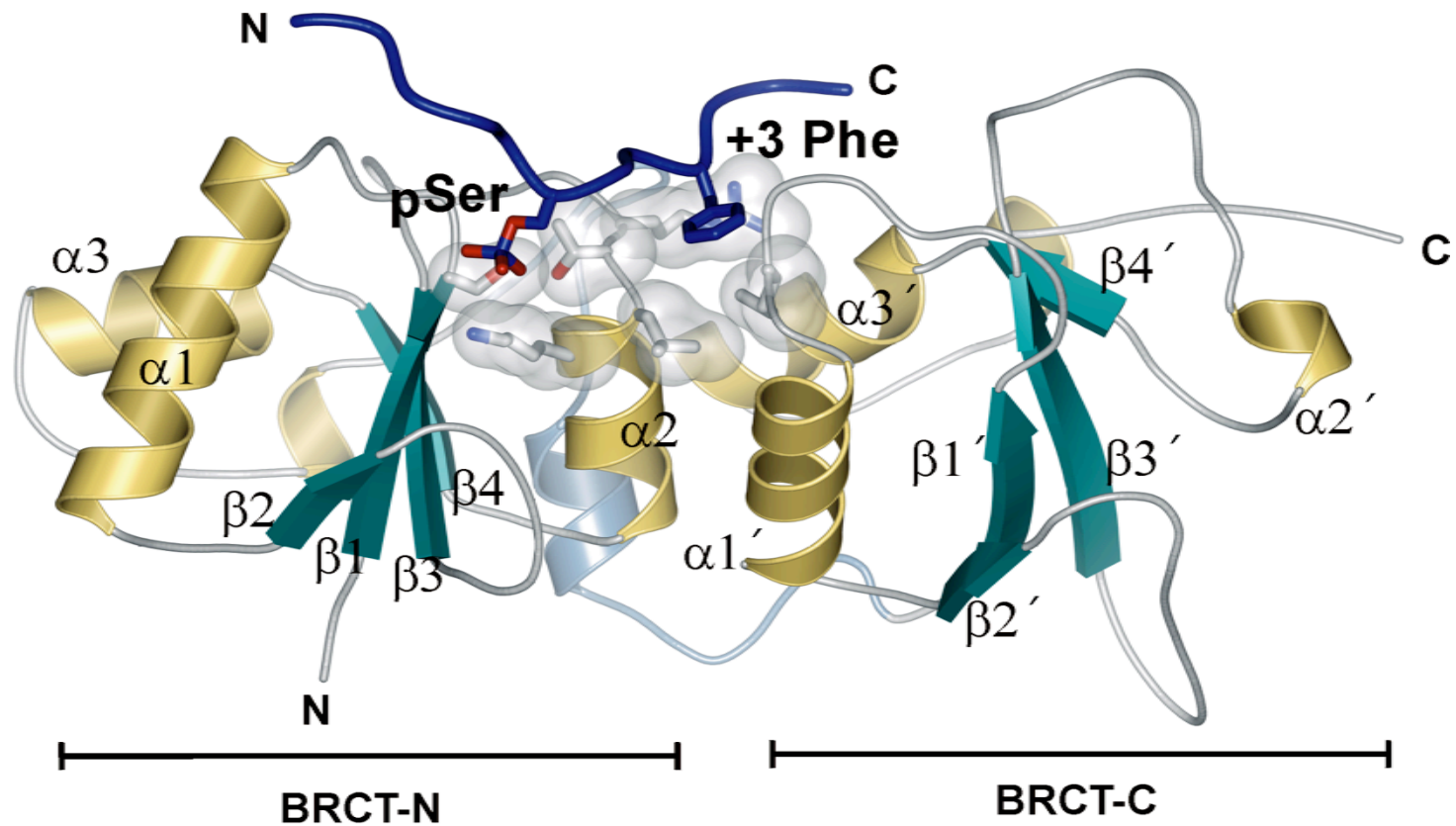
QVFPF...



BRCA1 BRCT interactions mediate BRCA1 integration into multiple protein complexes

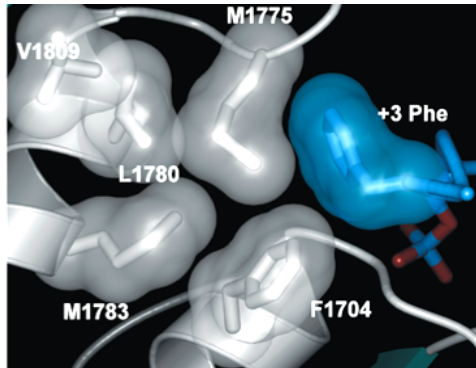


Structure of the hBRCA1-phosphoprotein complex

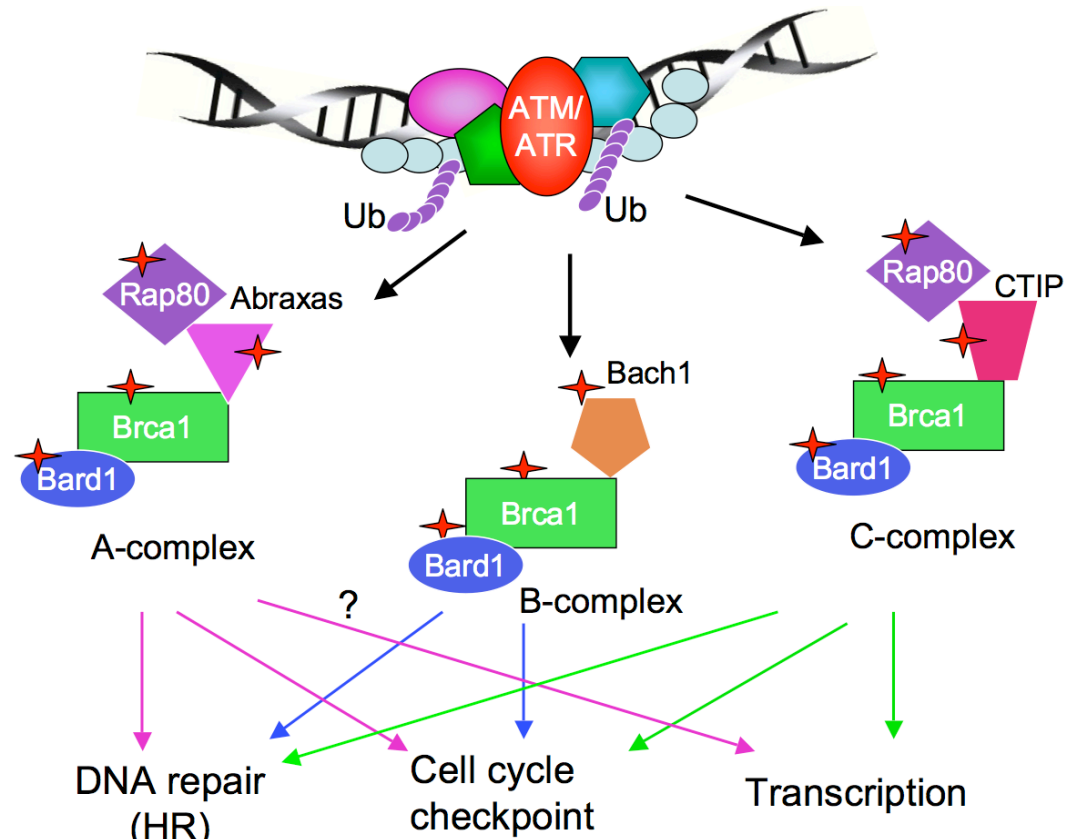
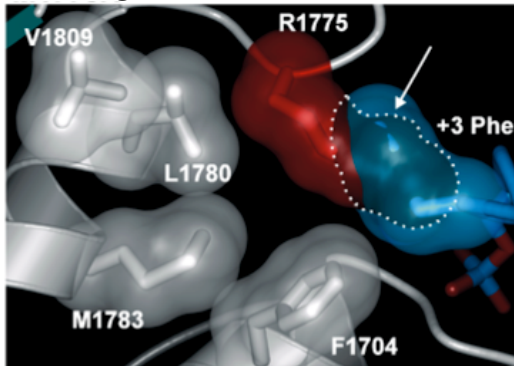


BRCA1 mutations occlude the phosphoprotein binding pocket

WT



M1775R



Wang et al Science, 2007

Questions:

Part 1.

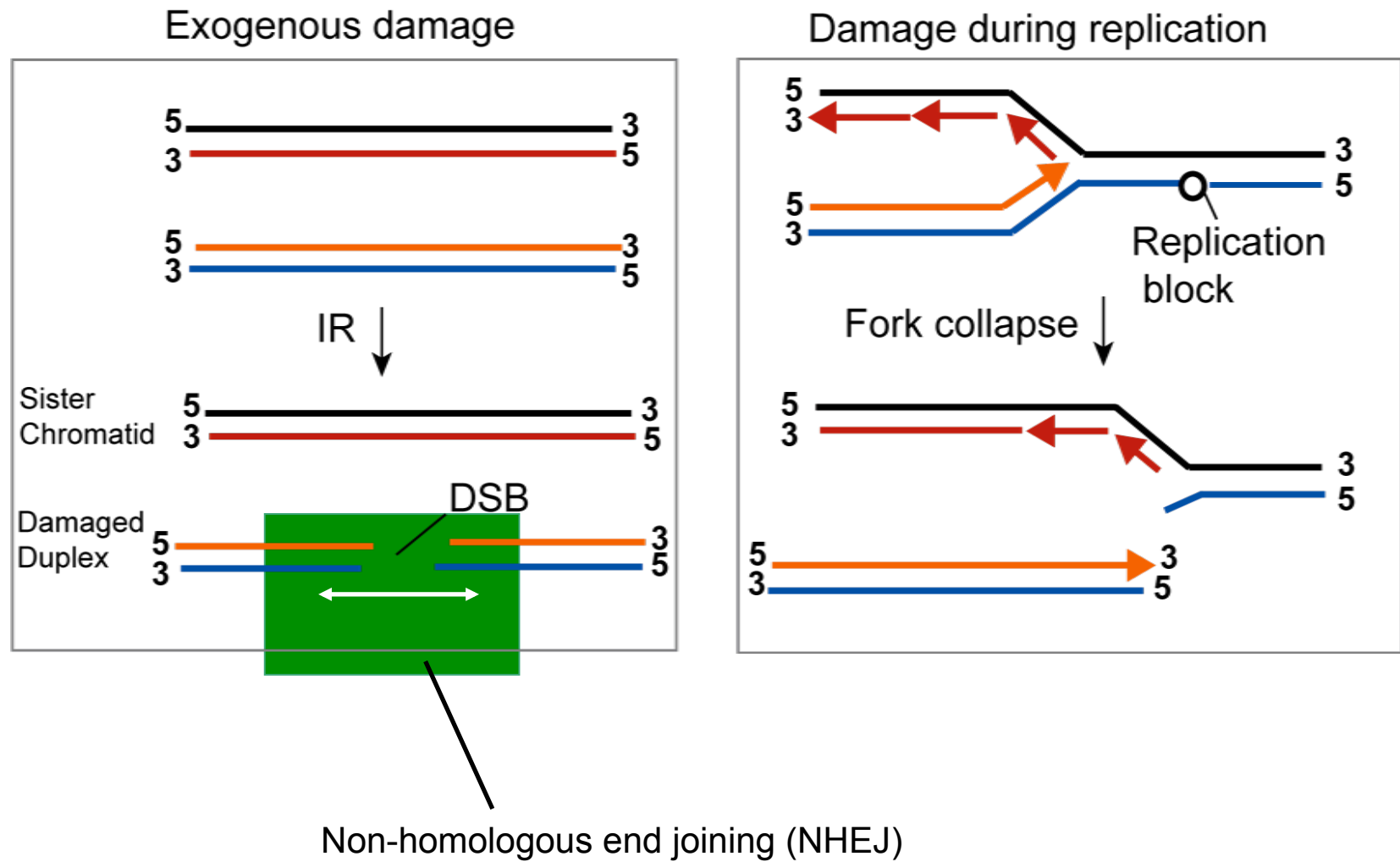
1. How do BRCT domains integrate into multidomain/multiprotein complexes?
2. Are BRCT phosphoprotein interactions regulated?
 - Structure/function studies of Nijmegen breakage syndrome protein Nbs1

Part 2.

How do BRCT proteins recognize unique targets?

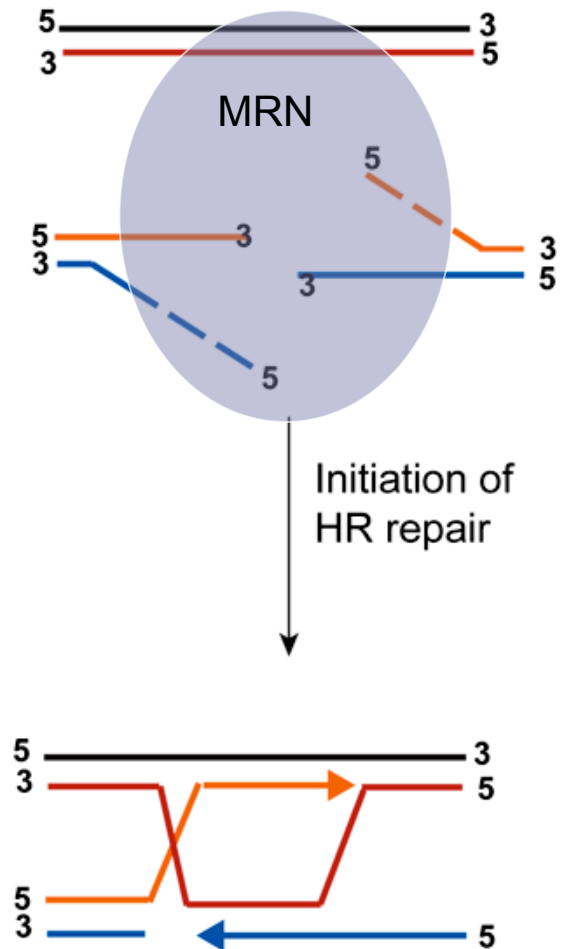
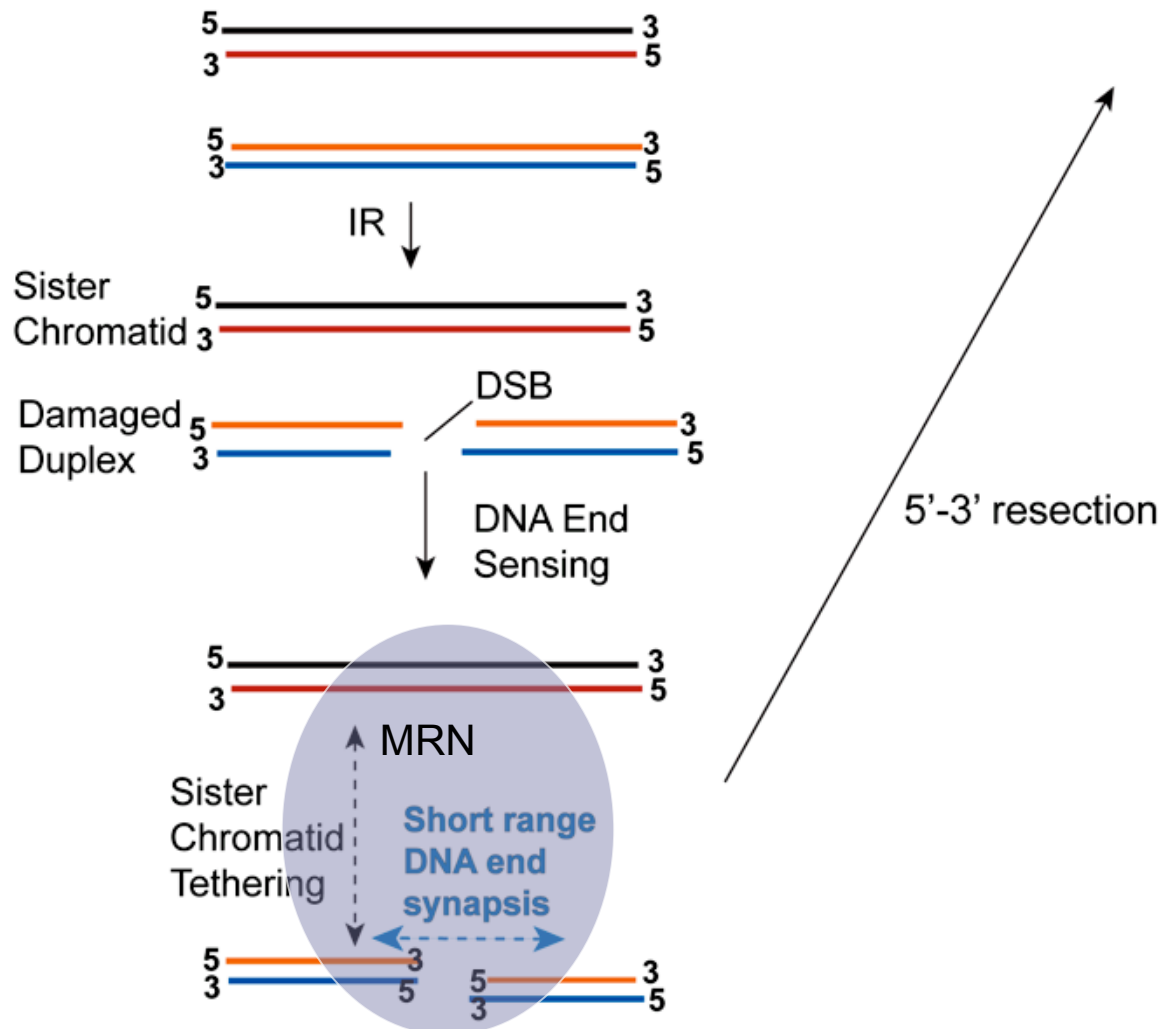
- Identification of a fission yeast S-phase phospho-H2A binding BRCT protein

DNA double strand breaks



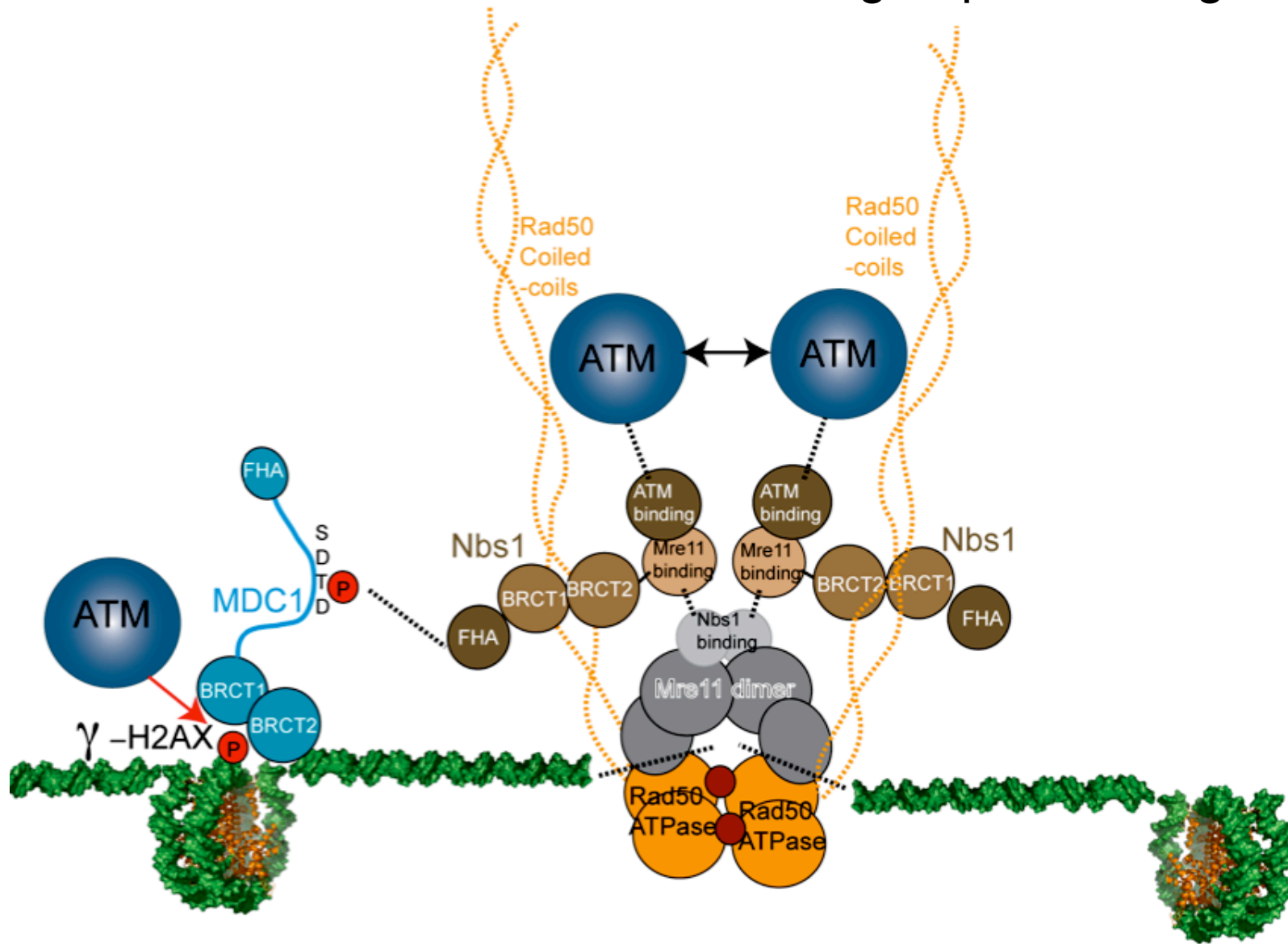
Homologous Recombination repair of DNA double strand breaks

2. Catalysis

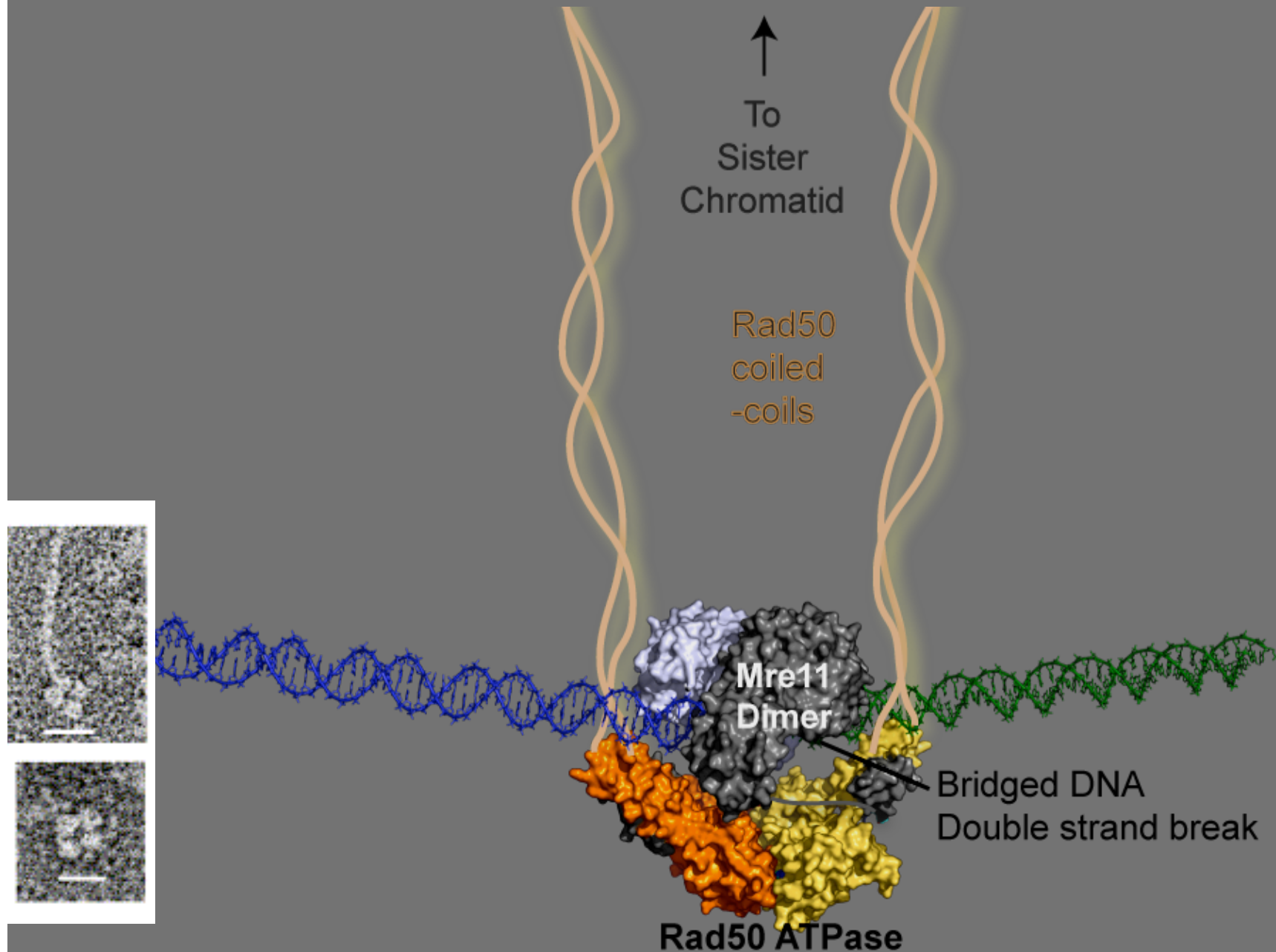


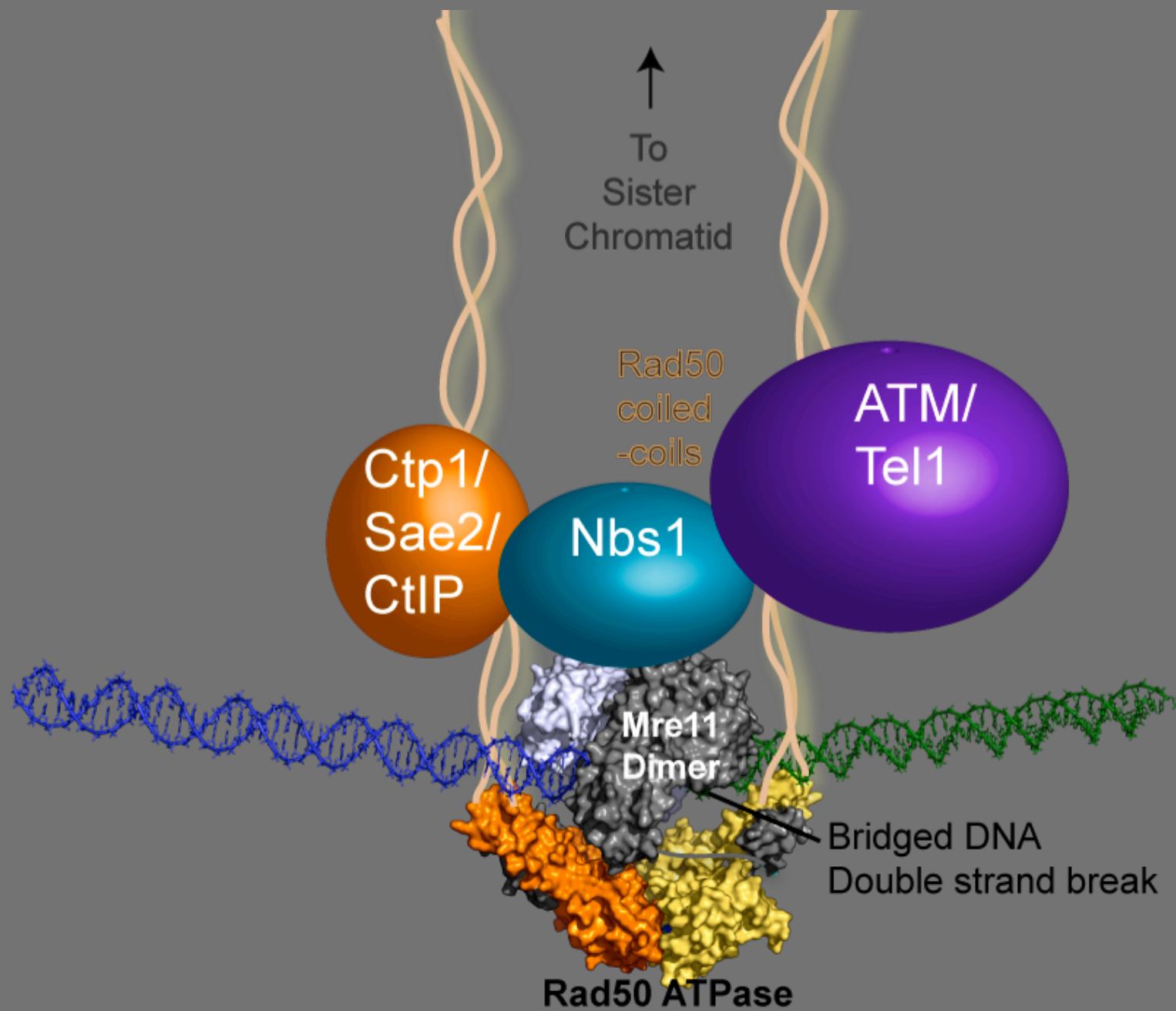
1. DNA Bridging Architecture

The Mre11/Rad50/Nbs1 complex integrates DNA double strand break sensing, repair and signaling



Composite Model of the Mre11-Rad50-DNA complex





Nijmegen Breakage Syndrome (NBS)

- Radiation sensitivity
- Immunodeficiency
- Strong predisposition to lymphoid malignancy
- Malignancies develop before patients are aged 20 years (mean age, 9 y).
- Cancer appears prior to the diagnosis of NBS in approximately 20-30% of patients.

Microcephaly



Preaxial polydactyly



Vitilego



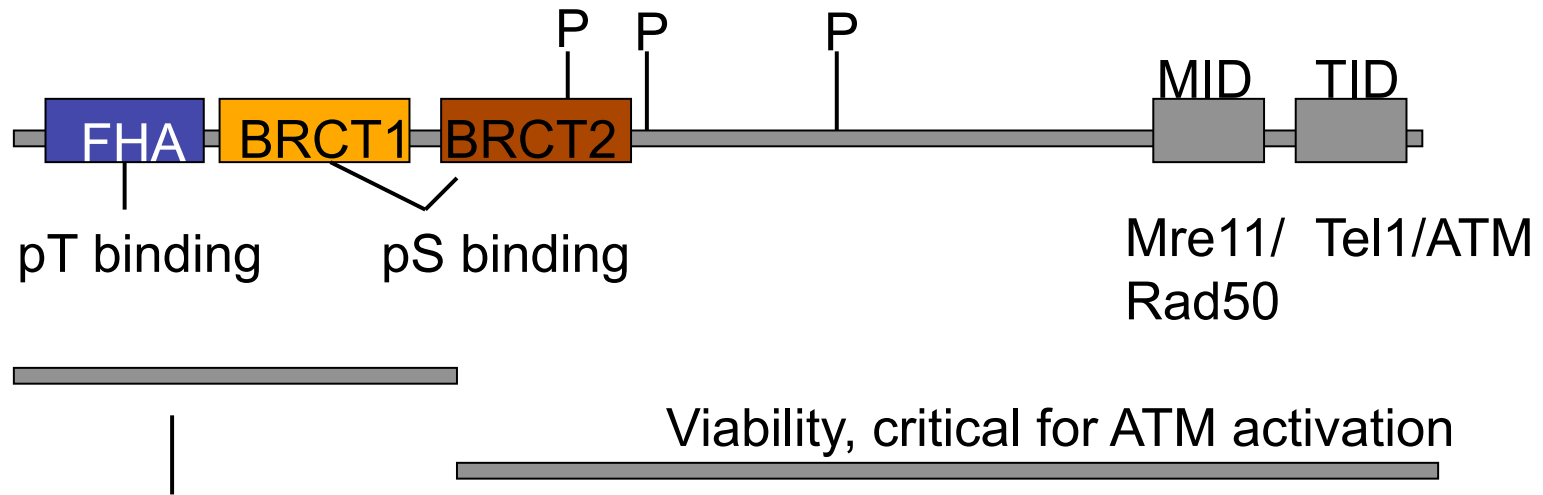
Cutaneous sarcoidosis



Cranio-facial abnormalities



Nbs1- domain architecture / interactions



- T-cell, oocyte development,
- Efficient damage signaling
- IRIF formation

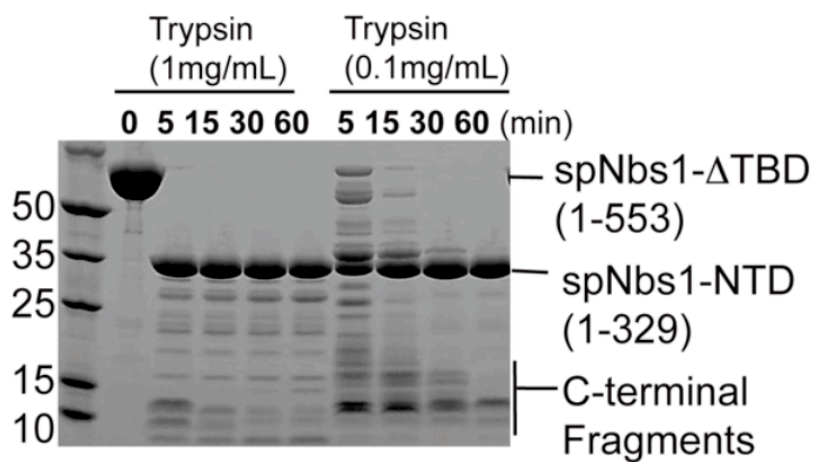
FHA, BRCT Binding targets:

-MDC1, CtIP

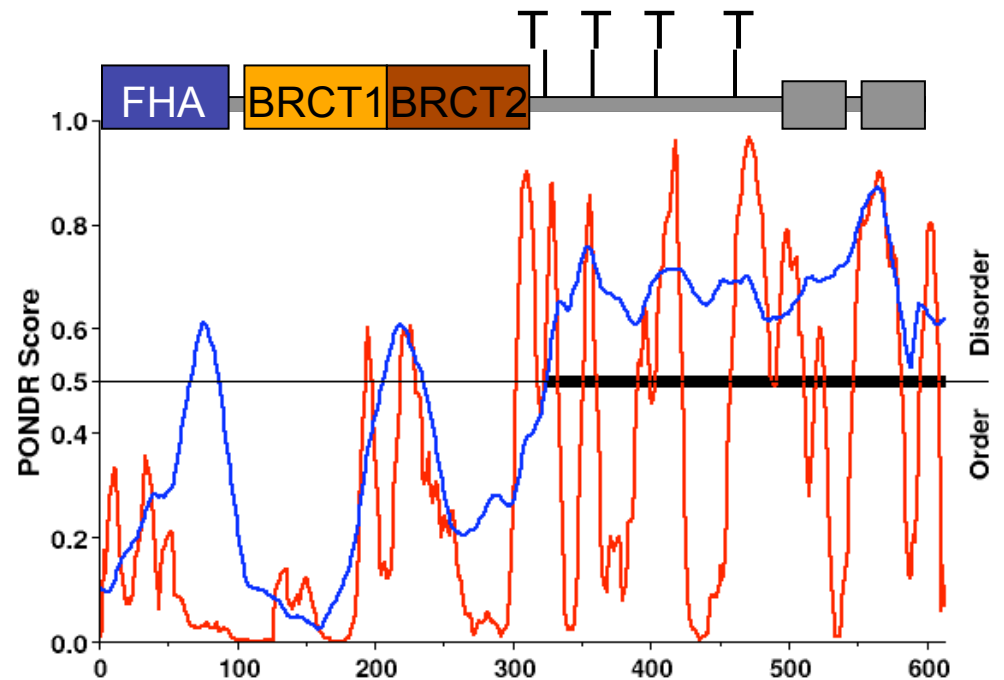
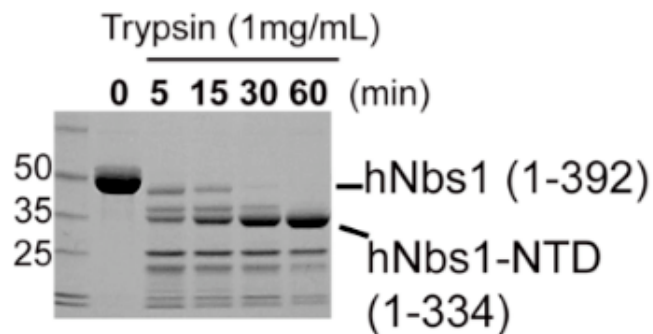
Mapping structured domains in Nbs1



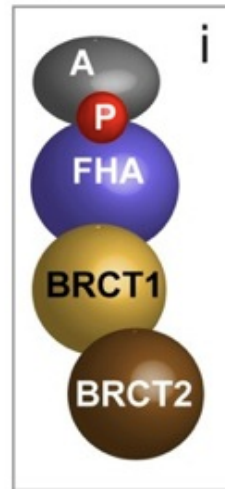
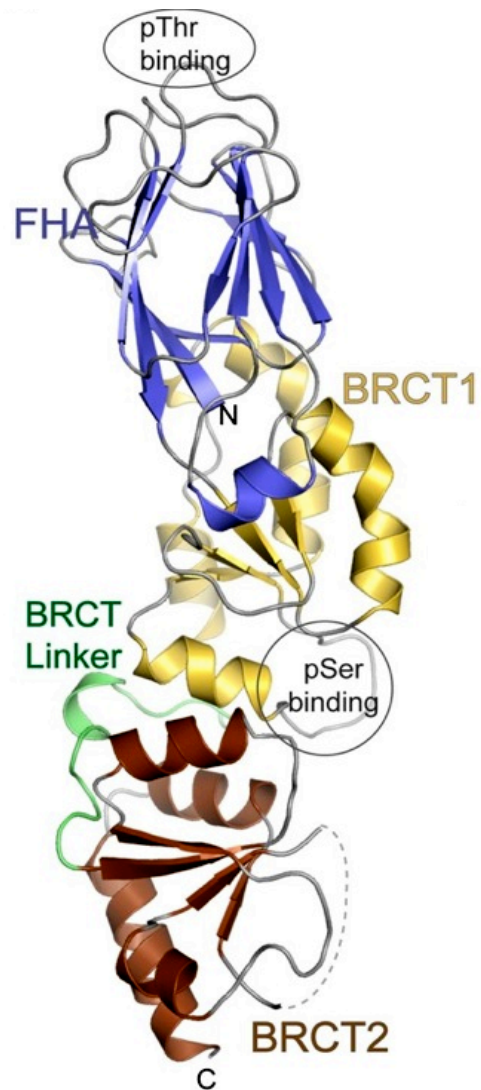
S. Pombe Nbs1



Human Nbs1



The Nbs1 N-terminus is a divalent phosphoprotein interaction scaffold



S. pombe FHA binding Targets???

hNbs1: hMDC1

scXrs2: Lif1

The Nbs1 FHA domain binds phosphorylated Ctp1

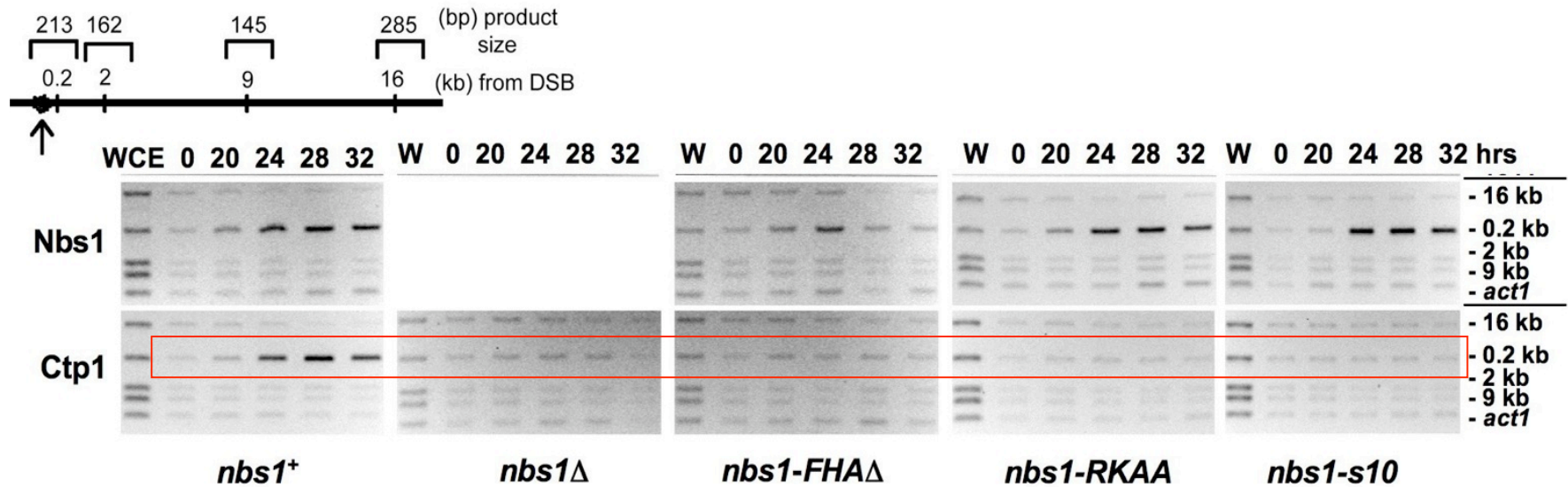
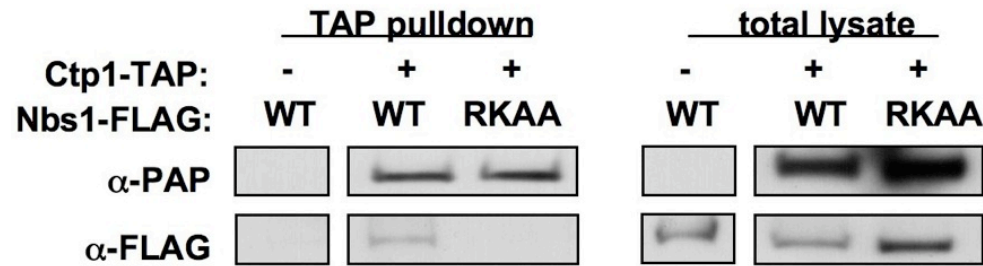
Ctp1-Nbs1

1. Ctp1 is a member of the MRN epistasis group.
2. Ctp1 is a high copy suppressor of Nbs1 FHA mutations
3. hCtIP co-IPs with MRN
4. Ctp1 is phosphorylated

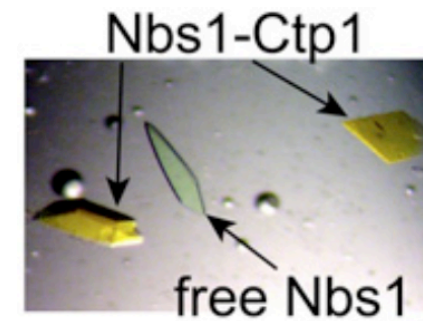
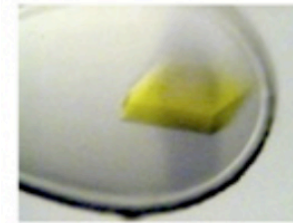
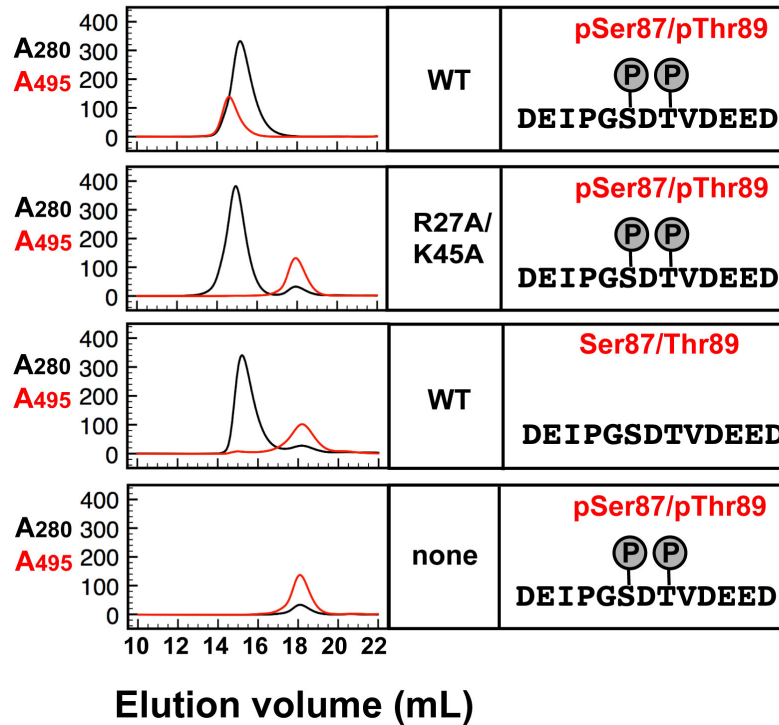


hMdc1	215-NLNSDTDVEE
hMdc1	296-GEDSDTDVDD
hMdc1	326-FIDSDTDAEE
hMdc1	373-QAGSDTDVEE
hMdc1	399-VINSDTDDEE
hMdc1	450-ERDSDTDVEE
spCtp1	74-ELD STT DEDE
spCtp1	84-IPGSDTVDEE
scLif1	384-GSESETDASA
scLif1	414-QTESETDIET

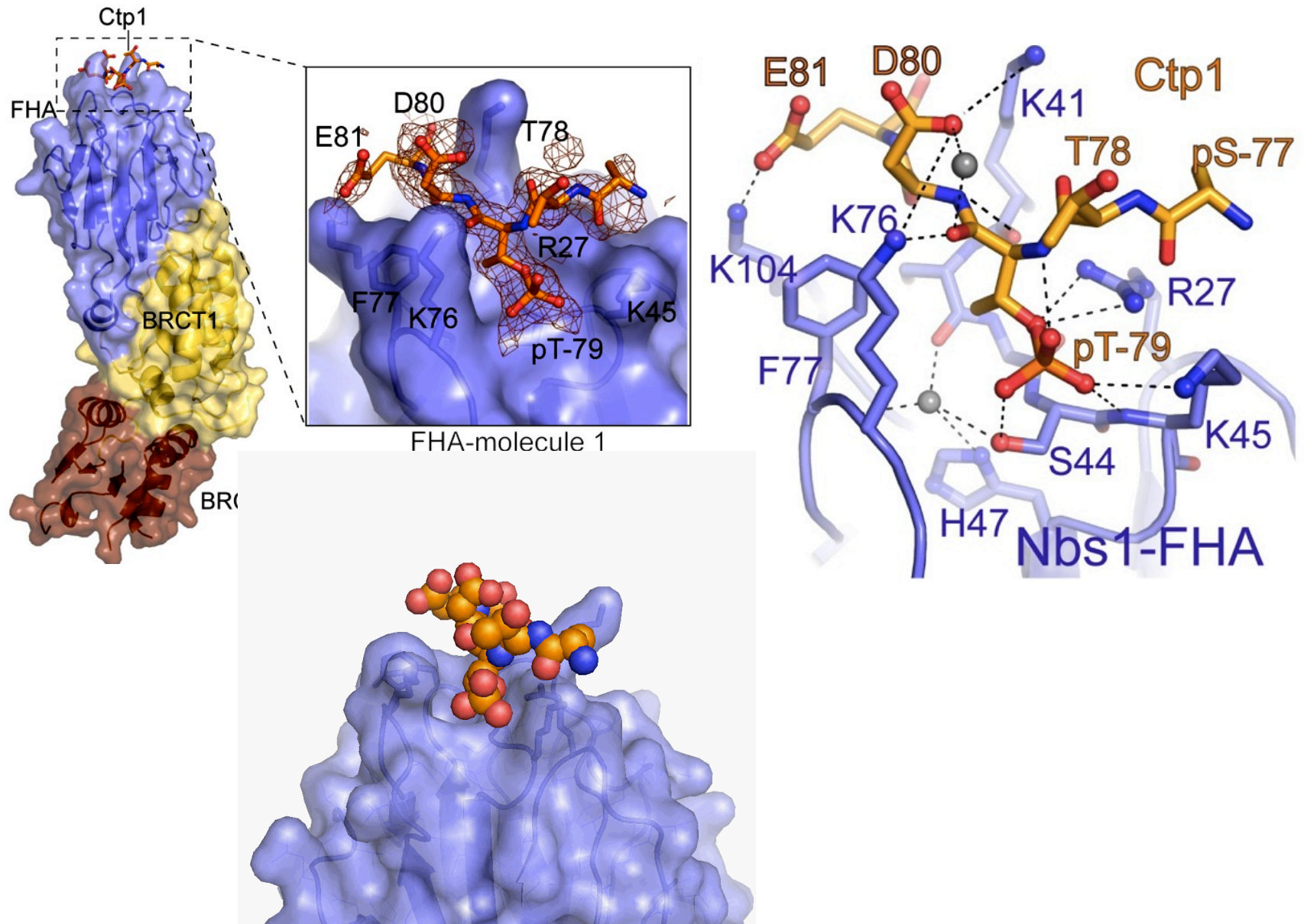
FHA domain mutations in Nbs1 impair Ctp1 recruitment to a DSB



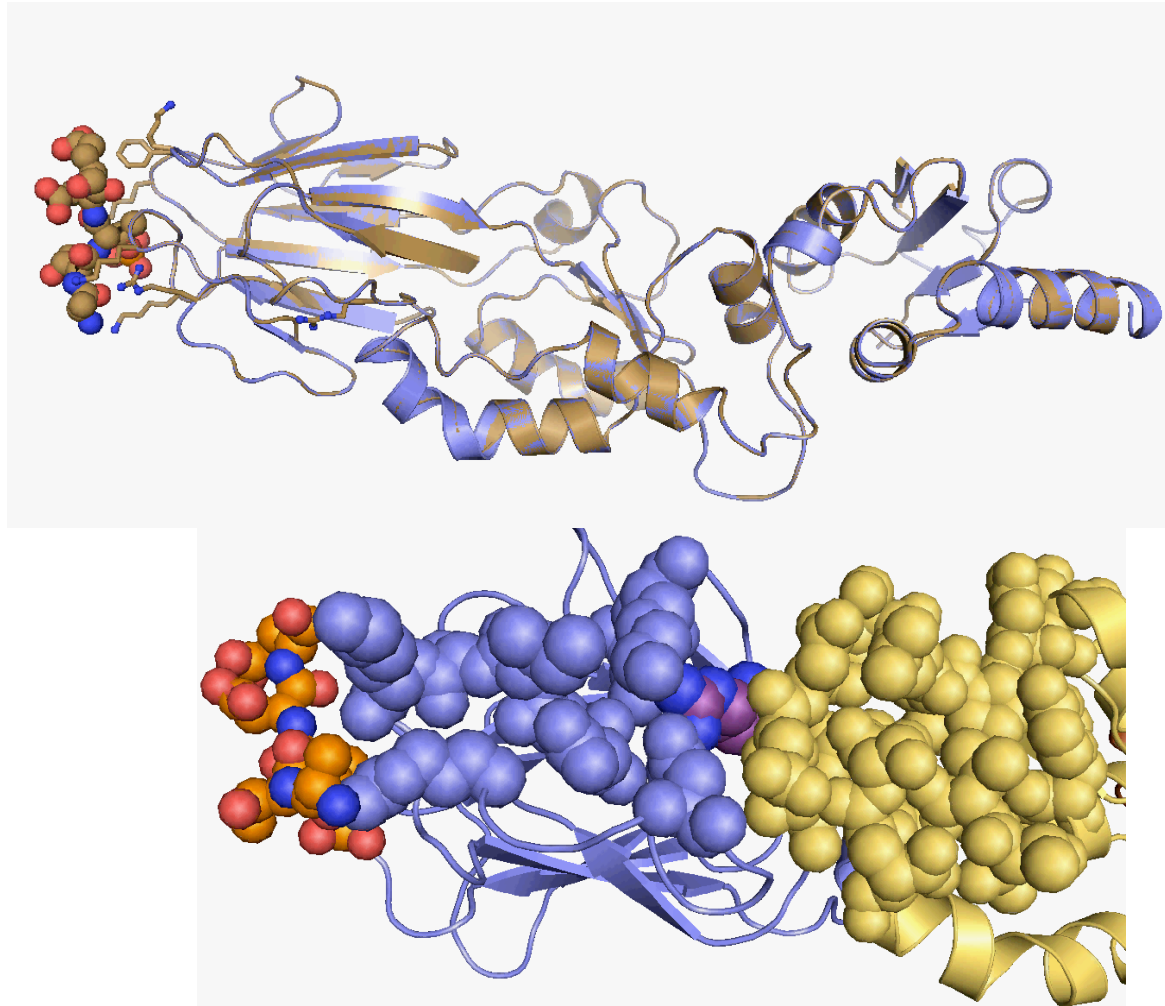
The Nbs1 FHA domain binds phosphorylated Ctp1



X-ray Structure of the Nbs1-Ctp1 complex

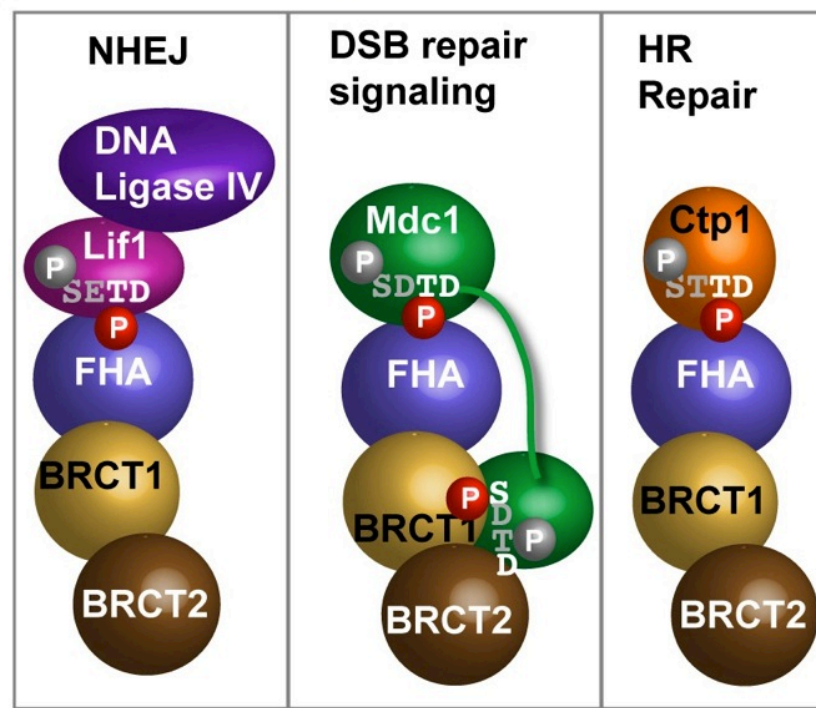


Ctp1-binding in the FHA modulates tandem BRCT conformations



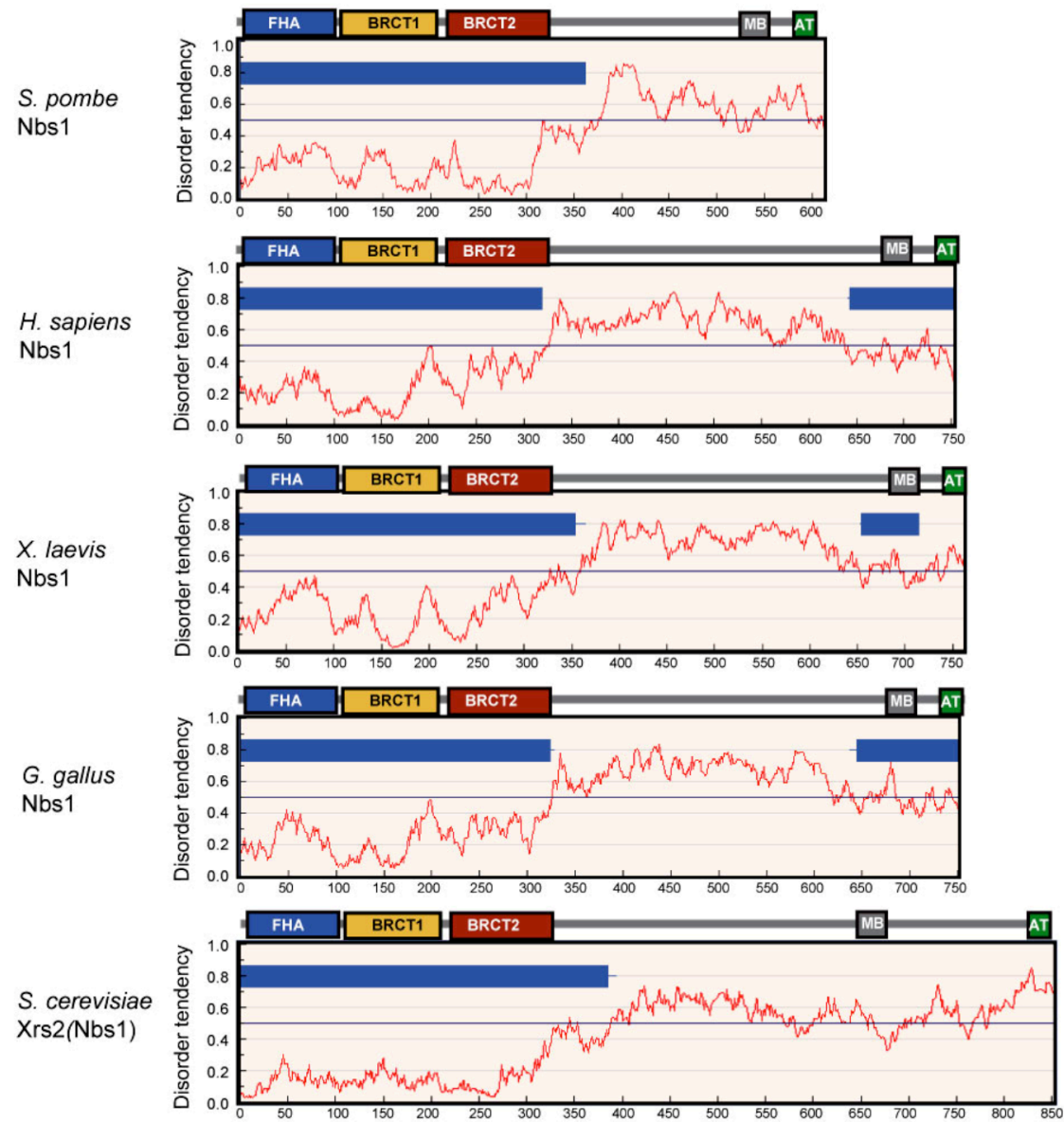
Hypothesis: FHA phosphoprotein interactions can allosterically regulate interactions in the BRCT domains of Nbs1

Nbs1 docks with multiple partners to regulate DSB repair

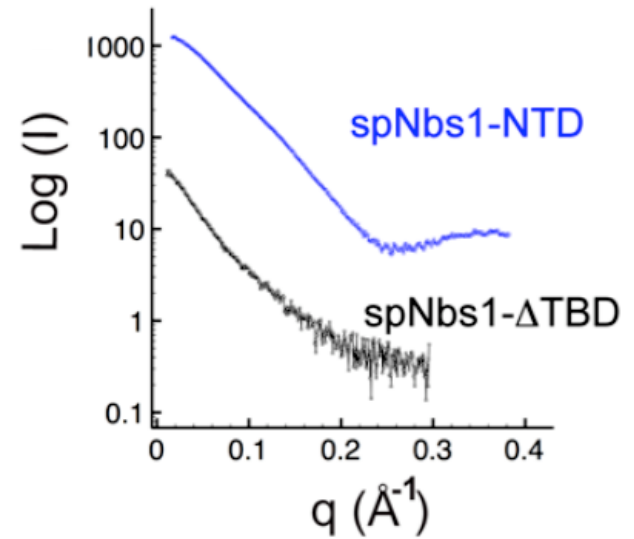
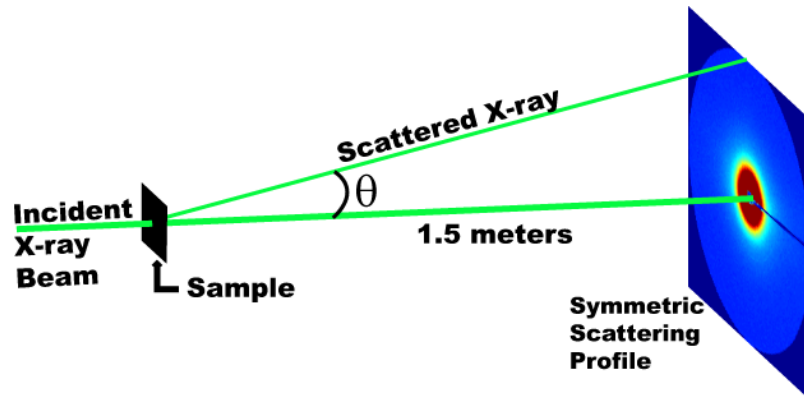


Partnering of Tandem BRCTs with an FHA expands the Nbs1 regulatory repertoire

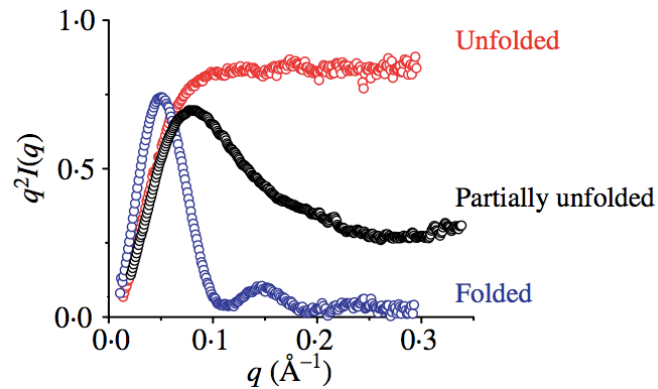
Protein order/disorder predictions for Nbs1 homologs



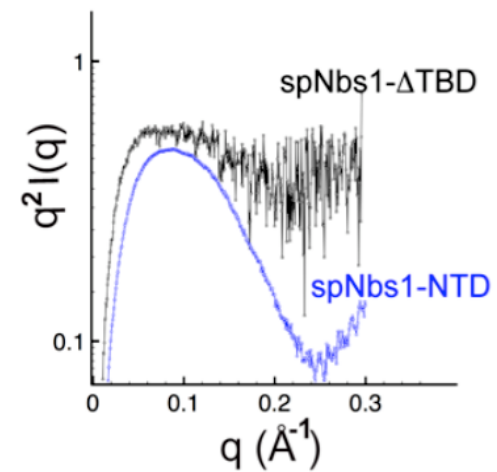
The Nbs1 C-terminal region is flexible



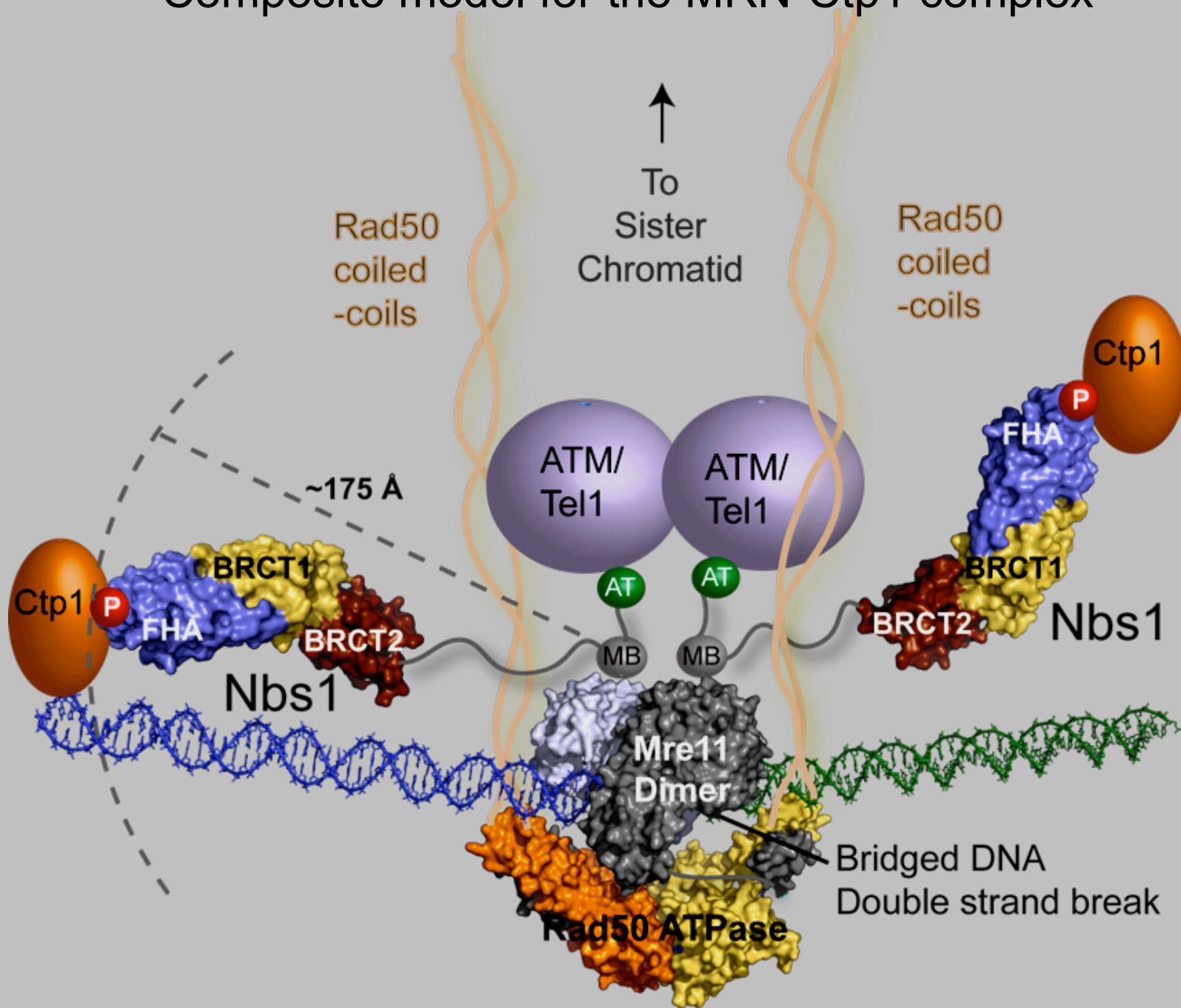
↓ Kratky plot



↓ Kratky plot



Composite model for the MRN-Ctp1 complex



Some answers to the Questions ...

Part 1.

A. How do BRCT domains integrate into multidomain/multiprotein complexes?

- Fusion of BRCTs with an FHA expands the substrate binding repertoire of Nbs1
- FHA/BRCTs of Nbs1 flexibly link to enzymatic DSB repair effectors

B. Are BRCT phosphoprotein interactions regulated?

- Possibly. The FHA-BRCT fusion provides a mechanism for allosteric regulation of phosphoprotein binding function

Part 2.

How do BRCT proteins recognize unique targets?

- Identification of a fission yeast S-phase phospho-H2A binding BRCT protein

hBRCA1(BACH1 CtIP)

hMDC1- γ H2AX

pSxxF
pSxxY

pSxxY(coo-)

NOT

NOT
pSxxL

pSxxF(coo-)
pSxxL(coo-)

What about yeast γ H2A BRCT effectors?

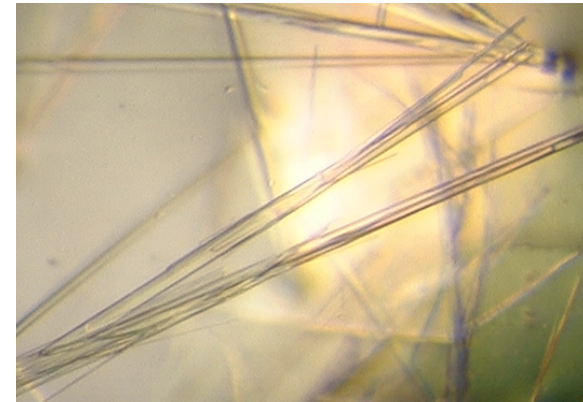
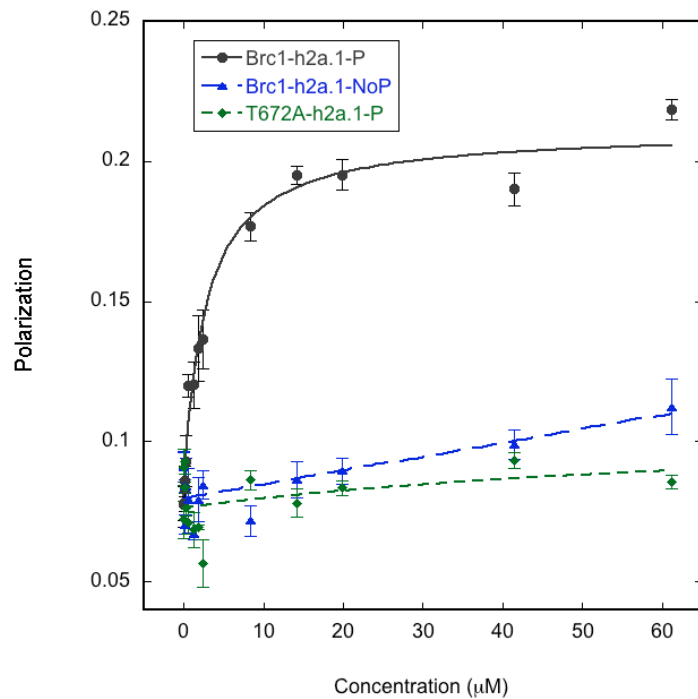
human H2AX	LPNIQAVLLPKKTSATVGPKAPSGGKKATQASQ	EY
mouse H2AX	LPNIQAVLLPKKSSATVGPKAPAVGKKASQASQ	EY
<i>T. thermophila</i> H2A.1	LPNINPMLLPKSKKTESRG-----QASQ	DL
<i>S. cerevisiae</i> H2A.1	LPNIHQNLLPKKSAKATKA-----SQ	EL
<i>S. cerevisiae</i> H2A.2	LPNIHQNLLPKKSAKTAKA-----SQ	EL
<i>S. pombe</i> H2A.1	VPNINAHLLPKTSGRTGKP-----SQ	EL
<i>S. pombe</i> H2A.2	VPNINAHLLPKQSGK-GKP-----SQ	EL

S. pombe Brc1

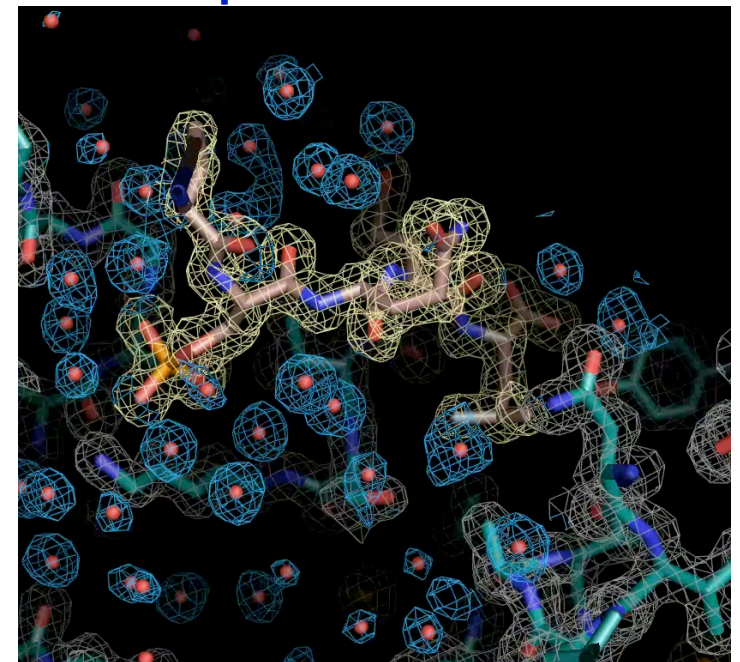
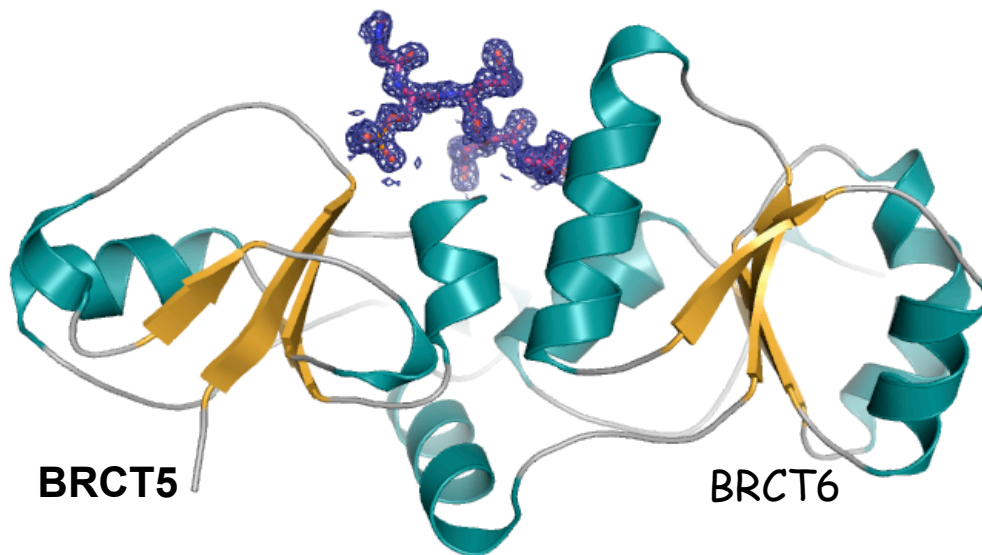


- Brc1^{Rtt107/PTIP} forms spontaneous and DNA damage-induced nuclear foci by binding γ H2A.
- Brc1 foci colocalize predominantly with ribosomal DNA repeats
- DNA damage-induced foci colocalize with DSB response factors. The Brc1- γ H2A interaction is critical for recovery from replication fork collapse.
- Brc1 docking to γ H2A is a critical chromatin-specific response to replication-associated DNA damage.

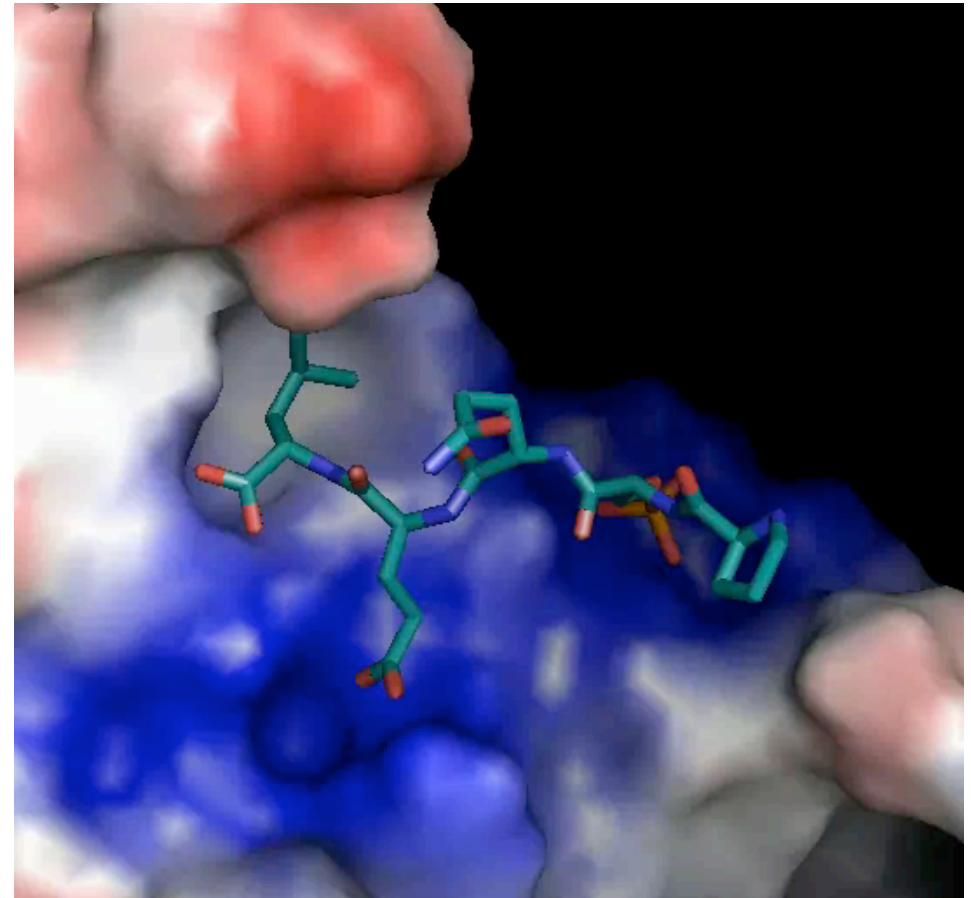
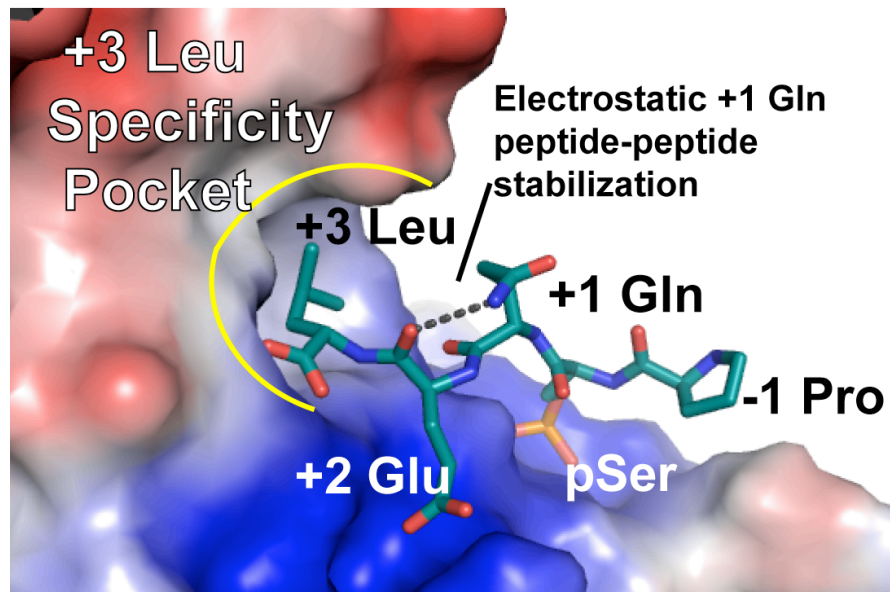
BRC1 directly binds the SpH2A.1 phosphorylated tail



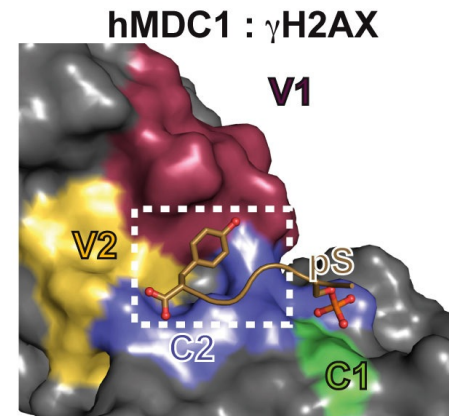
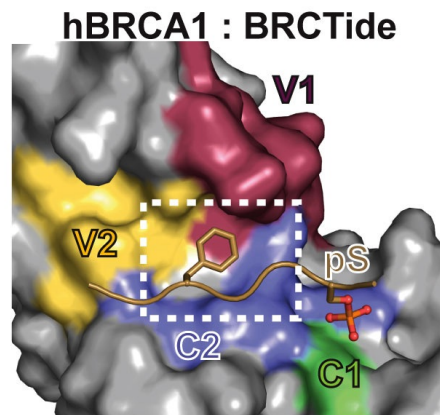
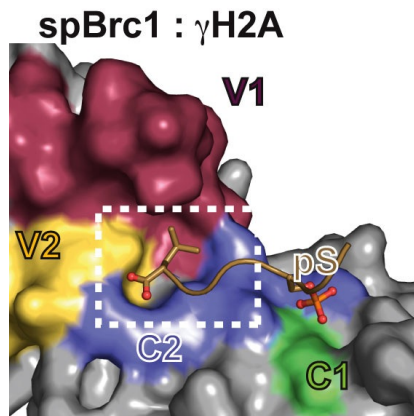
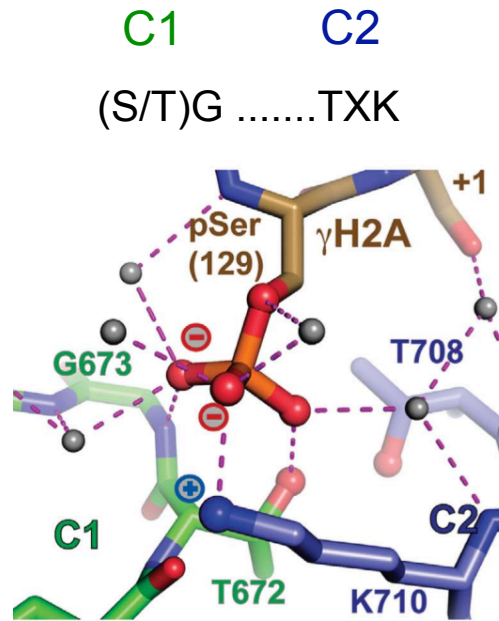
**BRC1:phospho-H2A.1
complex at 1.45 Å**



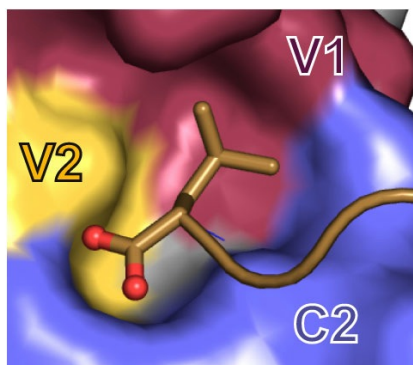
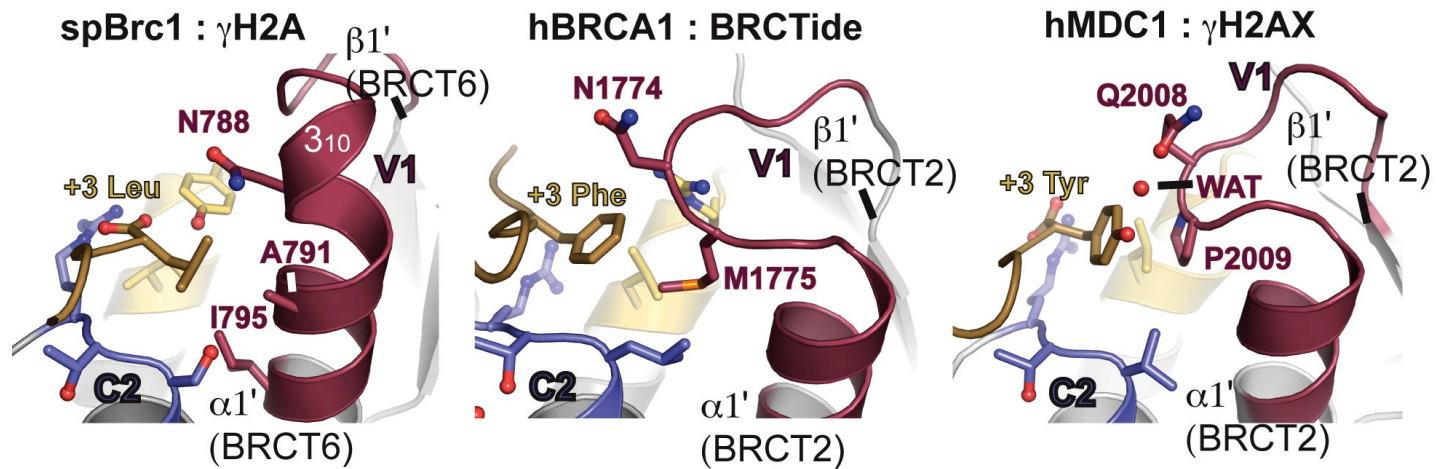
Specificity of the Brc1 BRCT5-6: phospho-H2A.1 complex



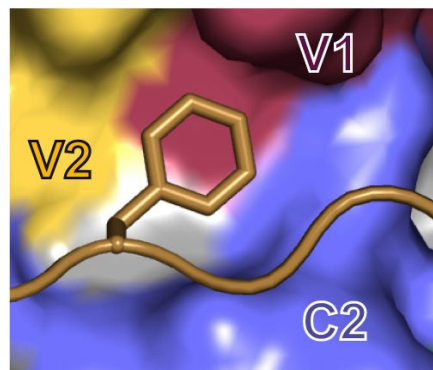
Constant regions bind pSer, Variable regions bind pSer +3



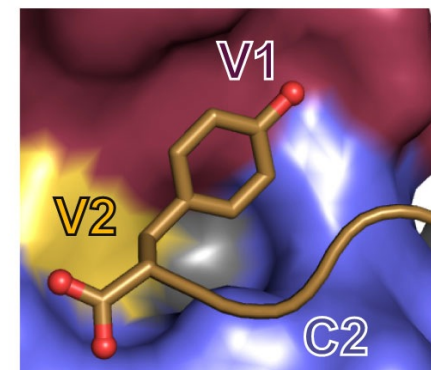
Variability of V1 loops dictates pSer +3 binding specificity



pSxxL (coo-)



....pSxxF ...



....pSxxY (coo-)

Some answers to the Questions ...

Part 1.

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- Fusion of BRCTs with an FHA expands the substrate binding repertoire of Nbs1
- FHA/BRCTs of Nbs1 flexibly link to enzymatic DSB repair effectors

B. Are BRCT phosphoprotein interactions regulated?

- Possibly. The FHA-BRCT fusion provides a mechanism for allosteric regulation of phosphoprotein binding function

Part 2.

A. How do BRCT proteins recognize unique targets?

- BRCTs utilize a two-point specificity
 - Two constant regions bind pSer
 - Variable sequence/structural insertions dictate binding specificity at pSer +3

Acknowledgements



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Percy Tumbale



Denise Appel



Patrick Robertson



Tainer Lab

(Scripps)

John Tainer

Grant Guenther

Russell Lab

Jessica Williams

Gerry Dodson

Oliver Limbo