

Supplemental Information

Architecture and DNA Recognition Elements of the Fanconi Anemia FANCM-FAAP24 Complex

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Inventory of Supplemental Information

Supplementary Figure S1. Electron density and structure B-factors.

[Links to Results.](#)

Supplementary Figure S2. Comparison of protein binding functions for FANCM (HhH)₂ domain and DNA binding for FAAP24 (HhH)₂ domain.

[Links to Figure 2](#)

Supplementary Figure 3. Heterodimeric interfaces within the FANCM_{CTD}FAAP24 complex

[Links to Results.](#)

Supplementary Figure 4. Comparison of FANCM metal-ion ligands to those of A.pernix XPF and BamH1 bound to cognate DNA.

[Links to Figure 4.](#)

Supplementary Figure 5. Structural comparison of monomeric FAAP24-(HhH)₂ with heterodimeric FANCM_{CTD}-FAAP24-(HhH)₂.

[Links to Results.](#)

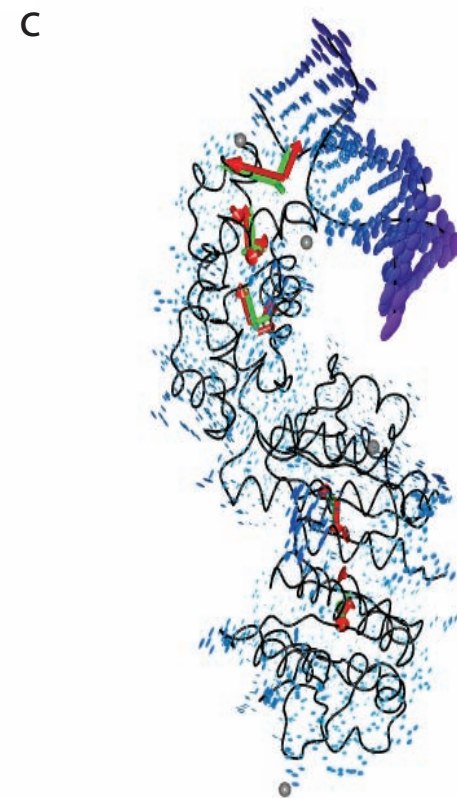
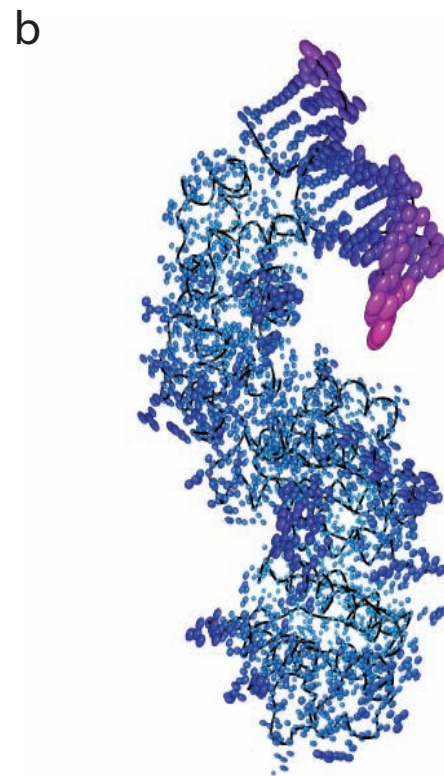
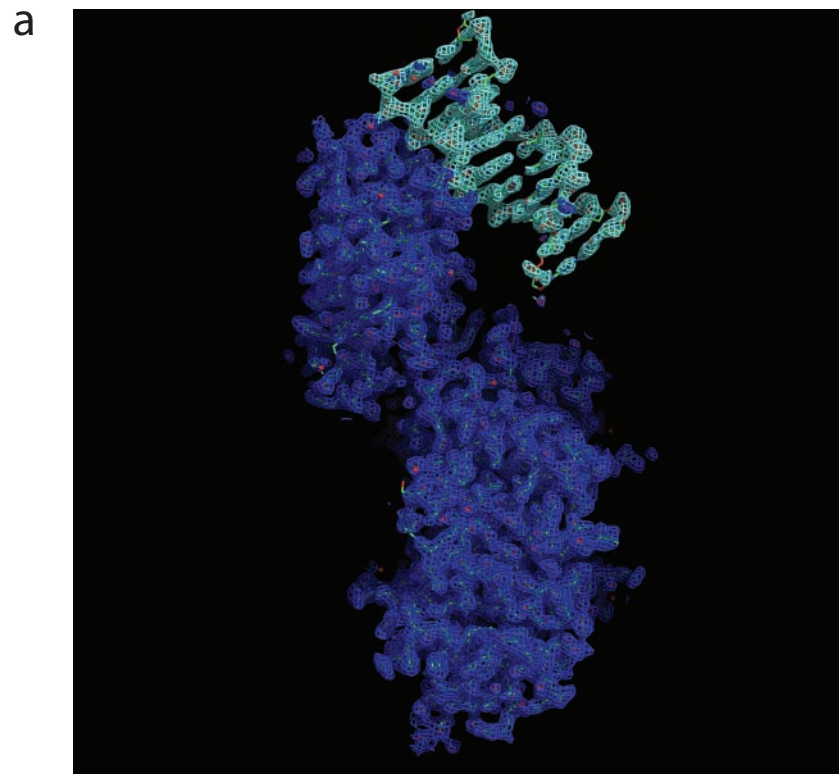
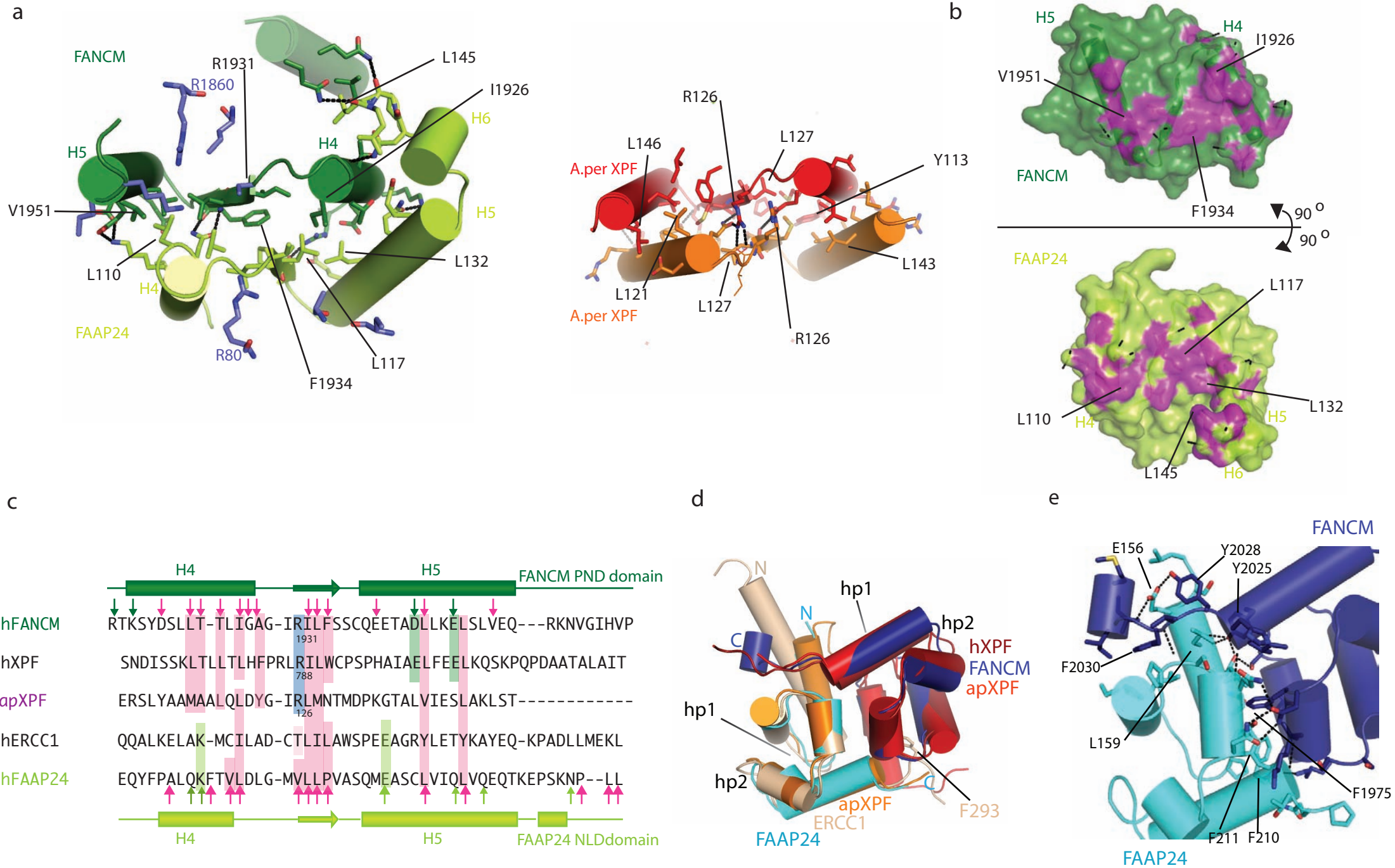
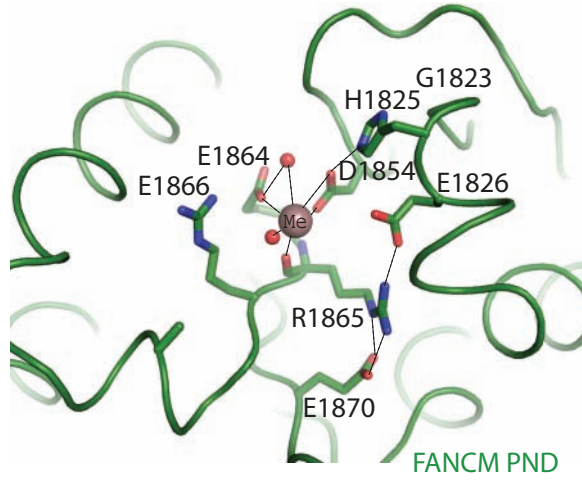


Figure S3

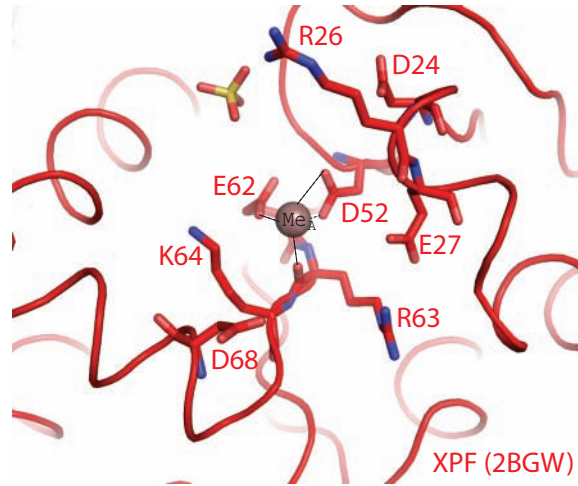
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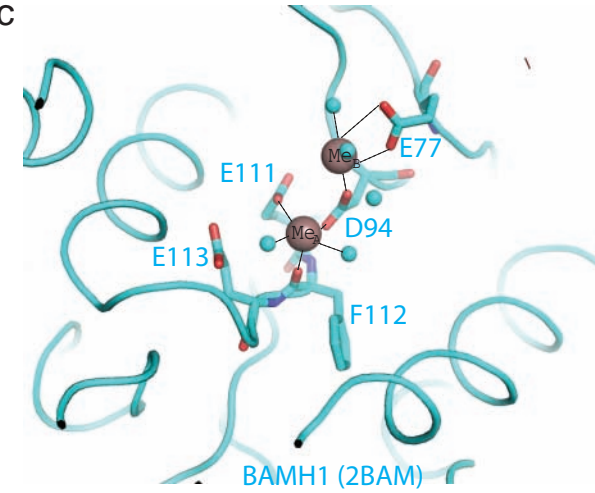
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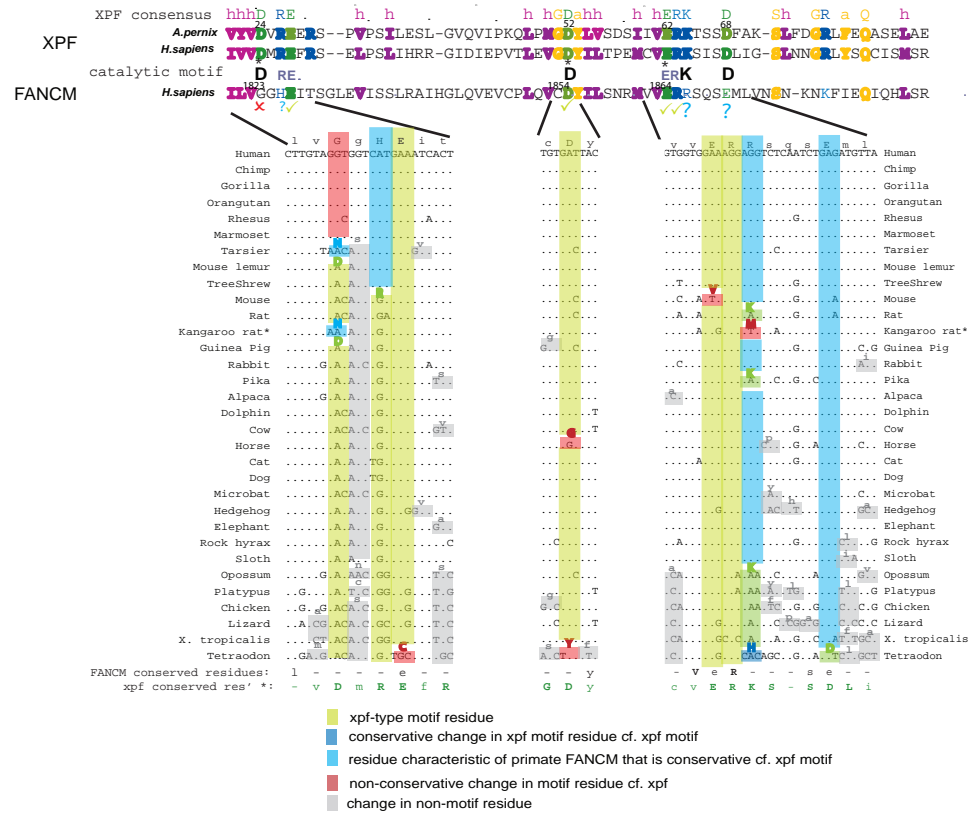
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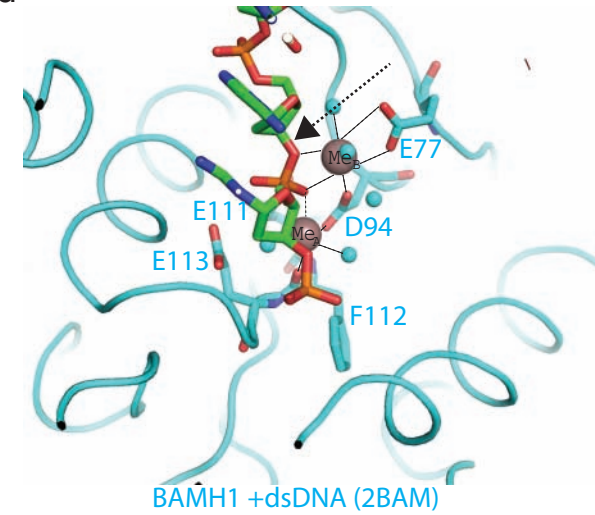
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e



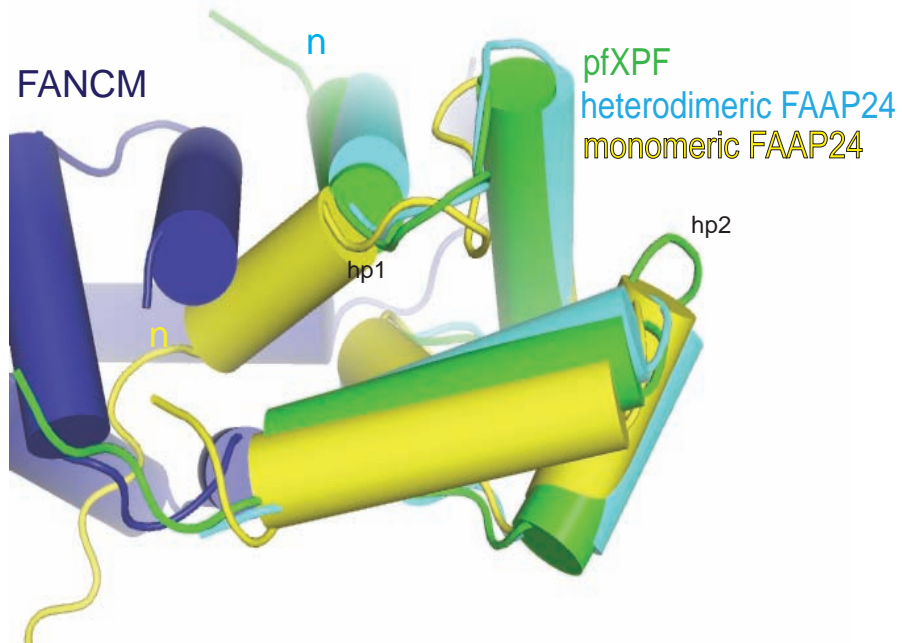
d



a

input \ aligned with		FAAP24 monomer	pfXPF	apXPF	hXPF	ERCC1	RuvA	DNA pol-iota
heterodimeric FAAP24	aligned PDB	2LHY	1x2i-B	2bhn-A	2kn7-A	1z00-B	1d8l-A	3epg
	Z-score	4.4	11.8	9.9	10	8.4	7.2	6.4
	rmsd (Å)	2.3	0.9	1.1	1.5	1.6	2.4	2.1
	% seq identity	100	30	28	23	23	26	31
	aligned residues	51	60	60	60	60	58	52
FAAP24 monomer	aligned PDB		zx2i-A	2bgw-A	2a1j-A	1z00-B	2ztd-B	4ebd
	Z-score		4.9	4.4	4.2	3.6	2.1	2.9
	rmsd (Å)		2	10.4	2.9	2.7	3	8.5
	% seq identity		33	26	25	24	22	23
	aligned residues		52	62	53	55	55	71

b



c

