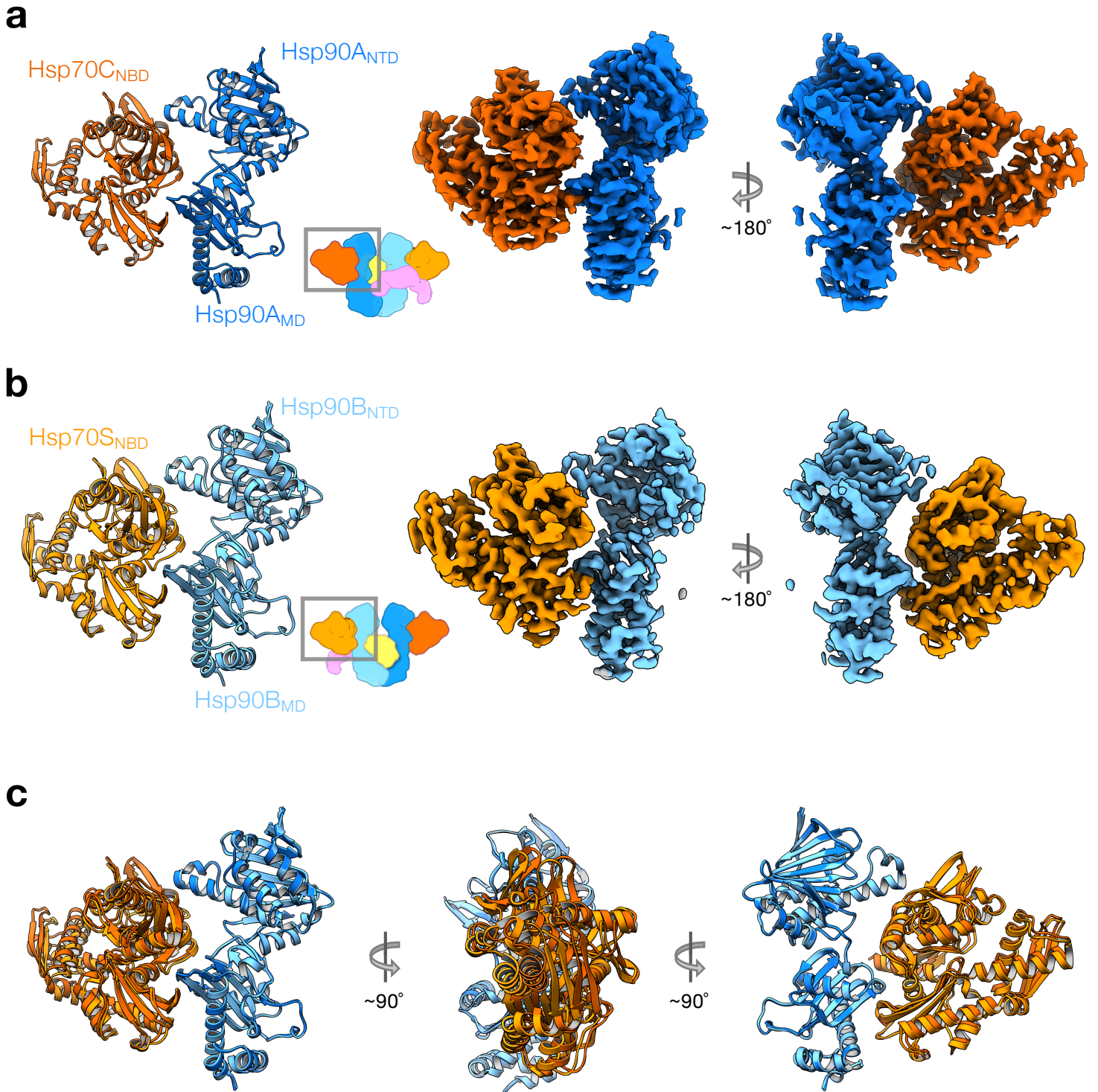


Supplementary Fig. 1



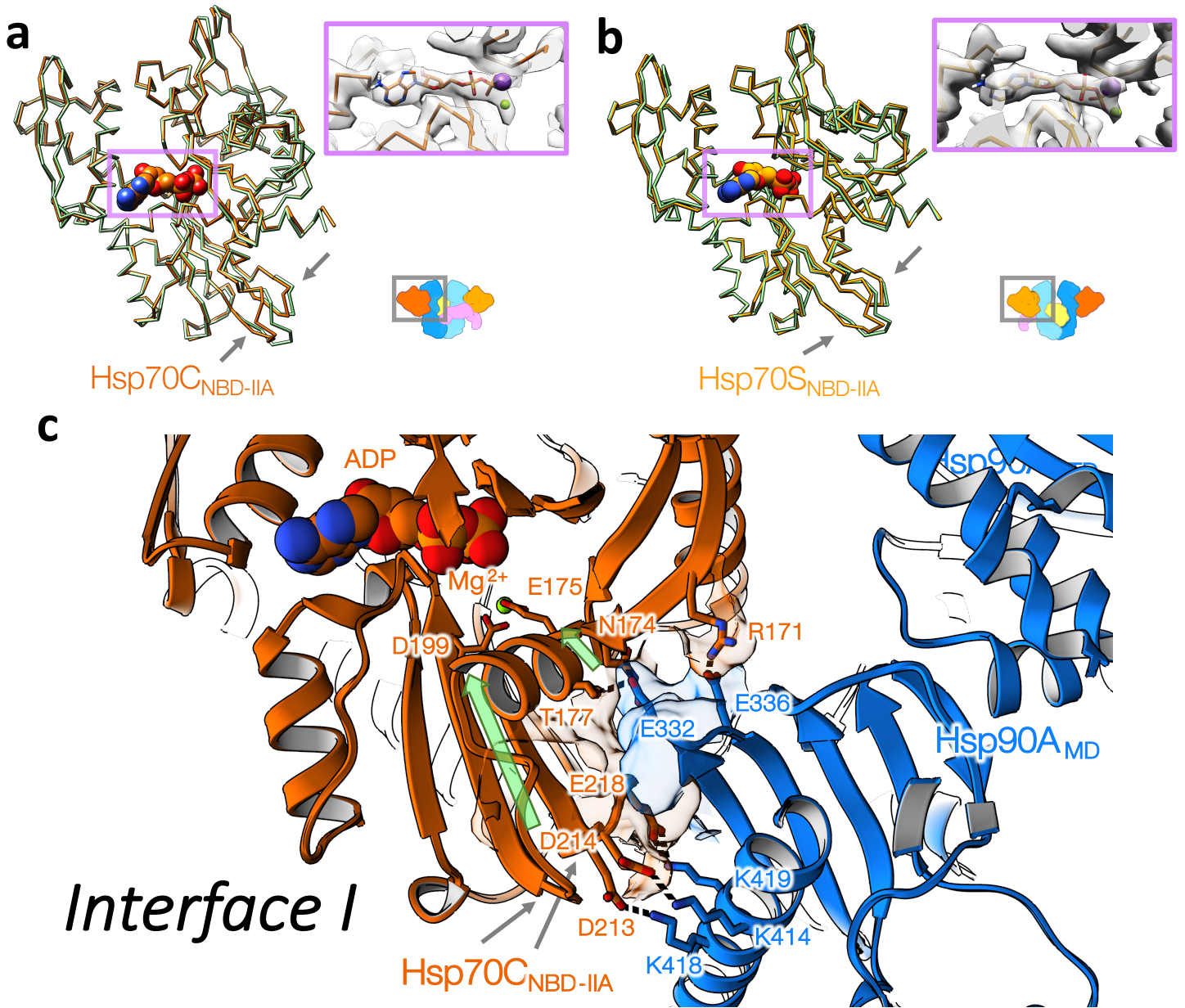


# Supplementary Fig. 2

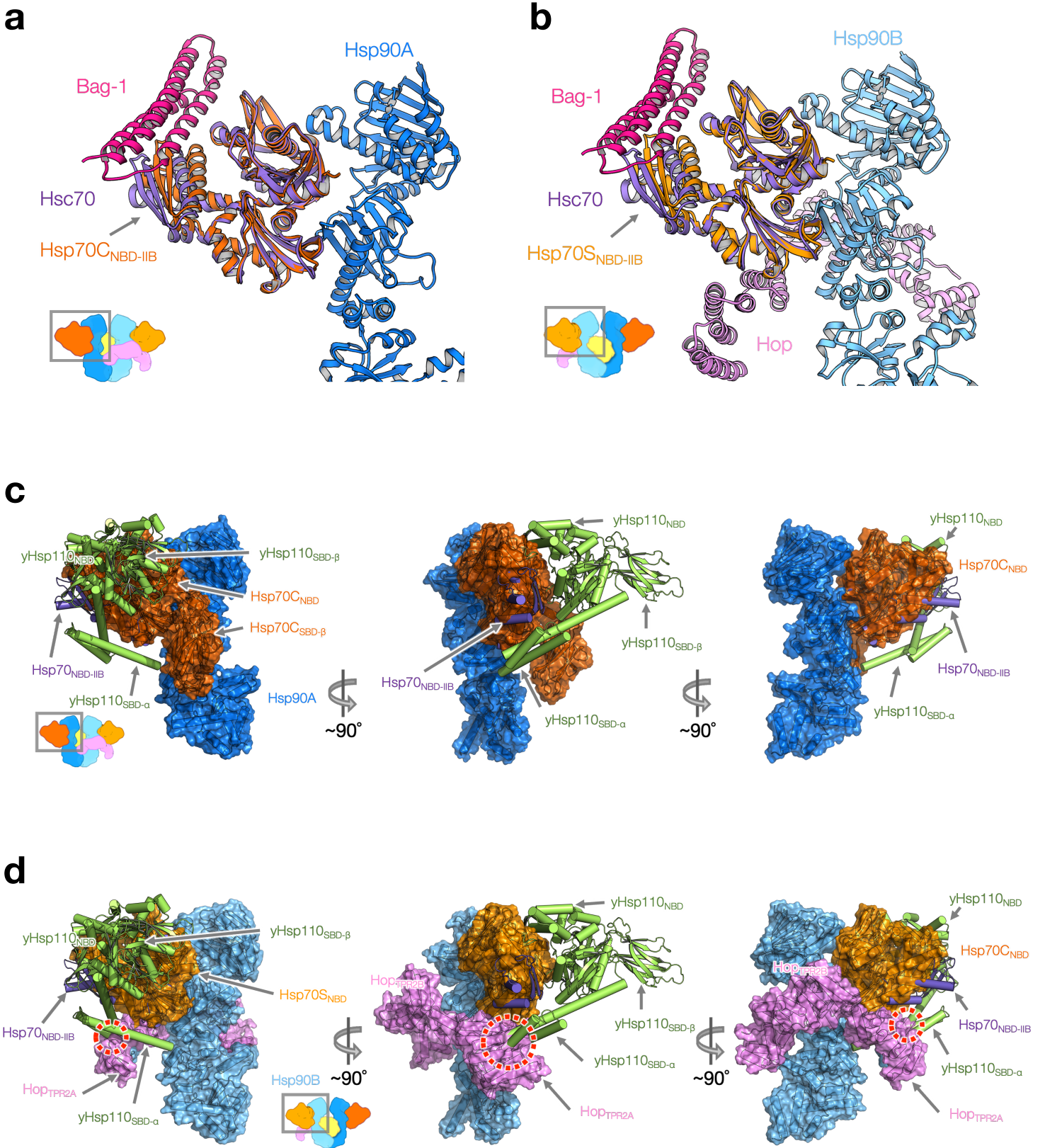
**b**

		-51	-41	-31	-21	-11	-1	10D	20V	
Hsp70/1-641	1	-----MAKAAAIGIDLGGTTCVGVFQHGK							25	
Hsc70/1-646	1	-----MSKGPVAVGIDLGGTTCVGVFQHGK							25	
SSA1/1-642	1	-----MSKAVGIDLGGTTCVVAHFANDR							23	
BIP/1-654	1	-----MKLSLVAAMLLLSAARAEEEDKKEDEVGVVVDLGGTTCVGVFKNGR							49	
Mortalin/1-679	1	MISASRAAAARLVGAAASRGPTAARHQDSWNGLSHEAFRLV---SRRDYASEAIGKAVVVDLGGTTCVAVMEGKQ							74	
DnaK/1-638	1	-----MGKIGIDLGGTTCVVAIMDGT							23	
		30A	40S	49R	59V	69D	79G	89H	99D	
Hsp70/1-641	26	VEI IANDQGNRTTPSYVAFTD-TERLIGDAAKNQVALNPONTVFDAKRLIGRKFDDPVVQSDMKHWPFOVINDDGDKP	101							
Hsc70/1-646	26	VEI IANDQGNRTTPSYVAFTD-TERLIGDAAKNQVAMNPNTVFDAKRLIGRRFDDAVVQSDMKHWPFMVVDNAGR	101							
SSA1/1-642	24	VDI IANDQGNRTTPSYVAFTD-TERLIGDAAKNQAMNPNTVFDAKRLIGRNFNDPEVQADMKHFPKLIDVDGKP	99							
BIP/1-654	50	VEI IANDQGNRTTPSYVAFTDEGERLIGDAAKNQLTSPENTVFDKRLIGRTWNPVQDDIKFLPKVVEKKTTP	126							
Mortalin/1-679	75	AKVLENAEGARTTPSYVAFTADGERLVGMPAKRQAVTNPNTFYATKRLIGRRYDDPEVQDKIKNVFKIVRASNGD	151							
DnaK/1-638	24	PRVLENAEGDRTTPSI IAYTQDGETLVGQPAKRQAVTNPQNTLFAIKRLIGRRFQDEEVQRDVSIMPFKIIAADNGD	100							
		109-	118E	128K	138P	148A	158T	168N		
Hsp70/1-641	102	KVQVSYK-GETKAFYP E EISSMVLTKMKEIAEAYLGYPVTVNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPT	177							
Hsc70/1-646	102	KVQVEYK-GETKSFYP E EISSMVLTKMKEIAEAYLGKTVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPT	177							
SSA1/1-642	100	QIQVEFK-GETKNFTPE EISSMVLGKMKETAESYLGAKVNDVAVTVPAYFNDSQRQATKDAGVIAGLNVLRIINEPT	175							
BIP/1-654	127	YIQVDIGGGQTKTFAP E EISAMVLTMKKETA EAYLGKVTTHAVTVPAYFNDAQRQATKDAGVIAGLNVMRIINEPT	203							
Mortalin/1-679	152	A-WVE---AHGKLYSP SQIGAFVLMKMKETAENYLGHAKNAVITVPAYFNDSQRQATKDAGVISGLNVLRIINEPT	224							
DnaK/1-638	101	A-WVE---VKGQKMAP PQISA E V L K M K K T A E D Y L G E P V T E A V I T V P A Y F N D A Q R Q A T K D A G R I A G L E V K R I I N E P T	173							
		178A	188T	198F	208S	215	224G	234D	244E	
Hsp70/1-641	178	AAAIAYGLDRTGKGERNVLI FDLGGGTFDVSILTI DD---GIFEVKATAGDTHLGGEDFDNR LVNHVFEEFKRKHK	250							
Hsc70/1-646	178	AAAIAYGLDKKVGAEENVLI FDLGGGTFDVSILTI ED---GIFEVKSTAGDTHLGGEDFDNRMVNHVIAEFKRRKHK	250							
SSA1/1-642	176	AAAIAYGLDKKGGK-EEHVLIFDLGGGTFDVSLLSIED---GIFEVKATAGDTHLGGEDFDNR LVNHVIAEFKRRKHK	247							
BIP/1-654	204	AAAIAYGLDKRE-GEKNI LV FDLGGGTFDVSLLTIDN---GVFEVATNGDTHLGGEDFDQRVMEHFIKLYKKTG	275							
Mortalin/1-679	225	AAALAYGLDKS E--DKVIAVYDLGGGTFDISLEIQK---GVFEVKSTNGDTHLGGEDFDQALLRHVKEFKRET	295							
DnaK/1-638	174	AAALAYGLDKGT-GNRTIAVYDLGGGTFDISIIEIDVDEGKTFEVKATNGDTHLGGEDFDSRLINYLVEEFKDKQD	249							
		254S	264R	274L	284I	290G	300A	310F	320A	
Hsp70/1-641	251	KDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFE---GIDFYTSITRARFEELCSDLFRSTLEPVEKALRD	323							
Hsc70/1-646	251	KDISENKRAVRRLRTACERAKRTLSSSTQASLEIDSLFE---GIDFYTSITRARFEELNADLFRGTLDPVEKALRD	323							
SSA1/1-642	248	KDLSTNQRALRRLRTACERAKRTLSSSAQTSVEIDSLFE---GIDFYTSITRARFEELNADLFRSTLDPVEKALRD	320							
BIP/1-654	276	KDVRKDNRAVQLRRERVEKAKRALSSQHQARIEIESFYE---GEDFSETLRAKFEELNADLFRSTMKPVQKVL	348							
Mortalin/1-679	296	VDLTKDNMALQRVREAAEKAKCE LSSSVQTDINLPYLTMDSSGPKHLNMLTRAQFEGIVTDLIRRTIAPCQKAMQD	372							
DnaK/1-638	250	IDLRLNDP LAMQRLKEAAEKAKI E L S S A Q Q T D V N L P Y I T A D A T G P K H M N I K V T R A K L E S L V E D L V N R S I E P L K V A L Q D	326							
		330Q	340S	350L	360N	370A	380L	390D		
Hsp70/1-641	324	AKLDKAQIHDLVLVGGSTRIPKVQLLQDFNNGRDLNKSINPDEAVAYGAAVQAAI LMGDKSENVDL LLDVAPLS	400							
Hsc70/1-646	324	AKLDKSIHDLVLVGGSTRIPKIQKLQDFNNGKELNKSINPDEAVAYGAAVQAAI LSGDKSENVDL LLDVTPLS	400							
SSA1/1-642	321	AKLDKSQVDEIVLVGGSTRIPKVQLVTDYFNGKEPNRSINPDEAVAYGAAVQAAI LTGDESSKTQD LLDVAPLS	397							
BIP/1-654	349	SDLKSSDIDEIVLVGGSTRIPKIQKLVEFFNGKEPSRGINPDEAVAYGAAVQAGVLSGDQD--TGDVLLDVCPL	423							
Mortalin/1-679	373	AEVSKSDIEGIVLVGGTRMPKVQQTVDLFG-GRAPSKAVNPDEAVAYGAAIQGGVLAGD---VTDVLLDVTPL	444							
DnaK/1-638	327	AGLSVSDIDDVIVLVGGTRMPMVQKVAEFF-GKEPRKDVNPDEAVAYGAAVQGGVLTGD---VKDVL LLDVTPLS	398							
		410M	420I	430T	440I	450T	460E	470G		
Hsp70/1-641	401	LGL ETAGGVMTALIKRNTIPTKQTQIFTTYSDNQPVLIQVYEGERAMTKDNNLLGRFELSGIPAPRGVPQIEVT	477							
Hsc70/1-646	401	LGI ETAGGVMTVLIKRNNTIPTKQTQFTTTYSDNQPVLIQVYEGERAMTKDNNLLGKFEELTGIPAPRGVPQIEVT	477							
SSA1/1-642	398	LGI ETAGGVMTKLI PRNSTIPTKKEIFSTYADNQPVLIQVFEGERAKTKDNNLLGKFEELSGIPAPRGVPQIEVT	474							
BIP/1-654	424	LGI ETAGGVMTKLI PRNTVVPTKKSQIFSTASDNQPTVLIQVYEGERLTKDNNLLGTFDLTGIPAPRGVPQIEVT	500							
Mortalin/1-679	445	LGI ETLGGVFTKLI NRNTIPTKKSQVFSTAADGQTQVEIKVCGGEREMAGDNKLLGQFTLIGIPAPRGVPQIEVT	521							
DnaK/1-638	399	LGI ETMGGVMTL IAKNNTIPTKHSQVFSTAEDNQSAVTIHLVQGERKRAADNKS LGQFNLDGINPAPRGMPQIEVT	475							
		480I	490A	500K	510L	520Q	530E	540N	550K	
Hsp70/1-641	478	FDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAKEYKA EDEVQRERVS AKNALESYAFNMKSAVE	554							
Hsc70/1-646	478	FDIDANGILNVS AVDKSTGKENKITITNDKGRLSKEDI ERMVQEAKEYKA EDEKQRDKVSSKNSLESYAFNMKATVE	554							
SSA1/1-642	475	FDVDSNGILNVS AVKGTGKSNKITITNDKGRLSKEDI EKMVAEAEKFEDEKESQR IASKNQLLES IAYS LKNTIS	551							
BIP/1-654	501	FEIDVNGILRVTAEDKGTGNKKNKITITNDQNR LTP E E I E R M V N D A E K F A E D K K L K E R I D T R N E L E S Y A S L K N Q I G	577							
Mortalin/1-679	522	FDIDANGIVHVS AKDKGTGR EQQIVIQSS-GGLSKDDI ENMVKNAKEYAEEDRRKKERVEAVNMAEGIIHDTETKME	597							
DnaK/1-638	476	FDIDADGILHVS AKDKNSGKEQKITIKAS-SGLNEDEIQKMRDAEANA EADRKF EELVQTRNQGDHLLHSTRKQVE	551							
		559K	569K	579S	589K	599L	609G	618-	623G	
Hsp70/1-641	555	D-EGLKGGKISEADKKKVLDKQCEVSWLDANTLAEKDEFEHKKREL EQVCNP I ISGLYQAGGPP---G---PGGF G-	623							
Hsc70/1-646	555	D-EKLQGGKINDEDKQKILDKCNEIINWLDKNQTAKEE E FEHQQKLEKVCNP IITKLYQSAGGM---PGGMPGGFP	627							
SSA1/1-642	552	E-AG--DKLEQADKDKVTKKA EETISWLD SNTTASKEEFDKLLKELQDIANPIMSKLYQAGGAPGGAAGGAPGGFP	625							
BIP/1-654	578	DKKELGGKLSSEDKETMEKAVEEKIEWLESHQDADIEDFKAKKLEEEIVQPIISKLYGSAGPPPTGEED-----	647							
Mortalin/1-679	598	E---FKDQLPADECNKLEEKISKMR ELLARKDSETGENIRQAASSLQQASLKL FEMAYKKMASEREGSGSSGTG---	668							
DnaK/1-638	552	E---AGDKLPADDKTAIESALTALETA LKGEDKA---AIEAKMQELAQVSQKLMEIAQQQHAQQQTAGADASAN---	619							
		631S	641D							
Hsp70/1-641	624	-AQQPKGGSGSGPTIEEVD---	641							
Hsc70/1-646	628	GGAPP SGGASSGPTIEEVD---	646							
SSA1/1-642	626	GAPPA--PEAE GPTVEEVD---	642							
BIP/1-654	648	TAE-----KDEL---	654							
Mortalin/1-679	669	---EQKEDQKEEKQ-----	679							
DnaK/1-638	620	---NAKDDDDVDAEFEEVKDKK	638							

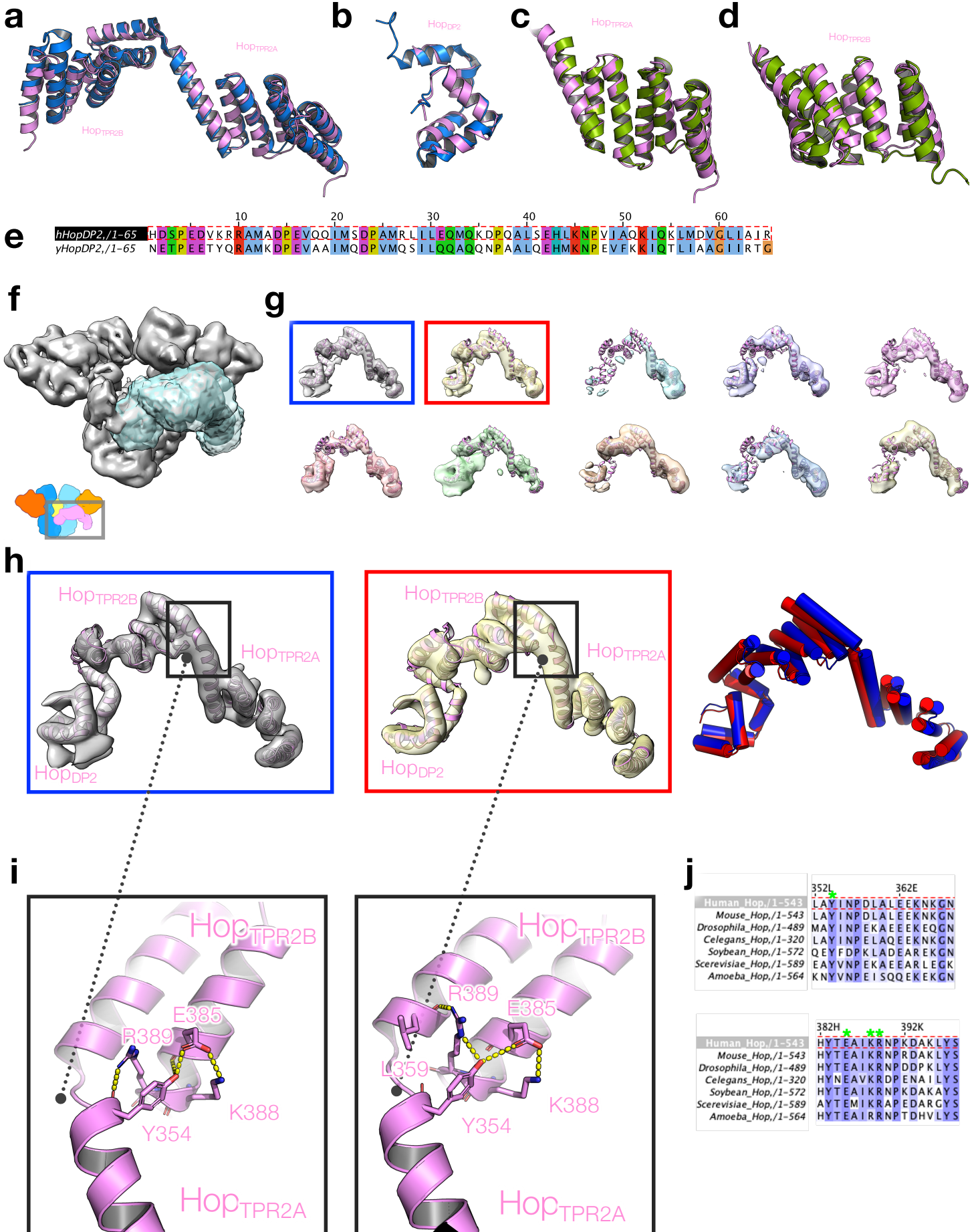
Supplementary Fig. 3



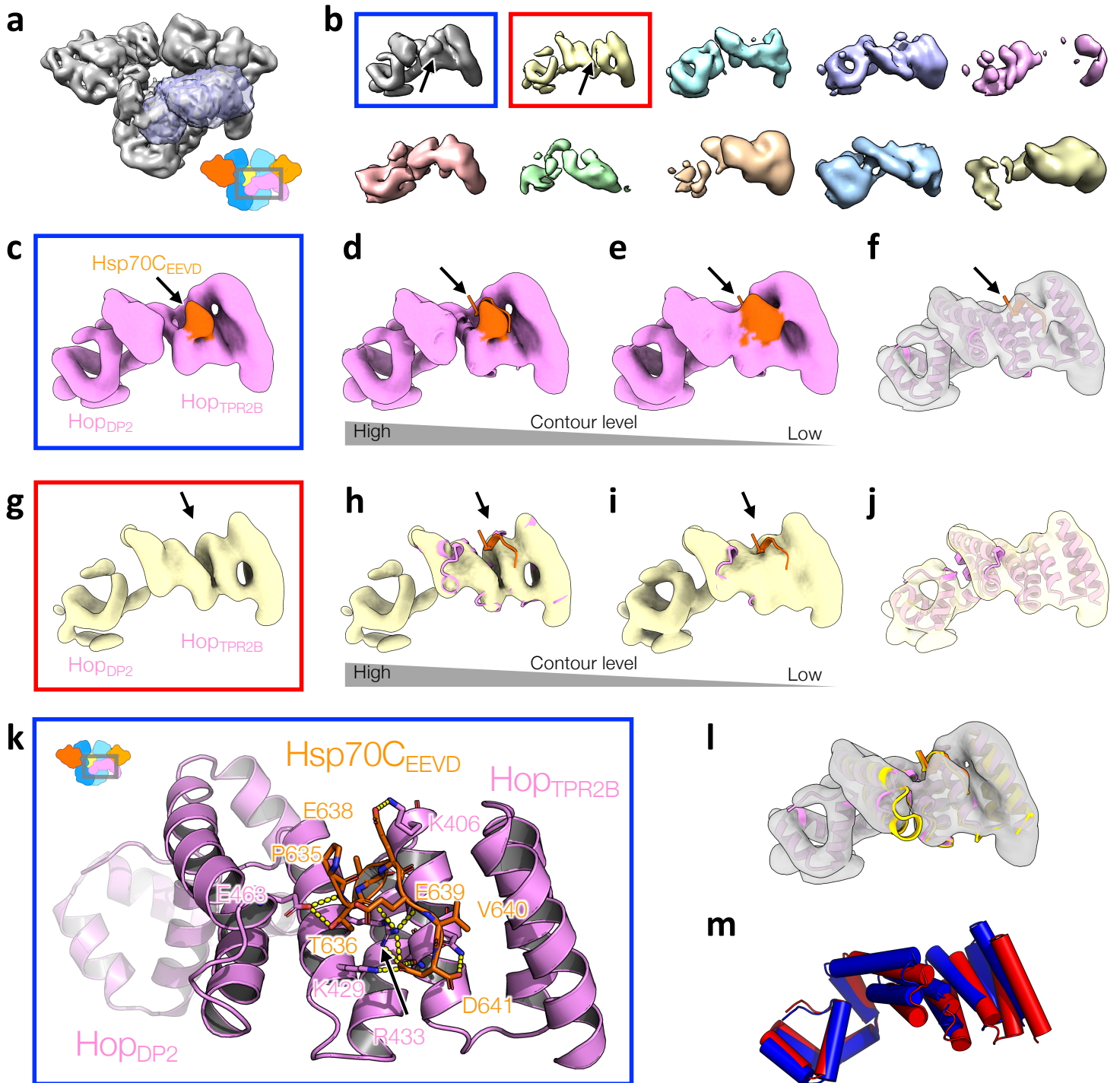
Supplementary Fig. 4



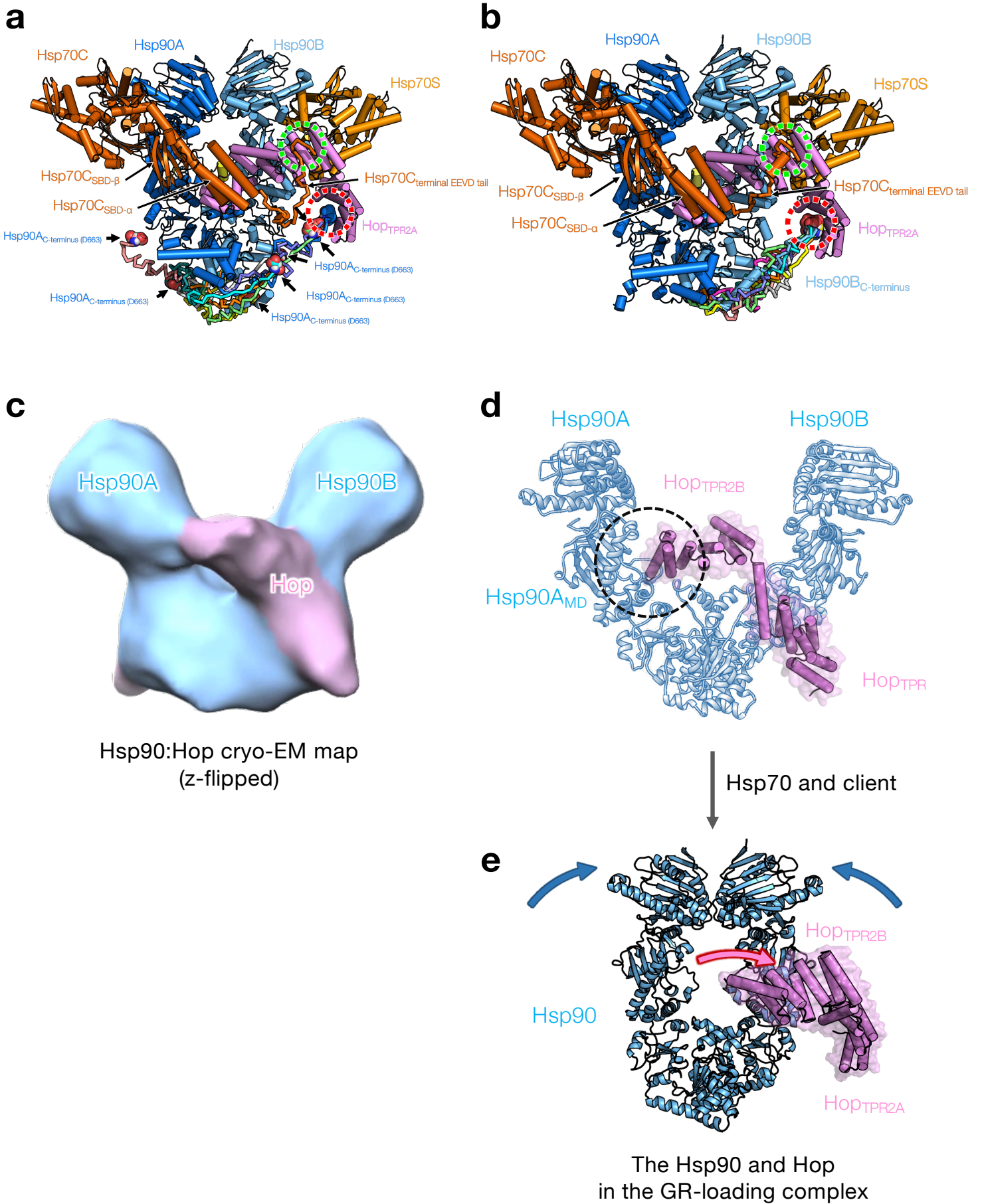
# Supplementary Fig. 5



Supplementary Fig. 6

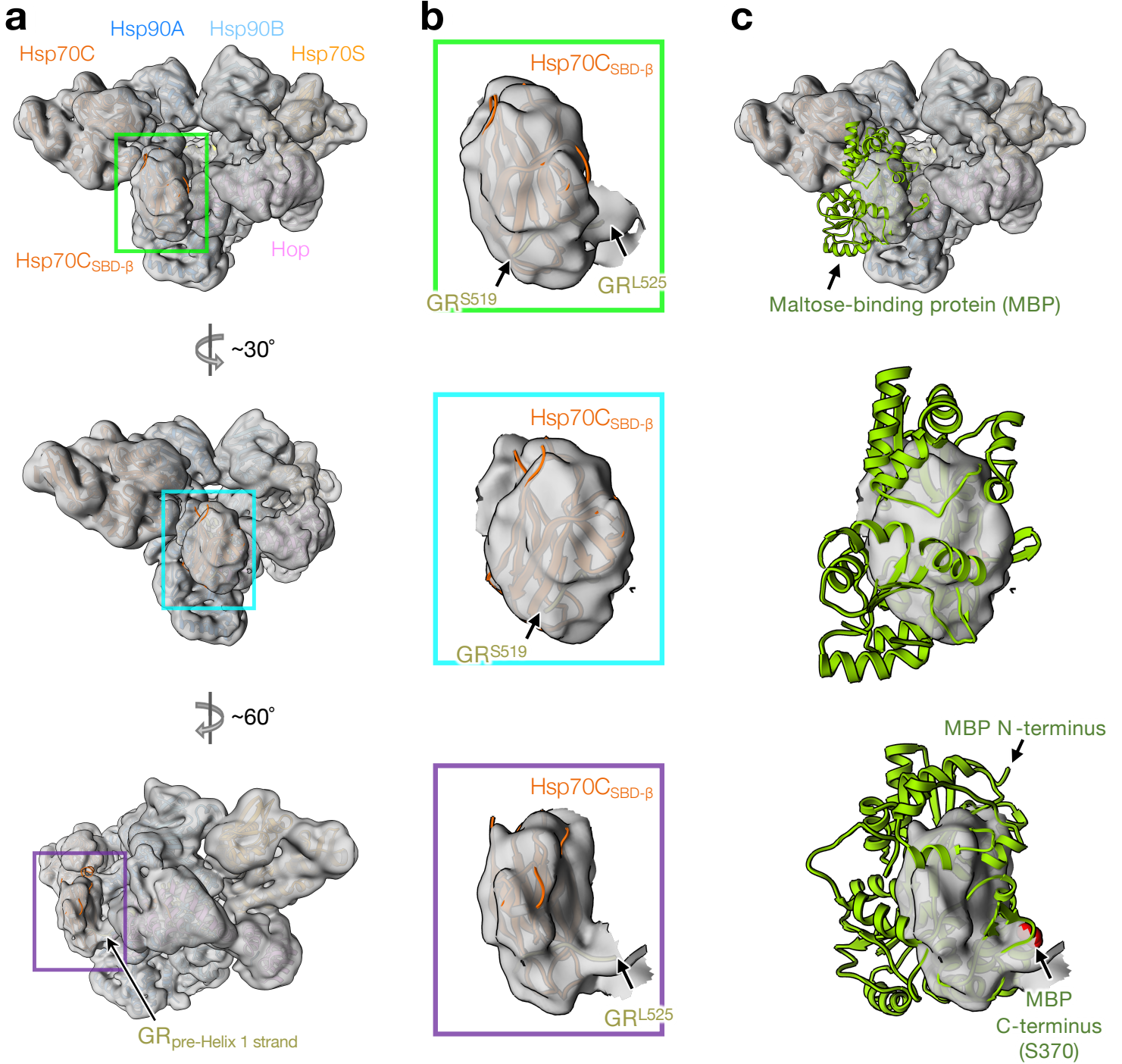


Supplementary Fig. 7

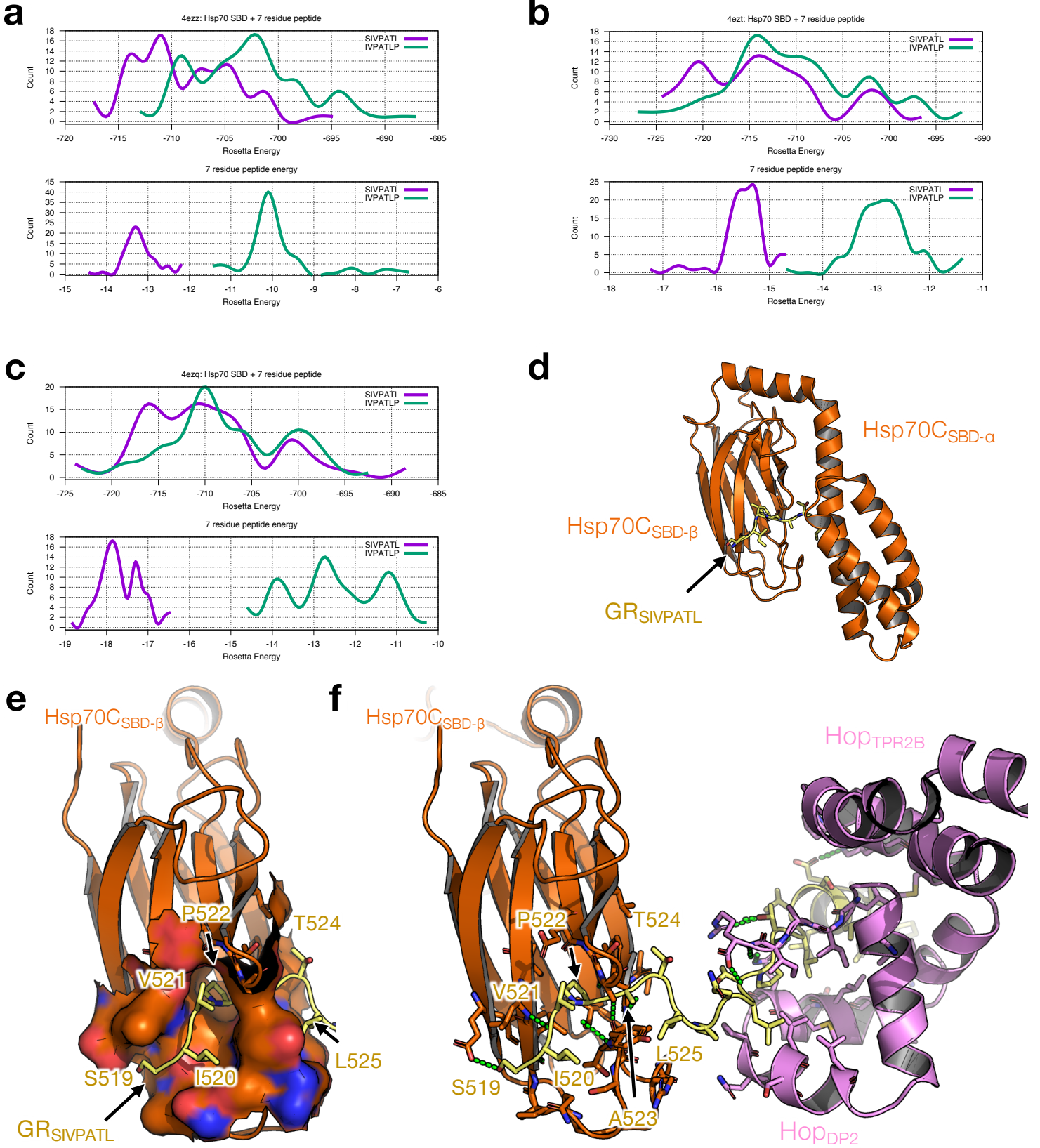




Supplementary Fig. 8

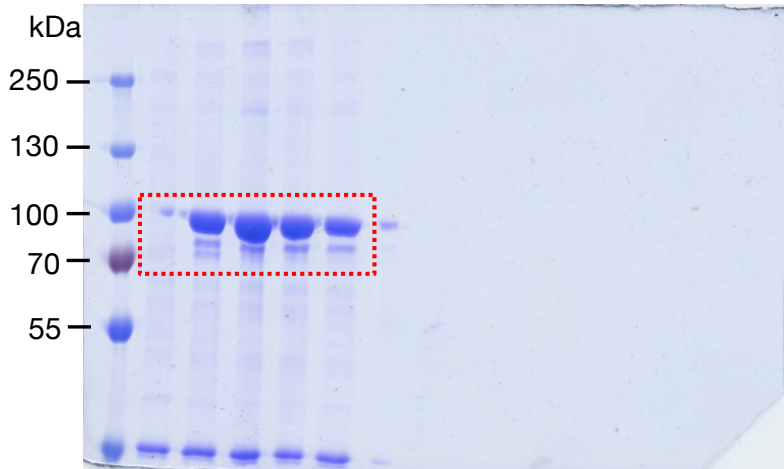


# Supplementary Fig. 9

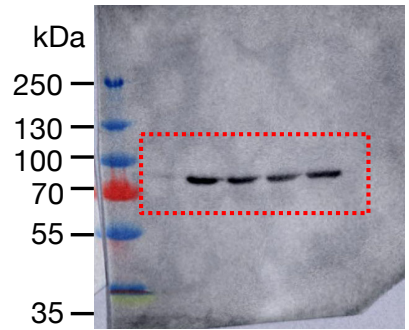


Supplementary Fig. 10

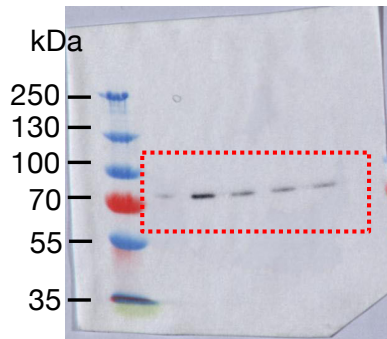
ED fig. 4f



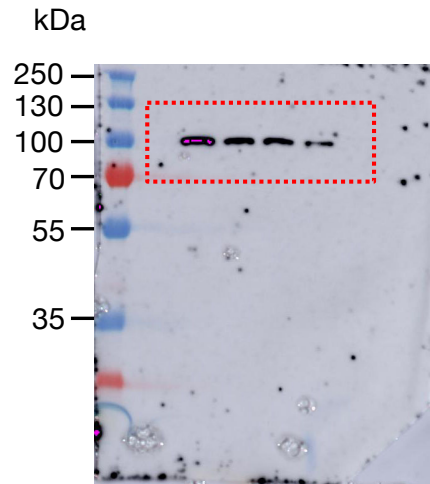
His-Hsc82 resin



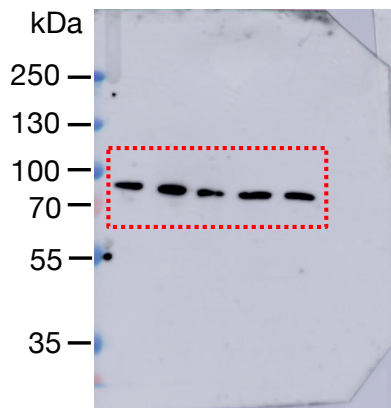
Sti1 resin



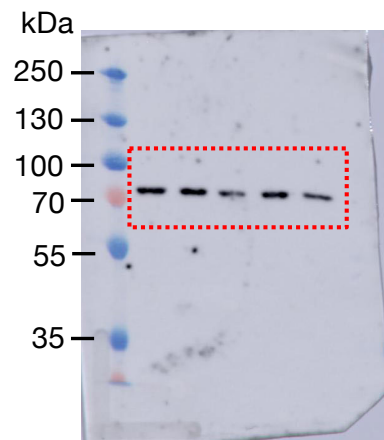
Ssa1/2 resin



His-Hsc82 lysates



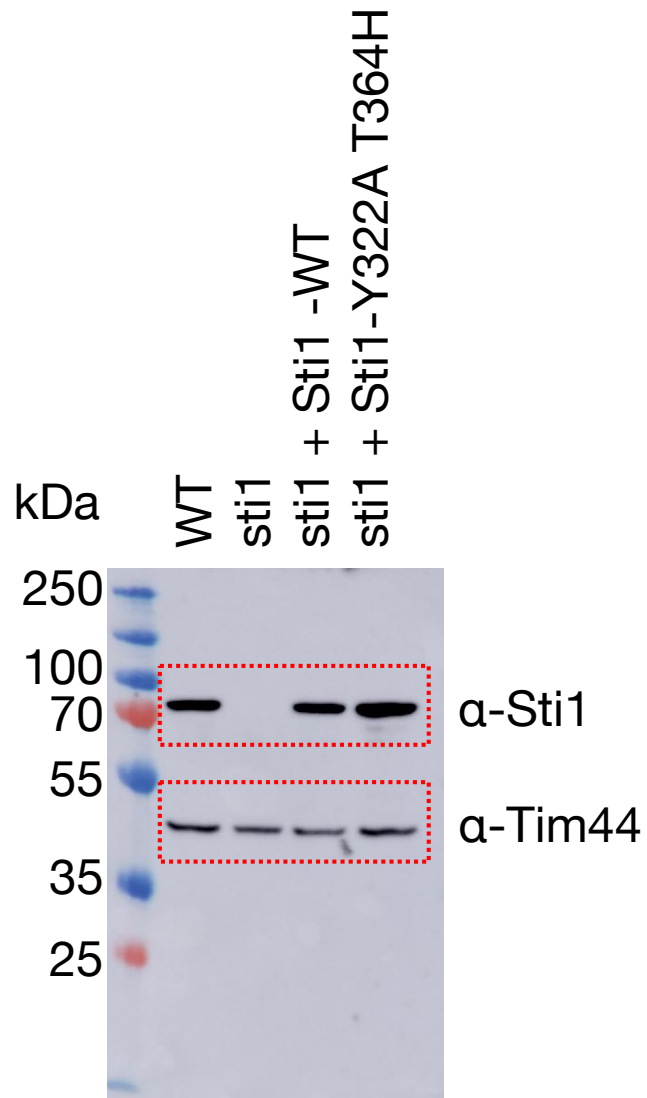
Sti1 lysates



Ssa1 lysates

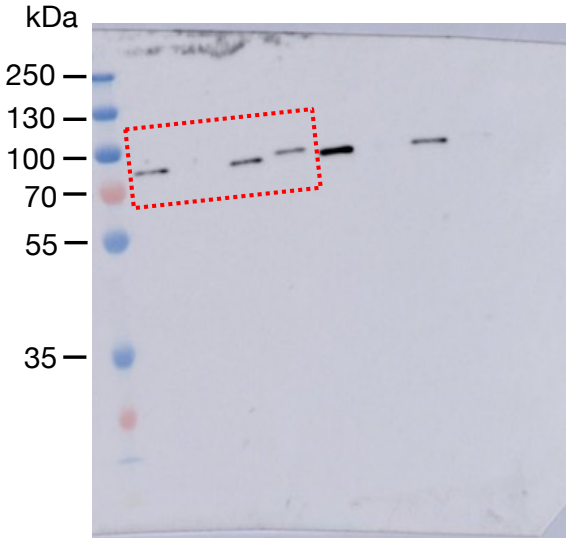
Supplementary Fig. 10

ED fig. 6h

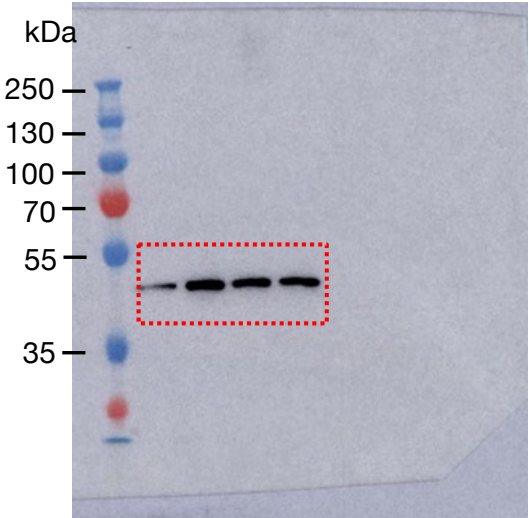


Supplementary Fig. 10

ED fig. 8f



$\alpha$ -Sti1



$\alpha$ -Tim44