

Supplementary Materials for
Substrate recognition principles for the PP2A-B55 protein phosphatase

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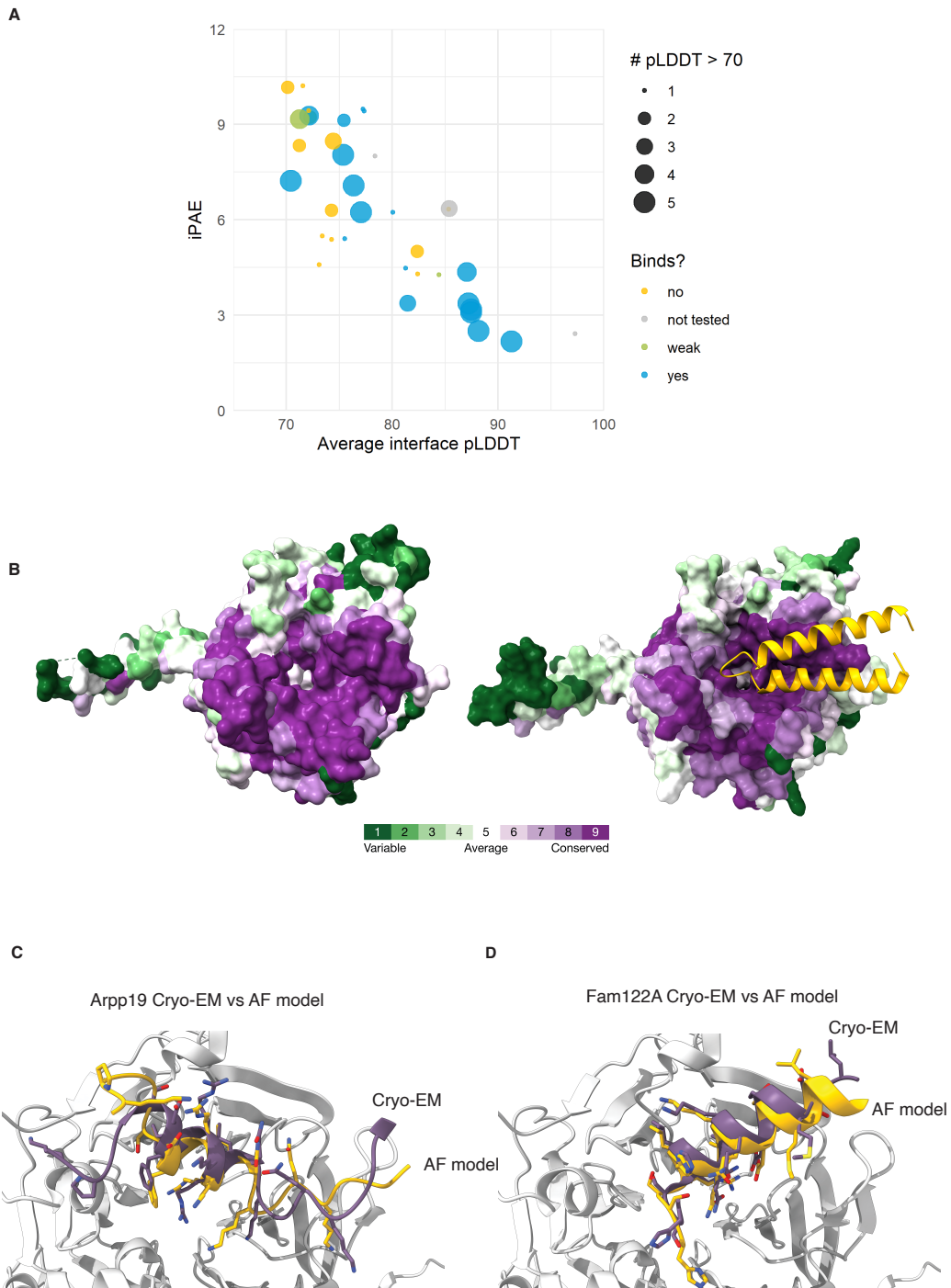
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The PDF file includes:

Figs. S1 to S17
Table S1
Legends for tables S2 to S4
Legend for data S1

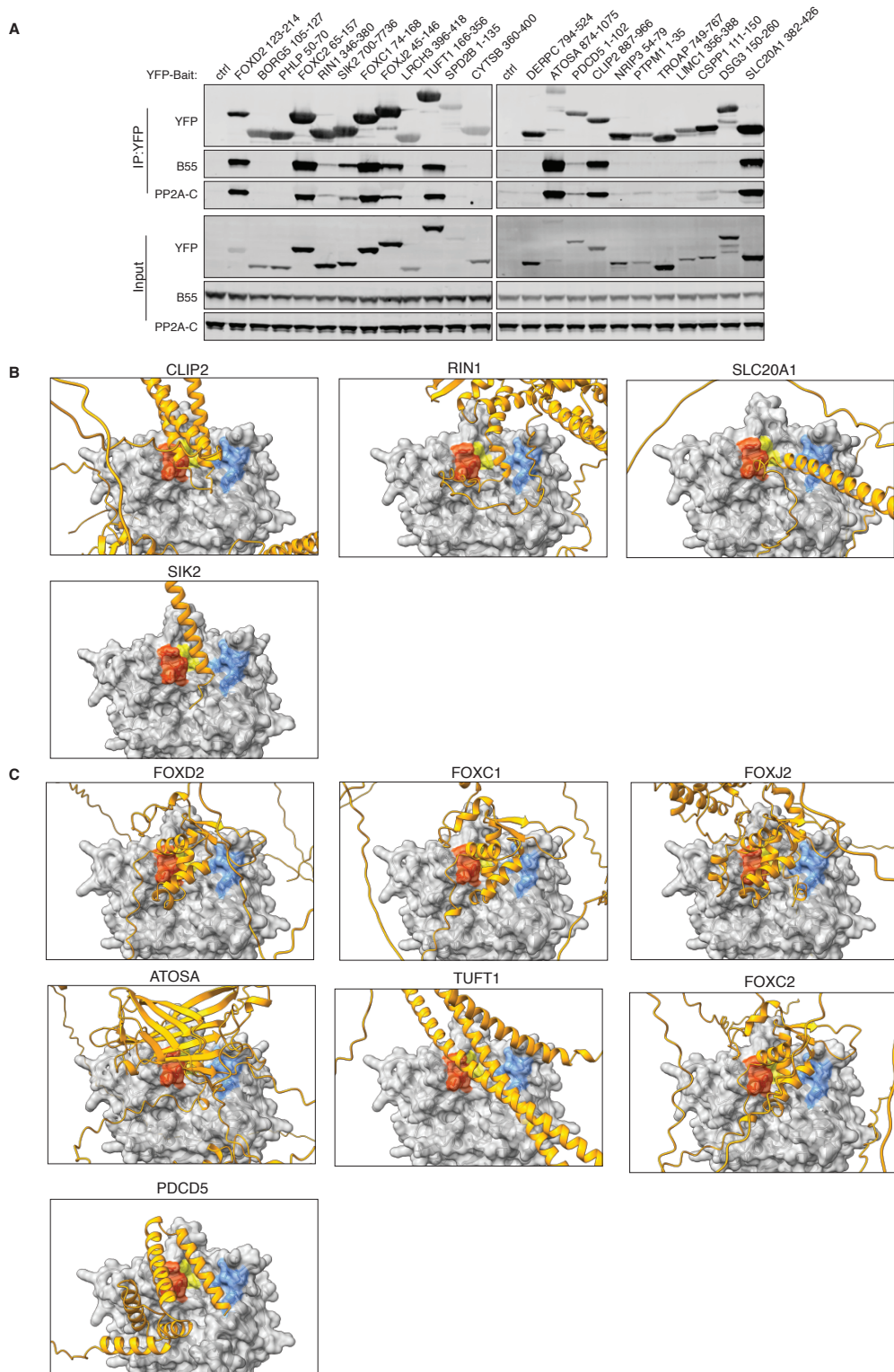
Other Supplementary Material for this manuscript includes the following:

Tables S2 to S4
Data S1



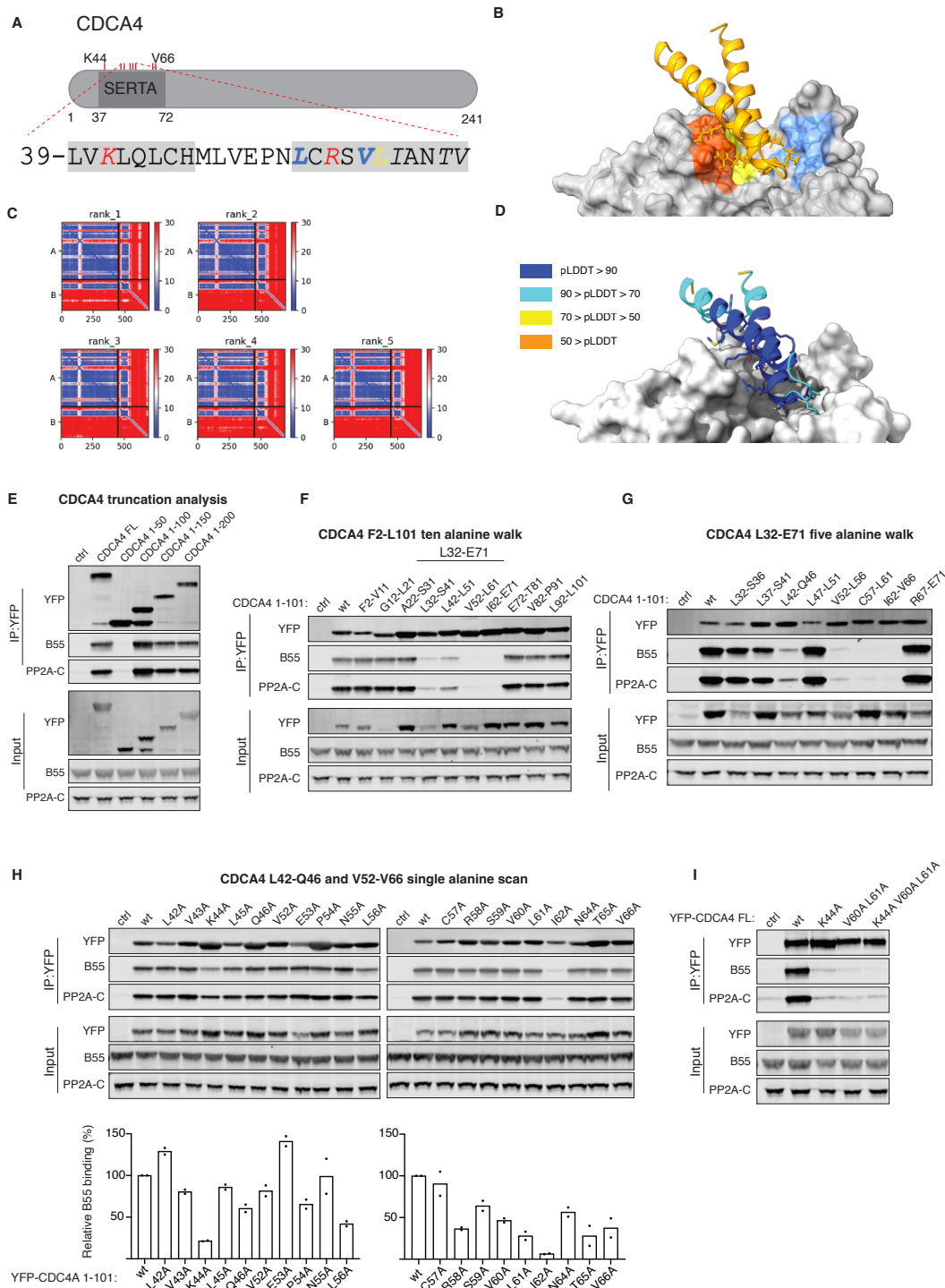
Supplemental Figure S1. AF score plots and comparison to cryo-EM models.

A) Plot showing iPAE and pLDDT score for the 36 models and whether they were binding to PP2A-B55 α in immunoprecipitation experiments. The size of the dot indicates number of models with a pLDDT above 70. **B)** Surface conservation of B55 α with CDCA4 modeled **C)** Overlay of the Arpp19 cryo-EM structure (PDB: 8TTB) with the AF2 model focusing on the helix binding B55. **D)** Overlay of the FAM122A cryo-EM structure (PDB: 8SO0) with the AF2 model focusing on the helix binding B55.



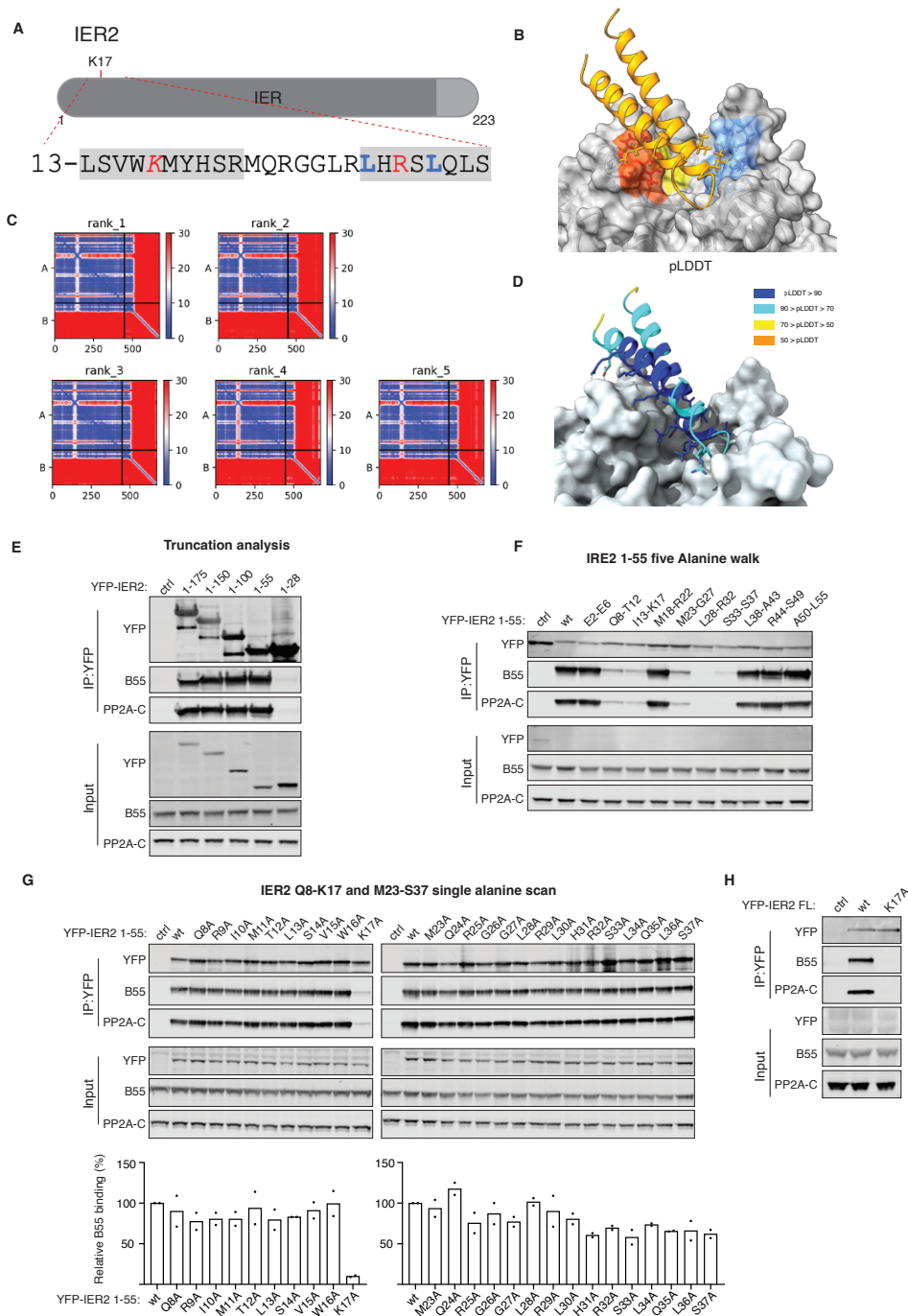
Supplemental Figure S2. Validation of novel binders and AF models of distinct binding mechanisms.

A) The indicated YFP tagged protein fragments were expressed in HeLa cells and following immunoprecipitation they were probed for binding to PP2A-B55 α by western blot. B55 refers to B55 α **B)** AF2 models of the indicated proteins binding to PP2A-B55 in a common manner. **C)** AF2 models of the indicated proteins binding to PP2A-B55 in a distinct manner.



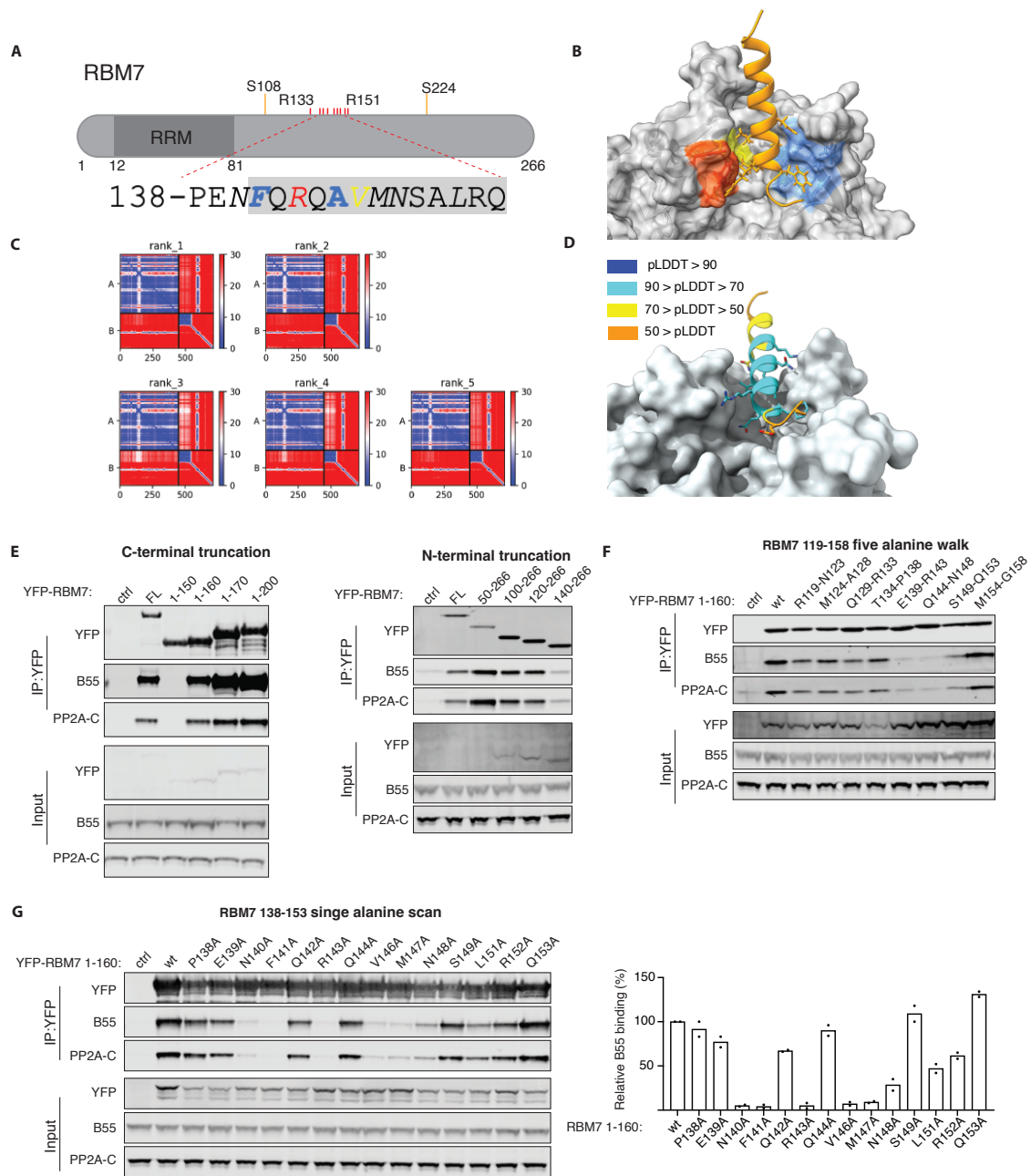
Supplemental Figure S3. CDCA4 data.

A) Schematic of CDCA4 and sequence binding PP2A-B55 α . Amino acids crucial for binding are indicated by a red line in the schematic. **B)** AF2 model of CDCA4 bound to B55. **C)** Predicted aligned error (PAE) score for the 5 models. **D)** pLDDT score mapped onto model. **E-I)** The indicated YFP tagged protein fragments were expressed in HeLa cells and following immunoprecipitation they were probed for binding to PP2A-B55 by western blot. B55 refers to B55 α . In H) the quantification of two biological replicates is shown with binding normalized to wild type protein. Bars visualize the average of the two biological replicates.



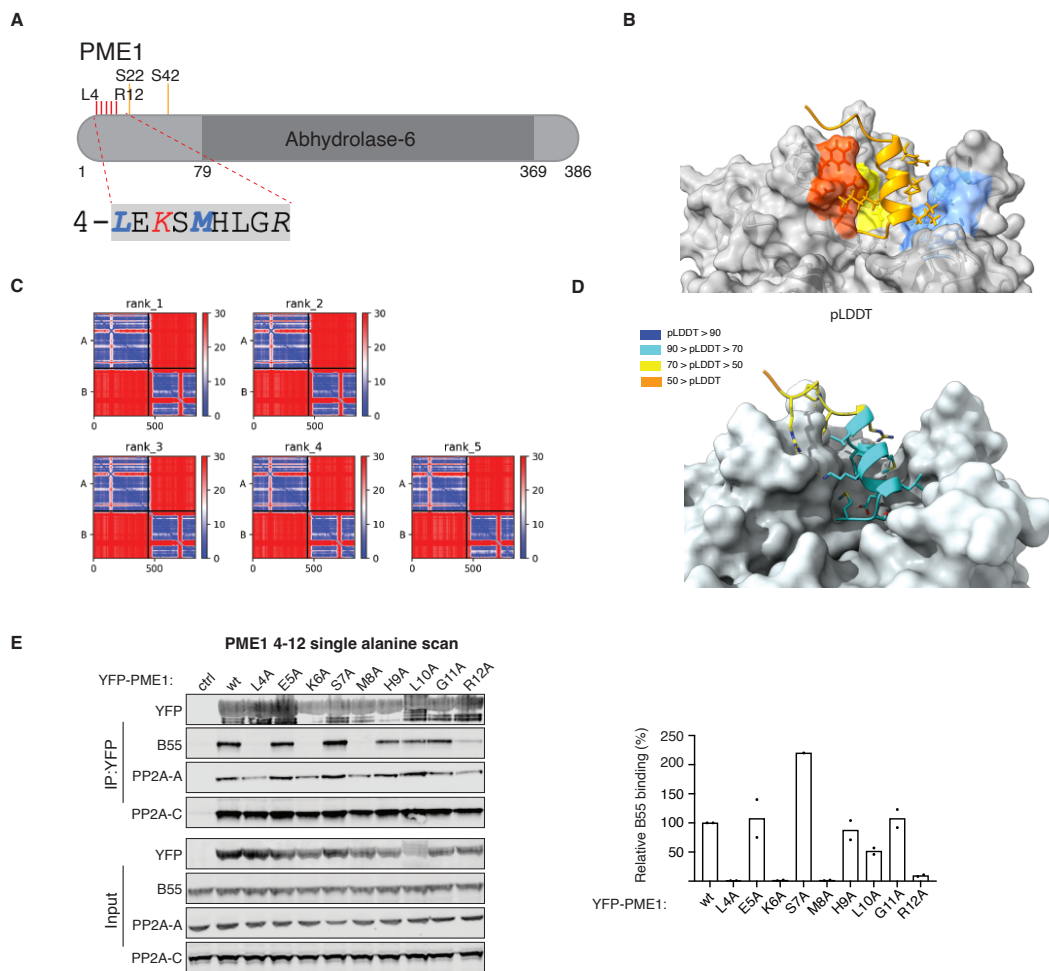
Supplemental Figure S4. IER2 data.

A) Schematic of IER2 and sequence binding PP2A-B55 α . Amino acids crucial for binding are indicated by a red line in the schematic. **B)** AF2 model of IER2 bound to B55. **C)** Predicted aligned error (PAE) score for the 5 models. **D)** pLDDT score mapped onto model. **E-H)** The indicated YFP tagged protein fragments were expressed in HeLa cells and following immunoprecipitation they were probed for binding to PP2A-B55 by western blot. B55 refers to B55 α . In G) the quantification of two biological replicates is shown with binding normalized to wild type protein. Bars visualize the average of the two biological replicates.



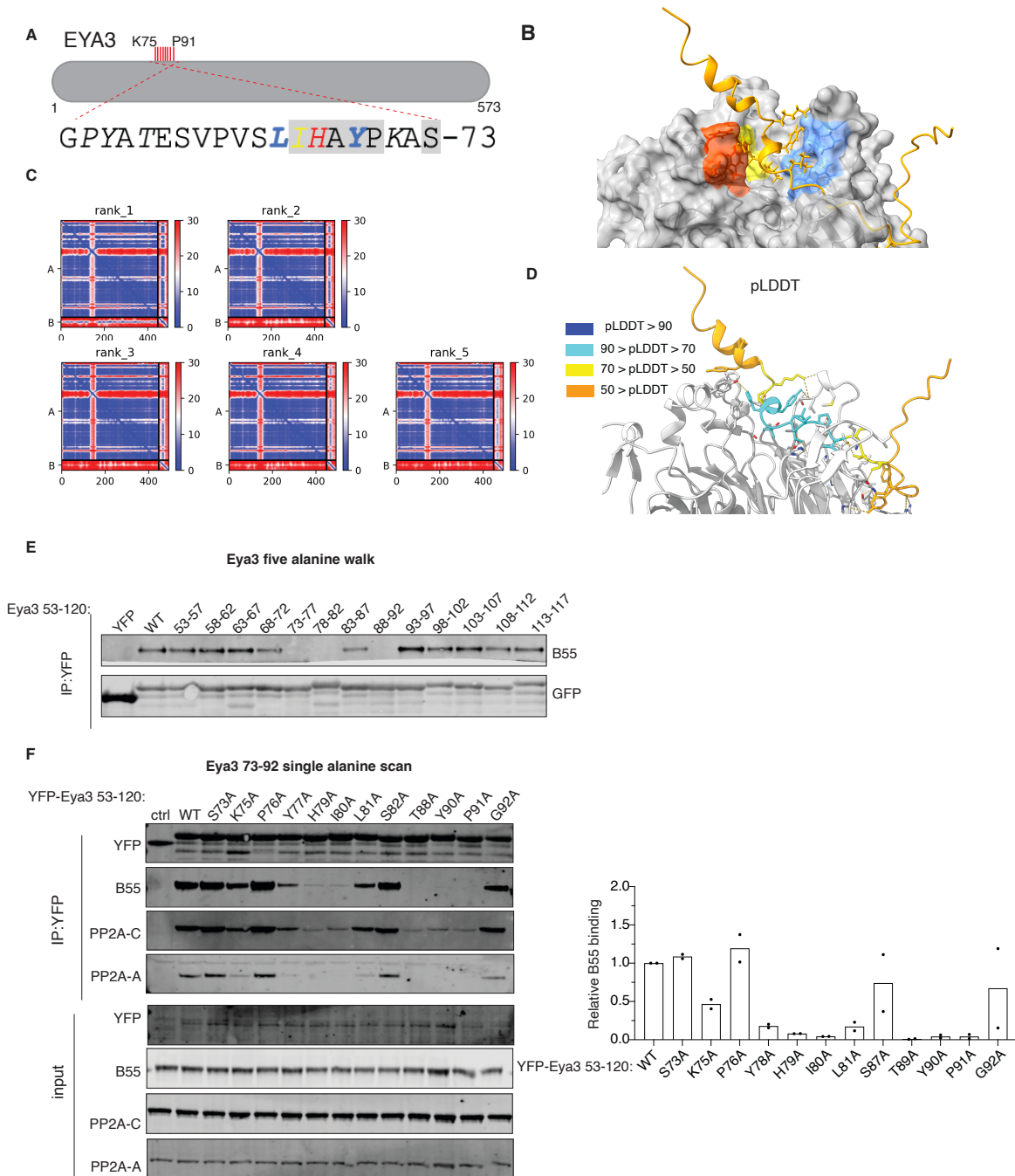
Supplemental Figure S5. RBM7 data.

A) Schematic of RBM7 and sequence binding PP2A-B55. Amino acids crucial for binding are indicated by a red line in the schematic. Phosphorylation sites with higher occupancy in RBM7 R143A indicated with yellow lines and amino acid. **B)** AF2 model of RBM7 bound to B55. **C)** Predicted aligned error (PAE) score for the 5 models. **D)** pLDDT score mapped onto model. **E-G)** The indicated YFP tagged protein fragments were expressed in HeLa cells and following immunoprecipitation they were probed for binding to PP2A-B55 by western blot. B55 refers to B55 α . The quantification of two biological replicates is shown with binding normalized to wild type protein. Bars visualize the average of the two biological replicates.



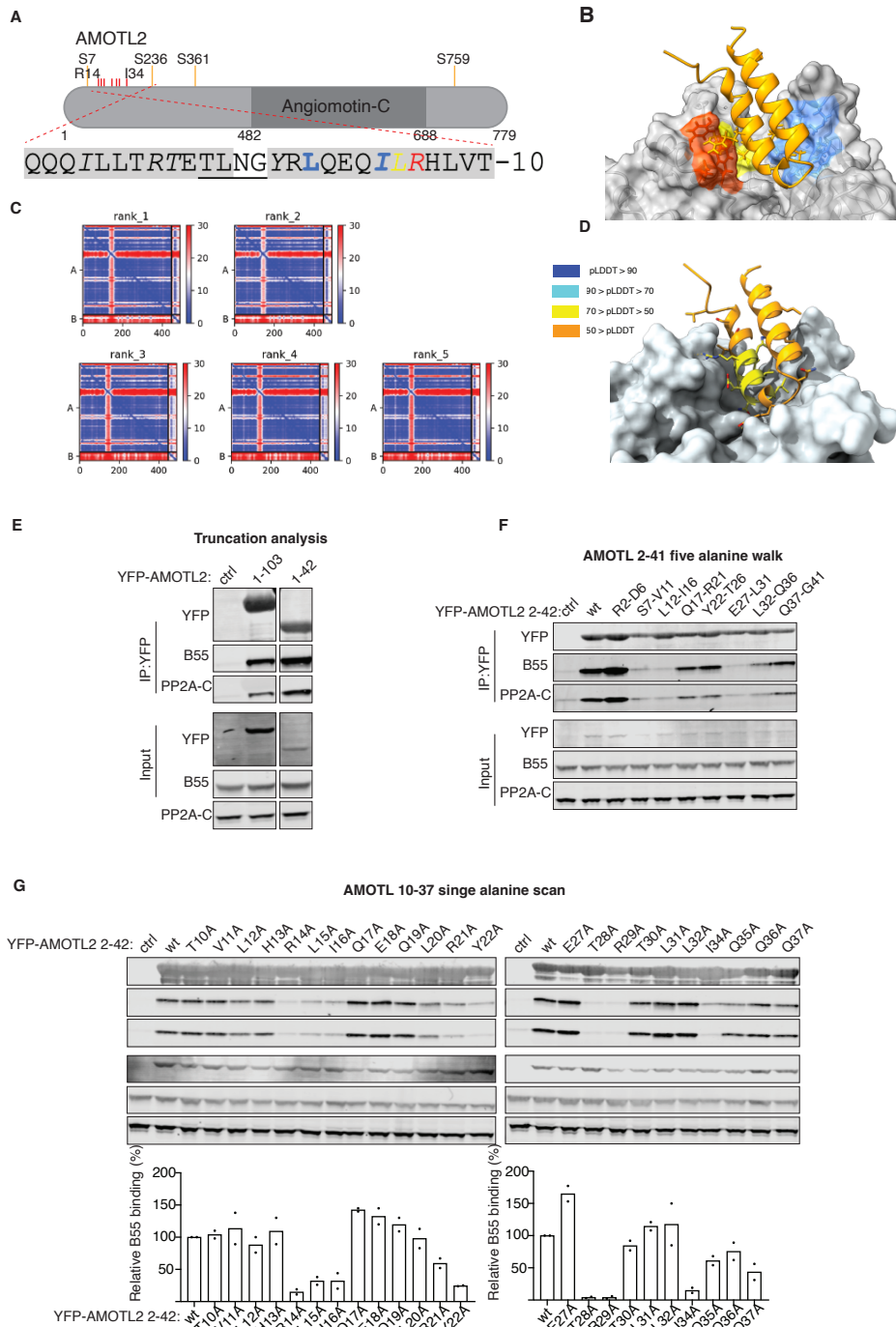
Supplemental Figure S6. PME1 data.

A) Schematic of PME1 and sequence binding PP2A-B55. Amino acids crucial for binding are indicated by a red line in the schematic. Phosphorylation sites with higher occupancy in PME1 L4A indicated with yellow lines and amino acid number. **B)** AF2 model of PME1 binding helix bound to B55. **C)** Predicted aligned error (PAE) score for the 5 models. **D)** pLDDT score mapped onto model. **E)** The indicated YFP tagged proteins were expressed in HeLa cells and following immunoprecipitation they were probed for binding to PP2A-B55 by western blot. B55 refers to B55 α . The quantification of two biological replicates is shown with binding normalized to wild type protein. Bars visualize the average of the two biological replicates.



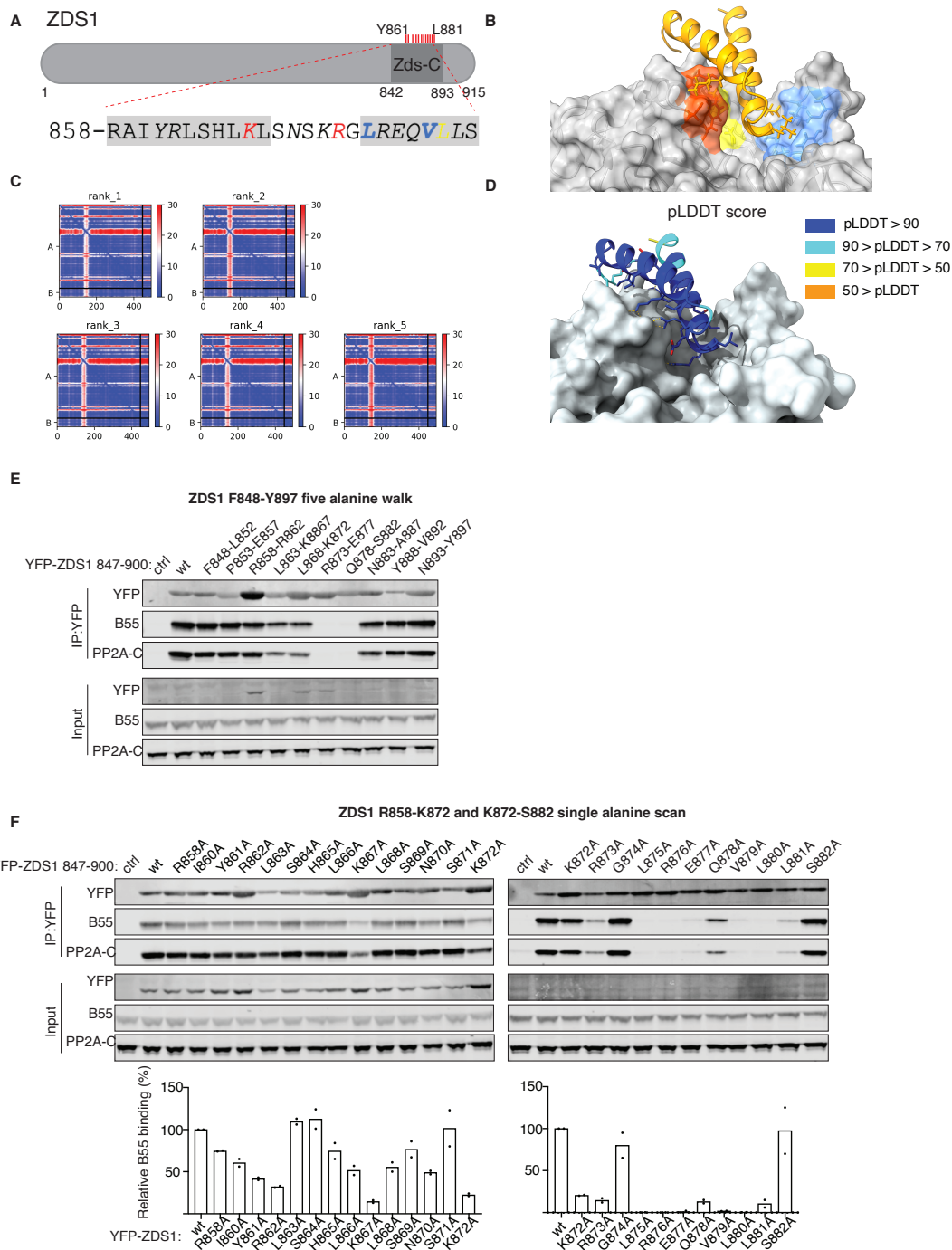
Supplemental Figure S7. EYA3 data.

A) Schematic of EYA3 and sequence binding PP2A-B55 α . **B)** AF2 model of EYA binding helix bound to B55. **C)** Predicted aligned error (PAE) score for the 5 models. **D)** pLDDT score mapped onto model. **E-F)** The indicated YFP tagged protein fragments were expressed in HeLa cells and following immunoprecipitation they were probed for binding to PP2A-B55 by western blot. B55 refers to B55 α . In F) The quantification of two biological replicates is shown with binding normalized to wild type protein. Bars visualize the average of the two biological replicates.



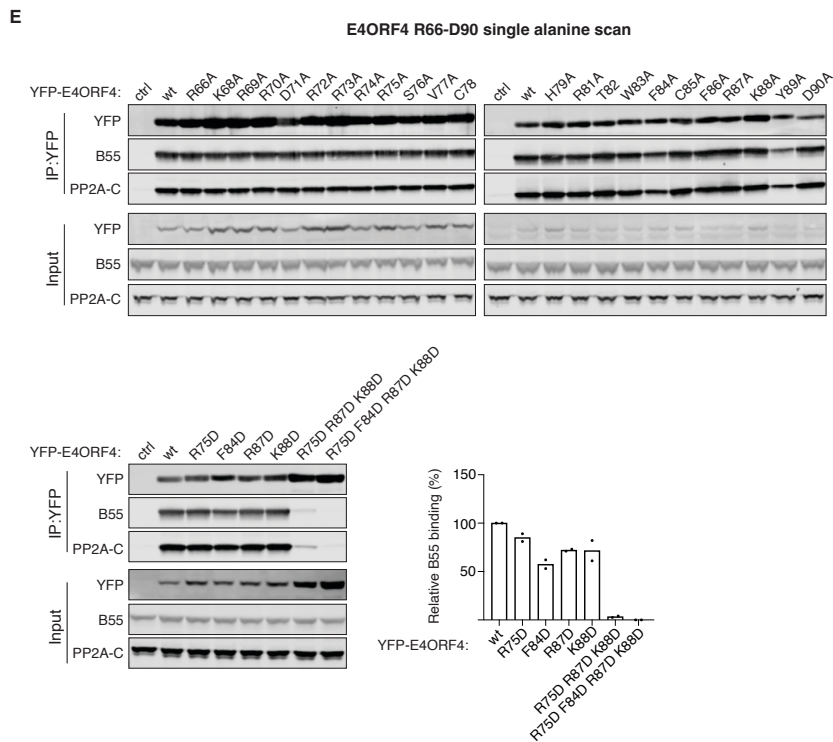
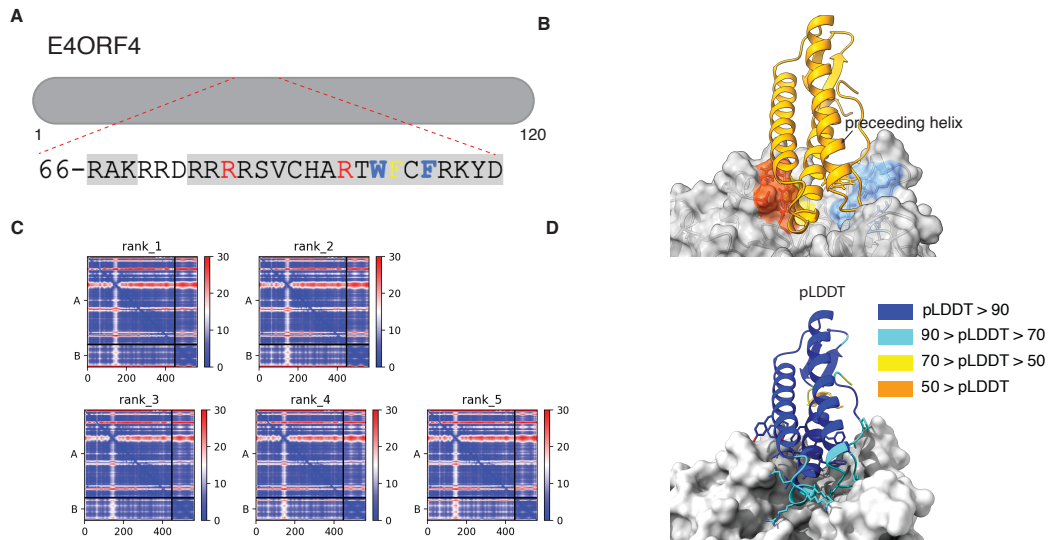
Supplemental Figure S8. AMOTL2 data.

A) Schematic of AMOTL2 and sequence binding PP2A-B55 α . Amino acids crucial for binding are indicated by a red line in the schematic. Phosphorylation sites with higher occupancy in AMOTL2 T28A/R29A indicated with yellow lines and amino acid number **B)** AF2 model of AMOTL2 bound to B55. **C)** Predicted aligned error (PAE) score for the 5 models. **D)** pLDDT score mapped onto model. **E-G)** The indicated YFP tagged protein fragments were expressed in HeLa cells and following immunoprecipitation they were probed for binding to PP2A-B55 by western blot. B55 refers to B55 α . The quantification of two biological replicates is shown with binding normalized to wild type protein. Bars visualize the average of the two biological replicates.



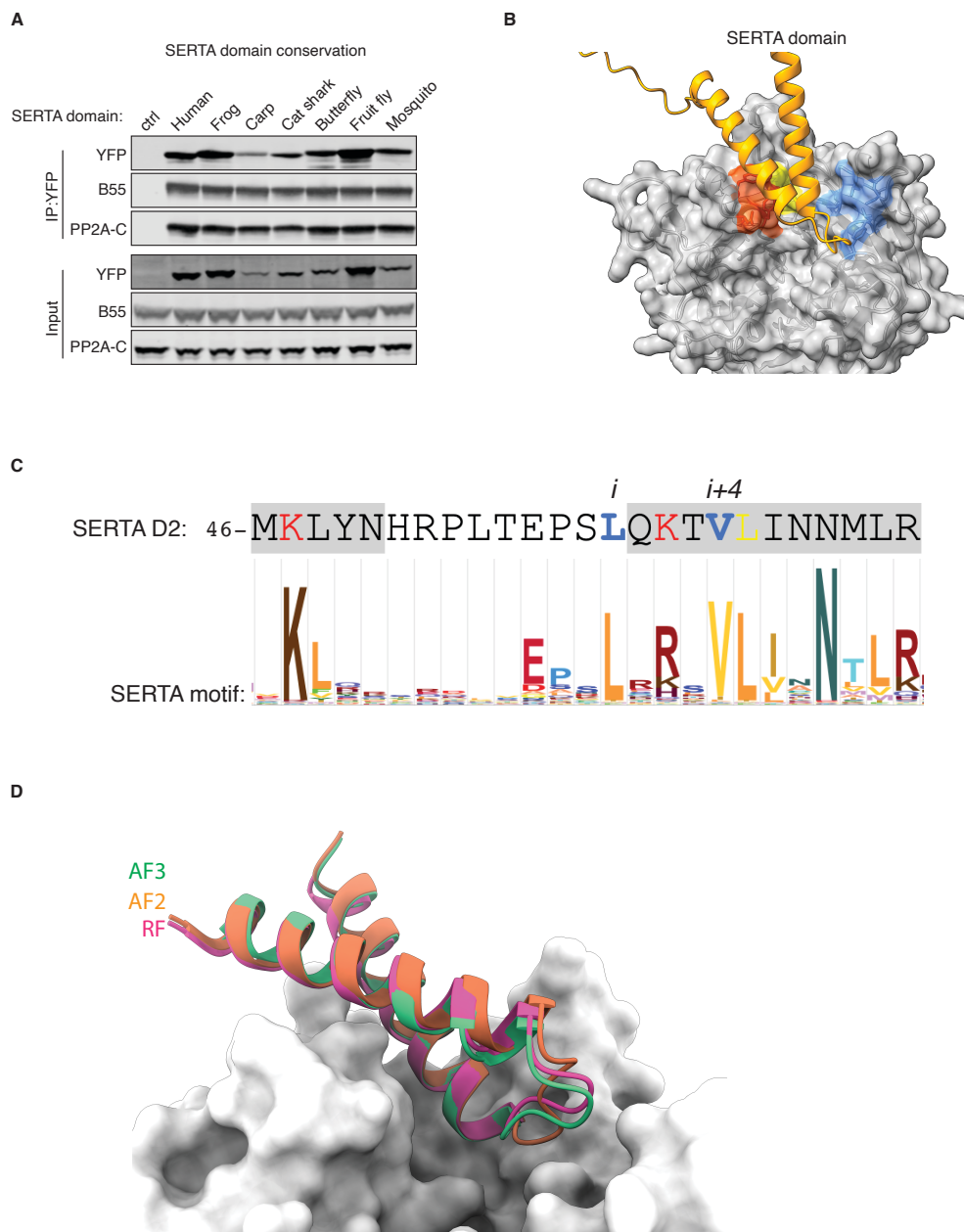
Supplemental Figure S9. Zds1 data.

A) Schematic of Zds1 and sequence binding PP2A-B55 α . Amino acids crucial for binding are indicated by a red line in the schematic. **B)** AF2 model of Zds1 binding helices bound to B55. **C)** Predicted aligned error (PAE) score for the 5 models. **D)** pLDDT score mapped onto model. **E-F)** The indicated YFP tagged protein fragments were expressed in HeLa cells and following immunoprecipitation they were probed for binding to PP2A-B55 by western blot. B55 refers to B55 α . In F) The quantification of two biological replicates is shown with binding normalized to wild type protein. Bars visualize the average of the two biological replicates.



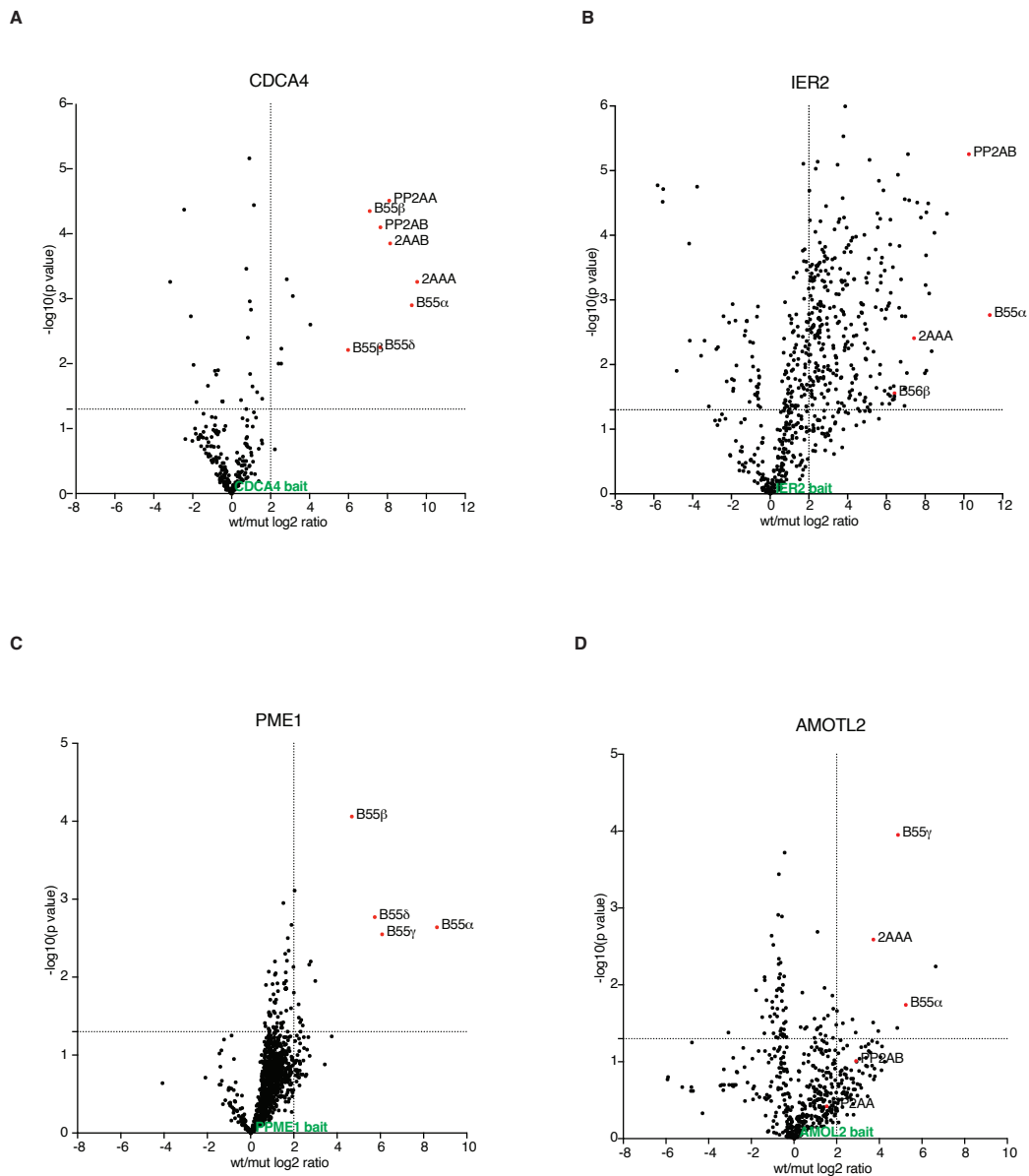
Supplemental Figure S10. E4ORF4 data.

A) Schematic of E4ORF4 and sequence binding PP2A-B55. **B)** AF2 model of E4ORF4 bound to B55. **C)** Predicted aligned error (PAE) score for the 5 models. **D)** pLDDT score mapped onto model. **E)** The indicated YFP tagged protein fragments were expressed in HeLa cells and following immunoprecipitation they were probed for binding to PP2A-B55 by western blot. B55 refers to B55 α . **E)** Bottom panel the quantification of two biological replicates is shown with binding normalized to wild type protein. Bars visualize the average of the two biological replicates.



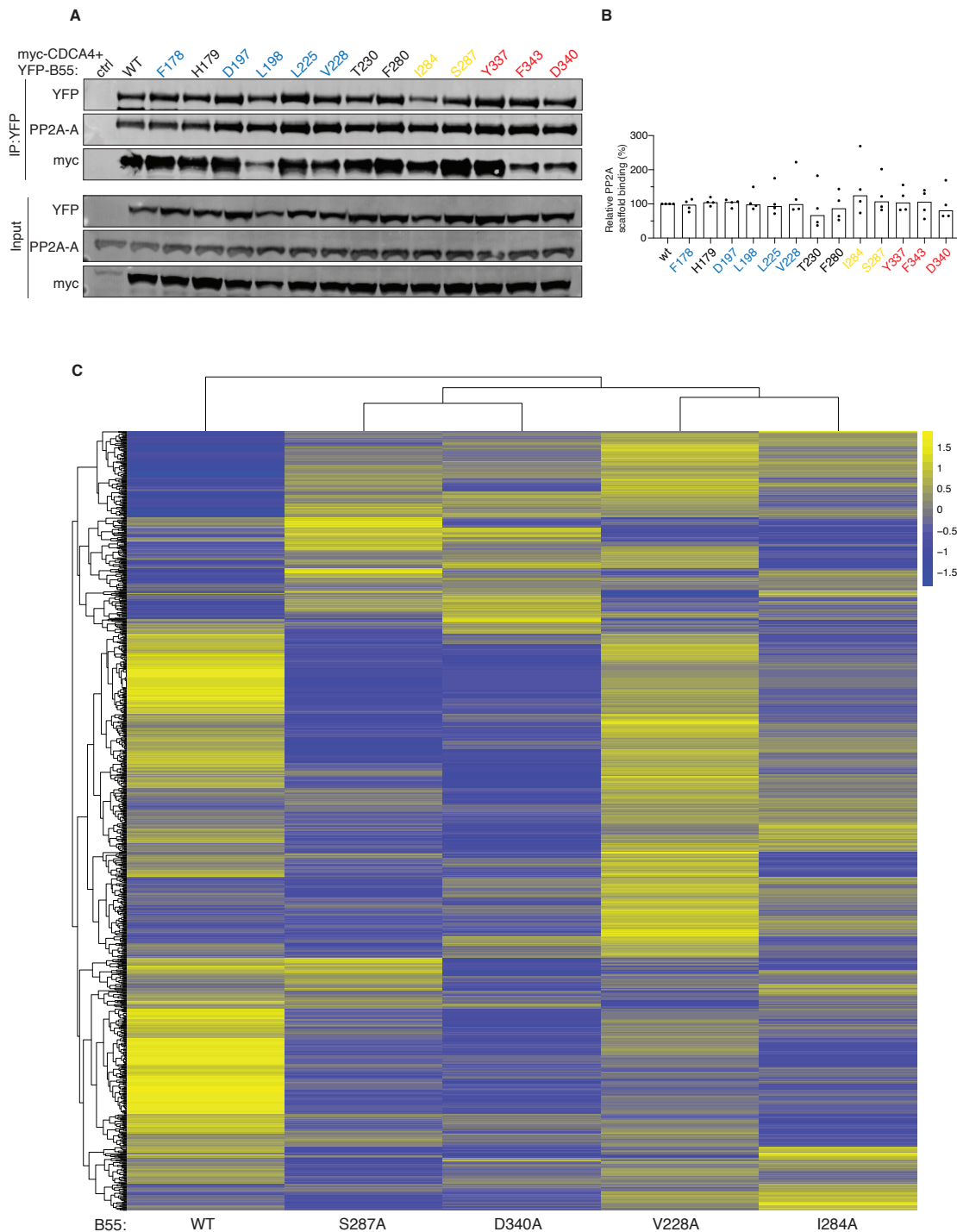
Supplemental Figure S11. Conservation of SERTA domains.

A) YFP tagged SERTA domains from different species were expressed in HeLa cells and binding to PP2A-B55 determined by western-blot. B55 refers to B55 α . **B)** AF2 model of the CDCA4 SERTA domain bound to B55. **C)** Signature of all SERTA domains in the Pfam database showing conservation of key residues (data from Pfam entry 06031) **D)** AF2, AF3 and RosettaFold (RF) predictions of CDCA4 bound to B55. Models are overlaid.



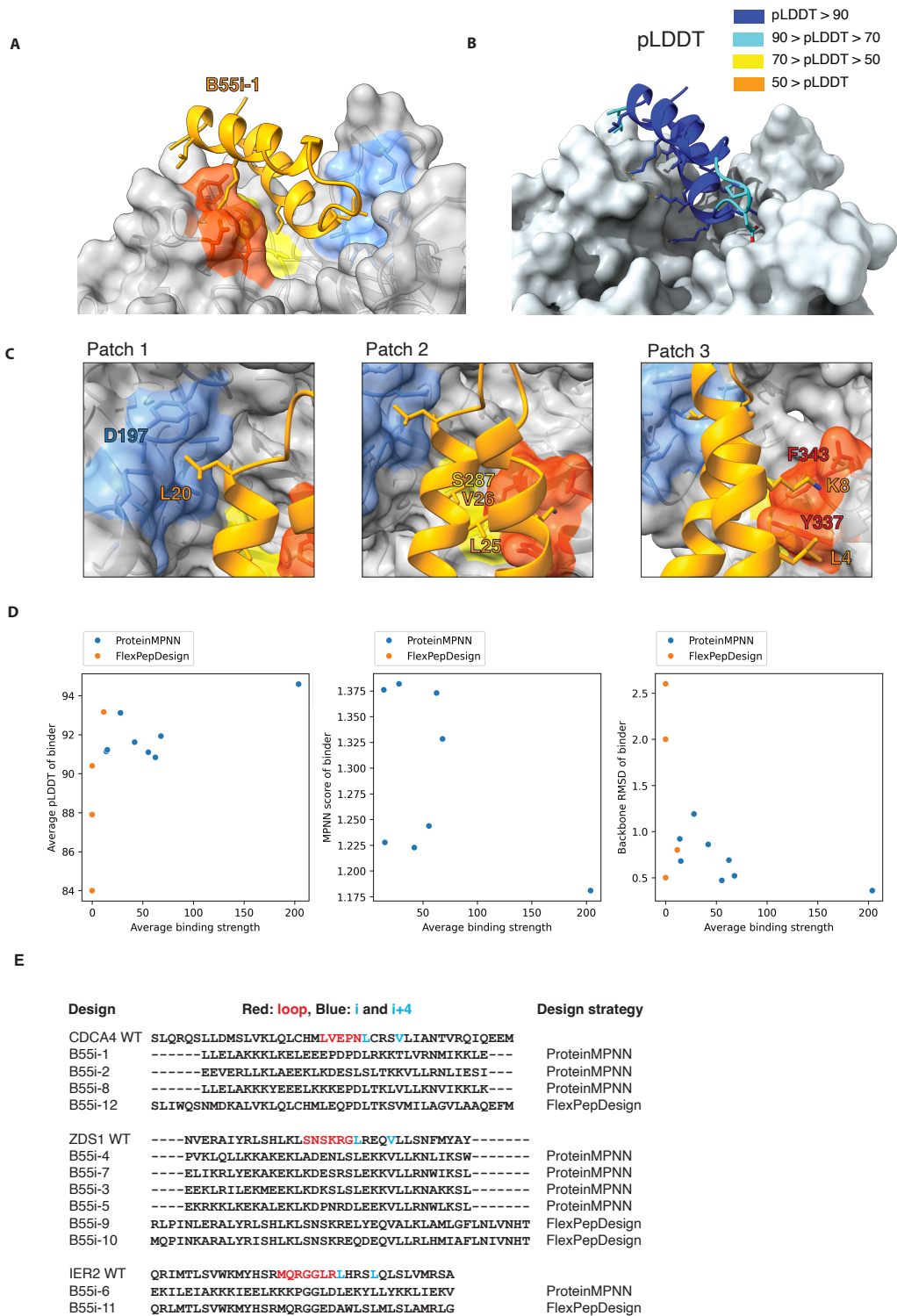
Supplemental Figure S12. Volcano plots of MS data.

A-D) Volcano plots of mass spectrometry analysis of immunopurifications (n=4 technical replicates) of the indicated proteins comparing wild type to a mutant form with the key B55 interacting residues mutated (CDCA4 K44A/V60A/L61A; AMOTL2 T28A/R29A; PME1 L4A; IER2 K17A). PP2AA/B: catalytic subunit, 2AAA: scaffold subunit. See supplemental Table S3 for data.



Supplemental Figure S13. B55 mutant IPs with CDCA4.

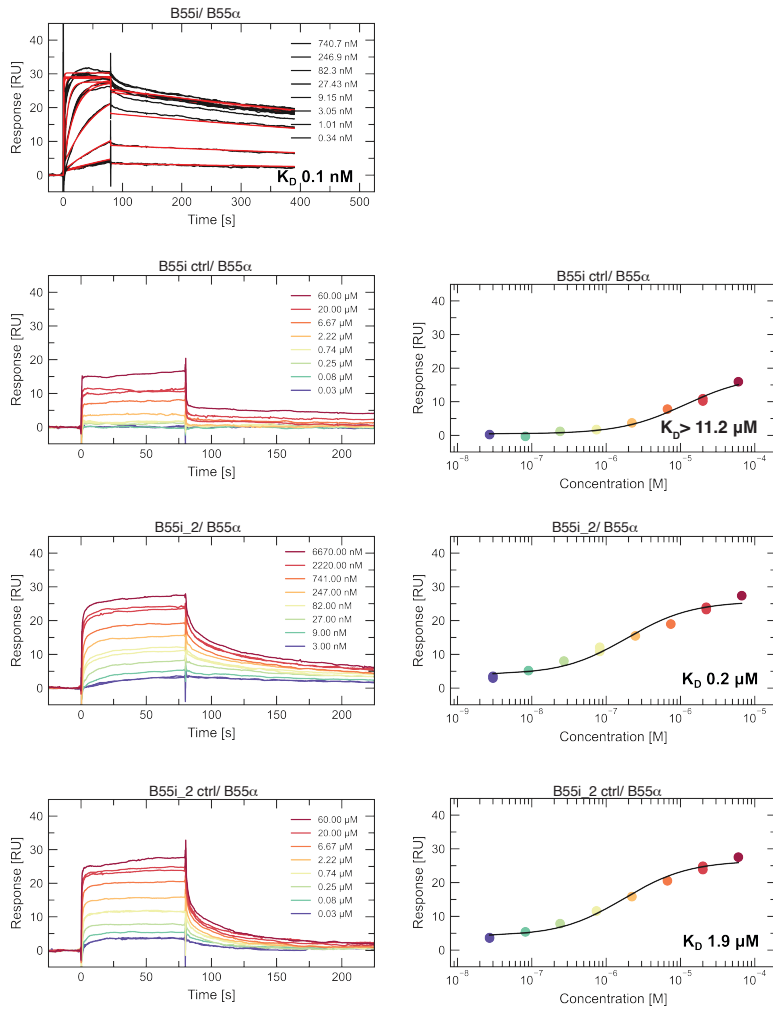
A) Immunoprecipitation of indicated YFP tagged B55 α mutants. Binding to myc-CDCA4 determined by western blot **B)** Quantification of **A)** Relative binding of PP2A scaffold and B55 α to CDCA4; median shown, n=4 biological replicates. **C)** HEAT map relating to Figure 2 showing all proteins identified by mass spectrometry for the indicated B55 α mutants. Scale bar is log₂ and n=4 technical replicates. See Supplemental Table S3 for full data.



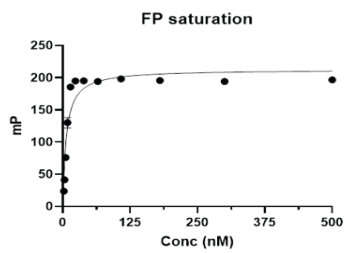
Supplemental Figure S14. B55i and Protein MPNN scores in relation to binding.

A-B) AF model of B55i-1 bound to B55 and pLDDT score. **C)** Zoom in on interactions of B55i-1 with the different patches. **D)** Plots of design scores and binding strength based on immunoprecipitations from HeLa cells of YFP tagged de novo B55 binders. **E)** Amino acid sequence of MPNN and FlexPep generated B55 binding designs.

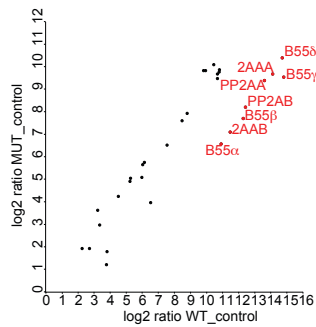
F



G

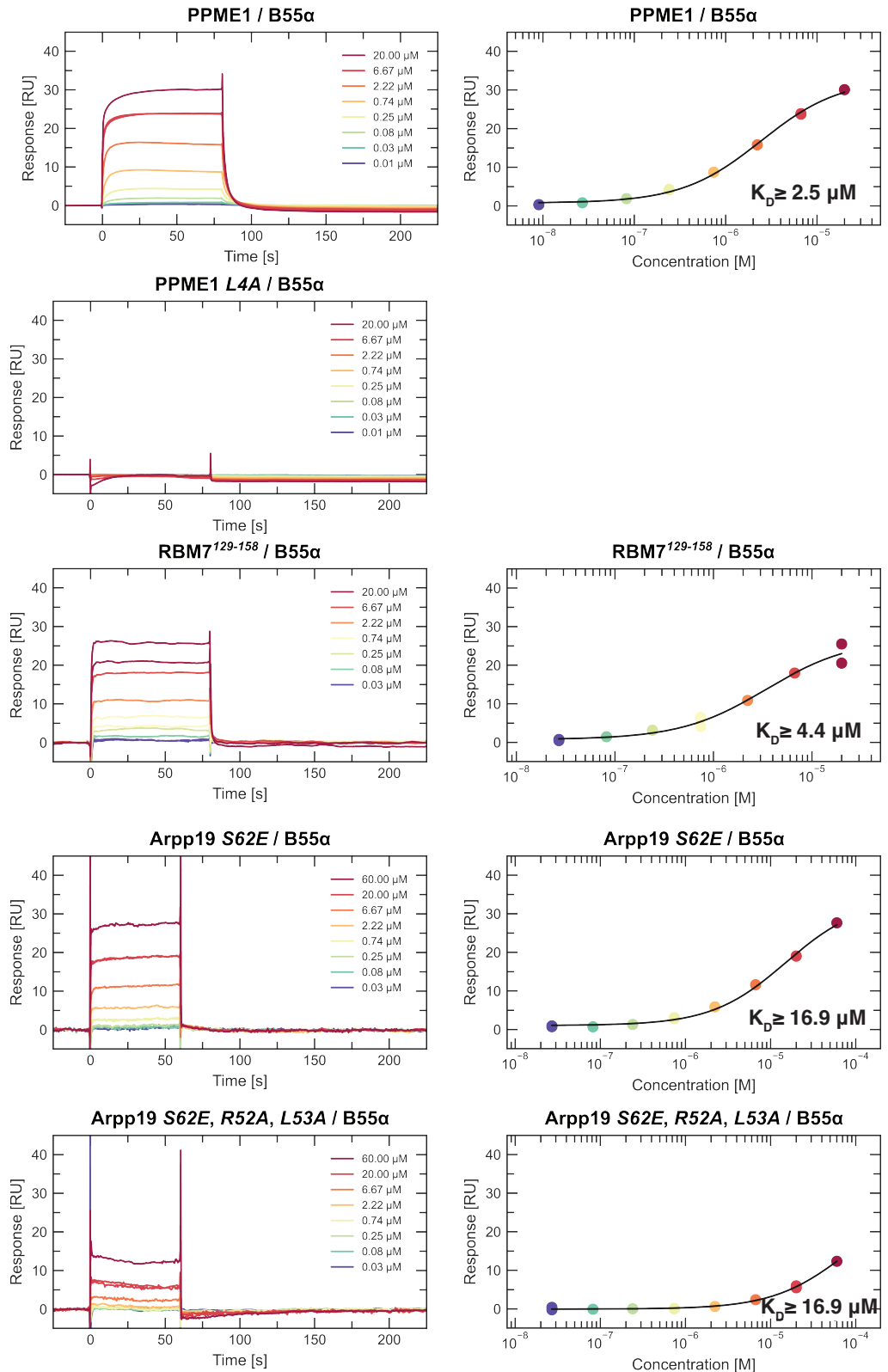


H

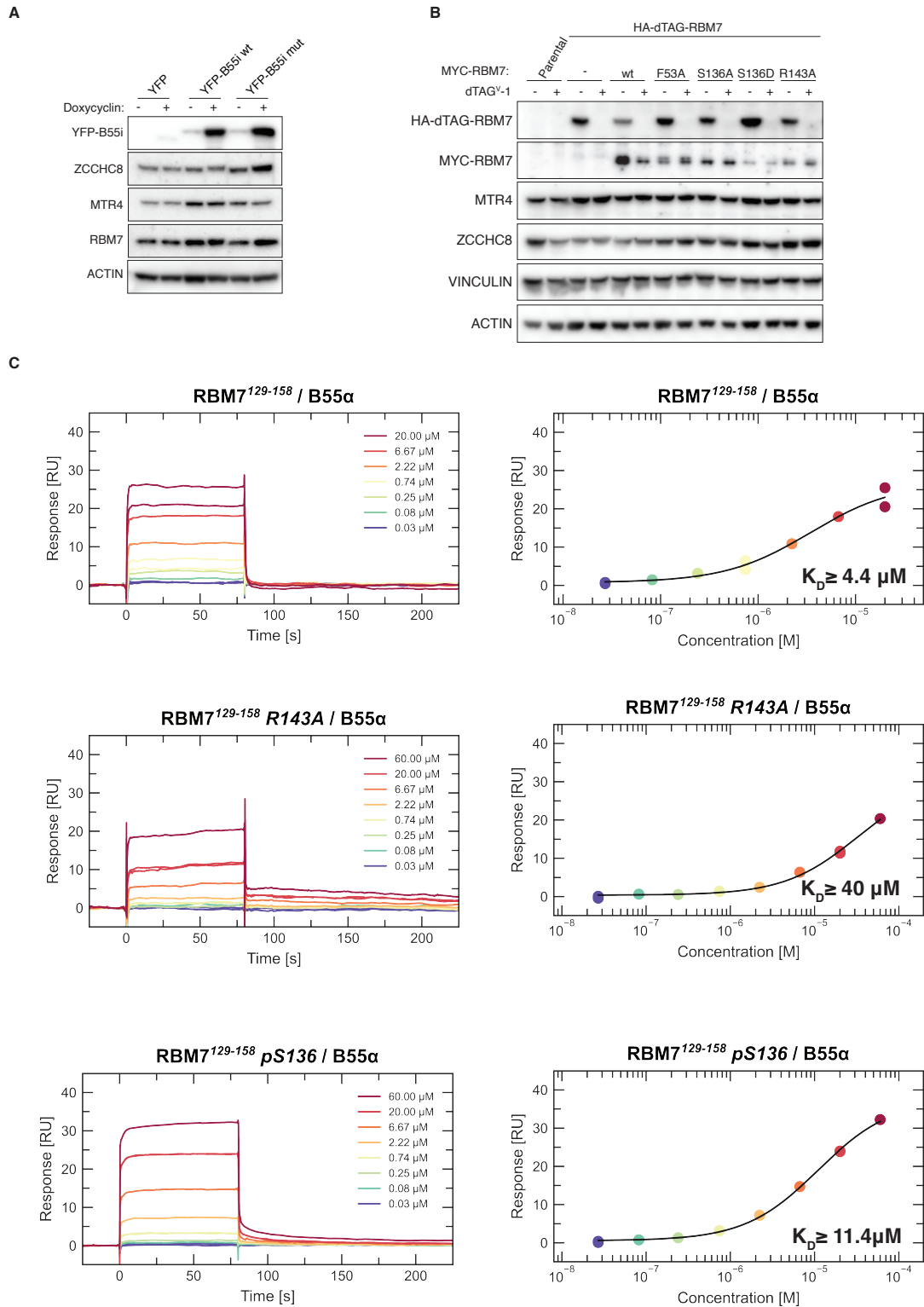


Supplemental Figure S14-continued. SPR and MS data for B55i.

F) SPR data for B55i-1 and B55i-2 peptides binding to B55. **G)** FP measurements for B55i (n=3). **H)** Mass spectrometry analysis of B55i and B55i CTRL based on n=4 technical replicates.



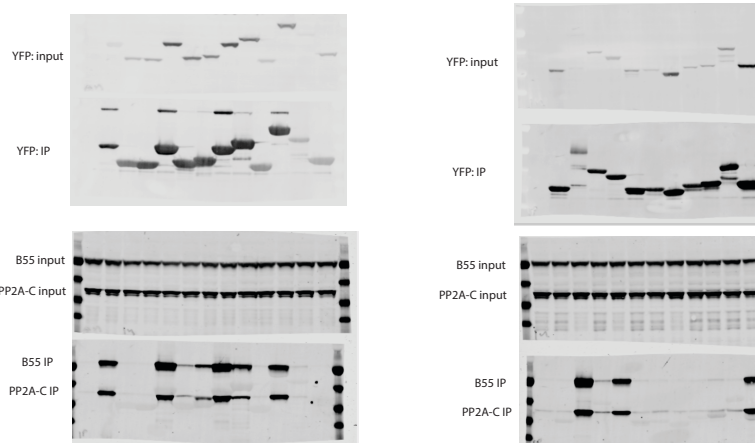
Supplemental Figure S15. SPR data for PME1, Arpp19 and RBM7.
 SPR data for the indicated proteins binding to B55.



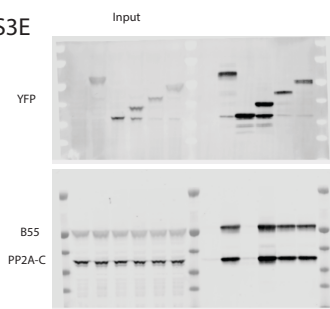
Supplemental Figure S16. Western blots relating to RBM7 biology and RBM7 SPR data.

A) Western blots of B55i-1 expression from inducible HeLa cells. **B)** Removal of HA-dTAG-RBM7 with dTAG-1 and complementation with myc-RBM7 variants. **C)** SPR data for the indicated RBM7 peptides binding to B55.

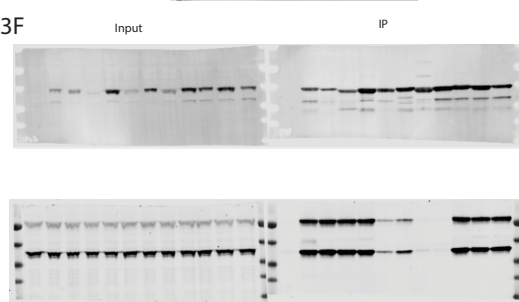
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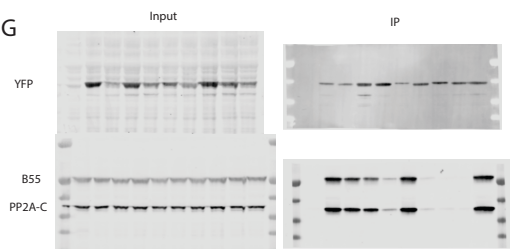
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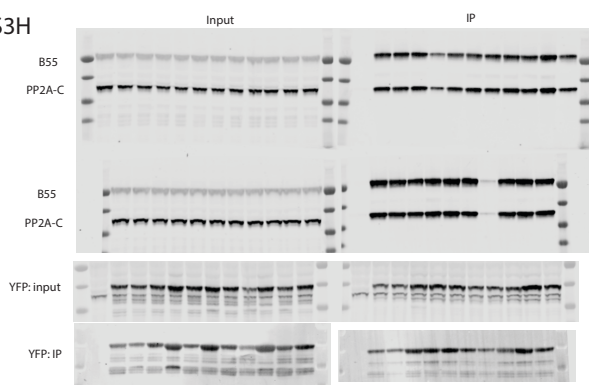
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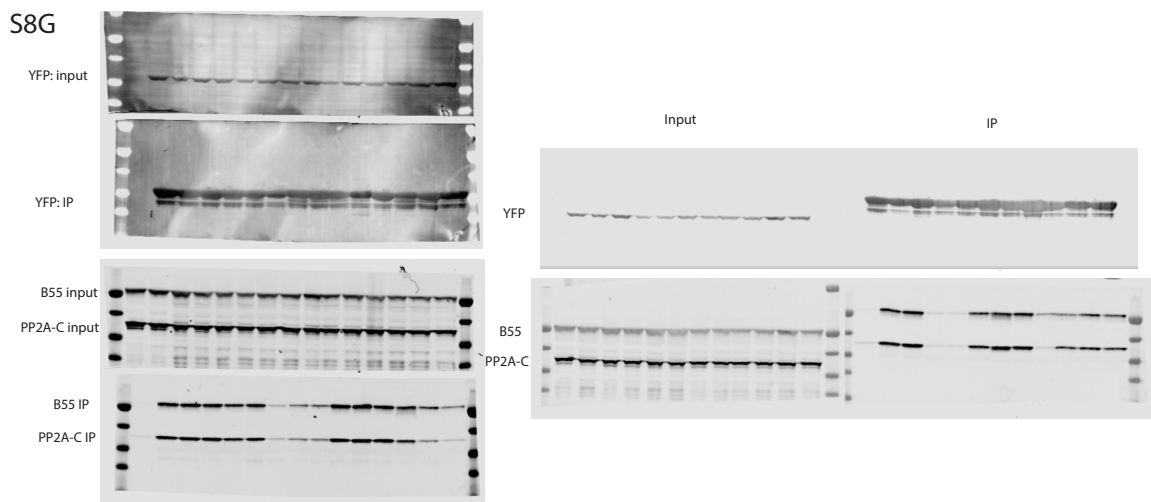
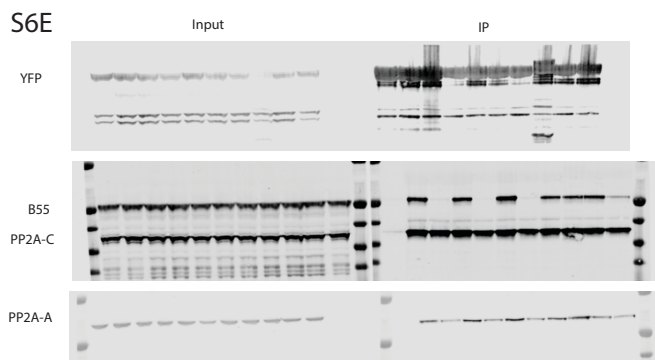
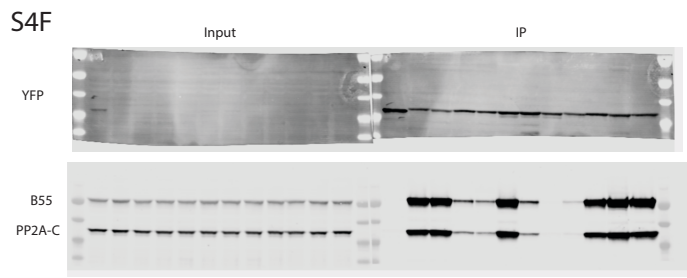
S3G



S3H

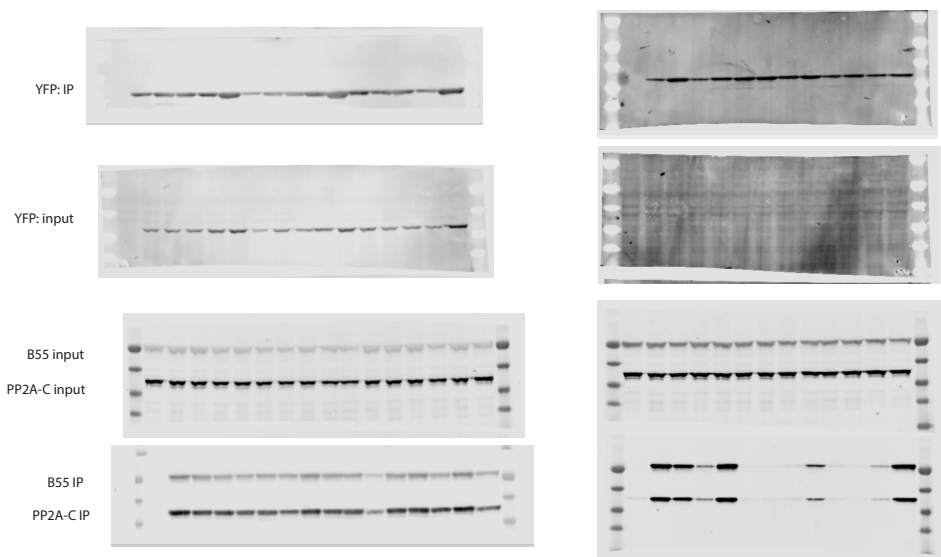


Supplemental Figure S17. Uncropped western blots of selected panels.

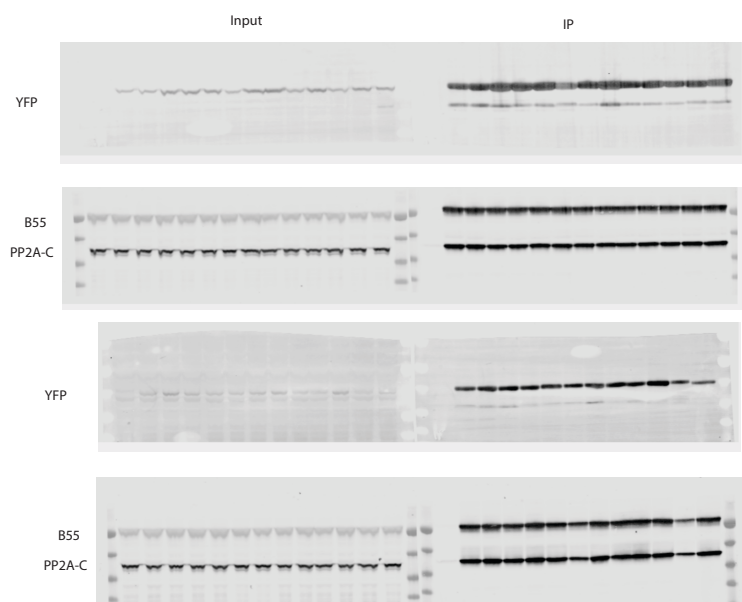


Supplemental Figure S17 continued. Uncropped western blots of selected panels.

S9F



S10E



Supplemental Figure S17 continued. Uncropped western blots of selected panels.

af2_scores

pdb	int_plddt	iPAE
b55_A1X283-SPD2B_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	73.73	9.26
b55_A2A3K4-PTPC1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0.0	24.55
b55_A3KMH1-VWA8_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	65.31	26.28
b55_A3KN83-SBNO1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0.0	22.28
b55_A7KAX9-RHG32_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	58.69	15.41
b55_A8MPP1-D11L8_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	72.52	27.19
b55_O00165-HAX1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0	30
b55_O00311-CDC7_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_2_seed_000.pdb	62.44	22.7
b55_O00505-IMA4_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_2_seed_000.pdb	0.0	25.27
b55_O14530-TXND9_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_3_seed_000.pdb	73.14	26.31
b55_O14734-ACOT8_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_1_seed_000.pdb	0	18.86
b55_O14737-PDCD5_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	84.41	4.27
b55_O14795-UN13B_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	65.47	10.72
b55_O14907-TX1B3_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	71.1	22.62
b55_O15061-SYNEM_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0	30
b55_O43166-SI1L1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	69.19	21.58
b55_O43593-HAIR_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	65.95	8.05
b55_O43768-ENSA_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb	77.41	5.06
b55_O43819-SCO2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0.0	14.35
b55_O60343-TBCD4_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	64.14	14.22
b55_O60548-FOXO2_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb	79.68	6.23
b55_O60610-DIAP1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0	30
b55_O60884-DNJA2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0	30
b55_O60925-PFD1_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	0	12.97
b55_O75190-DNJB6_HUMAN_unrelaxed_rank_005_alphafold2_multimer_v3_model_2_seed_000.pdb	64.31	23.16
b55_O75376-NCOR1_HUMAN_unrelaxed_alphafold2_multimer_v3_model_2_seed_000.pdb	0	12.58
b55_O75665-OFD1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0	30
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b55_O95071-UBR5_HUMAN_unrelaxed_alphafold2_multimer_v3_model_1_seed_000.pdb	0	30
b55_O95263-PDE8B_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_2_seed_000.pdb	77.47	26.86
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b55_P01215-GLHA_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_3_seed_000.pdb	0	24.62
b55_P04792-HSPB1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0.0	7.35
b55_P07900-HS90A_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	62.79	22.92
b55_P08238-HS90B_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	66.88	22.44
b55_P0CG12-DERPC_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	82.4	3.89

Supplemental Table S1. AF2 scores for models with pLDDT and iPAE indicated after pdb file.

b55_P11498-PYC_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	72.93	26.23
b55_P12036-NFH_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0	30
b55_P12270-TPR_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0	30
b55_P13051-UNG_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb	79.4	25.72
b55_P17987-TCPA_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0	30
b55_P19387-RPB3_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	0	30
b55_P23458-JAK1_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	67.14	27.44
b55_P27540-ARNT_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	57.84	15.93
b55_P27708-PYR1_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	75.68	27.66
b55_P29218-IMPA1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	72.58	26.89
b55_P30876-RPB2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0	30
b55_P31689-DNJA1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	66.39	26.02
b55_P31948-STIP1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	63.17	22.95
b55_P32926-DSG3_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	84.95	5.93
b55_P36873-PP1G_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	78.52	19.84
b55_P40227-TCPZ_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_3_seed_000.pdb	0	26.66
b55_P42345-MTOR_HUMAN_unrelaxed_alphafold2_multimer_v3_model_1_seed_000.pdb	83.96	27.75
b55_P48552-NRIP1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	53.92	12.51
b55_P48643-TCPE_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0	16.91
b55_P48681-NEST_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0	30
b55_P49368-TCPG_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0	30
b55_P50990-TCPQ_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0.0	25.45
b55_P50991-TCPD_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_4_seed_000.pdb	0	26.36
b55_P53041-PPP5_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	68.24	24.08
b55_P53634-CATC_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	66.76	26.22
b55_P53814-SMTN_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb	70.95	20.64
b55_P55789-ALR_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0	11.52
b55_P56211-ARP19_HUMAN_unrelaxed_rank_005_alphafold2_multimer_v3_model_4_seed_000.pdb	77.56	4.71
b55_P56524-HDAC4_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	54.55	12.74
b55_P60510-PP4C_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	78.39	8.01
b55_P61758-PFD3_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_4_seed_000.pdb	65.94	30
b55_P62136-PP1A_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	79.75	22.11
b55_P62140-PP1B_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	0.0	13.51
b55_P63151-2ABA_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_3_seed_000.pdb	72.77	23.09
b55_P78371-TCPB_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	65.46	26.69
b55_P86791-CCZ1_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	0.0	16.38
b55_Q00005-2ABB_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	75.07	21.14
b55_Q00587-BORG5_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	70.91	7.94
b55_Q05209-PTN12_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_3_seed_000.pdb	76.67	20.7
b55_Q08209-PP2BA_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_1_seed_000.pdb	0.0	26.68

Supplemental Table S1 continued. AF2 scores for models with pLDDT and iPAE indicated after pdb file.

b55_Q08AF3-SLFN5_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	69.07	27.17
b55_Q0VG06-FP100_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	68.07	26.7
b55_Q12815-TROAP_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	73.87	5.38
b55_Q12851-M4K2_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb	71.28	25.25
b55_Q12948-FOXC1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	84.19	4.39
b55_Q13015-AF1Q_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	0	30
b55_Q13049-TRI32_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_4_seed_000.pdb	67.48	24.38
b55_Q13322-GRB10_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	68.71	26.3
b55_Q13371-PHLP_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	75.4	7.03
b55_Q13451-FKBP5_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	74.06	19.1
b55_Q13523-PRP4B_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	60.56	12.73
b55_Q13671-RIN1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	72.99	5.86
b55_Q14140-SRTD2_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	92.53	2.16
b55_Q14678-KANK1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	0	9.57
b55_Q15031-SYLM_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_3_seed_000.pdb	75.96	26.16
b55_Q15438-CYH1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	69.31	11.83
b55_Q15468-STIL_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb	0.0	13.74
b55_Q15773-MLF2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	68.78	9.06
b55_Q16342-PDCD2_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_5_seed_000.pdb	82.2	24.47
b55_Q16563-SYPL1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	59.95	12.11
b55_Q16584-M3K11_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	66.74	24.78
b55_Q1MSJ5-CSPP1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	77.31	5.68
b55_Q2KHR3-QSER1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	59.27	23.66
b55_Q2M3G4-SHRM1_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_3_seed_000.pdb	73.59	15.77
b55_Q32MH5-ATOSA_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb	89.82	3.27
b55_Q3YEC7-RABL6_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0.0	17.72
b55_Q53ET0-CRTC2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	0	30
b55_Q58FF8-H90B2_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	0.0	22.53
b55_Q58WW2-DCAF6_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	0.0	26.14
b55_Q5M775-CYTSB_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	71.56	9.81
b55_Q5T447-HECD3_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	71.27	27.62
b55_Q5T5U3-RHG21_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	0.0	8.52
b55_Q5T953-IER5L_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	90.5	2.03
b55_Q5T9S5-CCD18_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0	30
b55_Q5VT52-RPRD2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0.0	8.1
b55_Q5VY09-IER5_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	90.91	2.43
b55_Q63ZY3-KANK2_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	56.69	13.2
b55_Q66LE6-2ABD_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	74.6	21.59
b55_Q6BDS2-BLT3A_HUMAN_unrelaxed_rank_005_alphafold2_multimer_v3_model_4_seed_000.pdb	80.91	26.42
b55_Q6NYC8-PPR18_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0	30

Supplemental Table S1 continued. AF2 scores for models with pLDDT and iPAE indicated after pdb file.

b55_Q6NZY4-ZCHC8_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0	30
b55_Q6P3X3-TTC27_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_3_seed_000.pdb	74.7	28.36
b55_Q6P996-PDXD1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	80.79	27.48
b55_Q6PID6-TTC33_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	73.23	25.44
b55_Q6UUV7-CRTC3_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	0	30
b55_Q70CQ4-UBP31_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb	0.0	10.02
b55_Q70EL4-UBP43_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	63.92	9.12
b55_Q7RTV0-PHF5A_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0.0	20.2
b55_Q7Z401-MYCPP_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_1_seed_000.pdb	68.42	27.59
b55_Q7Z7K0-COXM1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb	59.97	22.11
b55_Q86SQ0-PHLB2_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	0.0	25.94
b55_Q86TC9-MYPN_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_5_seed_000.pdb	0.0	21.66
b55_Q86U70-LDB1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0.0	24.52
b55_Q86UU1-PHLB1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_3_seed_000.pdb	73.11	13.88
b55_Q8IY67-RAVR1_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_2_seed_000.pdb	0.0	23.84
b55_Q8N157-AHI1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	80.41	13.94
b55_Q8N163-CCAR2_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	0	27.78
b55_Q8N5M4-TTC9C_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	75.21	17.14
b55_Q8N612-FHI1B_HUMAN_unrelaxed_rank_005_alphafold2_multimer_v3_model_2_seed_000.pdb	86.14	28.33
b55_Q8N8E3-CE112_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_1_seed_000.pdb	67.59	26.52
b55_Q8NDG6-TDRD9_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	75.26	26.09
b55_Q8NHY2-COP1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	83.5	10.85
b55_Q8TBC3-SHKB1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_3_seed_000.pdb	69.2	24.78
b55_Q8TCS8-PNPT1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb	0.0	27.75
b55_Q8TEP8-CE192_HUMAN_unrelaxed_alphafold2_multimer_v3_model_1_seed_000.pdb	68.18	27.75
b55_Q8TEU7-RPGF6_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0.0	27.08
b55_Q8TF61-FBX41_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	68.55	8.16
b55_Q8WUF5-IASPP_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	60.77	9.71
b55_Q8WUI4-HDAC7_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	69.85	26.27
b55_Q8WUK0-PTPM1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	82.57	4.2
b55_Q8WUM9-S20A1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	79.37	3.87
b55_Q8WV74-NUDT8_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	64.39	12.93
b55_Q8WW01-SEN15_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	68.47	20.39
b55_Q8WXG6-MADD_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0.0	28.11
b55_Q92526-TCPW_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0	30
b55_Q92540-SMG7_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb	64.35	15.07
b55_Q92771-DDX12_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb	0.0	27.2
b55_Q96A73-P33MX_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	62.11	10.34
b55_Q96AT1-K1143_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0	13.99
b55_Q96D53-COQ8B_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_3_seed_000.pdb	0.0	23.81

Supplemental Table S1 continued. AF2 scores for models with pLDDT and iPAE indicated after pdb file.

b55_Q96D71-REPS1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	0	13.81
b55_Q96DF8-ESS2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	63.71	10.33
b55_Q96E09-PBIR1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	82.4	2.99
b55_Q96FC9-DDX11_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb	75.57	26.98
b55_Q96HB5-CC120_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_3_seed_000.pdb	0	22.55
b55_Q96I18-LRCH3_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	72.13	9.43
b55_Q96IU2-ZBED3_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_3_seed_000.pdb	0	25.5
b55_Q96N67-DOCK7_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0	30
b55_Q96PE3-INP4A_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	82.04	25.95
b55_Q96QU8-XPO6_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_2_seed_000.pdb	76.56	27.92
b55_Q96RT1-ERBIN_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0	26.28
b55_Q99471-PFD5_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	0	30
b55_Q99504-EYA3_HUMAN_unrelaxed_rank_005_alphafold2_multimer_v3_model_4_seed_000.pdb	76.04	25.12
b55_Q99550-MPP9_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	59.99	11.63
b55_Q99832-TCPH_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_3_seed_000.pdb	83.41	28.53
b55_Q99933-BAG1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb	65.63	20.67
b55_Q99958-FOXC2_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	75.17	8.7
b55_Q99959-PKP2_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_3_seed_000.pdb	77.97	25.11
b55_Q9BQ95-ECSIT_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	73.54	25.25
b55_Q9BRK5-CAB45_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb	71.53	25.22
b55_Q9BRQ8-FSP1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	96.89	2.41
b55_Q9BSJ6-PIMRE_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	0	9.49
b55_Q9BSV6-SEN34_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0	30
b55_Q9BTL4-IER2_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	89.46	2.4
b55_Q9BU02-THTPA_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	69.75	21.19
b55_Q9BU61-NDUF3_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	0	24.95
b55_Q9BUP3-HTAI2_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_5_seed_000.pdb	62.21	18.39
b55_Q9BW92-SYTM_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	77.53	23.48
b55_Q9BWT7-CAR10_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	59.56	19.12
b55_Q9BXF6-RFIP5_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_2_seed_000.pdb	55.96	17.81
b55_Q9BXL8-CDCA4_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb	94.28	1.73
b55_Q9BYV8-CEP41_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_2_seed_000.pdb	0.0	26.64
b55_Q9BZL6-KPCD2_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_3_seed_000.pdb	64.39	25.06
b55_Q9C0B7-TNG6_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	0	30
b55_Q9H0K1-SIK2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	82.48	3.58
b55_Q9H0R5-GBP3_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	0.0	26.39
b55_Q9H1H9-KI13A_HUMAN_unrelaxed_rank_005_alphafold2_multimer_v3_model_4_seed_000.pdb	66.54	26.64
b55_Q9H2J4-PDCL3_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_3_seed_000.pdb	0.0	23.97
b55_Q9H4G0-E41L1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	84.2	5.02
b55_Q9H4M9-EHD1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	69.63	19.06

Supplemental Table S1 continued. AF2 scores for models with pLDDT and iPAE indicated after pdb file.

b55_Q9H5N1-RABE2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	61.69	17.72
b55_Q9H5Z1-DHX35_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	76.47	12.42
b55_Q9H845-ACAD9_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	0.0	18.16
b55_Q9H910-JUPI2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	0	11.65
b55_Q9HCN8-SDF2L_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	83.72	24.62
b55_Q9NXX1-TUFT1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	77.25	9.48
b55_Q9NQ35-NRIP3_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	73.09	4.59
b55_Q9NQI0-DDX4_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	82.5	23.61
b55_Q9NQP4-PFD4_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	0	26.58
b55_Q9NQT8-KI13B_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	65.89	9.77
b55_Q9NR46-SHLB2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	65.73	8.98
b55_Q9NRA8-4ET_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	69.39	7.13
b55_Q9NRL3-STRN4_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	0.0	25.8
b55_Q9NRV9-HEBP1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	0.0	17.03
b55_Q9NSY1-BMP2K_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	64.61	13.47
b55_Q9NTX5-ECHD1_HUMAN_unrelaxed_rank_005_alphafold2_multimer_v3_model_2_seed_000.pdb	76.48	25.95
b55_Q9NUJ3-T11L1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb	61.26	26.64
b55_Q9NUP9-LIN7C_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0.0	23.45
b55_Q9NZ71-RTLE1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	69.82	12.29
b55_Q9NZW5-PALS2_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb	0.0	24.89
b55_Q9P0K8-FOXJ2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	77.34	9.42
b55_Q9P202-WHRN_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	64.86	9.99
b55_Q9P227-RHG23_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb	58.69	13.43
b55_Q9P270-SLAI2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	62.22	14.93
b55_Q9P210-CPSF2_HUMAN_unrelaxed_rank_004_alphafold2_multimer_v3_model_1_seed_000.pdb	69.28	27.06
b55_Q9UBI6-GBG12_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	0	30
b55_Q9UDT6-CLIP2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	80.87	4.48
b55_Q9UDY4-DNJB4_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	73.09	27.41
b55_Q9UGU0-TCF20_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0.0	9.26
b55_Q9UHB6-LIMA1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	60.0	11.67
b55_Q9UJY1-HSPB8_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_2_seed_000.pdb	0	25.83
b55_Q9UKY7-CDV3_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	0	11.74
b55_Q9UL15-BAG5_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	69.34	25.44
b55_Q9UNE7-CHIP_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_1_seed_000.pdb	66.98	25.16
b55_Q9UPQ0-LIMC1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	73.4	5.49
b55_Q9UPQ4-TRI35_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	72.63	27.3
b55_Q9UQL6-HDAC5_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	0.0	12.86
b55_Q9Y2H2-SAC2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0	14.95
b55_Q9Y2H5-PKHA6_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_4_seed_000.pdb	68.3	8.59
b55_Q9Y2J4-AMOL2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	64.32	11.27

Supplemental Table S1 continued. AF2 scores for models with pLDDT and iPAE indicated after pdb file.

b55_Q9Y2K2-SIK3_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	63.81	10.37
b55_Q9Y2Q3-GSTK1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_5_seed_000.pdb	69.74	22.84
b55_Q9Y2Z0-SGT1_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_2_seed_000.pdb	0.0	25.17
b55_Q9Y371-SHLB1_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_3_seed_000.pdb	64.44	19.0
b55_Q9Y375-CIA30_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_2_seed_000.pdb	62.51	16.86
b55_Q9Y3X0-CCDC9_HUMAN_unrelaxed_rank_003_alphafold2_multimer_v3_model_5_seed_000.pdb	0	21.68
b55_Q9Y446-PKP3_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_1_seed_000.pdb	0.0	11.04
b55_Q9Y4R8-TELO2_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	0	30
b55_Q9Y570-PPME1_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb	75.52	5.41
b55_Q9Y580-RBM7_HUMAN_unrelaxed_rank_002_alphafold2_multimer_v3_model_1_seed_000.pdb	79.41	5.69
b55_Q9Y597-KCTD3_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb	65.54	18.64
b55_Q9Y618-NCOR2_HUMAN_unrelaxed_alphafold2_multimer_v3_model_1_seed_000.pdb	66.88	6.69
b55_Q9Y6Q9-NCOA3_HUMAN_unrelaxed_rank_001_alphafold2_multimer_v3_model_4_seed_000.pdb	64.93	6.14

Supplemental Table S1 continued. AF2 scores for models with pLDDT and iPAE indicated after pdb file.

Table S2: Metrics of designed binders

Table S3: Mass spectrometry data

Table S4: Computational alanine scanning of B55 binders

Supplemental dataset 1: Alphafold models pdb files.