

Supplemental information

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non-catalytic subunit PPP1R15B**

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Figures S1-S6 and accompanying text

Table S2

Figure S1 Multiple sequence alignment of R15B orthologs. Related to Figure 1

Sequences were aligned using Mafft⁷⁶ and coloured according to Clustal⁸⁰ colouring scheme. Colour intensity indicates sequence conservation. A black arrow shows the beginning of the fragment used in this study.

Figure S2 HDX-MS analyses of eIF2 in the presence of R15B⁴¹⁴⁻⁶¹³. Related to Figure 2

(A-C) Sequence coverage map in HDX-MS analyses of eIF2 α (A), β (B) and γ (C) in presence of R15B⁴¹⁴⁻⁶¹³. Bars represent the peptic peptides of eIF2 plotted against the amino acid sequence.

(D-L) Woods plots showing differences in deuterium uptake for eIF2 in the presence or absence of R15B⁴¹⁴⁻⁶¹³. Deprotected, protected and non-significantly different peptides are in red, blue and grey respectively plotted as Δ fraction exchanged (Y-axis). Bar length corresponds to peptide length plotted against the sequence position (X-axis). Dashed and dotted lines indicate 98 and 99% confidence intervals applied to identify peptides with statistically significant deuteration differences. Data for eIF2 α 3 sec, 30 sec, 50 min; eIF2 β 30 sec, 5 min, 50 min and eIF2 γ 30 sec, 5 min and 50 min are shown in panels (D-L) respectively. Error bars denote combined uncertainty of peptide deuteration calculated based on triplicate experiments.

Figure S3 HDX-MS analyses for R15B⁴¹⁴⁻⁶¹³. Related to Figure 3

(A) Plot showing HDX for a given R15B⁴¹⁴⁻⁶¹³ peptide following 3 sec incubation with D₂O. Bars indicate the peptic peptides of R15B⁴¹⁴⁻⁶¹³ plotted against the amino acid sequence (X-axis). Y-axis: fraction of deuteration peptide compared to maximum level of measured deuteration. Error bars represent combined uncertainty calculated on triplicate experiments.

(B) Sequence coverage of R15B⁴¹⁴⁻⁶¹³ in presence of eIF2 in HDX analyses. Bars indicate the peptic peptides of R15B⁴¹⁴⁻⁶¹³ plotted on the amino acid sequence.

Figure S4 ^{15}N backbone relaxation of R15B⁴¹⁴⁻⁶¹³ alone and in the presence of 10% eIF2. Related to Figure 4.

- (A-E) Experimental ^{15}N backbone relaxation data for R15B⁴¹⁴⁻⁶¹³ at 281.5K.
(G-K) Experimental ^{15}N backbone relaxation data for R15B⁴¹⁴⁻⁶¹³ in the presence of eIF2 at 281.5K.
- (A, G) $\{\text{H}\}-^{15}\text{N}$ NOE,
(B, H) R_2
(C, I) η_{xy}
(D, J) R_1
(E, K) Superposition of measured R_2 (black line) and calculated exchange free R_2^0 (blue). Exchange contribution (Rex, red line).
(F) Peak intensity ratio of $^1\text{H}, ^{15}\text{N}$ 2D spectra of R15B⁴¹⁴⁻⁶¹³ on its own and after addition of 10% eIF2, only a modest degree of local attenuation was observed.

Figure S5 Sequence alignments of R15B⁴¹⁴⁻⁶³⁹. Related to Figure 5

- (A) Pair-wise sequence alignments of the human R15B sequence repeats.
(B) Multiple sequence alignments of the first R15B repeat and the homologous sequence repeats identified in human R15A.
(C) Same as in (B) with the addition of R15 from Drosophila melanogaster (dm), ICP34 from the human Herpes simplex virus 1 (hhv1) and DP71L from the African swine fever virus (asfv).

Figure S6 pLDDT of R15B-eIF2 AlphaFold2 model. Related to Figure 7

- (A) pLDDT scores shown for R15B⁴¹⁴⁻⁶¹³, eIF2 α 1-315, eIF2 β 167-333, eIF2 γ 1-472 as a contiguous representation.
(B) As in (A) with R15B⁴¹⁴⁻⁵⁰⁰.

Table S2 Oligonucleotides used in this study. Related to STAR methods.

Figure S1

PR15B_HUMAN	340 RD N P T Q F V P A A G D I P G N T Q E S - T E E K I E L L T T E V P L A L E E E S P - S E G C P S S E I P M E - - - K E P G E G R I S V V D Y S Y L E G D L P I S A R P A C S N K L I D Y I 429
A0A2R9BET9_PANPA	340 RD N P T Q F V P A A G G I P G N T Q E S - T E E K I E L L T T E V P L A L E E E S P - S E G C P S S E I P M E - - - K E P G E G R I S V V D Y S Y L E G D L P I S A R P A C S N K L I D Y I 429
H2Q0Y9_PANTR	340 RD N P T Q F V P A A G G I P G N T Q E S - T E E K I E L L T T E V P L A L E E E S P - S E G C P S S E I P M E - - - K E P G E G R I S V V D Y S Y L E G D L P I S A R P A C S N K L I D Y I 429
H2N419_PONAB	340 RD N P T Q F V P A A G D I P G N T Q E P - T E G K I E L L T T E V P L A L E E E S P - S E G C P S C E I P M E - - - K E P G E G R I S V V D Y S Y L E N D L P V S A R P A C S N K L I D Y I 429
E1BKX2_BOVIN	331 G D S P T Q C V P A A G V P G T A Q E P - T E E K T E L L I R E V P F G L E R Q G P - S G G I L S C E L P V E - - - T G - - - Q E L G E D Q I S V V D S S D I E D D L P I S A R P A C S N K L I D Y I 418
PR15B_MOUSE	333 T D N P A Q A V S P A A D R P - - - E P - T E K K P E L V I Q E V S - - - - Q S P - Q G S S L S C E L S V Q - - - K E C E E D H T N A T D L S D R C E S L P V S T R P V C S N K L I D Y I 413
D3ZP67_RAT	334 T D K A A Q A V S P A G A S P - - - Q P - T E K K V E L V V E E V L - - - - Q S P - Q G S S L S C E L S V Q - - - K E C E - - - - - D Y S D I G G N L P V S T R P A C T N K L I D Y I 407
E2RII3_CANLF	331 G D S P A Q C V P S A G V V P R R A Q D P - A E E D P P V I S A K E A P L A L E R Q G P S S E G C P S A G V P A G V P A S K E P G E D Q V S V G D S S D L E D S I P A S T R P A C S N R L I D Y I 425
M3WUP7_FELCA	339 G D S P T Q C V P S A G A V P G T A O K P G T E E E V A L V T T E D P L A V E K F G P - S E G C P S R E V P V E - - - - K E P G E D Q I S V V D S S D L E D D I P L S S R P A C S N R L I D Y I 429
G1L2H7_AILME	335 G D S P T Q C V P S V G A A P G A A Q K P - T E - - - - L T K E V P L A P E K F G P - S E G C P S G E L P V E - - - - K E P G E D Q R Q S A G D S S D L E D D I P T S T R P A C S N R L I D Y I 419
I3LIA2_PIG	340 R D S P T Q C I P V - - - P G T A Q E P - T E E K I E L L T T E V P L A L E R H D S - S E S C A S C E F P A E - - - - Q E P G E D Q I S V V D S S D I E D D L P T S A R P A C S N K L I D Y I 425
HOX5S2_OTOGA	342 R D N T T Q F V P V P A G A I P G T T Q E L - T E E K I E L L T T E I P H A L E K Q S P - L E S C P S C E V P M V - - - - K E P R E D Q I S V V D Y S C - K D D L P I S T R P A C S N K L I D Y I 430
HOV6Q0_CAVPO	338 G A I P - - - - A G A V P G N N Q S - G E E K R E L L E T E I P L A L E Q G P - L G S P F S V E V A V E - - - - K E P G E D Q V S V V D S C D I E D G L P L S A R P A C G N K L I D Y I 421
G7NVE1_MACFA	337 R D N P T Q F V P A A R E D I P G T T Q E S - T E E K I E L L T T E V P L A L E Q S P - S E S C P S C E I P M E - - - - K E P G E G R I S V V D Y S Y L K D D L P I S A R P A C S N K L I D Y I 426
W5NWS5_SHEEP	336 G D S P T Q C V P A A G V P G T A Q E P - T E E K T E L L I R E V P F G L E R Q S P - S G G I P S C E - - - - T G - - - - Q E L G E D Q I S V V D P P D I D D L P I S A R P A C S N K L I D Y I 423
A0A2K6RYB9_SAIBB	340 R G N P T Q F V P V P A G D I P G T T Q E S - T E E K I E L L T T E V P L A L E Q S P - S E S C P S C E I P M E - - - - K E P G E D G I S V I D Y S C I G N A L P I S A R P A C S N K L I D Y I 429
A0A2K5F0R6_AOTNA	340 R D N P T Q F V P S P A G D I P G T T Q E S - T E E K I A L L T T E V P L A L E Q S S - S E S C P S C E I P M E - - - - K E P G E D R I S V V G Y S C I G D D L P I S A R P A C S N K L I D Y I 429
A0A5F7ZW85_MACMU	338 R D N P T Q F V P A A R E D I P G T T Q E S - T E E K I E L L T T E V P L A L E Q S P - S E S F P S C E I P M E - - - - K E P G E G R I S V V D Y S Y L K D D L P I S A R P A C S N K L I D Y I 427
PR15B_HUMAN	430 L G G A S S D L E T S S D P E G E D D I D D F E E A E D D G F D S D S S L S D S D L B Q D P E G L H L W N S F C I S V D P Y N P Q N F T A T I T I T A A R I V P E E P S D S E K D L L G K S D L E N S Q 525
A0A2R9BET9_PANPA	430 L G G A S S D L E T S S D P E G E D D W D D E E A E D D G F D S D S S L S D S D L B Q D P E G L H L W N S F C I S V D P Y N P Q N F T A T I T I T A A R I V P E E P S D S E K D L L G K S D L E N S Q 525
H2Q0Y9_PANTR	430 L G G A S S D L E T S S D P E G E D D W D D E E A E D D G F D S D S S L S D S D L B Q D P E G L H L W N S F C I S V D P Y N P Q N F T A T I T I T A A R I V P E E P S D S E K D L L G K S D L E N S Q 525
H2N419_PONAB	430 L G G A S S D L E T S S D P E G E D D W D D E E A E D D G F D S D S S L S D S D L B Q D P E G L H L W N S F C I S V D P Y N P Q N F T A T I T I T A A R I V P E E P S D S E K D L L G K S D L E N S Q 525
E1BKX2_BOVIN	419 L G G A S S D L E T S S D S E D V D N D E D V E D D G F D S D S S F S D S D L E Q D S E G L H L W N S F Y S V D P Y N P Q N F T A T I T I T A A R I L P G N P S D S E K D L L G K S D L G N S P Q 514
PR15B_MOUSE	414 L G G A S S D L E T S S D S E S E D W G E E P E D D G F D S D G S L S D S D V E Q D S E G L H L W N S F H S V D P Y N P Q N F T A T I T I T A A R I A P R D P S D S G T S W L G S C G V G - S C Q 508
D3ZP67_RAT	408 L G G A S S D L D T S S D S E S E D W D D E E P E D D G F D S D G S L S D S D V E Q D S E G L H L W N S F H S V D P Y N P Q N F T A T I T I T A A R I A P R D P S D S E K S W L G S D V G - S Q 502
E2RII3_CANLF	426 L G G T S S D L E T S S D S S G G E T W D E E A E D D G F D S D S P L S A S D L E Q D P E G L H L W N S F Y S V D P Y N D P Q N F T A T I T I S A A R I V P G D S S D S E K N L L G K S G L E N S P Q 521
M3WUP7_FELCA	430 L G G A S S D P E T S S D S E G E G G D E E D D G F D S D S F S D S D L E Q D S E G L Q L W N S F Y S V D P Y N P Q N F T A T I T I T A A R I V P G A P S D S E K D L L D K S D L E N S P Q 525
G1L2H7_AILME	429 L G G A P S N L E T S S D S E D V D N D E E A E D D G F D S D S A V S E D E L E B H G S E - - - - L W N S F C S V D P Y N P Q N F T A T I T I T A A R I V P G D P S D E K E S D K S D L E N S P Q 512
I3LIA2_PIG	426 L G G A A S D L E T S S D S E G E G D W D E E A E D D G F D S D G S L S D S D L E R D S E G L H L W N S F Y S V D P Y N P Q N F T A T I T I T A A R I L P R E S S D S E K D L L D Q S D V E N S P Q 521
HOX5S2_OTOGA	431 L G G A S S D L E T S S D S E G E G D W D E E A E D D G F D S D S S L S A S D L E Q D S E G L H L W N S F Y S V D P Y N P Q N F T A T I T I T A A R I V S E D L S D S E N D L L D R S D L E N S Q 526
HOV6Q0_CAVPO	422 L G G A S S D L E T S S D S E G E G W D D E E E D D G F D S D G P L S D S D L E Q D S E E L H L W N S F Y S V D P Y N P Q N F T A T I T I T A P K I V P G E P S D S G K E L L D K S D L E N S - Q 516
G7NVE1_MACFA	427 L G G A S S D L E T S S D S P E G E D W D E E A E D D G F D S D S L S D S D L E Q D P E G L H L W N S F Y S V D P Y N P Q N F T A T I T I T A A R I V P E E P S D S E K D L L G E S D L E N S P Q 522
W5NWS5_SHEEP	424 L G G A A S D L E T S S D S E D E D W D D E E D D G F D S D S F S E D E L E Q D S E G L H L W N S F Y S V D P Y N P Q N F T A T I T I T A A R I L P G N P S D S E K D L L G K S D L E N S P H 519
A0A2K6RYB9_SAIBB	430 L G G A S S D L E T S S D S P E G E D W D D E E A E D D G F D S D S L S D S D L E Q D P E G L H L W N S F Y S V D P Y N P Q N F T A T I T I T A A R I V P E E P S D S E K D L L G K S D L E N S Q 525
A0A2K5F0R6_AOTNA	430 L G G A S S D L E T S S D S P E G E D W D D E E A E D D G F D S D S L S D S D L E Q D P E G L H L W N S F Y S V D P Y N P Q N F T A T I T I T A A R I V P E E P S D S E K D L L G K S D L E N S Q 525
A0A5F7ZW85_MACMU	428 L G G A S S D L E T S S D S P E G E D W D D E E A E D D G F D S D S L S D S D L E Q D P E G L H L W N S F Y S V D P Y N P Q N F T A T I T I T A A R I V P E E P S D S E K D L L G E S D L E N S Q 523
PR15B_HUMAN	526 S G S L P E T P H S S G E E D D W D S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E N E R K G C R D S K T P S S I V A I S E C H T L L S C K V Q L L G S Q E S E C P D 621
A0A2R9BET9_PANPA	526 S G S L P E T P H S S G E E D D W D S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E N E R K G C R D S K T P S S I V A I S E C H T L L S C K V Q L L G S Q E S E C P D 621
H2Q0Y9_PANTR	526 S G S L P E T P H S S G E E D D W D S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E N E R K G C R D S K T P S S I V A I S E C H T L L S C K V Q L L G S Q E S E C P D 621
H2N419_PONAB	526 S G S L P E T P H S S G E E D D W D S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E N E R K G C R D S K T P S S I V A I S E C H T L L S C K V Q L L G S Q E S E C P D 621
E1BKX2_BOVIN	515 T E S L P E F P D H N S G D D D W E S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E N E R K G C R D S K T P S S I V A I S E C H T L L S C K V Q L L G S Q E T E C P D 606
PR15B_MOUSE	509 E G P L P E T P D H S S G E E D D W D S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E N E R K G C R D S K T P S S I V A I S E C H T L L S C K V Q L L G S P E S K C P D 604
D3ZP67_RAT	503 A T L L P Q T P D H S S G E E D D W E S S A D E E A E A E N I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E N E R K G C R D S K T P S S I V A I S E C H T L L S C K V Q L L G S Q E D N C P G 595
E2RII3_CANLF	522 T G S L P E S P D Y N E G E E D D W E S S A D E E A S I L Q L W N S F C N S D D P Y N P L N F T K A P E T T S G E N E R K W R G C R D S E K P S E P T V A I S D R H T F L L S C E V Q L L G S R E S E G P D 617
M3WUP7_FELCA	526 T G S L P E S P D Y N E G E E D D W E S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E N K I W K G C C D P E R P S E P A A P I S E Y H T L L S C E V H L L G S R E T E G P D 621
G1L2H7_AILME	513 T G S L P E S P D C N S G E E D D W E S S A D E E A S I L E W N S F C N S D D P Y N D L L N F T K A P E T T S G E N K N W T G C H D S E R P S E P T V A I S D C H T L L S C E V Q L L G S R K S E G P D 608
I3LIA2_PIG	522 T G S L P E S P D H N S G E D D D W E S S A D E E A S I L R L W N S F C N S D D P Y N L N L F T K A P E T T S G E N K N G K C R D S E R P P S S I V T I S D C H S L L S C E V H L L G S R E N E C P D 617
HOX5S2_OTOGA	527 T G S L P E S P D H S S G E E D D W E S S A D E E A S I L K L W N S F C N S D D P Y N L N L F T K A P E T T S G E N K N W R G S C D T K R L P F S I V G I S D S C T L L S C K V Q L L G S Q E S G C P D 622
HOV6Q0_CAVPO	517 A D T F P E T P D H S S G E E D D W E S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E N K D S K C L D S K R L P F S L V A I S E C H T L L S C K V Q L L G H Q E D C P N 612
G7NVE1_MACFA	523 S G S L P E T P H S S G E E D D W E S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E N G K C R D S K T P S S I V A I S E C H T L L S C K V Q L L G S Q E S E C P D 618
W5NWS5_SHEEP	520 T G S L P E S P D H N S G D D D W E S S A D E E A S I L K L W N S F C N S D D P Y N L N L F T K A P E T T S G E N K W R G S C L D S K A Q P S P - - - - I S E C H T L L S C K V Q L L G S R E S K C P D 611
A0A2K6RYB9_SAIBB	526 S G S L S E T P E H S S G E E D D W E S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E G N W K R G C C D S K A P S P S I V A I S E C H T L L S C K V Q L L G S Q E S E C P D 621
A0A2K5F0R6_AOTNA	526 S G S L P E T P E H S S G E E D D W E S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E G N W K R G C C D S K A P S P I V P I S E C H T L L S C K V Q L L G S Q E S E C P D 621
A0A5F7ZW85_MACMU	524 S G S L P E T P E H S S G E E D D W E S S A D E E A S I L K L W N S F C N S D D P Y N P L N F T K A P E T T S G E G N G K C R D S K T P S S I V A I S E C H T L L S C K V Q L L G S Q E S E C P D 619
PR15B_HUMAN	622 S V Q R D V L S G G R H T H V K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V L F K Q C - 713
A0A2R9BET9_PANPA	622 S V Q R D V L S G G R H T H V K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F K Q C - 713
H2Q0Y9_PANTR	622 S V Q R D V L S G G R H T H V K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F K Q C - 713
H2N419_PONAB	622 S V Q R D V L S G G R H T H V K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F K Q C - 713
E1BKX2_BOVIN	607 L T V R G V V L S G E T H T I R R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F E Q C - 698
PR15B_MOUSE	605 C G L G E A L A G E R Y T H I K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F E Q C - 696
D3ZP67_RAT	596 C G L G E A L S G E R Y T H I K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F E Q C - 688
E2RII3_CANLF	618 L V Q G G V L S G E R H A R I K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F E Q C - 709
M3WUP7_FELCA	622 L G Q G G V L S G G R H T R I K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L T A F E Q C - 713
G1L2H7_AILME	609 L I P G E V L S G E R R A H T K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F K Q C - 700
I3LIA2_PIG	618 L V Q G G V L S G E R H T H T Q R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F E Q C - 709
HOX5S2_OTOGA	623 L V Q R E V L S G E R H T H I K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R V Y N D L Q G T C F K G L H V F E Q C - 714
HOV6Q0_CAVPO	613 L L Q R E F V - - E K H T S I K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R V F S I L Q D H V S K D L L L Y S S A K - 702
G7NVE1_MACFA	619 S V L R D V L S G G R Q T H V K R R K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F K Q C - 710
W5NWS5_SHEEP	612 L V Q G V F L S R E R H T H I K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q Q T C F K G L N V F E Q Y - 703
A0A2K6RYB9_SAIBB	622 L L Q R E V L S G G R H T H V K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G K C F K G L N V F K Q C - 713
A0A2K5F0R6_AOTNA	622 L L Q R E V L S G G R H T H V K R K K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G K C F K G L N V F K Q C - 713
A0A5F7ZW85_MACMU	620 S V L R D V L S G G R Q T H V K R R K V T F L E E V T E Y Y I S G D E D R K G P W E E F A R D G C F F Q K R I D E T B D A I G Y C L T F E H R E R M F N I L Q G T C F K G L N V F K Q C - 711

Figure S2

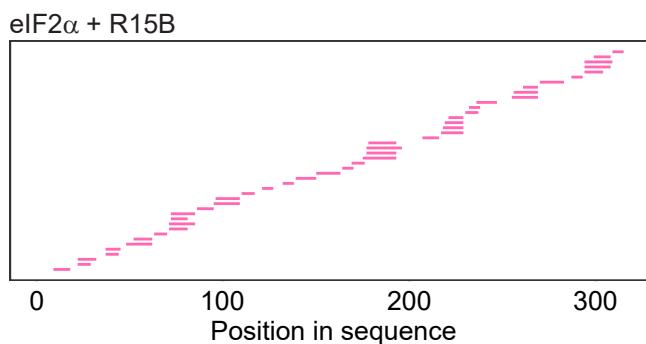
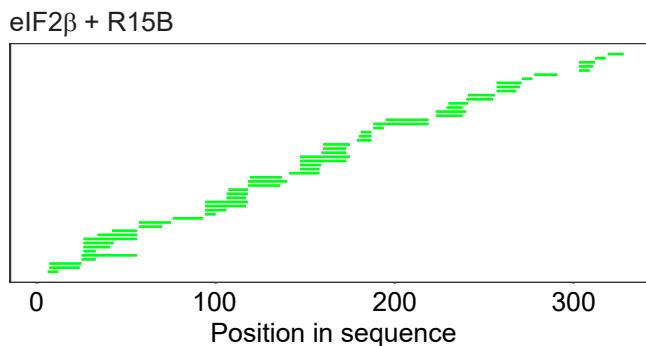
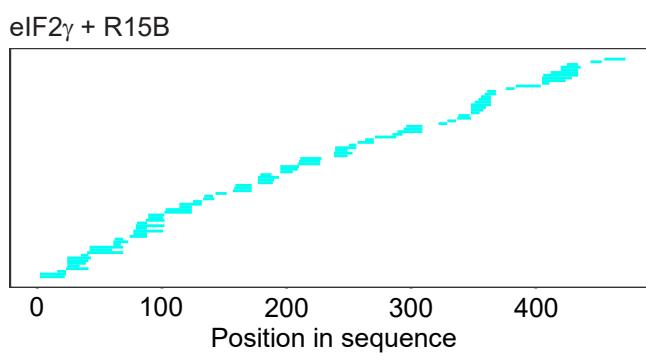
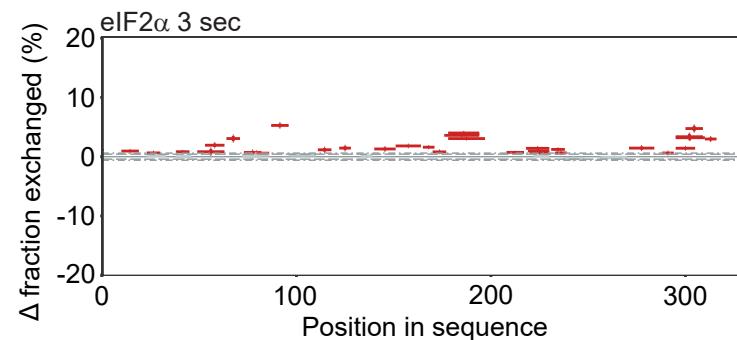
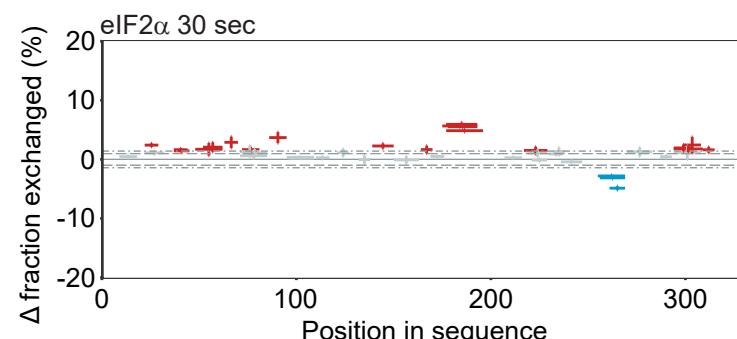
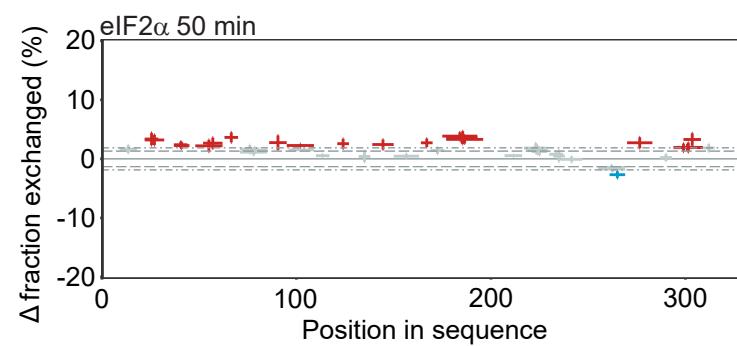
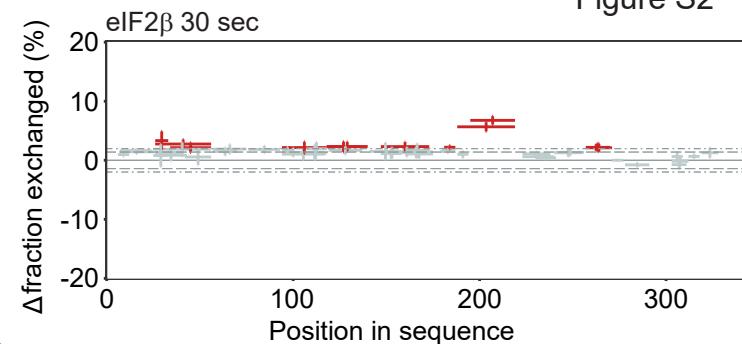
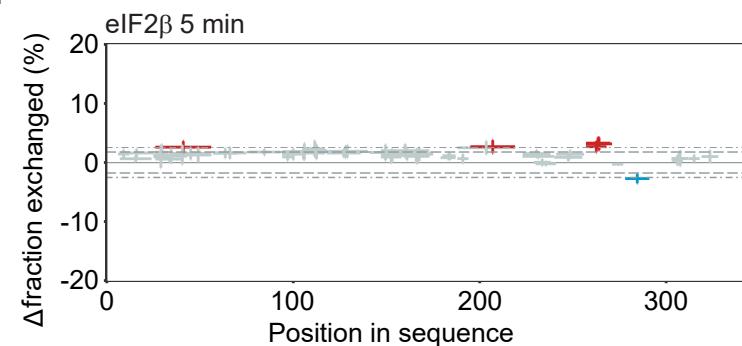
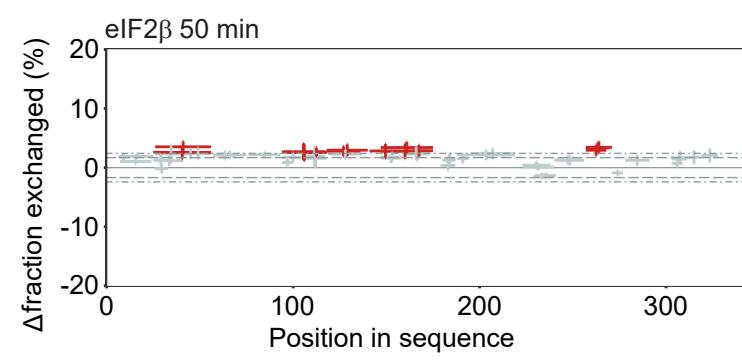
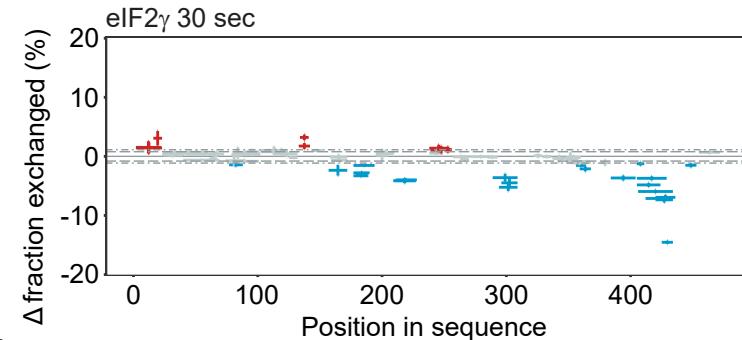
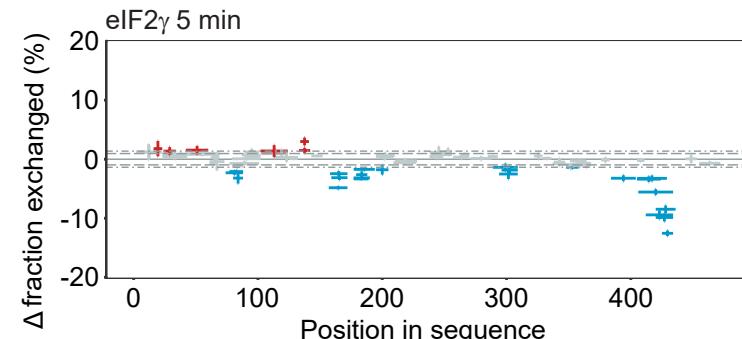
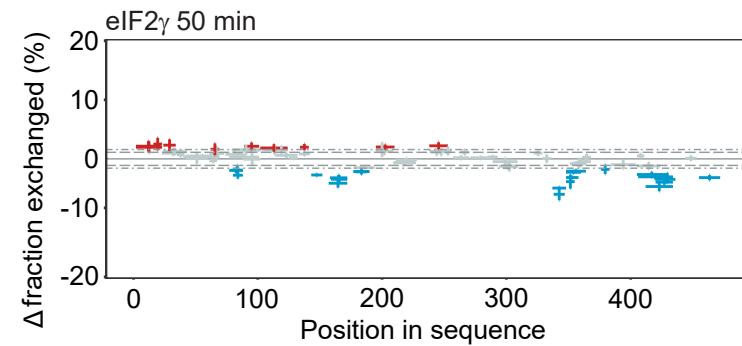
A**B****C****D****E****F****G****H****I****J****K****L**

Figure S3

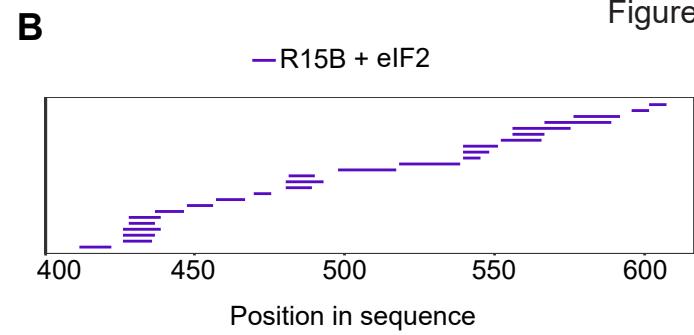
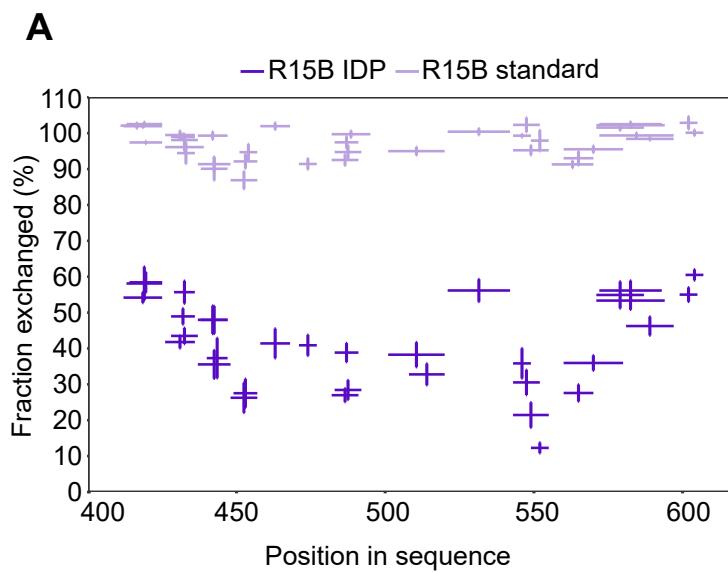


Figure S4

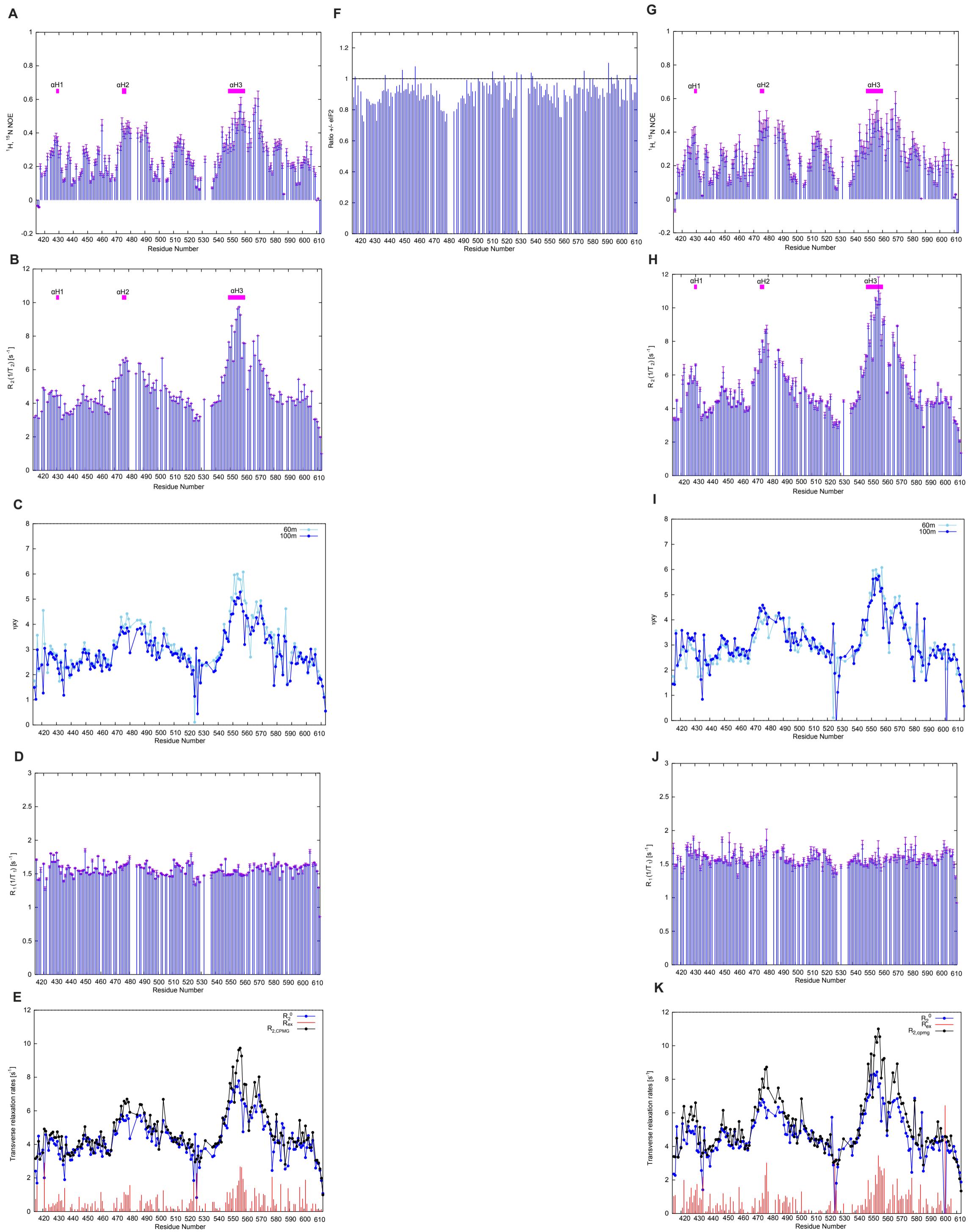


Figure S5

A

R15B	414	P I S A R P A C S N K L I D Y I L G G A S S D L E T S S D - - - P E G E D W D E E A E D D G F D S D S S L S D S D L E	469
R15B	499	A A R I V P E E P S D S E K D L - - S G K S D L E N S S Q S G S L P E T P E H S S G E E D D - W E S S A - - - - -	547
R15B	470	Q D P E G L H L W N S F C - S V D P Y N P Q N F T A T I Q T	498
R15B	548	D E A E S L K L W N S F C N S D D P Y N P L N F K A P F Q T	577

B

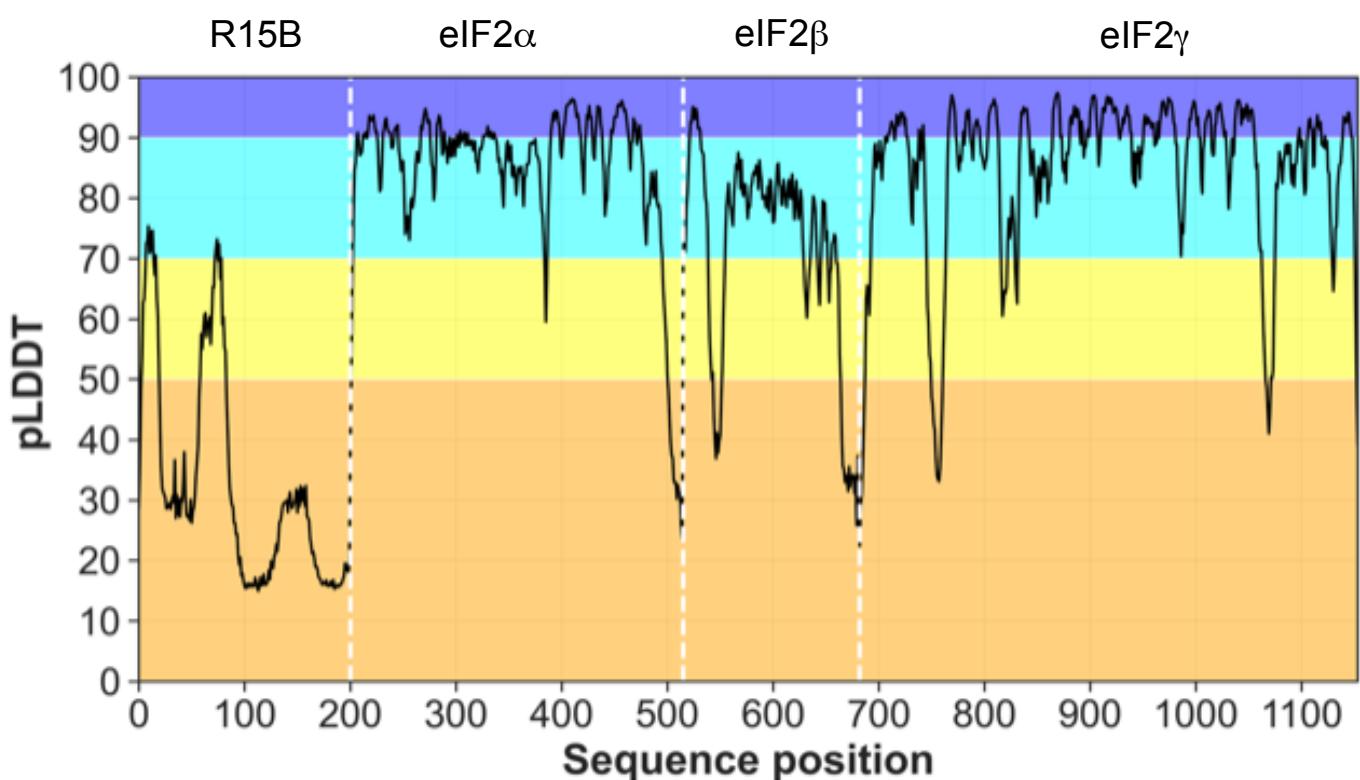
R15B	415	I S A R P A C S N K L I D Y I L G G A S S D L E T S S D P E G E D W D E - - - E A E D D G F D S D S S L S D S D L E	469
R15A	329	P P C I P P P S A F L K A W V Y - - - - - - - - - W P G E D T E E E E E D E E E D S D S G S D E E E G E A E	374
R15A	376	S S S T P A T G V F L K S W V Y - - - - - - - - - Q P G E D T E E - - - E E D E D S D T G S A E D E R E A E	417
R15A	419	S A S T P P P A S A F L K A W V Y - - - - - - - - - R P G E D T E E - - - E E D E D V D S E D K E D D S E A A	460
R15A	469	H P S H P D Q R A H F R G W G Y - - - - - - - - - R P G K E T E - - - E E E - - - - - A A E D W G E A E	503

C

hs-R15B	415	I S A R P A C S N K L I D Y I L G G A S S D L E T S S D P E G E D W D E - - - E A E D D G F D S D S S L S D S D L E	469
hs-R15A	419	S A S T P P P A S A F L K A W V Y - - - - - - - - - R P G E D T E E - - - E E D E D V D S E D K E D D S E A A	460
hs-R15A	376	S S S T P A T G V F L K S W V Y - - - - - - - - - Q P G E D T E E - - - E E D E D S D T G S A E D E R E A E	417
hs-R15A	329	P P C I P P P S A F L K A W V Y - - - - - - - - - W P G E D T E E E E E D E E E D S D S G S D E E E G E A E	374
hs-R15A	469	H P S H P D Q R A H F R G W G Y - - - - - - - - - R P G K E T E - - - E E A A E D W G E A E - - - - -	503
dm_R15	129	- C V P S S C Y F F I D L H P H - - - - - - - - - H G F K - - - - - D T A E D C P T S Q A S S D R N N N	165
hhv1_ICP34	54	- G P P P S C S L L L R Q W L H - - - - - - - - - V P E S A S D D - - - D D D D D W P D - - - - - - - - -	84
asfv_DP71L	44	I G T N P T - - - - - L A F I L G G - - - - - N E D L - - - S D D S D W D E N F S L E N T L - - -	76

Figure S6

A



B

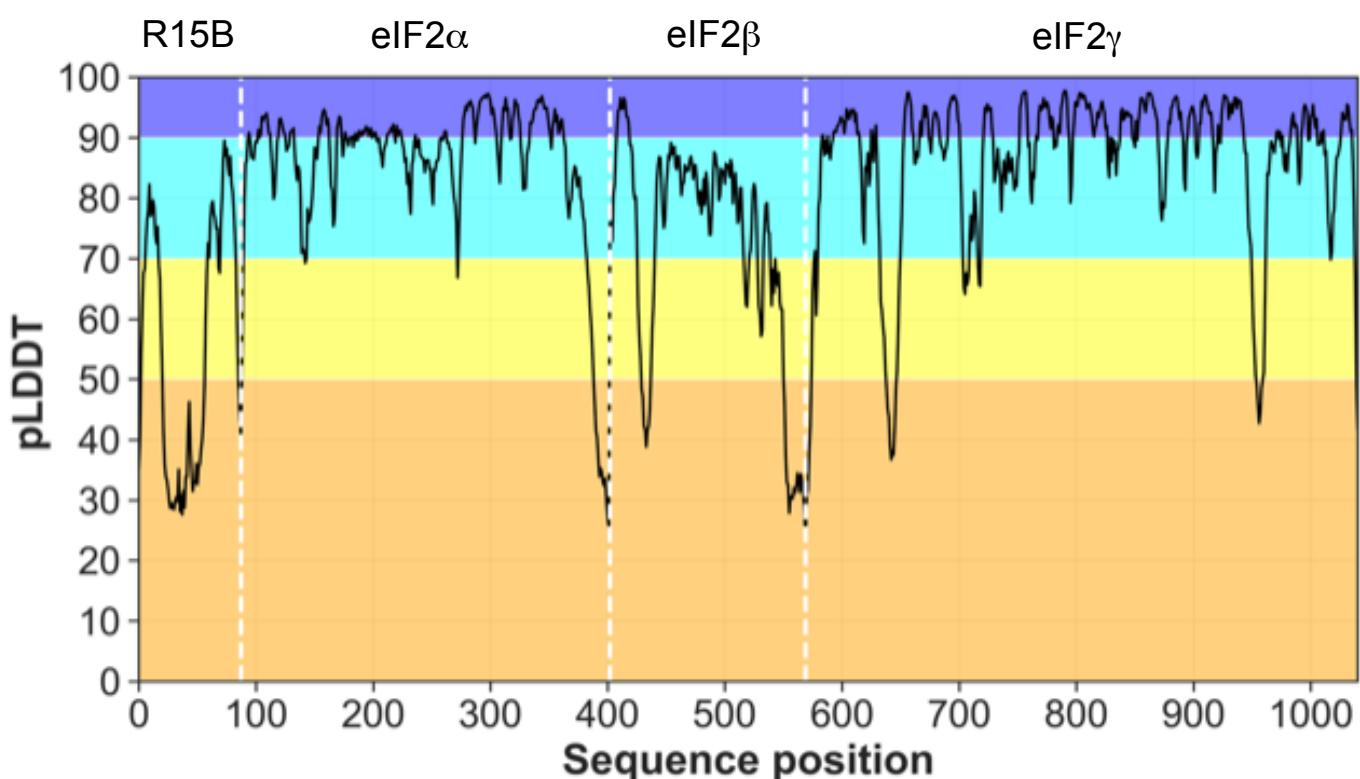


Table S2 : Oligonucleotides used in this study

Primer 5'-3'	SOURCE
R15B Forward aa1 PXJ41 ggatgacgacgataagATGGAGCCGGGGACAGGC	Sigma-Aldrich
R15B Forward aa411 PXJ41 ggatgacgacgataagGGTGACCTTCCCATTCTGCCAGAC	Sigma-Aldrich
R15B Forward aa414 PXJ41 ggatgacgacgataagCCCATTCTGCCAGACC	Sigma-Aldrich
R15B Reverse aa414 PXJ41 gtaccctcgagaactatcaGGGAAGGTACCTTAGGTATGAGTAATCA	Sigma-Aldrich
R15B Reverse aa613 PXJ41 gtaccctcgagaactatcaCCCCAACAGCTGCACCTACAAGAAAG	Sigma-Aldrich
R15B Reverse aa639 PXJ41 gtaccctcgagaactatcaTTTCTTTGACATGTGTGTG	Sigma-Aldrich
R15B N423D site directed mutagenesis Forward AGACCAGCTTGTAGTGACAAACTGATAGATTAT	Sigma-Aldrich
R15B N423D site directed mutagenesis Reverse ATAATCTATCAGTTGTCACTACAAGCTGGTCT	Sigma-Aldrich
R15B Forward aa414 pET-47b cagggaccggtCCCATTTCTGCCAGACCAGC	Sigma-Aldrich
R15B Forward aa632 pET-47b cagggaccggtAGACACACACATGTCAAAAG	Sigma-Aldrich
R15B Reverse aa613 pET-47b ggcaccagagcgtaCCCCAACAGCTGCACCTTAC	Sigma-Aldrich
R15B Reverse aa664 pET-47b ggcaccagagcgtaCCATGGTCCTTGCATCCTC	Sigma-Aldrich
R15B Reverse aa705 pET-47b ggcaccagagcgtaTTGAAGCATGTTCCCTGGAGT	Sigma-Aldrich