**Supplementary Information.**

# HDX-MS reveals dysregulated checkpoints that compromise discrimination against self RNA during RIG-I mediated autoimmunity

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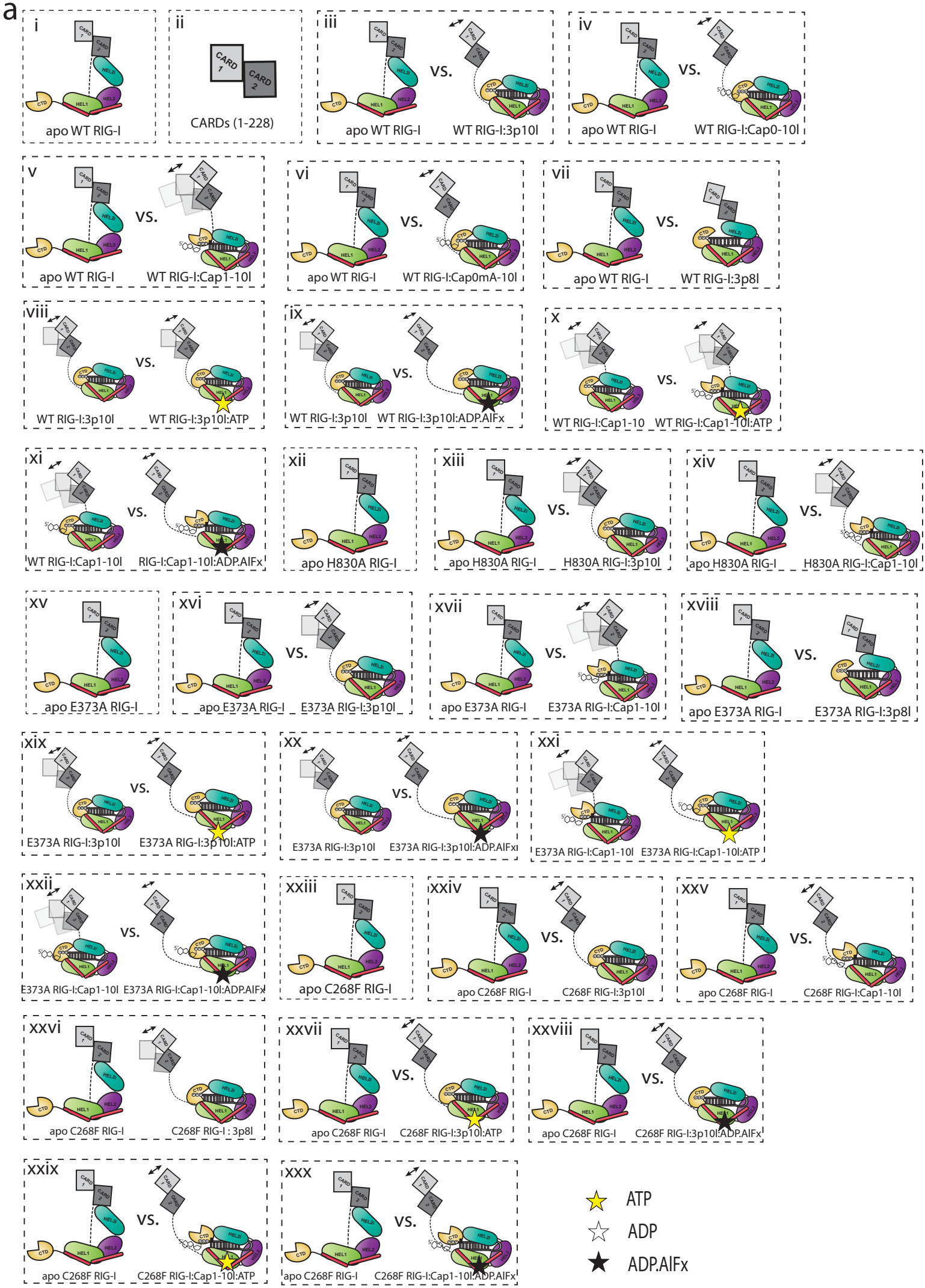



Supplementary Fig. 1a

Supplementary Fig. 1b

# Supplementary Fig. 1c

| WT RIG-I peptide sequence | charge | start | end | structure | (i) | (ii) | (iii) | (iv) | (v) | (vi) | (vii) | (viii) | (ix) | (x) | (xi) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| QDYIRKTLDPTYIL | 3 | 13 | 26 | CARD1 | 36 (3) | 65 (3) | 15 (5) | 21 (4) | 9 (4) | 17 (3) | 4 (4)* | -1 (4)* | 9 (5) | -1 (2)* | 10 (4) |
| IRKTLDPTYIL | 3 | 16 | 26 | | 32 (2) | 63 (5) | 21 (2) | 23 (5) | 10 (5) | 22 (3) | 6 (4) | -1 (4)* | 7 (3) | 0 (2)* | 13 (4) |
| SYMAPWFRE | 2 | 27 | 35 | | 41 (3) | 72 (5) | 21 (4) | 24 (4) | 11 (3) | 22 (3) | 2 (4)* | -4 (4)* | 3 (3)* | 0 (2)* | 15 (3) |
| YMAPWFREEEVQ | 2 | 28 | 39 | | 44 (2) | 76 (4) | 19 (4) | 23 (3) | 10 (2) | 19 (3) | 3 (3)* | -2 (5)* | 2 (4)* | -1 (2)* | 9 (3) |
| VQYIQA | 2 | 38 | 43 | | 25 (2) | 56 (4) | 20 (4) | 18 (4) | 3 (3)* | 13 (4) | 0 (2)* | -5 (4) | 1 (5)* | 2 (3)* | 7 (5) |
| YIQAEKNNKGPMEA | 3 | 40 | 53 | | 43 (4) | 71 (5) | 13 (5) | 17 (3) | 7 (4) | 12 (7) | -2 (4)* | -2 (3)* | 1 (4)* | -2 (4)* | 1 (6)* |
| EKNNKGPMEAATL | 2 | 44 | 56 | | 39 (3) | 55 (7) | 15 (4) | 15 (4) | 5 (4) | 16 (5) | 2 (5)* | -3 (3)* | 3 (5)* | -1 (3)* | 8 (5) |
| LQEEGWFRGFL | 2 | 64 | 74 | | 47 (4) | 56 (8) | 11 (5) | 17 (4) | 8 (4) | 9 (4) | 3 (4)* | 2 (5)* | 9 (4) | -3 (2)* | 0 (4)* |
| QEEGWFRGFL | 2 | 65 | 74 | | 46 (2) | 53 (4) | 10 (3) | 9 (6) | 10 (5) | 6 (6) | 4 (7)* | -2 (4)* | 6 (3) | -1 (3)* | 4 (4)* |
| FRGFLDA | 2 | 70 | 76 | | 15 (1) | | 7 (2) | 18 (2) | 11 (3) | 24 (3) | 1 (3)* | 4 (3)* | 14 (5) | 1 (2)* | 12 (3) |
| DALDHAGYSGL | 2 | 75 | 85 | | 27 (2) | 54 (5) | 16 (3) | 20 (3) | 9 (3) | 21 (3) | 2 (4)* | -1 (4)* | 5 (3) | 0 (2)* | 7 (5) |
| LDHAGYSGL | 2 | 77 | 85 | | 32 (2) | 50 (6) | 11 (4) | 11 (4) | 5 (3)* | 14 (4) | 4 (5)* | -1 (5)* | 5 (4)* | -1 (3)* | 7 (3) |
| YEAIESW | 1 | 86 | 92 | | 22 (2) | 66 (4) | 29 (3) | 32 (3) | 19 (4) | 30 (3) | 2 (4)* | -2 (4)* | 7 (3) | -1 (3)* | 16 (4) |
| YEAIESWD | 1 | 86 | 93 | | 19 (2) | 64 (6) | 25 (4) | 32 (3) | 16 (3) | 33 (3) | 2 (4)* | 1 (5)* | 10 (6) | 0 (3)* | 17 (3) |
| FKKIEKLEE | 3 | 94 | 102 | | 64 (3) | 72 (5) | 8 (4) | 13 (3) | 4 (2)* | 6 (3) | -4 (5)* | -2 (4)* | 3 (4)* | -2 (2)* | 4 (4)* |
| YRLLL | 2 | 103 | 107 | Latch region | 8 (1) | 52 (3) | 21 (2) | 26 (2) | 7 (2) | 28 (2) | 3 (5)* | 0 (4)* | 7 (7) | 1 (3)* | 20 (2) |
| YRLLLKRLQPEF | 3 | 103 | 114 | | 13 (1) | 60 (4) | 31 (3) | 38 (4) | 18 (5) | 34 (3) | 5 (4)* | 2 (6)* | 6 (3) | 0 (3)* | 13 (5) |
| LLKRLQPEF | 2 | 106 | 114 | | 17 (3) | 66 (6) | 30 (5) | 37 (5) | 21 (4) | 37 (5) | 6 (4) | -1 (5)* | 7 (4) | 0 (3)* | 15 (5) |
| LLKRLQPEF | 3 | 106 | 114 | | 14 (3) | 65 (6) | 35 (3) | 38 (6) | 17 (7) | 38 (4) | 6 (4) | -3 (4)* | 7 (3) | 1 (4)* | 19 (9) |
| KRLQPEF | 2 | 108 | 114 | | 21 (3) | 76 (5) | 31 (5) | 34 (5) | 18 (6) | 34 (5) | 6 (5) | -2 (6)* | 4 (5)* | 1 (4)* | 13 (7) |
| KTRIIPTDIISDL | 2 | 115 | 127 | CARD2 | 53 (3) | 73 (5) | 19 (4) | 22 (3) | 13 (3) | 19 (3) | 2 (4)* | -3 (4)* | 3 (4)* | -2 (2)* | 6 (3) |
| KTRIIPTDIISDL | 3 | 115 | 127 | | 46 (2) | 72 (5) | 19 (4) | 21 (3) | 12 (3) | 18 (3) | 3 (4)* | -3 (4)* | 3 (4)* | -2 (3)* | 6 (4) |
| KTRIIPTDIISD | 3 | 115 | 126 | | 47 (2) | 71 (4) | 15 (5) | 12 (4) | 8 (4) | 15 (4) | 1 (4)* | 2 (5)* | 2 (5)* | -2 (3)* | 7 (4) |
| ILQICSTKGMMAGAEKLVE | 3 | 139 | 157 | | 28 (1) | 57 (4) | 22 (2) | 25 (2) | 12 (2) | 23 (2) | 5 (3) | -1 (4)* | 7 (2) | 0 (2)* | 13 (2) |
| LLRSDKENWPKTLKL | 4 | 159 | 173 | | 36 (0) | 75 (3) | 12 (7) | 29 (2) | 14 (4) | 12 (3) | -2 (3)* | -1 (5)* | -1 (2)* | 0 (2)* | 13 (5) |
| RSDKENWPKTLKL | 3 | 161 | 173 | | 34 (4) | 65 (5) | 16 (6) | 18 (4) | 10 (5) | 20 (5) | 3 (0)* | 0 (4)* | 4 (4)* | -2 (16)* | 10 (5) |
| RSDKENWPKTLKLAL | 4 | 161 | 175 | | 28 (3) | 59 (5) | 23 (4) | 26 (3) | 10 (5) | 21 (4) | -3 (4)* | 3 (4)* | 2 (4)* | 3 (3)* | |
| ALEKERNKFSEL | 3 | 174 | 185 | | 57 (1) | 82 (6) | 19 (3) | 20 (3) | 10 (3) | 17 (3) | 0 (4)* | -3 (4)* | 4 (5)* | -3 (5)* | 6 (5) |
| EKERNKFSEL | 3 | 176 | 185 | | 56 (2) | 77 (5) | 13 (4) | 15 (4) | 7 (3) | 11 (4) | 0 (3)* | -2 (4)* | 4 (5)* | -2 (3)* | 5 (4) |
| WIVEKGIKDVETEDLED | 2 | 186 | 202 | linker | 88 (2) | 87 (6) | 5 (2) | 0 (4)* | -2 (5)* | -1 (5)* | -2 (3)* | -1 (2)* | -3 (2)* | 0 (1)* | -2 (5)* |
| WIVEKGIKDVE | 3 | 186 | 196 | | 86 (4) | 85 (6) | 2 (3)* | 2 (4)* | 0 (4)* | -1 (7)* | -1 (3)* | -1 (3)* | 0 (1)* | -2 (4)* | -2 (5)* |
| WIVEKGIKDVETEDL | 3 | 186 | 200 | | 86 (1) | 84 (3) | 4 (6)* | 2 (6)* | -1 (6)* | -1 (6)* | -1 (6)* | -4 (5)* | -2 (6)* | -3 (5)* | -1 (5)* |
| IVEKGIKDVETEDL | 3 | 187 | 200 | | 84 (1) | 81 (6) | 5 (2)* | 3 (4)* | 2 (4)* | -1 (4)* | -1 (6)* | -4 (3)* | 5 (2) | -2 (4)* | 0 (3)* |
| EDKMETSDIQIF | 2 | 201 | 212 | | 70 (4) | 75 (6) | 4 (5)* | 3 (4)* | 2 (5)* | 1 (5)* | -2 (5)* | -2 (4)* | 0 (6)* | -2 (5)* | 1 (4)* |
| FYQEDPECQNL | 2 | 212 | 222 | | 73 (1) | 63 (5) | 3 (3)* | 1 (3)* | -10 (5) | -4 (4)* | -1 (3)* | -1 (3)* | 5 (5)* | -2 (5)* | 1 (5)* |
| YQEDPECQNL | 2 | 213 | 222 | | 67 (3) | 70 (5) | 2 (5)* | -2 (5)* | -11 (6) | 1 (5)* | 1 (2)* | -3 (5)* | -1 (5)* | -2 (5)* | -3 (3)* |
| SENSCPPSEVSDTNL | 2 | 223 | 237 | | 71 (5) | | 5 (6)* | -2 (4)* | -9 (7) | -2 (5)* | -2 (6)* | -4 (5)* | -3 (5)* | -2 (6)* | -1 (5)* |
| VSDTNL | 1 | 232 | 237 | | 72 (5) | | 4 (6)* | -2 (3)* | -13 (7) | -2 (6)* | | -3 (5)* | -2 (4)* | -2 (6)* | -1 (5)* |
| YSPFKPRNYQLE | 2 | 238 | 249 | HEL1 | 79 (4) | | 0 (4)* | 3 (4)* | -1 (5)* | -6 (4) | 1 (5)* | -4 (5)* | -3 (4)* | -6 (4) | -3 (4)* |
| YSPFKPRNYQLE | 3 | 238 | 249 | | 62 (3) | | 1 (4)* | 3 (4)* | -2 (4)* | -6 (4) | 2 (5)* | -4 (5)* | -4 (4)* | -6 (3) | -4 (4)* |
| YSPFKPRN | 3 | 238 | 245 | | 62 (3) | | 4 (6)* | -1 (3)* | -2 (5)* | 3 (6)* | -3 (2)* | -9 (6) | -10 (5) | -7 (5) | -11 (4) |
| LALPAMKGKNTIICAPTGCGKTFVSLL | 3 | 250 | 276 | | 46 (2) | | 0 (3)* | 3 (2)* | 4 (3)* | -4 (3)* | 3 (3)* | -1 (4)* | -12 (3) | 3 (7)* | -9 (4) |
| LALPAMKGKNTIICAPTGCGKTFVSLLL | 4 | 250 | 276 | | 51 (1) | | -5 (1)* | 3 (1)* | -3 (3)* | 2 (6)* | 0 (5)* | -3 (4)* | -11 (3) | -4 (3)* | |
| APTGCGKTF | 2 | 264 | 272 | | 72 (3) | | 2 (4)* | 0 (3)* | -3 (8)* | 4 (5)* | -5 (3)* | | -46 (6) | -10 (5) | -32 (5) |
| ICEHHLKKFPQGQKGKVVF | 3 | 277 | 295 | | 34 (2) | | 2 (3)* | 1 (2)* | -2 (3)* | -1 (2)* | -3 (3)* | -1 (3)* | -3 (2)* | | -3 (3)* |
| PQGQKGKVVF | 3 | 286 | 295 | | 63 (3) | | -4 (4)* | -3 (3)* | 4 (5)* | 4 (3)* | -2 (2)* | 0 (4)* | 2 (4)* | -2 (4)* | 0 (6)* |
| FANQIPVYEQQ | 2 | 296 | 306 | motif Ia | 57 (2) | | -12 (3) | -12 (4) | -10 (6) | -16 (4) | -4 (4)* | 6 (5) | -9 (5) | -4 (5)* | -26 (6) |
| FANQIPVYEQQKSVF | 2 | 296 | 310 | | 56 (1) | | -14 (3) | -12 (5) | -6 (4) | -18 (3) | -6 (3) | 6 (5) | -10 (5) | -3 (4)* | -22 (6) |
| FANQIPVYEQQKSVFSKY | 3 | 296 | 313 | | 53 (1) | | -13 (3) | -12 (5) | -14 (4) | -21 (4) | -6 (4) | 6 (3) | -10 (5) | 4 (5)* | -19 (6) |
| FERHGYRVTGISGATAENVPVEQIVENND | 3 | 314 | 342 | | 59 (2) | | -14 (2) | -3 (3)* | -2 (4)* | -6 (3) | -1 (4)* | -2 (4)* | 0 (3)* | | -1 (3)* |
| GYRVTGISGATAENVPVEQIVENN | 4 | 318 | 341 | | 69 (2) | | -3 (2)* | 0 (2)* | 0 (6)* | -6 (3) | -3 (5)* | 3 (2)* | 1 (4)* | -1 (3)* | 4 (0)* |
| YRVTGISGATAENVPVEQIVE | 3 | 319 | 339 | | 72 (4) | | 3 (5)* | 0 (6)* | -3 (4)* | -3 (6)* | -3 (3)* | -3 (4)* | -4 (4)* | -5 (5) | -1 (7)* |
| IIILTPQILVNNLKKGTIPSL | 2 | 343 | 363 | | 28 (2) | | -6 (4) | -8 (3) | -3 (4)* | -10 (3) | -3 (3)* | -2 (4)* | -10 (3) | -4 (4)* | -16 (4) |
| IIILTPQILVN | 2 | 343 | 353 | | 41 (2) | | -3 (3)* | -6 (4) | -3 (2)* | -9 (4) | 3 (3)* | 1 (3)* | -7 (2) | -4 (2)* | -13 (2) |
| IIILTPQILVNNL | 2 | 343 | 355 | motif Ic | 58 (2) | | -8 (3) | -11 (3) | -5 (3) | -11 (3) | -1 (3)* | -1 (3)* | -10 (2) | -5 (3) | -20 (3) |
| IIILTPQILVNNLKKGTIPSL | 3 | 343 | 363 | | 58 (2) | | -6 (3) | -9 (3) | -3 (4)* | -11 (3) | -3 (3)* | -2 (4)* | -9 (3) | -5 (4) | -16 (3) |
| IIILTPQILVNNLKKGTIPSLSI | 3 | 343 | 365 | | 57 (2) | | -6 (3) | -7 (2) | -2 (3)* | -9 (3) | -3 (3)* | -2 (4)* | -9 (3) | -5 (4) | -15 (3) |
| IIILTPQILVNNLKKGTIPSLSIF | 3 | 343 | 366 | | 54 (2) | | -5 (3) | -7 (2) | -1 (2)* | -8 (2) | -1 (3)* | -1 (4)* | -8 (3) | -5 (4)* | -14 (2) |
| LMIFDECHNTSKQHPYNM | 3 | 368 | 385 | motif IIa | 29 (2) | | -6 (2) | -4 (2)* | -2 (2)* | -10 (2) | 3 (5)* | 2 (3)* | -6 (3) | -1 (2)* | -10 (3) |
| IFDECHNTSKQHPYNMIM | 2 | 370 | 387 | | 30 (1) | | -5 (2) | -4 (2)* | -1 (2)* | -10 (2) | 2 (5)* | 3 (7)* | -7 (2) | 2 (7)* | -10 (3) |
| IFDECHNTSKQHPYNMIM | 3 | 370 | 387 | | 29 (2) | | -6 (2) | -4 (2)* | -2 (2)* | -10 (2) | 3 (5)* | 2 (3)* | -6 (3) | -1 (2)* | -10 (3) |
| FNYLDQKLGGSSGPLPQVIGL | 2 | 388 | 408 | | 33 (2) | | 1 (2)* | 4 (3)* | 2 (4)* | -5 (2) | 3 (3)* | 0 (4)* | 3 (3)* | 0 (3)* | 3 (4)* |
| FNYLDQKLGGSSGPLPQVIG | 2 | 388 | 407 | | 33 (1) | | 2 (2)* | 3 (2)* | 2 (4)* | -6 (4) | 4 (4)* | -1 (4)* | 2 (2)* | -1 (3)* | 3 (4)* |
| DQKLGGSSGPLPQVIGL | 2 | 392 | 408 | | 39 (2) | | 0 (2)* | 4 (3)* | 1 (4)* | -3 (2)* | 1 (3)* | 0 (3)* | 2 (3)* | -1 (3)* | 2 (4)* |
| TASVGVGDAKNTDEALD | 2 | 409 | 425 | | 61 (3) | | -2 (4)* | -3 (4)* | -1 (4)* | -7 (4) | -3 (5)* | -1 (5)* | -8 (4) | -4 (4)* | -11 (4) |
| TASVGVGDAKNTDEAL | 2 | 409 | 424 | | 59 (3) | | -3 (4)* | -3 (4)* | -2 (5)* | -6 (4) | -4 (2)* | -1 (5)* | -8 (4) | -5 (4)* | -10 (4) |
| DYICKL | 1 | 425 | 430 | | 1 (1) | | -1 (1)* | 1 (1)* | 1 (1)* | -3 (1)* | 0 (2)* | 0 (0)* | 0 (2)* | 0 (1)* | 0 (0)* |
| DYICKL | 2 | 425 | 430 | | 3 (1) | | -1 (1)* | -1 (1)* | -3 (1)* | -2 (1)* | 0 (1)* | 1 (1)* | 1 (2)* | 0 (1)* | 0 (1)* |
| CASLDASVIATVKHNLEEL | 2 | 431 | 449 | | 43 (2) | | -5 (3)* | -1 (3)* | 0 (3)* | -5 (2)* | 3 (4)* | 1 (4)* | 2 (3)* | -3 (2)* | -2 (3)* |
| SVIATVKHNLEE | 2 | 437 | 448 | | 55 (3) | | -2 (3)* | -1 (3)* | 1 (3)* | -2 (3)* | -3 (4)* | -3 (3)* | -2 (3)* | -4 (3)* | 1 (2)* |
| EQVVYKPQKF | 3 | 450 | 459 | | 55 (4) | | 3 (4)* | 3 (4)* | 2 (5)* | 5 (5)* | 4 (6)* | -8 (3) | -5 (3)* | -12 (4) | 2 (6)* |
| VVYKPQKF | 2 | 452 | 459 | | 60 (3) | | 1 (4)* | 4 (4)* | 4 (4)* | 2 (4)* | -1 (6)* | -3 (4)* | -3 (4)* | -6 (4) | -4 (4)* |
| VVYKPQKF | 3 | 452 | 459 | | 61 (2) | | 2 (4)* | 0 (4)* | 1 (4)* | 1 (4)* | 0 (6)* | -4 (6)* | -1 (3)* | -8 (4) | -5 (4) |
| FRKVESRISDKFKYIIAQL | 3 | 460 | 478 | HEL2i | 39 (3) | | 1 (3)* | -1 (3)* | -5 (4) | -2 (3)* | -1 (6)* | -1 (3)* | -4 (2)* | | -13 (6) |
| MRDTESL | 2 | 479 | 485 | | 5 (2) | | -1 (2)* | -1 (2)* | -3 (2)* | -2 (2)* | -1 (2)* | 0 (1)* | 0 (4)* | 0 (1)* | 0 (1)* |
| AKRICKDLENL | 3 | 486 | 496 | | 69 (3) | | -4 (5)* | -4 (4)* | -1 (4)* | -11 (4) | 2 (6)* | -2 (5)* | -1 (5)* | -4 (3)* | -6 (4) |
| SQIQNREFGTQKYEQW | 3 | 497 | 512 | | 68 (2) | | -1 (4)* | -1 (4)* | -1 (4)* | -7 (4) | 0 (5)* | -2 (4)* | 1 (3)* | -2 (4)* | 0 (4)* |
| SQIQNREFGTQKYEQ | 3 | 497 | 511 | | 62 (3) | | -1 (4)* | -4 (3)* | -1 (2)* | -13 (3) | -2 (5)* | -3 (4)* | -1 (3)* | -2 (4)* | -1 (4)* |
| WIVTVQKACM | 2 | 512 | 521 | | 9 (2) | | -3 (2)* | -2 (3)* | 0 (2)* | -8 (2) | 5 (2)* | -3 (5)* | 0 (5)* | 1 (7)* | -2 (3)* |
| IVTVQKACM | 2 | 513 | 521 | | 13 (2) | | -4 (2)* | -3 (3)* | -2 (3)* | -9 (2) | 5 (3)* | 2 (4)* | 3 (5)* | -1 (2)* | 1 (3)* |
| VFQMPDKDEESRICKA | 3 | 522 | 537 | CTD:HEL2i | 60 (2) | | -9 (3) | -12 (3) | -4 (4)* | -15 (3) | 1 (6)* | -2 (4)* | -11 (3) | -8 (3) | -24 (3) |
| VFQMPDKDEESRICKALF | 4 | 522 | 539 | | 51 (2) | | -6 (3) | -10 (2) | -1 (2)* | -14 (3) | 3 (5)* | -2 (4)* | -9 (3) | -7 (3) | -21 (2) |
| FQMPDKDEESRICKA | 3 | 523 | 537 | | 62 (3) | | -7 (4) | -18 (3) | -4 (4)* | -19 (4) | 2 (8)* | -2 (4)* | -11 (3) | -8 (3) | -24 (3) |
| FQMPDKDEESRICKALF | 4 | 523 | 539 | | 49 (2) | | -6 (3) | -11 (3) | -3 (3)* | -20 (4) | 2 (4)* | -2 (4)* | -10 (3) | -7 (2) | -24 (2) |
| LYTSHLRKYNDAL | 3 | 540 | 552 | | 11 (2) | | -1 (3)* | 5 (5)* | 2 (6)* | -5 (3) | 3 (2)* | 1 (5)* | 2 (2)* | 0 (4)* | 0 (6)* |
| LYTSHLRKYNDAL | 4 | 540 | 552 | | 12 (2) | | -1 (4)* | 3 (5)* | 2 (5)* | -5 (3)* | 4 (3)* | 2 (4)* | 2 (3)* | 1 (4)* | -1 (5)* |
| YTSHLRKYNDAL | 2 | 541 | 552 | | 13 (2) | | -1 (3)* | 5 (5)* | 1 (6)* | -1 (4)* | 4 (2)* | 2 (5)* | 3 (4)* | 0 (5)* | 2 (7)* |
| IISEHARMKDALD | 3 | 553 | 565 | | 24 (2) | | -2 (2)* | 1 (3)* | -1 (3)* | -5 (3) | 3 (4)* | 1 (3)* | 2 (3)* | 0 (2)* | -1 (3)* |
| HARMKDALD | 2 | 557 | 565 | | 30 (2) | | 0 (3)* | 0 (3)* | -2 (3)* | -4 (2)* | 3 (3)* | 0 (3)* | 0 (3)* | 1 (3)* | 0 (2)* |
| HARMKDALD | 3 | 557 | 565 | | 32 (2) | | -1 (3)* | -1 (3)* | -2 (3)* | -5 (3)* | 0 (3)* | 0 (3)* | 0 (3)* | -2 (2)* | -1 (2)* |
| DYLKDFFSNVRAAGF | 3 | 565 | 579 | Gate motif | 34 (2) | | 14 (3) | 12 (4) | 9 (3) | | 2 (3)* | 0 (5)* | 2 (2)* | -1 (4)* | 2 (3)* |
| YLKDFFSNV | 2 | 566 | 574 | | 16 (1) | | 10 (2) | 14 (3) | 10 (2) | 9 (2) | 5 (4)* | 0 (2)* | 2 (2)* | -1 (1)* | 1 (2)* |
| YLKDFFSNVRAAGF | 3 | 566 | 579 | | 35 (2) | | 14 (4) | 17 (3) | 12 (3) | 11 (3) | 3 (4)* | -3 (3)* | 1 (3)* | -4 (2)* | -1 (2)* |
| FFSNV | 1 | 570 | 574 | | | | | 30 (2) | 21 (3) | 6 (3) | 3 (3)* | 0 (5)* | 2 (3)* | -2 (2)* | 3 (3)* |
| FFSNVRAAGFD | 2 | 570 | 580 | | 49 (1) | | 15 (5) | 18 (4) | 15 (5) | 14 (4) | -1 (4)* | 3 (6)* | 2 (3)* | | -2 (8)* |
| FFSNVRAAGF | 2 | 570 | 579 | | 49 (2) | | 17 (3) | 19 (3) | 13 (3) | 17 (3) | 4 (4)* | -2 (4)* | 0 (4)* | -1 (4)* | 1 (5)* |

WT RIG-I

| peptide sequence | charge | start | end | structure | (i) | (ii) | (iii) | (iv) | (v) | (vi) | (vii) | (viii) | (ix) | (x) | (xi) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DEIEQDLTQRFEEKLQE | 3 | 580 | 596 | HEL2i | 25 (2) | | 3 (2)* | 11 (3) | 2 (3)* | 2 (2)* | 5 (3)* | 0 (2)* | 0 (2)* | -3 (2)* | -1 (2)* |
| DEIEQDLTQRFEEKLQEL | 3 | 580 | 597 | | 25 (1) | | 4 (2)* | 8 (1) | 3 (2)* | 2 (3)* | 3 (2)* | 0 (3)* | 0 (2)* | -1 (1)* | 0 (2)* |
| DEIEQDLTQRFEEKLQELES | 3 | 580 | 599 | | 27 (1) | | 4 (2)* | 7 (1) | 3 (2)* | 1 (2)* | 3 (3)* | 0 (3)* | 0 (3)* | -1 (2)* | -2 (2)* |
| QELESVSRDPSNENPKLED | 3 | 595 | 613 | | 47 (2) | | 2 (3)* | 1 (2)* | 1 (5)* | -3 (3)* | -1 (3)* | -1 (4)* | -7 (4) | -3 (4)* | -6 (5) |
| ESVSRDPSNENPKLEDLC | 3 | 598 | 615 | | 40 (1) | | 0 (1)* | 3 (3)* | 2 (3)* | 0 (2)* | 4 (6)* | -3 (3)* | -6 (7) | 1 (3)* | -6 (3) |
| VSRDPSNENPKLED | 2 | 600 | 613 | | 58 (2) | | 3 (4)* | 2 (4)* | 1 (4)* | -1 (5)* | -2 (5)* | -3 (4)* | -7 (4) | -2 (4)* | -6 (4) |
| VSRDPSNENPKL | 3 | 600 | 611 | | 51 (3) | | 4 (4)* | 3 (6)* | 2 (5)* | 1 (10)* | -2 (4)* | -5 (4) | -10 (4) | -3 (5)* | -6 (5) |
| FILQEEYHLNPET | 2 | 616 | 628 | HEL2 | 33 (3) | | -4 (3)* | -1 (3)* | -2 (3)* | -3 (2)* | -1 (3)* | 1 (4)* | -2 (3)* | 0 (2)* | -4 (2)* |
| ILQEEYHLNPETITIL | 2 | 617 | 632 | | 22 (1) | | -1 (1)* | 1 (1)* | 1 (1)* | -3 (1)* | 2 (3)* | 1 (2)* | -2 (3)* | -1 (2)* | -3 (2)* |
| EEYHLNPETITILFVKTR | 2 | 620 | 637 | | 38 (2) | | 1 (2)* | 5 (3)* | 2 (5)* | -6 (3) | 5 (4) | 0 (4)* | 3 (3)* | 0 (4)* | 4 (5)* |
| FVKTRALVDALKNWIEGNPKL | 3 | 633 | 653 | | 31 (2) | | -3 (3)* | -2 (2)* | -1 (3)* | -8 (3) | -2 (2)* | 1 (3)* | -6 (3) | 3 (3)* | -11 (2) |
| FVKTRALVDALKNWIEGNPKLSF | 3 | 633 | 655 | | 35 (2) | | -3 (2)* | -3 (2)* | -2 (2)* | -10 (2) | | 1 (3)* | -6 (2) | 4 (4)* | -10 (2) |
| FVKTRALVDALKNWIEGNPKLSFLKPGIL | 4 | 633 | 661 | motif IV | 36 (2) | | -3 (3)* | 0 (2)* | 5 (2) | -12 (2) | -3 (0)* | 2 (5)* | -6 (3) | | -12 (4) |
| SFLKPGIL | 2 | 654 | 661 | | 40 (2) | | 1 (2)* | 3 (3)* | 1 (5)* | -2 (3)* | 0 (2)* | -1 (5)* | -8 (2) | -5 (5) | -12 (5) |
| TGRGKTNQNTGMTLPAQKCIL | 3 | 662 | 682 | | 72 (4) | | 3 (5)* | 0 (6)* | -4 (5)* | -3 (5)* | -4 (5)* | -3 (4)* | -4 (4)* | -6 (5) | -1 (7)* |
| TGRGKTNQNTGMTLPAQKCIL | 4 | 662 | 682 | | 67 (3) | | 4 (4)* | -3 (4)* | -5 (3)* | -1 (4)* | -2 (5)* | -4 (4)* | -3 (3)* | -6 (5) | 0 (0)* |
| PAQKCIL | 2 | 676 | 682 | | 85 (3) | | -1 (5)* | 1 (3)* | 0 (4)* | -3 (6)* | -2 (4)* | 1 (2)* | -1 (3)* | -14 (6) | -4 (5)* |
| DAFKASGDHNIL | 2 | 683 | 694 | | 46 (3) | | 0 (3)* | 2 (4)* | -2 (3)* | -2 (4)* | -1 (4)* | -2 (3)* | -1 (2)* | -4 (3)* | 0 (4)* |
| DAFKASGDHNIL | 3 | 683 | 694 | | 47 (2) | | 0 (3)* | 0 (4)* | -3 (3)* | -2 (5)* | 0 (3)* | -2 (3)* | -2 (3)* | -4 (3)* | 1 (4)* |
| FKASGDHNIL | 3 | 685 | 694 | | 39 (3) | | -1 (3)* | 0 (4)* | -3 (3)* | -3 (4)* | 1 (5)* | -1 (3)* | 0 (3)* | -2 (2)* | 0 (4)* |
| IATSVADEGID | 2 | 695 | 705 | Pincer | 71 (2) | | 0 (4)* | -4 (3)* | -5 (4) | -3 (6)* | 0 (6)* | -2 (3)* | -49 (5) | -9 (4) | -39 (5) |
| IATSVADEGIDIAQCNLVILYEYVGNVIKM | 3 | 695 | 724 | | 68 (2) | | 1 (3)* | -1 (3)* | -3 (4)* | -2 (1)* | 0 (2)* | -3 (4)* | -38 (4) | -4 (4)* | -24 (3) |
| YEYVGNVIKM | 2 | 715 | 724 | | 83 (4) | | 0 (6)* | -5 (4)* | -2 (4)* | -8 (4) | -2 (6)* | -4 (5)* | -39 (5) | -12 (4) | -40 (3) |
| YVGNVIKM | 2 | 717 | 724 | | 72 (3) | | 2 (5)* | -1 (4)* | 2 (4)* | 0 (3)* | -1 (6)* | -4 (5)* | -34 (4) | -12 (4) | -35 (3) |
| IQTRGRGRARGSKC | 4 | 725 | 738 | | 74 (2) | | 3 (4)* | -3 (4)* | -3 (7)* | 0 (5)* | 3 (0)* | -7 (4) | -38 (5) | 2 (7)* | -31 (6) |
| FLLTSNAGVIEKEQINM | 2 | 739 | 755 | | 44 (3) | | -1 (4)* | 2 (4)* | 0 (5)* | -23 (3) | 3 (5)* | 2 (4)* | -9 (3) | -4 (3)* | -12 (4) |
| LTSNAGVIEKEQINM | 2 | 741 | 755 | | 55 (3) | | -3 (5)* | -1 (4)* | -2 (4)* | -7 (3) | -1 (6)* | 0 (1)* | -10 (4) | -5 (3)* | -15 (3) |
| AGVIEKE | 2 | 745 | 751 | | 51 (3) | | 4 (4)* | 2 (3)* | -3 (5)* | | -3 (1)* | -2 (1)* | -7 (3) | -1 (5)* | -2 (5)* |
| KEQINM | 2 | 750 | 755 | | 41 (3) | | 2 (4)* | 3 (4)* | 2 (5)* | -3 (3)* | -5 (7)* | 4 (5)* | -24 (2) | -10 (3) | -26 (6) |
| YKEKMMNDSIL | 2 | 756 | 766 | | 18 (2) | | 4 (3)* | 10 (3) | 3 (5)* | -1 (3)* | 5 (5) | 6 (4) | 2 (3)* | -1 (3)* | 1 (5)* |
| YKEKMMNDSIL | 3 | 756 | 766 | | 18 (3) | | 5 (4)* | 6 (3) | 3 (5)* | -1 (3)* | 5 (4) | 6 (4) | 1 (3)* | -1 (3)* | 1 (5)* |
| RLQTWDEAVF | 2 | 767 | 776 | | 52 (2) | | -5 (4)* | -1 (3)* | -4 (3)* | 1 (4)* | 0 (3)* | 0 (4)* | 5 (2) | -1 (2)* | 3 (2)* |
| WDEAVF | 1 | 771 | 776 | | 50 (3) | | 0 (4)* | -4 (2)* | 4 (2)* | 2 (2)* | 1 (4)* | -2 (3)* | 0 (4)* | -1 (7)* | 1 (5)* |
| FREKILHIQTHEKF | 4 | 776 | 789 | | 19 (4) | | -6 (4) | 1 (4)* | 0 (5)* | -7 (4) | -2 (0)* | 2 (4)* | 4 (5)* | 1 (3)* | -4 (5)* |
| REKILHIQTHEKF | 3 | 777 | 789 | | 22 (2) | | -7 (4) | 0 (3)* | 0 (5)* | -8 (4) | 0 (3)* | 3 (4)* | 0 (3)* | | -6 (5) |
| RDSQEKPKPVPDK | 2 | 791 | 803 | CTD | 81 (4) | | 1 (4)* | 0 (5)* | -2 (4)* | -5 (7) | 0 (6)* | -11 (5) | -15 (3) | | -18 (3) |
| VRVIEE | 2 | 823 | 828 | | 62 (3) | | 0 (4)* | 4 (4)* | 0 (4)* | -13 (4) | -3 (4)* | 0 (4)* | -3 (7)* | -1 (2)* | -2 (2)* |
| VRVIEECHY | 2 | 823 | 831 | | 41 (2) | | -6 (4) | 3 (3)* | 4 (3)* | | -3 (4)* | 1 (4)* | 2 (5)* | -1 (3)* | -2 (3)* |
| VRVIEECHYTVLGDA | 3 | 823 | 837 | | 42 (4) | | -1 (2)* | 1 (2)* | -2 (4)* | -8 (4) | -2 (2)* | -1 (2)* | | 0 (3)* | 0 (5)* |
| VRVIEECHY | 3 | 823 | 831 | | 35 (2) | | -7 (5) | -2 (4)* | 0 (5)* | -9 (5) | -2 (6)* | -1 (4)* | 3 (4)* | -2 (3)* | -2 (5)* |
| CHYTVLGDA | 2 | 829 | 837 | | 26 (1) | | 2 (2)* | 3 (2)* | 1 (2)* | 0 (2)* | 3 (3)* | -1 (3)* | 0 (4)* | 0 (2)* | -1 (2)* |
| TVLGDAFKECF | 2 | 832 | 842 | | 49 (2) | | -3 (3)* | -1 (3)* | -1 (3)* | -6 (3) | -1 (3)* | 0 (4)* | 0 (3)* | 1 (4)* | 0 (4)* |
| FKECF | 1 | 838 | 842 | | 31 (3) | | -8 (3) | -3 (4)* | -2 (5)* | -10 (4) | 3 (7)* | 1 (5)* | -1 (3)* | 5 (3)* | -1 (5)* |
| FKECF | 2 | 838 | 842 | | 34 (2) | | -9 (3) | -6 (4) | -9 (5) | -9 (4) | -2 (5)* | 2 (6)* | 0 (5)* | 5 (4)* | 0 (5)* |
| FVSRPHPKPKQFSS | 4 | 842 | 855 | Capping loop | 77 (4) | | -12 (5) | -13 (6) | -4 (4)* | -13 (6) | -21 (5) | 1 (5)* | 4 (3)* | -3 (6)* | -4 (5)* |
| VSRPHPKPKQFSSF | 3 | 843 | 856 | | 74 (5) | | -10 (6) | -15 (5) | -4 (5)* | -12 (6) | -24 (4) | 0 (5)* | 2 (6)* | -3 (6)* | -3 (6)* |
| VSRPHPKPKQFSSF | 4 | 843 | 856 | | 77 (4) | | -12 (5) | -13 (6) | -2 (4)* | -13 (6) | -22 (6) | 1 (5)* | 4 (3)* | -3 (6)* | -4 (5)* |
| EKRAKIF | 2 | 857 | 863 | | 43 (3) | | -5 (4)* | -4 (5)* | -5 (5)* | -11 (4) | -2 (4)* | -1 (6)* | -3 (3)* | -1 (4)* | -5 (5) |
| EKRAKIFC | 2 | 857 | 864 | | 40 (3) | | -3 (3)* | -1 (5)* | -6 (5) | -9 (6) | 0 (4)* | 0 (3)* | 0 (2)* | | -3 (5)* |
| EKRAKIFC | 3 | 857 | 864 | | 41 (4) | | -6 (4) | -3 (5)* | -4 (6)* | -11 (5) | 2 (4)* | 0 (5)* | -1 (3)* | 0 (4)* | 0 (6)* |
| CARQNCSHDWGIHVKYKT | 4 | 864 | 881 | | 37 (3) | | -1 (3)* | -3 (4)* | -3 (5)* | -7 (4) | | 0 (5)* | -2 (2)* | 2 (3)* | -1 (4)* |
| FEIPVIKIESF | 2 | 882 | 892 | | 11 (2) | | -7 (2) | -5 (2)* | -4 (3)* | -10 (2) | -1 (4)* | 1 (2)* | 1 (2)* | -1 (2)* | -1 (3)* |
| FEIPVIKIES | 2 | 882 | 891 | | 16 (2) | | -8 (2) | -3 (2)* | -2 (2)* | -6 (2) | -1 (5)* | 3 (2)* | 3 (2)* | -1 (2)* | 1 (2)* |
| EIPVIKIESF | 2 | 883 | 892 | | 11 (2) | | -8 (2) | -4 (2)* | -2 (2)* | -6 (2) | | 3 (2)* | 3 (2)* | -1 (2)* | 1 (2)* |
| VVEDIATGVQTL | 1 | 893 | 904 | RNA binding region | 65 (2) | | -12 (4) | -9 (3) | -6 (3) | -14 (3) | -5 (3) | -1 (3)* | -3 (4)* | -5 (4)* | -10 (2) |
| VVEDIATGVQTL | 2 | 893 | 904 | | 65 (3) | | -10 (4) | -14 (3) | -11 (4) | -16 (4) | -6 (3) | 3 (3)* | -1 (4)* | -5 (4)* | -10 (3) |
| IATGVQTL | 2 | 897 | 904 | | 66 (3) | | -8 (5) | -20 (5) | -22 (5) | -18 (4) | -6 (3) | -1 (6)* | -6 (3) | -7 (5) | -6 (4) |
| YSKWKDFHFEKIPFDPAE | 3 | 905 | 922 | | 54 (3) | | -9 (4) | -6 (3) | -3 (3)* | -5 (4)* | -1 (1)* | 2 (4)* | 1 (3)* | 3 (4)* | -10 (4) |
| EKIPFDPAE | 2 | 914 | 922 | | 35 (3) | | 2 (3)* | 1 (3)* | -1 (3)* | -3 (3)* | 2 (5)* | 0 (4)* | -1 (4)* | -1 (4)* | 1 (3)* |
| EKIPFDPAEMSK | 2 | 914 | 925 | | 54 (3) | | -2 (4)* | -1 (4)* | -3 (4)* | -5 (4)* | -5 (3) | -1 (3)* | -1 (2)* | -2 (5)* | -1 (5)* |
| EKIPFDPAEMSK | 3 | 914 | 925 | | 57 (3) | | 0 (4)* | 0 (4)* | -2 (4)* | -5 (4)* | -3 (3)* | -2 (3)* | -2 (3)* | -2 (4)* | -2 (6)* |

HDX Dynamics Key

HDX Perturbation Key

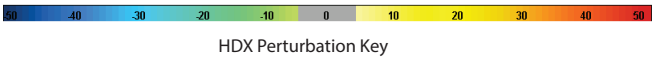
H830A RIG-I

| peptide sequence | charge | start | end | structure | (xii) | (xiii) | (xiv) |
|---|---|---|---|---|---|---|---|
| FQDYIRKTLDPTYILS | 3 | 12 | 27 | CARD1 | 52 (3) | 11 (3) | 11 (3) |
| QDYIRKTLDPTYIL | 3 | 13 | 26 | | 78 (3) | 11 (3) | 10 (5) |
| IRKTLDPTYIL | 3 | 16 | 26 | | 46 (3) | 17 (4) | 16 (6) |
| SYMAPWFRE | 2 | 27 | 35 | | 53 (3) | 14 (4) | 14 (4) |
| YMAPWFREEEVQ | 2 | 28 | 39 | | 55 (3) | 14 (4) | 14 (4) |
| VQYIQA | 2 | 38 | 43 | | 66 (4) | 8 (5) | 8 (5) |
| YIQAEKNNKGPMEA | 3 | 40 | 53 | | 51 (3) | 9 (4) | 8 (4) |
| EKNNKGPMEAATL | 2 | 44 | 56 | | 45 (2) | 11 (3) | 11 (5) |
| LQEEGWFRGFL | 2 | 64 | 74 | | 48 (2) | 9 (4) | 6 (6) |
| QEEGWFRGFL | 2 | 65 | 74 | | 52 (1) | 9 (3) | 8 (4) |
| FRGFLDA | 2 | 70 | 76 | | 16 (2) | 20 (3) | 19 (4) |
| DALDHAGYSGL | 2 | 75 | 85 | | 34 (2) | 13 (3) | 13 (3) |
| LDHAGYSGL | 2 | 77 | 85 | | 36 (2) | 10 (3) | 9 (3) |
| YEAIESW | 1 | 86 | 92 | Latch region | 35 (2) | 25 (5) | 23 (4) |
| YEAIESWD | 1 | 86 | 93 | | 29 (3) | 23 (5) | 22 (5) |
| YRLLL | 2 | 103 | 107 | | 12 (3) | 24 (5) | 23 (5) |
| YRLLLKRLQPEF | 3 | 103 | 114 | | 17 (3) | 33 (5) | 33 (5) |
| LLKRLQPEF | 2 | 106 | 114 | | 21 (4) | 30 (5) | 28 (6) |
| LLKRLQPEF | 3 | 106 | 114 | | 18 (4) | 33 (5) | 34 (6) |
| LLKRLQPEFKTRIIPTDIISD | 4 | 106 | 126 | | 7 (1) | 10 (1) | 8 (2) |
| KRLQPEF | 2 | 108 | 114 | | 21 (4) | 34 (5) | 33 (6) |
| KRLQPEF | 3 | 108 | 114 | | 18 (4) | 33 (4) | 33 (6) |
| KTRIIPTDIISD | 3 | 115 | 126 | CARD2 | 62 (2) | 12 (4) | 11 (4) |
| KTRIIPTDIISDL | 2 | 115 | 127 | | 59 (2) | 14 (4) | 13 (4) |
| KTRIIPTDIISDL | 3 | 115 | 127 | | 58 (3) | 14 (4) | 13 (4) |
| KTRIIPTDIISDLSE | 3 | 115 | 129 | | 63 (2) | 11 (4) | 11 (4) |
| EEILQICSTKGMMAGAEKL | 3 | 137 | 155 | | 31 (1) | 17 (3) | 8 (5) |
| ILQICSTKGMMAGA | 2 | 139 | 152 | | 40 (2) | 20 (2) | 20 (3) |
| ILQICSTKGMMAGAEKL | 3 | 139 | 155 | | 37 (2) | 16 (3) | 15 (4) |
| ILQICSTKGMMAGAEKLVE | 3 | 139 | 157 | | 29 (1) | 19 (2) | 18 (3) |
| LLRSDKENWPKTLKL | 4 | 159 | 173 | | 29 (2) | 10 (3) | 18 (3) |
| RSDKENWPKTLKL | 3 | 161 | 173 | | 28 (2) | 13 (4) | 10 (6) |
| ALEKERNKFSEL | 4 | 174 | 185 | | 67 (1) | 15 (5) | 13 (8) |
| ALEKERNKFSEL | 3 | 174 | 185 | | 61 (3) | 8 (3) | 8 (4) |
| EKERNKFSEL | 3 | 176 | 185 | | 65 (2) | 10 (4) | 10 (6) |
| WIVEKGIKDVE | 3 | 186 | 196 | linker | 102 (3) | 0 (5)* | 0 (6)* |
| WIVEKGIKDVETEDL | 3 | 186 | 200 | | 98 (2) | -2 (5)* | 2 (3)* |
| WIVEKGIKDVETEDLED | 2 | 186 | 202 | | 97 (3) | 0 (4)* | 1 (5)* |
| WIVEKGIKDVETEDLEDKMETSD | 3 | 186 | 208 | | 95 (2) | 0 (3)* | -1 (6)* |
| IVEKGIKDVETEDL | 3 | 187 | 200 | | 95 (5) | -2 (5)* | 1 (5)* |
| EDKMETSDIQIF | 2 | 201 | 212 | | 84 (3) | 1 (4)* | 1 (6)* |
| IQIFYQEDPECQNLSE | 2 | 209 | 224 | | 70 (2) | 0 (3)* | -2 (6)* |
| FYQEDPECQNL | 2 | 212 | 222 | | 81 (2) | -2 (3)* | -2 (6)* |
| YQEDPECQNL | 2 | 213 | 222 | | 81 (3) | -1 (4)* | -3 (6)* |
| SENSCPPSEVSDTNL | 2 | 223 | 237 | | 83 (4) | -2 (6)* | -1 (4)* |
| NSCPPSEVSDTNL | 2 | 225 | 237 | | 82 (4) | -1 (6)* | -1 (3)* |
| VSDTNL | 1 | 232 | 237 | | 92 (5) | -2 (6)* | -2 (3)* |
| YSPFKPRN | 3 | 238 | 245 | HEL1 | 100 (4) | -2 (5)* | -1 (7)* |
| YSPFKPRNYQLE | 3 | 238 | 249 | | 74 (3) | 4 (4)* | 3 (5)* |
| YSPFKPRNYQLE | 2 | 238 | 249 | | 73 (3) | 3 (4)* | 3 (5)* |
| LALPAMKGKNTIIC | 2 | 250 | 263 | | 32 (3) | -1 (4)* | 1 (5)* |
| LALPAMKGKNTIICAPTGCGKTFVSLL | 4 | 250 | 276 | | 47 (2) | 4 (3)* | 2 (5)* |
| LALPAMKGKNTIICAPTGCGKTFVSLL | 3 | 250 | 276 | | 43 (2) | -1 (3)* | -5 (3) |
| APTGCGKTF | 2 | 264 | 272 | | 84 (3) | -1 (5)* | -1 (6)* |
| LICEHHLKKFPQGQKGKVVF | 3 | 276 | 295 | | 29 (1) | 0 (2)* | 0 (3)* |
| ICEHHLKKFPQGQKGKVVF | 3 | 277 | 295 | | 28 (2) | -3 (2)* | -3 (4)* |
| PQGQKGKVVF | 3 | 286 | 295 | | 79 (4) | -1 (4)* | -1 (7)* |
| FANQIPVYEQQ | 2 | 296 | 306 | motif Ia | 74 (2) | -18 (3) | -15 (4) |
| FANQIPVYEQQKSVF | 2 | 296 | 310 | | 66 (2) | -16 (4) | -14 (5) |
| FANQIPVYEQQKSVFSKY | 3 | 296 | 313 | | 56 (1) | -10 (2) | -11 (3) |
| FERHGYRVTGISGATAENVPVEQIVENND | 4 | 314 | 342 | | 66 (3) | -4 (4)* | -3 (4)* |
| FERHGYRVTGISGATAENVPVEQIVENND | 3 | 314 | 342 | | 65 (3) | -4 (4)* | 0 (7)* |
| GYRVTGISGATAENVPVEQIVENN | 4 | 318 | 341 | | 71 (2) | -3 (5)* | -5 (6)* |
| YRVTGISGATAENVPVEQIVE | 3 | 319 | 339 | | 84 (5) | -2 (7)* | -2 (8)* |
| IIILTPQIL | 2 | 343 | 351 | | 38 (1) | -5 (2)* | -4 (2)* |
| IIILTPQIL | 1 | 343 | 351 | | 35 (1) | -4 (2)* | -3 (2)* |
| IIILTPQILVN | 2 | 343 | 353 | | 38 (1) | -6 (2) | -5 (2)* |
| IIILTPQILVNN | 2 | 343 | 354 | | 43 (2) | -8 (3) | -8 (4) |
| IIILTPQILVNNL | 2 | 343 | 355 | motif Ic | 52 (1) | -11 (2) | -10 (3) |
| IIILTPQILVNNLKKGTIPSL | 3 | 343 | 363 | | 72 (3) | -10 (3) | -8 (4) |
| IIILTPQILVNNLKKGTIPSL | 2 | 343 | 363 | | 68 (2) | -7 (4) | -6 (4) |
| IIILTPQILVNNLKKGTIPSLSI | 3 | 343 | 365 | | 68 (2) | -9 (3) | -7 (4) |
| IIILTPQILVNNLKKGTIPSLSIF | 3 | 343 | 366 | | 65 (2) | -9 (3) | -7 (3) |
| KGTIPSLSIFT | 2 | 357 | 367 | | 61 (1) | 4 (3)* | 4 (3)* |
| KGTIPSLSIFT | 3 | 357 | 367 | | 61 (1) | 4 (3)* | 4 (3)* |
| LMIFDECHNTSKQHPYNM | 3 | 368 | 385 | motif IIa | 36 (1) | -6 (2) | -6 (2) |
| IFDECHNTSKQHPYNMIM | 3 | 370 | 387 | | 36 (2) | -6 (2) | -6 (2) |
| IFDECHNTSKQHPYNMIM | 2 | 370 | 387 | | 36 (1) | -6 (2) | -6 (3) |
| FNYLDQKLGGSSGPLPQVIG | 2 | 388 | 407 | | 37 (1) | 0 (2)* | 0 (3)* |
| FNYLDQKLGGSSGPLPQVIGL | 2 | 388 | 408 | | 36 (1) | 0 (2)* | 0 (3)* |
| DQKLGGSSGPLPQVIGL | 2 | 392 | 408 | | 43 (1) | 0 (2)* | 0 (3)* |
| LTASVGVGDAKNTDEAL | 2 | 408 | 424 | | 70 (3) | -5 (4) | -5 (5)* |
| TASVGVGDAKNTDEAL | 2 | 409 | 424 | | 72 (3) | -5 (4) | -5 (5)* |
| TASVGVGDAKNTDEALD | 2 | 409 | 425 | | 69 (3) | -5 (4)* | -4 (5)* |
| DYICKL | 2 | 425 | 430 | | 3 (1) | 0 (1)* | 1 (1)* |
| DYICKL | 1 | 425 | 430 | | 3 (0) | 0 (2)* | 1 (2)* |
| CASLDASVIATVKHNLEEL | 2 | 431 | 449 | | 37 (1) | 0 (2)* | 0 (3)* |
| SVIATVKHNLEE | 2 | 437 | 448 | | 62 (2) | -1 (3)* | -1 (3)* |
| EQVVYKPQKF | 3 | 450 | 459 | | 76 (2) | 1 (4)* | 1 (4)* |
| VVYKPQKF | 2 | 452 | 459 | | 83 (3) | -1 (5)* | -1 (5)* |
| VVYKPQKF | 3 | 452 | 459 | | 83 (3) | -1 (4)* | -1 (5)* |
| FRKVESRISDKF | 3 | 460 | 471 | HEL2i | 71 (2) | 0 (3)* | -3 (16)* |
| QLMRDTESL | 2 | 477 | 485 | | 9 (2) | 0 (2)* | -1 (5)* |
| MRDTESL | 2 | 479 | 485 | | 7 (0) | 1 (1)* | 1 (1)* |
| AKRICKDLENL | 3 | 486 | 496 | | 76 (3) | -8 (3) | -6 (5) |
| SQIQNREFGTQKYEQ | 3 | 497 | 511 | | 76 (3) | -4 (5)* | -4 (5)* |
| SQIQNREFGTQKYEQW | 3 | 497 | 512 | | 70 (3) | -3 (4)* | -3 (5)* |
| WIVTVQKACM | 2 | 512 | 521 | | 11 (4) | 0 (6)* | 0 (5)* |
| IVTVQKACM | 2 | 513 | 521 | | 12 (1) | -2 (2)* | -1 (2)* |
| VFQMPDKDEESRICKA | 3 | 522 | 537 | CTD:HEL2i | 66 (2) | -11 (3) | -11 (4) |
| VFQMPDKDEESRICKALF | 4 | 522 | 539 | | 58 (2) | -10 (3) | -9 (3) |
| FQMPDKDEESRICKA | 3 | 523 | 537 | | 64 (2) | -11 (3) | -11 (4) |
| FQMPDKDEESRICKALF | 4 | 523 | 539 | | 53 (2) | -9 (2) | -9 (3) |
| LYTSHLRKYNDAL | 4 | 540 | 552 | | 8 (2) | 2 (4)* | 2 (4)* |
| LYTSHLRKYNDAL | 3 | 540 | 552 | | 8 (2) | 2 (3)* | 2 (4)* |

H830A RIG-I

| peptide sequence | charge | start | end | structure | (xii) | (xiii) | (xiv) |
|---|---|---|---|---|---|---|---|
| LYTSHLRKYNDAL | 4 | 540 | 552 | HEL2i | 8 (2) | 2 (4)* | 2 (4)* |
| LYTSHLRKYNDAL | 3 | 540 | 552 | | 8 (2) | 2 (3)* | 2 (4)* |
| IISEHARMKDALD | 3 | 553 | 565 | | 23 (2) | 2 (3)* | 2 (3)* |
| HARMKDALD | 2 | 557 | 565 | | 32 (2) | 1 (2)* | 1 (3)* |
| HARMKDALD | 3 | 557 | 565 | | 31 (2) | 1 (2)* | 1 (3)* |
| DYLKDFFSNVRAAGF | 3 | 565 | 579 | | 49 (2) | 14 (4) | 12 (4) |
| YLKDFFSNV | 2 | 566 | 574 | Gate motif | 18 (1) | 14 (2) | 13 (2) |
| YLKDFFSNVRAAGF | 3 | 566 | 579 | | 46 (5) | 12 (5) | 12 (3) |
| FFSNV | 1 | 570 | 574 | | 36 (2) | 27 (4) | 25 (4) |
| FFSNVRAAGF | 2 | 570 | 579 | | 58 (2) | 19 (5) | 17 (5) |
| FFSNVRAAGFD | 2 | 570 | 580 | | 63 (5) | 15 (6) | 14 (6) |
| FSNVRAAGF | 2 | 571 | 579 | | 65 (2) | 19 (4) | 17 (5) |
| DEIEQDLTQRFEEKLQE | 3 | 580 | 596 | | 25 (0) | 5 (2) | 6 (2) |
| DEIEQDLTQRFEEKLQEL | 3 | 580 | 597 | | 25 (1) | 6 (2) | 6 (2) |
| DEIEQDLTQRFEEKLQELES | 3 | 580 | 599 | | 28 (1) | 5 (2) | 6 (2) |
| QELESVSRDPSNENPKLED | 3 | 595 | 613 | | 53 (2) | 0 (3)* | 0 (4)* |
| ESVSRDPSNENPKLEDLC | 3 | 598 | 615 | | 45 (1) | 0 (2)* | 0 (2)* |
| VSRDPSNENPKL | 3 | 600 | 611 | | 68 (4) | 0 (6)* | -2 (6)* |
| VSRDPSNENPKLED | 2 | 600 | 613 | | 58 (3) | 1 (4)* | 0 (5)* |
| FILQEEYHLNPET | 2 | 616 | 628 | HEL2 | 31 (1) | 0 (2)* | 0 (2)* |
| ILQEEYHLNPETITIL | 2 | 617 | 632 | | 26 (1) | 0 (1)* | 0 (2)* |
| EEYHLNPETITILFVKTR | 2 | 620 | 637 | | 40 (1) | 0 (2)* | 1 (3)* |
| FVKTRALVDALKNWIEGNPKL | 3 | 633 | 653 | motif IV | 30 (1) | -1 (2)* | -2 (3)* |
| FVKTRALVDALKNWIEGNPKLSF | 3 | 633 | 655 | | 32 (1) | -1 (3)* | -3 (4)* |
| FVKTRALVDALKNWIEGNPKLSFLKPGIL | 4 | 633 | 661 | | 33 (1) | 0 (2)* | -2 (5)* |
| WIEGNPKL | 2 | 646 | 653 | | 42 (1) | 0 (2)* | 1 (3)* |
| WIEGNPKLSFLKPGIL | 2 | 646 | 661 | | 44 (2) | 4 (2)* | 1 (4)* |
| SFLKPGIL | 2 | 654 | 661 | | 43 (2) | 1 (2)* | 2 (4)* |
| KPGILTGRGKTNQNTG | 3 | 657 | 672 | | 30 (4) | -4 (5)* | -1 (5)* |
| TGRGKTNQNTGMTLPAQKCIL | 3 | 662 | 682 | | 84 (3) | -3 (4)* | -3 (5)* |
| PAQKCIL | 2 | 676 | 682 | | 77 (1) | -4 (2)* | 3 (6)* |
| DAFKASGDHNIL | 3 | 683 | 694 | | 55 (3) | -1 (4)* | -1 (4)* |
| DAFKASGDHNIL | 2 | 683 | 694 | | 52 (3) | 0 (4)* | 0 (5)* |
| FKASGDHNIL | 3 | 685 | 694 | | 46 (3) | 0 (4)* | -1 (4)* |
| IATSVADEGID | 2 | 695 | 705 | Pincer | 84 (3) | -5 (5)* | -3 (4)* |
| IATSVADEGIDIAQCNL | 2 | 695 | 711 | | 85 (3) | -2 (6)* | 0 (5)* |
| SVADEGIDIAQ | 2 | 698 | 708 | | 38 (2) | 4 (3)* | 4 (4)* |
| CNLVILYEYVGNV | 4 | 709 | 721 | | 23 (2) | 1 (3)* | 1 (4)* |
| VILYEYVGNVIKM | 2 | 712 | 724 | | 72 (3) | -2 (5)* | 0 (4)* |
| YEYVGNVIKM | 2 | 715 | 724 | | 97 (3) | -5 (6)* | -5 (6)* |
| YVGNVIKM | 2 | 717 | 724 | | 91 (3) | -4 (5)* | -4 (6)* |
| IQTRGRGRARGSKC | 4 | 725 | 738 | | 66 (3) | -4 (4)* | -4 (5)* |
| FLLTSNAGVIE | 2 | 739 | 749 | | 65 (1) | -5 (2)* | -2 (3)* |
| FLLTSNAGVIEKEQINM | 2 | 739 | 755 | | 46 (3) | 4 (4)* | 1 (4)* |
| LTSNAGVIEKEQINM | 2 | 741 | 755 | | 60 (2) | 3 (5)* | 0 (3)* |
| AGVIEKE | 2 | 745 | 751 | | 62 (2) | 0 (4)* | 0 (6)* |
| KEQINM | 2 | 750 | 755 | | 59 (2) | 4 (3)* | 3 (3)* |
| YKEKMMNDSIL | 3 | 756 | 766 | | 21 (2) | 11 (3) | 11 (4) |
| YKEKMMNDSIL | 2 | 756 | 766 | | 21 (2) | 11 (3) | 11 (4) |
| SILRLQT | 2 | 764 | 770 | | 26 (2) | 1 (3)* | 2 (4)* |
| RLQTWDEAVF | 2 | 767 | 776 | | 51 (1) | -2 (3)* | 0 (3)* |
| WDEAVF | 1 | 771 | 776 | | 75 (2) | 0 (3)* | -1 (3)* |
| FREKILHIQTHEKF | 4 | 776 | 789 | | -18 (1) | -2 (2)* | -1 (3)* |
| REKILHIQTHEKF | 3 | 777 | 789 | | 9 (2) | 0 (4)* | -2 (3)* |
| THEKFIRDS | 2 | 785 | 793 | CTD | 18 (1) | 14 (2) | 13 (2) |
| EKFIRDSQEK | 2 | 787 | 796 | | 63 (2) | 10 (4) | 4 (4)* |
| RDSQEKPKPVPDK | 2 | 791 | 803 | | 98 (2) | 0 (4)* | 0 (5)* |
| VRVIEE | 2 | 823 | 828 | | 65 (2) | -4 (3)* | -4 (3)* |
| TVLGDAFKECF | 2 | 832 | 842 | | 56 (2) | -5 (3)* | -3 (3)* |
| FKECF | 1 | 838 | 842 | | 46 (2) | -14 (3) | -10 (4) |
| FKECF | 2 | 838 | 842 | | 44 (2) | -14 (3) | -10 (4) |
| FVSRPHPKPKQFSS | 4 | 842 | 855 | Capping loop | 77 (2) | -19 (4) | -3 (4)* |
| VSRPHPKPKQFSSF | 4 | 843 | 856 | | 78 (3) | -19 (4) | -3 (4)* |
| VSRPHPKPKQFSSF | 3 | 843 | 856 | | 77 (2) | -22 (4) | -4 (4)* |
| EKRAKIF | 2 | 857 | 863 | | 49 (2) | -14 (2) | -9 (3) |
| EKRAKIFC | 3 | 857 | 864 | | 44 (3) | -13 (3) | -10 (3) |
| EKRAKIFC | 2 | 857 | 864 | | 43 (2) | -13 (4) | -8 (3) |
| CARQNCSHDWGIHVKYKT | 4 | 864 | 881 | | 15 (2) | -3 (2)* | -2 (2)* |
| DWGIHVKYKTFEIPVIKIESFVV | 4 | 872 | 894 | | 47 (2) | 4 (3)* | 3 (5)* |
| FEIPVIKIESF | 2 | 882 | 892 | | 14 (1) | -5 (3) | -5 (3)* |
| FVVEDIATGVQTL | 2 | 892 | 904 | RNA binding region | 64 (2) | -12 (4) | -11 (5) |
| VVEDIATGVQTL | 2 | 893 | 904 | | 74 (2) | -14 (3) | -12 (4) |
| VVEDIATGVQTL | 1 | 893 | 904 | | 72 (2) | -15 (3) | -12 (4) |
| YSKWKDFHFEKIPFDPAE | 3 | 905 | 922 | | 52 (2) | -4 (2)* | -4 (6)* |
| EKIPFDPAE | 2 | 914 | 922 | | 46 (3) | 1 (3)* | 1 (4)* |
| EKIPFDPAEMSK | 2 | 914 | 925 | | 65 (4) | -2 (5)* | -3 (6)* |
| EKIPFDPAEMSK | 3 | 914 | 925 | | 66 (4) | -1 (5)* | -2 (6)* |

HDX Dynamics Key




HDX Perturbation Key

E373A RIG-I

| peptide sequence | charge | start | end | structure | (xv) | (xvi) | (xvii) | (xviii) | (xix) | (xx) | (xxi) | (xxii) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FQDYIRKTLDPTYIL | 2 | 12 | 26 | CARD1 | 34 (2) | 14 (3) | 6 (3) | 0 (3)* | 2 (2)* | 1 (2)* | 7 (3) | 13 (3) |
| FQDYIRKTLDPTYIL | 3 | 12 | 26 | | 33 (2) | 14 (3) | 6 (3) | 0 (3)* | 2 (2)* | 1 (2)* | 7 (3) | 13 (3) |
| FQDYIRKTLDPTYILS | 3 | 12 | 27 | | 49 (1) | 10 (1) | 3 (2)* | 0 (1)* | 3 (1)* | 2 (3)* | 7 (4) | 24 (4) |
| SYMAPWFREEEVQ | 2 | 27 | 39 | | 45 (2) | 15 (3) | 7 (3) | 0 (2)* | 4 (3)* | 2 (3)* | 8 (2) | 12 (3) |
| YMAPWFRE | 2 | 28 | 35 | | 52 (2) | 12 (3) | 5 (3)* | -1 (2)* | 4 (3)* | -1 (3)* | 8 (3) | 10 (4) |
| YMAPWFREEE | 2 | 28 | 37 | | 51 (2) | 13 (3) | 6 (3) | 1 (2)* | 3 (4)* | 1 (4)* | 7 (3) | 8 (4) |
| YMAPWFREEEVQ | 2 | 28 | 39 | | 47 (2) | 15 (3) | 7 (3) | 0 (2)* | 4 (3)* | 1 (4)* | 8 (2) | 11 (3) |
| VQYIQA | 1 | 38 | 43 | | 48 (2) | 16 (3) | 6 (3) | -3 (3)* | 3 (2)* | 2 (3)* | 8 (3) | 16 (4) |
| YIQAEKNNKGPMEAATL | 3 | 40 | 56 | | 38 (2) | 14 (3) | 7 (3) | 0 (3)* | 4 (3)* | 3 (3)* | 8 (3) | 13 (3) |
| LQEEGWFRGFL | 2 | 64 | 74 | | 38 (1) | 17 (1) | 13 (2) | 1 (2)* | 1 (4)* | -1 (3)* | 1 (4)* | 14 (3) |
| QEEGWFRGFL | 2 | 65 | 74 | | 47 (2) | 8 (2) | 4 (3)* | 2 (2)* | 3 (3)* | 0 (3)* | 4 (3)* | 6 (3) |
| QEEGWFRGFLDAL | 2 | 65 | 77 | | 45 (3) | 21 (3) | 10 (4) | 0 (4)* | 3 (3)* | 0 (4)* | 8 (3) | 14 (4) |
| FRGFL | 2 | 70 | 74 | | 19 (1) | 14 (2) | 6 (2) | -2 (2)* | 3 (1)* | 0 (2)* | 7 (2) | 13 (2) |
| FRGFLDA | 2 | 70 | 76 | | 15 (1) | 15 (2) | 7 (2) | -2 (1)* | 3 (1)* | 1 (1)* | 7 (2) | 13 (2) |
| DALDHAGYSGL | 2 | 75 | 85 | | 30 (2) | 12 (2) | 5 (2) | 0 (3)* | 3 (2)* | 2 (3)* | 7 (2) | 10 (3) |
| LDHAGYSGL | 2 | 77 | 85 | | 34 (2) | 8 (2) | 5 (3)* | 0 (2)* | 5 (2) | 5 (3)* | 8 (3) | 9 (3) |
| YEAIESWD | 1 | 86 | 93 | | 28 (2) | 18 (2) | 7 (2) | -3 (2)* | 4 (3)* | 2 (2)* | 9 (3) | 17 (2) |
| YEAIESWDFKKIEKLEE | 3 | 86 | 102 | | 52 (2) | 7 (2) | 0 (3)* | -3 (3)* | 0 (2)* | -5 (5)* | 0 (4)* | |
| EAIESWDFKKIEKLEEY | 4 | 87 | 103 | | 55 (3) | 10 (3) | 5 (3)* | 2 (2)* | 2 (3)* | | 4 (4)* | 6 (4) |
| DFKKIEKLEE | 3 | 93 | 102 | | 69 (2) | 6 (3) | 2 (3)* | 1 (2)* | 1 (5)* | -2 (6)* | 1 (4)* | 3 (4)* |
| FKKIEKLEE | 3 | 94 | 102 | | 63 (2) | 5 (3) | 2 (3)* | 1 (2)* | -2 (4)* | -3 (4)* | 1 (3)* | 3 (4)* |
| YRLLL | 2 | 103 | 107 | Latch region | 11 (4) | 19 (4) | 8 (5) | 0 (4)* | 2 (2)* | 0 (2)* | 8 (5) | 15 (3) |
| YRLLLKRLQPEF | 3 | 103 | 114 | | 15 (3) | 32 (4) | 9 (5) | 3 (3)* | -1 (2)* | 5 (2)* | 14 (4) | 14 (4) |
| LLKRLQPEF | 2 | 106 | 114 | | 19 (4) | 26 (5) | 13 (5) | 3 (5)* | 4 (2)* | 7 (2) | 15 (3) | 22 (3) |
| KRLQPEF | 2 | 108 | 114 | | 19 (5) | 31 (5) | 15 (6) | 5 (6)* | 2 (2)* | 7 (3) | 23 (4) | 24 (4) |
| KRLQPEF | 3 | 108 | 114 | | 15 (5) | 31 (5) | 16 (6) | 0 (6)* | 4 (2)* | 2 (3)* | 13 (4) | 22 (4) |
| KTRIIPTD | 2 | 115 | 122 | | 53 (3) | 15 (5) | 8 (4) | 2 (4)* | 1 (5)* | -1 (6)* | 5 (4) | 8 (5) |
| KTRIIPTDIISD | 3 | 115 | 126 | | 54 (2) | 13 (4) | 8 (4) | -1 (3)* | 3 (4)* | 0 (5)* | 5 (4) | 7 (4) |
| KTRIIPTDIISDL | 2 | 115 | 127 | | 52 (2) | 14 (3) | 8 (3) | 2 (2)* | 2 (4)* | 1 (4)* | 6 (3) | 9 (4) |
| KTRIIPTDIISDL | 3 | 115 | 127 | | 51 (2) | 14 (3) | 8 (3) | 1 (2)* | 2 (4)* | 1 (4)* | 6 (3) | 9 (4) |
| KTRIIPTDIISDLSE | 3 | 115 | 129 | | 56 (2) | 15 (4) | 11 (3) | -1 (2)* | 2 (3)* | 3 (4)* | 12 (3) | 8 (3) |
| ILQICSTKGMMAGAEKL | 3 | 139 | 155 | CARD2 | 34 (2) | 16 (2) | 8 (2) | 3 (3)* | 3 (3)* | 0 (2)* | 5 (4) | 12 (3) |
| ILQICSTKGMMAGAEKLVE | 3 | 139 | 157 | | 27 (2) | 20 (3) | 10 (2) | 3 (2)* | 4 (2)* | 1 (2)* | 8 (2) | 14 (3) |
| ICSTKGMMAGAEKL | 3 | 142 | 155 | | 34 (2) | 21 (3) | 12 (3) | 3 (3)* | 4 (3)* | 1 (3)* | 8 (3) | 13 (3) |
| LRSDKENWPKTLKL | 4 | 160 | 173 | | 29 (3) | 20 (3) | 8 (3) | 2 (3)* | -6 (3) | -6 (4) | 2 (4)* | 11 (2) |
| LRSDKENWPKTLKLAL | 4 | 160 | 175 | | 26 (3) | 21 (3) | 8 (4) | 4 (3)* | -4 (3)* | -8 (3) | 3 (4)* | 6 (2) |
| ALEKERNKFSEL | 3 | 174 | 185 | | 62 (2) | 10 (4) | 12 (4) | 1 (2)* | 1 (4)* | 1 (4)* | -1 (6)* | 4 (5)* |
| EKERNKFSEL | 3 | 176 | 185 | | 59 (1) | 10 (4) | 6 (3) | 1 (2)* | -9 (4) | -3 (5)* | -2 (4)* | 4 (4)* |
| LWIVEKGIKDVETED | 3 | 185 | 199 | linker | 88 (2) | 2 (4)* | 3 (6)* | 1 (5)* | 0 (2)* | -1 (4)* | 1 (5)* | -1 (6)* |
| WIVEKGIKD | 3 | 186 | 194 | | 76 (3) | 3 (5)* | 4 (5)* | 1 (4)* | 4 (4)* | 2 (3)* | 3 (5)* | 1 (5)* |
| WIVEKGIKDVE | 2 | 186 | 196 | | 89 (1) | 2 (4)* | 3 (5)* | 2 (4)* | 1 (3)* | -1 (3)* | 1 (3)* | -1 (6)* |
| WIVEKGIKDVE | 3 | 186 | 196 | | 89 (1) | 2 (4)* | 4 (5)* | 2 (4)* | 1 (2)* | 0 (9)* | 2 (5)* | 0 (6)* |
| WIVEKGIKDVETEDLED | 2 | 186 | 202 | | 85 (3) | 2 (5)* | 3 (6)* | 4 (5)* | 1 (5)* | -1 (5)* | 1 (5)* | -2 (5)* |
| EDKMETSD | 2 | 201 | 208 | | 75 (1) | 1 (4)* | 1 (1)* | 0 (4)* | 1 (1)* | 0 (3)* | 0 (1)* | -5 (1)* |
| IQIFYQEDPECQNL | 2 | 209 | 222 | | 82 (2) | 4 (5)* | 5 (5)* | -7 (4) | 1 (5)* | 1 (5)* | 2 (6)* | -2 (5)* |
| YQEDPECQNL | 2 | 213 | 222 | | 77 (3) | 1 (5)* | 2 (6)* | -10 (5) | 1 (4)* | 0 (6)* | 2 (6)* | -1 (7)* |
| YQEDPECQNLSE | 2 | 213 | 224 | | 76 (3) | 1 (5)* | 2 (6)* | -9 (5) | 0 (6)* | 0 (6)* | 2 (6)* | 0 (5)* |
| SENSCPPSEVSDTNL | 2 | 223 | 237 | | 77 (3) | 0 (5)* | 2 (6)* | -9 (6) | 1 (4)* | 0 (5)* | 2 (6)* | 0 (7)* |
| YSPFKPRN | 2 | 238 | 245 | HEL1 | 89 (2) | 2 (6)* | 2 (6)* | 1 (5)* | -5 (4) | -8 (4) | -5 (7) | -10 (6) |
| YSPFKPRN | 3 | 238 | 245 | | 89 (2) | 2 (6)* | 2 (6)* | 1 (5)* | -3 (4)* | -8 (6) | -4 (5)* | -8 (6) |
| YSPFKPRNYQLE | 2 | 238 | 249 | | 60 (2) | 7 (4) | 5 (4) | 2 (4)* | -4 (4)* | -9 (5) | -3 (4)* | -9 (4) |
| LALPAMKGKN | 3 | 250 | 259 | | 45 (4) | 3 (5)* | 2 (6)* | 3 (6)* | 2 (4)* | 0 (5)* | 2 (5)* | 2 (5)* |
| LALPAMKGKNTIIC | 3 | 250 | 263 | | 32 (4) | 2 (5)* | 1 (5)* | 3 (5)* | -2 (4)* | -4 (5)* | 0 (5)* | -2 (5)* |
| LALPAMKGKNTIICA | 3 | 250 | 264 | | 67 (2) | 4 (3)* | 4 (3)* | 1 (4)* | -1 (4)* | -4 (5)* | 0 (5)* | -5 (4)* |
| LALPAMKGKNTIICAPTGCGKT | 4 | 250 | 271 | | 52 (3) | -3 (4)* | -1 (4)* | -6 (3) | -5 (3)* | -17 (3) | -9 (4) | -24 (4) |
| LALPAMKGKNTIICAPTGCGKTFVSL | 3 | 250 | 275 | | 46 (2) | 3 (3)* | 2 (4)* | -2 (4)* | -5 (3) | -12 (3) | -6 (4) | -17 (4) |
| LALPAMKGKNTIICAPTGCGKTFVSL | 4 | 250 | 275 | | 43 (2) | 2 (3)* | -1 (3)* | -6 (3) | -2 (3)* | -9 (3) | -5 (2)* | -11 (3) |
| LICEHHLKKFPQGQKGKVVF | 4 | 276 | 295 | | 32 (2) | 1 (3)* | -3 (3)* | -4 (2)* | -15 (3) | -23 (3) | -10 (5) | -23 (3) |
| ICEHHLKKFPQGQKGKVVF | 4 | 277 | 295 | | 33 (2) | 0 (3)* | -6 (3) | -10 (3) | -15 (3) | -28 (3) | -11 (5) | -25 (3) |
| FANQIPVYEQQKSVF | 2 | 296 | 310 | | 65 (2) | -16 (3) | -6 (4) | -10 (4) | 2 (3)* | -5 (4) | -3 (4)* | -29 (4) |
| FANQIPVYEQQKSVFSKY | 3 | 296 | 313 | | 57 (2) | -14 (3) | -8 (3) | -3 (4)* | 2 (3)* | -6 (3) | 3 (3)* | -21 (4) |
| FERHGYRVTGISGATAENVPVEQ | 3 | 314 | 336 | | 66 (2) | 0 (4)* | 0 (4)* | -2 (3)* | -2 (4)* | -2 (3)* | -1 (5)* | -3 (4)* |
| FERHGYRVTGISGATAENVPVEQ | 4 | 314 | 336 | | 71 (5) | 2 (5)* | 1 (5)* | -3 (5)* | 2 (3)* | -7 (4) | 1 (3)* | -3 (4)* |
| IIILTPQIL | 2 | 343 | 351 | | 32 (2) | -2 (3)* | 0 (3)* | -10 (2) | -1 (2)* | -3 (2)* | -1 (3)* | -13 (3) |
| IIILTPQILVNNL | 2 | 343 | 355 | | 47 (2) | -8 (3) | -4 (3)* | -10 (3) | -2 (2)* | -6 (2) | 1 (3)* | -23 (3) |
| IIILTPQILVNNLKKGTIPSL | 3 | 343 | 363 | motif Ia | 61 (2) | -6 (3) | -2 (3)* | -6 (3) | -2 (4)* | -5 (4)* | -2 (3)* | -16 (3) |
| IIILTPQILVNNLKKGTIPSLSIF | 3 | 343 | 366 | | 59 (2) | -6 (3) | -2 (3)* | -11 (4) | -2 (3)* | -5 (3)* | -2 (3)* | -14 (3) |
| VNNLKKGTIPSL | 2 | 352 | 363 | | 71 (2) | -7 (4) | -3 (4)* | -5 (4)* | -2 (5)* | -5 (5) | -3 (4)* | -11 (4) |
| VNNLKKGTIPSL | 3 | 352 | 363 | | 71 (2) | -7 (4) | -3 (4)* | -5 (4) | -2 (4)* | -5 (5) | -3 (4)* | -11 (4) |
| IFDACHNTSKQHPYNM | 4 | 370 | 385 | | 40 (1) | -5 (2)* | 0 (3)* | -2 (2)* | 0 (2)* | -2 (3)* | -1 (3)* | -15 (3) |
| IFDACHNTSKQHPYNMIM | 3 | 370 | 387 | | 34 (1) | -4 (2)* | 0 (2)* | -1 (2)* | 1 (2)* | -2 (2)* | 0 (3)* | -13 (3) |
| IFDACHNTSKQHPYNMIM | 4 | 370 | 387 | | 34 (1) | -4 (2)* | 1 (2)* | -1 (2)* | 2 (2)* | -1 (2)* | 0 (2)* | -13 (3) |
| FNYLDQKLGGSSGPLPQVIG | 2 | 388 | 407 | | 34 (2) | 1 (3)* | 1 (4)* | 0 (3)* | 1 (2)* | 0 (3)* | 3 (3)* | 2 (3)* |
| DQKLGGSSGPLPQVIG | 2 | 392 | 407 | | 42 (2) | 2 (3)* | 0 (3)* | 2 (2)* | 2 (3)* | 1 (4)* | 4 (3)* | 6 (3) |
| DQKLGGSSGPLPQVIGL | 2 | 392 | 408 | | 39 (2) | 2 (3)* | 1 (4)* | 0 (3)* | 0 (2)* | 0 (3)* | 3 (3)* | 2 (3)* |
| TASVGVGDAKNTD | 2 | 409 | 421 | motif Ic | 77 (3) | -1 (6)* | 2 (12)* | | -2 (7)* | -6 (8) | -3 (5)* | -15 (5) |
| TASVGVGDAKNTDEAL | 2 | 409 | 424 | | 64 (3) | 1 (5)* | 1 (4)* | -1 (4)* | -2 (5)* | -6 (6) | -2 (4)* | -12 (4) |
| TASVGVGDAKNTDEALD | 2 | 409 | 425 | | 61 (3) | 1 (5)* | 1 (4)* | -1 (4)* | -1 (5)* | -6 (5) | -2 (4)* | -11 (4) |
| DYICKL | 2 | 425 | 430 | motif IIa | 3 (3) | 1 (3)* | 0 (4)* | -1 (3)* | 0 (2)* | -1 (2)* | 1 (4)* | -1 (3)* |
| YICKL | 2 | 426 | 430 | | 4 (3) | 1 (4)* | 1 (5)* | -1 (3)* | 0 (2)* | -1 (2)* | 1 (5)* | -1 (4)* |
| CASLDASVIATVKHNLEEL | 2 | 431 | 449 | | 39 (1) | 4 (2)* | 2 (2)* | 1 (2)* | -3 (3)* | -11 (2) | -3 (2)* | 3 (2)* |
| SVIATVKHNLEE | 2 | 437 | 448 | | 54 (2) | 3 (3)* | 2 (3)* | 0 (2)* | -3 (4)* | -5 (3)* | -2 (3)* | -4 (3)* |
| SVIATVKHNLEEL | 2 | 437 | 449 | | 54 (2) | 5 (3)* | 3 (3)* | 2 (2)* | -6 (4) | -8 (3) | -5 (3)* | -7 (3) |
| LEQVVYKPQKF | 3 | 449 | 459 | | 63 (2) | 10 (4) | 6 (3) | 0 (4)* | -9 (4) | -16 (4) | -11 (3) | -17 (3) |
| EQVVYKPQKF | 2 | 450 | 459 | | 53 (2) | 16 (4) | 13 (4) | 3 (2)* | -12 (5) | -10 (5) | -6 (3) | -10 (4) |
| EQVVYKPQKF | 3 | 450 | 459 | | 62 (2) | 12 (4) | 8 (3) | 0 (3)* | -7 (5) | -14 (5) | -9 (3) | -14 (4) |
| LMRDTESLAKRICKDLEN | 4 | 478 | 495 | | 44 (2) | 0 (2)* | 1 (2)* | -1 (3)* | -7 (2) | -12 (1) | -16 (2) | |
| MRDTESLAKRICKDLENL | 4 | 479 | 496 | HEL2i | 44 (2) | 0 (2)* | 1 (2)* | -1 (3)* | -6 (2) | -12 (1) | -16 (2) | -6 (2) |
| AKRICKDLENL | 3 | 486 | 496 | | 69 (3) | 0 (4)* | 1 (4)* | 1 (3)* | -4 (5)* | -4 (3)* | -3 (4)* | -6 (4) |
| SQIQNREFGTQKYEQ | 3 | 497 | 511 | | 70 (2) | 0 (5)* | 1 (4)* | 0 (4)* | 0 (5)* | -2 (6)* | 1 (4)* | -3 (5)* |
| SQIQNREFGTQKYEQW | 3 | 497 | 512 | | 64 (2) | 0 (4)* | 2 (4)* | 0 (3)* | 0 (4)* | -2 (5)* | 1 (4)* | -4 (4)* |
| WIVTVQKACM | 2 | 512 | 521 | CTD:HEL2i | 49 (4) | -4 (9)* | 1 (6)* | 3 (2)* | -2 (4)* | -1 (4)* | -1 (2)* | -4 (2)* |
| VFQMPDKDEE | 2 | 522 | 531 | | 70 (3) | -1 (6)* | 0 (5)* | 0 (4)* | -1 (5)* | -4 (5)* | -3 (5)* | -18 (5) |
| VFQMPDKDEESRICKA | 3 | 522 | 537 | | 61 (2) | -4 (4)* | -1 (4)* | 1 (3)* | -1 (4)* | -5 (4) | -3 (3)* | -22 (3) |
| VFQMPDKDEESRICKA | 4 | 522 | 537 | | 61 (2) | -4 (4)* | -1 (3)* | 0 (3)* | -2 (4)* | -6 (4) | -4 (3)* | -23 (3) |
| VFQMPDKDEESRICKALF | 3 | 522 | 539 | | 54 (1) | -4 (3)* | -1 (3)* | 1 (2)* | -2 (3)* | -5 (3) | -3 (3)* | -19 (3) |
| SRICKALF | 3 | 532 | 539 | | 26 (2) | -5 (2)* | -2 (2)* | 1 (2)* | -3 (2)* | -5 (2) | -4 (3)* | -16 (3) |
| YTSHLRKYNDALI | 3 | 541 | 553 | Gate motif | 7 (2) | 2 (4)* | 2 (4)* | 3 (4)* | 0 (4)* | -1 (4)* | 0 (4)* | -1 (4)* |
| IISEHARMKDAL | 3 | 553 | 564 | | 25 (2) | 3 (3)* | 1 (4)* | 1 (2)* | -2 (2)* | -5 (3)* | -1 (4)* | -3 (4)* |
| IISEHARMKDALD | 3 | 553 | 565 | | 22 (2) | 2 (3)* | 3 (3)* | 1 (2)* | 0 (3)* | -2 (3)* | 0 (4)* | -2 (3)* |
| DYLKDFFSNVRAAGF | 3 | 565 | 579 | | 44 (2) | 11 (3) | 12 (3) | -1 (3)* | -3 (2)* | -3 (3)* | 2 (3)* | -5 (4)* |
| YLKDFFSNV | 2 | 566 | 574 | | 19 (2) | 11 (2) | 8 (3) | 3 (2)* | 1 (2)* | 0 (2)* | 2 (3)* | 2 (3)* |
| YLKDFFSNVRAAGF | 3 | 566 | 579 | | 43 (2) | 15 (3) | 13 (2) | -1 (4)* | | 3 (4)* | 11 (3) | 4 (3)* |
| FFSNVRAAGF | 2 | 570 | 579 | | 55 (2) | 17 (4) | 12 (3) | 3 (3)* | 3 (6)* | 0 (6)* | 9 (3) | 5 (5)* |
| FDEIEQDLTQRF | 2 | 579 | 590 | | 21 (2) | 7 (2) | 4 (3)* | 2 (2)* | 0 (2)* | -3 (2)* | -3 (3)* | -3 (2)* |
| FDEIEQDLTQRFEEKL | 3 | 579 | 594 | | 15 (1) | 5 (2) | 2 (2)* | 5 (2)* | 2 (3)* | 4 (3)* | 5 (2) | 1 (2)* |
| DEIEQDLTQRFEEKLQEL | 3 | 580 | 597 | | 24 (2) | 5 (2)* | 2 (2)* | 2 (1)* | 1 (2)* | -1 (2)* | 0 (2)* | -1 (3)* |
| DEIEQDLTQRFEEKLQELES | 3 | 580 | 599 | | 26 (2) | 4 (2)* | 2 (2)* | 4 (5)* | 1 (2)* | -1 (2)* | 0 (2)* | -2 (2)* |

E373A RIG-I

| peptide sequence | charge | start | end | structure | (xv) | (xvi) | (xvii) | (xviii) | (xix) | (xx) | (xxi) | (xxii) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LESVSRDPSNENPKLED | 3 | 597 | 613 | HEL2 | 53 (2) | 2 (4)* | 1 (4)* | -2 (4)* | 0 (4)* | -4 (5)* | -1 (4)* | -8 (4) |
| ESVSRDPSNENPKLED | 3 | 598 | 613 | | 52 (2) | 1 (4)* | 1 (4)* | -3 (3)* | 0 (4)* | -4 (5)* | -1 (3)* | -8 (4) |
| VSRDPSNENPKLED | 3 | 600 | 613 | | 54 (3) | 2 (5)* | 1 (4)* | -2 (4)* | 0 (5)* | -4 (5)* | -1 (4)* | -7 (4) |
| FILQEEYHLNPET | 2 | 616 | 628 | | 31 (2) | 0 (2)* | 0 (3)* | 3 (2)* | -1 (2)* | -5 (2)* | -2 (3)* | -6 (2) |
| ILQEEYHLNPET | 2 | 617 | 628 | | 32 (2) | 1 (2)* | 2 (3)* | 0 (2)* | 0 (2)* | -3 (2)* | -1 (3)* | -6 (3) |
| ILQEEYHLNPETIT | 2 | 617 | 630 | | 33 (1) | 0 (1)* | -1 (2)* | 0 (1)* | -2 (1)* | -3 (2)* | -3 (2)* | -7 (2) |
| ILQEEYHLNPETITIL | 2 | 617 | 632 | | 24 (1) | 0 (2)* | 0 (3)* | -1 (2)* | 0 (2)* | -3 (2)* | -1 (3)* | -5 (2) |
| EYHLNPET | 2 | 621 | 628 | | 53 (2) | 0 (4)* | 1 (3)* | 0 (3)* | 2 (3)* | -1 (3)* | 1 (2)* | -4 (3)* |
| YHLNPET | 2 | 622 | 628 | | 61 (2) | 0 (3)* | 2 (3)* | -1 (3)* | -1 (3)* | -10 (4) | -2 (3)* | -15 (3) |
| FVKTRALVDALKNWIEGNPKL | 3 | 633 | 653 | motif IV | 32 (1) | -1 (2)* | -1 (2)* | -5 (2) | -7 (2) | -19 (3) | -11 (4) | -19 (2) |
| FVKTRALVDALKNWIEGNPKL | 4 | 633 | 653 | | 32 (2) | -1 (2)* | -1 (2)* | -5 (2) | -5 (2) | -17 (3) | -10 (3) | -19 (2) |
| RALVDALKNWIEGNPKLSFLK | 3 | 637 | 657 | | 32 (1) | -1 (2)* | -1 (2)* | -3 (7)* | -7 (2) | -19 (3) | -11 (4) | -19 (2) |
| SFLKPGIL | 2 | 654 | 661 | | 41 (3) | 4 (4)* | 2 (5)* | 3 (5)* | -2 (4)* | -7 (4) | -4 (5)* | -15 (5) |
| LKPGIL | 2 | 656 | 661 | | 64 (2) | 4 (4)* | 2 (7)* | 0 (3)* | -4 (6)* | -11 (4) | -7 (7) | -25 (7) |
| TGRGKTNQNTGMTLPAQ | 3 | 662 | 678 | | 78 (4) | 3 (7)* | 1 (5)* | -1 (5)* | -3 (7)* | -2 (7)* | 0 (6)* | 0 (7)* |
| TGRGKTNQNTGMTLPAQK | 4 | 662 | 679 | | 78 (3) | 1 (6)* | 0 (6)* | -5 (4) | 0 (4)* | -2 (6)* | 0 (6)* | -2 (5)* |
| MTLPAQK | 2 | 673 | 679 | | 85 (3) | 4 (4)* | 0 (6)* | -4 (7)* | -3 (5)* | -1 (7)* | 0 (6)* | -2 (7)* |
| DAFKASGDHNIL | 2 | 683 | 694 | | 47 (2) | 2 (4)* | 2 (3)* | 1 (3)* | 2 (4)* | -1 (4)* | 1 (3)* | -1 (4)* |
| LIATSVADEGIDIAQCN | 2 | 694 | 710 | Pincer | 75 (2) | 5 (4)* | 2 (3)* | 3 (4)* | -1 (6)* | -15 (5) | -5 (3) | -39 (3) |
| IAQCNL | 1 | 706 | 711 | | 71 (2) | 3 (4)* | 1 (4)* | -2 (3)* | -1 (6)* | -11 (5) | -5 (4)* | -30 (3) |
| YEYVGNVIKM | 2 | 715 | 724 | | 86 (3) | 4 (5)* | 3 (4)* | 3 (4)* | -1 (7)* | -12 (5) | -7 (4) | -34 (4) |
| LTSNAGVIEKEQINM | 2 | 741 | 755 | | 54 (2) | 11 (4) | 7 (3) | 3 (3)* | -1 (5)* | -10 (6) | -10 (4) | -23 (3) |
| KEQINM | 2 | 750 | 755 | | 48 (2) | 15 (4) | 9 (3) | -2 (3)* | 1 (4)* | -12 (4) | -8 (3) | -34 (3) |
| YKEKMMNDSIL | 2 | 756 | 766 | | 17 (3) | 20 (4) | 13 (5) | 5 (4)* | 0 (2)* | -5 (3) | -1 (4)* | -8 (4) |
| YKEKMMNDSIL | 3 | 756 | 766 | | 17 (4) | 20 (4) | 13 (5) | 4 (4)* | 1 (2)* | -6 (3) | 0 (4)* | -8 (4) |
| SILRL | 2 | 764 | 768 | | 11 (4) | 1 (5)* | 0 (5)* | 1 (4)* | -1 (3)* | -2 (3)* | 3 (6)* | 0 (5)* |
| SILRLQT | 2 | 764 | 770 | | 25 (3) | 4 (3)* | 2 (4)* | 0 (4)* | 2 (2)* | 3 (2)* | 7 (4) | 8 (3) |
| RLQTWDEAV | 2 | 767 | 775 | | 53 (2) | 3 (3)* | 2 (3)* | 1 (3)* | 0 (4)* | -2 (6)* | 5 (3) | 5 (4) |
| RLQTWDEAVF | 2 | 767 | 776 | | 45 (2) | 1 (2)* | 2 (2)* | -4 (2)* | 4 (2)* | 5 (4) | 5 (2) | 7 (3) |
| DEAVF | 1 | 772 | 776 | | 24 (2) | -4 (3)* | -2 (3)* | 4 (3)* | 2 (7)* | -1 (4)* | -2 (4)* | -11 (4) |
| RDSQEKPKPVPDK | 2 | 791 | 803 | CTD | 78 (2) | 12 (5) | 10 (4) | 5 (3)* | -9 (6) | -20 (5) | -14 (4) | -23 (4) |
| KALACYTADVRVIE | 3 | 814 | 827 | | 45 (2) | -1 (4)* | -3 (4)* | | -5 (6)* | | -8 (5) | 0 (2)* |
| VRVIE | 2 | 823 | 827 | | 33 (2) | 2 (3)* | 1 (3)* | 0 (3)* | -1 (3)* | -2 (3)* | 1 (3)* | -2 (3)* |
| VRVIEE | 2 | 823 | 828 | | 62 (3) | 1 (3)* | 2 (4)* | -2 (4)* | -2 (2)* | -3 (3)* | -1 (4)* | -2 (3)* |
| VRVIEECHY | 3 | 823 | 831 | | 40 (2) | -2 (2)* | 2 (3)* | -6 (2) | 0 (2)* | -3 (2)* | -1 (4)* | -3 (3)* |
| CHYTVLGDA | 2 | 829 | 837 | | 31 (1) | 1 (2)* | 0 (2)* | -3 (2)* | 0 (2)* | 2 (4)* | 2 (2)* | 0 (2)* |
| TVLGDA | 1 | 832 | 837 | | 52 (2) | 1 (4)* | 0 (3)* | -2 (3)* | 0 (5)* | -1 (5)* | 2 (3)* | 0 (4)* |
| TVLGDAFKECF | 2 | 832 | 842 | | 51 (2) | -3 (3)* | -2 (3)* | -5 (3)* | 1 (3)* | -1 (4)* | 2 (3)* | 1 (3)* |
| FKECF | 2 | 838 | 842 | Capping loop | 38 (2) | -9 (3) | -5 (4) | -10 (4) | 0 (3)* | -2 (3)* | 0 (5)* | -4 (4)* |
| VSRPHPKPKQFSSF | 3 | 843 | 856 | | 77 (3) | -11 (5) | -1 (5)* | -13 (4) | -22 (6) | -7 (6) | -16 (5) | -3 (4)* |
| VSRPHPKPKQFSSF | 4 | 843 | 856 | | 77 (3) | -11 (5) | -2 (5)* | -11 (5) | -22 (5) | -7 (6) | -17 (4) | -2 (3)* |
| KPKQFSSFEKRA | 2 | 849 | 860 | | 59 (2) | 5 (3) | 3 (3)* | 2 (2)* | -6 (5) | -10 (4) | -5 (3) | -3 (5)* |
| FEIPVIKIES | 2 | 882 | 891 | | 16 (2) | -7 (2) | 3 (4)* | 1 (2)* | 1 (2)* | 0 (2)* | 0 (4)* | -3 (3)* |
| FEIPVIKIESF | 2 | 882 | 892 | | 16 (2) | -7 (2) | -5 (3)* | -7 (2) | 0 (1)* | 0 (1)* | -1 (2)* | -3 (2)* |
| FVVED | 1 | 892 | 896 | | 17 (1) | -5 (2) | -3 (4)* | -9 (2) | 0 (3)* | -1 (2)* | 0 (4)* | -3 (4)* |
| VVEDIATGVQTL | 2 | 893 | 904 | RNA binding region | 69 (2) | -10 (3) | -6 (3) | -16 (3) | -1 (3)* | -5 (3) | -3 (4)* | -12 (3) |
| YSKWKDFHF | 3 | 905 | 913 | | 66 (2) | -11 (3) | -9 (5) | -10 (2) | -23 (3) | -32 (5) | -17 (6) | -35 (7) |
| YSKWKDFHFEKIPFDPAE | 4 | 905 | 922 | | 55 (2) | -9 (3) | -10 (3) | -11 (3) | -24 (5) | -35 (4) | -25 (4) | -33 (9) |
| EKIPFDPAE | 2 | 914 | 922 | | 43 (2) | -1 (3)* | 0 (4)* | -5 (4) | -1 (3)* | -2 (4)* | 1 (4)* | -1 (4)* |
| EKIPFDPAEMSK | 2 | 914 | 925 | | 59 (3) | -1 (5)* | 0 (4)* | -4 (5)* | 1 (5)* | -1 (6)* | 1 (4)* | -2 (5)* |
| EKIPFDPAEMSK | 3 | 914 | 925 | | 60 (3) | -1 (5)* | 0 (4)* | -3 (4)* | 1 (5)* | -1 (6)* | 2 (4)* | -1 (5)* |

HDX Dynamics Key

HDX Perturbation Key

| C268F RIG-I peptide sequence | charge | start | end | structure | (xxiii) | (xxiv) | (xxv) | (xxvi) | (xxvii) | (xxviii) | (xxix) | (xxx) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FQDYIRKTLDPTYILS | 3 | 12 | 27 | | 38 (2) | 23 (3) | 17 (3) | 8 (2) | 1 (1)* | -5 (3)* | 1 (2)* | 1 (3)* |
| IRKTLDPTYIL | 3 | 16 | 26 | | 36 (2) | 27 (3) | 21 (3) | 8 (3) | 0 (2)* | -6 (3) | | 0 (3)* |
| SYMAPWFRE | 2 | 27 | 35 | | 47 (2) | 21 (3) | 20 (3) | 8 (2) | -4 (3)* | -1 (3)* | -2 (4)* | -5 (4)* |
| YMAPWFREEEVQ | 2 | 28 | 39 | | 45 (2) | 24 (3) | 20 (3) | 10 (2) | -3 (3)* | -4 (4)* | 0 (3)* | -1 (3)* |
| VQYIQA | 2 | 38 | 43 | | 34 (2) | | 12 (3) | 0 (4)* | -5 (2)* | 0 (4)* | 0 (2)* | -1 (2)* |
| YIQAEKNNKGPMEA | 3 | 40 | 53 | CARD1 | 47 (3) | 12 (4) | 10 (4) | -3 (3)* | -4 (4)* | -2 (4)* | -2 (6)* | -4 (4)* |
| LQEEGWFRGFL | 2 | 64 | 74 | | 52 (1) | 19 (6) | 7 (3) | 0 (2)* | 2 (5)* | -3 (5)* | 1 (3)* | 2 (3)* |
| FRGFLDA | 2 | 70 | 76 | | 15 (1) | 23 (2) | 21 (1) | 5 (3)* | -1 (2)* | 0 (2)* | 0 (2)* | -2 (1)* |
| DALDHAGYSGL | 2 | 75 | 85 | | 28 (2) | 19 (3) | 15 (3) | 5 (2) | -3 (3)* | -3 (3)* | 0 (4)* | -1 (3)* |
| LDHAGYSGL | 2 | 77 | 85 | | 33 (3) | 14 (4) | 10 (4) | -2 (4)* | -3 (4)* | -4 (3)* | 0 (5)* | -1 (3)* |
| YEAIESW | 1 | 86 | 92 | | 25 (2) | 33 (3) | 30 (3) | 14 (4) | -1 (3)* | -2 (3)* | 0 (2)* | -1 (2)* |
| YEAIESWD | 1 | 86 | 93 | | 26 (3) | 30 (3) | 26 (3) | 12 (3) | -2 (3)* | -4 (3)* | -1 (2)* | -1 (3)* |
| FKKIEKLEE | 3 | 94 | 102 | | 64 (1) | 9 (4) | 6 (4) | 2 (2)* | -3 (3)* | -1 (4)* | 0 (0)* | -2 (4)* |
| YRLLL | 2 | 103 | 107 | | 9 (1) | 28 (2) | 25 (3) | 8 (4) | -2 (2)* | -1 (2)* | -2 (1)* | -3 (4)* |
| YRLLLKRLQPEF | 3 | 103 | 114 | Latch region | 12 (4) | 41 (4) | 37 (5) | 23 (5) | -3 (3)* | -6 (2) | -1 (4)* | -3 (4)* |
| LLKRLQPEF | 2 | 106 | 114 | | 12 (4) | 35 (5) | 36 (4) | 23 (4) | -2 (2)* | -4 (4)* | 0 (3)* | -1 (3)* |
| LLKRLQPEF | 3 | 106 | 114 | | 16 (4) | 46 (5) | 40 (5) | 22 (5) | -3 (3)* | -6 (4) | 0 (4)* | -1 (4)* |
| KRLQPEF | 2 | 108 | 114 | | 21 (5) | 38 (6) | 42 (6) | 23 (5) | -1 (1)* | -4 (4)* | -4 (4)* | -9 (5) |
| KRLQPEF | 3 | 108 | 114 | | 20 (5) | 41 (6) | 41 (6) | 13 (6) | 0 (1)* | -6 (3) | -2 (2)* | -6 (5) |
| KTRIIPTDIISDL | 2 | 115 | 127 | | 51 (2) | 22 (3) | 17 (3) | 8 (2) | 2 (4)* | -6 (4) | -2 (2)* | 1 (4)* |
| KTRIIPTDIISDL | 3 | 115 | 127 | CARD2 | 51 (2) | 22 (3) | 17 (4) | 7 (2) | -1 (4)* | -6 (4) | -5 (6) | 1 (4)* |
| KTRIIPTDIISDLSE | 3 | 115 | 129 | | 58 (1) | 21 (3) | 13 (6) | 4 (2)* | 2 (4)* | -2 (4)* | 2 (2)* | 3 (4)* |
| ILQICSTKGMMAGA | 2 | 139 | 152 | | 37 (2) | 30 (3) | 25 (4) | 12 (2) | -2 (4)* | -3 (3)* | 2 (3)* | 0 (4)* |
| ILQICSTKGMMAGAEKL | 3 | 139 | 155 | | 34 (4) | 26 (4) | 21 (4) | 10 (4) | -2 (2)* | -2 (2)* | 1 (1)* | 0 (3)* |
| ILQICSTKGMMAGAEKLVE | 3 | 139 | 157 | | 26 (2) | 29 (3) | 26 (3) | 13 (3) | -2 (2)* | -2 (3)* | 1 (3)* | -1 (3)* |
| LLRSDKENWPKTLKL | 4 | 159 | 173 | | 28 (2) | 32 (3) | 26 (4) | 14 (2) | -5 (4)* | -2 (4)* | -2 (3)* | 0 (3)* |
| RSDKENWPKTLKLAL | 4 | 161 | 175 | | 26 (3) | 24 (4) | 14 (3) | 18 (3) | 2 (2)* | -3 (5)* | -1 (4)* | -3 (3)* |
| ALEKERNKFSEL | 3 | 174 | 185 | | 51 (2) | 23 (4) | 12 (3) | 7 (3) | 0 (1)* | -9 (4) | 2 (2)* | 1 (2)* |
| EKERNKFSEL | 3 | 176 | 185 | | 60 (2) | 17 (3) | 11 (4) | 6 (2) | 0 (3)* | -8 (4) | 0 (1)* | 0 (5)* |
| WIVEKGIKDVE | 3 | 186 | 196 | | 89 (3) | 5 (5)* | -1 (6)* | -7 (5) | 0 (5)* | -11 (5) | 2 (6)* | 3 (6)* |
| WIVEKGIKDVETEDL | 3 | 186 | 200 | | 92 (3) | 3 (4)* | 0 (5)* | -5 (5) | -1 (4)* | -8 (4) | -1 (6)* | 2 (5)* |
| WIVEKGIKDVETEDLED | 2 | 186 | 202 | | 86 (3) | 4 (4)* | 0 (5)* | -6 (4) | 5 (2)* | -11 (5) | 1 (3)* | 1 (6)* |
| WIVEKGIKDVETEDLEDKMETSD | 3 | 186 | 208 | linker | 87 (2) | 3 (3)* | 0 (5)* | -7 (3) | 3 (4)* | -8 (6) | 1 (5)* | 1 (4)* |
| IVEKGIKDVETEDL | 3 | 187 | 200 | | 85 (3) | 4 (4)* | 0 (5)* | -5 (4)* | -3 (6)* | -5 (4) | 2 (5)* | 1 (5)* |
| EDKMETSDIQIF | 2 | 201 | 212 | | 79 (2) | 4 (4)* | 1 (4)* | -3 (2)* | -2 (5)* | -3 (2)* | 1 (5)* | 2 (5)* |
| IQIFYQEDPECQNLSE | 2 | 209 | 224 | | 87 (3) | 2 (6)* | -3 (6)* | -11 (4) | -2 (4)* | -14 (6) | 2 (6)* | 3 (6)* |
| FYQEDPECQNL | 2 | 212 | 222 | | 72 (3) | 4 (5)* | 0 (6)* | -14 (5) | -2 (6)* | -18 (6) | 1 (6)* | 2 (6)* |
| YQEDPECQNL | 2 | 213 | 222 | | 79 (4) | 3 (5)* | 0 (6)* | -17 (5) | -1 (6)* | -17 (6) | 1 (7)* | 1 (7)* |
| SENSCPPSEVSDTNL | 2 | 223 | 237 | | 78 (3) | 3 (5)* | 0 (6)* | -16 (5) | 0 (5)* | -17 (5) | 1 (5)* | 2 (6)* |
| NSCPPSEVSDTNL | 2 | 225 | 237 | | 81 (4) | 2 (4)* | -1 (5)* | -16 (5) | -2 (6)* | -15 (5) | 1 (5)* | 1 (6)* |
| VSDTNL | 1 | 232 | 237 | | 83 (3) | 1 (5)* | 0 (6)* | -13 (5) | 0 (5)* | -9 (5) | 1 (6)* | 1 (6)* |
| YSPFKPRN | 3 | 238 | 245 | | 94 (3) | -3 (5)* | 0 (7)* | -12 (5) | -4 (6)* | -6 (4) | -2 (6)* | |
| YSPFKPRNYQLE | 3 | 238 | 249 | | 65 (3) | 0 (3)* | -3 (4)* | -5 (3)* | -3 (4)* | -8 (4) | 1 (4)* | 6 (4) |
| YSPFKPRNYQLE | 2 | 238 | 249 | HEL1 | 65 (2) | 0 (3)* | -6 (4) | -5 (3) | -4 (4)* | -8 (3) | -2 (0)* | 8 (5) |
| LICEHHLKKFPQGQKGKVVF | 3 | 276 | 295 | | 31 (3) | -14 (4) | 1 (4)* | -3 (3)* | 4 (1)* | -4 (3)* | -1 (2)* | -15 (5) |
| ICEHHLKKFPQGQKGKVVF | 3 | 277 | 295 | | 28 (1) | -13 (4) | 3 (2)* | -2 (2)* | 3 (3)* | | -4 (3)* | -16 (3) |
| FANQIPVYEQQ | 2 | 296 | 306 | | 74 (3) | -42 (5) | -33 (4) | -29 (4) | -4 (4)* | -7 (4) | -1 (4)* | -18 (4) |
| FANQIPVYEQQKSVF | 2 | 296 | 310 | motif Ia | 68 (3) | -37 (4) | -31 (4) | -21 (4) | -4 (4)* | -5 (4)* | 0 (4)* | -15 (4) |
| FANQIPVYEQQKSVFSKY | 3 | 296 | 313 | | 62 (2) | -31 (3) | -27 (3) | -19 (3) | -3 (3)* | | 0 (3)* | -11 (3) |
| FERHGYRVTGISGATAENVPVEQIVENND | 4 | 314 | 342 | | 59 (1) | -1 (1)* | -5 (2)* | -9 (2) | | -10 (4) | 0 (4)* | |
| GYRVTGISGATAENVPVEQIVENN | 4 | 318 | 341 | | 60 (1) | 0 (2)* | -2 (5)* | -9 (2) | -3 (2)* | -9 (3) | 1 (4)* | -2 (2)* |
| YRVTGISGATAENVPVEQIVE | 3 | 319 | 339 | | 78 (3) | 2 (4)* | -5 (2) | -9 (5) | -5 (4) | -10 (5) | 1 (6)* | 0 (6)* |
| IIILTPQIL | 2 | 343 | 351 | | 32 (1) | -15 (2) | -12 (2) | -15 (1) | -2 (2)* | -5 (1)* | -1 (2)* | -5 (2) |
| IIILTPQIL | 1 | 343 | 351 | | 32 (1) | -16 (2) | -13 (2) | -7 (1) | -2 (2)* | 0 (2)* | -1 (2)* | -6 (2) |
| IIILTPQILVN | 2 | 343 | 353 | | 34 (1) | -16 (2) | -14 (2) | -22 (2) | -2 (2)* | -4 (2)* | 0 (2)* | -5 (2)* |
| IIILTPQILVNNL | 2 | 343 | 355 | | 48 (2) | -26 (2) | -21 (3) | -13 (2) | -3 (3)* | -5 (3) | -2 (3)* | -10 (3) |
| IIILTPQILVNNLKKGTIPSL | 3 | 343 | 363 | | 64 (3) | -17 (3) | -16 (3) | -15 (3) | -4 (3)* | -11 (3) | -1 (3)* | -8 (3) |
| IIILTPQILVNNLKKGTIPSL | 2 | 343 | 363 | motif Ic | 62 (3) | -18 (3) | -17 (4) | -15 (3) | -4 (3)* | -11 (3) | -1 (3)* | -8 (3) |
| IIILTPQILVNNLKKGTIPSLSI | 3 | 343 | 365 | | 61 (2) | -16 (3) | -14 (3) | -14 (3) | -4 (3)* | -12 (3) | -1 (3)* | -8 (3) |
| IIILTPQILVNNLKKGTIPSLSIF | 3 | 343 | 366 | | 59 (2) | -15 (3) | -14 (3) | -13 (3) | -3 (3)* | -17 (3) | -1 (3)* | -7 (3) |
| LMIFDECHNTSKQHPYNM | 3 | 368 | 385 | | 30 (2) | -11 (2) | -11 (3) | -5 (2) | -1 (4)* | -3 (3)* | 1 (3)* | -1 (2)* |
| IFDECHNTSKQHPYNMIM | 3 | 370 | 387 | motif IIa | 33 (2) | -11 (2) | -11 (3) | -6 (2) | -1 (3)* | -3 (3)* | 0 (2)* | -1 (2)* |
| FNYLDQKLGGSSGPLPQVIG | 2 | 388 | 407 | | 36 (2) | 1 (3)* | -1 (4)* | -2 (3)* | -2 (3)* | -5 (2)* | 1 (3)* | 3 (3)* |
| FNYLDQKLGGSSGPLPQVIGL | 2 | 388 | 408 | | 33 (3) | 0 (3)* | -1 (4)* | -2 (3)* | -2 (3)* | -3 (3)* | 1 (3)* | 3 (3)* |
| DQKLGGSSGPLPQVIGL | 2 | 392 | 408 | | 37 (3) | 1 (3)* | -2 (4)* | -3 (3)* | -2 (3)* | -3 (2)* | 1 (3)* | 3 (3)* |
| LTASVGVGDAKNTDEAL | 2 | 408 | 424 | | 63 (3) | -17 (3) | -17 (3) | -6 (8) | -2 (5)* | -3 (3)* | 1 (9)* | -3 (3)* |
| TASVGVGDAKNTDEAL | 2 | 409 | 424 | | 64 (3) | -13 (4) | -14 (4) | -12 (4) | -3 (3)* | -7 (3) | 0 (4)* | -3 (4)* |
| TASVGVGDAKNTDEALD | 2 | 409 | 425 | | 61 (3) | -14 (4) | -14 (5) | -10 (4) | -4 (3)* | -8 (3) | 0 (4)* | -2 (4)* |
| DYICKL | 2 | 425 | 430 | | -23 (2) | 0 (2)* | 0 (3)* | -1 (2)* | 0 (2)* | 1 (1)* | 1 (3)* | 0 (3)* |
| DYICKL | 1 | 425 | 430 | | -11 (2) | -1 (2)* | 0 (4)* | -1 (2)* | 0 (3)* | 2 (1)* | 0 (4)* | 0 (4)* |
| CASLDASVIATVKHNLEEL | 2 | 431 | 449 | | 35 (1) | -1 (1)* | -2 (2)* | -1 (1)* | -1 (2)* | -4 (1)* | 1 (2)* | 12 (2) |
| SVIATVKHNLEE | 2 | 437 | 448 | | 60 (2) | -5 (2)* | -6 (3) | -7 (4) | -1 (3)* | -5 (3)* | -2 (12)* | 10 (4) |
| EQVVYKPQKF | 3 | 450 | 459 | | 69 (2) | -19 (3) | -16 (4) | -16 (3) | -3 (3)* | -1 (3)* | 0 (3)* | 21 (4) |
| VVYKPQKF | 2 | 452 | 459 | | 75 (3) | -14 (3) | -12 (4) | -12 (4) | -4 (3)* | -3 (4)* | 1 (4)* | 10 (4) |
| VVYKPQKF | 3 | 452 | 459 | | 75 (3) | -14 (4) | -10 (4) | -10 (4) | -4 (3)* | -3 (4)* | 0 (4)* | 8 (5) |
| FRKVESRISDKFKYIIAQL | 3 | 460 | 478 | HEL2i | 32 (2) | -16 (3) | 3 (3)* | -4 (2)* | 0 (2)* | -4 (1)* | 0 (2)* | 1 (2)* |
| QLMRDTESL | 2 | 477 | 485 | | 47 (2) | -1 (4)* | 0 (4)* | -14 (3) | -1 (3)* | -2 (1)* | | -5 (3)* |
| MRDTESL | 2 | 479 | 485 | | 8 (1) | 0 (1)* | 0 (2)* | -2 (1)* | -1 (2)* | 0 (1)* | 0 (2)* | -1 (2)* |
| AKRICKDLENL | 3 | 486 | 496 | | 68 (1) | -2 (2)* | -6 (3) | -4 (3)* | 3 (1)* | -7 (4) | 1 (4)* | 2 (3)* |
| SQIQNREFGTQ | 2 | 497 | 507 | | 79 (3) | -5 (6) | -7 (5) | -17 (4) | -2 (7)* | -2 (4)* | 2 (5)* | 0 (5)* |
| SQIQNREFGTQKYEQ | 3 | 497 | 511 | | 73 (2) | -6 (3) | -8 (3) | -9 (3) | -3 (4)* | -5 (4)* | 1 (4)* | 3 (4)* |
| SQIQNREFGTQKYEQW | 3 | 497 | 512 | | 65 (2) | -2 (5)* | -8 (4) | -4 (4)* | -2 (4)* | -2 (4)* | 2 (4)* | 5 (5) |
| WIVTVQKACM | 2 | 512 | 521 | | 9 (1) | -5 (2) | -8 (4) | 0 (2)* | 1 (3)* | 1 (7)* | 0 (4)* | 1 (2)* |
| IVTVQKACM | 2 | 513 | 521 | | 12 (2) | -6 (2) | -7 (2) | -1 (2)* | -1 (2)* | 1 (2)* | 1 (2)* | 0 (2)* |
| VFQMPDKDEESRICKA | 3 | 522 | 537 | | 58 (2) | -23 (5) | -18 (5) | -11 (2) | -3 (4)* | -7 (2) | -1 (3)* | -7 (3) |
| VFQMPDKDEESRICKALF | 4 | 522 | 539 | CTD:HEL2i | 53 (2) | -18 (2) | -17 (3) | -9 (2) | 0 (3)* | -7 (2) | -1 (3)* | -5 (3) |
| FQMPDKDEESRICKA | 3 | 523 | 537 | | 60 (2) | -19 (3) | -19 (4) | -11 (3) | -5 (3)* | -7 (4) | -3 (3)* | -5 (3) |
| LYTSHLRKYNDAL | 4 | 540 | 552 | | 9 (3) | 1 (4)* | 0 (4)* | 2 (4)* | -3 (2)* | -2 (4)* | 0 (3)* | 0 (3)* |
| LYTSHLRKYNDAL | 3 | 540 | 552 | | 9 (3) | 2 (4)* | 0 (4)* | 2 (4)* | -2 (3)* | -2 (4)* | 0 (3)* | 1 (4)* |
| IISEHARMKDALD | 3 | 553 | 565 | | 23 (1) | 2 (3)* | -1 (2)* | -1 (2)* | -3 (6)* | -4 (3)* | 0 (1)* | 1 (2)* |
| HARMKDALD | 2 | 557 | 565 | | 34 (1) | 1 (2)* | -4 (2)* | -3 (2)* | -2 (2)* | -4 (2)* | -3 (1)* | 0 (2)* |
| YLKDFFSNV | 2 | 566 | 574 | | 16 (1) | 14 (2) | 12 (2) | 6 (1) | -2 (2)* | -5 (2) | 0 (2)* | 0 (2)* |
| YLKDFFSNVRAAGF | 3 | 566 | 579 | Gate motif | 40 (3) | 20 (4) | 12 (5) | 2 (5)* | -3 (2)* | -15 (5) | -3 (14)* | 2 (4)* |
| FFSNV | 1 | 570 | 574 | | 33 (2) | 28 (2) | 27 (3) | 13 (2) | -4 (3)* | -5 (3)* | 0 (4)* | -2 (4)* |
| FFSNVRAAGF | 2 | 570 | 579 | | 51 (2) | 21 (4) | 18 (5) | 5 (3)* | -2 (5)* | -9 (5) | 1 (5)* | -1 (5)* |
| DEIEQDLTQRFEEKLQE | 3 | 580 | 596 | | 17 (1) | 10 (1) | 6 (1) | 3 (2)* | -2 (2)* | -7 (2) | -1 (3)* | -5 (3) |
| DEIEQDLTQRFEEKLQEL | 3 | 580 | 597 | | 22 (1) | 9 (2) | 6 (2) | 3 (1)* | -2 (2)* | -10 (2) | 0 (2)* | -3 (2)* |
| DEIEQDLTQRFEEKLQELES | 3 | 580 | 599 | | 24 (1) | 8 (2) | 5 (2) | 1 (1)* | -2 (2)* | -10 (2) | 0 (2)* | -4 (2)* |
| ESVSRDPSNENPKLEDLC | 3 | 598 | 615 | | 44 (2) | 4 (2)* | 4 (2)* | -4 (3)* | -1 (1)* | -10 (3) | 2 (4)* | -2 (2)* |
| VSRDPSNENPKL | 3 | 600 | 611 | | 63 (4) | 3 (5)* | 1 (6)* | -8 (5) | -3 (5)* | -9 (4) | -2 (6)* | -9 (6) |
| VSRDPSNENPKLED | 2 | 600 | 613 | | 56 (3) | 3 (4)* | 0 (5)* | -8 (4) | -3 (4)* | -9 (3) | -1 (5)* | -5 (5) |
| FILQEEYHLNPET | 2 | 616 | 628 | HEL2 | 26 (1) | 0 (2)* | -2 (1)* | 4 (2)* | -1 (2)* | -5 (2) | 1 (2)* | -2 (2)* |
| ILQEEYHLNPETITIL | 2 | 617 | 632 | | 22 (1) | 0 (2)* | -3 (1)* | -2 (1)* | -1 (2)* | -4 (2)* | 1 (1)* | -2 (2)* |
| EEYHLNPETITILFVKTR | 3 | 620 | 637 | | 37 (3) | 0 (3)* | -2 (4)* | -2 (3)* | -2 (3)* | -4 (3)* | 1 (3)* | 3 (3)* |
| FVKTRALVDALKNWIEGNPKL | 3 | 633 | 653 | | 25 (1) | -12 (2) | -6 (1) | -5 (1)* | -1 (2)* | -6 (2) | -1 (2)* | -6 (1) |
| FVKTRALVDALKNWIEGNPKLSF | 3 | 633 | 655 | motif IV | 24 (1) | -15 (2) | -4 (2)* | -4 (1)* | 0 (2)* | -6 (4) | 2 (3)* | |
| FVKTRALVDALKNWIEGNPKLSFLKPGIL | 4 | 633 | 661 | | 30 (1) | -18 (2) | -3 (2)* | -3 (2)* | -2 (2)* | -11 (3) | -5 (2)* | -12 (1) |
| SFLKPGIL | 2 | 654 | 661 | | 33 (4) | -2 (5)* | -5 (5)* | -5 (5) | -3 (3)* | -3 (5)* | -5 (5) | -13 (4) |
| KPGILTGRGKTNQNTG | 3 | 657 | 672 | | 50 (2) | -5 (3)* | -3 (3)* | -11 (3) | 2 (3)* | -11 (3) | -2 (2)* | -9 (2) |
| TGRGKTNQNTGMTLPAQKCIL | 4 | 662 | 682 | | 78 (3) | 2 (4)* | 0 (6)* | -12 (5) | 0 (3)* | -13 (5) | 1 (4)* | 0 (4)* |
| TGRGKTNQNTGMTLPAQKCIL | 3 | 662 | 682 | | 78 (3) | 2 (4)* | -3 (1)* | -9 (5) | -1 (4)* | -10 (5) | 1 (6)* | -1 (1)* |
| PAQKCIL | 2 | 676 | 682 | | 86 (2) | 3 (5)* | 2 (6)* | -10 (6) | 0 (4)* | -7 (5) | -1 (6)* | 2 (7)* |
| DAFKASGDHNIL | 3 | 683 | 694 | | 43 (3) | 2 (2)* | -1 (3)* | -5 (3)* | -2 (4)* | -6 (3) | 0 (4)* | 1 (4)* |
| DAFKASGDHNIL | 2 | 683 | 694 | | 48 (2) | 0 (4)* | -1 (4)* | 0 (3)* | -1 (5)* | -6 (5) | | -2 (5)* |
| FKASGDHNIL | 3 | 685 | 694 | | 29 (2) | 3 (3)* | -1 (2)* | -4 (5)* | 0 (3)* | -8 (3) | 2 (3)* | 3 (4)* |

C268F RIG-I

| peptide sequence | charge | start | end | structure | (xxiii) | (xxiv) | (xxv) | (xxvi) | (xxvii) | (xxviii) | (xxix) | (xxx) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| IATSVADEGID | 2 | 695 | 705 | Pincer | 77 (2) | -6 (3) | -8 (5) | -20 (3) | -3 (4)* | -23 (3) | -3 (5)* | -38 (5) |
| IATSVADEGIDIAQCNL | 2 | 695 | 711 | | 78 (2) | -5 (3)* | -5 (4)* | -12 (3) | -4 (4)* | -26 (4) | -3 (4)* | -40 (4) |
| IATSVADEGIDIAQCNLVILYEYVGNVIKM | 3 | 695 | 724 | | 66 (2) | -8 (2) | -6 (3) | -12 (3) | -2 (3)* | -23 (2) | -2 (3)* | -45 (3) |
| VILYEYVGNVIKM | 2 | 712 | 724 | | 68 (2) | -21 (2) | -18 (2) | -13 (3) | -3 (3)* | -19 (4) | -2 (2)* | -11 (2) |
| YEYVGNVIKM | 2 | 715 | 724 | | 86 (2) | -27 (3) | -21 (3) | -12 (3) | -4 (3)* | -8 (3) | -3 (3)* | -17 (3) |
| YVGNVIKM | 2 | 717 | 724 | | 84 (2) | -28 (3) | -21 (3) | -12 (3) | -3 (3)* | -6 (3) | -4 (3)* | -17 (3) |
| IQTRGRGRARGSKC | 4 | 725 | 738 | | 77 (4) | -21 (4) | -15 (4) | -20 (5) | -5 (3) | -18 (4) | -2 (5)* | -20 (5) |
| FLLTSNAGVIE | 2 | 739 | 749 | | 57 (2) | -21 (2) | -14 (3) | -19 (2) | 3 (2)* | 0 (1)* | 2 (2)* | |
| FLLTSNAGVIEKEQINM | 2 | 739 | 755 | | 58 (1) | -28 (2) | -26 (1) | -24 (4) | -2 (2)* | -4 (3)* | 0 (2)* | 0 (2)* |
| LTSNAGVIEKEQINM | 2 | 741 | 755 | | 57 (1) | -31 (3) | -28 (2) | -22 (2) | -1 (3)* | -3 (2)* | -1 (3)* | 0 (3)* |
| KEQINM | 2 | 750 | 755 | | 58 (2) | -38 (4) | -33 (5) | -23 (3) | -2 (4)* | -3 (3)* | -1 (4)* | -2 (5)* |
| YKEKMMNDSIL | 3 | 756 | 766 | | 21 (3) | -4 (4)* | -6 (4) | 0 (4)* | 0 (1)* | 0 (4)* | 0 (4)* | 5 (3) |
| YKEKMMNDSIL | 2 | 756 | 766 | | 21 (3) | -4 (4)* | -6 (4) | -2 (4)* | 1 (3)* | -1 (4)* | 0 (4)* | 5 (4)* |
| SILRLQT | 2 | 764 | 770 | | 27 (3) | -4 (3)* | -3 (5)* | -4 (3)* | -1 (3)* | -3 (3)* | 1 (4)* | 10 (2) |
| RLQTWDEAVF | 2 | 767 | 776 | | 46 (1) | -6 (2) | -7 (2) | -4 (2)* | 1 (2)* | 2 (2)* | 2 (3)* | 7 (2) |
| WDEAVF | 1 | 771 | 776 | | 66 (3) | -1 (3)* | -2 (3)* | -6 (4) | -2 (4)* | -4 (2)* | 2 (3)* | 3 (3)* |
| RDSQEKPKPVPDK | 2 | 791 | 803 | CTD | 90 (2) | -13 (3) | -18 (5) | -12 (2) | -3 (3)* | -7 (3) | 1 (3)* | 1 (2)* |
| VRVIEE | 2 | 823 | 828 | | 59 (1) | 1 (2)* | 3 (2)* | -12 (2) | -1 (2)* | -7 (2) | -1 (2)* | -2 (2)* |
| VRVIEECHY | 3 | 823 | 831 | | 43 (1) | -1 (2)* | 0 (3)* | -8 (1) | -2 (3)* | -10 (3) | 1 (3)* | 0 (3)* |
| VRVIEECHYTVLGDA | 3 | 823 | 837 | | 34 (1) | -1 (2)* | 2 (0)* | -11 (1) | -1 (2)* | -9 (2) | -1 (2)* | -1 (2)* |
| CHYTVLGDA | 2 | 829 | 837 | | 30 (1) | 1 (2)* | 2 (2)* | -3 (2)* | -1 (2)* | -3 (1)* | 0 (2)* | -2 (2)* |
| TVLGDAFKECF | 2 | 832 | 842 | | 52 (2) | -4 (3)* | -3 (3)* | -8 (3) | -3 (3)* | -14 (3) | 0 (3)* | -1 (3)* |
| FKECF | 1 | 838 | 842 | | 42 (3) | -8 (4) | -7 (4) | -10 (3) | -3 (4)* | -9 (4) | -2 (5)* | -4 (4)* |
| FKECF | 2 | 838 | 842 | | 39 (3) | -8 (4) | -6 (4) | -12 (4) | -4 (4)* | -2 (4)* | -1 (4)* | -5 (4)* |
| FVSRPHPKPKQFSS | 4 | 842 | 855 | | 79 (3) | -6 (4) | -4 (5)* | -14 (4) | -4 (4)* | -10 (4) | 0 (4)* | 2 (5)* |
| VSRPHPKPKQFSSF | 4 | 843 | 856 | Capping loop | 77 (3) | -6 (4) | -4 (5)* | -14 (4) | -4 (4)* | -10 (4) | 2 (5)* | 4 (6)* |
| VSRPHPKPKQFSSF | 3 | 843 | 856 | | 75 (2) | -7 (4) | -4 (5)* | -18 (4) | -2 (4)* | -11 (5) | 2 (4)* | 3 (6)* |
| EKRAKIF | 2 | 857 | 863 | | 49 (2) | -13 (3) | -13 (3) | -14 (3) | -3 (0)* | -4 (4)* | -1 (4)* | -3 (3)* |
| EKRAKIFC | 3 | 857 | 864 | | 26 (2) | -11 (3) | -12 (4) | -12 (3) | -2 (2)* | 0 (5)* | -2 (0)* | -4 (4)* |
| EKRAKIFC | 2 | 857 | 864 | | 48 (3) | -10 (4) | -14 (3) | -19 (3) | -1 (2)* | -3 (2)* | 0 (1)* | 3 (4)* |
| CARQNCSHDWGIHVKYKT | 4 | 864 | 881 | | 35 (2) | -16 (3) | -2 (2)* | -8 (2) | -2 (3)* | 2 (5)* | -3 (3)* | 3 (4)* |
| FEIPVIKIES | 2 | 882 | 891 | | 14 (1) | -10 (2) | -6 (1) | -9 (1) | 0 (1)* | 1 (1)* | 4 (6)* | 1 (2)* |
| FEIPVIKIESF | 2 | 882 | 892 | | 18 (1) | -8 (2) | -8 (2) | -8 (1) | 0 (1)* | 1 (1)* | 0 (1)* | 0 (1)* |
| EIPVIKIESF | 2 | 883 | 892 | | 14 (1) | -6 (3) | -6 (1) | -9 (1) | 0 (1)* | 1 (1)* | 4 (6)* | 1 (2)* |
| FVVEDIATGVQTL | 2 | 892 | 904 | RNA binding region | 63 (2) | -16 (3) | -17 (2) | -23 (2) | -3 (3)* | -21 (4) | 0 (3)* | -2 (3)* |
| VVEDIATGVQTL | 2 | 893 | 904 | | 72 (2) | -19 (3) | -17 (2) | -24 (2) | -3 (3)* | -11 (3) | -2 (2)* | -5 (3) |
| VVEDIATGVQTL | 1 | 893 | 904 | | 71 (2) | -19 (3) | -20 (3) | -19 (2) | -3 (3)* | -9 (4) | -1 (3)* | -3 (3)* |
| EKIPFDPAE | 2 | 914 | 922 | | 51 (4) | -1 (4)* | -1 (5)* | -7 (4) | -3 (4)* | -9 (3) | 0 (5)* | -3 (4)* |
| EKIPFDPAEMSK | 2 | 914 | 925 | | 61 (4) | -2 (4)* | -4 (6)* | -10 (4) | -3 (5)* | -9 (4) | 0 (6)* | -1 (5)* |
| EKIPFDPAEMSK | 3 | 914 | 925 | | 62 (4) | -2 (4)* | -4 (6)* | -10 (4) | -3 (5)* | -6 (3) | 0 (5)* | -1 (5)* |

HDX Dynamics Key

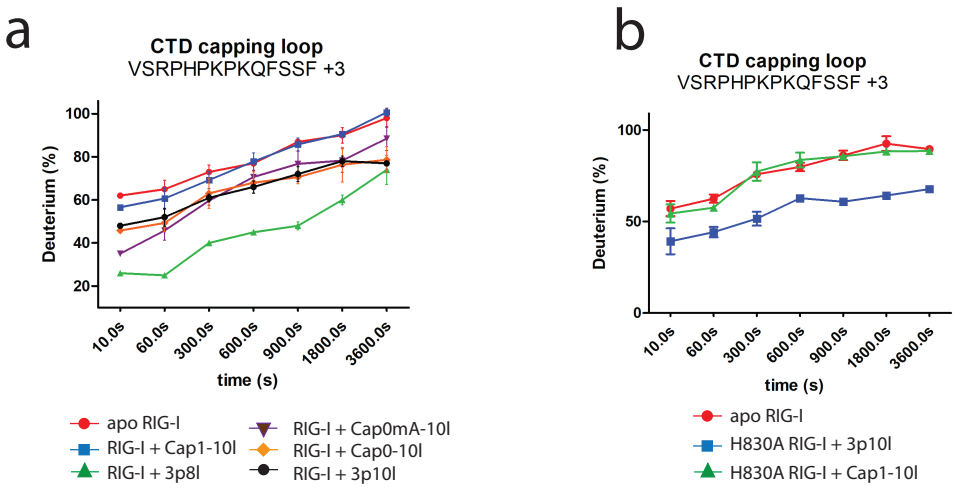
HDX Perturbation Key

**Supplementary Figure 1**

A summary of all HDX experiments. (**a**) Schematic representations of all HDX characterizations performed in this study. (**b**) HDX consolidation view for all studied conformational states of WT/H830A/E373A/C268F RIG-I with the experimental order in **Supplementary Fig 1a**. (**c**) HDX Experimental view for all studied conformational states of WT/H830A/E373A/C268F RIG-I with the experimental order in **Supplementary Fig 1a**. In Supplementary Fig 1c, specific RIG-I domain/motifs are defined in Fig 1a (CARD2 latch region is the region that intra-molecularly interacts with HEL2i gate motif in the apo receptor state. In HEL2i, the CTD:HEL2i region is the HEL2i region that CTD clashes with upon RNA agonist binding).

The values listed under each HDX experiments demonstrate the averaged difference in percentage of deuterium incorporation of that corresponding peptide either derived from apo protein or between two different states across all exchange time points (i.e., 0s, 10s, 60s, 300s, 600s, 900s, 1500s and 3600s). Including time 0s there were 8 time points and each time point was replicated with two independent MS runs per conformational state of receptor or receptor complex. HDX analyses were performed duplicate or triplicate, with single preparations of each protein ligand complex. The intensity weighted mean m/z centroid value of each peptide envelope was calculated and subsequently converted into a percentage of deuterium incorporation. Corrections for back-exchange were made on the basis of an estimated 70% deuterium recovery, and accounting for the known 80% deuterium content of the deuterium exchange buffer. When comparing the two samples, the perturbation %D is determined by calculating the difference between the two samples. HDX Workbench colors each peptide according to the smooth color gradient HDX perturbation key (D%) shown in each indicated figure. Differences in %D between -5% to 5% are considered non-significant and are colored gray according to the HDX perturbation key [1]. In addition to the -5% to 5% test, Unpaired t-tests are calculated to detect statistically significant ($p<0.05$) differences between samples at each time point. At least one time point with a p value less than 0.05 was present in the data set further confirming that the difference is significant. A negative value represents decreased deuterium incorporation or

stabilization while a positive value represents increased deuterium incorporation or de-stabilization in the corresponding region of the receptor when a binding event takes place. Peptides exhibiting statistically insignificant or undetectable changes are colored gray. Blank region represents undetected peptide for corresponding experiment. The deuterium incorporation data from all overlapping peptides were consolidated to individual amino acid values using a residue averaging approach [2]. HDX Workbench was used to automate mapping of gradient colors to pymol structure model [3]. For HDX experiments – i, ii, xii, xv and xxiii – measuring apo receptor dynamics, colors are coded according to HDX dynamics key. For the rest differential HDX experimental comparison views, colors are coded according to HDX perturbation key.

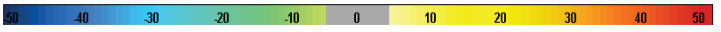



Supplementary Figure 2

C

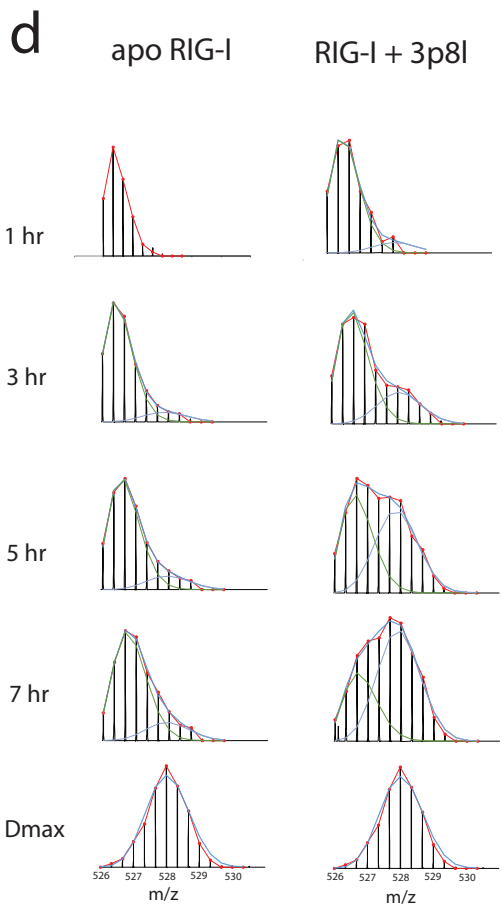
| sequence | charge | start | end | structure | RIG-I ± 3p8l |
|---|---|---|---|---|---|
| QDYIRKTLDPTYIL | 3 | 13 | 26 | | 1 (2)* |
| IRKTLDPTYIL | 3 | 16 | 26 | | 0 (3)* |
| SYMAPWFRE | 2 | 27 | 35 | | 3 (2)* |
| YMAPWFREEEVQ | 2 | 28 | 39 | | 3 (2)* |
| VQYIQA | 2 | 38 | 43 | | 1 (2)* |
| YIQAEKNNKGPMEA | 3 | 40 | 53 | | -1 (4)* |
| EKNNKGPMEAATL | 2 | 44 | 56 | | -1 (3)* |
| LQEEGWFRGFL | 2 | 64 | 74 | | 1 (3)* |
| QEEGWFRGFL | 2 | 65 | 74 | | 2 (3)* |
| FRGFLDA | 2 | 70 | 76 | | 3 (1)* |
| DALDHAGYSGL | 2 | 75 | 85 | | 1 (4)* |
| LDHAGYSGL | 2 | 77 | 85 | | 0 (6)* |
| YEAIESW | 1 | 86 | 92 | | -1 (1)* |
| YEAIESWD | 1 | 86 | 93 | | -1 (2)* |
| FKKIEKLEE | 3 | 94 | 102 | | 0 (3)* |
| YRLLL | 2 | 103 | 107 | | 11 (4) |
| YRLLLKRLQPEF | 3 | 103 | 114 | | 15 (4) |
| LLKRLQPEF | 2 | 106 | 114 | latch region | 15 (5) |
| LLKRLQPEF | 3 | 106 | 114 | | 22 (6) |
| KRLQPEF | 2 | 108 | 114 | | 21 (6) |
| KRLQPEF | 3 | 108 | 114 | | 22 (5) |
| KTRIIPTDIISD | 3 | 115 | 126 | | 4 (3)* |
| KTRIIPTDIISDL | 2 | 115 | 127 | | 3 (3)* |
| KTRIIPTDIISDL | 3 | 115 | 127 | | 3 (3)* |
| KTRIIPTDIISDLSE | 3 | 115 | 129 | | 3 (2)* |
| EEILQICSTKGMMAGAEKL | 3 | 137 | 155 | | 8 (2) |
| ILQICSTKGMMAGA | 2 | 139 | 152 | | 7 (2) |
| ILQICSTKGMMAGAEKL | 3 | 139 | 155 | CARD2 | 5 (2) |
| ILQICSTKGMMAGAEKLVE | 3 | 139 | 157 | | 8 (2) |
| LLRSDKENWPKTLKL | 4 | 159 | 173 | | 1 (1)* |
| RSDKENWPKTLKLAL | 4 | 161 | 175 | | 5 (2) |
| ALEKERNKFSEL | 3 | 174 | 185 | | 3 (4)* |
| ALEKERNKFSEL | 4 | 174 | 185 | | 3 (3)* |
| EKERNKFSEL | 3 | 176 | 185 | | 2 (4)* |
| WIVEKGIKDVE | 3 | 186 | 196 | | 0 (5)* |
| WIVEKGIKDVETEDL | 3 | 186 | 200 | | 0 (6)* |
| WIVEKGIKDVETEDLEDKMETSD | 3 | 186 | 208 | | -1 (5)* |
| IVEKGIKDVETEDL | 3 | 187 | 200 | | 0 (1)* |
| EDKMETSDIQIF | 2 | 201 | 212 | | 0 (4)* |
| FYQEDPECQNL | 2 | 212 | 222 | | -1 (3)* |
| YQEDPECQNL | 2 | 213 | 222 | | 0 (4)* |
| SENSCPPSEVSDTNL | 2 | 223 | 237 | | 0 (6)* |
| NSCPPSEVSDTNL | 2 | 225 | 237 | | -1 (6)* |
| VSDTNL | 1 | 232 | 237 | | 0 (5)* |
| YSPFKPRN | 3 | 238 | 245 | | 0 (5)* |
| YSPFKPRNYQLE | 2 | 238 | 249 | | 4 (5)* |
| YSPFKPRNYQLE | 3 | 238 | 249 | | 4 (5)* |
| LALPAMKGKNTIIC | 2 | 250 | 263 | | 1 (1)* |
| LALPAMKGKNTIICAPTGCGKTFVSLL | 3 | 250 | 276 | | 1 (4)* |
| LALPAMKGKNTIICAPTGCGKTFVSLL | 4 | 250 | 276 | | -2 (2)* |
| APTGCGKTF | 2 | 264 | 272 | | 1 (4)* |
| PQGQKGKVVF | 3 | 286 | 295 | | -1 (3)* |
| FANQIPVYEQQ | 2 | 296 | 306 | | 0 (4)* |
| FANQIPVYEQQKSVF | 2 | 296 | 310 | | -3 (5)* |
| FANQIPVYEQQKSVFSKY | 3 | 296 | 313 | | 0 (2)* |
| FERHGYRVTGISGATAENVPVEQIVENND | 4 | 314 | 342 | | -1 (2)* |
| GYRVTGISGATAENVPVEQIVENN | 4 | 318 | 341 | | 0 (3)* |
| YRVTGISGATAENVPVEQIVE | 3 | 319 | 339 | | 1 (4)* |
| IIILTPQIL | 1 | 343 | 351 | | -3 (1)* |
| IIILTPQIL | 2 | 343 | 351 | | -3 (1)* |
| IIILTPQILVN | 2 | 343 | 353 | motif Ic | -6 (1) |
| IIILTPQILVNN | 2 | 343 | 354 | | -6 (2) |
| IIILTPQILVNNL | 2 | 343 | 355 | | -5 (2)* |
| IIILTPQILVNNLKKGTIPSL | 2 | 343 | 363 | | -3 (5)* |
| IIILTPQILVNNLKKGTIPSL | 3 | 343 | 363 | | -3 (5)* |
| IIILTPQILVNNLKKGTIPSLSI | 3 | 343 | 365 | | -3 (5)* |
| IIILTPQILVNNLKKGTIPSLSIF | 3 | 343 | 366 | | -3 (4)* |
| KGTIPSLSIFT | 2 | 357 | 367 | | 0 (2)* |
| KGTIPSLSIFT | 3 | 357 | 367 | | 0 (2)* |
| LMIFDECHNTSKQHPYNM | 3 | 368 | 385 | | -2 (2)* |
| IFDECHNTSKQHPYNMIM | 2 | 370 | 387 | | -3 (3)* |
| IFDECHNTSKQHPYNMIM | 3 | 370 | 387 | | -2 (2)* |
| FNYLDQKLGGSSGPLPQVIG | 2 | 388 | 407 | | 0 (1)* |
| FNYLDQKLGGSSGPLPQVIGL | 2 | 388 | 408 | | 0 (1)* |
| DQKLGGSSGPLPQVIGL | 2 | 392 | 408 | | 0 (2)* |
| LTASVGVGDAKNTDEAL | 2 | 408 | 424 | | 0 (3)* |
| TASVGVGDAKNTDEAL | 2 | 409 | 424 | | 1 (4)* |
| TASVGVGDAKNTDEALD | 2 | 409 | 425 | | 0 (5)* |
| TASVGVGDAKNTDEALDYICKL | 3 | 409 | 430 | | 3 (2)* |
| DYICKL | 1 | 425 | 430 | | 0 (1)* |
| DYICKL | 2 | 425 | 430 | | 0 (0)* |
| CASLDASVIATVKHNLEE | 2 | 431 | 448 | | 1 (4)* |
| CASLDASVIATVKHNLEEL | 2 | 431 | 449 | | -1 (1)* |
| SVIATVKHNLEE | 2 | 437 | 448 | | -1 (1)* |
| EQVVYKPQKF | 3 | 450 | 459 | | 0 (3)* |
| VVYKPQKF | 2 | 452 | 459 | | 2 (3)* |
| VVYKPQKF | 3 | 452 | 459 | | 2 (3)* |
| MRDTESL | 2 | 479 | 485 | | 0 (1)* |
| AKRICKDLENL | 3 | 486 | 496 | | 1 (3)* |
| SQIQNREFGTQ | 2 | 497 | 507 | | 1 (4)* |
| SQIQNREFGTQKYEQ | 3 | 497 | 511 | | 0 (6)* |
| SQIQNREFGTQKYEQW | 3 | 497 | 512 | | 0 (5)* |
| WIVTVQKACM | 2 | 512 | 521 | | 0 (5)* |
| IVTVQKACM | 2 | 513 | 521 | | 0 (1)* |
| VFQMPDKDEESRICKA | 3 | 522 | 537 | | 0 (5)* |
| VFQMPDKDEESRICKALF | 4 | 522 | 539 | | 0 (4)* |
| FQMPDKDEESRICKA | 3 | 523 | 537 | | 1 (4)* |
| FQMPDKDEESRICKALF | 4 | 523 | 539 | | 1 (4)* |
| LYTSHLRKYNDAL | 3 | 540 | 552 | | 0 (4)* |
| LYTSHLRKYNDAL | 4 | 540 | 552 | | 0 (4)* |
| YTSHLRKYNDAL | 2 | 541 | 552 | | 0 (4)* |
| IISEHARMKDALD | 3 | 553 | 565 | | 0 (1)* |
| HARMKDALD | 2 | 557 | 565 | | -1 (2)* |
| HARMKDALD | 3 | 557 | 565 | | 0 (1)* |
| DYLKDFFSNVRAAGF | 3 | 565 | 579 | | 2 (3)* |
| YLKDFFSNV | 2 | 566 | 574 | | 0 (0)* |
| YLKDFFSNVRAAGF | 3 | 566 | 579 | | -1 (3)* |
| FFSNV | 1 | 570 | 574 | | 1 (2)* |
| FFSNVRAAGF | 2 | 570 | 579 | | 1 (2)* |
| AAGFDEIEQDLT | 2 | 576 | 587 | | -2 (3)* |
| DEIEQDLTQRFEEKLQE | 3 | 580 | 596 | | 2 (1)* |
| DEIEQDLTQRFEEKLQEL | 3 | 580 | 597 | | 2 (1)* |
| DEIEQDLTQRFEEKLQELES | 3 | 580 | 599 | | 2 (1)* |
| QELESVSRDPSNENPKLED | 3 | 595 | 613 | | -1 (5)* |
| ESVSRDPSNENPKLEDLC | 3 | 598 | 615 | | 0 (6)* |
| VSRDPSNENPKL | 3 | 600 | 611 | | 2 (3)* |
| VSRDPSNENPKLED | 2 | 600 | 613 | | 0 (5)* |
| FILQEEYHLNPET | 2 | 616 | 628 | | -1 (2)* |
| ILQEEYHLNPETITIL | 2 | 617 | 632 | | 0 (1)* |
| EEYHLNPETITILFVKTR | 2 | 620 | 637 | | 0 (2)* |
| FVKTRALVDALKNWIEGNPKL | 3 | 633 | 653 | | 0 (3)* |
| WIEGNPKL | 2 | 646 | 653 | | 0 (4)* |
| WIEGNPKLSFLKPGIL | 2 | 646 | 661 | | 1 (5)* |
| SFLKPGIL | 2 | 654 | 661 | | 0 (6)* |
| KPGILTGRGKTNQNTG | 3 | 657 | 672 | | 1 (3)* |
| TGRGKTNQNTGMTLPAQKCIL | 3 | 662 | 682 | | 1 (4)* |
| TGRGKTNQNTGMTLPAQKCIL | 4 | 662 | 682 | | 1 (4)* |
| PAQKCIL | 2 | 676 | 682 | | 1 (2)* |
| DAFKASGDHNIL | 2 | 683 | 694 | | 0 (5)* |
| DAFKASGDHNIL | 3 | 683 | 694 | | 0 (5)* |

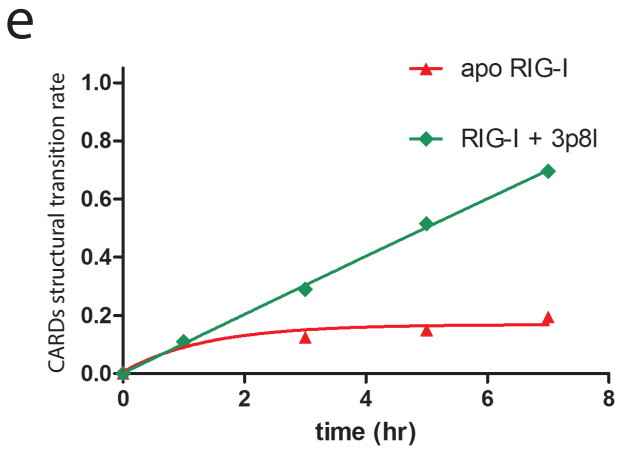
| sequence | charge | start | end | structure | RIG-I ± 3p8l |
|---|---|---|---|---|---|
| FKASGDHNIL | 3 | 685 | 694 | | 0 (5)* |
| IATSVADEGID | 2 | 695 | 705 | | 0 (5)* |
| IATSVADEGIDIAQCNL | 2 | 695 | 711 | | -5 (4)* |
| IATSVADEGIDIAQCNLVILYEYVGNVIKM | 3 | 695 | 724 | | 0 (6)* |
| SVADEGIDIAQ | 2 | 698 | 708 | | -1 (4)* |
| VILYEYVGNVIKM | 2 | 712 | 724 | | 2 (4)* |
| YEYVGNVIKM | 2 | 715 | 724 | | 0 (4)* |
| YVGNVIKM | 2 | 717 | 724 | | 0 (4)* |
| IQTRGRGRARGSKC | 4 | 725 | 738 | | 1 (4)* |
| FLLTSNAGVIE | 2 | 739 | 749 | | 1 (3)* |
| FLLTSNAGVIEKEQINM | 2 | 739 | 755 | | 1 (4)* |
| LTSNAGVIEKEQINM | 2 | 741 | 755 | | 0 (5)* |
| AGVIEKE | 2 | 745 | 751 | | -1 (5)* |
| KEQINM | 2 | 750 | 755 | | 0 (4)* |
| YKEKIMMNDSIL | 2 | 756 | 766 | | 3 (2)* |
| YKEKIMMNDSIL | 3 | 756 | 766 | | 2 (3)* |
| SILRLQT | 2 | 764 | 770 | | 3 (2)* |
| RLQTWDEAVF | 2 | 767 | 776 | | -2 (2)* |
| WDEAVF | 1 | 771 | 776 | | -3 (2)* |
| FREKILHIQTHEKF | 4 | 776 | 789 | | 1 (1)* |
| THEKFIRDS | 2 | 785 | 793 | CTD | 0 (0)* |
| EKFIRDSQEK | 2 | 787 | 796 | | 2 (3)* |
| VRVIEE | 2 | 823 | 828 | | -5 (2)* |
| VRVIEECHY | 2 | 823 | 831 | RNA binding region | -6 (2) |
| VRVIEECHY | 3 | 823 | 831 | | -8 (1) |
| VRVIEECHYTVLGDA | 3 | 823 | 837 | | -3 (1)* |
| CHYTVLGDA | 2 | 829 | 837 | | -1 (2)* |
| TVLGDAFKECF | 2 | 832 | 842 | RNA binding region | -12 (5) |
| FKECF | 1 | 838 | 842 | | -25 (5) |
| FKECF | 2 | 838 | 842 | | -27 (5) |
| FVSRPHPKPKQFSS | 4 | 842 | 855 | | 1 (5)* |
| VSRPHPKPKQFSSF | 3 | 843 | 856 | | 2 (5)* |
| VSRPHPKPKQFSSF | 4 | 843 | 856 | | 1 (5)* |
| EKRAKIF | 2 | 857 | 863 | RNA binding region | -12 (4) |
| EKRAKIFC | 3 | 857 | 864 | | -12 (2) |
| CARQNCSHDWGIHVKYKT | 4 | 864 | 881 | | -3 (1)* |
| DWGIHVKYKTFEIPVIKIESFVV | 4 | 872 | 894 | | -2 (3)* |
| FEIPVIKIES | 2 | 882 | 891 | RNA binding region | -19 (3) |
| FEIPVIKIESF | 2 | 882 | 892 | | -32 (1) |
| EIPVIKIESF | 2 | 883 | 892 | | -19 (3) |
| FVVEDIATGVQTL | 2 | 892 | 904 | | -3 (2)* |
| VVEDIATGVQTL | 1 | 893 | 904 | | -4 (4)* |
| VVEDIATGVQTL | 2 | 893 | 904 | | -4 (3)* |
| IATGVQTL | 2 | 897 | 904 | | 3 (5)* |
| YSKWKDFHFEKIPFDPAE | 3 | 905 | 922 | | 2 (3)* |
| EKIPFDPAEMSK | 2 | 914 | 925 | | -3 (4)* |
| EKIPFDPAEMSK | 3 | 914 | 925 | | -4 (5)* |

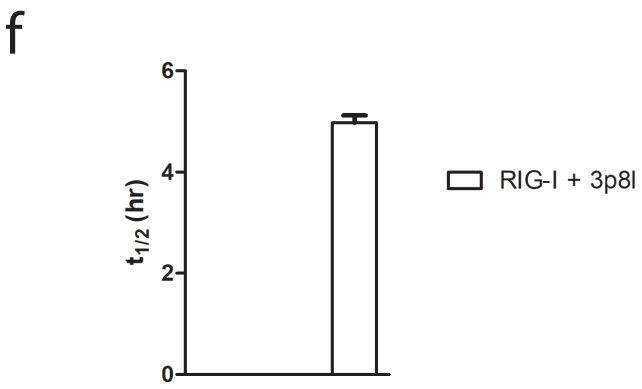


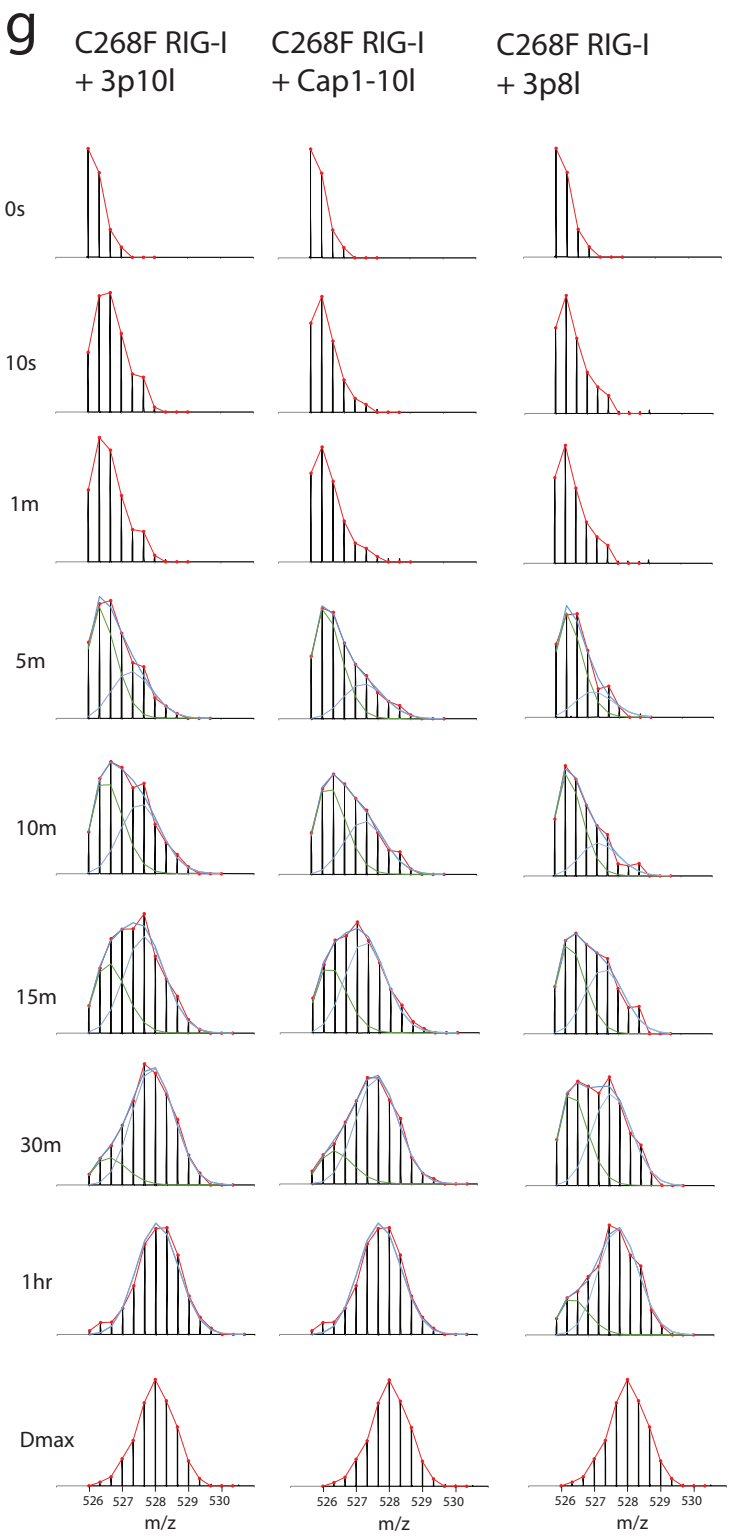

HDX perturbation key

Supplementary Figure 2



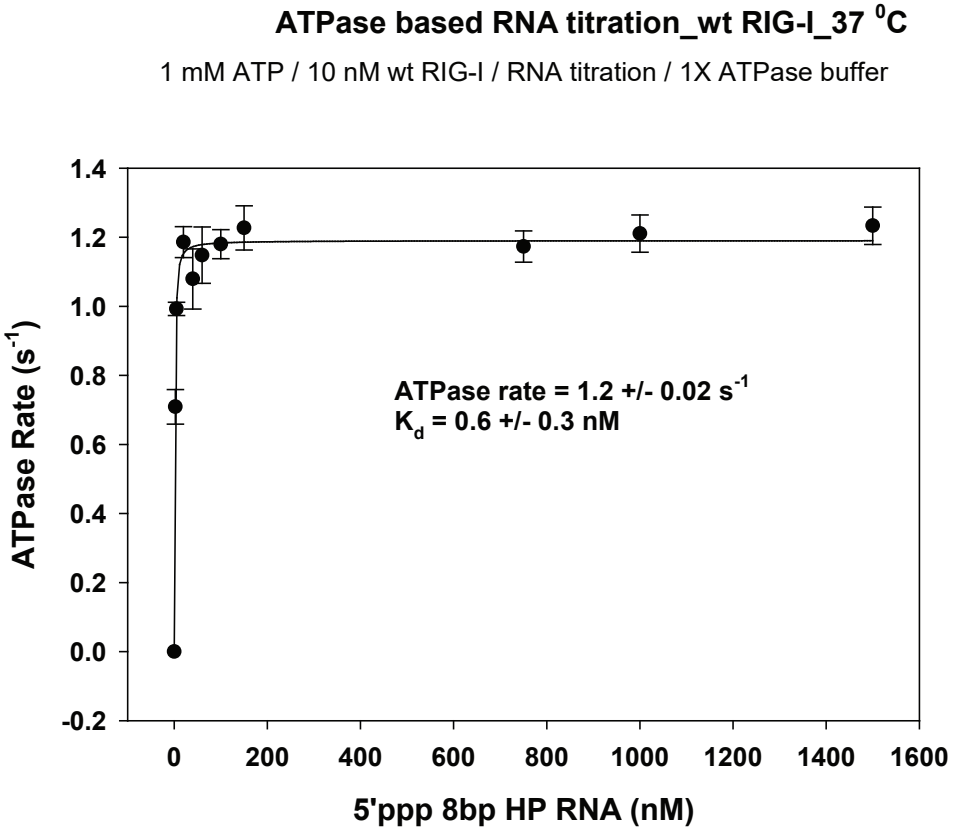



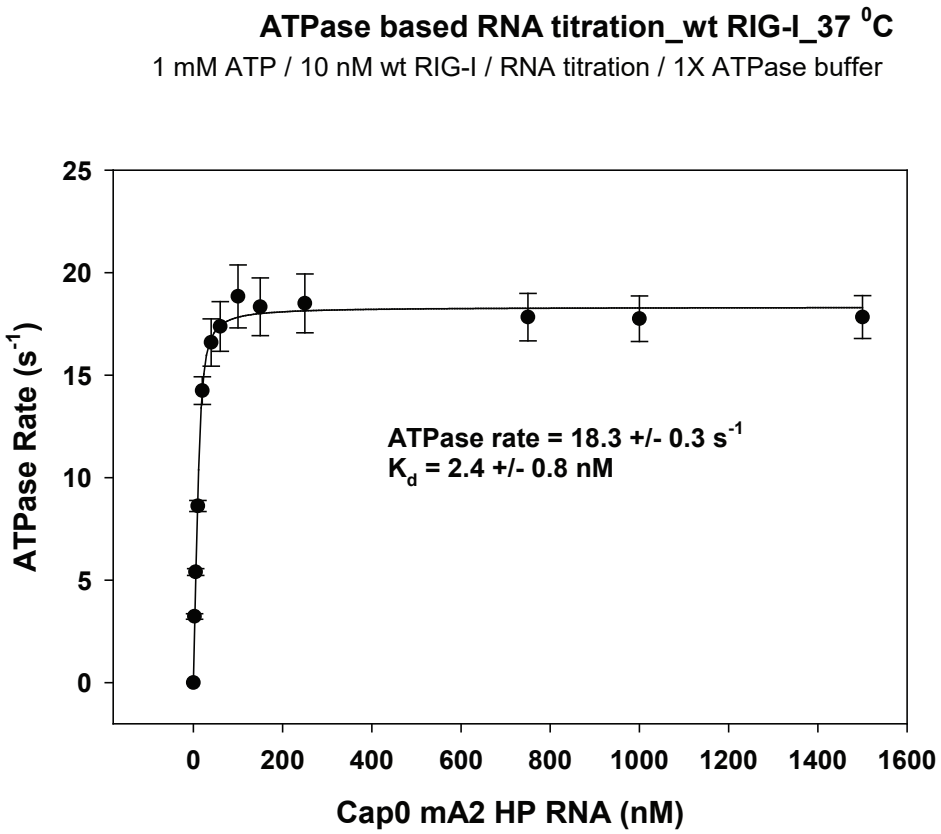




Supplementary Figure 2

**Supplementary Figure 2**

Differential deuterium uptake plots of CTD capping loop peptide region (VSRPHPKPKQFSSF, +3) of WT (a) and H830A RIG-I (b) upon receptor perturbed by indicated RNAs. The data are plotted as percent deuterium uptake verse time on a logarithmic scale. The HDX plots of this CTD capping loop peptide between indicated groups were statistically analysis by HDX Workbench (Supplementary Fig. 1c) [1]. (c) HDX perturbation view of RIG-I with and without 3p8l in longer HDX-MS time points (3 hr and 5 hr). This HDX perturbation view is presented as Supplementary Fig. 1c. (d) MS spectra of RIG-I CARD2 latch peptide Y103-114 derived from indicated complexes in indicated on-exchange time points. The quantity of each mass population was determined as Fig. 2a. (e) In each indicated state, the fraction of RIG-I CARDs molecules in the higher MS population (open conformation) to the total amount is plotted against the incubation HDX time points as Fig.2c. (f) Half-life ($t_{1/2}$) of respective partial unfolding event is determined by fitting an exponential curve as Fig. 2d. No half-life ($t_{1/2}$) of partial unfolding event is predicted I apo RIG-I in the indicated time points. (g) MS spectra of C268F RIG-I CARD2 latch peptide Y103-114 derived from indicated complexes in indicated on-exchange time points. The quantity of each mass population was determined as Fig. 2a.




Supplementary Figure 3

**Supplementary Figure 3 (related to Table 1)**

$K_d$, ATPase hydrolysis activity of WT RIG-I for 3p8l and Cap0mA-10l. The data is derived from radiometric ATPase assay wherein a fixed concentration of protein is titrated with increasing concentration of RNA. The curves are fit to the quadratic equation to obtain the $k_{atpase}$ and $k_{d,\ app}$ values. Error bars are from the time courses of the ATPase rate measurements at each RNA concentration.

**Supplementary Table 1.** Primers for generating RIG-I mutants

| RIG-I mutants | Prime sequence |
|---|---|
| **H830A** | 5'-GAGTGATAGAGGAATGCGCTTACACTGTGCTTGGAGATG-3'<br>5'-CATCTCCAAGCACAGTGTAAGCGCATTCCTCTATCACTC-3' |
| **E373A** | 5'-CTTTGATGATATTTGATGCGTGCCACAACACTAGTAAACAAC-3'<br>5'-GTTGTTTACTAGTGTTGTGGCACGCATCAAATATCATCAAAG-3' |
| **C268F** | 5'-ATATGTGCTCCTACAGGTTTTGGAAAAACCTTTGTTTCACTGC-3'<br>5'-GCAGTGAAACAAAGGTTTTTCCAAAACCTGTAGGAGCACATAT-3' |

## References:


1. Pascal, B.D. et al. HDX workbench: software for the analysis of H/D exchange MS data. *J Am Soc Mass Spectrom* **23**, 1512-21 (2012).
2. Keppel, T.R. & Weis, D.D. Mapping residual structure in intrinsically disordered proteins at residue resolution using millisecond hydrogen/deuterium exchange and residue averaging. *J Am Soc Mass Spectrom* **26**, 547-54 (2015).
3. Zheng, J. et al. High-resolution HDX-MS reveals distinct mechanisms of RNA recognition and activation by RIG-I and MDA5. *Nucleic Acids Res* **43**, 1216-30 (2015).