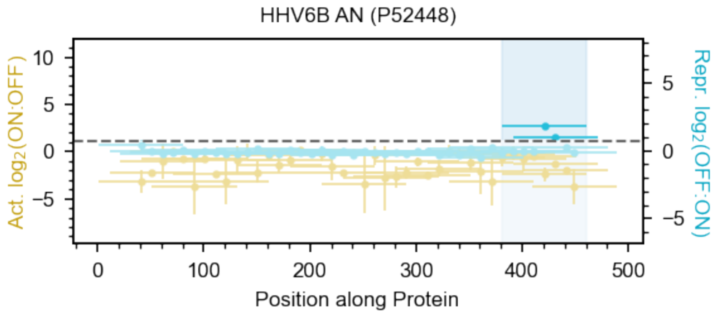
# Herpesvirus Tiling and Perturbation Screen Data from Ludwig, C.H. et al. 2023

## HHV6B AN (P52448)

Gene: U70 ; Protein Family: AN



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Extended repression domain from residues 381 to 470:
INDHSNPEYIESTEVPSVHIVTALFRRRTEEERSLHLVIDETEYIEEEIPLALIVTPVAPNPEFTCRVITDICNLWENNICKQTSLQVWA

Max tile of repression domain from residues 381 to 460 (estimated 34.9% to 41.3% of cells repressed):
INDHSNPEYIESTEVPSVHIVTALFRRRTEEERSLHLVIDETEYIEEEIPLALIVTPVAPNPEFTCRVITDICNLWENNI

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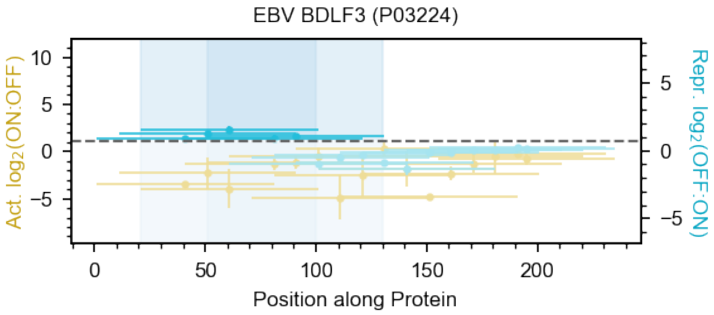
# EBV BDLF3 (P03224)

Gene: BDLF3 ; Protein Family: BDLF3



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Extended repression domain from residues 1 to 100:
MAHARDKAGAVMAMILICETSLIWTSSGSSTASAGNVTGTTAVTTPSPSASGPSTNQSTTLTTTSAPITTTAILSTNTTTVTFTGTTVTPVPTTSNASTI

Max tile of repression domain from residues 21 to 100 (estimated 24.9% to 39.8% of cells repressed):
SLIWTSSGSSTASAGNVTGTTAVTTPSPSASGPSTNQSTTLTTTSAPITTTAILSTNTTTVTFTGTTVTPVPTTSNASTI

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Extended repression domain from residues 41 to 130:
TAVTTPSPSASGPSTNQSTTLTTTSAPITTTAILSTNTTTVTFTGTTVTPVPTTSNASTINVTTKVTAQNITATEAGTGTSTGVTSNVTT

Max tile of repression domain from residues 51 to 130 (estimated 18.3% to 24.4% of cells repressed):
SGPSTNQSTTLTTTSAPITTTAILSTNTTTVTFTGTTVTPVPTTSNASTINVTTKVTAQNITATEAGTGTSTGVTSNVTT

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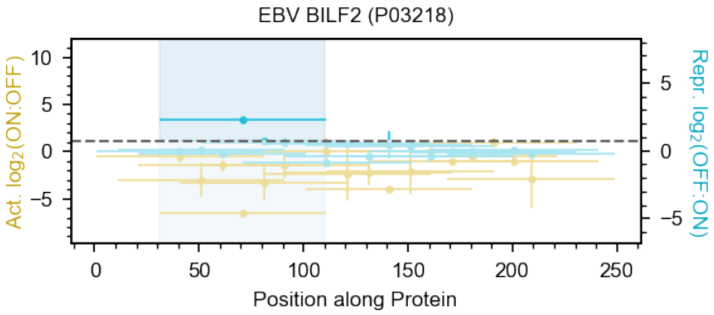
## EBV BILF2 (P03218)

Gene: BILF2 ; Protein Family: BILF2



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Extended repression domain from residues 31 to 120:
HAGARVNLTCSVPSNESVSRIELGRGYTPGDGQLPLAVATSNNGTHITNGGYNYSLTLEWVNDSNTSVSLIIPNVTLAHAGYYTCNVTLR

Max tile of repression domain from residues 31 to 110 (estimated 50.3% to 54.2% of cells repressed):
HAGARVNLTCSVPSNESVSRIELGRGYTPGDGQLPLAVATSNNGTHITNGGYNYSLTLEWVNDSNTSVSLIIPNVTLAHA

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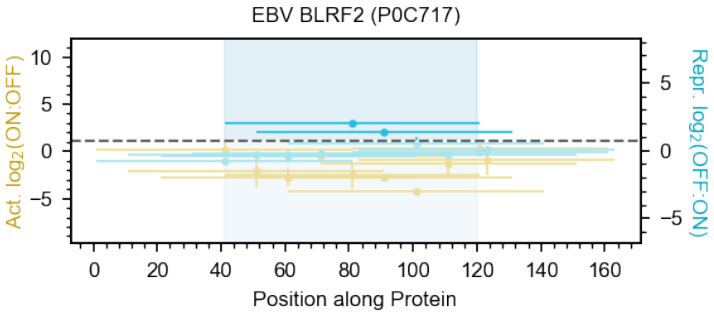
# EBV BLRF2 (P0C717)

Gene: BLRF2 ; Protein Family: BLRF2



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Extended repression domain from residues 41 to 130:
LRGGACASSTSVPSAPVPPPEPLTARQREVMITQATGRLASQAMKKIEDKVRKSVDGVTTRNEMENILQNLTLRIQVSMLGAKGQPSPGE

Max tile of repression domain from residues 41 to 120 (estimated 41.3% to 44.7% of cells repressed):
LRGGACASSTSVPSAPVPPPEPLTARQREVMITQATGRLASQAMKKIEDKVRKSVDGVTTRNEMENILQNLTLRIQVSML

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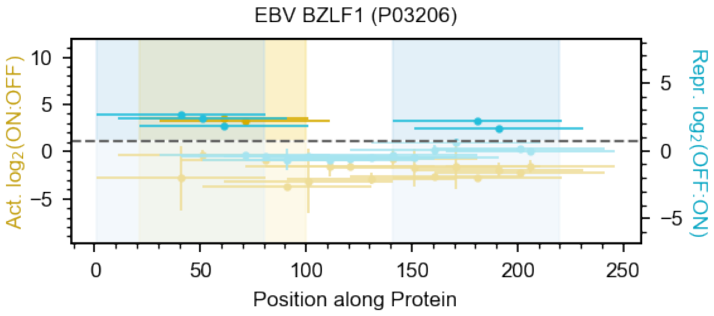
# EBV BZLF1 (P03206)

Gene: BZLF1 ; Protein Family: BZLF1



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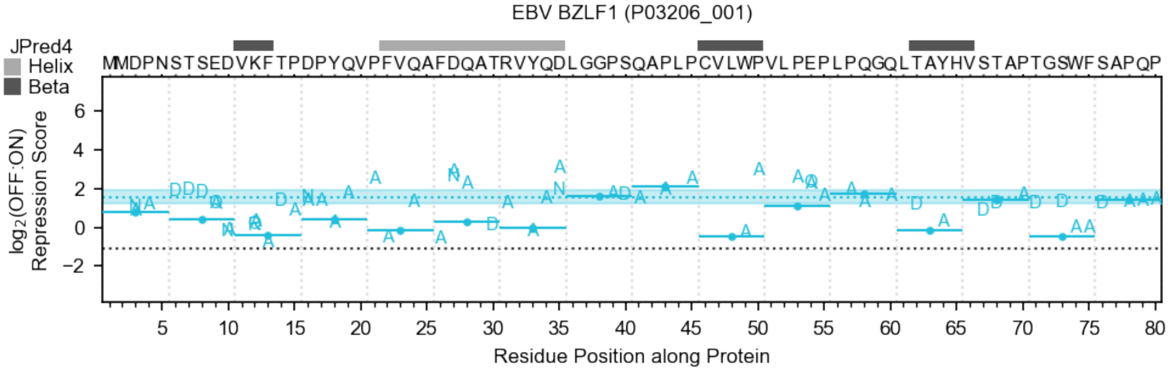
Extended repression domain from residues 1 to 100:
MMDPNSTSEDVKFTPDPYQVPFVQAFDQATRVYQDLGGPSQAPLPCVLWPVLPEPLPQGQLTAYHVSTAPTGSWFSAPQPAPENAYQAYAAPQLFPVSDI

Max tile of repression domain from residues 1 to 80 (estimated 60.3% to 62.5% of cells repressed):
MMDPNSTSEDVKFTPDPYQVPFVQAFDQATRVYQDLGGPSQAPLPCVLWPVLPEPLPQGQLTAYHVSTAPTGSWFSAPQP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_rev | 6 | 14 | STSEDVKFT | No | - | - | |

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Extended activation domain from residues 21 to 110:
PFVQAFDQATRVYQDLGGPSQAPLPCVLWPVLPEPLPQGQLTAYHVSTAPTGSWFSAPQPAPENAYQAYAAPQLFPVSDITQNQQTNQAG

Max tile of activation domain from residues 21 to 100 (estimated 10.6% to 13.5% of cells activated):
PFVQAFDQATRVYQDLGGPSQAPLPCVLWPVLPEPLPQGQLTAYHVSTAPTGSWFSAPQPAPENAYQAYAAPQLFPVSDI

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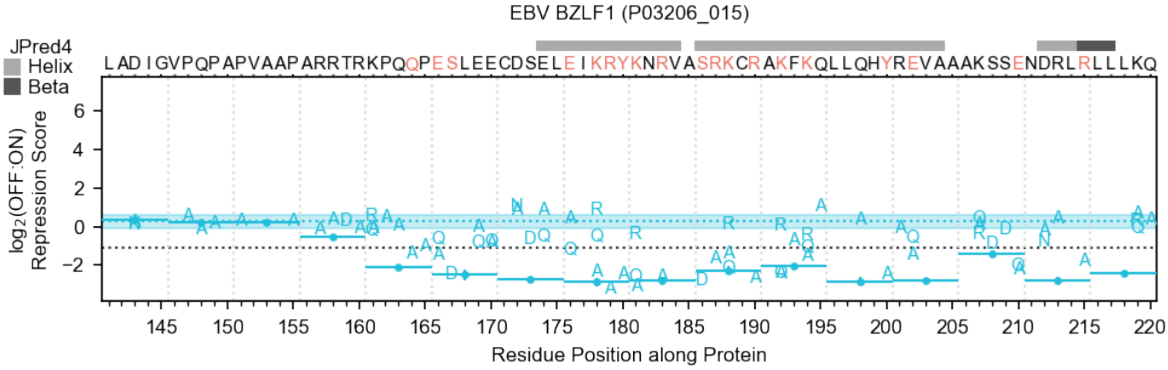
Extended repression domain from residues 141 to 230:
LADIGVPQPAPVAAPARRTRKPQQPESLEECDSELEIKRYKNRVASRKCRAKFKQLLQHYREVAAAKSSENDRLRLLLKQMCPSLDVDSI

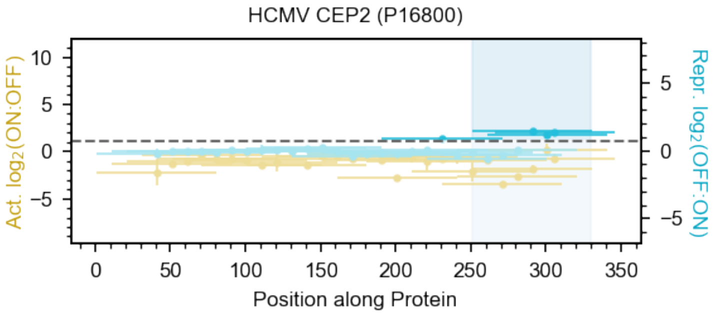
Max tile of repression domain from residues 141 to 220 (estimated 42.3% to 55.6% of cells repressed):
LADIGVPQPAPVAAPARRTRKPQQPESLEECDSELEIKRYKNRVASRKCRAKFKQLLQHYREVAAAKSSENDRLRLLLKQ



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| CtBP_expanded | 165 | 169 | PESLE | Yes | 161 | 220 | KPQQPESLEECDSELEIKRYKNRVASRKCRAKFKQLLQHYREVAAAKSSENDRLRLLLKQ |
| flexi_NRBOX | 192 | 198 | KFKQLLQ | Yes | 161 | 220 | KPQQPESLEECDSELEIKRYKNRVASRKCRAKFKQLLQHYREVAAAKSSENDRLRLLLKQ |
| LIG_NRBOX | 213 | 219 | RLRLLLK | Yes | 161 | 220 | KPQQPESLEECDSELEIKRYKNRVASRKCRAKFKQLLQHYREVAAAKSSENDRLRLLLKQ |

## HCMV CEP2 (P16800)

Gene: UL94 ; Protein Family: CEP2



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Extended repression domain from residues 251 to 345:
LCYVPCGPMTQSLIHNEEPATFFCESDDAKYLCAVGSKTAAQVTLGDGLDYHIGVKDSEGRWLPVKTDVWDLVKVEEPVSRMIVCSCPVLKNLVH

Max tile of repression domain from residues 251 to 330 (estimated 26.6% to 30.5% of cells represed):
LCYVPCGPMTQSLIHNEEPATFFCESDDAKYLCAVGSKTAAQVTLGDGLDYHIGVKDSEGRWLPVKTDVWDLVKVEEPVS

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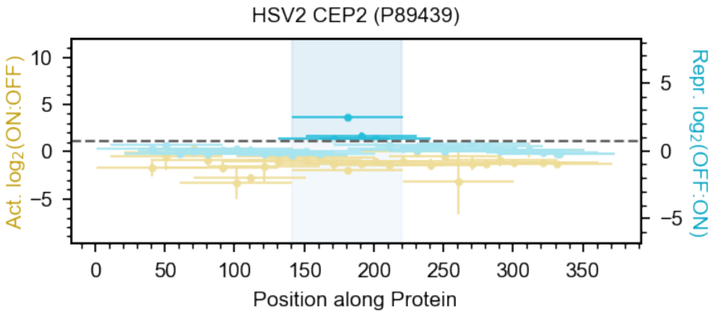
## HSV2 CEP2 (P89439)

Gene: UL16 ; Protein Family: CEP2



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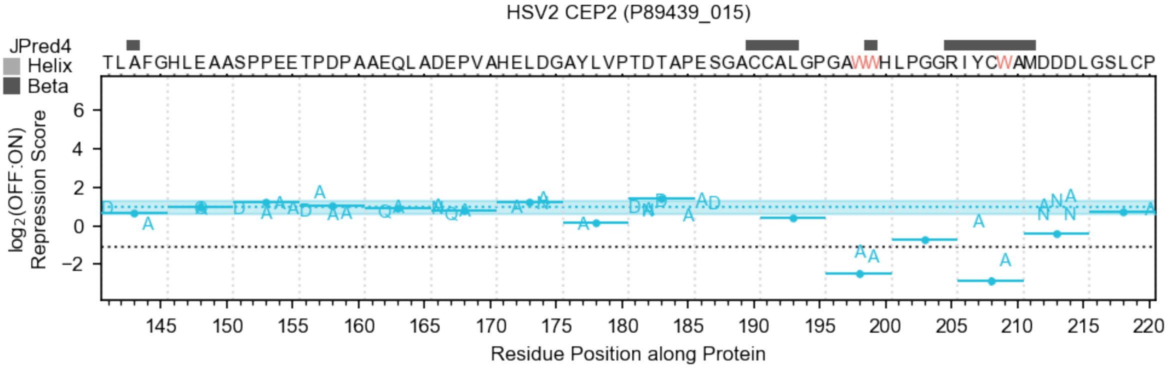
Extended repression domain from residues 131 to 240:
VTHPRTPLLCTLAFGHLEAASPPEETPDPAAEQLADEPVAHELDGAYLVPTDTAPESGACCALGPGAWWHLPGGRIYCWAMDDDLGSLCPPGSRARHLGWLLSRITDPPG

Max tile of repression domain from residues 141 to 220 (estimated 56.5% to 56.7% of cells repressed):
TLAFGHLEAASPPEETPDPAAEQLADEPVAHELDGAYLVPTDTAPESGACCALGPGAWWHLPGGRIYCWAMDDDLGSLCP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| Sin3A_SID | 160 | 164 | AAEQL | No | - | - | |
| | - | - | | No | 196 | 200 | GAWWH |
| | - | - | | No | 206 | 210 | IYCWA |

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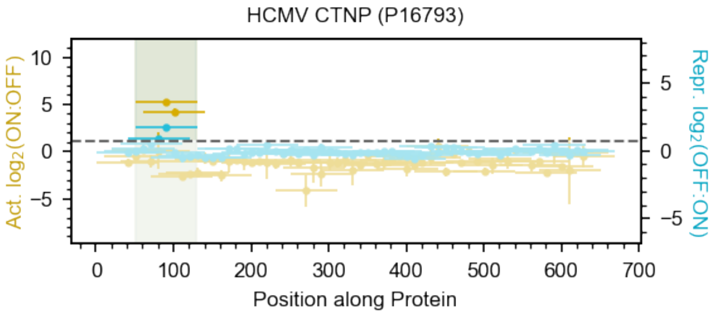
# HCMV CTNP (P16793)

Gene: UL52 ; Protein Family: CTNP



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Extended repression domain from residues 41 to 130:
LCSPQRQAVSRYSGWSTEYTQWHSDLTTELLWHAHPRQVPMDEALAAAAAASYQVNPQHPANRYRHYEFQTLSLGTSEVDELLNCCAEET

Max tile of repression domain from residues 51 to 130 (estimated 35.3% to 39.0% of cells repressed):
RYSGWSTEYTQWHSDLTTELLWHAHPRQVPMDEALAAAAAASYQVNPQHPANRYRHYEFQTLSLGTSEVDELLNCCAEET

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Extended activation domain from residues 51 to 140:
RYSGWSTEYTQWHSDLTTELLWHAHPRQVPMDEALAAAAAASYQVNPQHPANRYRHYEFQTLSLGTSEVDELLNCCAEETTCGGTQSTVL

Max tile of activation domain from residues 51 to 130 (estimated 38.8% to 41.5% of cells activated):
RYSGWSTEYTQWHSDLTTELLWHAHPRQVPMDEALAAAAAASYQVNPQHPANRYRHYEFQTLSLGTSEVDELLNCCAEET

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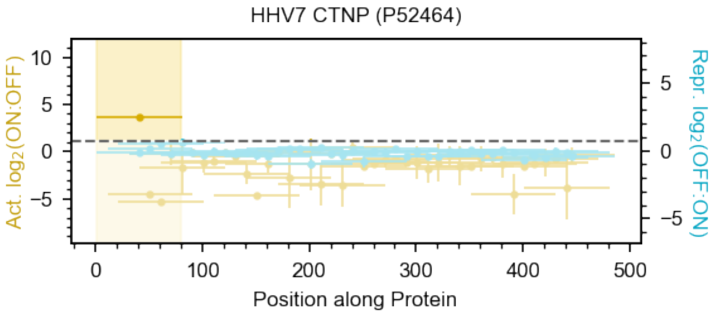
## HHV7 CTNP (P52464)

Gene: U36 ; Protein Family: CTNP



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Extended activation domain from residues 1 to 80:
MAYKGWNSDSFSMNSELFNEILLYAHLDSSGIDSDDLNTNPNTLENEINSVEKTLNIEELKKITTALNIDNRCNICSIIN

Max tile of activation domain from residues 1 to 80 (estimated 11.4% to 15.3% of cells activated):
MAYKGWNSDSFSMNSELFNEILLYAHLDSSGIDSDDLNTNPNTLENEINSVEKTLNIEELKKITTALNIDNRCNICSIIN

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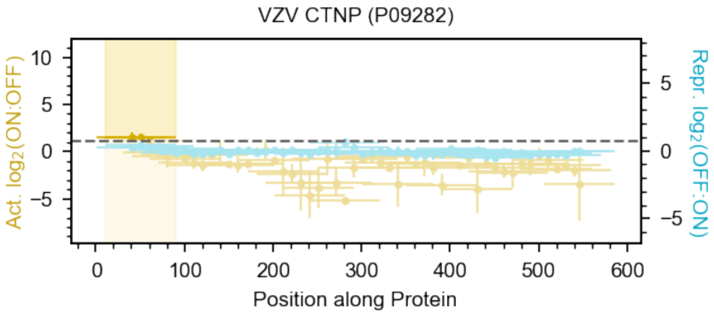
## VZV CTNP (P09282)

Gene: ORF26 ; Protein Family: CTNP



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Extended activation domain from residues 1 to 100:
MDRVESEEPMDGFESPVFSENTSSNSGWCSDAFSDSYIAYNPALLLKNDLLFSELLFASHLINVPRAIENNVTYEASSAVGVDNEMTSSTTEFIEEIGDV

Max tile of activation domain from residues 11 to 90 (estimated 2.6% to 3.9% of cells activated):
DGFESPVFSENTSSNSGWCSDAFSDSYIAYNPALLLKNDLLFSELLFASHLINVPRAIENNVTYEASSAVGVDNEMTSST

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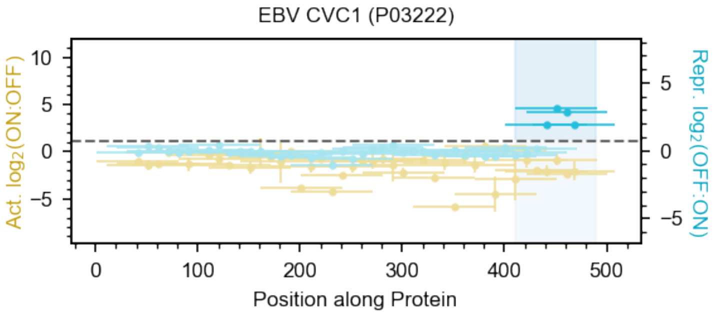
## EBV CVC1 (P03222)

Gene: BGLF1 ; Protein Family: CVC1



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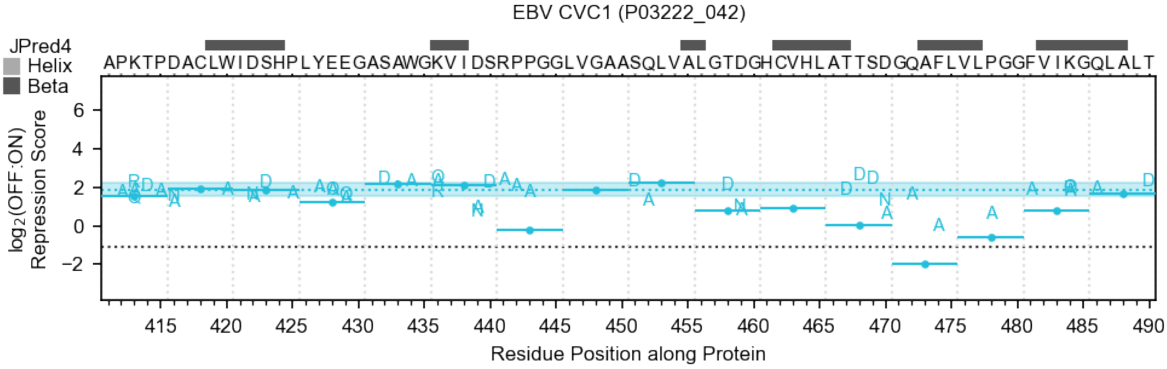
Extended repression domain from residues 401 to 507:
SCWVKATISNAPKTPDACLWIDSHPLYEEGASAWGKVIDSRPPGGLVGAASQLVALGTDGHCVHLATTSDGQAFLVLPGGFVIKGQLALTPEERGYILARHGIRREQ

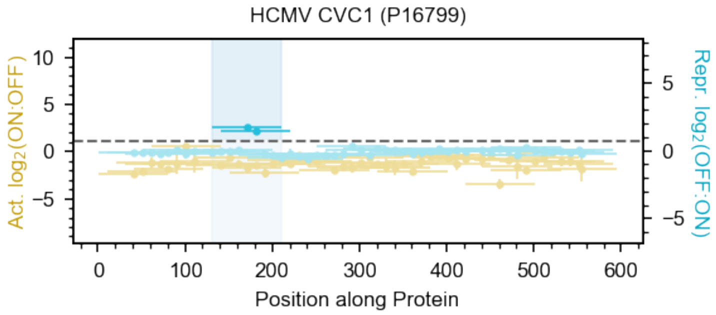
Max tile of repression domain from residues 411 to 490 (estimated 73.3% to 73.7% of cells represented):
APKTPDACLWIDSHPLYEEGASAWGKVIDSRPPGGLVGAASQLVALGTDGHCVHLATTSDGQAFLVLPGGFVIKGQLALT



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 433 | 439 | AWGKVID | No | - | - | |
| Sin3A_SID | 449 | 453 | AASQL | No | - | - | |
| SUMO_SIM_par | 451 | 459 | SQLVALGTD | No | - | - | |
| | - | - | | No | 471 | 475 | GQAFL |

## HCMV CVC1 (P16799)

Gene: UL93 ; Protein Family: CVC1



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Extended repression domain from residues 131 to 220:
TLGLRCPDNRLSGAQTLHLRLVWPDGSYRDWEFLARDLLREEMEANKRDRQHQLATTTNHRRRGGLRNNLDNGSDRRLPEAAVASLETAV

Max tile of repression domain from residues 131 to 210 (estimated 36.4% to 37.4% of cells repressed):
TLGLRCPDNRLSGAQTLHLRLVWPDGSYRDWEFLARDLLREEMEANKRDRQHQLATTTNHRRRGGLRNNLDNGSDRRLPE

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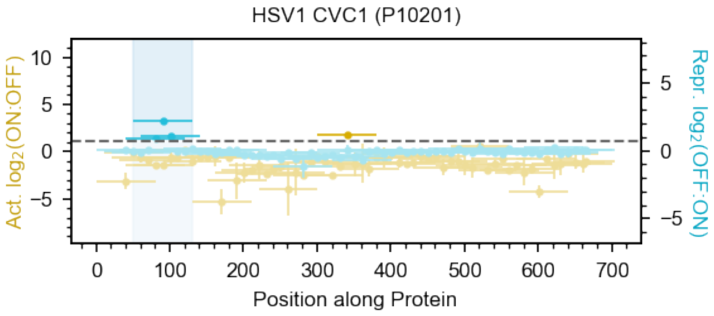
## HSV1 CVC1 (P10201)

Gene: UL17 ; Protein Family: CVC1



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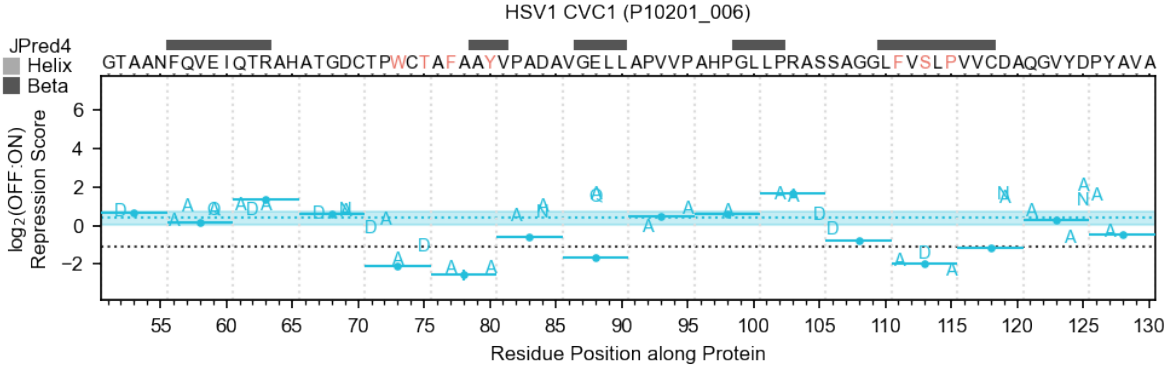
Extended repression domain from residues 41 to 140:
AALMRGRPGLGTAANFQVEIQTRAHATGDCTPWCTAFAAYVPADAVGELLAPVVPAHPGLLPRASSAGGLFVSLPVVCDAQGVYDPYAVAALRLAWGSGA

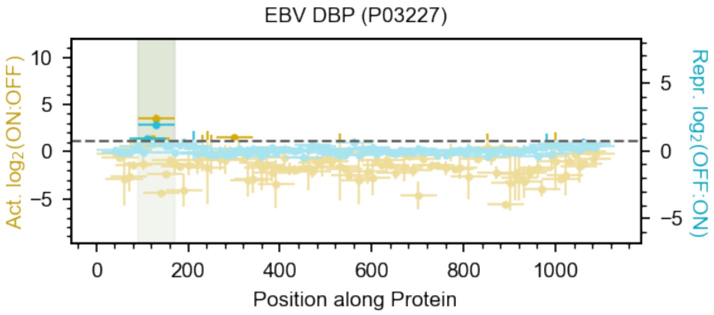
Max tile of repression domain from residues 51 to 130 (estimated 48.4% to 49.7% of cells repressed):
GTAANFQVEIQTRAHATGDCTPWCTAFAAYVPADAVGELLAPVVPAHPGLLPRASSAGGLFVSLPVVCDAQGVYDPYAVA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 71 | 80 | TPWCTAFAAY |
| flexi_NRBOX | 85 | 91 | AVGELLA | Yes | 86 | 90 | VGELL |
| MYND_1 | 98 | 102 | PGLLP | No | - | - | |
| | - | - | | No | 111 | 120 | FVSLPVVCDA |

## EBV DBP (P03227)

Gene: BALF2 ; Protein Family: DBP



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Extended repression domain from residues 91 to 180:
YVFHNAHMVPPIFEGPGLEALCGETREVFGYDAYSALPRESSKPGDFFPEGLDPSAYLGAVAITEAFKERLYSGNLVAIPSLKQEVAVGQ

Max tile of repression domain from residues 91 to 170 (estimated 41.6% to 42.1% of cells repressed):
YVFHNAHMVPPIFEGPGLEALCGETREVFGYDAYSALPRESSKPGDFFPEGLDPSAYLGAVAITEAFKERLYSGNLVAIP

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Extended activation domain from residues 81 to 170:
LRATSYHRDIYVFHNAHMVPPIFEGPGLEALCGETREVFGYDAYSALPRESSKPGDFFPEGLDPSAYLGAVAITEAFKERLYSGNLVAIP

Max tile of activation domain from residues 91 to 170 (estimated 9.2% to 16.2% of cells activated):
YVFHNAHMVPPIFEGPGLEALCGETREVFGYDAYSALPRESSKPGDFFPEGLDPSAYLGAVAITEAFKERLYSGNLVAIP

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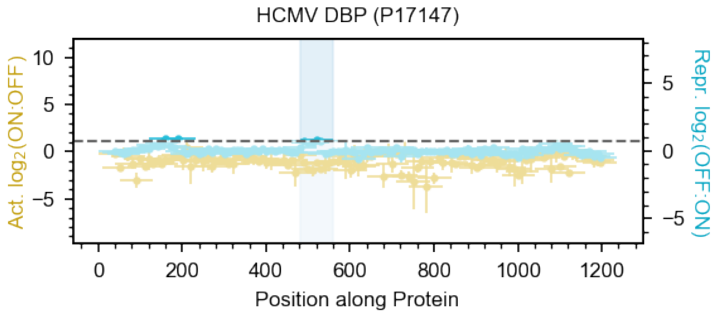
# HCMV DBP (P17147)

Gene: UL57 ; Protein Family: DBP



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Extended repression domain from residues 481 to 570:
HTCYQTAFVRVRTRLPVVPKQPKKEPCVITVQSRFLNDVDILGSFGRRYNVDAKDGGLDGKGDDGVPGGGAGGGGGRDVSGGPSDGLGGG

Max tile of repression domain from residues 481 to 560 (estimated 15.7% to 17.1% of cells repressed):
HTCYQTAFVRVRTRLPVVPKQPKKEPCVITVQSRFLNDVDILGSFGRRYNVDAKDGGLDGKGDDGVPGGGAGGGGGRDVS

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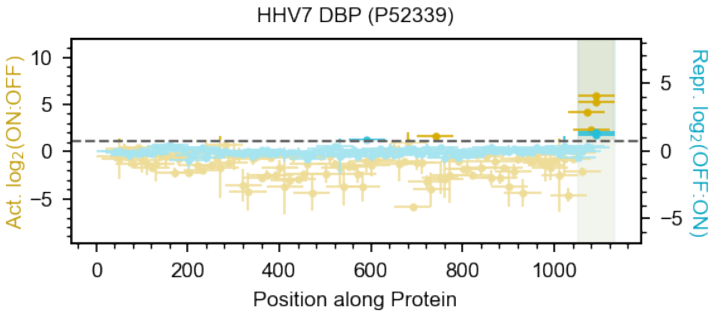
## HHV7 DBP (P52339)

Gene: U41 ; Protein Family: DBP



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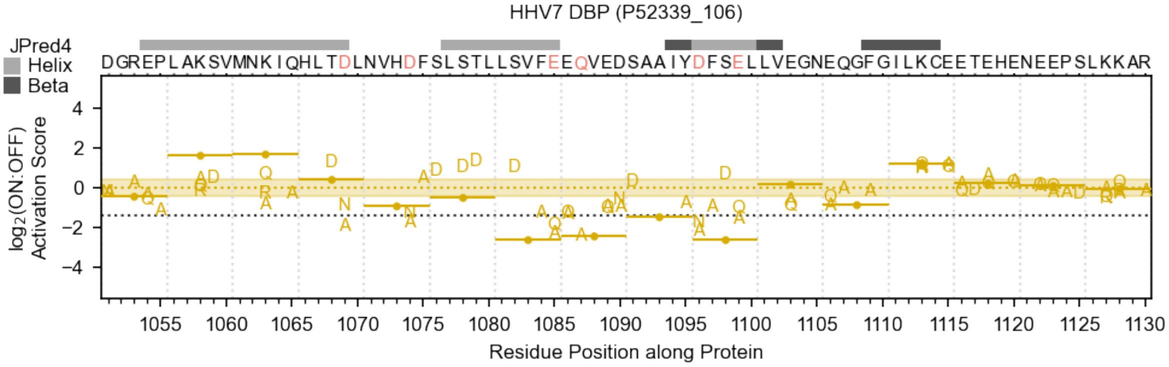
Extended activation domain from residues 1031 to 1131:
AEVMKDRDSKPTMDDMLFYVDGREPLAKSVMNKIQHLTDLNVHDFSLSTLLSVFEEQVEDSAAIYDFSELLVEGNEQGFGILKCEETEHENEEPSLKKARL

Max tile of activation domain from residues 1051 to 1130 (estimated 52.6% to 56.1% of cells activated):
DGREPLAKSVMNKIQHLTDLNVHDFSLSTLLSVFEEQVEDSAAIYDFSELLVEGNEQGFGILKCEETEHENEEPSLKKAR



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| LIG_NRBOX | 1076 | 1082 | SLSTLLS | Yes | 1081 | 1100 | LSVFEEQVEDSAAIYDFSEL |
| SUMO_SIM_par | 1078 | 1086 | STLLSVFEE | Yes | 1081 | 1100 | LSVFEEQVEDSAAIYDFSEL |
| flexi_NRBOX | 1079 | 1085 | TLLSVFE | Yes | 1081 | 1100 | LSVFEEQVEDSAAIYDFSEL |
| flexi_NRBOX | 1096 | 1102 | DFSELLV | Yes | 1081 | 1100 | LSVFEEQVEDSAAIYDFSEL |
| SUMO_for | 1112 | 1115 | LKCE | No | - | - | |

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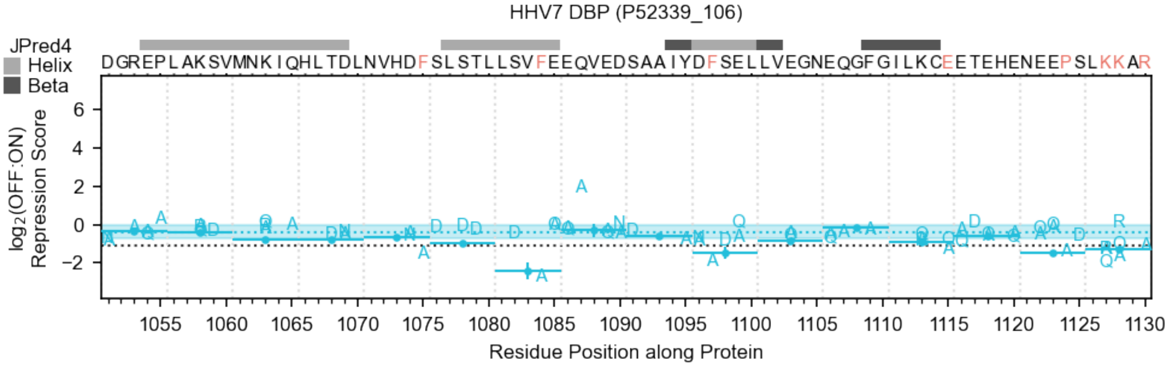
Extended repression domain from residues 1051 to 1131:
DGREPLAKSVMNKIQHLTDLNVHDFSLSTLLSVFEEQVEDSAAIYDFSELLVEGNEQGFGILKCEETEHENEEPSLKKARL

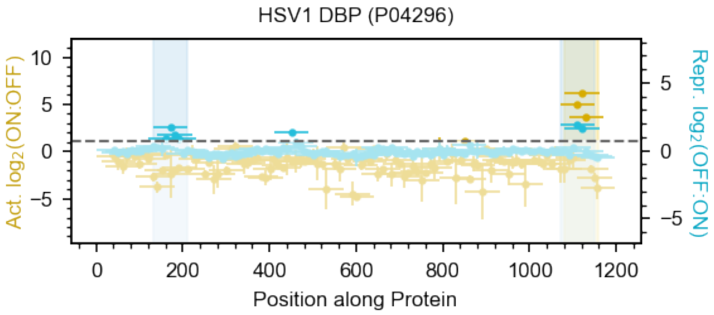
Max tile of repression domain from residues 1052 to 1131 (estimated 24.8% to 28.8% of cells repressed):
GREPLAKSVMNKIQHLTDLNVHDFSLSTLLSVFEEQVEDSAAIYDFSELLVEGNEQGFGILKCEETEHENEEPSLKKARL
Neighboring tile of repression domain from 1052 to 1131:



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| LIG_NRBOX | 1076 | 1082 | SLSTLLS | Yes | 1081 | 1085 | LSVFE |
| SUMO_SIM_par | 1078 | 1086 | STLLSVFEE | Yes | 1081 | 1085 | LSVFE |
| flexi_NRBOX | 1079 | 1085 | TLLSVFE | Yes | 1081 | 1085 | LSVFE |
| flexi_NRBOX | 1096 | 1102 | DFSELLV | Yes | 1096 | 1100 | DFSEL |
| SUMO_for | 1112 | 1115 | LKCE | No | - | - |  |
|  | - | - |  | No | 1121 | 1130 | NEEPSLKKAR |

## HSV1 DBP (P04296)

Gene: UL29 ; Protein Family: DBP



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Extended repression domain from residues 121 to 230:
RHFGFSDYTPRPGDLKHETTGEALCERLGLDPDRALLYLVVTEGFKEAVCINNTFLHLGGSDKVTIGGAEVHRIPVYPLQLFMPDFSRVIAEPFNANHRSIGEKFTYPLP

Max tile of repression domain from residues 131 to 210 (estimated 33.3% to 38.3% of cells repressed):
RPGDLKHETTGEALCERLGLDPDRALLYLVVTEGFKEAVCINNTFLHLGGSDKVTIGGAEVHRIPVYPLQLFMPDFSRVI

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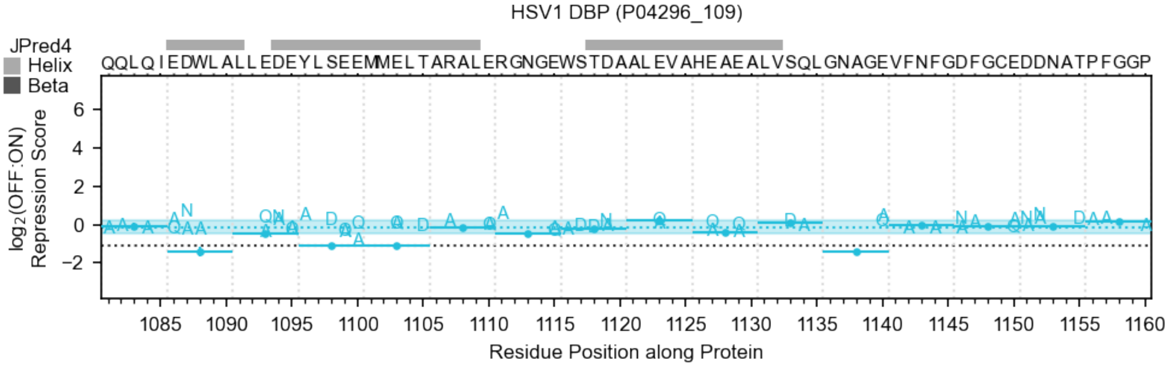
Extended repression domain from residues 1071 to 1160:
ATVKSLGPRTQQLQIEDWLALLEDEYLSEEMMELTARALERGNGEWSTDAALEVAHEAEALVSQLGNAGEVFNFGDFGCEDDNATPFGGP

Max tile of repression domain from residues 1071 to 1150 (estimated 41.1% to 43.0% of cells repressed):
ATVKSLGPRTQQLQIEDWLALLEDEYLSEEMMELTARALERGNGEWSTDAALEVAHEAEALVSQLGNAGEVFNFGDFGCE
Neighboring tile of repression domain from 1081 to 1160:



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_anti | 1086 | 1095 | EDWLALLEDE | Yes | 1086 | 1090 | EDWLA |
| flexi_NRBOX | 1087 | 1093 | DWLALLE | Yes | 1086 | 1090 | EDWLA |
|  | - | - |  | No | 1096 | 1105 | YLSEEMMELT |
|  | - | - |  | No | 1136 | 1140 | GNAGE |

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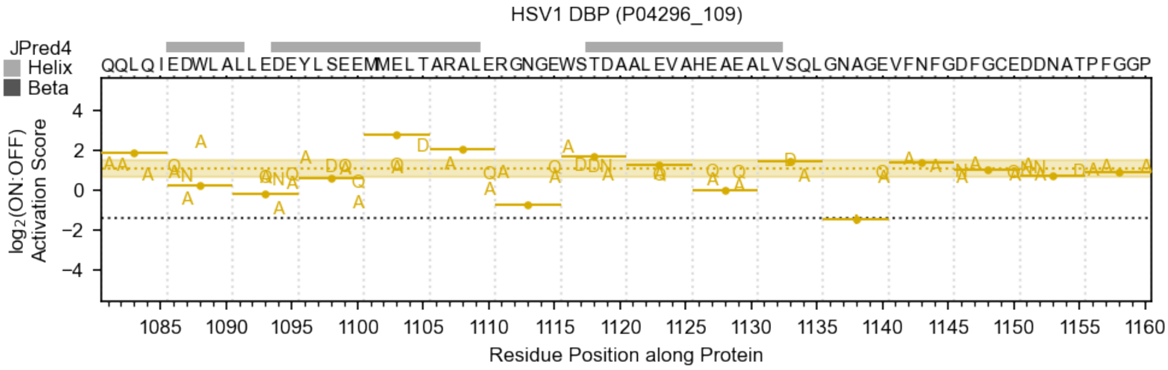
Extended activation domain from residues 1071 to 1170:
ATVKSLGPRTQQLQIEDWLALLEDEYLSEEMMELTARALERGNGEWSTDAALEVAHEAEALVSQLGNAGEVFNFGDFGCEDDNATPFGGPGAPGPAFAGR

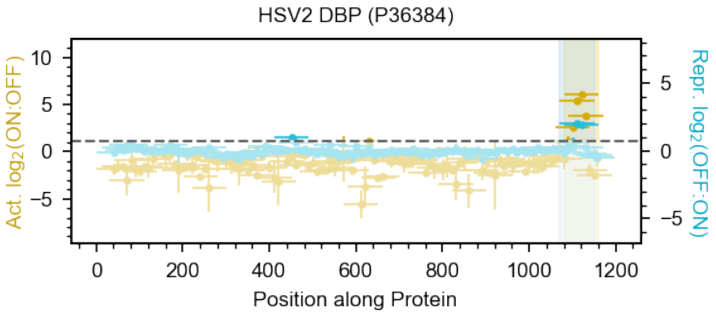
Max tile of activation domain from residues 1081 to 1160 (estimated 58.4% to 61.9% of cells activated):
QQLQIEDWLALLEDEYLSEEMMELTARALERGNGEWSTDAALEVAHEAEALVSQLGNAGEVFNFGDFGCEDDNATPFGGP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_anti | 1086 | 1095 | EDWLALLEDE | No | - | - | |
| flexi_NRBOX | 1087 | 1093 | DWLALLE | No | - | - | |
| | - | - | | No | 1136 | 1140 | GNAGE |

## HSV2 DBP (P36384)

Gene: UL29 ; Protein Family: DBP



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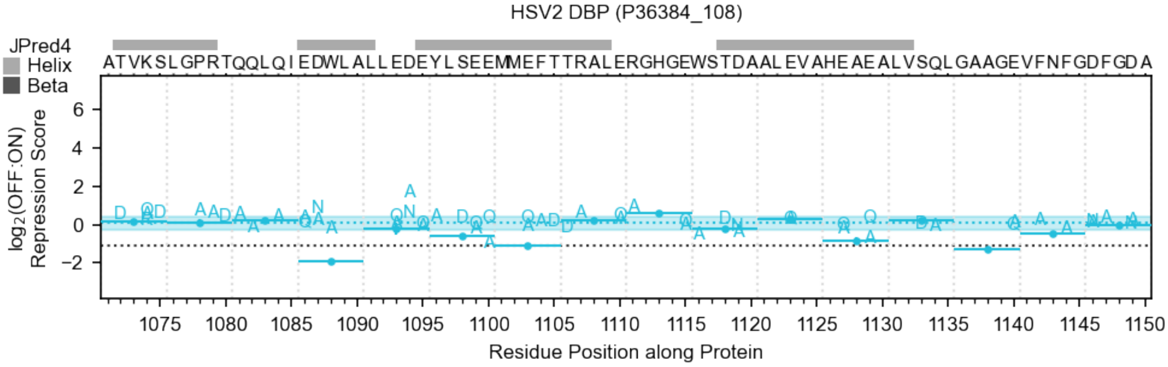
Extended repression domain from residues 1071 to 1160:
ATVKSLGPRTQQLQIEDWLALLEDEYLSEEMMEFTTRALERGHGEWSTDAALEVAHEAEALVSQLGAAGEVFNFGDFGDADDHAASFGGL

Max tile of repression domain from residues 1071 to 1150 (estimated 41.0% to 44.5% of cells repressed):
ATVKSLGPRTQQLQIEDWLALLEDEYLSEEMMEFTTRALERGHGEWSTDAALEVAHEAEALVSQLGAAGEVFNFGDFGDA

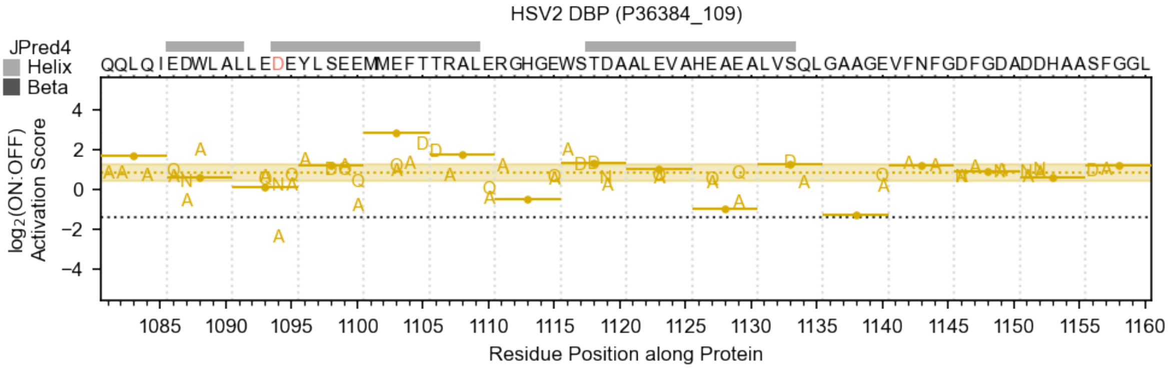


| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_anti | 1086 | 1095 | EDWLALLEDE | Yes | 1086 | 1090 | EDWLA |
| flexi_NRBOX | 1087 | 1093 | DWLALLE | Yes | 1086 | 1090 | EDWLA |
|  | - | - |  | No | 1101 | 1105 | MMEFT |
|  | - | - |  | No | 1136 | 1140 | GAAGE |

---

Extended activation domain from residues 1061 to 1170:
GAAVASSVFVATVKSLGPRTQQLQIEDWLALLEDEYLSEEMMEFTTRALERGHGEWSTDAALEVAHEAEALVSQLGAAGEVFNFGDFGDADDHAASFGGLAAAAAGAAGV

Max tile of activation domain from residues 1081 to 1160 (estimated 55.7% to 56.4% of cells activated):
QQLQIEDWLALLEDEYLSEEMMEFTTRALERGHGEWSTDAALEVAHEAEALVSQLGAAGEVFNFGDFGDADDHAASFGGL



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_anti | 1086 | 1095 | EDWLALLEDE | No | - | - | |
| flexi_NRBOX | 1087 | 1093 | DWLALLE | No | - | - | |

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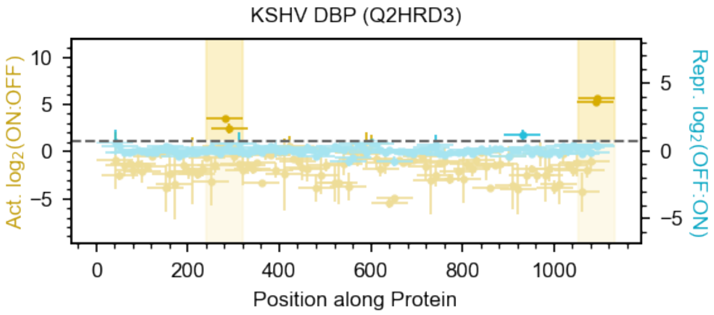
## KSHV DBP (Q2HRD3)

Gene: ORF6 ; Protein Family: DBP



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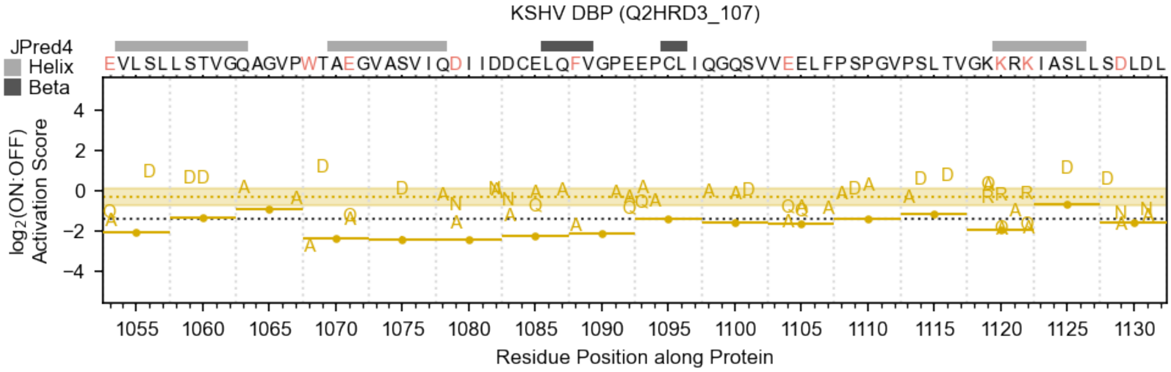
Extended activation domain from residues 241 to 330:
SERQFVHDQYKIPKLVQAKDFPQCASRGTDGSTLMVIDSLVAELGMSYGLSFIEGPQDSCEVLNYDTWPIFENCETPDARLRALEVWHAE

Max tile of activation domain from residues 241 to 320 (estimated 9.9% to 15.0% of cells activated):
SERQFVHDQYKIPKLVQAKDFPQCASRGTDGSTLMVIDSLVAELGMSYGLSFIEGPQDSCEVLNYDTWPIFENCETPDAR

---

Extended activation domain from residues 1051 to 1132:
GDEVLSLLSTVGQAGVPWTAEGVASVIQDIIDDCELQFVGPEEPCLIQGQSVVEELFPSPGVPSLTVGKKRKIASLLSDLDL

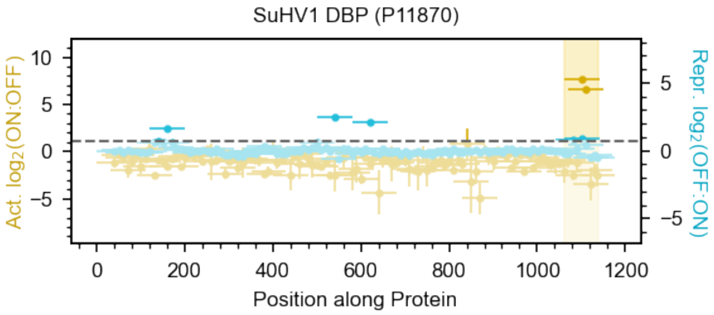
Max tile of activation domain from residues 1053 to 1132 (estimated 42.9% to 51.7% of cells activated):
EVLSLLSTVGQAGVPWTAEGVASVIQDIIDDCELQFVGPEEPCLIQGQSVVEELFPSPGVPSLTVGKKRKIASLLSDLDL



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 1053 | 1059 | EVLSLLS | Yes | 1053 | 1057 | EVLSL |
| SUMO_SIM_par | 1053 | 1060 | EVLSLLST | Yes | 1053 | 1057 | EVLSL |
| SUMO_SIM_anti | 1053 | 1060 | EVLSLLST | Yes | 1053 | 1057 | EVLSL |
| flexi_NRBOX | 1076 | 1082 | VIQDIID | Yes | 1068 | 1092 | WTAEGVASVIQDIIDDCELQFVGPE |
| flexi_NRBOX | 1072 | 1078 | GVASVIQ | Yes | 1068 | 1092 | WTAEGVASVIQDIIDDCELQFVGPE |
|  | - | - |  | No | 1098 | 1107 | QGQSVVEELF |
| flexi_NRBOX | 1122 | 1128 | KIASLLS | Yes | 1118 | 1122 | GKKRK |
| flexi_NRBOX | 1122 | 1128 | KIASLLS | Yes | 1128 | 1132 | SDLDL |

## SuHV1 DBP (P11870)

Gene: UL29 ; Protein Family: DBP



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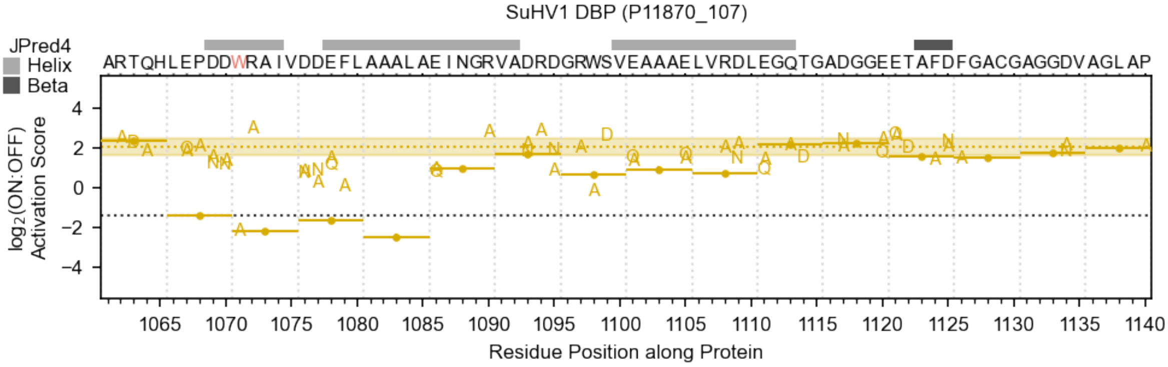
Extended activation domain from residues 1061 to 1150:
ARTQHLEPDDWRAIVDDEFLAAALAEINGRVADRDGRWSVEAAAELVRDLEGQTGADGGEETAFDFGACGAGGDVAGLAPASLVPAELGG

Max tile of activation domain from residues 1061 to 1140 (estimated 82.7% to 85.4% of cells activated):
ARTQHLEPDDWRAIVDDEFLAAALAEINGRVADRDGRWSVEAAAELVRDLEGQTGADGGEETAFDFGACGAGGDVAGLAP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 1070 | 1076 | DWRAIVD | Yes | 1066 | 1085 | LEPDDWRAIVDDEFLAAALA |
| Sin3A_SID | 1102 | 1106 | AAAEL | No | - | - | |

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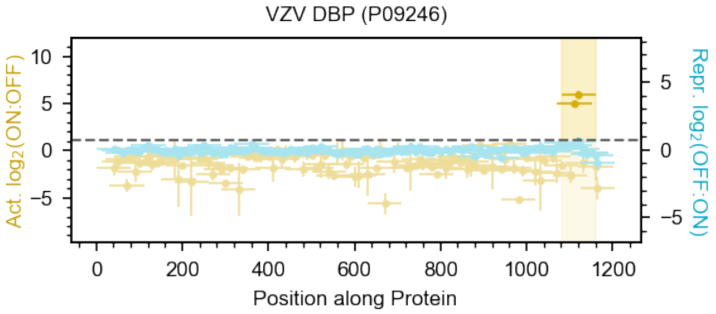
## VZV DBP (P09246)

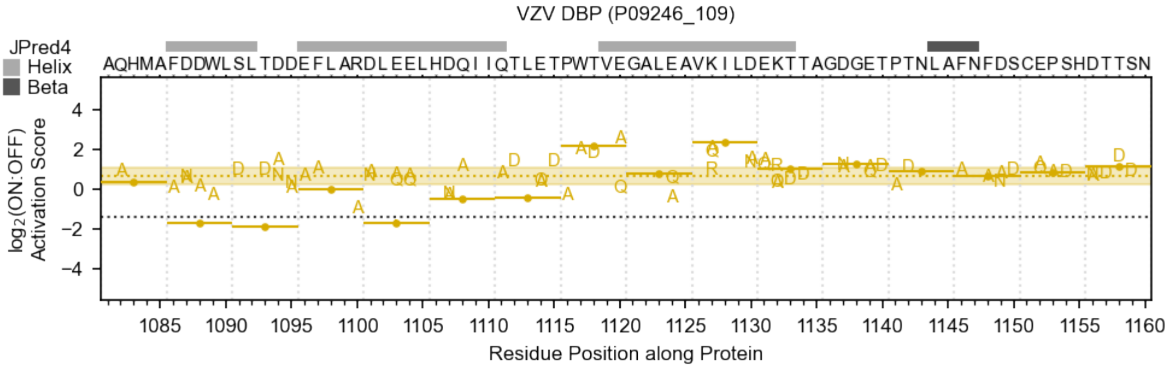
Gene: ORF29 ; Protein Family: DBP



---

Extended activation domain from residues 1071 to 1160:
ATVVRAVGARAQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGALEAVKILDEKTTAGDGETPTNLAFNFDSCEPSHDTTSN

Max tile of activation domain from residues 1081 to 1160 (estimated 48.5% to 62.9% of cells activated):
AQHMAFDDWLSLTDDEFLARDLEELHDQIIQTLETPWTVEGALEAVKILDEKTTAGDGETPTNLAFNFDSCEPSHDTTSN



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 1086 | 1095 | FDDWLSLTDD |
| | - | - | | No | 1101 | 1105 | DLEEL |
| SUMO_rev | 1124 | 1134 | EAVKILDEKTT | No | - | - | |
| CtBP_expanded | 1141 | 1145 | PTNLA | No | - | - | |

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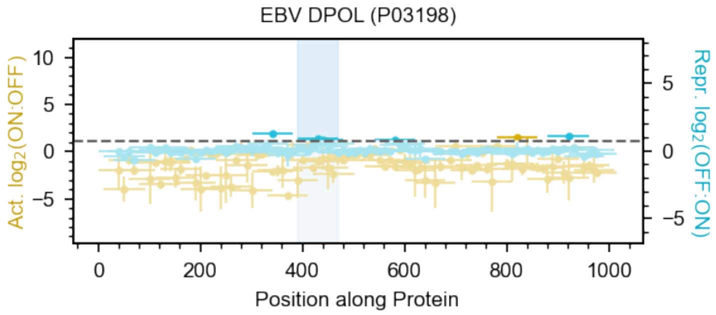
## EBV DPOL (P03198)

Gene: BALF5 ; Protein Family: DPOL



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Extended repression domain from residues 391 to 480:
RARHIYSINPASLGKIRAGGVCEVRRPHDAGKGFLRANTKVRITGLIPIDMYAVCRDKLSLSDYKLDTVARHLLGAKKEDVHYKEIPRLF

Max tile of repression domain from residues 391 to 470 (estimated 18.0% to 18.3% of cells repressed):
RARHIYSINPASLGKIRAGGVCEVRRPHDAGKGFLRANTKVRITGLIPIDMYAVCRDKLSLSDYKLDTVARHLLGAKKED

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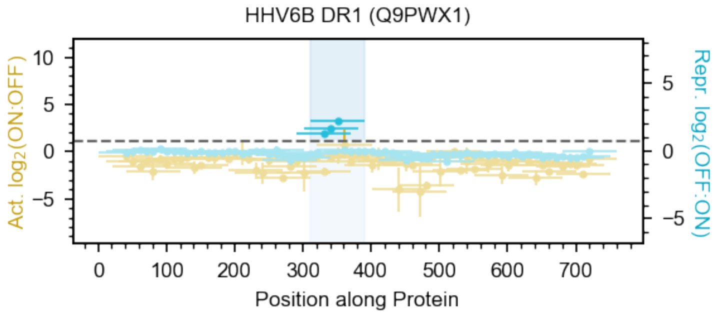
## HHV6B DR1 (Q9PWX1)

Gene: DR1 ; Protein Family: DR1



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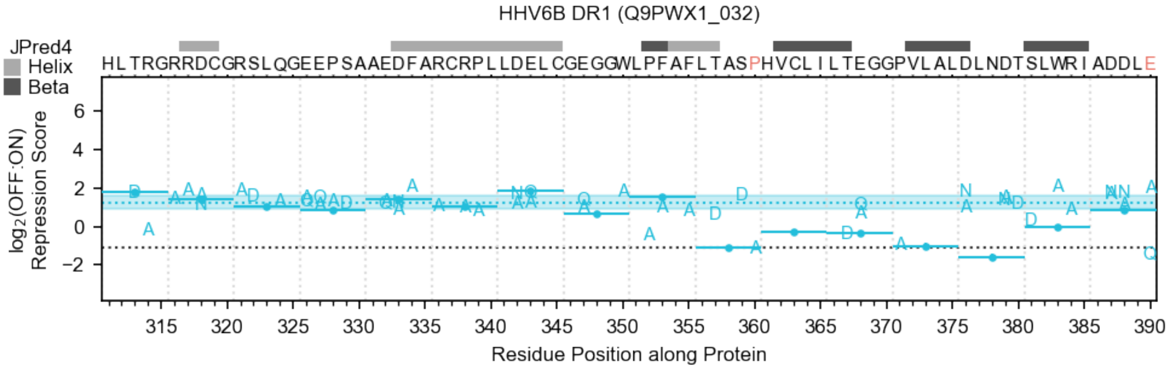
Extended repression domain from residues 291 to 390:
GKEEAERGGRQQATDRLASPHLTRGRRDCGRSLQGEEPSAAEDFARCRPLLDELCGEGGWLPFAFLTASPHVCLILTEGGPVLALDLNDTSLWRIADDLE

Max tile of repression domain from residues 311 to 390 (estimated 46.9% to 51.4% of cells repressed):
HLTRGRRDCGRSLQGEEPSAAEDFARCRPLLDELCGEGGWLPFAFLTASPHVCLILTEGGPVLALDLNDTSLWRIADDLE



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 356 | 360 | LTASP |
| flexi_NRBOX | 361 | 367 | HVCLILT | No | - | - | |
| SUMO_SIM_par | 371 | 376 | PVLALD | Yes | 376 | 380 | DLNDT |

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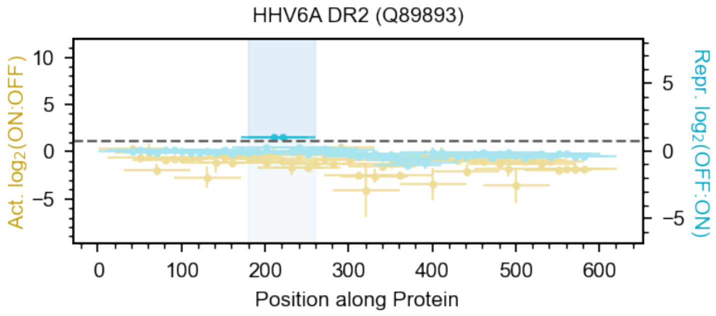
## HHV6A DR2 (Q89893)

Gene: DR2 ; Protein Family: DR2



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Extended repression domain from residues 171 to 260:
PVLEWESTELVLTDWRRGRNEAQRDAPSVAEHFARCRPLLDELCGEGGWLPFAFLSTSPHVWLILTEGGPVLAVDVNDTSVWRIADDLEL

Max tile of repression domain from residues 181 to 260 (estimated 18.4% to 20.2% of cells repressed):
VLTDWRRGRNEAQRDAPSVAEHFARCRPLLDELCGEGGWLPFAFLSTSPHVWLILTEGGPVLAVDVNDTSVWRIADDLEL

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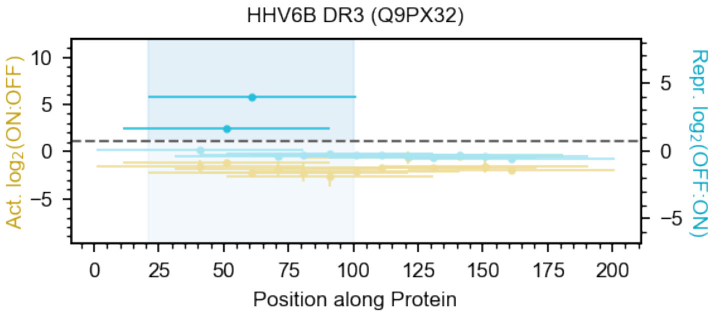
## HHV6B DR3 (Q9PX32)

Gene: DR3 ; Protein Family: DR3



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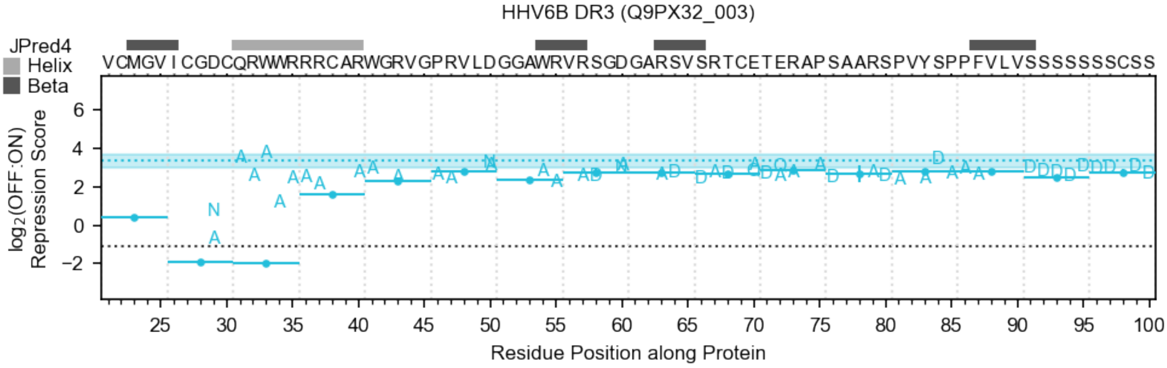
Extended repression domain from residues 11 to 100:
ACVCAGLCCWVCMGVICGDCQRWWRRRCARWGRVGPRVLDGGAWRVRSGDGARSVSRTCETERAPSAARSPVYSPPFVLVSSSSSSSSCSS

Max tile of repression domain from residues 21 to 100 (estimated 86.5% to 87.7% of cells repressed):
VCMGVICGDCQRWWRRRCARWGRVGPRVLDGGAWRVRSGDGARSVSRTCETERAPSAARSPVYSPPFVLVSSSSSSSSCSS



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
|  | - | - |  | No | 26 | 35 | ICGDCQRWWR |

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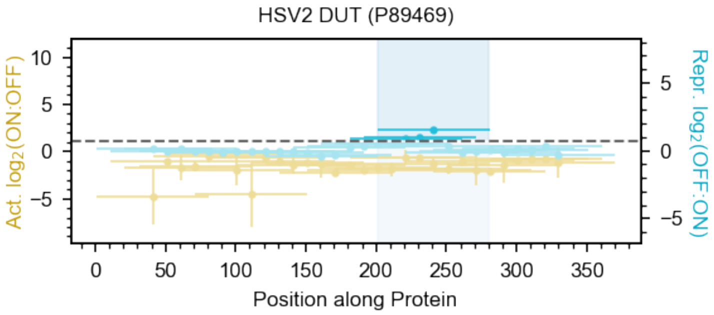
# HSV2 DUT (P89469)

Gene: UL50 ; Protein Family: DUT



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Extended repression domain from residues 181 to 280:
RRGGSLVYAGELTQVTTEHGDCVHEAPAFLPKREEDAGFDILIHRAVTVPANGATVIQPSLRVLRAADGPEACYVLGRSSLNARGLLVMPTRWPSGHAC
A

Max tile of repression domain from residues 201 to 280 (estimated 28.8% to 36.5% of cells repressed):
DCVHEAPAFLPKREEDAGFDILIHRAVTVPANGATVIQPSLRVLRAADGPEACYVLGRSSLNARGLLVMPTRWPSGHACA

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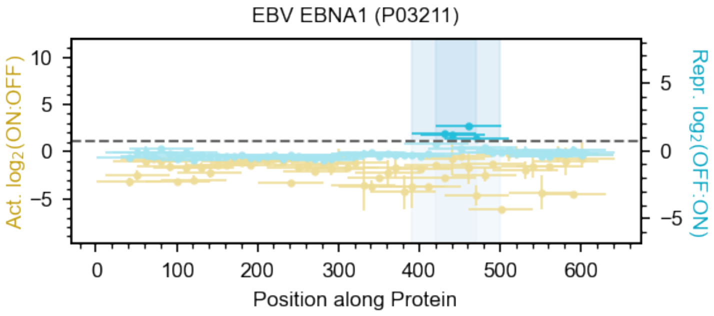
## EBV EBNA1 (P03211)

Gene: BKRF1 ; Protein Family: EBNA ; EBV Strain: B95-8 (Type 1)



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Extended repression domain from residues 391 to 480:
SGSPPRRPPPGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPSTGPRGQGDGGRRKKGGWFGKHRGQGGSNPKFEN

Max tile of repression domain from residues 391 to 470 (estimated 22.4% to 28.8% of cells repressed):
SGSPPRRPPPGRRPFFHPVGEADYFEYHQEGGPDGEPDVPPGAIEQGPADDPGEGPSTGPRGQGDGGRRKKGGWFGKHRG

---

Extended repression domain from residues 421 to 510:
GGPDGEPDVPPGAIEQGPADDPGEGPSTGPRGQGDGGRRKKGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWVAGVFVY

Max tile of repression domain from residues 421 to 500 (estimated 35.2% to 41.0% of cells repressed):
GGPDGEPDVPPGAIEQGPADDPGEGPSTGPRGQGDGGRRKKGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDE

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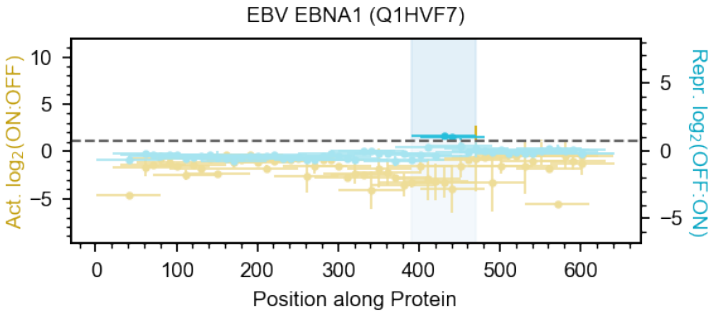
# EBV EBNA1 (Q1HVF7)

Gene: BKRF1 ; Protein Family: EBNA ; EBV Strain: AG876 (Type 2)



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Extended repression domain from residues 391 to 480:
SGSPPRRPPPGRRPFFHPVAEADYFEYHQEGGPDGEPDMPPGAIEQGPADDPGEGPSTGPRGQGDGGRRKKGGWYGKHRGEGGSSQKFEN

Max tile of repression domain from residues 391 to 470 (estimated 16.3% to 26.0% of cells repressed):
SGSPPRRPPPGRRPFFHPVAEADYFEYHQEGGPDGEPDMPPGAIEQGPADDPGEGPSTGPRGQGDGGRRKKGGWYGKHRG

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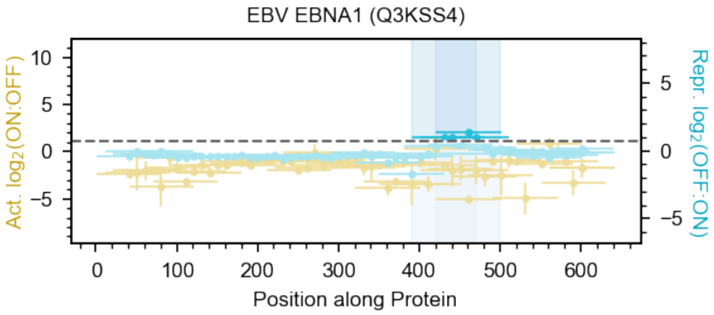
# EBV EBNA1 (Q3KSS4)

Gene: BKRF1 ; Protein Family: EBNA ; EBV Strain: GD1 (Type 1)



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Extended repression domain from residues 391 to 480:
SGSPPRRPPPGRRPFFHPVGDADYFEYLQEGGPDGEPDVPPGAIEQGPTDDPGEGPSTGPRGQGDGGRRKKGGWFGKHRGQGGSNPKFEN

Max tile of repression domain from residues 391 to 470 (estimated 18.2% to 20.2% of cells repressed):
SGSPPRRPPPGRRPFFHPVGDADYFEYLQEGGPDGEPDVPPGAIEQGPTDDPGEGPSTGPRGQGDGGRRKKGGWFGKHRG

---

Extended repression domain from residues 421 to 510:
GGPDGEPDVPPGAIEQGPTDDPGEGPSTGPRGQGDGGRRKKGGWFGKHRGQGGSNPKFENIAEGLRVLLARSHVERTTEEGNWVAGVFVY

Max tile of repression domain from residues 421 to 500 (estimated 25.7% to 29.8% of cells repressed):
GGPDGEPDVPPGAIEQGPTDDPGEGPSTGPRGQGDGGRRKKGGWFGKHRGQGGSNPKFENIAEGLRVLLARSHVERTTEE

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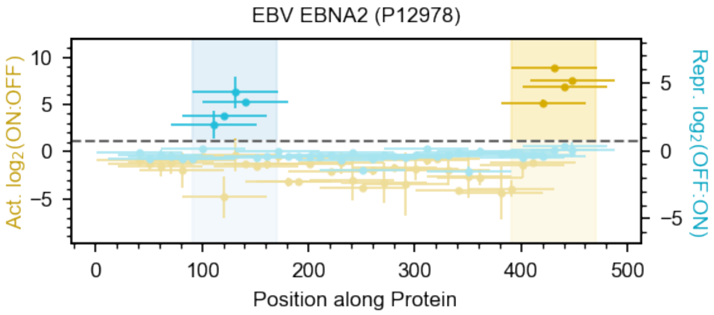
## EBV EBNA2 (P12978)

Gene: BYRF1 ; Protein Family: EBNA ; EBV Strain: B95-8 (Type 1)



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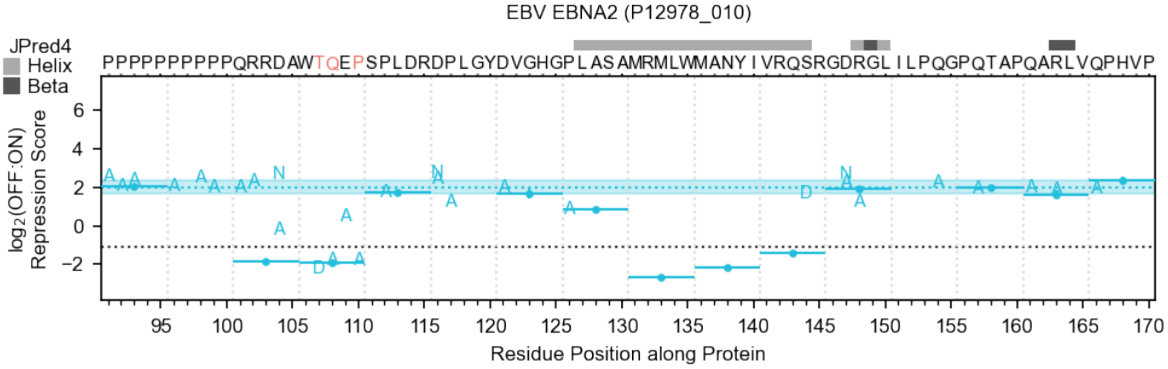
Extended repression domain from residues 71 to 180:
PPPPPPPPPPPPPPPPPPSPPPPPPPPPPPQRRDAWTQEPSPLDRDPLGYDVGHGPLASAMRMLWMANYIVRQSRGDRGLILPQGPQTAPQARLVQPHVPPLRPTAPTIL

Max tile of repression domain from residues 91 to 170 (estimated 73.9% to 98.2% of cells repressed):
PPPPPPPPPPQRRDAWTQEPSPLDRDPLGYDVGHGPLASAMRMLWMANYIVRQSRGDRGLILPQGPQTAPQARLVQPHVP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 101 | 110 | QRRDAWTQEP |
| | - | - | | No | 131 | 145 | MRMLWMANYIVRQSR |

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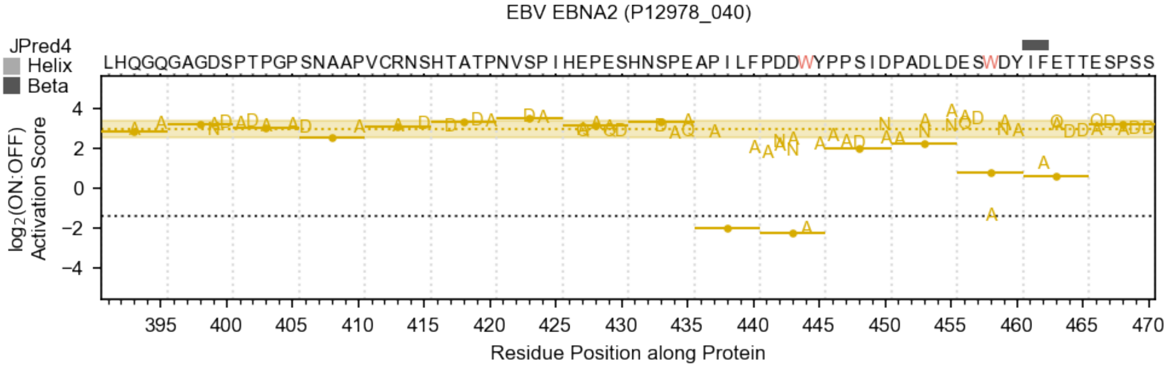
Extended activation domain from residues 381 to 487:
SMPELSPVLGLHQGQGAGDSPTPGPSNAAPVCRNSHTATPNVSPIHEPESHNSPEAPILFPDDWYPPSIDPADLDESWDYIFETTESPSSDEDYVEGPSKRPRPSIQ

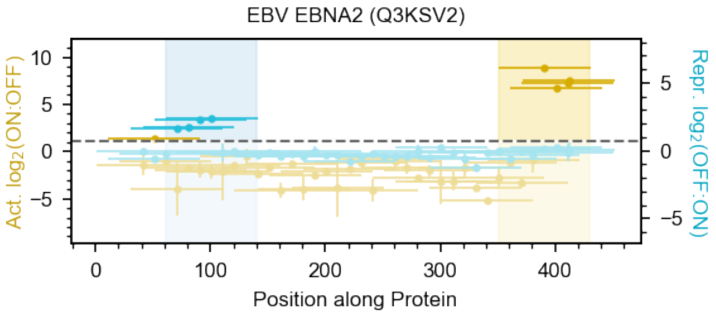
Max tile of activation domain from residues 391 to 470 (estimated 92.3% to 93.7% of cells activated):
LHQGQGAGDSPTPGPSNAAPVCRNSHTATPNVSPIHEPESHNSPEAPILFPDDWYPPSIDPADLDESWDYIFETTESPSS



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| MYND_1 | 437 | 441 | PILFP | Yes | 436 | 445 | APILFPDDWY |
| CtBP_expanded | 451 | 455 | PADLD | No | - | - | |
| flexi_NRBOX | 457 | 463 | SWDYIFE | No | - | - | |

# EBV EBNA2 (Q3KSV2)

Gene: BYRF1 ; Protein Family: EBNA ; EBV Strain: GD1 (Type 1)



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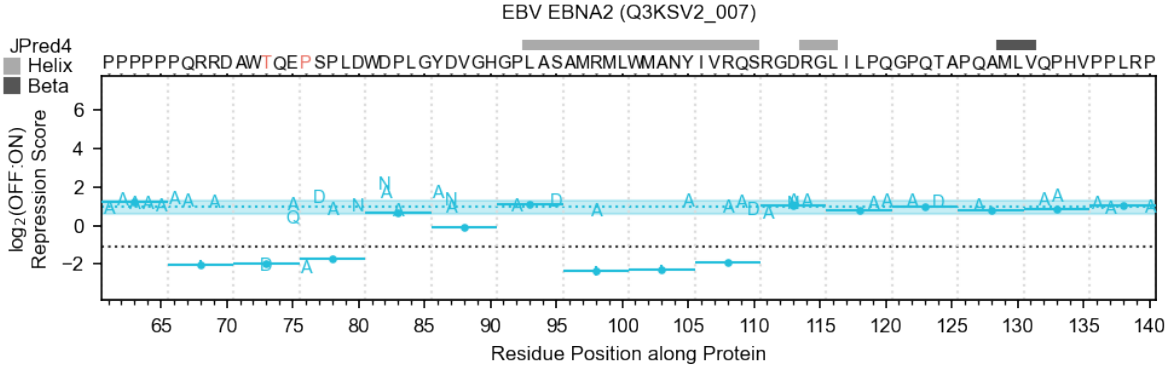
Extended repression domain from residues 31 to 140:
IPSNPYQEQLSDTPLIPLTIFVGENTGVPPPPPPPPQRRDAWTQEPSPLDWDPLGYDVGHGPLASAMRMLWMANYIVRQSRGDRGLILPQGPQTAPQA
MLVQPHVPPLRP

Max tile of repression domain from residues 61 to 140 (estimated 47.2% to 60.1% of cells repressed):
PPPPPPQRRDAWTQEPSPLDWDPLGYDVGHGPLASAMRMLWMANYIVRQSRGDRGLILPQGPQTAPQAMLVQPHVPPLRP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 66 | 80 | PQRRDAWTQEPSPLD |
| | - | - | | No | 96 | 110 | AMRMLWMANYIVRQS |
| MYND_1 | 136 | 140 | PPLRP | No | - | - | |

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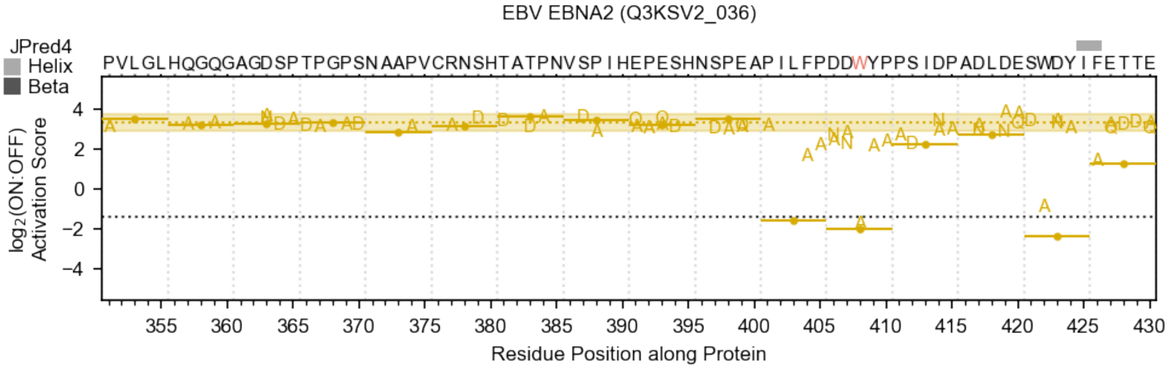
Extended activation domain from residues 351 to 451:
PVLGLHQGQGAGDSPTPGPSNAAPVCRNSHTATPNVSPIHEPESHNSPEAPILFPDDWYPPSIDPADLDESWDYIFETTESPSSDEDYVEGPSKRPRPSI
Q

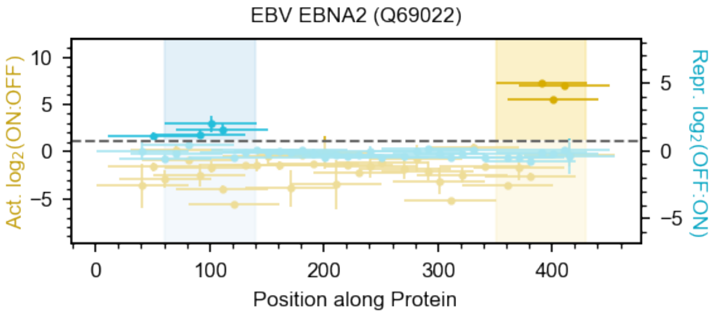
Max tile of activation domain from residues 351 to 430 (estimated 92.9% to 92.9% of cells activated):
PVLGLHQGQGAGDSPTPGPSNAAPVCRNSHTATPNVSPIHEPESHNSPEAPILFPDDWYPPSIDPADLDESWDYIFETTE



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| MYND_1 | 401 | 405 | PILFP | Yes | 401 | 410 | PILFPDDWYP |
| CtBP_expanded | 415 | 419 | PADLD | No | - | - | |
| flexi_NRBOX | 421 | 427 | SWDYIFE | Yes | 421 | 425 | SWDYI |

## EBV EBNA2 (Q69022)

Gene: BYRF1 ; Protein Family: EBNA ; EBV Strain: AG876 (Type 2)



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Extended repression domain from residues 51 to 150:
VVGENTGAPAPPQPPPPPPPPPPPPERRDAWTQEPLPLDMNPLGSDASQGPLASSIRMLCMAQYLLRNARGQQGLLRPLGPQTRSQVTLERQPVHNPRQEA

Max tile of repression domain from residues 61 to 140 (estimated 27.3% to 59.3% of cells repressed):
PPQPPPPPPPPPPPPERRDAWTQEPLPLDMNPLGSDASQGPLASSIRMLCMAQYLLRNARGQQGLLRPLGPQTRSQVTLER

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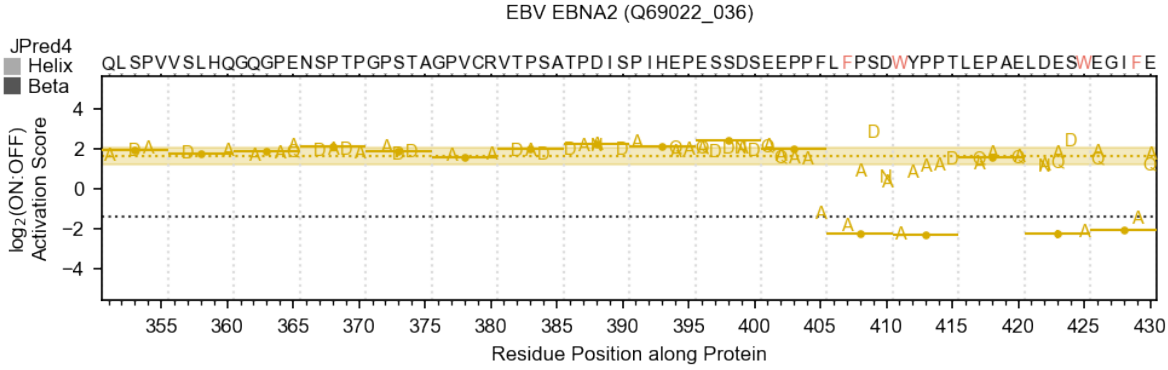
Extended activation domain from residues 351 to 450:
QLSPVVSLHQGQGPENSPTPGPSTAGPVCRVTPSATPDISPIHEPESSDSEEPPFLFPSDWYPPTLEPAELDESWEGIFETTESHSSDEENVGGPSKRPR

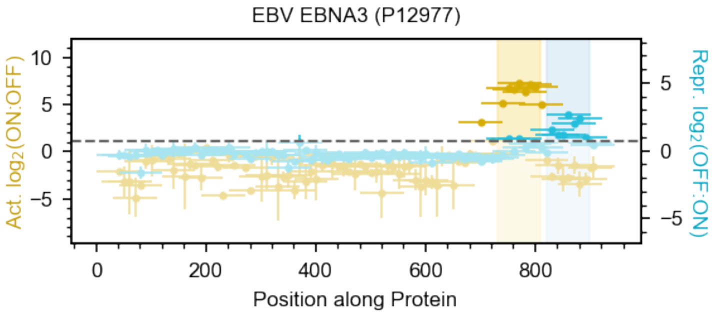
Max tile of activation domain from residues 351 to 430 (estimated 76.5% to 83.1% of cells activated):
QLSPVVSLHQGQGPENSPTPGPSTAGPVCRVTPSATPDISPIHEPESSDSEEPPFLFPSDWYPPTLEPAELDESWEGIFE



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| HP1 | 354 | 358 | PVVSL | No | - | - | |
| MYND_1 | 404 | 408 | PFLFP | Yes | 406 | 415 | LFPSDWYPPT |
| MYND_1 | 414 | 418 | PTLEP | Yes | 406 | 415 | LFPSDWYPPT |
| CtBP_expanded | 418 | 422 | PAELD | Yes | 421 | 430 | LDESWEGIFE |
| flexi_NRBOX | 424 | 430 | SWEGIFE | Yes | 421 | 430 | LDESWEGIFE |

## EBV EBNA3 (P12977)

Gene: BLRF3-BERF1 ; Protein Family: EBNA ; EBV Strain: B95-8 (Type 1)



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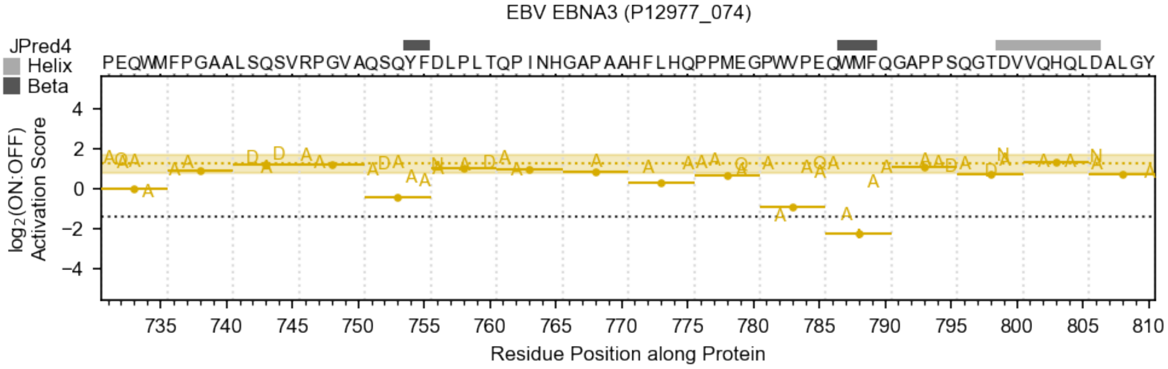
Extended activation domain from residues 701 to 850:
YFDIPLTEPINQGASAAHFLPQQPMEGPLVPEQWMFPGAALSQSVRPGVAQSQYFDLPLTQPINHGAPAAHFLHQPPMEGPWVPEQWMFQGAPPSQGTDVVQHQLDALGYTLHGLNHPGVPVSPAVNQYHLSQAAFGLPIDEDESGEGSD

Max tile of activation domain from residues 731 to 810 (estimated 79.1% to 81.2% of cells activated):
PEQWMFPGAALSQSVRPGVAQSQYFDLPLTQPINHGAPAAHFLHQPPMEGPWVPEQWMFQGAPPSQGTDVVQHQLDALGY



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| Sin3A_SID | 769 | 773 | AAHFL | No | - | - | |
| CSL_BTD_1 | 781 | 784 | PWVP | No | - | - | |
| | - | - | | No | 786 | 790 | QWMFQ |

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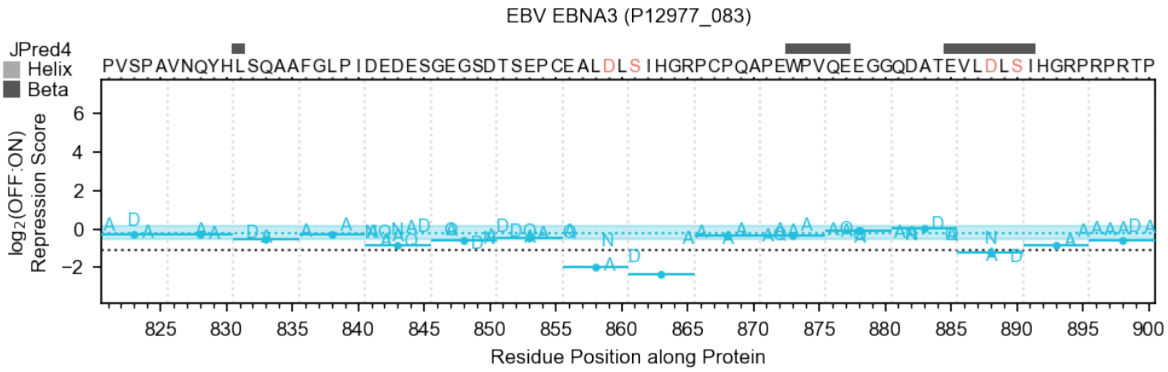
Extended repression domain from residues 791 to 930:
GAPPSQGTDVVQHQLDALGYTLHGLNHPGVPVSPAVNQYHLSQAAFGLPIDEDESGEGSDTSEPCEALDLSIHGRPCPQAPEWPVQEEGGQDATEVLDLSIHGRPRPRTPEWPVQGEGGQNVTGPETRRVVVSAVVHMCQ

Max tile of repression domain from residues 821 to 900 (estimated 60.1% to 62.5% of cells repressed):
PVSPAVNQYHLSQAAFGLPIDEDESGEGSDTSEPCEALDLSIHGRPCPQAPEWPVQEEGGQDATEVLDLSIHGRPRPRTP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| Sin3A_SID | 834 | 838 | AAFGL | No | - | - | |
| CtBP_EBNA3 | 858 | 861 | LDLS | Yes | 856 | 865 | EALDLSIHGR |
| SUMO_SIM_par | 884 | 890 | TEVLDLS | Yes | 886 | 890 | VLDLS |

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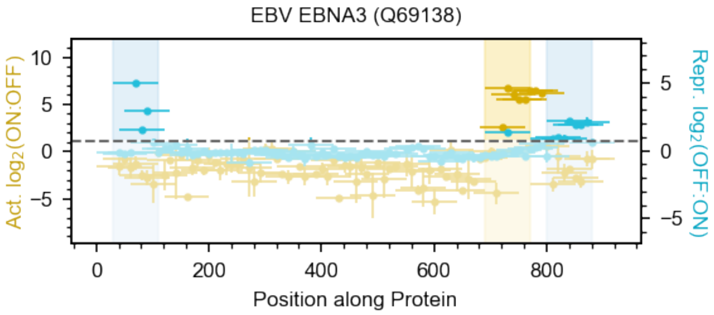
## EBV EBNA3 (Q69138)

Gene: BLRF3-BERF1 ; Protein Family: EBNA ; EBV Strain: AG876 (Type 2)



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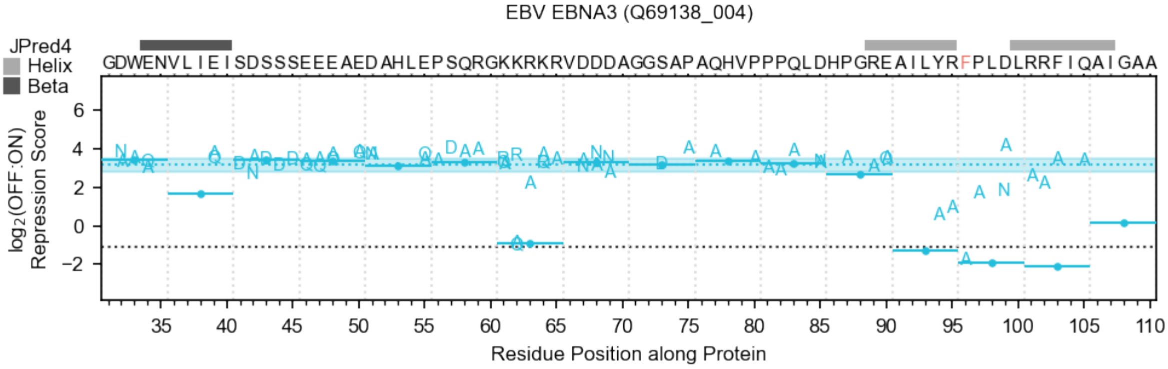
Extended repression domain from residues 31 to 130:
GDWENVLIEISDSSSEEEAEDAHLEPSQRGKKRKRVDDDAGGSAPAQHVPPPQLDHPGREAILYRFPLDLRRFIQAIGAAATHPDTRAIDQFFGSQISNT

Max tile of repression domain from residues 31 to 110 (estimated 95.9% to 96.6% of cells repressed):
GDWENVLIEISDSSSEEEAEDAHLEPSQRGKKRKRVDDDAGGSAPAQHVPPPQLDHPGREAILYRFPLDLRRFIQAIGAA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 32 | 38 | DWENVLI | No | - | - | |
| SUMO_SIM_par | 36 | 48 | VLIEISDSSSEEE | No | - | - | |
| CtBP_expanded | 97 | 101 | PLDLR | Yes | 91 | 105 | AILYRFPLDLRRFIQ |
| flexi_NRBOX | 99 | 105 | DLRRFIQ | Yes | 91 | 105 | AILYRFPLDLRRFIQ |

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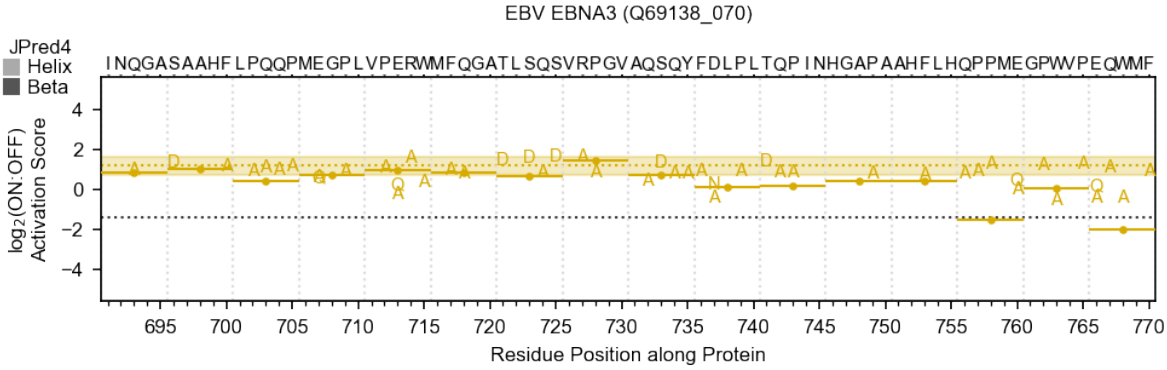
Extended activation domain from residues 681 to 830:
QYFDIPLTEPINQGASAAHFLPQQPMEGPLVPERWMFQGATLSQSVRPGVAQSQYFDLPLTQPINHGAPAAHFLHQPPMEGPWVPEQWMFQGAPPSQGTDVVQHQLDDLGYPLHDLNHPGVPVSPAVNQYHFSQAAFGLPIDEDESGERS

Max tile of activation domain from residues 691 to 770 (estimated 70.1% to 70.3% of cells activated):
INQGASAAHFLPQQPMEGPLVPERWMFQGATLSQSVRPGVAQSQYFDLPLTQPINHGAPAAHFLHQPPMEGPWVPEQWMF



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| Sin3A_SID | 697 | 701 | AAHFL | No | - | - | |
| | - | - | | No | 756 | 760 | QPPME |
| CSL_BTD_1 | 762 | 765 | PWVP | No | - | - | |
| | - | - | | No | 766 | 770 | EQWMF |

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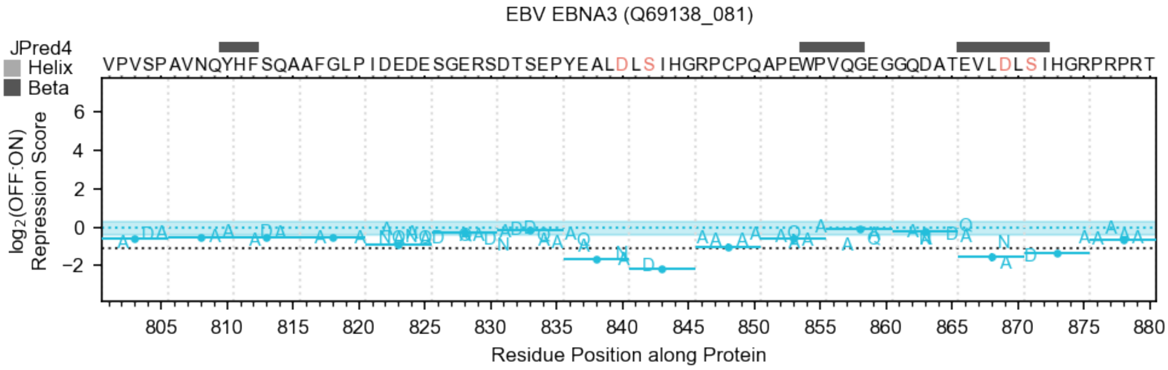
Extended repression domain from residues 771 to 910:
QGAPPSQGTDVVQHQLDDLGYPLHDLNHPGVPVSPAVNQYHFSQAAFGLPIDEDESGERSDTSEPYEALDLSIHGRPCPQAPEWPVQGEGGQDATEVLDLSIHGRPRPRTPEWPVQGESGQNVTDHEPRRVVVSAIVHMC

Max tile of repression domain from residues 801 to 880 (estimated 46.6% to 53.0% of cells repressed):
VPVSPAVNQYHFSQAAFGLPIDEDESGERSDTSEPYEALDLSIHGRPCPQAPEWPVQGEGGQDATEVLDLSIHGRPRPRT



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| Sin3A_SID | 815 | 819 | AAFGL | No | - | - | |
| CtBP_EBNA3 | 839 | 842 | LDLS | Yes | 836 | 845 | YEALDLSIHG |
| SUMO_SIM_par | 865 | 871 | TEVLDLS | Yes | 866 | 875 | EVLDLSIHGR |

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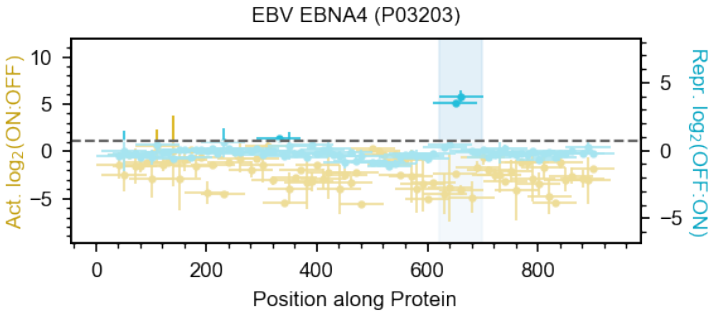
# EBV EBNA4 (P03203)

Gene: BERF2A-BERF2B ; Protein Family: EBNA ; EBV Strain: B95-8 (Type 1)



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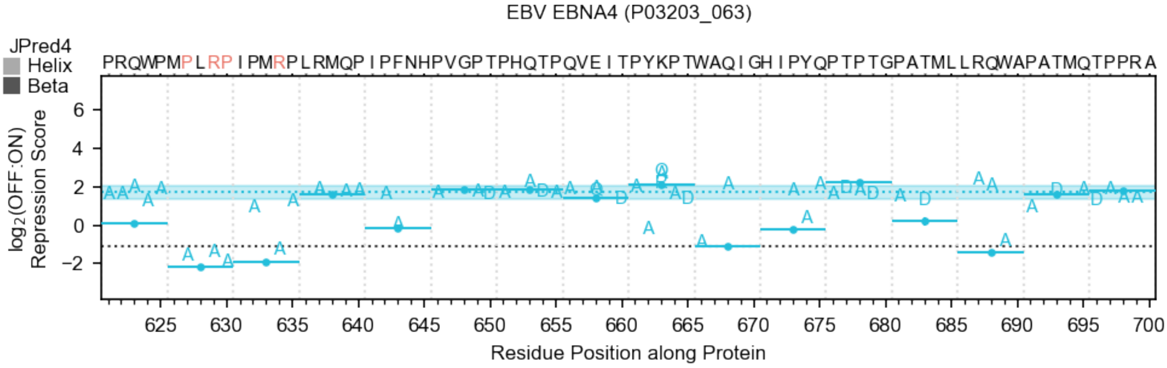
Extended repression domain from residues 611 to 700:
KQSRPPETAAPRQWPMPLRPIPMRPLRMQPIPFNHPVGPTPHQTPQVEITPYKPTWAQIGHIPYQPTPTGPATMLLRQWAPATMQTPPRA

Max tile of repression domain from residues 621 to 700 (estimated 82.2% to 92.2% of cells repressed):
PRQWPMPLRPIPMRPLRMQPIPFNHPVGPTPHQTPQVEITPYKPTWAQIGHIPYQPTPTGPATMLLRQWAPATMQTPPRA

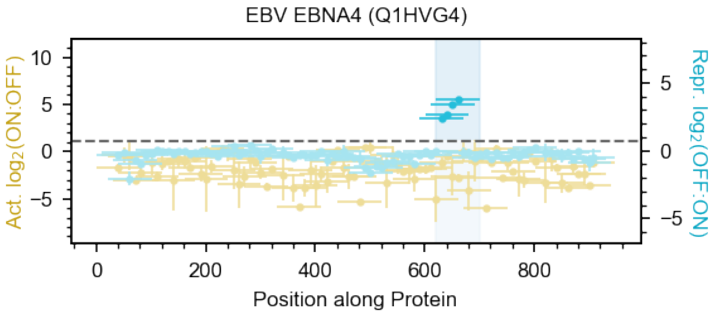


| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 626 | 635 | MPLRPIPMRP |
| | - | - | | No | 666 | 670 | WAQIG |
| | - | - | | No | 686 | 690 | LRQWA |
| WW_3 | 696 | 700 | TPPRA | No | - | - | |

**Herpesvirus Tiling and Perturbation Screen Data from Ludwig, C.H. et al. 2023**

## EBV EBNA4 (Q1HVG4)

Gene: BERF2A-BERF2B ; Protein Family: EBNA ; EBV Strain: AG876 (Type 2)



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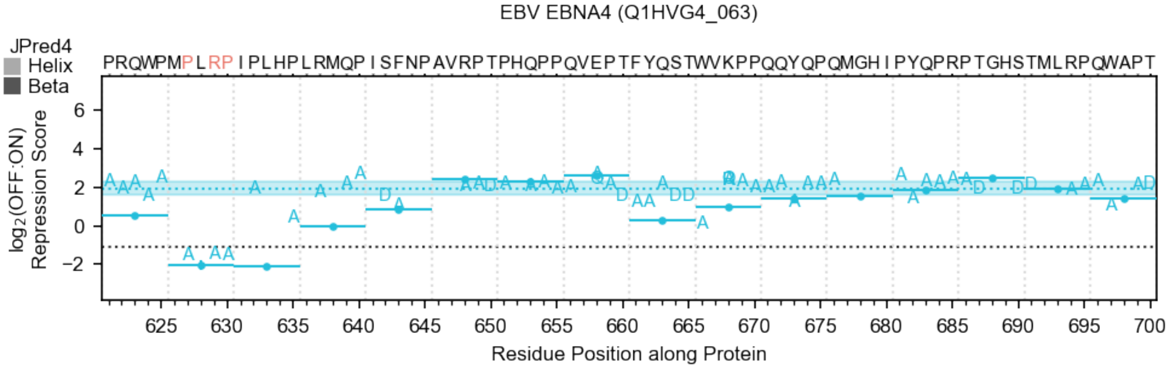
Extended repression domain from residues 591 to 700:
SHAQTPWPVTHPSQTPGGPTTQSLAPETEAPRQWPMPLRPIPLHPLRMQPISFNPAVRPTPHQPPQVEPTFYQSTWVKPPQQYQPQMGHIPYQPRPTGHSTMLRPQWAPT

Max tile of repression domain from residues 621 to 700 (estimated 83.6% to 86.3% of cells repressed):
PRQWPMPLRPIPLHPLRMQPISFNPAVRPTPHQPPQVEPTFYQSTWVKPPQQYQPQMGHIPYQPRPTGHSTMLRPQWAPT



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 626 | 635 | MPLRPIPLHP |

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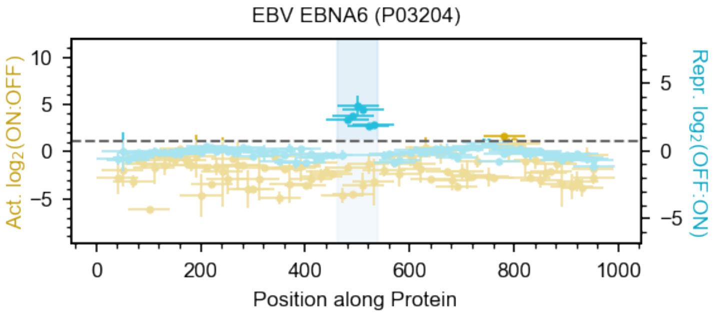
## EBV EBNA6 (P03204)

Gene: BERF3-BERF4 ; Protein Family: EBNA ; EBV Strain: B95-8 (Type 1)



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Extended repression domain from residues 441 to 570:
DKAEAQSTPERPGPSEQSSVTVEPAHPTPVEMPMVILHQPPPVPKPVPVKPTPPPSRRRRGACVVYDDDVIEVIDVETTEDSSSVSQPNKPHRKHQDGFQRSGRRQKRAAPPTVSPSDTGPPAVGPPAAG

Max tile of repression domain from residues 461 to 540 (estimated 59.5% to 88.4% of cells repressed):
TVEPAHPTPVEMPMVILHQPPPVPKPVPVKPTPPPSRRRRGACVVYDDDVIEVIDVETTEDSSSVSQPNKPHRKHQDGFQ

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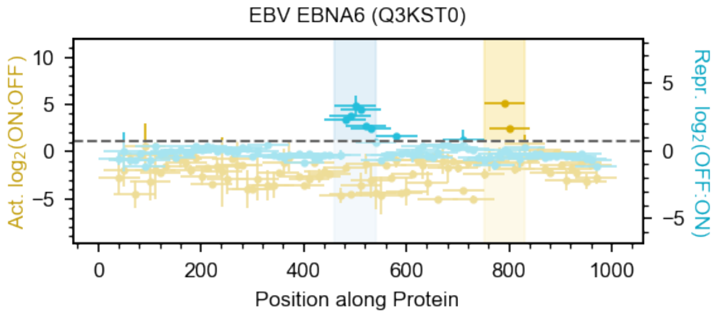
**Herpesvirus Tiling and Perturbation Screen Data from Ludwig, C.H. et al. 2023**

## EBV EBNA6 (Q3KST0)

Gene: BERF3-BERF4 ; Protein Family: EBNA ; EBV Strain: GD1 (Type 1)



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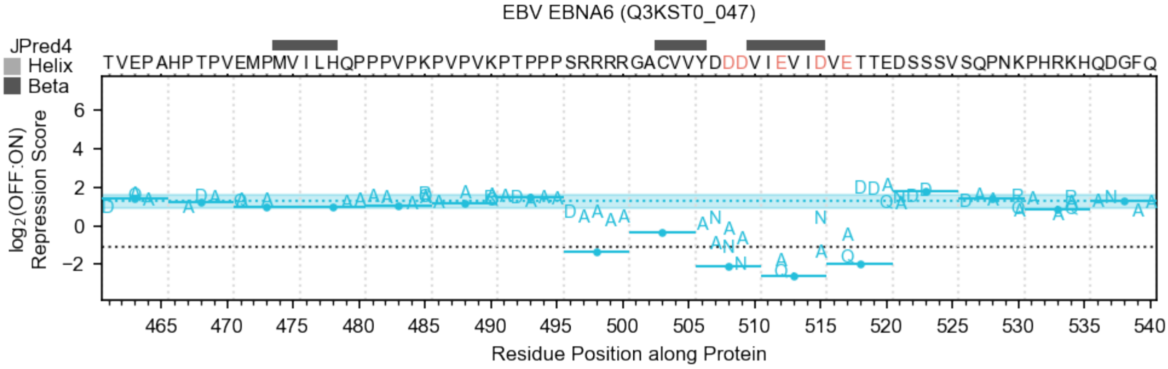
Extended repression domain from residues 441 to 570:
DKAEAQSTPERPGPSEQSSVTVEPAHPTPVEMPMVILHQPPPVPKPVPVKPTPPPSRRRRGACVVYDDDVIEVIDVETTEDSSSVSQPNKPHRKHQDGFQRSGRRQKRAAPPTVSPSDTGPPAAGPPAAG

Max tile of repression domain from residues 461 to 540 (estimated 59.5% to 88.4% of cells repressed):
TVEPAHPTPVEMPMVILHQPPPVPKPVPVKPTPPPSRRRRGACVVYDDDVIEVIDVETTEDSSSVSQPNKPHRKHQDGFQ



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| CtBP_expanded | 469 | 473 | PVEMP | No | - | - | |
| HP1 | 473 | 477 | PMVIL | No | - | - | |
| | - | - | | No | 496 | 500 | SRRRR |
| SUMO_SIM_par | 512 | 524 | EVIDVETTEDSSS | Yes | 506 | 520 | YDDDVIEVIDVETTE |
| flexi_NRBOX | 509 | 515 | DVIEVID | Yes | 506 | 520 | YDDDVIEVIDVETTE |
| SUMO_SIM_par | 507 | 515 | DDDVIEVID | Yes | 506 | 520 | YDDDVIEVIDVETTE |
| SUMO_SIM_anti | 507 | 515 | DDDVIEVID | Yes | 506 | 520 | YDDDVIEVIDVETTE |

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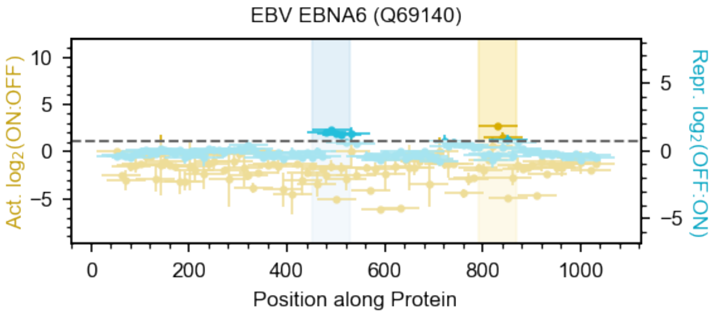
Extended activation domain from residues 751 to 840:
YQGYQEQPAPQAPYQGYQEQPPPQAPYQGYQEQPAPQAPYQGYQEPPAHGLQSSSYPGYAGPWTPRSQHPCYRHPWAPWSQDPVHGHTQG

Max tile of activation domain from residues 751 to 830 (estimated 34.6% to 37.2% of cells activated):
YQGYQEQPAPQAPYQGYQEQPPPQAPYQGYQEQPAPQAPYQGYQEPPAHGLQSSSYPGYAGPWTPRSQHPCYRHPWAPWS

## EBV EBNA6 (Q69140)

Gene: BERF3-BERF4 ; Protein Family: EBNA ; EBV Strain: AG876 (Type 2)



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Extended repression domain from residues 441 to 550:
DEAEEAQSTPERPGPSKQPSEPVEPAHTTPAGRSTVILHEPPREPEAVSFKPPPPPSRRRRGACVVYDDDIIEVIDVETTEEETTSMQRQPPLGQQPPPP VISTGSAMSS

Max tile of repression domain from residues 451 to 530 (estimated 25.8% to 37.2% of cells repressed):
ERPGPSKQPSEPVEPAHTTPAGRSTVILHEPPREPEAVSFKPPPPPSRRRRGACVVYDDDIIEVIDVETTEEETTSMQRQ

---

Extended activation domain from residues 791 to 880:
EEPRPPQAPFVGDYGFVQIPSAQWEPHPSQGTYQGHIDPQLPAALDLGPEQPRFPQDPYVYSGGQLSSCPGYAGPWPSRPQHPRYRHTLA

Max tile of activation domain from residues 791 to 870 (estimated 6.0% to 8.5% of cells activated):
EEPRPPQAPFVGDYGFVQIPSAQWEPHPSQGTYQGHIDPQLPAALDLGPEQPRFPQDPYVYSGGQLSSCPGYAGPWPSRP

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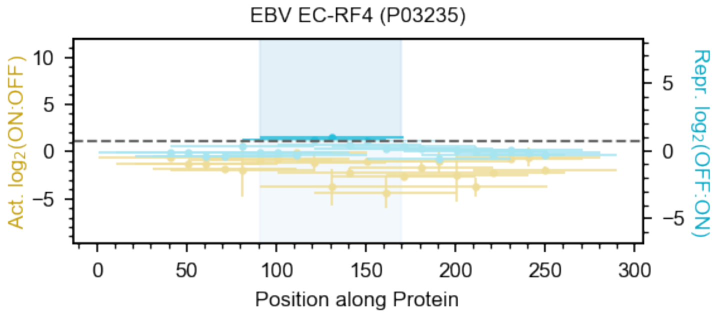
# EBV EC-RF4 (P03235)

Gene: EC-RF4 ; Protein Family: EC-RF4



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Extended repression domain from residues 81 to 170:
RQQDAPIAPGLLPCRPEDAGYLQDQVSLVGGRGEALLPQTLDIEGQGLVGGPGAVFTPDREVAHLTVVLELGVRVPVLEAGDGAAAAVPA

Max tile of repression domain from residues 91 to 170 (estimated 15.3% to 23.8% of cells repressed):
LLPCRPEDAGYLQDQVSLVGGRGEALLPQTLDIEGQGLVGGPGAVFTPDREVAHLTVVLELGVRVPVLEAGDGAAAAVPA

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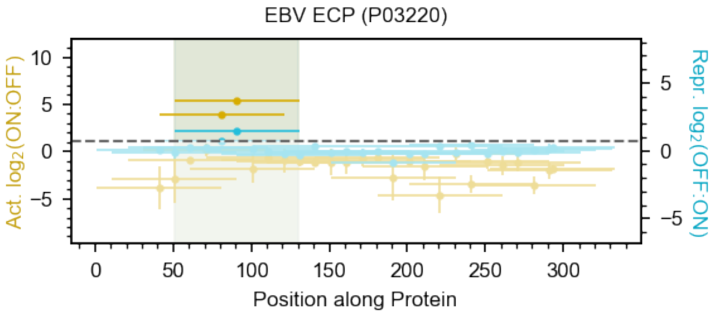
## EBV ECP (P03220)

Gene: BGLF3 ; Protein Family: ECP



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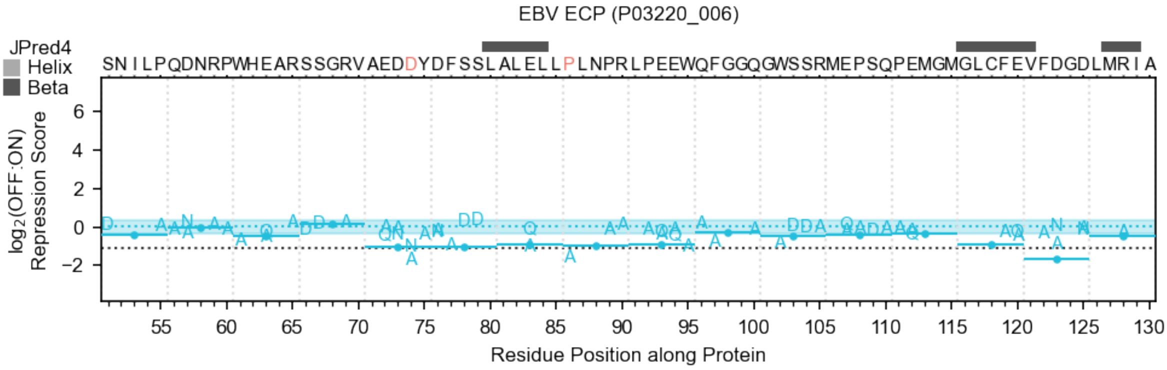
Extended repression domain from residues 41 to 130:
ETPLKSFLLVSNILPQDNRPWHEARSSGRVAEDDYDFSSLALELLPLNPRLPEEWQFGGQGWSSRMEPSQPEMGMGLCFEVFDGDLMRIA

Max tile of repression domain from residues 51 to 130 (estimated 25.5% to 31.9% of cells repressed):
SNILPQDNRPWHEARSSGRVAEDDYDFSSLALELLPLNPRLPEEWQFGGQGWSSRMEPSQPEMGMGLCFEVFDGDLMRIA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 121 | 125 | VFDGD |

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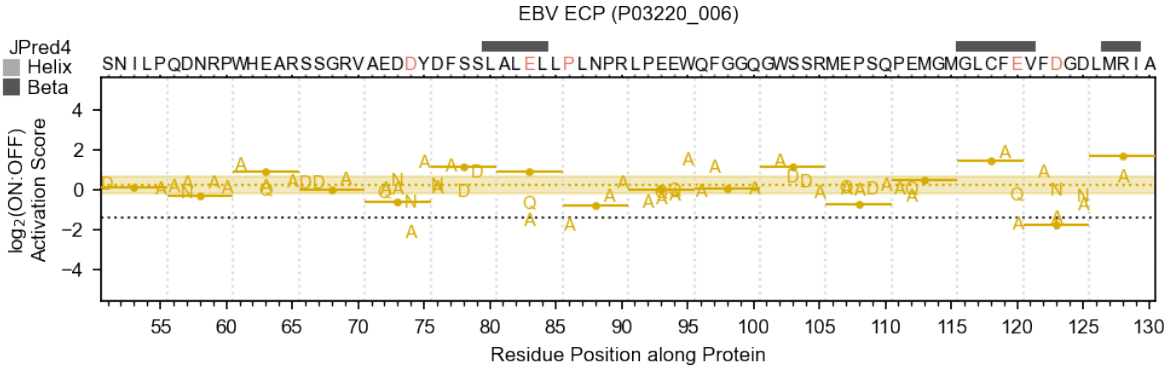
Extended activation domain from residues 41 to 130:
ETPLKSFLLVSNILPQDNRPWHEARSSGRVAEDDYDFSSLALELLPLNPRLPEEWQFGGQGWSSRMEPSQPEMGMGLCFEVFDGDLMRIA

Max tile of activation domain from residues 51 to 130 (estimated 41.2% to 43.4% of cells activated):
SNILPQDNRPWHEARSSGRVAEDDYDFSSLALELLPLNPRLPEEWQFGGQGWSSRMEPSQPEMGMGLCFEVFDGDLMRIA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 121 | 125 | VFDGD |

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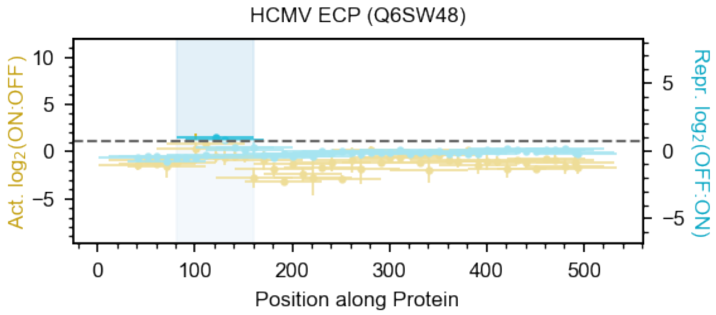
## HCMV ECP (Q6SW48)

Gene: UL95 ; Protein Family: ECP



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Extended repression domain from residues 81 to 170:
PSTAVRSPGSAGVSTSLCSVERMVELSAQSPAADFSVSEAWRFEEAVNMALVACEAVSPYDRFRLIETPDENFLLVTNVIPRESAEVPVL

Max tile of repression domain from residues 81 to 160 (estimated 18.2% to 20.2% of cells repressed):
PSTAVRSPGSAGVSTSLCSVERMVELSAQSPAADFSVSEAWRFEEAVNMALVACEAVSPYDRFRLIETPDENFLLVTNVI

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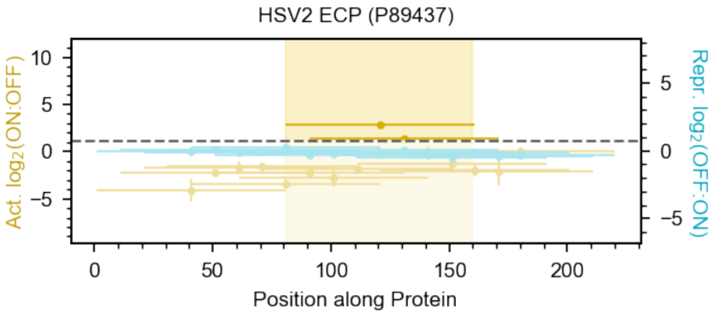
## HSV2 ECP (P89437)

Gene: UL14 ; Protein Family: ECP



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Extended activation domain from residues 81 to 170:
VEEQAARRDFLTAHRRYLDPALSERLDAADDRLADQEEQLEEAAANASLWGDGDLADGWMSPGDSDLLVMWQLTSAPKVHTDAPSRPGSR

Max tile of activation domain from residues 81 to 160 (estimated 6.8% to 7.7% of cells activated):
VEEQAARRDFLTAHRRYLDPALSERLDAADDRLADQEEQLEEAAANASLWGDGDLADGWMSPGDSDLLVMWQLTSAPKVH

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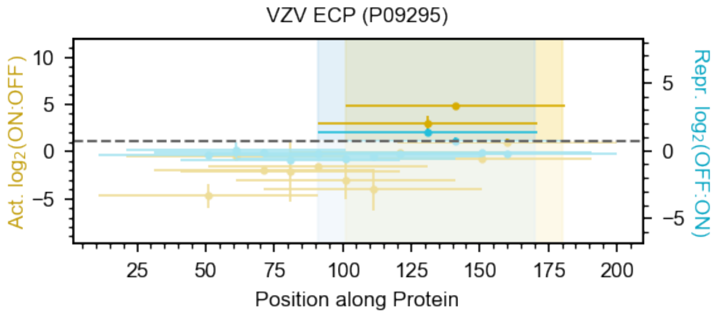
# VZV ECP (P09295)

Gene: ORF46 ; Protein Family: ECP



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Extended repression domain from residues 91 to 180:
IQQILNTNRRYIAPDFIRGLDKTEDDNTDNIDRLEDAVGPNIEHENHTWFGEDDEALLTQWMLTTHPPTSKYLQLQDLCVPTTIPTDMNQ

Max tile of repression domain from residues 91 to 170 (estimated 20.7% to 34.3% of cells repressed):
IQQILNTNRRYIAPDFIRGLDKTEDDNTDNIDRLEDAVGPNIEHENHTWFGEDDEALLTQWMLTTHPPTSKYLQLQDLCV

---

Extended activation domain from residues 91 to 180:
IQQILNTNRRYIAPDFIRGLDKTEDDNTDNIDRLEDAVGPNIEHENHTWFGEDDEALLTQWMLTTHPPTSKYLQLQDLCVPTTIPTDMNQ

Max tile of activation domain from residues 101 to 180 (estimated 26.9% to 37.7% of cells activated):
YIAPDFIRGLDKTEDDNTDNIDRLEDAVGPNIEHENHTWFGEDDEALLTQWMLTTHPPTSKYLQLQDLCVPTTIPTDMNQ

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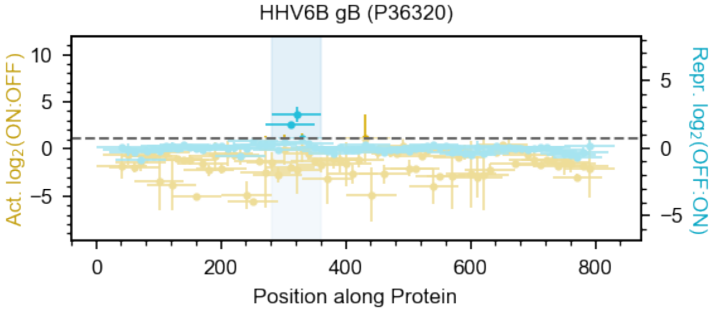
## HHV6B gB (P36320)

Gene: U39 ; Protein Family: gB



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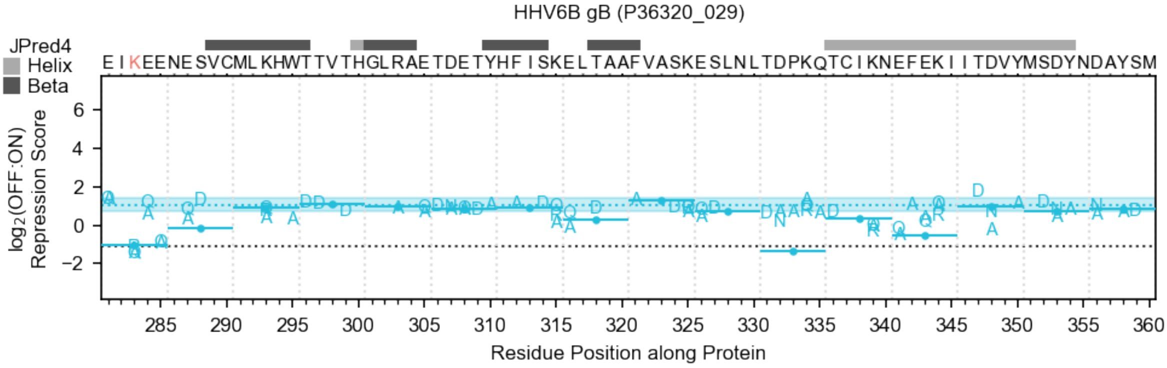
Extended repression domain from residues 271 to 370:
LEKGDTLFSWEIKEENESVCMLKHWTTVTHGLRAETDETYHFISKELTAAFVASKESLNLTDPKQTCIKNEFEKIITDVYMSDYNDAYSMNGSYQIFKTT

Max tile of repression domain from residues 281 to 360 (estimated 42.2% to 70.6% of cells repressed):
EIKEENESVCMLKHWTTVTHGLRAETDETYHFISKELTAAFVASKESLNLTDPKQTCIKNEFEKIITDVYMSDYNDAYSM



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 282 | 285 | IKEE | No | - | - | |
| SUMO_rev | 326 | 336 | ESLNLTDPKQT | Yes | 331 | 335 | TDPKQ |
| SUMO_for | 338 | 341 | IKNE | No | - | - | |
| flexi_NRBOX | 341 | 347 | EFEKIIT | No | - | - | |

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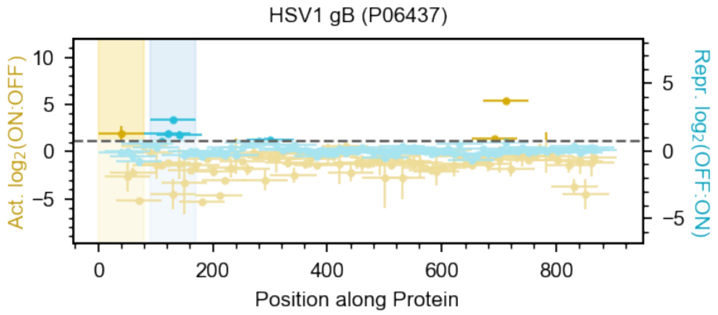
# HSV1 gB (P06437)

Gene: UL27 ; Protein Family: gB



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Extended activation domain from residues 1 to 80:
MHQGAPSWGRRWFVVWALLGLTLGVLVASAAPTSPGTPGVAAATQAANGGPATPAPPPLGAAPTGDPKPKKNKKPKNPTP

Max tile of activation domain from residues 1 to 80 (estimated 2.7% to 6.8% of cells activated):
MHQGAPSWGRRWFVVWALLGLTLGVLVASAAPTSPGTPGVAAATQAANGGPATPAPPPLGAAPTGDPKPKKNKKPKNPTP

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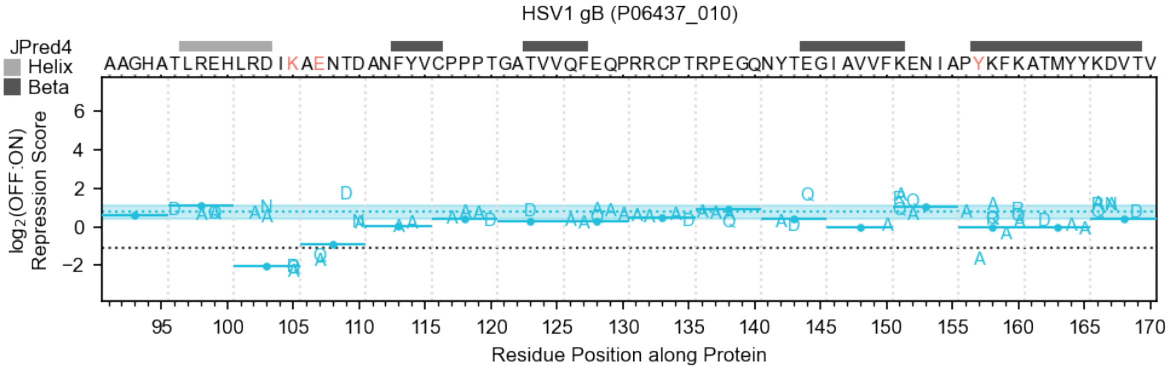
Extended repression domain from residues 81 to 180:
PRPAGDNATVAAGHATLREHLRDIKAENTDANFYVCPPPTGATVVQFEQPRRCPTRPEGQNYTEGIAVVFKENIAPYKFKATMYYKDVTVSQVWFGHRY
S

Max tile of repression domain from residues 91 to 170 (estimated 51.7% to 52.7% of cells repressed):
AAGHATLREHLRDIKAENTDANFYVCPPPTGATVVQFEQPRRCPTRPEGQNYTEGIAVVFKENIAPYKFKATMYYKDVTV



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_rev | 99 | 106 | EHLRDIKA | Yes | 101 | 105 | LRDIK |
| SUMO_for | 104 | 107 | IKAE | Yes | 101 | 105 | LRDIK |
| SUMO_SIM_anti | 143 | 150 | TEGIAVVF | No | - | - | |
| flexi_NRBOX | 145 | 151 | GIAVVFK | No | - | - | |

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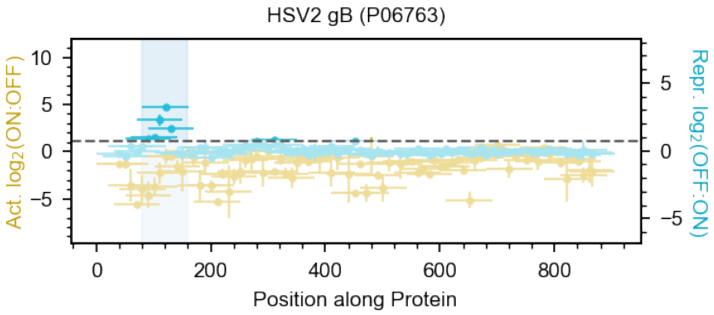
## HSV2 gB (P06763)

Gene: UL27 ; Protein Family: gB



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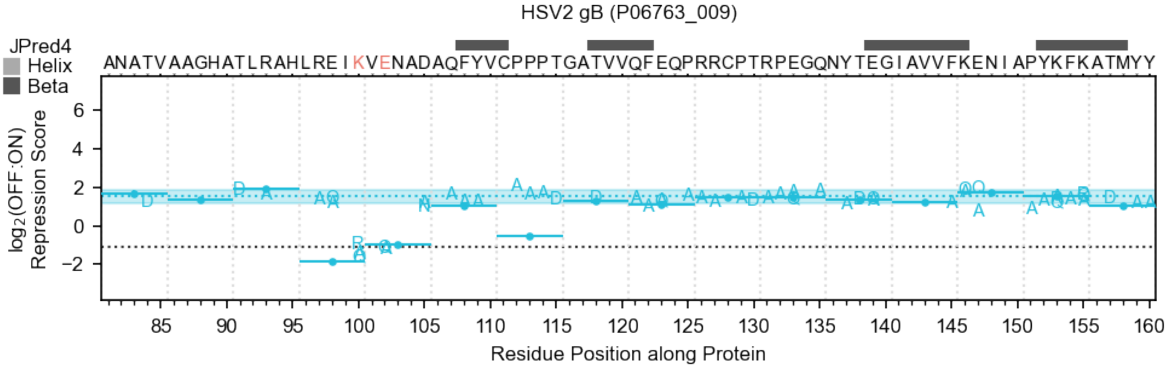
Extended repression domain from residues 51 to 170:
PPVPSPATTKARKRKTKKPPKRPEATPPPDANATVAAGHATLRAHLREIKVENADAQFYVCPPPTGATVVQFEQPRRCPTRPEGQNYTEGIAVVFKENIAPYKFKATMYYKDVTVSQVWF

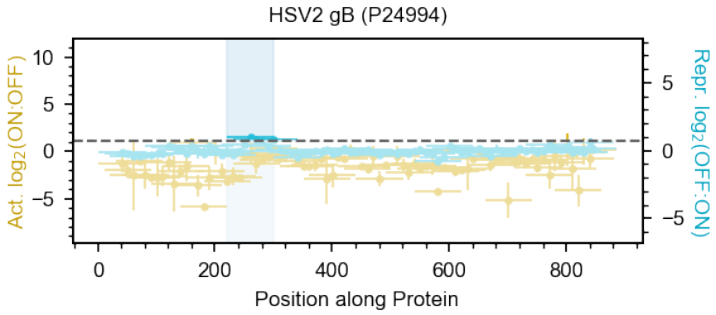
Max tile of repression domain from residues 81 to 160 (estimated 74.7% to 75.2% of cells repressed):
ANATVAAGHATLRAHLREIKVENADAQFYVCPPPTGATVVQFEQPRRCPTRPEGQNYTEGIAVVFKENIAPYKFKATMYY



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 99 | 102 | IKVE | Yes | 96 | 100 | LREIK |
| SUMO_SIM_anti | 138 | 145 | TEGIAVVF | No | - | - | |
| flexi_NRBOX | 140 | 146 | GIAVVFK | No | - | - | |

## HSV2 gB (P24994)

Gene: UL27 ; Protein Family: gB



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Extended repression domain from residues 221 to 310:
ATRTSRGWHTTDLKYNPARVEAFHRYGTTVNCIVEEVEARSVYPYDEFVLATGDFVYMSPFYGYRDGSHGEHTAYAADRFRQVDGYYERD

Max tile of repression domain from residues 221 to 300 (estimated 15.7% to 21.4% of cells repressed):
ATRTSRGWHTTDLKYNPARVEAFHRYGTTVNCIVEEVEARSVYPYDEFVLATGDFVYMSPFYGYRDGSHGEHTAYAADRF

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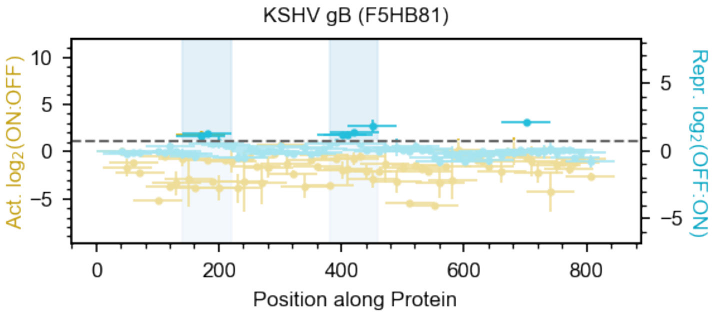
# KSHV gB (F5HB81)

Gene: ORF8 ; Protein Family: gB



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Extended repression domain from residues 131 to 220:
SAITNKYELPRPVPLYEISHMDSTYQCFSSMKVNVNGVENTFTDRDDVNTTVFLQPVEGLTDNIQRYFSQPVIYAEPGWFPGIYRVRTTV

Max tile of repression domain from residues 141 to 220 (estimated 23.6% to 24.7% of cells repressed):
RPVPLYEISHMDSTYQCFSSMKVNVNGVENTFTDRDDVNTTVFLQPVEGLTDNIQRYFSQPVIYAEPGWFPGIYRVRTTV

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Extended repression domain from residues 361 to 460:
SCLTSDINTTLNASKAKLASTHVPNGTVQYFHTTGGLYLVWQPMSAINLTHAQGDSGNPTSSPPPSASPMTTSASRRKRRSASTAAAGGGGSTDNLSYTQ

Max tile of repression domain from residues 381 to 460 (estimated 25.7% to 28.0% of cells repressed):
THVPNGTVQYFHTTGGLYLVWQPMSAINLTHAQGDSGNPTSSPPPSASPMTTSASRRKRRSASTAAAGGGGSTDNLSYTQ

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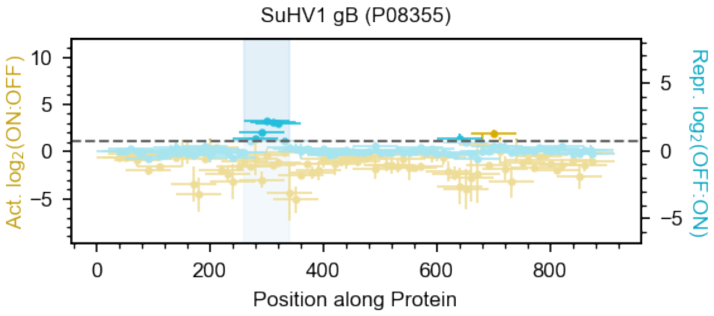
## SuHV1 gB (P08355)

Gene: - ; Protein Family: gB



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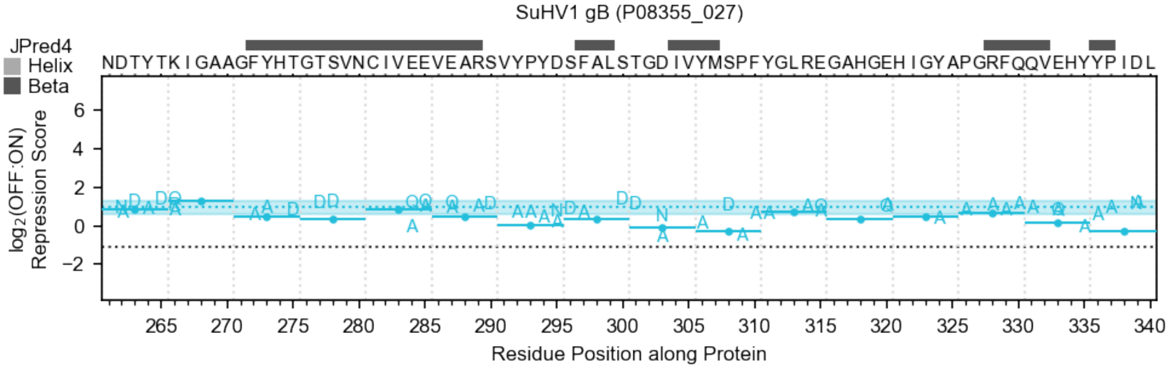
Extended repression domain from residues 231 to 370:
TAFDRDENPVEVDLRPSRLNALGTRGWHTTNDTYTKIGAAGFYHTGTSVNCIVEEVEARSVYPYDSFALSTGDIVYMSPFYGLREGAHGEHIGYAPGRFQQVEHYYPIDLDSRLRASESVTRNFLRTPHFTVAWDWAPKT

Max tile of repression domain from residues 261 to 340 (estimated 47.3% to 50.7% of cells represented):
NDTYTKIGAAGFYHTGTSVNCIVEEVEARSVYPYDSFALSTGDIVYMSPFYGLREGAHGEHIGYAPGRFQQVEHYYPIDL



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 278 | 284 | SVNCIVE | No | - | - | |

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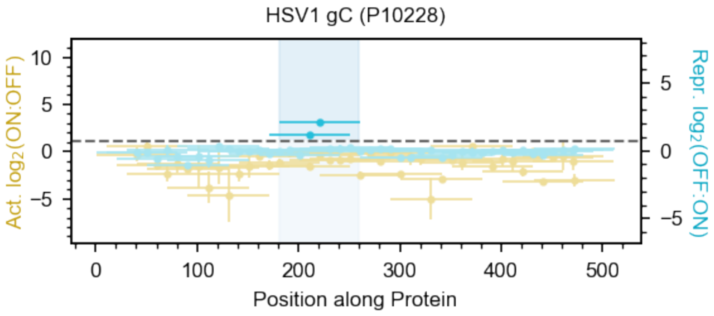
## HSV1 gC (P10228)

Gene: UL44 ; Protein Family: gC



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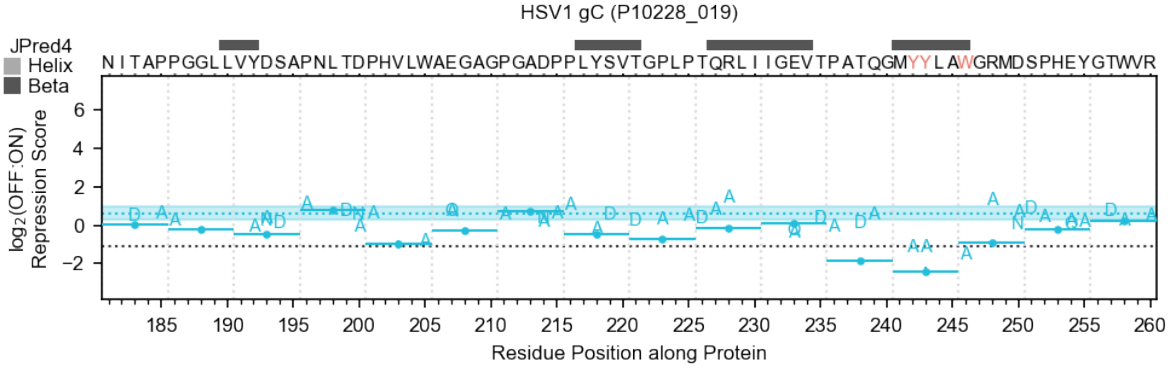
Extended repression domain from residues 171 to 260:
PAPDLEEVLTNITAPPGGLLVYDSAPNLTDPHVLWAEGAGPGADPPLYSVTGPLPTQRLIIGEVTPATQGMYYLAWGRMDSPHEYGTWVR

Max tile of repression domain from residues 181 to 260 (estimated 44.5% to 46.6% of cells repressed):
NITAPPGGLLVYDSAPNLTDPHVLWAEGAGPGADPPLYSVTGPLPTQRLIIGEVTPATQGMYYLAWGRMDSPHEYGTWVR



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| WW_1 | 215 | 218 | PPLY | No | - | - | |
| | - | - | | No | 236 | 245 | PATQGMYYLA |

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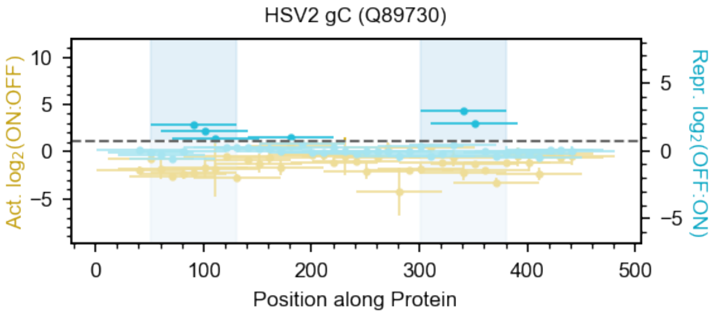
## HSV2 gC (Q89730)

Gene: UL44 ; Protein Family: gC



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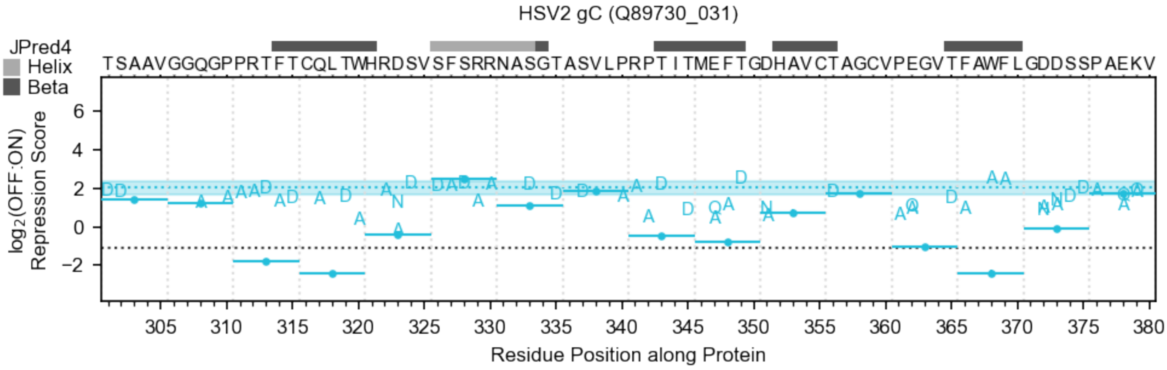
Extended repression domain from residues 51 to 150:
RNASAPRTTPTPPQPRKATKSKASTAKPAPPPKTGPPKTSSEPVRCNRHDPLARYGSRVQIRCRFPNSTRTEFRLQIWRYATATDAEIGTAPSLEEVMVN

Max tile of repression domain from residues 51 to 130 (estimated 35.8% to 45.4% of cells repressed):
RNASAPRTTPTPPQPRKATKSKASTAKPAPPPKTGPPKTSSEPVRCNRHDPLARYGSRVQIRCRFPNSTRTEFRLQIWRY

---

Extended repression domain from residues 301 to 390:
TSAAVGGQGPPRTFTCQLTWHRDSVSFSRRNASGTASVLPRPTITMEFTGDHAVCTAGCVPEGVTFAWFLGDDSSPAEKVAVASQTSCGR

Max tile of repression domain from residues 301 to 380 (estimated 67.1% to 71.2% of cells repressed):
TSAAVGGQGPPRTFTCQLTWHRDSVSFSRRNASGTASVLPRPTITMEFTGDHAVCTAGCVPEGVTFAWFLGDDSSPAEKV



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| WW_3 | 309 | 313 | GPPRT | Yes | 311 | 320 | PRTFTCQLTW |
| flexi_NRBOX | 365 | 371 | TFAWFLG | Yes | 366 | 370 | FAWFL |

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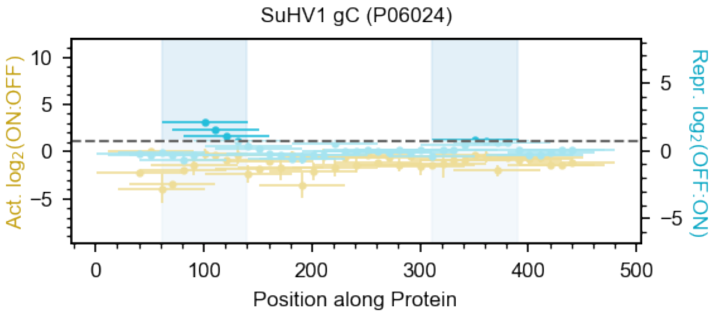
# SuHV1 gC (P06024)

Gene: - ; Protein Family: gC



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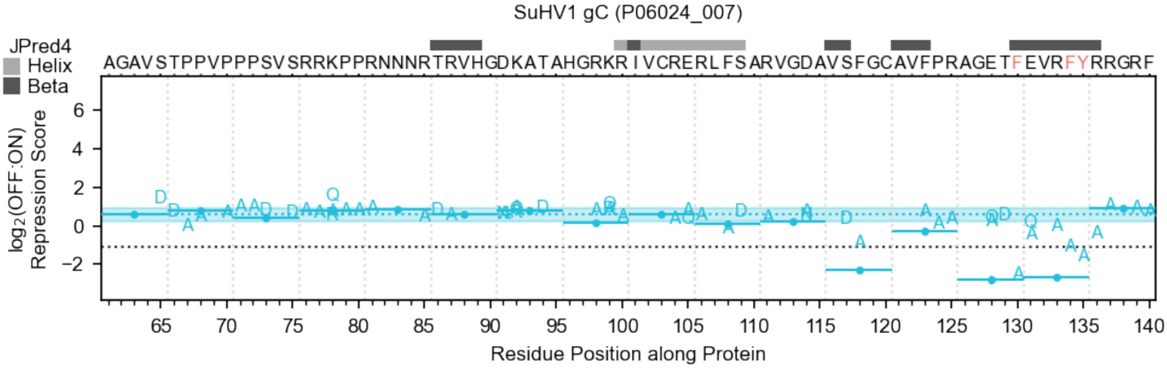
Extended repression domain from residues 61 to 160:
AGAVSTPPVPPPSVSRRKPPRNNNRTRVHGDKATAHGRKRIVCRERLFSARVGDAVSFGCAVFPRAGETFEVRFYRRGRFRSPDADPEYFDEPPRPELPR

Max tile of repression domain from residues 61 to 140 (estimated 47.1% to 48.2% of cells repressed):
AGAVSTPPVPPPSVSRRKPPRNNNRTRVHGDKATAHGRKRIVCRERLFSARVGDAVSFGCAVFPRAGETFEVRFYRRGRF



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| WW_3 | 78 | 82 | KPPRN | No | - | - | |
| | - | - | | No | 116 | 120 | VSFGC |
| | - | - | | No | 126 | 135 | AGETFEVRFY |

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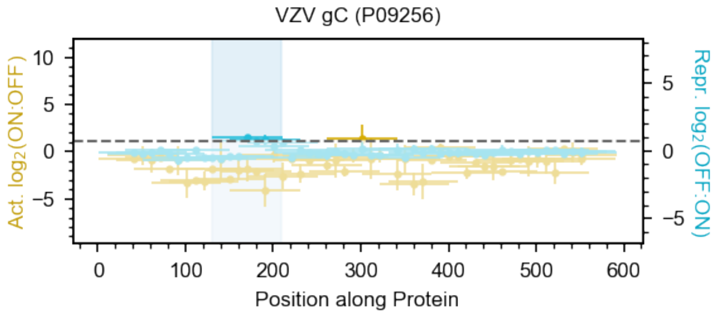
Extended repression domain from residues 311 to 400:
LAAADAADALAPSLRCEAVWYRDSVASQRFSEALRPHVYHPAAVSVRFVEGFAVCDGLCVPPEARLAWSDHAADTVYHLGACAEHPGLLN

Max tile of repression domain from residues 311 to 390 (estimated 14.5% to 18.6% of cells repressed):
LAAADAADALAPSLRCEAVWYRDSVASQRFSEALRPHVYHPAAVSVRFVEGFAVCDGLCVPPEARLAWSDHAADTVYHLG

## VZV gC (P09256)

Gene: ORF14 ; Protein Family: gC



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Extended repression domain from residues 131 to 230:
VAPTSAASRKPDPAVAPTSAATRKPDPAVAPTSAASRKPDPAANTQHSQPPFLYENIQCVHGGIQSIPYFHTFIMPCYMRLTTGQQAAFKQQQKTYEQYS

Max tile of repression domain from residues 131 to 210 (estimated 17.7% to 21.1% of cells repressed):
VAPTSAASRKPDPAVAPTSAATRKPDPAVAPTSAASRKPDPAANTQHSQPPFLYENIQCVHGGIQSIPYFHTFIMPCYMR

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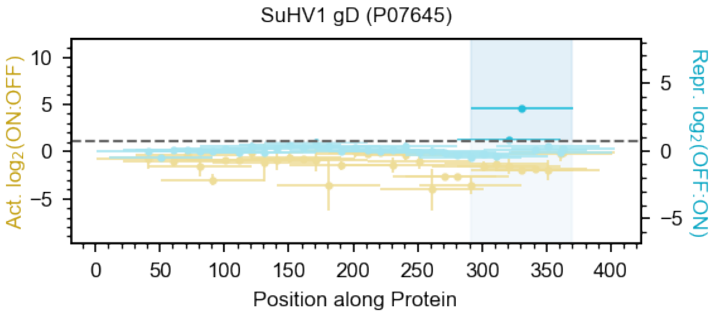
# SuHV1 gD (P07645)

Gene: - ; Protein Family: gD



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Extended repression domain from residues 281 to 370:
PEPAPATPAPPDRLPEPATRDHAAGGRPTPRPPRPETPHRPFAPPAVVPSGWPQPAEPFQPRTPAAPGVSRHRSVIVGTGTAMGALLVGV

Max tile of repression domain from residues 291 to 370 (estimated 70.4% to 75.8% of cells repressed):
PDRLPEPATRDHAAGGRPTPRPPRPETPHRPFAPPAVVPSGWPQPAEPFQPRTPAAPGVSRHRSVIVGTGTAMGALLVGV

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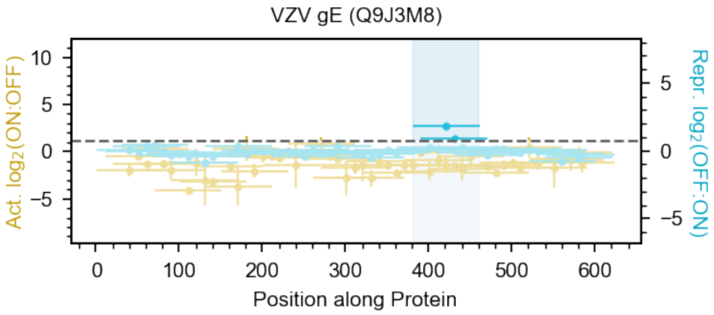
# VZV gE (Q9J3M8)

Gene: ORF68 ; Protein Family: gE



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Extended repression domain from residues 381 to 470:
VPIDPTCQPMRLYSTCLYHPNAPQCLSHMNSGCTFTSPHLAQRVASTVYQNCEHADNYTAYCLGISHMEPSFGLILHDGGTTLKFVDTPE

Max tile of repression domain from residues 381 to 460 (estimated 34.2% to 41.5% of cells repressed):
VPIDPTCQPMRLYSTCLYHPNAPQCLSHMNSGCTFTSPHLAQRVASTVYQNCEHADNYTAYCLGISHMEPSFGLILHDGG

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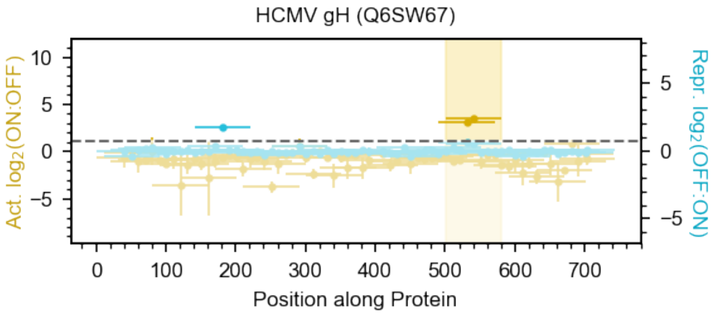
## HCMV gH (Q6SW67)

Gene: UL75 ; Protein Family: gH



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Extended activation domain from residues 491 to 580:
ETGLCSLAELSHFTQLLAHPHHEYLSDLYTPCSSSGRRDHSLERLTRLFPDATVPATVPAALSILSTMQPSTLETFPDLFCLPLGESFSA

Max tile of activation domain from residues 501 to 580 (estimated 9.7% to 15.8% of cells activated):
SHFTQLLAHPHHEYLSDLYTPCSSSGRRDHSLERLTRLFPDATVPATVPAALSILSTMQPSTLETFPDLFCLPLGESFSA

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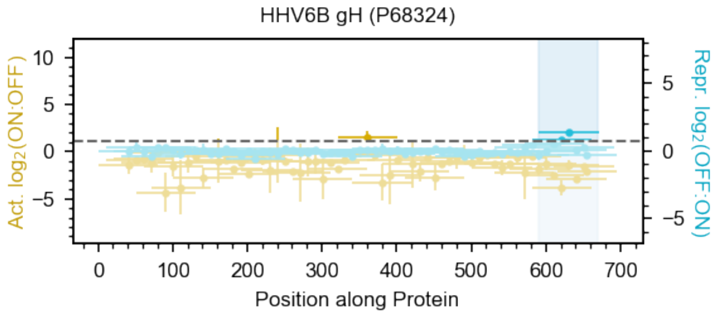
## HHV6B gH (P68324)

Gene: U48 ; Protein Family: gH



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Extended repression domain from residues 581 to 670:
YKYAGQDLLVLRNISSQTCEFCQSVVMEYDDIDGPLQYIYIKNIDELKTLTDPNNNLLVPNTRTHYLLLAKNGSVFEMSEVGIDIDQVSI

Max tile of repression domain from residues 591 to 670 (estimated 26.7% to 28.2% of cells repressed):
LRNISSQTCEFCQSVVMEYDDIDGPLQYIYIKNIDELKTLTDPNNNLLVPNTRTHYLLLAKNGSVFEMSEVGIDIDQVSI

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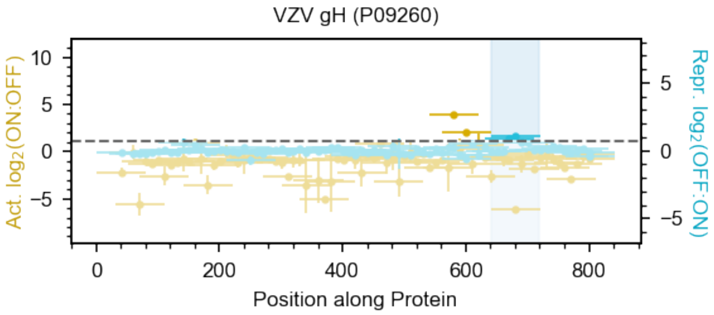
## VZV gH (P09260)

Gene: ORF37 ; Protein Family: gH



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Extended repression domain from residues 631 to 720:
AKDLHILHTHVPEVFTCQDAAARNGEYVLILPAVQGHSYVITRNKPQRGLVYSLADVDVYNPISVVYLSRDTCVSEHGVIETVALPHPDN

Max tile of repression domain from residues 641 to 720 (estimated 17.2% to 25.2% of cells repressed):
VPEVFTCQDAAARNGEYVLILPAVQGHSYVITRNKPQRGLVYSLADVDVYNPISVVYLSRDTCVSEHGVIETVALPHPDN

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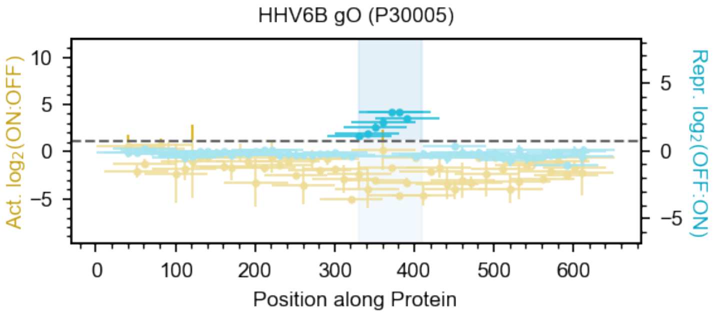
## HHV6B gO (P30005)

Gene: U47 ; Protein Family: gO



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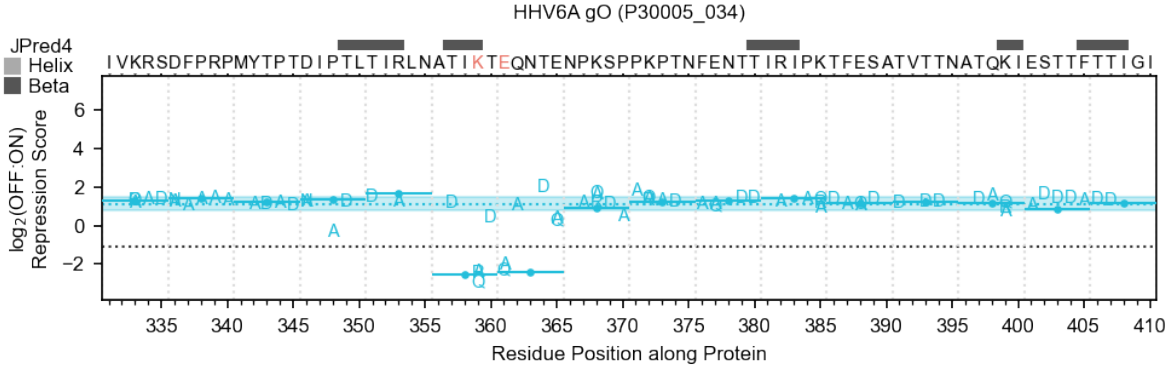
Extended repression domain from residues 291 to 430:
IPTPEPPPVTKNSTKLHTDTIKVTPNTPTITTQTTESIKKIVKRSDFPRPMYTPTDIPTLTIRLNATIKTEQNTENPKSPPKPTNFENTTIRIPKTFESATVTTNATQKIESTTFTTIGIKEINGNTYSSPKNSIYLKSK

Max tile of repression domain from residues 331 to 410 (estimated 62.7% to 69.2% of cells repressed):
IVKRSDFPRPMYTPTDIPTLTIRLNATIKTEQNTENPKSPPKPTNFENTTIRIPKTFESATVTTNATQKIESTTFTTIGI



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 358 | 361 | IKTE | Yes | 356 | 365 | ATIKTEQNTE |

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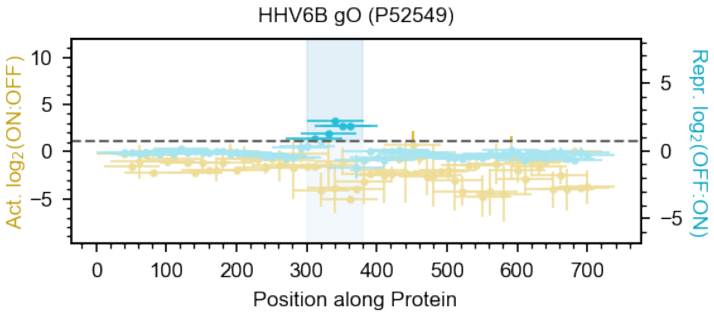
## HHV6B gO (P52549)

Gene: U47 ; Protein Family: gO



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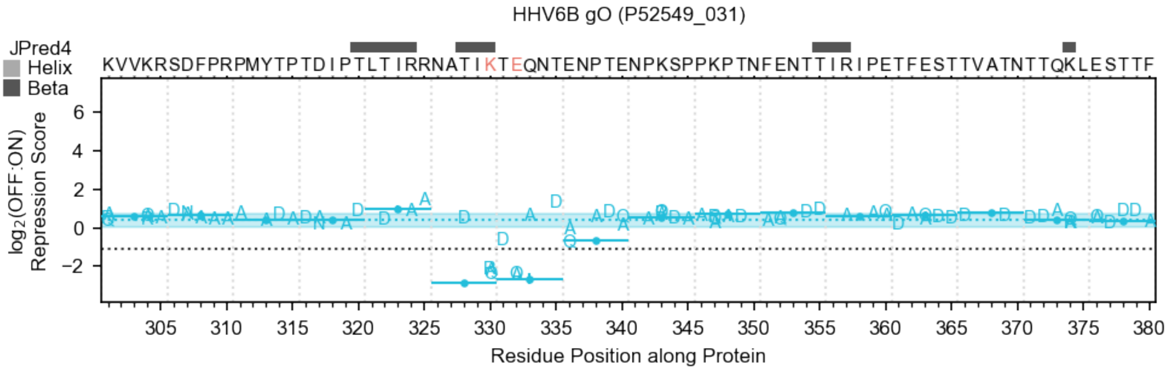
Extended repression domain from residues 271 to 400:
TKNFTELQTDTIKVTPNTPTITAQTTESIKKVVKRSDFPRPMYTPTDIPTLTIRRNATIKTEQNTENPTENPKSPPKPTNFENTTIRIPETFESTTVATNTTQKLESTTFATTIGIEEISDNIYSSPKNS

Max tile of repression domain from residues 301 to 380 (estimated 49.6% to 49.9% of cells represed):
KVVKRSDFPRPMYTPTDIPTLTIRRNATIKTEQNTENPTENPKSPPKPTNFENTTIRIPETFESTTVATNTTQKLESTTF



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 329 | 332 | IKTE | Yes | 326 | 335 | NATIKTEQNT |

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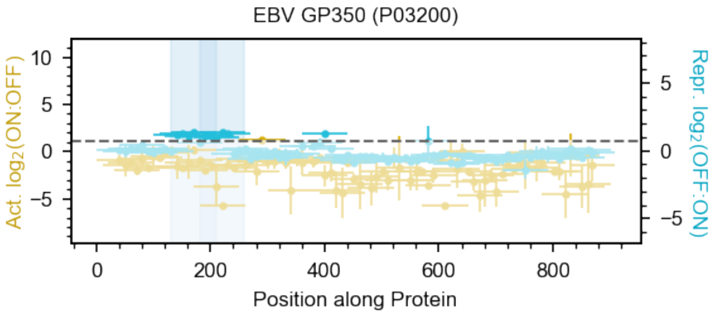
## EBV GP350 (P03200)

Gene: BLLF1 ; Protein Family: GP350



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Extended repression domain from residues 101 to 210:
ELALTMRSKKLPINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTNITAVVRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIE

Max tile of repression domain from residues 131 to 210 (estimated 26.9% to 27.0% of cells repressed):
YFQDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTNITAVVRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIE

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Extended repression domain from residues 151 to 270:
YLIPETVPYIKWDNCNSTNITAVVRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRP

Max tile of repression domain from residues 181 to 260 (estimated 22.1% to 30.9% of cells repressed):
VTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGTGY

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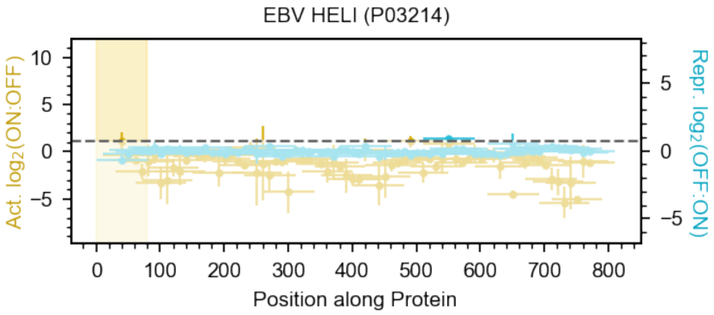
# EBV HELI (P03214)

Gene: BBLF4 ; Protein Family: HELI



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Extended activation domain from residues 1 to 80:
MAEEPRAPEALSSTFMLNMTSDASVRRIVRRIGTLARRRVQQLPDMETFSPEFDPELSEPPFLPFSAYVITGTAGAGKST

Max tile of activation domain from residues 1 to 80 (estimated 1.7% to 4.2% of cells activated):
MAEEPRAPEALSSTFMLNMTSDASVRRIVRRIGTLARRRVQQLPDMETFSPEFDPELSEPPFLPFSAYVITGTAGAGKST

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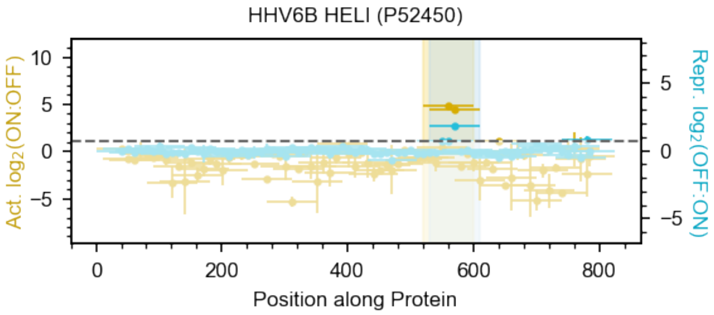
## HHV6B HELI (P52450)

Gene: U77 ; Protein Family: HELI



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Extended activation domain from residues 521 to 610:
CSEFTTPEVLMEIKNIKMPSIEFLESEMSRMSRDVQTVETDERYDFGLVDDGLSDMDLLEIDPCGDPFFTRYSKLPLTNSLSFEEISLLY

Max tile of activation domain from residues 521 to 600 (estimated 31.3% to 33.0% of cells activated):
CSEFTTPEVLMEIKNIKMPSIEFLESEMSRMSRDVQTVETDERYDFGLVDDGLSDMDLLEIDPCGDPFFTRYSKLPLTNS

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Extended repression domain from residues 511 to 610:
LMFGGMYSFCCSEFTTPEVLMEIKNIKMPSIEFLESEMSRMSRDVQTVETDERYDFGLVDDGLSDMDLLEIDPCGDPFFTRYSKLPLTNSLSFEEISLLY

Max tile of repression domain from residues 531 to 610 (estimated 37.3% to 40.3% of cells repressed):
MEIKNIKMPSIEFLESEMSRMSRDVQTVETDERYDFGLVDDGLSDMDLLEIDPCGDPFFTRYSKLPLTNSLSFEEISLLY

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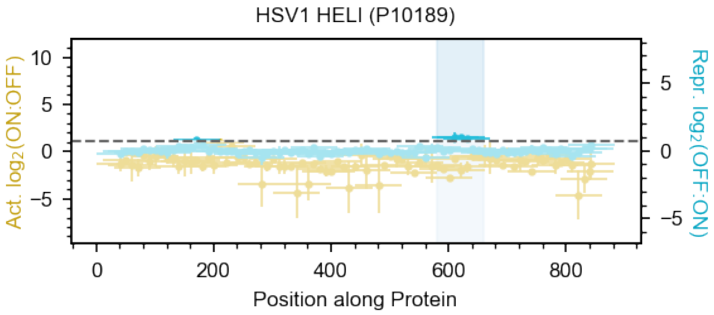
## HSV1 HELI (P10189)

Gene: UL5 ; Protein Family: HELI



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Extended repression domain from residues 571 to 670:
TLAYARMGELTAEILSLRPKSSGVPTQASVMADAGAPGERAFDFKQLGPRDGGPDDFPDDDLDVIFAGLDEQQLDVFYCHYTPGEPETTAAVHTQFALLK

Max tile of repression domain from residues 581 to 660 (estimated 17.8% to 20.5% of cells repressed):
TAEILSLRPKSSGVPTQASVMADAGAPGERAFDFKQLGPRDGGPDDFPDDDLDVIFAGLDEQQLDVFYCHYTPGEPETTA

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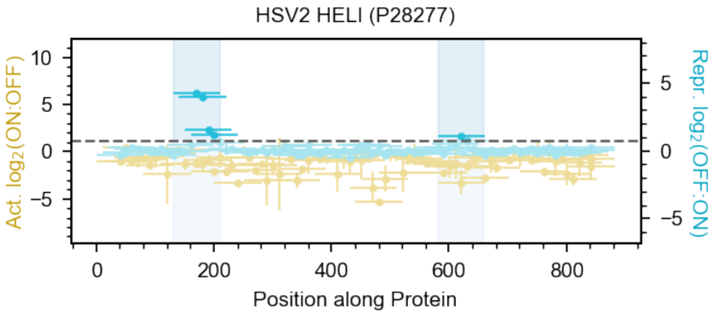
# HSV2 HELI (P28277)

Gene: UL5 ; Protein Family: HELI



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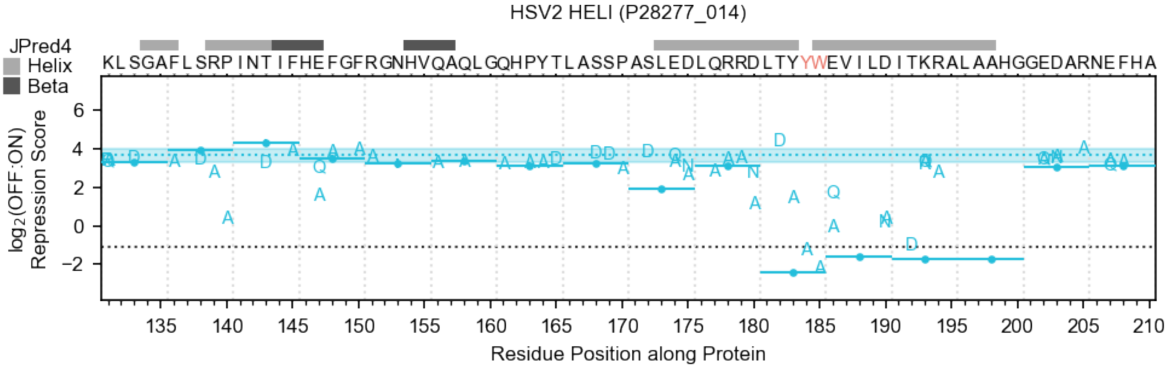
Extended repression domain from residues 131 to 240:
KLSGAFLSRPINTIFHEFGFRGNHVQAQLGQHPYTLASSPASLEDLQRRDLTYYWEVILDITKRALAAHGGEDARNEFHALTALEQTLGLGQGALTRLASVTHGALPAFT

Max tile of repression domain from residues 131 to 210 (estimated 90.9% to 91.1% of cells repressed):
KLSGAFLSRPINTIFHEFGFRGNHVQAQLGQHPYTLASSPASLEDLQRRDLTYYWEVILDITKRALAAHGGEDARNEFHA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| CtBP_expanded | 170 | 174 | PASLE | No | - | - | |
| flexi_NRBOX | 184 | 190 | YWEVILD | Yes | 181 | 200 | LTYYWEVILDITKRALAAHG |
| SUMO_SIM_par | 186 | 192 | EVILDIT | Yes | 181 | 200 | LTYYWEVILDITKRALAAHG |

---

Extended repression domain from residues 581 to 670:
AELLSLRRDAAGASATRAADTSDRSPGERAFNFKHLGPRDGGPDDFPDDDLDVIFAGLDEQQLDVFYCHYALEEPETTAAVHAQFGLLKR

Max tile of repression domain from residues 581 to 660 (estimated 20.5% to 20.6% of cells repressed):
AELLSLRRDAAGASATRAADTSDRSPGERAFNFKHLGPRDGGPDDFPDDDLDVIFAGLDEQQLDVFYCHYALEEPETTAA

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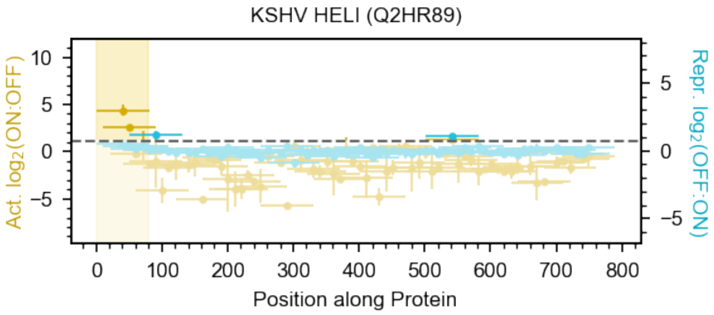
## KSHV HELI (Q2HR89)

Gene: ORF44 ; Protein Family: HELI



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Extended activation domain from residues 1 to 90:
MDSSEGCTDMDEPSPGFILNMTSDAKVRSVVEQIDRLSNITTSPPEMGWYDLEFDPLEDEGPFLPFSAYVITGTAGAGKSTSVSALHQNL

Max tile of activation domain from residues 1 to 80 (estimated 14.7% to 33.6% of cells activated):
MDSSEGCTDMDEPSPGFILNMTSDAKVRSVVEQIDRLSNITTSPPEMGWYDLEFDPLEDEGPFLPFSAYVITGTAGAGKS

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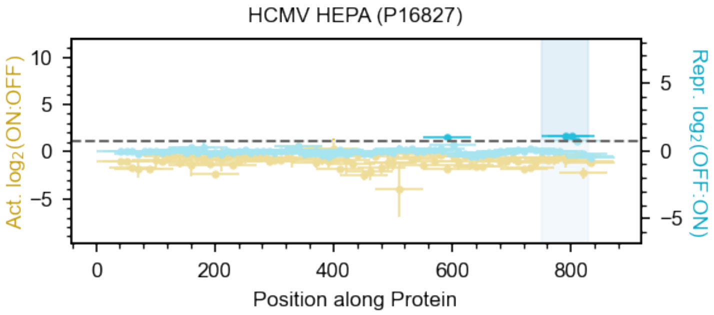
# HCMV HEPA (P16827)

Gene: UL102 ; Protein Family: HEPA



---

Extended repression domain from residues 751 to 850:
AEQGQIIVQSRDTALAADIGYGVYVDKAFAMLTACVEVWARELLSSSTASTTACSSSSVLSSALPSVTSSSSGTATVSPPSCSSSSATWLEERDEWVRSL

Max tile of repression domain from residues 751 to 830 (estimated 18.7% to 23.5% of cells repressed):
AEQGQIIVQSRDTALAADIGYGVYVDKAFAMLTACVEVWARELLSSSTASTTACSSSSVLSSALPSVTSSSSGTATVSPP

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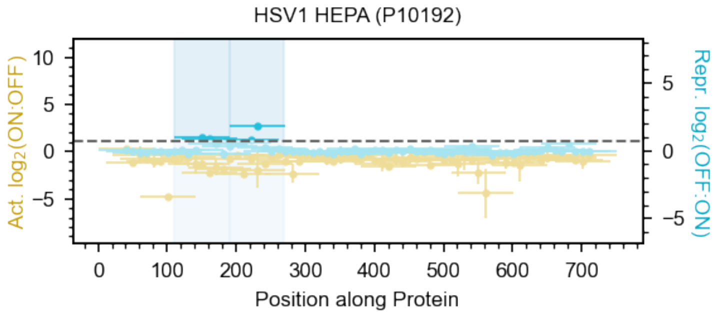
## HSV1 HEPA (P10192)

Gene: UL8 ; Protein Family: HEPA



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Extended repression domain from residues 111 to 200:
RQTGPVALFAPLRIGSDPRTGLVVKVERASWGPPAAPRAALLVAEANIDIDPMALAARVAEHPDARLAWARLAAIRDTPQCASAASLTVN

Max tile of repression domain from residues 111 to 190 (estimated 16.8% to 20.5% of cells repressed):
RQTGPVALFAPLRIGSDPRTGLVVKVERASWGPPAAPRAALLVAEANIDIDPMALAARVAEHPDARLAWARLAAIRDTPQ

---

Extended repression domain from residues 181 to 270:
RLAAIRDTPQCASAASLTVNITTGTALFAREYQTLAFPPIKKEGAFGDLVEVCEVGLRPRGHPQRVTARVLLPRDYDYFVSAGEKFSAPA

Max tile of repression domain from residues 191 to 270 (estimated 32.0% to 45.2% of cells repressed):
CASAASLTVNITTGTALFAREYQTLAFPPIKKEGAFGDLVEVCEVGLRPRGHPQRVTARVLLPRDYDYFVSAGEKFSAPA

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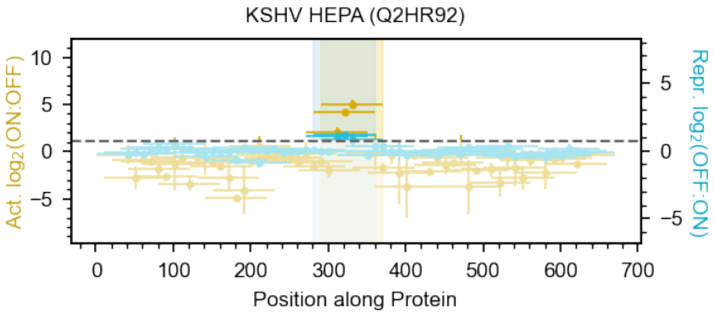
# KSHV HEPA (Q2HR92)

Gene: ORF40 ; Protein Family: HEPA



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Extended repression domain from residues 271 to 370:
EEGTAFAPLLPAFPCIPLRYGSPTSLDRASVQWDLFEPHILTHFDGIKRTSLADTVFGYDSLAISRECEDQYVWPTPVTDININLCTDSDTMAIVREPSG

Max tile of repression domain from residues 281 to 360 (estimated 20.0% to 27.5% of cells repressed):
PAFPCIPLRYGSPTSLDRASVQWDLFEPHILTHFDGIKRTSLADTVFGYDSLAISRECEDQYVWPTPVTDININLCTDSD

---

Extended activation domain from residues 271 to 370:
EEGTAFAPLLPAFPCIPLRYGSPTSLDRASVQWDLFEPHILTHFDGIKRTSLADTVFGYDSLAISRECEDQYVWPTPVTDININLCTDSDTMAIVREPSG

Max tile of activation domain from residues 291 to 370 (estimated 26.8% to 45.0% of cells activated):
GSPTSLDRASVQWDLFEPHILTHFDGIKRTSLADTVFGYDSLAISRECEDQYVWPTPVTDININLCTDSDTMAIVREPSG

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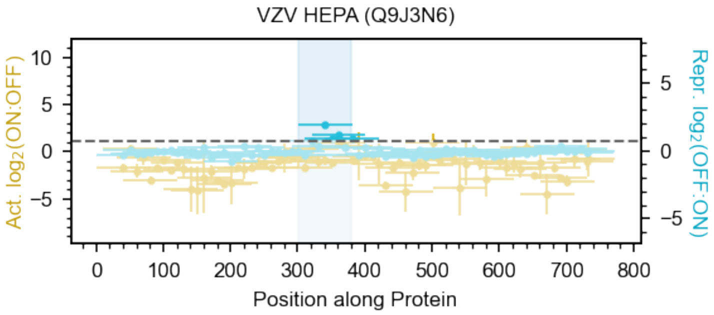
# VZV HEPA (Q9J3N6)

Gene: ORF52 ; Protein Family: HEPA



---

Extended repression domain from residues 301 to 400:
FAYLGPELNPKGEDRDYFCTVGFPGWTTLRTQTPAVESIRTATEMYMETDGLWPVTGIQAFHYLAPWGQHPPLPPRVQDLIGQIPQDTGHADATVNWDAG

Max tile of repression domain from residues 301 to 380 (estimated 39.5% to 41.3% of cells repressed):
FAYLGPELNPKGEDRDYFCTVGFPGWTTLRTQTPAVESIRTATEMYMETDGLWPVTGIQAFHYLAPWGQHPPLPPRVQDL

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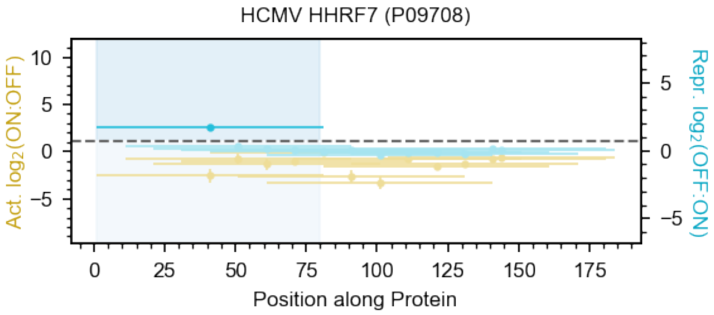
# HCMV HHRF7 (P09708)

Gene: US32 ; Protein Family: HHRF7



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Extended repression domain from residues 1 to 80:
MAMYTSESERDWRRVIHDSHGLWCDCGDWREHLYCVYDSHFQRRPTTRAERRAANWRRQMRRLHRLWCFCQDWKCHALYA

Max tile of repression domain from residues 1 to 80 (estimated 33.7% to 40.0% of cells repressed):
MAMYTSESERDWRRVIHDSHGLWCDCGDWREHLYCVYDSHFQRRPTTRAERRAANWRRQMRRLHRLWCFCQDWKCHALYA

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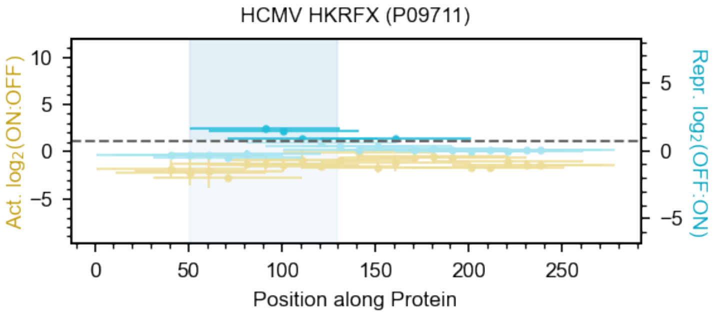
## HCMV HKRFX (P09711)

Gene: J1I ; Protein Family: HKRFX



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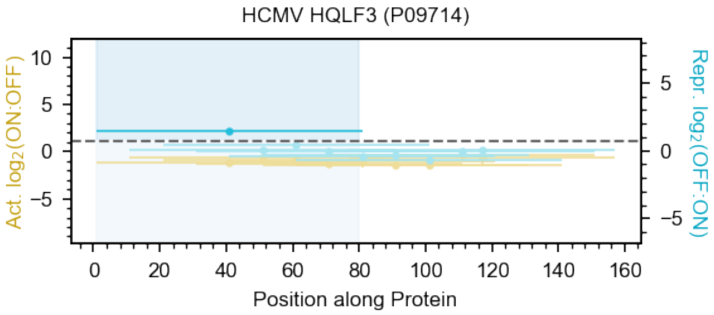
Extended repression domain from residues 51 to 150:
DTGKDRGTHRQRAETPSRSPVPTTNTVGRHAPAVRRQRRTQHAYGPQHSLEDPPRGPAPAVFWVCRGAAGWVCAGCVAGVCWVCRGCVGRVCQGVSRACA

Max tile of repression domain from residues 51 to 130 (estimated 31.2% to 39.2% of cells repressed):
DTGKDRGTHRQRAETPSRSPVPTTNTVGRHAPAVRRQRRTQHAYGPQHSLEDPPRGPAPAVFWVCRGAAGWVCAGCVAGV

---

## HCMV HQLF3 (P09714)

Gene: US1 ; Protein Family: HQLF3



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Extended repression domain from residues 1 to 80:
MASGLGDLSVGVSSLPMRELAWRRVADDSHDLWCCCMDWKAHVEYAHPASELRPGSGGWPEHAEAQWRQQVHAAHDVWCN

Max tile of repression domain from residues 1 to 80 (estimated 29.1% to 29.6% of cells repressed):
MASGLGDLSVGVSSLPMRELAWRRVADDSHDLWCCCMDWKAHVEYAHPASELRPGSGGWPEHAEAQWRQQVHAAHDVWCN

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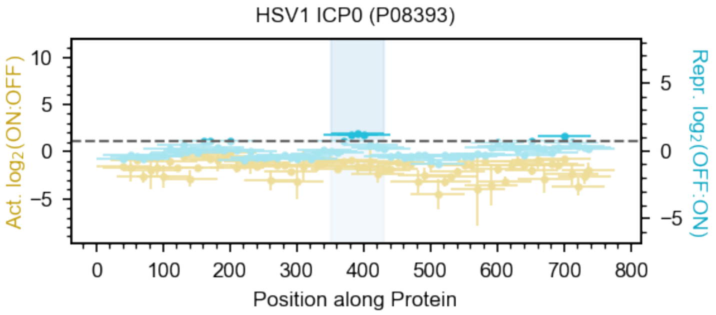
# HSV1 ICP0 (P08393)

Gene: RL2 ; Protein Family: ICP0



---

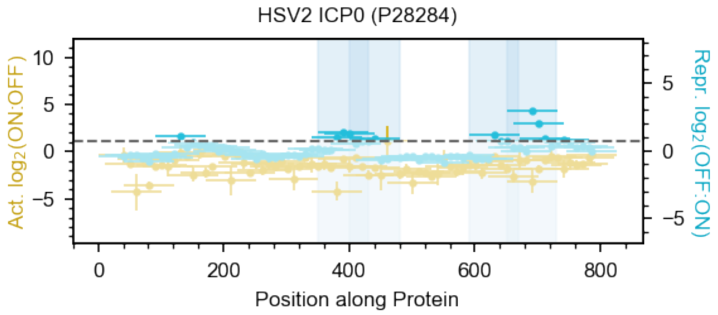
Extended repression domain from residues 331 to 440:
VGVVEAEAGRPRGRTGPLVNRPAPLANNRDPIVISDSPPASPHRPPAAPMPGSAPRPGPPASAAASGPARPRAAVAPCVRAPPPGPGPRAPAPGAEPAARPADARRVPQS

Max tile of repression domain from residues 351 to 430 (estimated 23.6% to 26.0% of cells repressed):
RPAPLANNRDPIVISDSPPASPHRPPAAPMPGSAPRPGPPASAAASGPARPRAAVAPCVRAPPPGPGPRAPAPGAEPAAR

---

## HSV2 ICP0 (P28284)

Gene: RL2 ; Protein Family: ICP0



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Extended repression domain from residues 341 to 440:
DAAAAEGRTPPARQPRAAQEPPIVISDSPPPSPRRPAGPGPLSFVSSSSAQVSSGPGGGGLPQSSGRAARPRAAVAPRVRSPPRAAAAPVVSASADAAGP

Max tile of repression domain from residues 351 to 430 (estimated 27.6% to 28.5% of cells repressed):
PARQPRAAQEPPIVISDSPPPSPRRPAGPGPLSFVSSSSAQVSSGPGGGGLPQSSGRAARPRAAVAPRVRSPPRAAAAPV

---

Extended repression domain from residues 381 to 480:
PLSFVSSSSAQVSSGPGGGGLPQSSGRAARPRAAVAPRVRSPPRAAAAPVVSASADAAGPAPPAVPVDAHRAPRSRMTQAQTDTQAQSLGRAGATDARGS

Max tile of repression domain from residues 401 to 480 (estimated 16.5% to 18.3% of cells repressed):
LPQSSGRAARPRAAVAPRVRSPPRAAAAPVVSASADAAGPAPPAVPVDAHRAPRSRMTQAQTDTQAQSLGRAGATDARGS

---

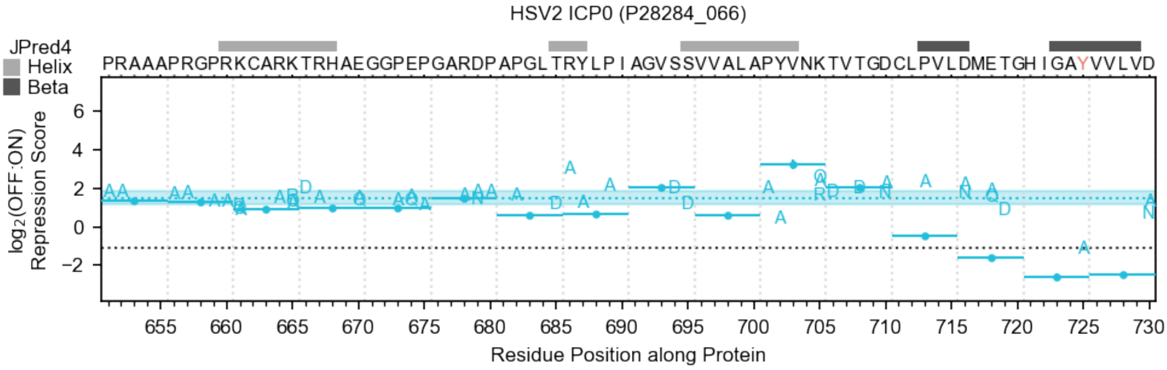
Extended repression domain from residues 591 to 690:
SSSASSSSASSSSASSSSASSSSASSSSASSSSASSSAGGAGGSVASASGAGERRETSLGPRAAAPRGPRKCARKTRHAEGGPEPGARDPAPGLTRYLPI

Max tile of repression domain from residues 591 to 670 (estimated 21.2% to 25.8% of cells repressed):
SSSASSSSASSSSASSSSASSSSASSSSASSSSASSSAGGAGGSVASASGAGERRETSLGPRAAAPRGPRKCARKTRHAE

---

Extended repression domain from residues 651 to 750:
PRAAAPRGPRKCARKTRHAEGGPEPGARDPAPGLTRYLPIAGVSSVVALAPYVNKTVTGDCLPVLDMETGHIGAYVVLVDQTGNVADLLRAAAPAWSRRT

Max tile of repression domain from residues 651 to 730 (estimated 68.8% to 70.6% of cells repressed):
PRAAAPRGPRKCARKTRHAEGGPEPGARDPAPGLTRYLPIAGVSSVVALAPYVNKTVTGDCLPVLDMETGHIGAYVVLVD



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 692 | 698 | GVSSVVA | No | - | - | |
| flexi_NRBOX | 721 | 727 | HIGAYVV | Yes | 716 | 730 | DMETGHIGAYVVLVD |
| SUMO_SIM_par | 725 | 730 | YVVLVD | Yes | 716 | 730 | DMETGHIGAYVVLVD |

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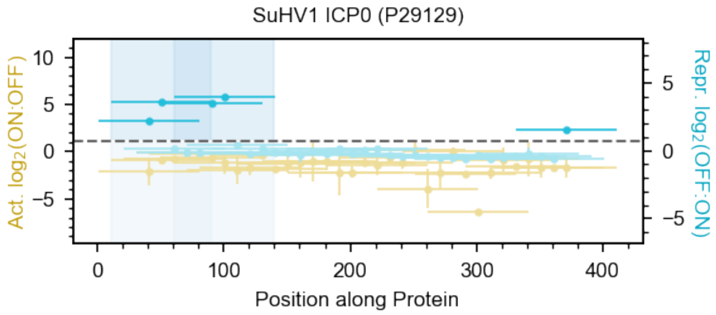
## SuHV1 ICP0 (P29129)

Gene: EP0 ; Protein Family: ICP0



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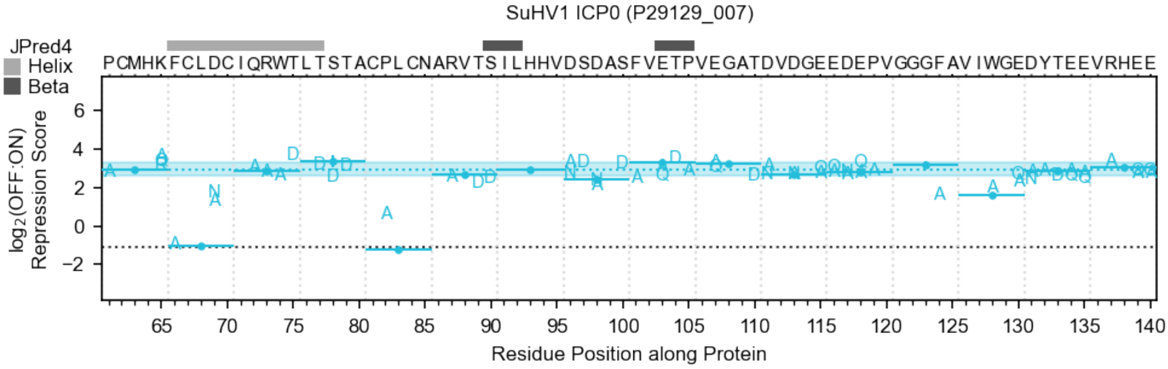
Extended repression domain from residues 1 to 90:
MGCTVSRRRTTTAEASSAWGIFGFYRPRSPSPPPQRLSLPLTVMDCPICLDVAATEAQTLPCMHKFCLDCIQRWTLTSTACPLCNARVTS

Max tile of repression domain from residues 11 to 90 (estimated 81.2% to 83.6% of cells repressed):
TTAEASSAWGIFGFYRPRSPSPPPQRLSLPLTVMDCPICLDVAATEAQTLPCMHKFCLDCIQRWTLTSTACPLCNARVTS

---

Extended repression domain from residues 51 to 140:
DVAATEAQTLPCMHKFCLDCIQRWTLTSTACPLCNARVTSILHHVDSDASFVETPVEGATDVDGEEDEPVGGGFAVIWGEDYTEEVRHEE

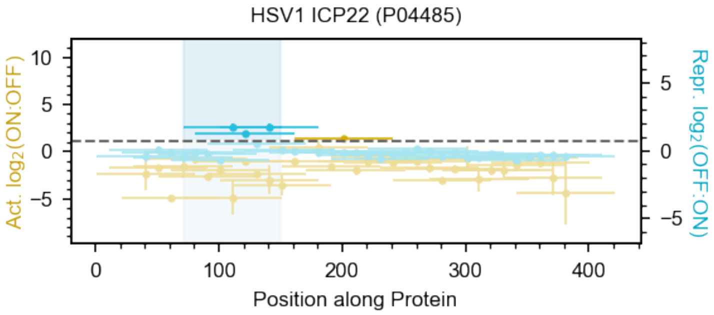
Max tile of repression domain from residues 61 to 140 (estimated 87.6% to 87.6% of cells repressed):
PCMHKFCLDCIQRWTLTSTACPLCNARVTSILHHVDSDASFVETPVEGATDVDGEEDEPVGGGFAVIWGEDYTEEVRHEE



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 81 | 85 | CPLCN |
| flexi_NRBOX | 87 | 93 | RVTSILH | No | - | - | |

## HSV1 ICP22 (P04485)

Gene: US1 ; Protein Family: ICP22



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Extended repression domain from residues 71 to 160:
PRIGGRRAPRRLGGRFFLDMSAESTTGTETDASVSDDPDDTSDWSYDDIPPRPKRARVNLRLTSSPDRRDGVIFPKMGRVRSTRETQPRA

Max tile of repression domain from residues 71 to 150 (estimated 31.0% to 43.6% of cells repressed):
PRIGGRRAPRRLGGRFFLDMSAESTTGTETDASVSDDPDDTSDWSYDDIPPRPKRARVNLRLTSSPDRRDGVIFPKMGRV

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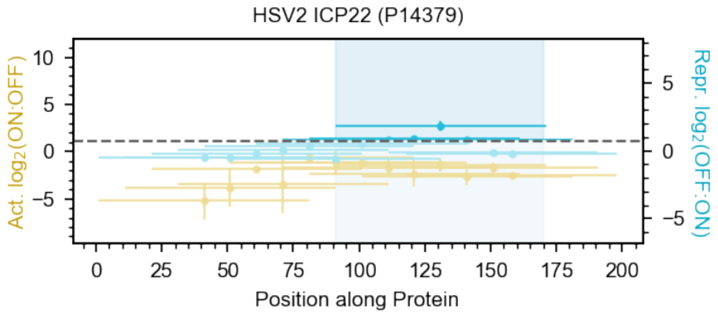
## HSV2 ICP22 (P14379)

Gene: US1 ; Protein Family: ICP22



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Extended repression domain from residues 71 to 180:
PPRELGGRYFLDLSAESTTGTESEGTGPSDDDDDDASDGWLVDTPPRKSKRPRINLRLTSSPDRRAGVVFPEVWRSDRPIRAAQPQAPAQSSGDRAHAPRRSARQAQMRS

Max tile of repression domain from residues 91 to 170 (estimated 28.6% to 50.0% of cells repressed):
TESEGTGPSDDDDDDASDGWLVDTPPRKSKRPRINLRLTSSPDRRAGVVFPEVWRSDRPIRAAQPQAPAQSSGDRAHAPR

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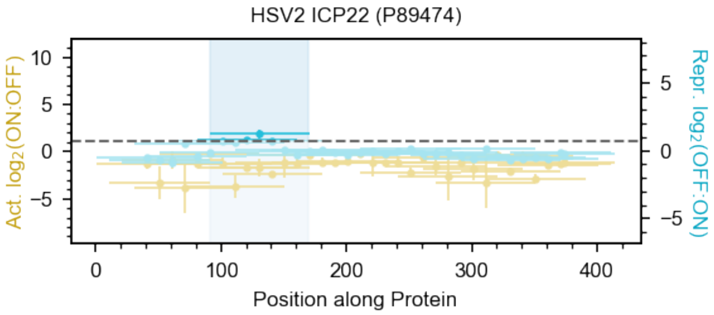
# HSV2 ICP22 (P89474)

Gene: US1 ; Protein Family: ICP22



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Extended repression domain from residues 81 to 180:
LDLSAESTTGTESEGTGPSDDDDDDASDGWLVDTPPRKSKRPRINLRLTSSPDRRAGVVFPEVWRSDRPIRAAQPQAPASLPGIAHAHRRSARQAQMRSG

Max tile of repression domain from residues 91 to 170 (estimated 18.2% to 32.0% of cells repressed):
TESEGTGPSDDDDDDASDGWLVDTPPRKSKRPRINLRLTSSPDRRAGVVFPEVWRSDRPIRAAQPQAPASLPGIAHAHRR

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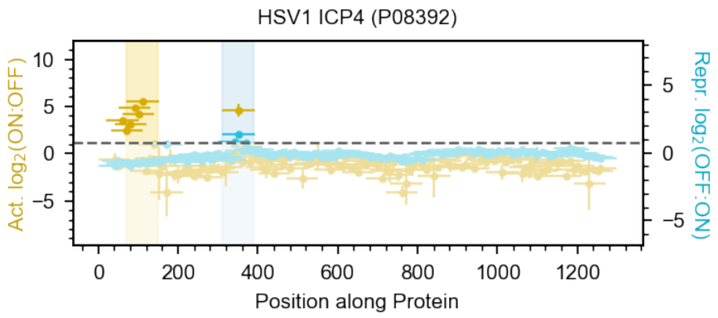
# HSV1 ICP4 (P08392)

Gene: RS1 ; Protein Family: ICP4



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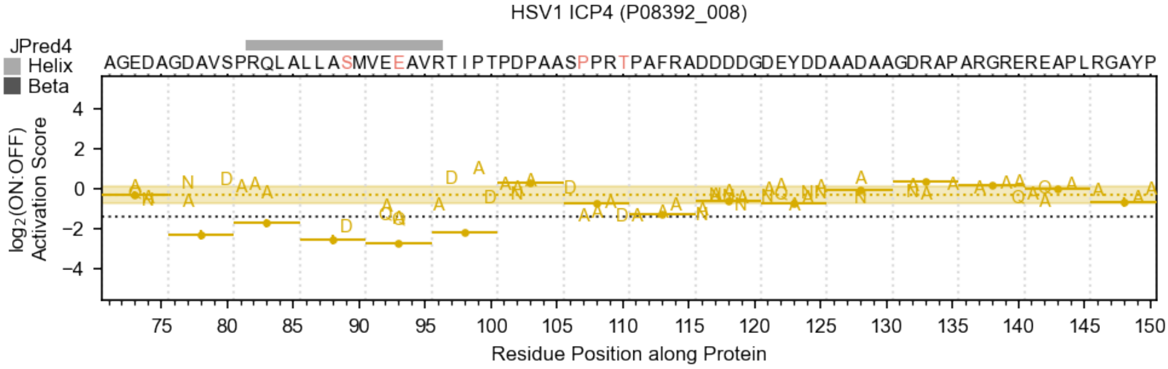
Extended activation domain from residues 21 to 150:
TPSPDRDERGALGWGAETEEGGDDPDHDPDHPHDLDDARRDGRAPAAGTDAGEDAGDAVSPRQLALLASMVEEAVRTIPTPDPAASPPRTPAFRADDDDGDEYDDAADAAGDRAPARGREREAPLRGAYP

Max tile of activation domain from residues 71 to 150 (estimated 39.1% to 49.6% of cells activated):
AGEDAGDAVSPRQLALLASMVEEAVRTIPTPDPAASPPRTPAFRADDDDGDEYDDAADAAGDRAPARGREREAPLRGAYP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 76 | 100 | GDAVSPRQLALLASMVEEAVRTIPT |
| WW_3 | 106 | 110 | SPPRT | No | - | - | |

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Extended repression domain from residues 301 to 390:
AFYARYRDGYVSGEPWPGAGPPPPGRVLYGGLGDSRPGLWGAPEAEEARRRFEASGAPAAVWAPELGDAAQQYALITRLLYTPDAEAMGW

Max tile of repression domain from residues 311 to 390 (estimated 25.0% to 27.9% of cells repressed):
VSGEPWPGAGPPPPGRVLYGGLGDSRPGLWGAPEAEEARRRFEASGAPAAVWAPELGDAAQQYALITRLLYTPDAEAMGW

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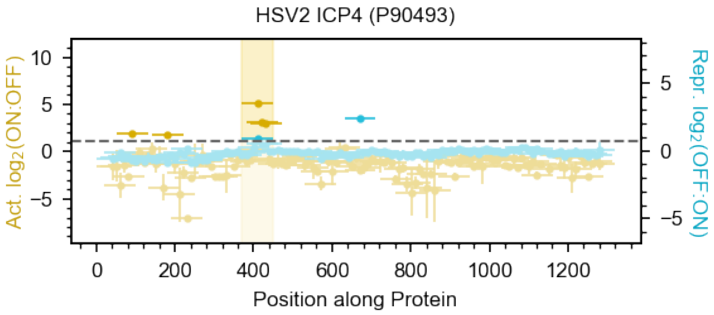
# HSV2 ICP4 (P90493)

Gene: RS1 ; Protein Family: ICP4



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Extended activation domain from residues 371 to 470:
EPWPGAGPPPPGRVLYGGLGDSRPGLWGAPEAEEARARFEASGAPAPVWAPELGDAAQQYALITRLLYTPDAEAMGWLQNPRVAPGDVALDQACFRISGA

Max tile of activation domain from residues 371 to 450 (estimated 33.3% to 39.7% of cells activated):
EPWPGAGPPPPGRVLYGGLGDSRPGLWGAPEAEEARARFEASGAPAPVWAPELGDAAQQYALITRLLYTPDAEAMGWLQN

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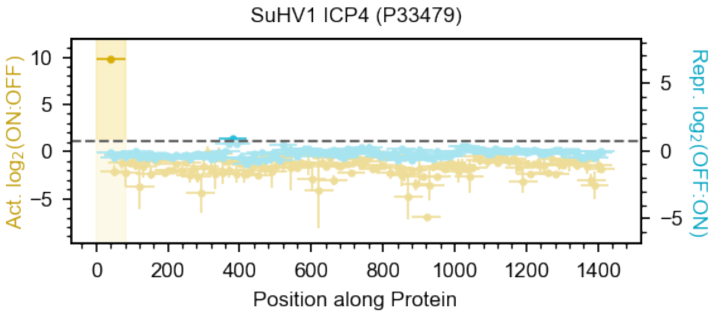
## SuHV1 ICP4 (P33479)

Gene: - ; Protein Family: ICP4



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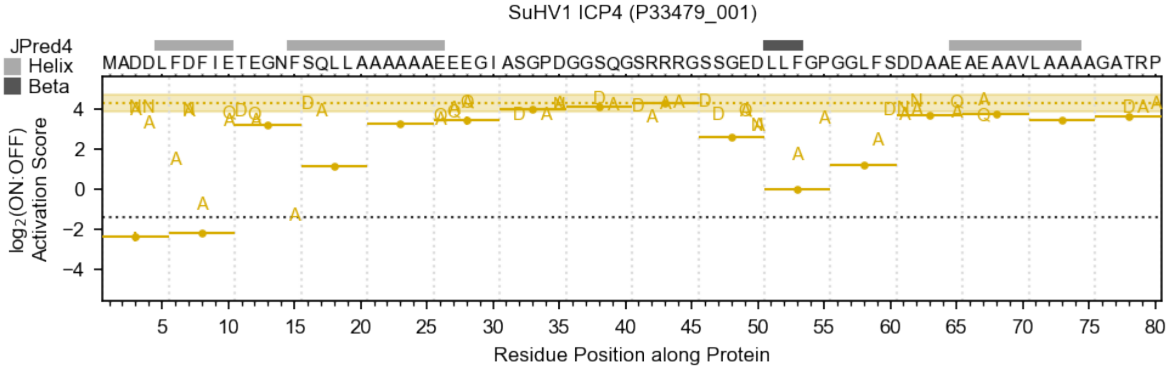
Extended activation domain from residues 1 to 80:
MADDLFDFIETEGNFSQLLAAAAAAEEEGIASGPDGGSQGSRRRGSSGEDLLFGPGGLFSDDAAEAEAAVLAAAAGATRP

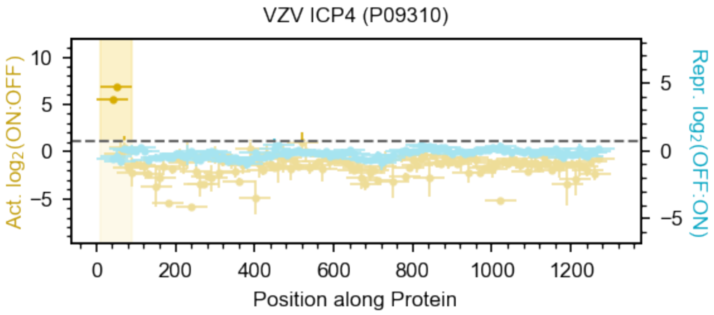
Max tile of activation domain from residues 1 to 80 (estimated 95.5% to 96.1% of cells activated):
MADDLFDFIETEGNFSQLLAAAAAAEEEGIASGPDGGSQGSRRRGSSGEDLLFGPGGLFSDDAAEAEAAVLAAAAGATRP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 4 | 10 | DLFDFIE | Yes | 1 | 10 | MADDLFDFIE |
| flexi_NRBOX | 14 | 20 | NFSQLLA | No | - | - | |

## VZV ICP4 (P09310)

Gene: ORF62/ORF71 ; Protein Family: ICP4



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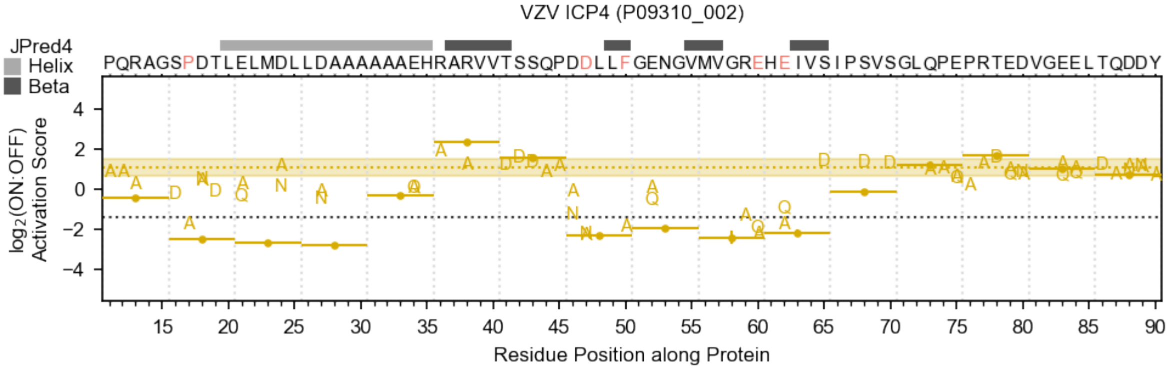
Extended activation domain from residues 1 to 90:
MDTPPMQRSTPQRAGSPDTLELMDLLDAAAAAAEHRARVVTSSQPDDLLFGENGVMVGREHEIVSIPSVSGLQPEPRTEDVGEELTQDDY

Max tile of activation domain from residues 11 to 90 (estimated 71.5% to 74.3% of cells activated):
PQRAGSPDTLELMDLLDAAAAAAEHRARVVTSSQPDDLLFGENGVMVGREHEIVSIPSVSGLQPEPRTEDVGEELTQDDY



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_anti | 18 | 24 | DTLELMD | Yes | 16 | 30 | SPDTLELMDLLDAAA |
| SUMO_SIM_par | 18 | 24 | DTLELMD | Yes | 16 | 30 | SPDTLELMDLLDAAA |
| LIG_NRBOX | 21 | 27 | ELMDLLD | Yes | 16 | 30 | SPDTLELMDLLDAAA |
| CtBP_expanded | 45 | 49 | PDDLL | Yes | 46 | 65 | DDLLFGENGVMVGREHEIVS |
| SUMO_SIM_par | 62 | 68 | EIVSIPS | Yes | 46 | 65 | DDLLFGENGVMVGREHEIVS |

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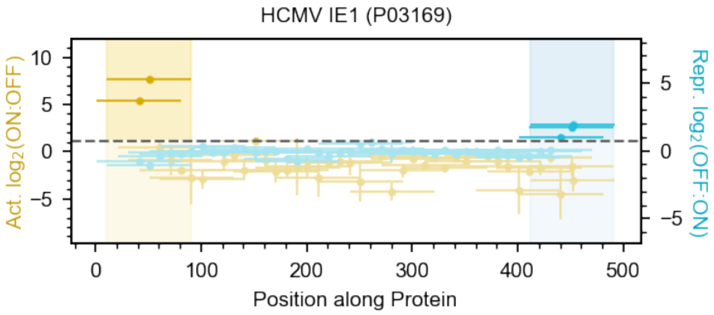
## HCMV IE1 (P03169)

Gene: UL123 ; Protein Family: IE



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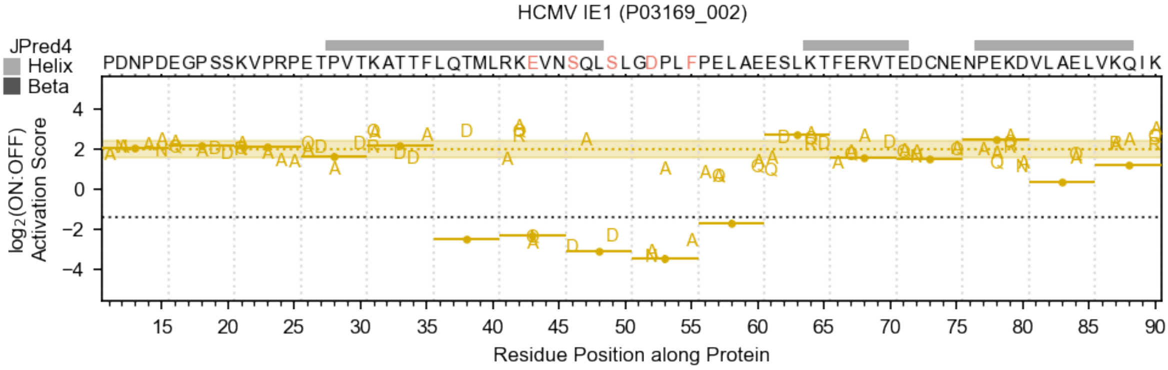
Extended activation domain from residues 1 to 90:
MESSAKRKMDPDNPDEGPSSKVPRPETPVTKATTFLQTMLRKEVNSQLSLGDPLFPELAEESLKTFERVTEDCNENPEKDVLAELVKQIK

Max tile of activation domain from residues 11 to 90 (estimated 83.3% to 84.5% of cells activated):
PDNPDEGPSSKVPRPETPVTKATTFLQTMLRKEVNSQLSLGDPLFPELAEESLKTFERVTEDCNENPEKDVLAELVKQIK



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 36 | 60 | LQTMLRKEVNSQLSLGDPLFPELAE |
| flexi_NRBOX | 81 | 87 | VLAELVK | No | - | - | |

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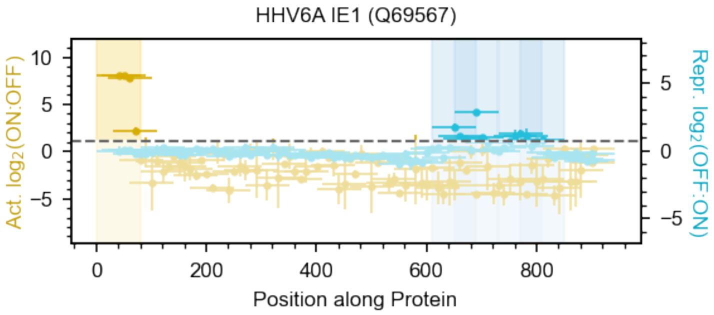
Extended repression domain from residues 401 to 491:
VSPPESPVPATIPLSSVIVAENSDQEESEQSDEEEEEGAQEEREDTVSVKSEPVSEIEEVAPEEEEDGAEEPTASGGKSTHPMVTRSKADQ

Max tile of repression domain from residues 412 to 491 (estimated 35.6% to 45.3% of cells repressed):
IPLSSVIVAENSDQEESEQSDEEEEEGAQEEREDTVSVKSEPVSEIEEVAPEEEEDGAEEPTASGGKSTHPMVTRSKADQ

## HHV6A IE1 (Q69567)

Gene: U90/U89 ; Protein Family: IE



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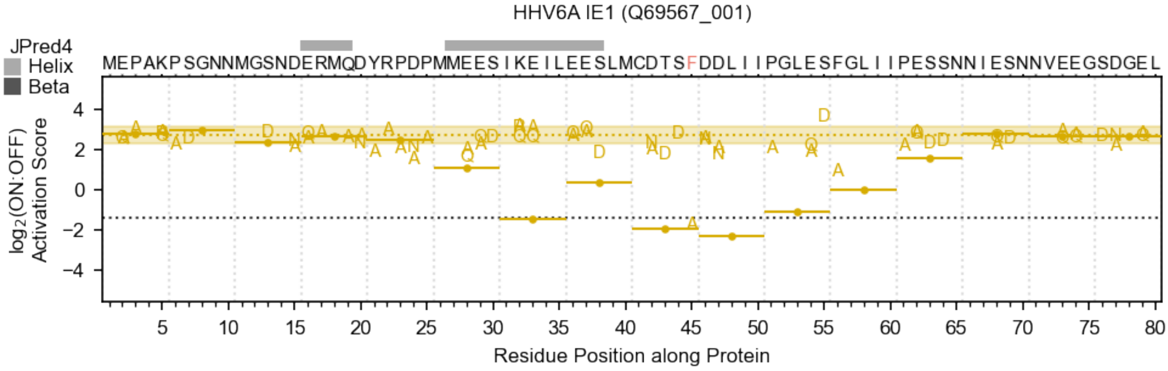
Extended activation domain from residues 1 to 110:
MEPAKPSGNNMGSNDERMQDYRPDPMMEESIKEILEESLMCDTSFDDLIIPGLESFGLIIPESSNNIESNNVEEGSDGELKTLAAQSAGNCIQSIGASVKAAMKQEQSDM

Max tile of activation domain from residues 1 to 80 (estimated 87.1% to 88.9% of cells activated):
MEPAKPSGNNMGSNDERMQDYRPDPMMEESIKEILEESLMCDTSFDDLIIPGLESFGLIIPESSNNIESNNVEEGSDGEL



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 30 | 36 | SIKEILE | Yes | 31 | 35 | IKEIL |
| flexi_NRBOX | 44 | 50 | SFDDLII | Yes | 41 | 50 | CDTSFDDLII |

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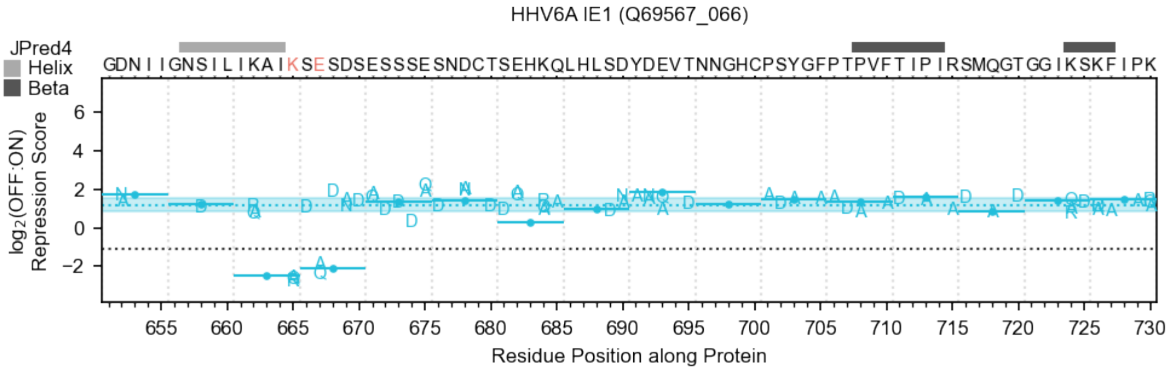
Extended repression domain from residues 611 to 710:
VAKRKHVSSKSPKNKKIKTDQLPKAADVIVISSESEDEEDGDNIIGNSILIKAIKSESDSESSSESNDCTSEHKQLHLSDYDEVTNNGHCPSYGFPTPVF

Max tile of repression domain from residues 611 to 690 (estimated 30.2% to 43.8% of cells repressed):
VAKRKHVSSKSPKNKKIKTDQLPKAADVIVISSESEDEEDGDNIIGNSILIKAIKSESDSESSSESNDCTSEHKQLHLSD

---

Extended repression domain from residues 651 to 740:
GDNIIGNSILIKAIKSESDSESSSESNDCTSEHKQLHLSDYDEVTNNGHCPSYGFPTPVFTIPIRSMQGTGGIKSKFIPKKNWIWYMKKT

Max tile of repression domain from residues 651 to 730 (estimated 61.7% to 69.0% of cells repressed):
GDNIIGNSILIKAIKSESDSESSSESNDCTSEHKQLHLSDYDEVTNNGHCPSYGFPTPVFTIPIRSMQGTGGIKSKFIPK



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 664 | 667 | IKSE | Yes | 661 | 670 | IKAIKSESDS |
| SUMO_rev | 676 | 686 | SNDCTSEHKQL | No | - | - | |

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Extended repression domain from residues 711 to 820:
TIPIRSMQGTGGIKSKFIPKKNWIWYMKKTHQVDNCPIHNSENVDAKDDSDGTEAKHCFMNHFVPIKTDDEDYDKNNVSYIYNKIQNSKIDSGDIIPTKKLIIDMVMDNF

Max tile of repression domain from residues 731 to 810 (estimated 20.3% to 32.4% of cells repressed):
KNWIWYMKKTHQVDNCPIHNSENVDAKDDSDGTEAKHCFMNHFVPIKTDDEDYDKNNVSYIYNKIQNSKIDSGDIIPTKK

---

Extended repression domain from residues 761 to 850:
DGTEAKHCFMNHFVPIKTDDEDYDKNNVSYIYNKIQNSKIDSGDIIPTKKLIIDMVMDNFMDLNDIIKQGITKHCQDLCNKYNVVTPTTC

Max tile of repression domain from residues 771 to 850 (estimated 10.3% to 21.4% of cells repressed):
NHFVPIKTDDEDYDKNNVSYIYNKIQNSKIDSGDIIPTKKLIIDMVMDNFMDLNDIIKQGITKHCQDLCNKYNVVTPTTC

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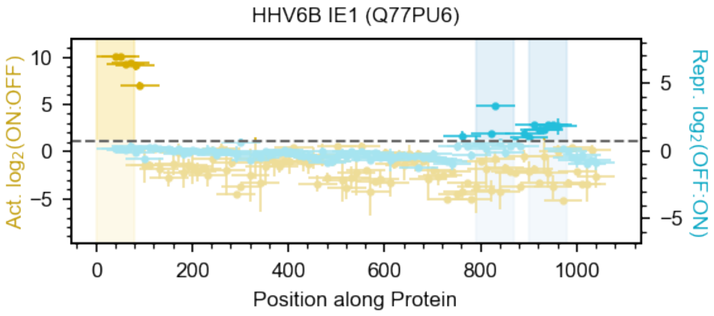
## HHV6B IE1 (Q77PU6)

Gene: U90 ; Protein Family: IE



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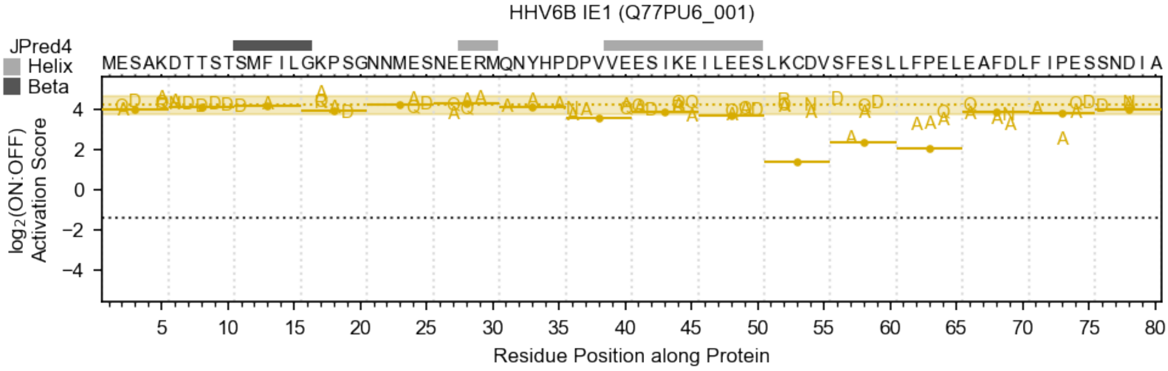
Extended activation domain from residues 1 to 130:
MESAKDTTSTSMFILGKPSGNNMESNEERMQNYHPDPVVEESIKEILEESLKCDVSFESLLFPELEAFDLFIPESSNDIASKNVSYSSNVEEGASDEFKTLVAQSVGNCIQSIGASVKAAMKQEQSNMED

Max tile of activation domain from residues 1 to 80 (estimated 96.0% to 96.6% of cells activated):
MESAKDTTSTSMFILGKPSGNNMESNEERMQNYHPDPVVEESIKEILEESLKCDVSFESLLFPELEAFDLFIPESSNDIA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 42 | 48 | SIKEILE | No | - | - | |
| flexi_NRBOX | 56 | 62 | SFESLLF | No | - | - | |

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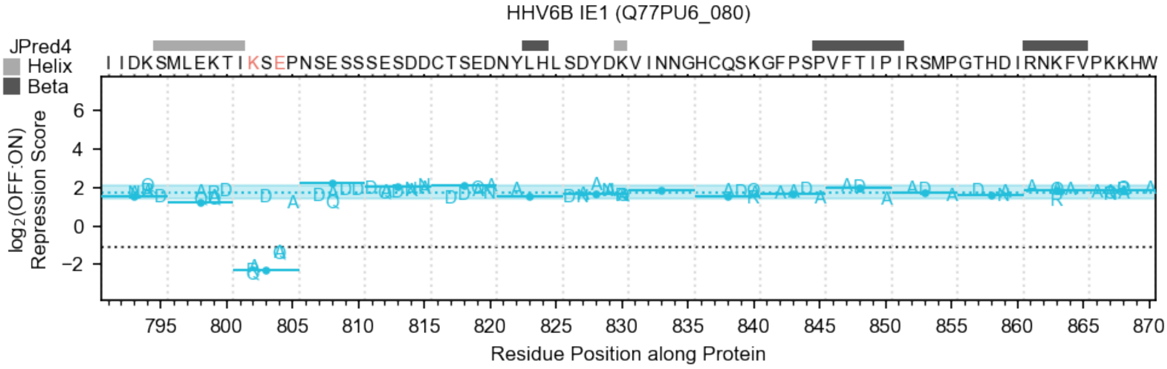
Extended repression domain from residues 781 to 870:
ESEDEEDGNNIIDKSMLEKTIKSEPNSESSSESDDCTSEDNYLHLSDYDKVINNGHCQSKGFPSPVFTIPIRSMPGTHDIRNKFVPKKHW

Max tile of repression domain from residues 791 to 870 (estimated 72.5% to 81.0% of cells repressed):
IIDKSMLEKTIKSEPNSESSSESDDCTSEDNYLHLSDYDKVINNGHCQSKGFPSPVFTIPIRSMPGTHDIRNKFVPKKHW



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 801 | 804 | IKSE | Yes | 801 | 805 | IKSEP |

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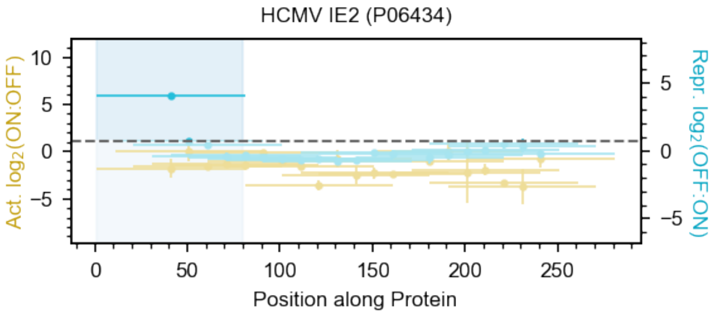
Extended repression domain from residues 851 to 1000:
IRSMPGTHDIRNKFVPKKHWLWFMRKTHKVDNCVIHSSAKMNVKNDSDVTEANHCFINHFVPIKTDDEEYEKENVSYTYSKIQDSKTDLEDITPTKKLITE

MVMENFMDLTDIIKHGIAKHCQDLSSKYTVITHTACEKNLNVANSQNLV

Max tile of repression domain from residues 901 to 980 (estimated 38.7% to 44.5% of cells repressed):
EANHCFINHFVPIKTDDEEYEKENVSYTYSKIQDSKTDLEDITPTKKLITEMVMENFMDLTDIIKHGIAKHCQDLSSKYT

## HCMV IE2 (P06434)

Gene: UL122 ; Protein Family: IE



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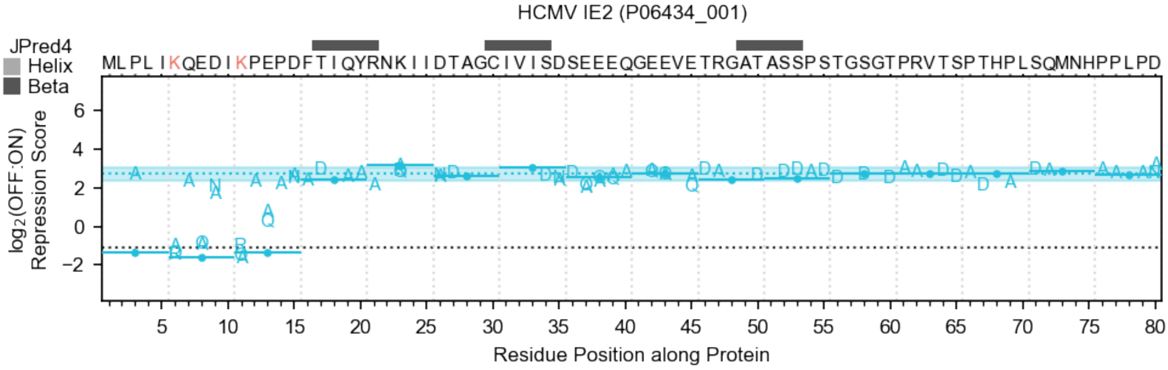
Extended repression domain from residues 1 to 80:
MLPLIKQEDIKPEPDFTIQYRNKIIDTAGCIVISDSEEEQGEEVETRGATASSPSTGSGTPRVTSPTHPLSQMNHPPLPD

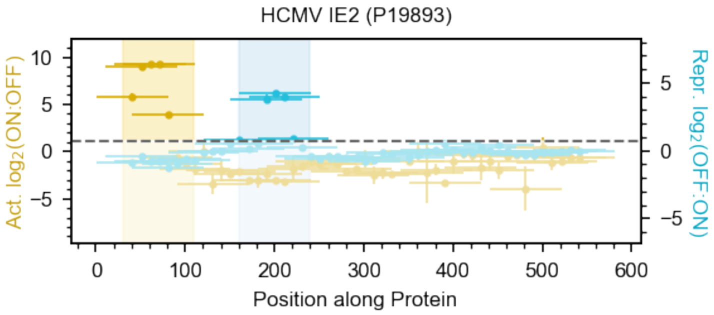
Max tile of repression domain from residues 1 to 80 (estimated 88.2% to 89.4% of cells repressed):
MLPLIKQEDIKPEPDFTIQYRNKIIDTAGCIVISDSEEEQGEEVETRGATASSPSTGSGTPRVTSPTHPLSQMNHPPLPD



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 10 | 13 | IKPE | Yes | 1 | 15 | MLPLIKQEDIKPEPD |
| SUMO_rev | 8 | 12 | EDIKP | Yes | 1 | 15 | MLPLIKQEDIKPEPD |
| SUMO_for | 5 | 8 | IKQE | Yes | 1 | 15 | MLPLIKQEDIKPEPD |
| WW_2 | 76 | 79 | PPLP | No | - | - | |

## HCMV IE2 (P19893)

Gene: UL122 ; Protein Family: IE



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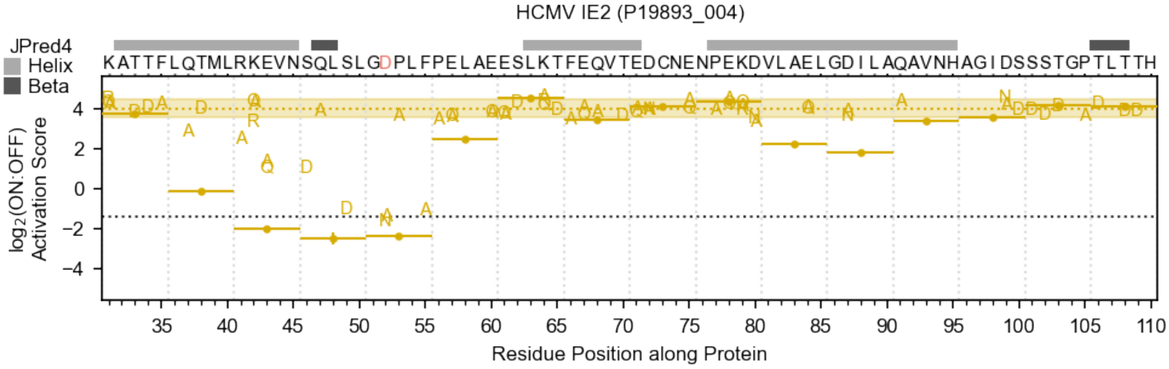
Extended activation domain from residues 1 to 120:
MESSAKRKMDPDNPDEGPSSKVPRPETPVTKATTFLQTMLRKEVNSQLSLGDPLFPELAEESLKTFEQVTEDCNENPEKDVLAELGDILAQAVNHAGIDSSSTGPTLTTHSCSVSSAPLN

Max tile of activation domain from residues 31 to 110 (estimated 94.3% to 94.6% of cells activated):
KATTFLQTMLRKEVNSQLSLGDPLFPELAEESLKTFEQVTEDCNENPEKDVLAELGDILAQAVNHAGIDSSSTGPTLTTH



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 41 | 55 | RKEVNSQLSLGDPLF |
| flexi_NRBOX | 84 | 90 | ELGDILA | No | - | - | |

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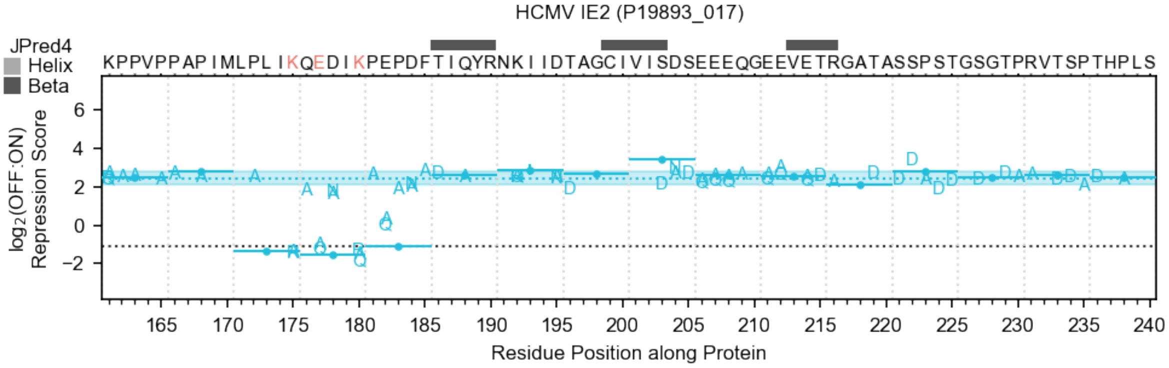
Extended repression domain from residues 151 to 260:
KTTRPFKVIIKPPVPPAPIMLPLIKQEDIKPEPDFTIQYRNKIIDTAGCIVISDSEEEQGEEVETRGATASSPSTGSGTPRVTSPTHPLSQMNHPPLPDPLGRPDEDSSS

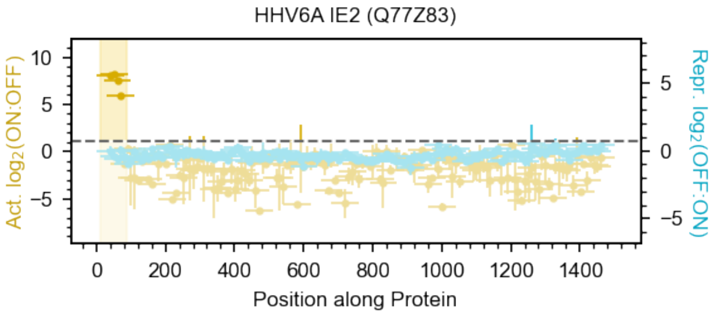
Max tile of repression domain from residues 161 to 240 (estimated 88.6% to 92.7% of cells repressed):
KPPVPPAPIMLPLIKQEDIKPEPDFTIQYRNKIIDTAGCIVISDSEEEQGEEVETRGATASSPSTGSGTPRVTSPTHPLS



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 179 | 182 | IKPE | Yes | 171 | 185 | LPLIKQEDIKPEPDF |
| SUMO_for | 174 | 177 | IKQE | Yes | 171 | 185 | LPLIKQEDIKPEPDF |
| SUMO_rev | 177 | 181 | EDIKP | Yes | 171 | 185 | LPLIKQEDIKPEPDF |

## HHV6A IE2 (Q77Z83)

Gene: U90/U87/U86 ; Protein Family: IE



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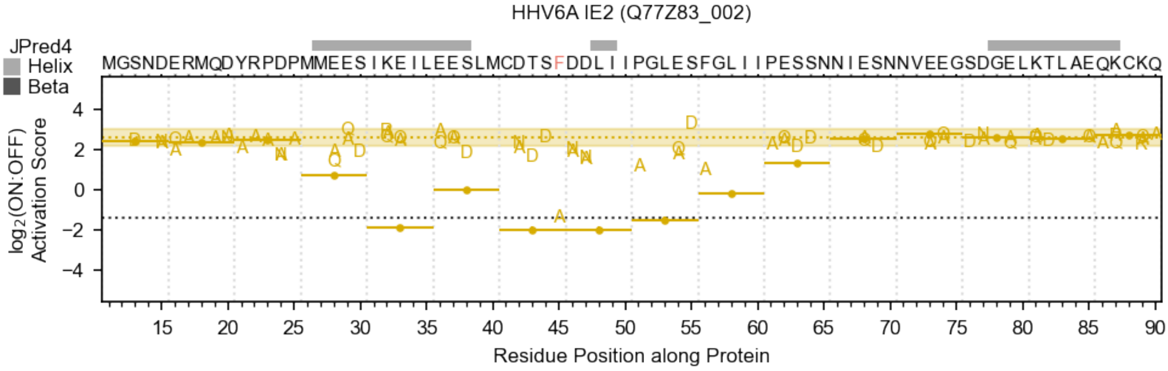
Extended activation domain from residues 1 to 110:
MEPAKPSGNNMGSNDERMQDYRPDPMMEESIKEILEESLMCDTSFDDLIIPGLESFGLIIPESSNNIESNNVEEGSDGELKTLAEQKCKQGNDNDVIQSAMKLSGLYCDA

Max tile of activation domain from residues 11 to 90 (estimated 86.5% to 91.0% of cells activated):
MGSNDERMQDYRPDPMMEESIKEILEESLMCDTSFDDLIIPGLESFGLIIPESSNNIESNNVEEGSDGELKTLAEQKCKQ



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 30 | 36 | SIKEILE | Yes | 31 | 35 | IKEIL |
| flexi_NRBOX | 44 | 50 | SFDDLII | Yes | 41 | 55 | CDTSFDDLIIPGLES |
| SUMO_rev | 73 | 83 | EEGSDGELKTL | No | - | - | |

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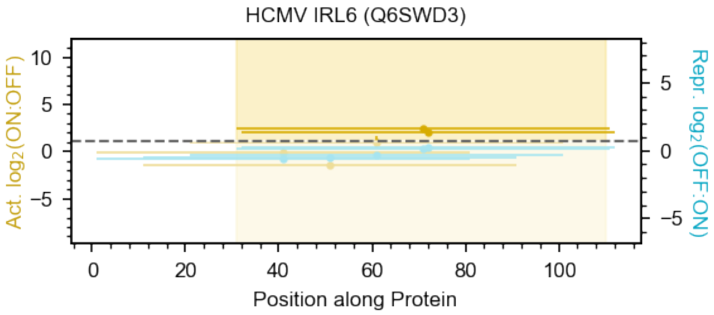
# HCMV IRL6 (Q6SWD3)

Gene: RL6 ; Protein Family: IRL6



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Extended activation domain from residues 31 to 111:
PLTTKWKTVFGNNGDQWLCNVTGIGNATVNGNATICVSSCGHNTLDLCNLKSGDSGFFDLSRWFGENMDEYSGDVWHLEVS

Max tile of activation domain from residues 31 to 110 (estimated 5.4% to 6.3% of cells activated):
PLTTKWKTVFGNNGDQWLCNVTGIGNATVNGNATICVSSCGHNTLDLCNLKSGDSGFFDLSRWFGENMDEYSGDVWHLEV

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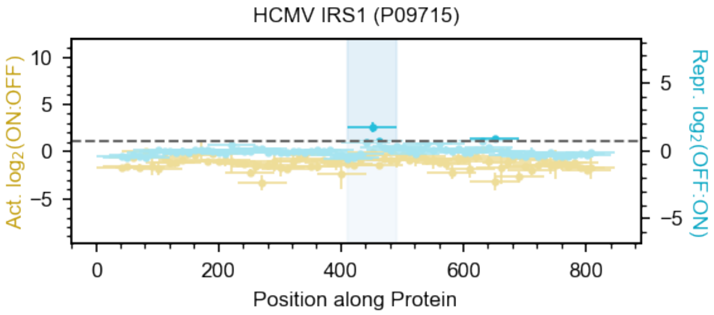
## HCMV IRS1 (P09715)

Gene: IRS1 ; Protein Family: IRS1



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Extended repression domain from residues 411 to 500:
AAGGGAICVPNADAHAVVGADAAAAAAPTVMVGSTAMAGPAASGTVPRAMLVVLLDELGAVFGYCPLDGHVYPLAAELSHFLRAGVLGAL

Max tile of repression domain from residues 411 to 490 (estimated 27.2% to 46.4% of cells repressed):
AAGGGAICVPNADAHAVVGADAAAAAAPTVMVGSTAMAGPAASGTVPRAMLVVLLDELGAVFGYCPLDGHVYPLAAELSH

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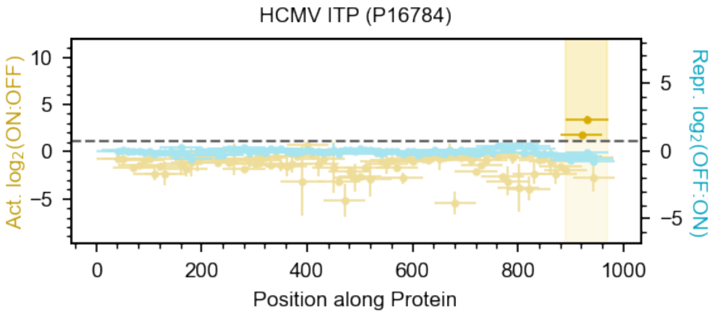
# HCMV ITP (P16784)

Gene: UL47 ; Protein Family: ITP



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Extended activation domain from residues 881 to 970:
AGTGVAAAAEADRALREFLEAPWESAPQPPRLRMTPDTDHEESTAGATSVPEVLGARYEPAHLAASDLLNWYIVPVSQAQQDILSSIDPP

Max tile of activation domain from residues 891 to 970 (estimated 9.0% to 14.5% of cells activated):
ADRALREFLEAPWESAPQPPRLRMTPDTDHEESTAGATSVPEVLGARYEPAHLAASDLLNWYIVPVSQAQQDILSSIDPP

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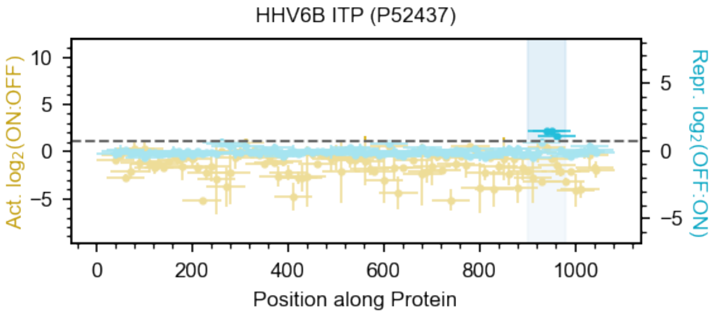
## HHV6B ITP (P52437)

Gene: U30 ; Protein Family: ITP



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Extended repression domain from residues 901 to 1000:
MLRNIITSVSSSKELLTNEALQKFIDTVQRISQHVNETYHSISVNLEKCKTSNDILIESLKKIIYIVDVLSSNAILNTSLASRCLEAANLAVSNNSFTIL

Max tile of repression domain from residues 901 to 980 (estimated 28.2% to 29.7% of cells repressed):
MLRNIITSVSSSKELLTNEALQKFIDTVQRISQHVNETYHSISVNLEKCKTSNDILIESLKKIIYIVDVLSSNAILNTSL

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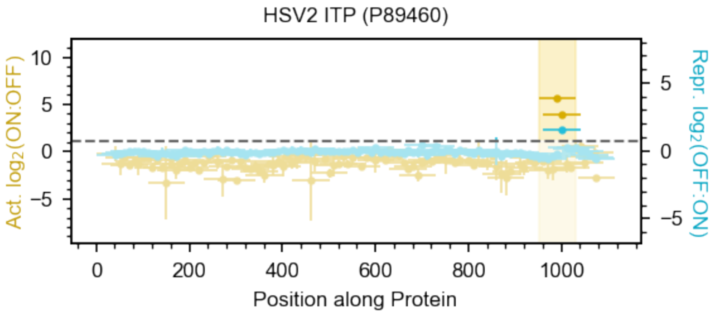
## HSV2 ITP (P89460)

Gene: UL37 ; Protein Family: ITP



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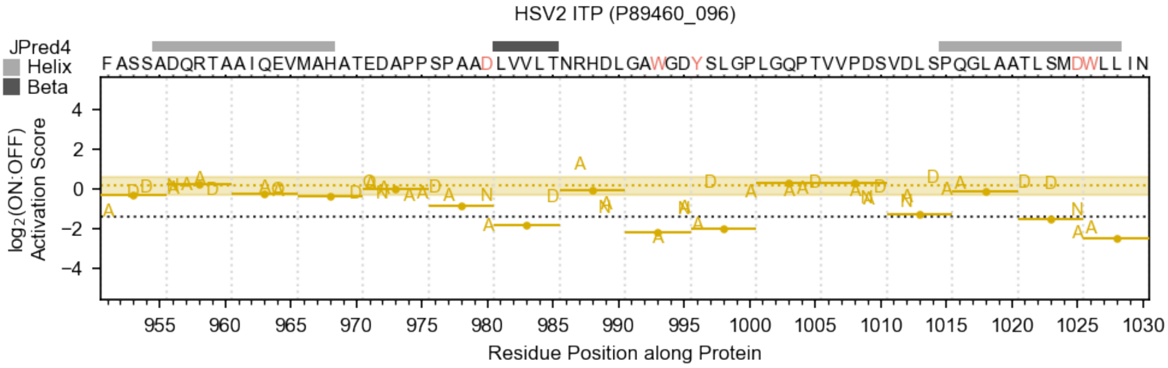
Extended activation domain from residues 951 to 1040:
FASSADQRTAAIQEVMAHATEDAPPSPAADLVVLTNRHDLGAWGDYSLGPLGQPTVVPDSVDLSPQGLAATLSMDWLLINELLQVTDGVF

Max tile of activation domain from residues 951 to 1030 (estimated 45.0% to 53.0% of cells activated):
FASSADQRTAAIQEVMAHATEDAPPSPAADLVVLTNRHDLGAWGDYSLGPLGQPTVVPDSVDLSPQGLAATLSMDWLLIN



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_anti | 980 | 985 | DLVVLT | Yes | 981 | 985 | LVVLT |
| SUMO_SIM_par | 980 | 985 | DLVVLT | Yes | 981 | 985 | LVVLT |
|  | - | - |  | No | 991 | 1000 | GAWGDYSLGP |
|  | - | - |  | No | 1021 | 1030 | TLSMDWLLIN |

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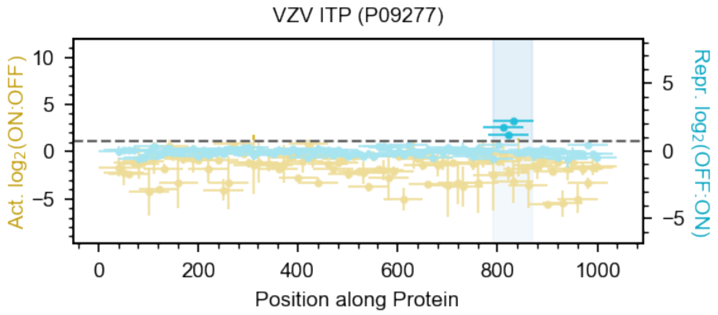
## VZV ITP (P09277)

Gene: ORF21 ; Protein Family: ITP



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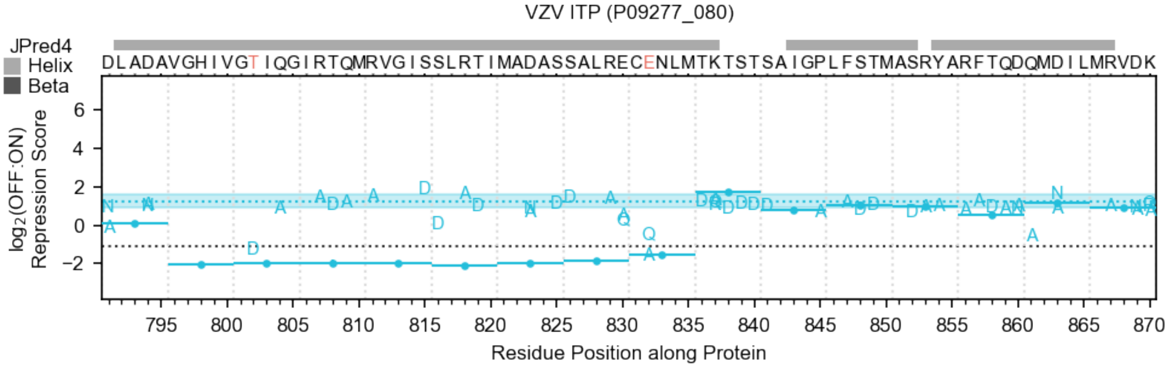
Extended repression domain from residues 771 to 870:
VGICNPKVERDEQFGVWRLNDLADAVGHIVGTIQGIRTQMRVGISSLRTIMADASSALRECENLMTKTSTSAIGPLFSTMASRYARFTQDQMDILMRVDK

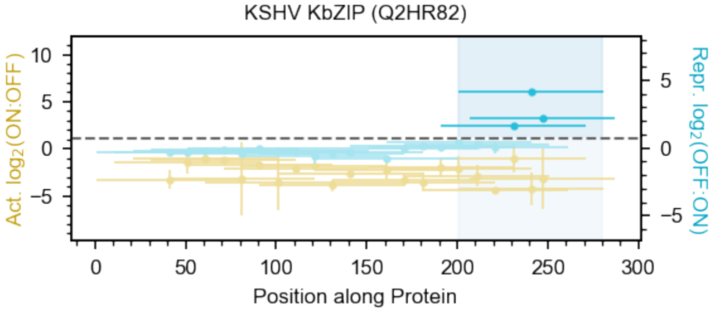
Max tile of repression domain from residues 791 to 870 (estimated 45.5% to 50.5% of cells repressed):
DLADAVGHIVGTIQGIRTQMRVGISSLRTIMADASSALRECENLMTKTSTSAIGPLFSTMASRYARFTQDQMDILMRVDK



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 795 | 801 | AVGHIVG | Yes | 796 | 835 | VGHIVGTIQGIRTQMRVGISSL<br>RTIMADASSALRECENLM |

## KSHV KbZIP (Q2HR82)

Gene: K8 ; Protein Family: KbZIP



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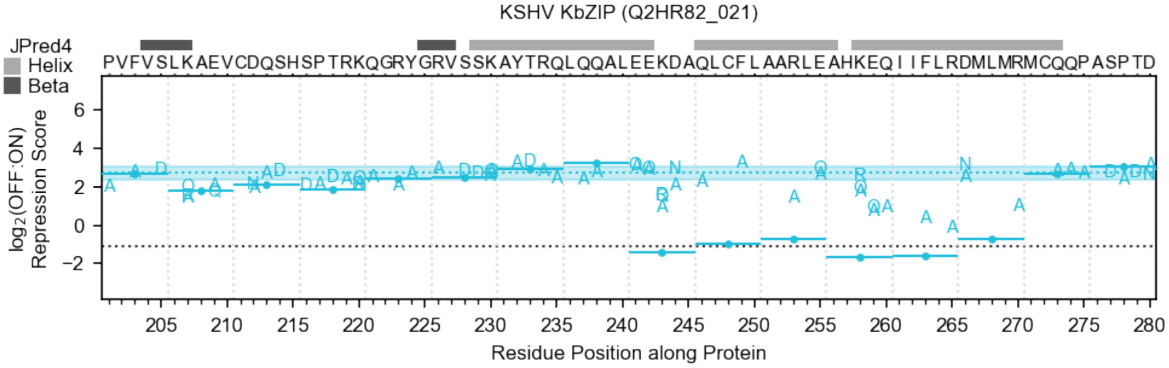
Extended repression domain from residues 191 to 286:
PAQPTHVLFSPVFVSLKAEVCDQSHSPTRKQGRYGRVSSKAYTRQLQQALEEKDAQLCFLAARLEAHKEQIIFLRDMLMRMCQQPASPTDAPLPPC

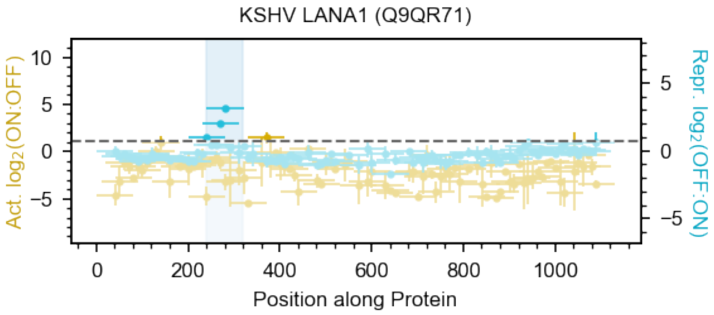
Max tile of repression domain from residues 201 to 280 (estimated 88.3% to 90.4% of cells repressed):
PVFVSLKAEVCDQSHSPTRKQGRYGRVSSKAYTRQLQQALEEKDAQLCFLAARLEAHKEQIIFLRDMLMRMCQQPASPTD



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 206 | 209 | LKAE | No | - | - | |
| | - | - | | No | 241 | 245 | EEKDA |
| | - | - | | No | 256 | 265 | AHKEQIIFLR |

# KSHV LANA1 (Q9QR71)

Gene: ORF73 ; Protein Family: LANA1



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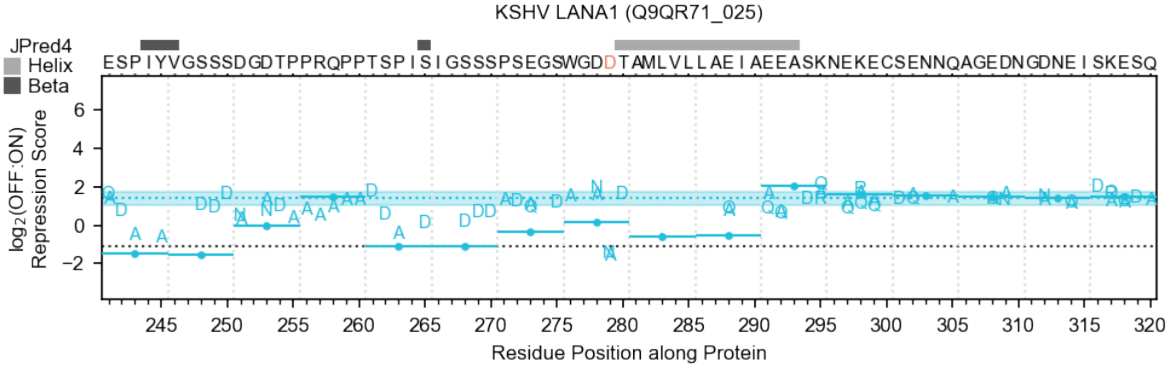
Extended repression domain from residues 231 to 320:
NRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGSSSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGEDNGDNEISKESQ

Max tile of repression domain from residues 241 to 320 (estimated 70.3% to 74.5% of cells repressed):
ESPIYVGSSSDGDTPPRQPPTSPISIGSSSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGEDNGDNEISKESQ



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
|  | - | - |  | No | 241 | 250 | ESPIYVGSSS |
| WW_3 | 254 | 258 | TPPRQ | No | - | - |  |
| SUMO_SIM_par | 261 | 270 | TSPISIGSSS | Yes | 261 | 270 | TSPISIGSSS |
| SUMO_SIM_par | 282 | 288 | MLVLLAE | No | - | - |  |

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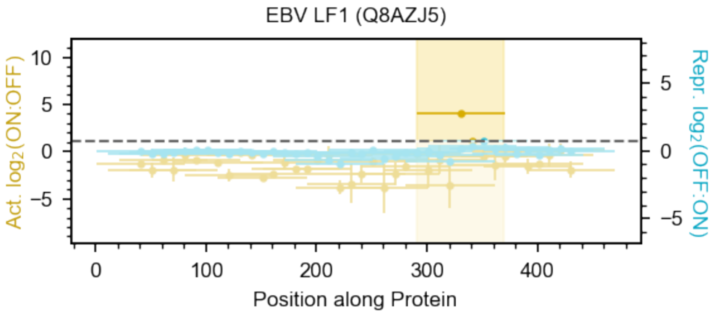
## EBV LF1 (Q8AZJ5)

Gene: LF1 ; Protein Family: LF1



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Extended activation domain from residues 291 to 380:
RAEEGWVCDVLLEPGPPTAREGCSLSMDPGLVTLKDAWTLFPLHPEHDAVVPPKEEIHVMAQGHLQGGTPSLWGFTFQEAACDQWVLRPR

Max tile of activation domain from residues 291 to 370 (estimated 17.0% to 21.2% of cells activated):
RAEEGWVCDVLLEPGPPTAREGCSLSMDPGLVTLKDAWTLFPLHPEHDAVVPPKEEIHVMAQGHLQGGTPSLWGFTFQEA

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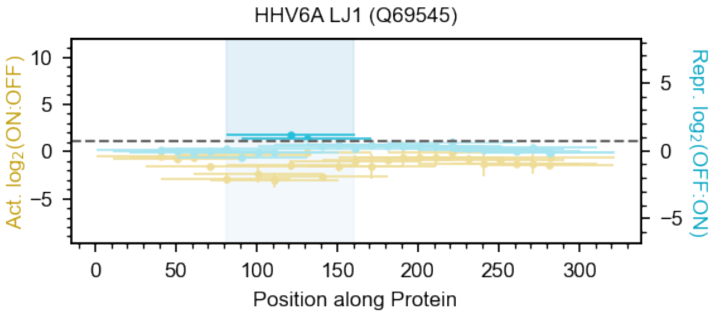
## HHV6A LJ1 (Q69545)

Gene: LJ1 ; Protein Family: LJ1



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Extended repression domain from residues 81 to 170:
PSSALSGGAGGGSRIHDTRVFRARRLGPQPMGSFFHASRSGARVGEKHGASHSGVRARVGGWVRVRVRVRVRVRVRVRVRVRVRVRVR

Max tile of repression domain from residues 81 to 160 (estimated 22.4% to 25.2% of cells repressed):
PSSALSGGAGGGSRIHDTRVFRARRLGPQPMGSFFHASRSGARVGEKHGASHSGVRARVGGWVRVRVRVRVRVRVRVRVR

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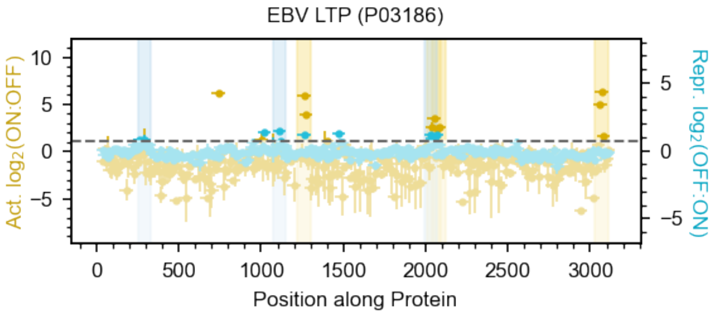
# EBV LTP (P03186)

Gene: BPLF1 ; Protein Family: LTP



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Extended repression domain from residues 241 to 330:
ETEDPRIFMLEHYGVYDFYEANGSGFDLVGPELVSSDGEAAGTPGADSSPPVMLPFERRIIPYNLRPLPSRSFTSDSFPAARYSPAKTNS

Max tile of repression domain from residues 251 to 330 (estimated 10.6% to 23.7% of cells repressed):
EHYGVYDFYEANGSGFDLVGPELVSSDGEAAGTPGADSSPPVMLPFERRIIPYNLRPLPSRSFTSDSFPAARYSPAKTNS

---

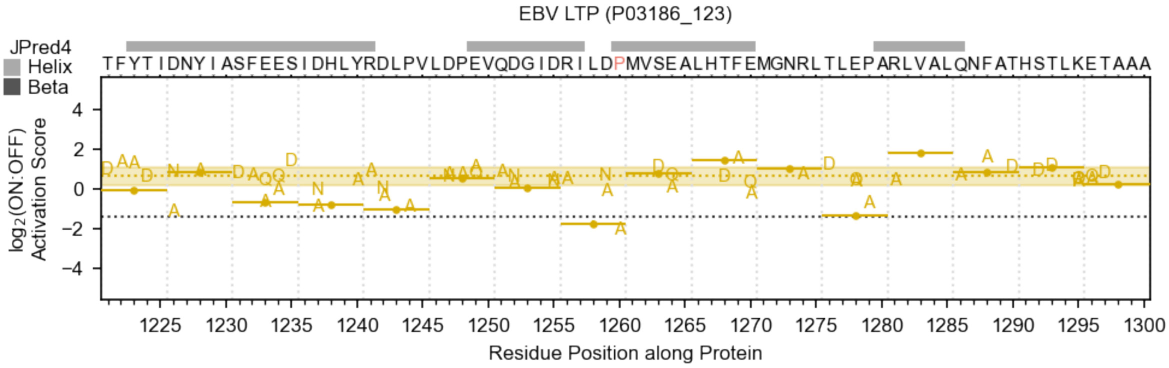
Extended repression domain from residues 1071 to 1160:
LGTALSDMSGIPWPLERVEEDDPSIAPLPEFETVAKKQKELETTRENEKRLRTILDDIEAMLGLAGVASAPGAPISPASPSATPANHDNP

Max tile of repression domain from residues 1071 to 1150 (estimated 28.1% to 31.6% of cells repressed):
LGTALSDMSGIPWPLERVEEDDPSIAPLPEFETVAKKQKELETTRENEKRLRTILDDIEAMLGLAGVASAPGAPISPASP

---

Extended activation domain from residues 1221 to 1310:
TFYTIDNYIASFEESIDHLYRDLPVLDPEVQDGIDRILDPMVSEALHTFEMGNRLTLEPARLVALQNFATHSTLKETAAAVNLLPGLLAV

Max tile of activation domain from residues 1221 to 1300 (estimated 50.6% to 56.1% of cells activated):
TFYTIDNYIASFEESIDHLYRDLPVLDPEVQDGIDRILDPMVSEALHTFEMGNRLTLEPARLVALQNFATHSTLKETAAA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 1224 | 1230 | TIDNYIA | No | - | - | |
| MYND_1 | 1244 | 1248 | PVLDP | No | - | - | |
| flexi_NRBOX | 1253 | 1259 | GIDRILD | Yes | 1256 | 1260 | RILDP |

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Extended repression domain from residues 1991 to 2080:
TGWGNGAPTRRAQFLAAAGPAKYAGTLWLETESPCDPLNPAYVSADTQEPLNYIPVYHNFLEYVMPTVLENPEAFSLTPAGRPQAIGPPQ

Max tile of repression domain from residues 1991 to 2070 (estimated 22.1% to 25.3% of cells repressed):
TGWGNGAPTRRAQFLAAAGPAKYAGTLWLETESPCDPLNPAYVSADTQEPLNYIPVYHNFLEYVMPTVLENPEAFSLTPA

---

Extended activation domain from residues 2001 to 2090:
RAQFLAAAGPAKYAGTLWLETESPCDPLNPAYVSADTQEPLNYIPVYHNFLEYVMPTVLENPEAFSLTPAGRPQAIGPPQDDQERRRRTL

Max tile of activation domain from residues 2011 to 2090 (estimated 9.6% to 15.2% of cells activated):
AKYAGTLWLETESPCDPLNPAYVSADTQEPLNYIPVYHNFLEYVMPTVLENPEAFSLTPAGRPQAIGPPQDDQERRRRTL

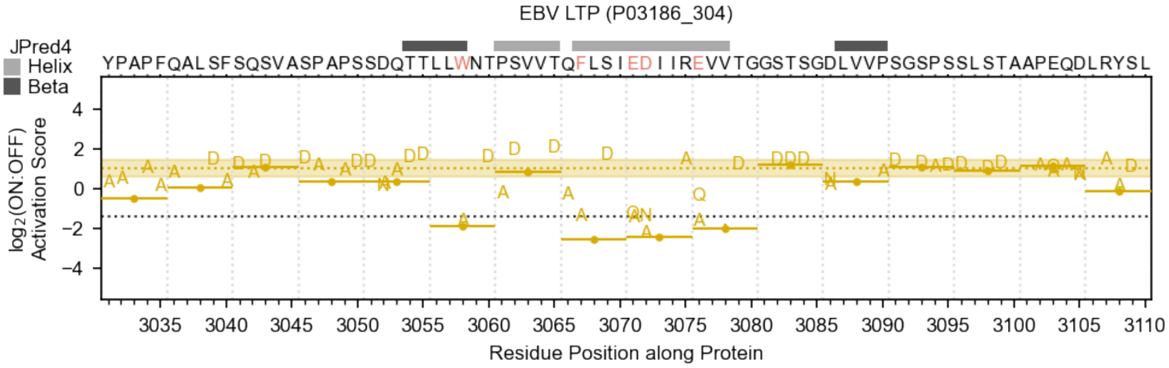
Extended activation domain from residues 2031 to 2120:
AYVSADTQEPLNYIPVYHNFLEYVMPTVLENPEAFSLTPAGRPQAIGPPQDDQERRRRTLASVASARLSAAAADSYWDTWPDVESNAGEL

Max tile of activation domain from residues 2041 to 2120 (estimated 5.8% to 6.3% of cells activated):
LNYIPVYHNFLEYVMPTVLENPEAFSLTPAGRPQAIGPPQDDQERRRRTLASVASARLSAAAADSYWDTWPDVESNAGEL

---

Extended activation domain from residues 3021 to 3120:
MYYPPSGSARYPAPFQALSFSQSVASPAPSSDQTTLLWNTPSVVTQFLSIEDIIREVVTGGSTSGDLVVPSGSPSSLSTAAPEQDLRYSLTLSQASRVLS

Max tile of activation domain from residues 3031 to 3110 (estimated 63.5% to 64.1% of cells activated):
YPAPFQALSFSQSVASPAPSSDQTTLLWNTPSVVTQFLSIEDIIREVVTGGSTSGDLVVPSGSPSSLSTAAPEQDLRYSL



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 3056 | 3060 | LLWNT |
| flexi_NRBOX | 3063 | 3069 | VVTQFLS | Yes | 3066 | 3080 | QFLSIEDIIREVVTG |
| flexi_NRBOX | 3069 | 3075 | SIEDIIR | Yes | 3066 | 3080 | QFLSIEDIIREVVTG |
| flexi_NRBOX | 3073 | 3079 | IIREVVT | Yes | 3066 | 3080 | QFLSIEDIIREVVTG |
| CtBP_expanded | 3094 | 3098 | PSSLS | No | - | - | |

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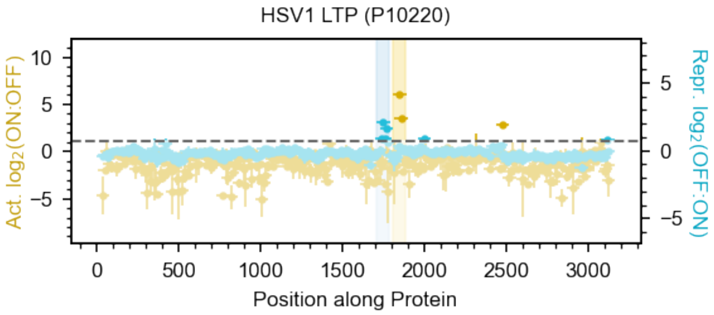
## HSV1 LTP (P10220)

Gene: UL36 ; Protein Family: LTP



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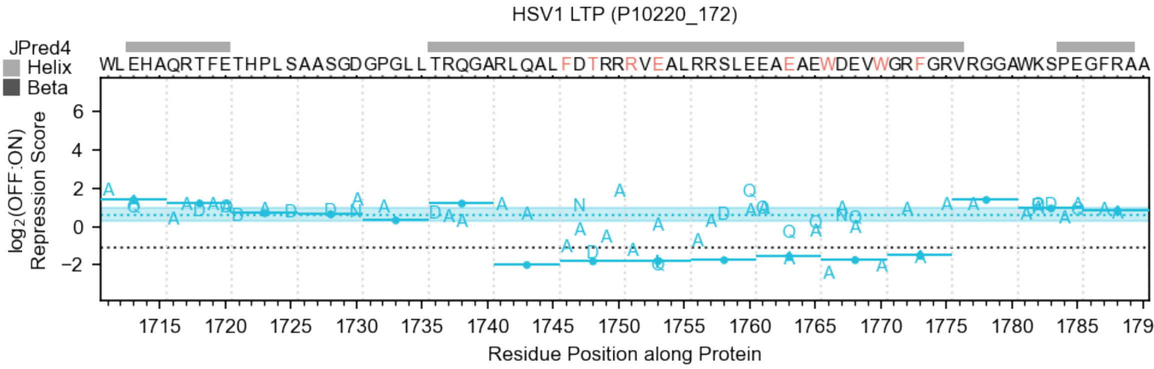
Extended repression domain from residues 1701 to 1810:
ARELDVQAVAWLEHAQRTFETHPLSAASGDGPGLLTRQGARLQALFDTRRRVEALRRSLEEAEAEWDEVWGRFGRVRGGAWKSPEGFRAACEQLRALQDTTNTVSGLRAQ

Max tile of repression domain from residues 1711 to 1790 (estimated 43.4% to 52.2% of cells repressed):
WLEHAQRTFETHPLSAASGDGPGLLTRQGARLQALFDTRRRVEALRRSLEEAEAEWDEVWGRFGRVRGGAWKSPEGFRAA

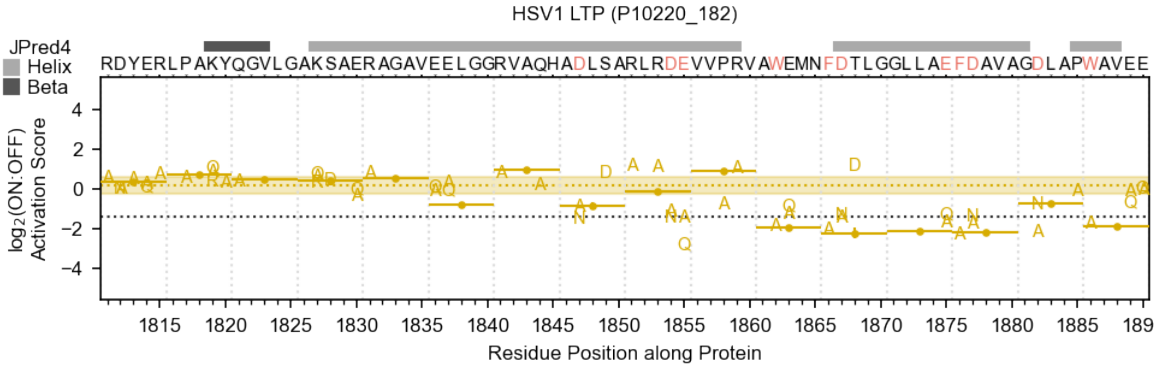


| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 1741 | 1747 | RLQALFD | Yes | 1741 | 1775 | RLQALFDTRRRVEALRRSLEEAEAEWDEVWGRFGR |

---

Extended activation domain from residues 1811 to 1900:
RDYERLPAKYQGVLGAKSAERAGAVEELGGRVAQHADLSARLRDEVVPRVAWEMNFDTLGGLLAEFDAVAGDLAPWAVEEFRGARELIQR

Max tile of activation domain from residues 1811 to 1890 (estimated 56.8% to 59.3% of cells activated):
RDYERLPAKYQGVLGAKSAERAGAVEELGGRVAQHADLSARLRDEVVPRVAWEMNFDTLGGLLAEFDAVAGDLAPWAVEE



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| LIG_NRBOX | 1868 | 1874 | TLGGLLA | Yes | 1861 | 1880 | AWEMNFDTLGGLLAEFDAVA |
|  | - | - |  | No | 1886 | 1890 | WAVEE |

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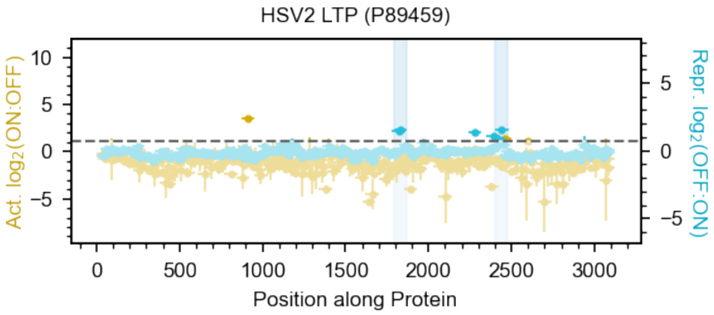
# HSV2 LTP (P89459)

Gene: UL36 ; Protein Family: LTP



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Extended repression domain from residues 1781 to 1870:
PAYERLSARYQGVLGAKGAERAEAVEELGARVTKHTALCARLRDEVVRRVPWEMNFDALGGLLAEFDAAAADLAPWAVEEFRGARELIQY

Max tile of repression domain from residues 1791 to 1870 (estimated 29.3% to 31.9% of cells repressed):
QGVLGAKGAERAEAVEELGARVTKHTALCARLRDEVVRRVPWEMNFDALGGLLAEFDAAAADLAPWAVEEFRGARELIQY

---

Extended repression domain from residues 2391 to 2480:
AQLPRLSALIAERPLADGPPCLVLVDISMTPVAVLWEAPEPPGPPDVRFVGSEATEELPFVATAGDVLAASAADADPFFARAILGRPFDA

Max tile of repression domain from residues 2401 to 2480 (estimated 31.8% to 32.2% of cells repressed):
AERPLADGPPCLVLVDISMTPVAVLWEAPEPPGPPDVRFVGSEATEELPFVATAGDVLAASAADADPFFARAILGRPFDA

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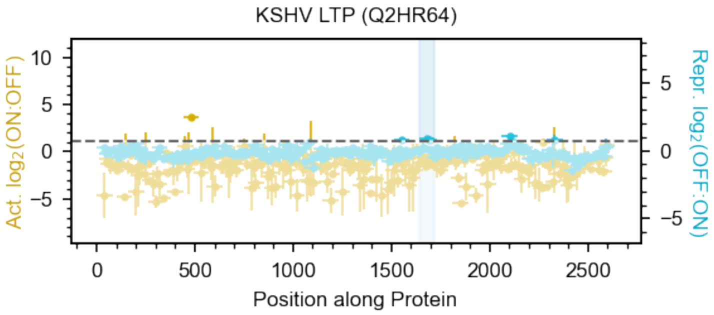
# KSHV LTP (Q2HR64)

Gene: ORF64 ; Protein Family: LTP



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Extended repression domain from residues 1641 to 1730:
HFEATQSVVFTAFPLTQEVTIPALHYAGPFDNLERLSRYLHIGQTQPAPGQWLLTLPTFDPTRPACVPAGGHEPPLHRQVVFSSFLEAQI

Max tile of repression domain from residues 1641 to 1720 (estimated 17.8% to 18.7% of cells repressed):
HFEATQSVVFTAFPLTQEVTIPALHYAGPFDNLERLSRYLHIGQTQPAPGQWLLTLPTFDPTRPACVPAGGHEPPLHRQV

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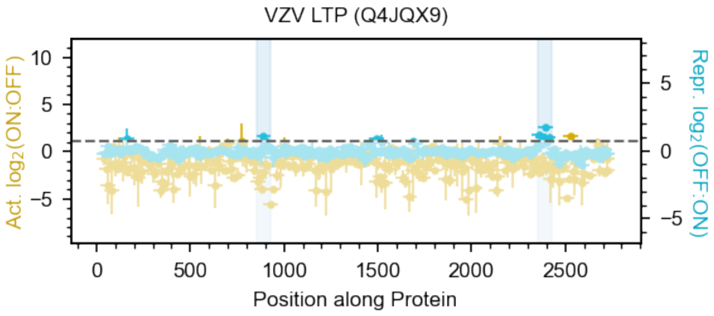
## VZV LTP (Q4JQX9)

Gene: ORF22 ; Protein Family: LTP



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Extended repression domain from residues 851 to 940:
KTINTRATQRASAEAELSCFNTLSAAVDQAVKDYETYNNGEVKYPEITRDDLLATIVRATDDLVRQIKILSDPMIQSGLQPSIKRRLETR

Max tile of repression domain from residues 851 to 930 (estimated 18.8% to 22.4% of cells repressed):
KTINTRATQRASAEAELSCFNTLSAAVDQAVKDYETYNNGEVKYPEITRDDLLATIVRATDDLVRQIKILSDPMIQSGLQ

---

Extended repression domain from residues 2341 to 2430:
SALIANKPLTNNPPCLLLLDEHMNPSYVLWERKDSIPAPDYVVFWGPESLIDLPYIDSDEDSFPSCPDDPFYSQIIAGYAPQGPPNLDTT

Max tile of repression domain from residues 2351 to 2430 (estimated 34.4% to 37.8% of cells repressed):
NNPPCLLLLDEHMNPSYVLWERKDSIPAPDYVVFWGPESLIDLPYIDSDEDSFPSCPDDPFYSQIIAGYAPQGPPNLDTT

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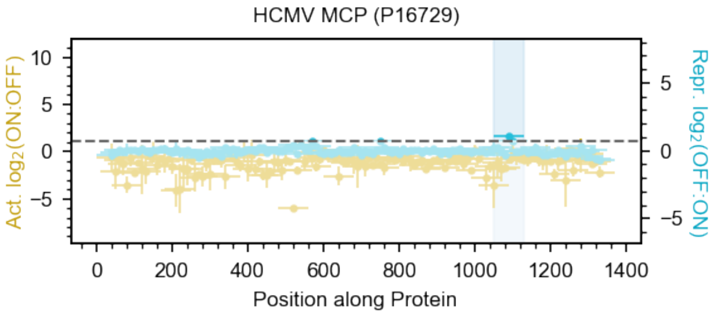
## HCMV MCP (P16729)

Gene: UL86 ; Protein Family: MCP



---

Extended repression domain from residues 1051 to 1140:
GKSCTSVIINNPIVTKEERDISTTYHVTQNINTVDMGLGYTSNTCVAYVNRVRTDMGVRVQDLFRVFPMNVYRHDEVDRWIRHAAGVERP

Max tile of repression domain from residues 1051 to 1130 (estimated 17.7% to 24.2% of cells repressed):
GKSCTSVIINNPIVTKEERDISTTYHVTQNINTVDMGLGYTSNTCVAYVNRVRTDMGVRVQDLFRVFPMNVYRHDEVDRW

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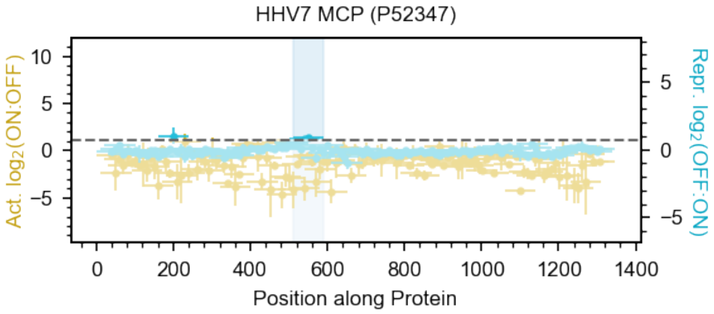
# HHV7 MCP (P52347)

Gene: U57 ; Protein Family: MCP



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Extended repression domain from residues 501 to 590:
MKKEIPKTTNMLKNELTTEDFYKSENFTLKTELHPFFDFTYIQKNRSTDVLCSPRILLGNIPLPLAPSSFHEARTNQMIEQAKTNNLNYD

Max tile of repression domain from residues 511 to 590 (estimated 14.1% to 19.4% of cells repressed):
MLKNELTTEDFYKSENFTLKTELHPFFDFTYIQKNRSTDVLCSPRILLGNIPLPLAPSSFHEARTNQMIEQAKTNNLNYD

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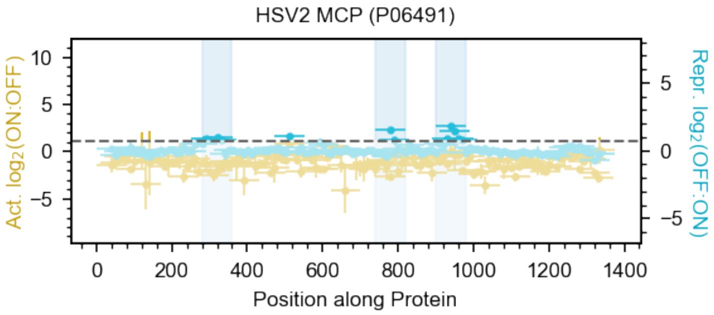
# HSV2 MCP (P06491)

Gene: UL19 ; Protein Family: MCP



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Extended repression domain from residues 251 to 370:
LTTATQPSVAVPRLTHADTRGRPVDGVLVTTAPIKQRLLQSFLKVEDTEADVPVTYGEMVLNGANLVTALVMGKAVRSLDDVGRHLLEMQEEQLDLNRQTLDELESAPQTTRVRADLVSI

Max tile of repression domain from residues 281 to 360 (estimated 17.3% to 19.8% of cells repressed):
TAPIKQRLLQSFLKVEDTEADVPVTYGEMVLNGANLVTALVMGKAVRSLDDVGRHLLEMQEEQLDLNRQTLDELESAPQT

---

Extended repression domain from residues 741 to 830:
ALMRRAALDRHRDCRVSAGGHDPVYAAACNVATADFNRNDGQLLHNTQARAADAADDRPHRGADWTVHHKIYYYVMVPAFSRGRCCTAGV

Max tile of repression domain from residues 741 to 820 (estimated 29.5% to 33.8% of cells repressed):
ALMRRAALDRHRDCRVSAGGHDPVYAAACNVATADFNRNDGQLLHNTQARAADAADDRPHRGADWTVHHKIYYYVMVPAF

---

Extended repression domain from residues 891 to 1010:
MLTLQVLAHNMAERTTALLCSAAPDAGANTASTTNMRIFDGALHAGILLMAPQHLDHTIQNGDYFYPLPVHALFAGADHVANAPNFPPALRDLSRQVPLVPPALGANYFSSIRQPVVQHV

Max tile of repression domain from residues 901 to 980 (estimated 40.0% to 40.2% of cells repressed):
MAERTTALLCSAAPDAGANTASTTNMRIFDGALHAGILLMAPQHLDHTIQNGDYFYPLPVHALFAGADHVANAPNFPPAL

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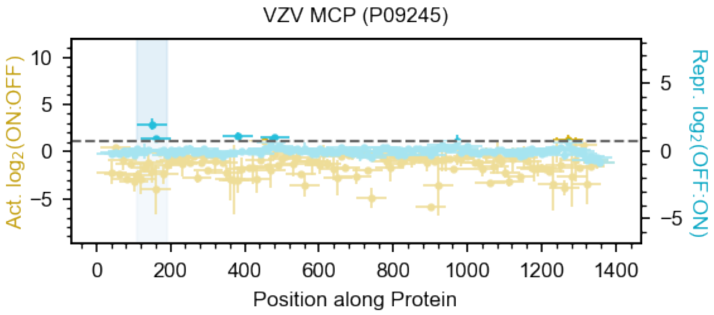
## VZV MCP (P09245)

Gene: ORF40 ; Protein Family: MCP



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Extended repression domain from residues 111 to 200:
VQQPMIARDGPHPVDQPVHNYMVKRIHKRSLSAAFAIASEALSLLSNTYVDGTEIDSSLRIRAIQQMARNLRTVLDSFERGTADQLLGVL

Max tile of repression domain from residues 111 to 190 (estimated 30.9% to 53.7% of cells repressed):
VQQPMIARDGPHPVDQPVHNYMVKRIHKRSLSAAFAIASEALSLLSNTYVDGTEIDSSLRIRAIQQMARNLRTVLDSFER

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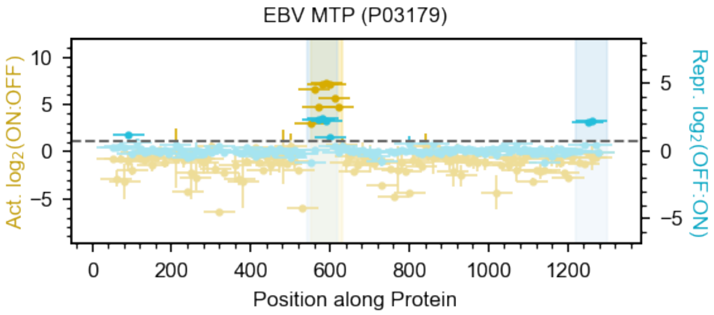
## EBV MTP (P03179)

Gene: BNRF1 ; Protein Family: MTP



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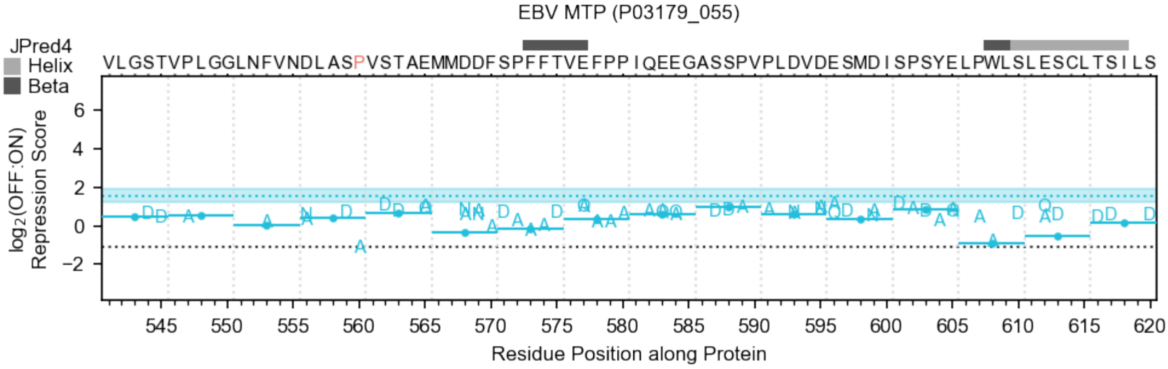
Extended repression domain from residues 531 to 640:
ACDMAGCQHYVLGSTVPLGGLNFVNDLASPVSTAEMMDDFSPFFTVEFPPIQEEGASSPVPLDVDESMDISPSYELPWLSLESCLTSILSHPTVGSKEHLVRHTDRVSGG

Max tile of repression domain from residues 541 to 620 (estimated 53.6% to 56.3% of cells repressed):
VLGSTVPLGGLNFVNDLASPVSTAEMMDDFSPFFTVEFPPIQEEGASSPVPLDVDESMDISPSYELPWLSLESCLTSILS



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_par | 590 | 597 | VPLDVDES | No | - | - | |
| flexi_NRBOX | 614 | 620 | CLTSILS | No | - | - | |

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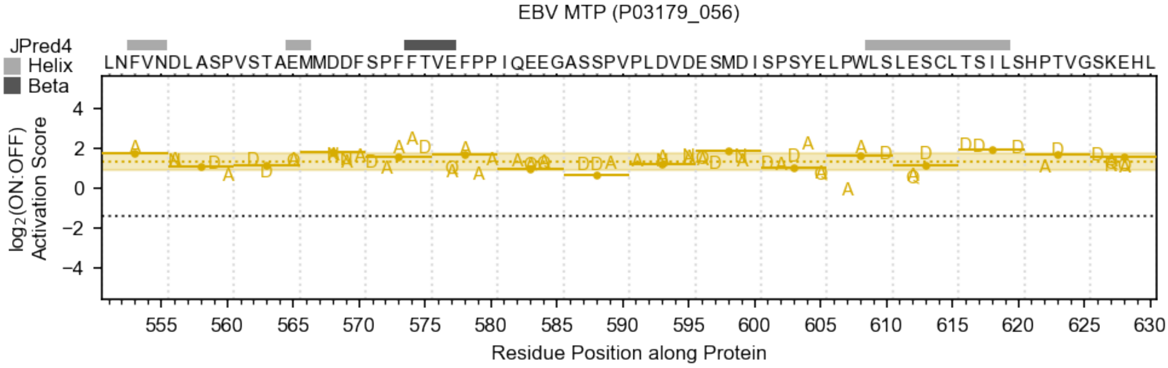
Extended activation domain from residues 511 to 660:
TVRQRGEKINGRTVLQALGRACDMAGCQHYVLGSTVPLGGLNFVNDLASPVSTAEMMDDFSPFFTVEFPPIQEEGASSPVPLDVDESMDISPSYELPWLSLESCLTSILSHPTVGSKEHLVRHTDRVSGGRVAQQPGVGPLDLPLADYAF

Max tile of activation domain from residues 551 to 630 (estimated 78.0% to 82.2% of cells activated):
LNFVNDLASPVSTAEMMDDFSPFFTVEFPPIQEEGASSPVPLDVDESMDISPSYELPWLSLESCLTSILSHPTVGSKEHL



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_par | 590 | 597 | VPLDVDES | No | - | - | |
| flexi_NRBOX | 614 | 620 | CLTSILS | No | - | - | |

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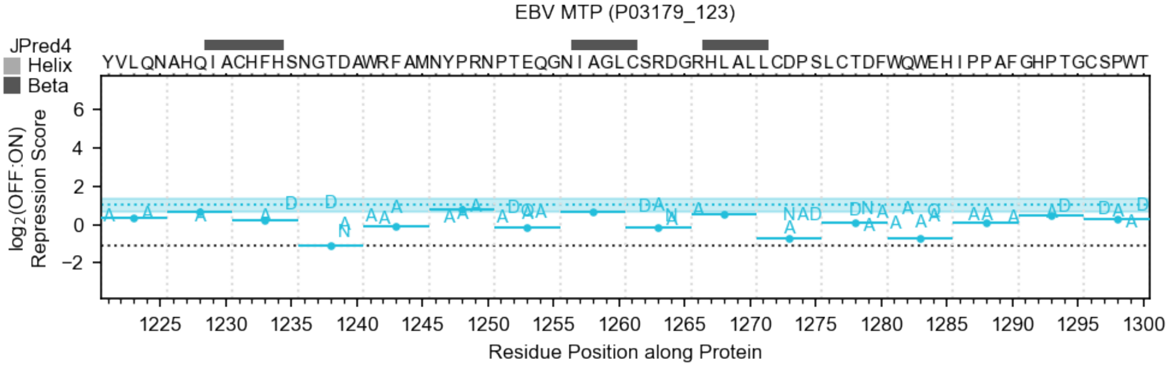
Extended repression domain from residues 1211 to 1300:
GLQFTNLGMPYVLQNAHQIACHFHSNGTDAWRFAMNYPRNPTEQGNIAGLCSRDGRHLALLCDPSLCTDFWQWEHIPPAFGHPTGCSPWT

Max tile of repression domain from residues 1221 to 1300 (estimated 47.6% to 48.7% of cells repressed):
YVLQNAHQIACHFHSNGTDAWRFAMNYPRNPTEQGNIAGLCSRDGRHLALLCDPSLCTDFWQWEHIPPAFGHPTGCSPWT



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | - | - | |

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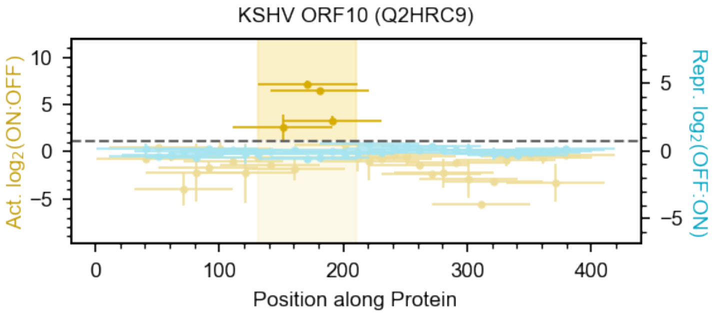
## KSHV ORF10 (Q2HRC9)

Gene: ORF10 ; Protein Family: ORF10



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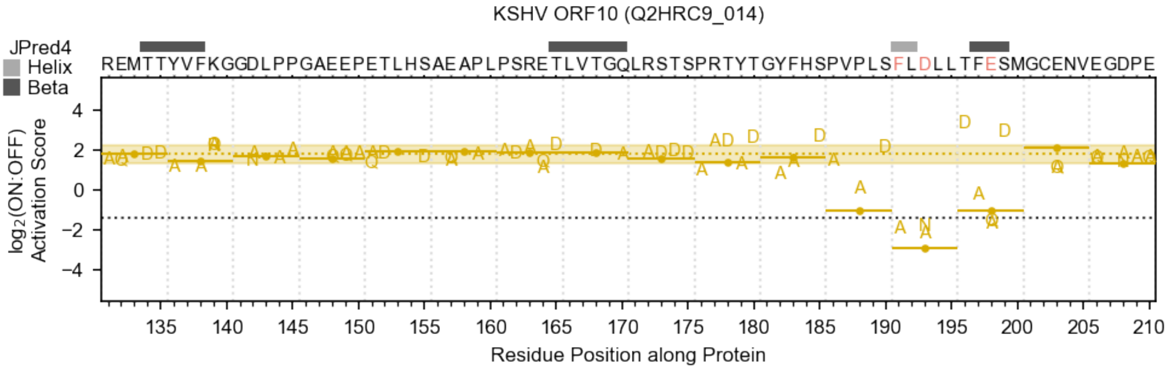
Extended activation domain from residues 131 to 230:
REMTTYVFKGGDLPPGAEEPETLHSAEAPLPSRETLVTGQLRSTSPRTYTGYFHSPVPLSFLDLLTFESMGCENVEGDPEPLTPKYLTFTQTGERLYKVT

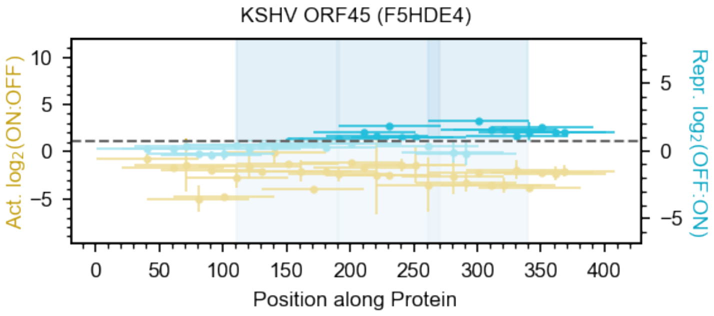
Max tile of activation domain from residues 131 to 210 (estimated 72.5% to 83.0% of cells activated):
REMTTYVFKGGDLPPGAEEPETLHSAEAPLPSRETLVTGQLRSTSPRTYTGYFHSPVPLSFLDLLTFESMGCENVEGDPE



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_anti | 190 | 196 | SFLDLLT | Yes | 191 | 195 | FLDLL |
| flexi_NRBOX | 190 | 196 | SFLDLLT | Yes | 191 | 195 | FLDLL |

## KSHV ORF45 (F5HDE4)

Gene: ORF45 ; Protein Family: ORF45



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Extended repression domain from residues 111 to 200:
EDEPEGYPADFFQPLSHLRPRPLARRAHTPKPVAVVAGRVRSSTDTAESEASMGWVSQDDGFSPAGLSPSDDEGVAILEPMAAYTGTGAY

Max tile of repression domain from residues 111 to 190 (estimated 13.1% to 16.6% of cells repressed):
EDEPEGYPADFFQPLSHLRPRPLARRAHTPKPVAVVAGRVRSSTDTAESEASMGWVSQDDGFSPAGLSPSDDEGVAILEP

---

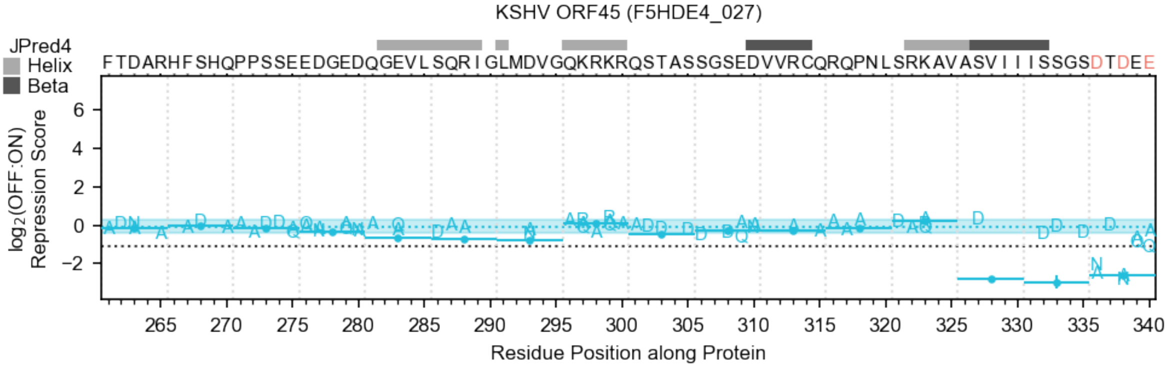
Extended repression domain from residues 171 to 290:
GFSPAGLSPSDDEGVAILEPMAAYTGTGAYGLSPASRNSVPGTQSSPYSDPDEGPSWRPLRAAPTAIVDLTSDSDSDDSSNSPDVNNEAAFTDARHFSHQPPSSEEDGEDQGEVLSQRIG

Max tile of repression domain from residues 191 to 270 (estimated 36.2% to 39.4% of cells repressed):
MAAYTGTGAYGLSPASRNSVPGTQSSPYSDPDEGPSWRPLRAAPTAIVDLTSDSDSDDSSNSPDVNNEAAFTDARHFSHQ

---

Extended repression domain from residues 261 to 407:
FTDARHFSHQPPSSEEDGEDQGEVLSQRIGLMDVGQKRKRQSTASSGSEDVVRCQRQPNLSRKAVASVIIISSGSDTDEEPSSAVSVIVSPSSTKGHLPTQSPSTSAHSISSGSTTTAGSRCSDPTRILASTPPLCGNGAYNWPWLD

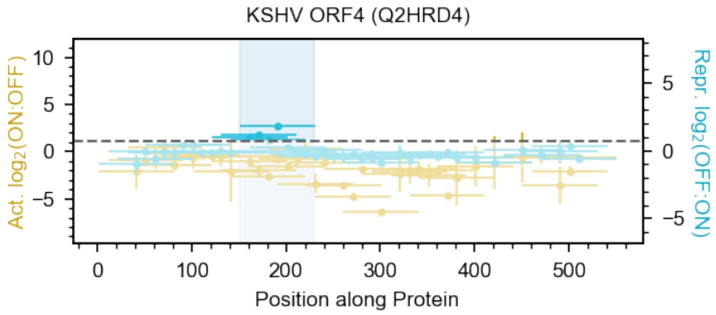
Max tile of repression domain from residues 261 to 340 (estimated 46.4% to 50.0% of cells repressed):
FTDARHFSHQPPSSEEDGEDQGEVLSQRIGLMDVGQKRKRQSTASSGSEDVVRCQRQPNLSRKAVASVIIISSGSDTDEE



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 324 | 330 | AVASVII | Yes | 326 | 340 | ASVIIISSGSDTDEE |
| SUMO_SIM_par | 327 | 333 | SVIIISS | Yes | 326 | 340 | ASVIIISSGSDTDEE |
| SUMO_SIM_anti | 327 | 333 | SVIIISS | Yes | 326 | 340 | ASVIIISSGSDTDEE |

## KSHV ORF4 (Q2HRD4)

Gene: ORF4 ; Protein Family: ORF4



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Extended repression domain from residues 121 to 230:
FLVGREYVRYCMIGASGQMAWSSSPPFCEKEKCHRPKIENGDFKPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPIQGFSLTY

Max tile of repression domain from residues 151 to 230 (estimated 37.4% to 40.8% of cells repressed):
EKCHRPKIENGDFKPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPIQGFSLTY

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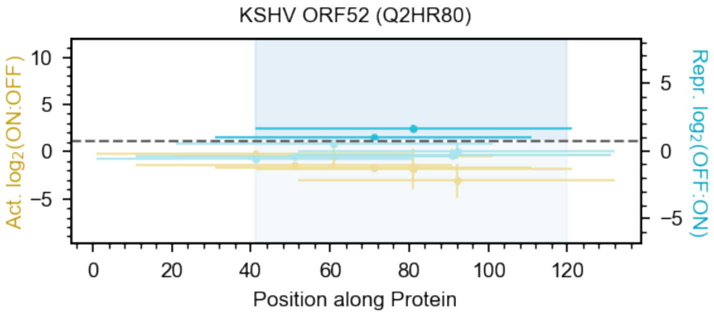
## KSHV ORF52 (Q2HR80)

Gene: ORF52 ; Protein Family: ORF52



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Extended repression domain from residues 31 to 120:
LRKALGSTADPRDRPLTATEKEAQLTATVGALSAAAAKKIEARVRTIFSKVVTQKQVDDALKGLSLRIDVCMSDGGTAKPPPGANNRRRR

Max tile of repression domain from residues 41 to 120 (estimated 26.1% to 41.1% of cells repressed):
PRDRPLTATEKEAQLTATVGALSAAAAKKIEARVRTIFSKVVTQKQVDDALKGLSLRIDVCMSDGGTAKPPPGANNRRRR

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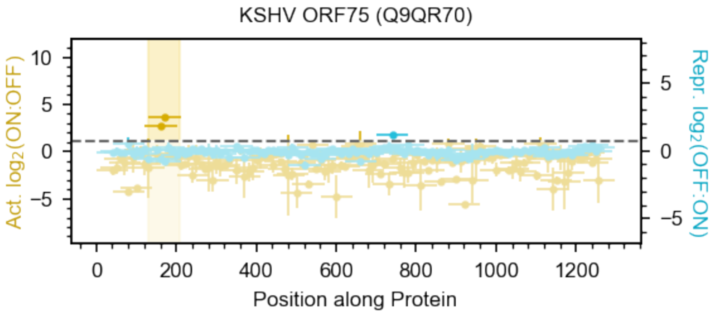
## KSHV ORF75 (Q9QR70)

Gene: ORF75 ; Protein Family: ORF75



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Extended activation domain from residues 121 to 210:
LGLQEWARVEVGRHLVSKITQTLLEPHPPQFIRAFTQNTDLVPYEGLEVPEGPQPVARPHIEDDVIMQAVMISLGADLLPLAVQASTGDN

Max tile of activation domain from residues 131 to 210 (estimated 12.9% to 13.4% of cells activated):
VGRHLVSKITQTLLEPHPPQFIRAFTQNTDLVPYEGLEVPEGPQPVARPHIEDDVIMQAVMISLGADLLPLAVQASTGDN

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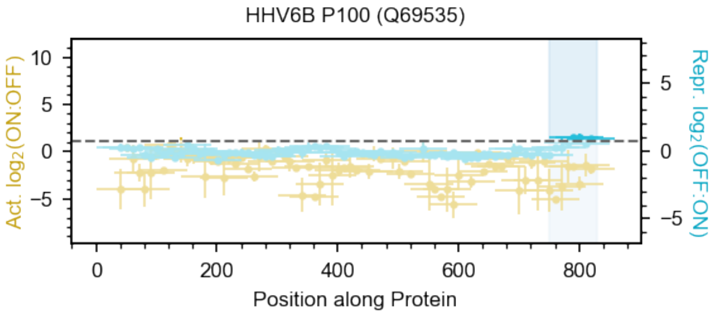
## HHV6B P100 (Q69535)

Gene: U11 ; Protein Family: P100



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Extended repression domain from residues 751 to 840:
LSRDLDSVSFKDALDVKLPGNGEREIDLALQKVKAGERETSDFKVGQDETLIPTQLMKVETPEEKDDVIEKMVLRIRQDGETDEETVPGP

Max tile of repression domain from residues 751 to 830 (estimated 17.4% to 22.0% of cells repressed):
LSRDLDSVSFKDALDVKLPGNGEREIDLALQKVKAGERETSDFKVGQDETLIPTQLMKVETPEEKDDVIEKMVLRIRQDG

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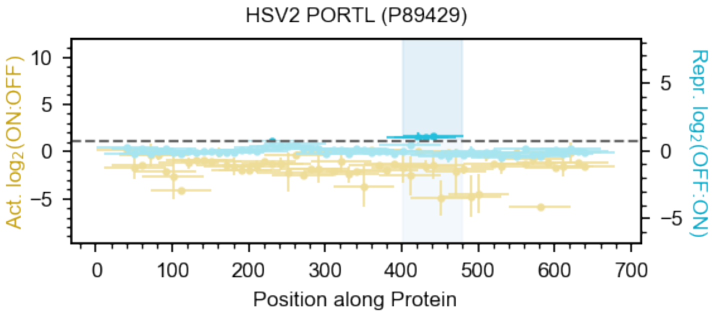
# HSV2 PORTL (P89429)

Gene: UL6 ; Protein Family: PORTL



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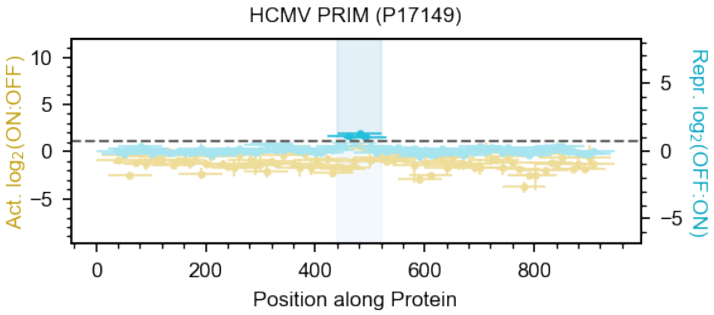
Extended repression domain from residues 381 to 480:
TLPGFGKGGTGRGSRPQDPGARPQQLRQAFQTAVVNNINGMLEGYINNLFGTIERLRETNAGLATQLQARDRELRRAQAGALEREQRAADRAAGGGAGRP

Max tile of repression domain from residues 401 to 480 (estimated 18.0% to 24.8% of cells repressed):
ARPQQLRQAFQTAVVNNINGMLEGYINNLFGTIERLRETNAGLATQLQARDRELRRAQAGALEREQRAADRAAGGGAGRP

---

# HCMV PRIM (P17149)

Gene: UL70 ; Protein Family: PRIM



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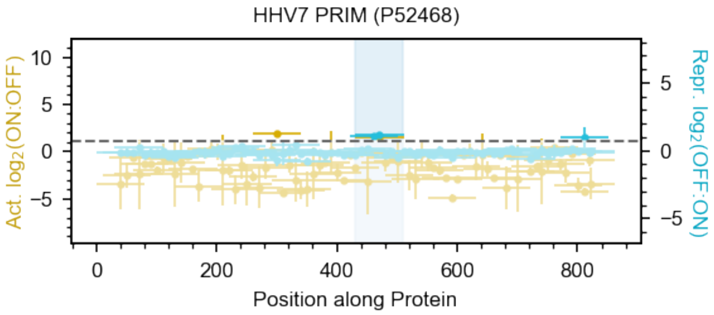
Extended repression domain from residues 441 to 530:
NDQHVFCAVASETWHRSLFPRDLLRHVPDSRFSDEALTETVWLHDDDVASTSPETQFYYTRHEVFNERLPVFNFVADFDLRLRDGVSGLA

Max tile of repression domain from residues 441 to 520 (estimated 23.8% to 24.5% of cells repressed):
NDQHVFCAVASETWHRSLFPRDLLRHVPDSRFSDEALTETVWLHDDDVASTSPETQFYYTRHEVFNERLPVFNFVADFDL

---

# HHV7 PRIM (P52468)

Gene: U43 ; Protein Family: PRIM



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Extended repression domain from residues 421 to 510:
YCFGSAESWYKNMGFDQVMQFLPNEYISDESLTSTFWLQDTTFLSDEIEKQFYVTRHEIFNEYLPVTNYIGDLDLPLQDSAIITESLFFS

Max tile of repression domain from residues 431 to 510 (estimated 18.8% to 25.6% of cells repressed):
KNMGFDQVMQFLPNEYISDESLTSTFWLQDTTFLSDEIEKQFYVTRHEIFNEYLPVTNYIGDLDLPLQDSAIITESLFFS

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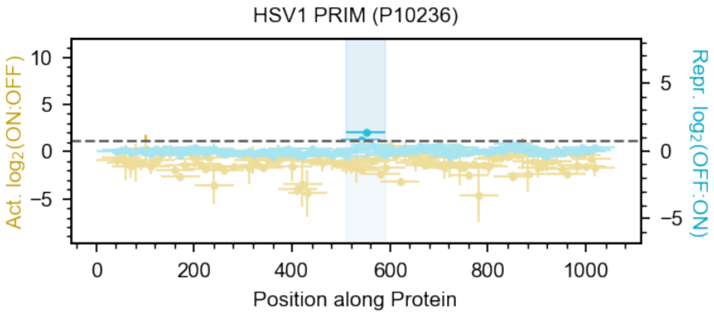
## HSV1 PRIM (P10236)

Gene: UL52 ; Protein Family: PRIM



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Extended repression domain from residues 501 to 590:
VKRLLRLAATEQQGPTPPAIAALIRNAAVQTPLPVYRISMVPTGQAFAALAWDDWARITRDARLAEAVVSAEAAAHPDHGALGRRLTDRI

Max tile of repression domain from residues 511 to 590 (estimated 22.9% to 30.4% of cells repressed):
EQQGPTPPAIAALIRNAAVQTPLPVYRISMVPTGQAFAALAWDDWARITRDARLAEAVVSAEAAAHPDHGALGRRLTDRI

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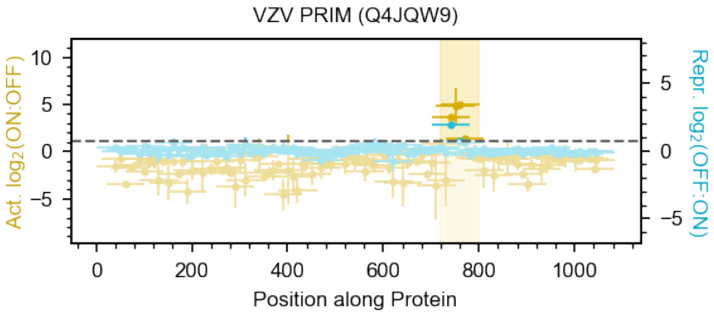
# VZV PRIM (Q4JQW9)

Gene: ORF6 ; Protein Family: PRIM



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Extended activation domain from residues 701 to 810:
LFPKAVVNPNKDPCYFYKTACPEPTVEVLDDDNLLDITSHSDIDFYIENGELYTCVEENYTEDVWFFDTQTTSEVHTHADVSNNENLHETLPCNCKEKIGFRVCVPIPNP

Max tile of activation domain from residues 721 to 800 (estimated 30.9% to 35.4% of cells activated):
CPEPTVEVLDDDNLLDITSHSDIDFYIENGELYTCVEENYTEDVWFFDTQTTSEVHTHADVSNNENLHETLPCNCKEKIG

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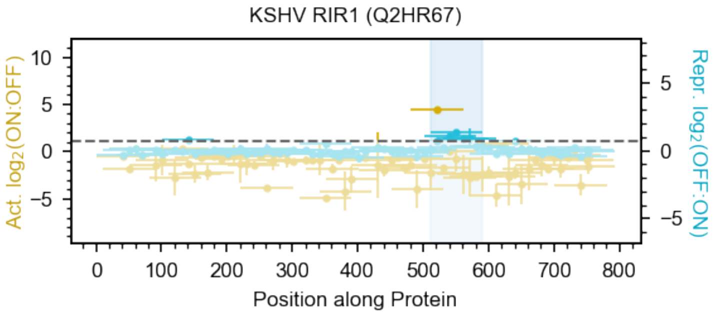
# KSHV RIR1 (Q2HR67)

Gene: ORF61 ; Protein Family: RIR1



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Extended repression domain from residues 501 to 610:
IGVQGLADVFAELGYGYLDAESAELDKNIFQSMYYTAVETSHNLVLEGQGVPFHGWEVSNFAKGRFHWQTWEGEDASFVPRHRWDALGKSIAEHGIFNSQFLAVMPTAGT

Max tile of repression domain from residues 511 to 590 (estimated 26.0% to 29.1% of cells repressed):
AELGYGYLDAESAELDKNIFQSMYYTAVETSHNLVLEGQGVPFHGWEVSNFAKGRFHWQTWEGEDASFVPRHRWDALGKS

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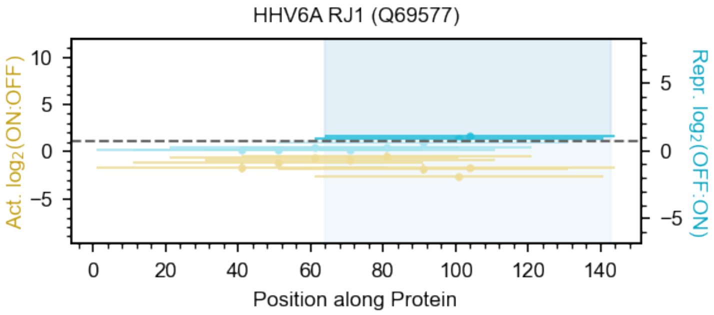
## HHV6A RJ1 (Q69577)

Gene: RJ1 ; Protein Family: RJ1



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Extended repression domain from residues 61 to 143:
RVRVRARPRVRVRVRARPRVRVRVRASPRVRVRVITPPFFSPPGGFDVIFKTRGIPSPGETVLDKKVSRPWRGLTSRRGATMI

Max tile of repression domain from residues 64 to 143 (estimated 17.8% to 23.6% of cells repressed):
VRARPRVRVRVRARPRVRVRVRASPRVRVRVITPPFFSPPGGFDVIFKTRGIPSPGETVLDKKVSRPWRGLTSRRGATMI

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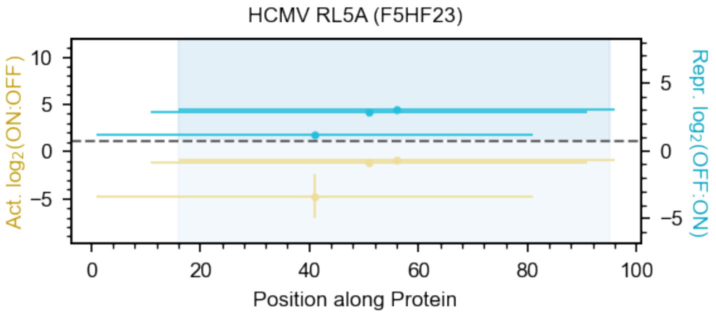
## HCMV RL5A (F5HF23)

Gene: RL5A ; Protein Family: RL5A



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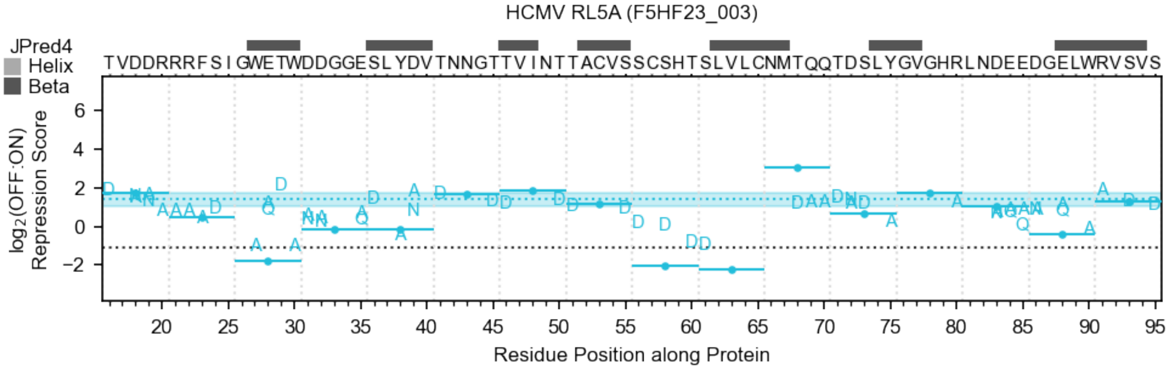
Extended repression domain from residues 1 to 95:
MDMRKLNTSQGRNLTTVDDRRRFSIGWETWDDGGESLYDVTNNGTTVINTTACVSSCSHTSLVLCNMTQQTDSLYGVGHRLNDEEDGELWRVSVS

Max tile of repression domain from residues 16 to 95 (estimated 70.0% to 72.0% of cells repressed):
TVDDRRRFSIGWETWDDGGESLYDVTNNGTTVINTTACVSSCSHTSLVLCNMTQQTDSLYGVGHRLNDEEDGELWRVSVS



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 26 | 30 | GWETW |
| | - | - | | No | 56 | 65 | SCSHTSLVLC |

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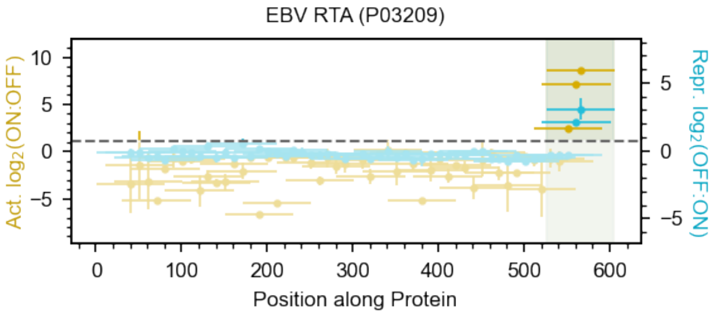
# EBV RTA (P03209)

Gene: BRLF1 ; Protein Family: RTA



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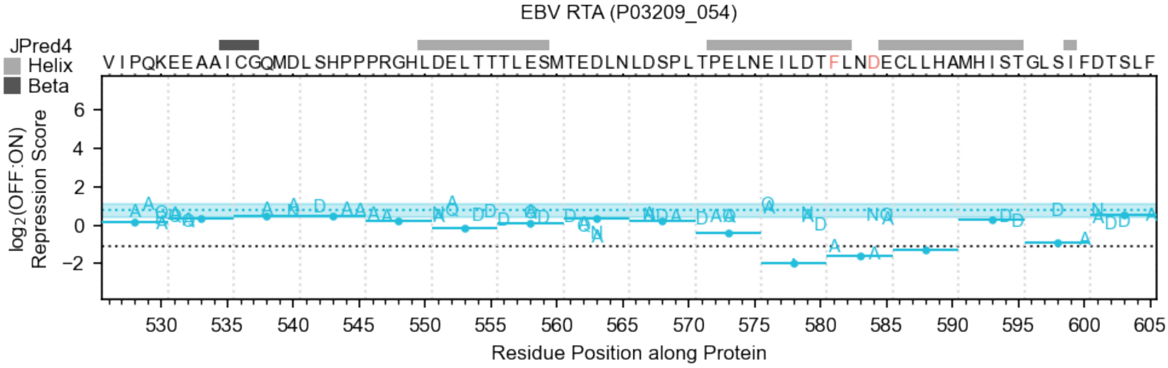
Extended repression domain from residues 521 to 605:
EMADTVIPQKEEAAICGQMDLSHPPPRGHLDELTTTLESMTEDLNLDSPLTPELNEILDTFLNDECLLHAMHISTGLSIFDTSLF

Max tile of repression domain from residues 526 to 605 (estimated 51.4% to 85.8% of cells repressed):
VIPQKEEAAICGQMDLSHPPPRGHLDELTTTLESMTEDLNLDSPLTPELNEILDTFLNDECLLHAMHISTGLSIFDTSLF



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| WW_3 | 544 | 548 | PPPRG | No | - | - | |
| flexi_NRBOX | 573 | 579 | ELNEILD | Yes | 576 | 590 | EILDTFLNDECLLHA |
| flexi_NRBOX | 577 | 583 | ILDTFLN | Yes | 576 | 590 | EILDTFLNDECLLHA |

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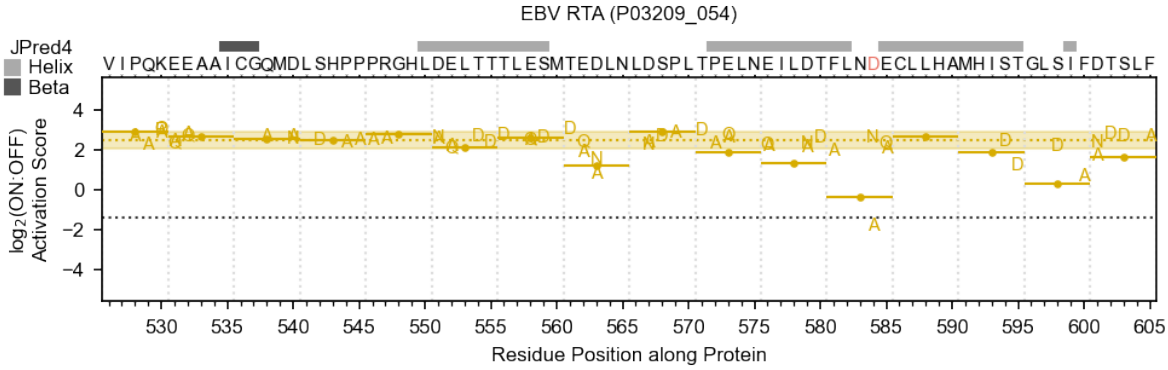
Extended activation domain from residues 511 to 605:
ETSQAVKALREMADTVIPQKEEAAICGQMDLSHPPPRGHLDELTTTLESMTEDLNLDSPLTPELNEILDTFLNDECLLHAMHISTGLSIFDTSLF

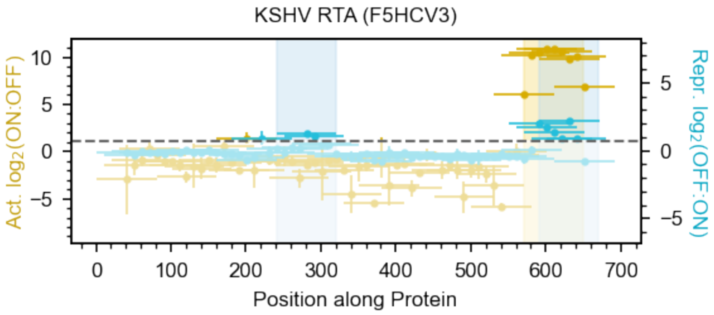
Max tile of activation domain from residues 526 to 605 (estimated 89.5% to 93.2% of cells activated):
VIPQKEEAAICGQMDLSHPPPRGHLDELTTTLESMTEDLNLDSPLTPELNEILDTFLNDECLLHAMHISTGLSIFDTSLF



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| WW_3 | 544 | 548 | PPPRG | No | - | - | |
| flexi_NRBOX | 573 | 579 | ELNEILD | No | - | - | |
| flexi_NRBOX | 577 | 583 | ILDTFLN | No | - | - | |

## KSHV RTA (F5HCV3)

Gene: ORF50 ; Protein Family: RTA



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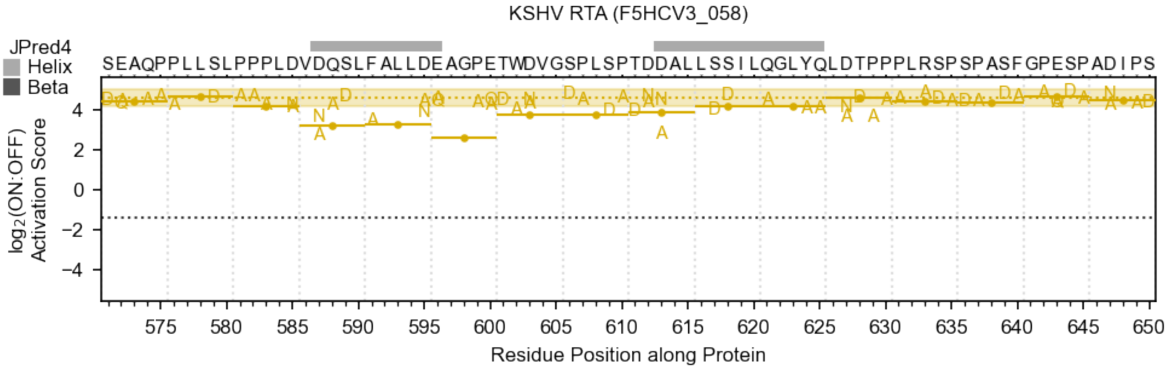
Extended repression domain from residues 241 to 330:
TGKVTGLSYPGSGLMPESLILPILEPGLLPASMVDLSDVLAKPAVILSAPALSQFVISKPHPNMPHTVSIIPFNPSGTDPAFISTWQAAS

Max tile of repression domain from residues 241 to 320 (estimated 22.4% to 26.9% of cells repressed):
TGKVTGLSYPGSGLMPESLILPILEPGLLPASMVDLSDVLAKPAVILSAPALSQFVISKPHPNMPHTVSIIPFNPSGTDP

---

Extended activation domain from residues 531 to 680:
ALTVPEADTTPSTTTPGTSLGSITTPQDVHATDVATSEGPSEAQPPLLSLPPPLDVDQSLFALLDEAGPETWDVGSPLSPTDDALLSSILQGLYQLDTPPPLRSPSPASFGPESPADIPSPSGGEYTQLQPVRATSATPANEVQESGTLY

Max tile of activation domain from residues 571 to 650 (estimated 97.2% to 97.2% of cells activated):
SEAQPPLLSLPPPLDVDQSLFALLDEAGPETWDVGSPLSPTDDALLSSILQGLYQLDTPPPLRSPSPASFGPESPADIPS



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_par | 582 | 587 | PPLDVD | No | - | - | |
| LIG_NRBOX | 589 | 595 | SLFALLD | No | - | - | |
| flexi_NRBOX | 615 | 621 | LLSSILQ | No | - | - | |

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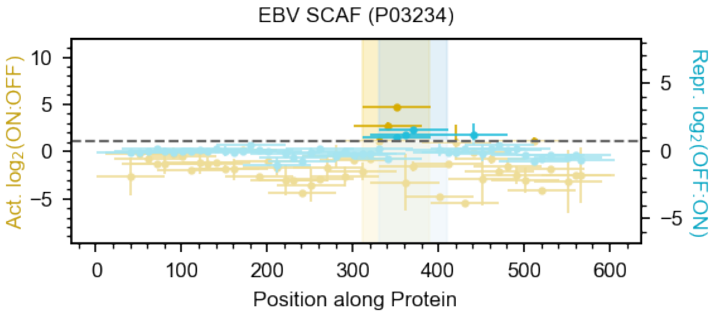
Extended repression domain from residues 551 to 680:
GSITTPQDVHATDVATSEGPSEAQPPLLSLPPPLDVDQSLFALLDEAGPETWDVGSPLSPTDDALLSSILQGLYQLDTPPPLRSPSPASFGPESPADIPSPSGGEYTQLQPVRATSATPANEVQESGTLY

Max tile of repression domain from residues 591 to 670 (estimated 45.2% to 52.2% of cells repressed):
FALLDEAGPETWDVGSPLSPTDDALLSSILQGLYQLDTPPPLRSPSPASFGPESPADIPSPSGGEYTQLQPVRATSATPA

## EBV SCAF (P03234)

Gene: BVRF2 ; Protein Family: SCAF



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Extended activation domain from residues 291 to 390:
FMTLLQTNLDNKPPRQTPLPYAAPLPPFSHQAIATAPSYGPGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAYFGLPGLFGPPP

Max tile of activation domain from residues 311 to 390 (estimated 26.1% to 34.6% of cells activated):
YAAPLPPFSHQAIATAPSYGPGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAYFGLPGLFGPPP

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Extended repression domain from residues 311 to 410:
YAAPLPPFSHQAIATAPSYGPGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAYFGLPGLFGPPPPVPPYYGSHLRADYVPAPSR

Max tile of repression domain from residues 331 to 410 (estimated 30.6% to 31.4% of cells repressed):
PGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAYFGLPGLFGPPPPVPPYYGSHLRADYVPAPSR

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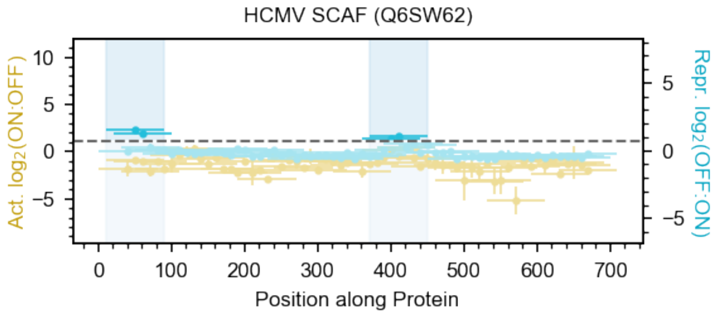
# HCMV SCAF (Q6SW62)

Gene: UL80 ; Protein Family: SCAF



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Extended repression domain from residues 11 to 100:
VAPVYVGGFLARYDQSPDEAELLLPRDVVEHWLHAQGQGQPSLSVALPLNINHDDTAVVGHVAAMQSVRDGLFCLGCVTSPRFLEIVRRA

Max tile of repression domain from residues 11 to 90 (estimated 27.9% to 33.6% of cells repressed):
VAPVYVGGFLARYDQSPDEAELLLPRDVVEHWLHAQGQGQPSLSVALPLNINHDDTAVVGHVAAMQSVRDGLFCLGCVTS

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Extended repression domain from residues 361 to 450:
AVSSLAWPHDGVYLPKDAFFSLLGASRSAAPVMYPGAVAAPPSASPAPLPLPSYPASYGAPVVGYDQLAARHFADYVDPHYPGWGRRYEP

Max tile of repression domain from residues 371 to 450 (estimated 20.4% to 20.5% of cells repressed):
GVYLPKDAFFSLLGASRSAAPVMYPGAVAAPPSASPAPLPLPSYPASYGAPVVGYDQLAARHFADYVDPHYPGWGRRYEP

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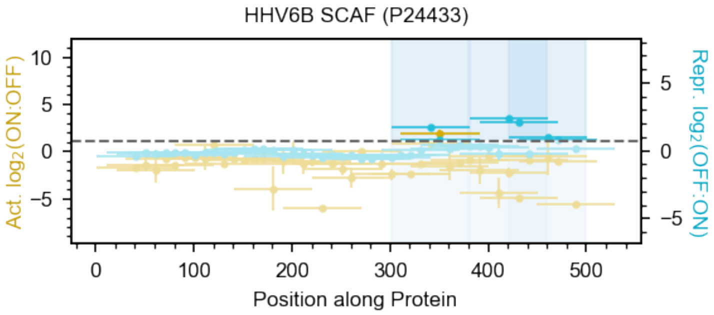
## HHV6B SCAF (P24433)

Gene: U53 ; Protein Family: SCAF



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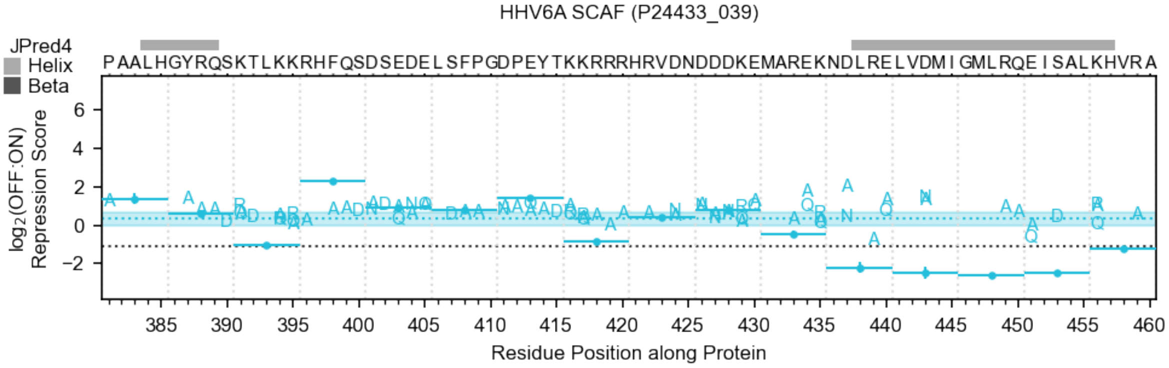
Extended repression domain from residues 301 to 390:
PFSDCVFLPKDAFFSLLNVTTGQQPKIVPPVSVHPPVTEQYQMLPYSESAAKIAEHESNRYHSPCQAMYPYWQYSPVPQYPAALHGYRQS

Max tile of repression domain from residues 301 to 380 (estimated 33.3% to 37.7% of cells repressed):
PFSDCVFLPKDAFFSLLNVTTGQQPKIVPPVSVHPPVTEQYQMLPYSESAAKIAEHESNRYHSPCQAMYPYWQYSPVPQY

---

Extended repression domain from residues 381 to 470:
PAALHGYRQSKTLKKRHFQSDSEDELSFPGDPEYTKKRRRHRVDNDDDKEMAREKNDLRELVDMIGMLRQEISALKHVRAQSPQRHIVPM

Max tile of repression domain from residues 381 to 460 (estimated 54.1% to 55.6% of cells repressed):
PAALHGYRQSKTLKKRHFQSDSEDELSFPGDPEYTKKRRRHRVDNDDDKEMAREKNDLRELVDMIGMLRQEISALKHVRA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_rev | 424 | 431 | DNDDDKEM | No | - | - | |
| flexi_NRBOX | 437 | 443 | DLRELVD | Yes | 436 | 460 | NDLRELVDMIGMLRQEISALKHVRA |

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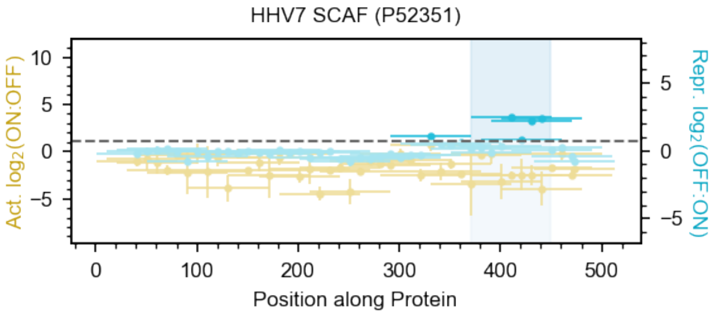
Extended repression domain from residues 421 to 510:
HRVDNDDDKEMAREKNDLRELVDMIGMLRQEISALKHVRAQSPQRHIVPMETLPTIEEKGAASPKPSILNASLAPETVNRSLAGQNESTD

Max tile of repression domain from residues 421 to 500 (estimated 16.9% to 22.9% of cells repressed):
HRVDNDDDKEMAREKNDLRELVDMIGMLRQEISALKHVRAQSPQRHIVPMETLPTIEEKGAASPKPSILNASLAPETVNR

# HHV7 SCAF (P52351)

Gene: U53 ; Protein Family: SCAF



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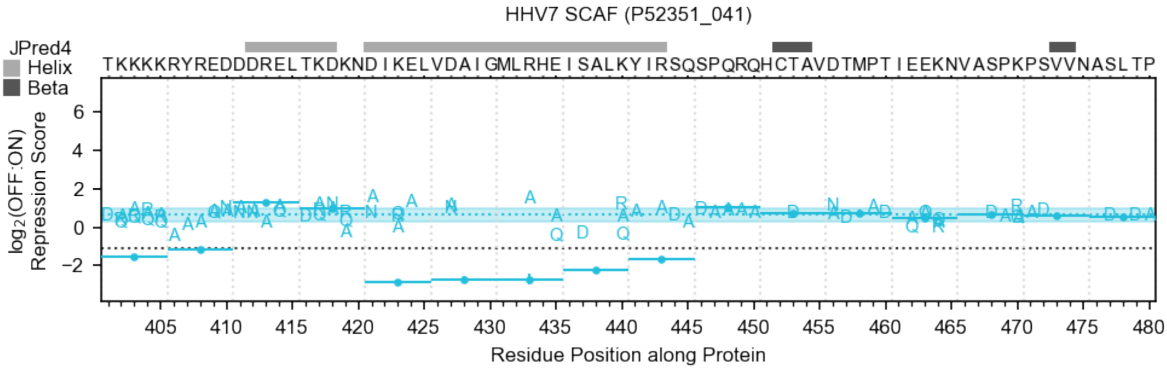
Extended repression domain from residues 371 to 480:
NYKSYRGSQKRCAPTDSDDEMSFPGDPDYTTKKKKRYREDDDRELTKDKNDIKELVDAIGMLRHEISALKYIRSQSPQRQHCTAVDTMPTIEEKNVASPKPSVVNASLTP

Max tile of repression domain from residues 371 to 450 (estimated 54.8% to 57.3% of cells repressed):
NYKSYRGSQKRCAPTDSDDEMSFPGDPDYTTKKKKRYREDDDRELTKDKNDIKELVDAIGMLRHEISALKYIRSQSPQRQ

---

Extended repression domain from residues 371 to 480:
NYKSYRGSQKRCAPTDSDDEMSFPGDPDYTTKKKKRYREDDDRELTKDKNDIKELVDAIGMLRHEISALKYIRSQSPQRQHCTAVDTMPTIEEKNVASPKPSVVNASLTP

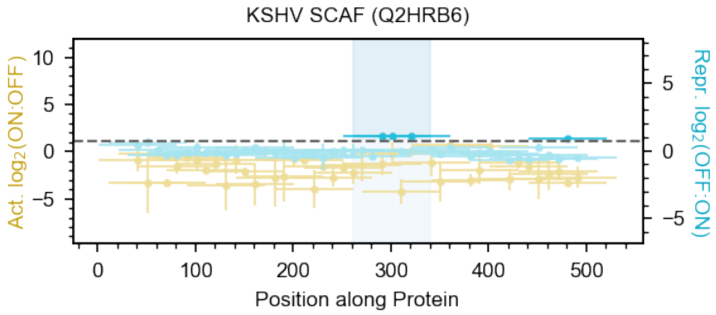
Max tile of repression domain from residues 401 to 480 (estimated 54.3% to 54.4% of cells repressed):
TKKKKRYREDDDRELTKDKNDIKELVDAIGMLRHEISALKYIRSQSPQRQHCTAVDTMPTIEEKNVASPKPSVVNASLTP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 401 | 410 | TKKKKRYRED |
| SUMO_rev | 418 | 425 | DKNDIKEL | Yes | 421 | 445 | DIKELVDAIGMLRHEISALKYIRSQ |
| flexi_NRBOX | 421 | 427 | DIKELVD | Yes | 421 | 445 | DIKELVDAIGMLRHEISALKYIRSQ |
| SUMO_rev | 456 | 466 | DTMPTIEEKNV | No | - | - | |

## KSHV SCAF (Q2HRB6)

Gene: ORF17 ; Protein Family: SCAF



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Extended repression domain from residues 251 to 340:
GQEDIISIPKSAFLSMLQSSIDGMKTTAAKMSHTLSGPGLMGCGGQMFPTDHHLPSYVSNPAPPYGYAYKNPYDPWYYSPQLPGYRTGKR

Max tile of repression domain from residues 261 to 340 (estimated 17.0% to 25.2% of cells repressed):
SAFLSMLQSSIDGMKTTAAKMSHTLSGPGLMGCGGQMFPTDHHLPSYVSNPAPPYGYAYKNPYDPWYYSPQLPGYRTGKR

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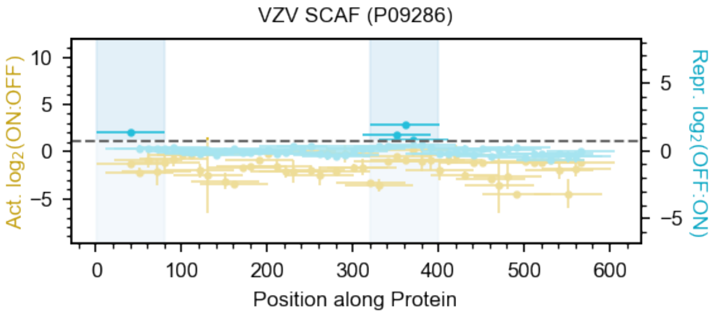
## VZV SCAF (P09286)

Gene: ORF33 ; Protein Family: SCAF



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Extended repression domain from residues 1 to 80:
MAAEADEENCEALYVAGYLALYSKDEGELNITPEIVRSALPPTSKIPINIDHRKDCVVGEVIAIIEDIRGPFFLGIVRCP

Max tile of repression domain from residues 1 to 80 (estimated 25.0% to 30.9% of cells repressed):
MAAEADEENCEALYVAGYLALYSKDEGELNITPEIVRSALPPTSKIPINIDHRKDCVVGEVIAIIEDIRGPFFLGIVRCP

---

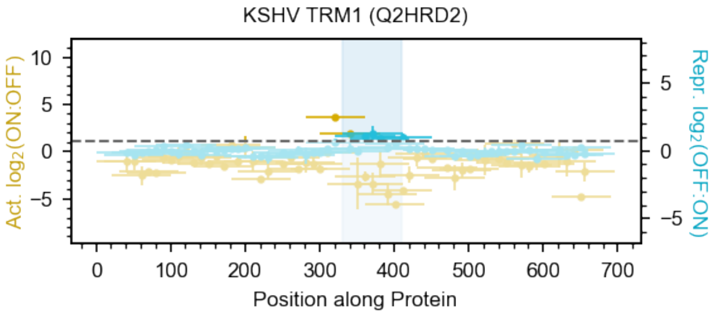
Extended repression domain from residues 311 to 410:
ASNISPQPPSGVPTGGEFVLIPTAYYSQLLTGQTKNPQVSIGAPNNGQYIVGPYGSPHPPAFPPNTGGYGCPPGHFGGPYGFPGYPPPNRLEMQMSAFMN

Max tile of repression domain from residues 321 to 400 (estimated 39.9% to 43.0% of cells repressed):
GVPTGGEFVLIPTAYYSQLLTGQTKNPQVSIGAPNNGQYIVGPYGSPHPPAFPPNTGGYGCPPGHFGGPYGFPGYPPPNR

---

# KSHV TRM1 (Q2HRD2)

Gene: ORF7 ; Protein Family: TRM1



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Extended repression domain from residues 321 to 420:
GCLGERGTPKHFFDCFRPDSLETLFCGGLFSSVEDTIESLQKDCSSAFYQQVNYTTALQKQNEFYVRLSKLLAAGQLNLGKCSTESCPSEARRQLVGGDK

Max tile of repression domain from residues 331 to 410 (estimated 15.0% to 37.8% of cells repressed):
HFFDCFRPDSLETLFCGGLFSSVEDTIESLQKDCSSAFYQQVNYTTALQKQNEFYVRLSKLLAAGQLNLGKCSTESCPSE

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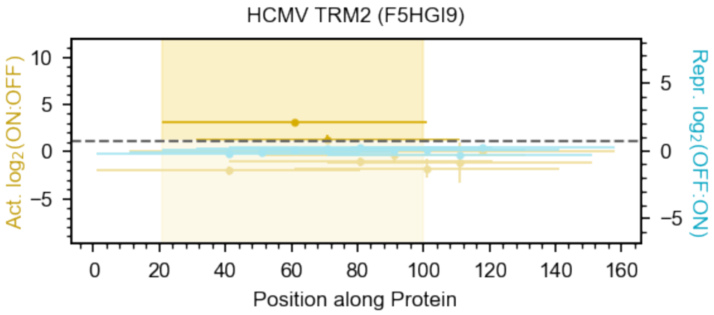
## HCMV TRM2 (F5HGI9)

Gene: UL51 ; Protein Family: TRM2



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Extended activation domain from residues 21 to 110:
DVQDDVDSPVPTRPLVIDEDAEPAAGTSGGLEGGGGDDEDGEDGHALPDLDDDLLLQFEPMLPRVYDLLLPSLDARLNFVNAGQKYAAFL

Max tile of activation domain from residues 21 to 100 (estimated 8.5% to 9.9% of cells activated):
DVQDDVDSPVPTRPLVIDEDAEPAAGTSGGLEGGGGDDEDGEDGHALPDLDDDLLLQFEPMLPRVYDLLLPSLDARLNFV

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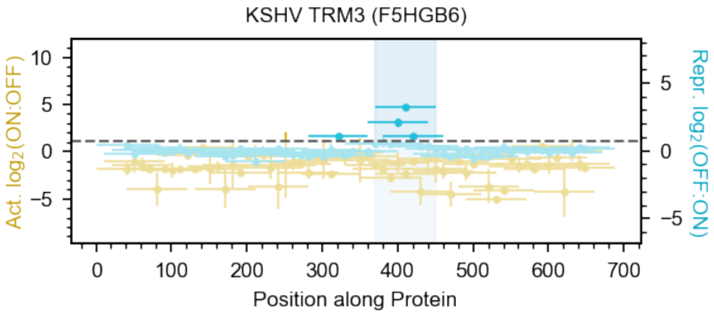
## KSHV TRM3 (F5HGB6)

Gene: ORF29 ; Protein Family: TRM3



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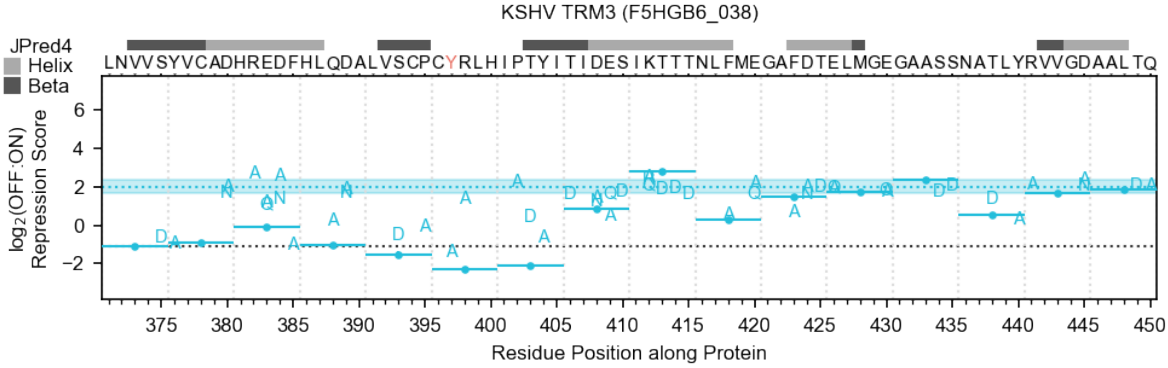
Extended repression domain from residues 361 to 460:
LNLRNAQEKMLNVVSYVCADHREDFHLQDALVSCPCYRLHIPTYITIDESIKTTTNLFMEGAFDTELMGEGAASSNATLYRVVGDAALTQFDMCRVDTTA

Max tile of repression domain from residues 371 to 450 (estimated 73.2% to 77.6% of cells repressed):
LNVVSYVCADHREDFHLQDALVSCPCYRLHIPTYITIDESIKTTTNLFMEGAFDTELMGEGAASSNATLYRVVGDAALTQ



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 372 | 378 | NVVSYVC | Yes | 371 | 375 | LNVVS |
| | - | - | | No | 391 | 405 | LVSCPCYRLHIPTYI |
| flexi_NRBOX | 438 | 444 | TLYRVVG | No | - | - | |

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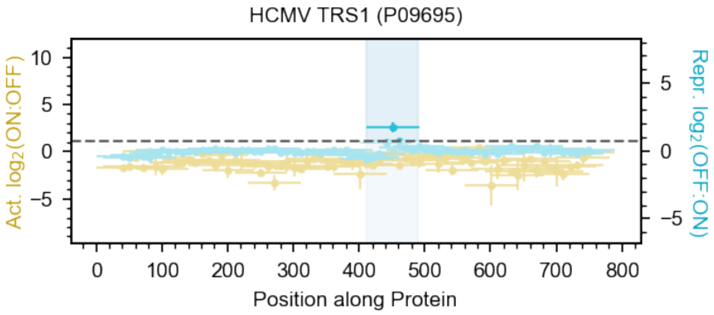
## HCMV TRS1 (P09695)

Gene: TRS1 ; Protein Family: TRS1



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Extended repression domain from residues 411 to 500:
AAGGGAICVPNADAHAVVGADAAAAAAPTVMVGSTAMAGPAASGTVPRAMLVVLLDELGAVFGYCPLDGHVYPLAAELSHFLRAGVLGAL

Max tile of repression domain from residues 411 to 490 (estimated 27.2% to 46.4% of cells repressed):
AAGGGAICVPNADAHAVVGADAAAAAAPTVMVGSTAMAGPAASGTVPRAMLVVLLDELGAVFGYCPLDGHVYPLAAELSH

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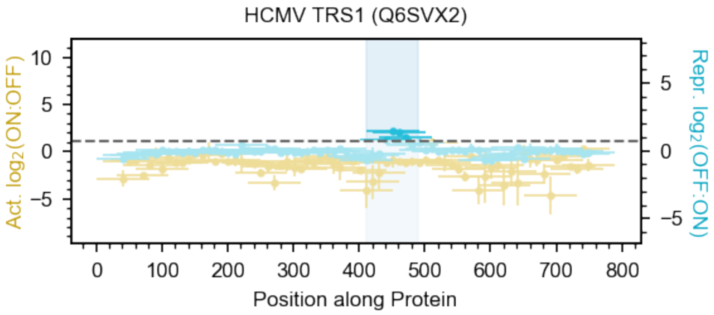
# HCMV TRS1 (Q6SVX2)

Gene: TRS1 ; Protein Family: TRS1



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Extended repression domain from residues 401 to 510:
PPQPYGGAGGSAICVPNADAHAVVGADATAAAAAAAAAPTVMVGPTAMAGPAASGTVPRAMLVVVLDELGAVFGYCPLDGHVYPLAAELSHFLRAGVLGALALGRESAPA

Max tile of repression domain from residues 411 to 490 (estimated 27.4% to 31.6% of cells repressed):
SAICVPNADAHAVVGADATAAAAAAAAAPTVMVGPTAMAGPAASGTVPRAMLVVVLDELGAVFGYCPLDGHVYPLAAELS

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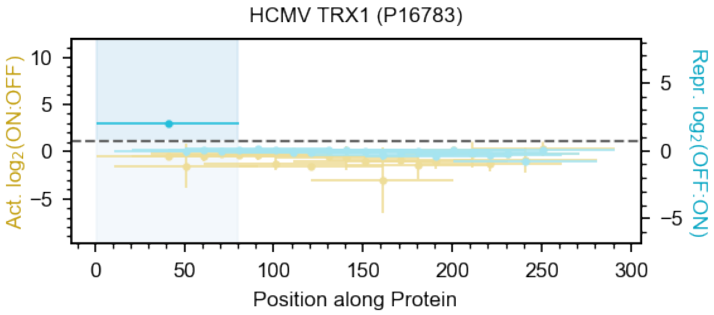
# HCMV TRX1 (P16783)

Gene: UL46 ; Protein Family: TRX1



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Extended repression domain from residues 1 to 80:
MDARAVAKRPRDPADEDNELVTALKAKREVNTISVRYLYHADHQALTARFFVPEGLVEFEAQPGALLIRMETGCDSPRHL

Max tile of repression domain from residues 1 to 80 (estimated 42.6% to 43.7% of cells repressed):
MDARAVAKRPRDPADEDNELVTALKAKREVNTISVRYLYHADHQALTARFFVPEGLVEFEAQPGALLIRMETGCDSPRHL

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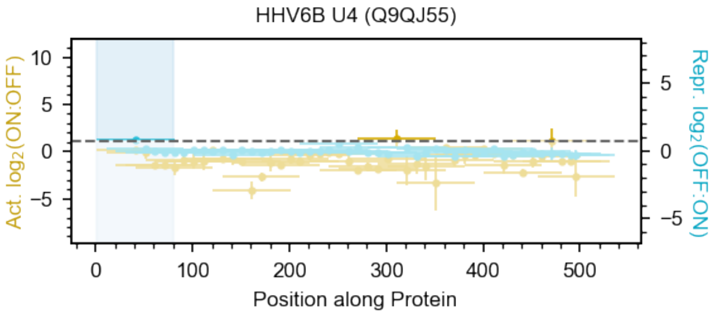
## HHV6B U4 (Q9QJ55)

Gene: U4 ; Protein Family: U4



---

Extended repression domain from residues 1 to 80:
MELLDHDIYKGPVRERVTYTIPNHPYLSLTVHHSRELDVDLKDITEEMIIDSGTLTAEDLFMTRGLRFCDDSVLWAALAE

Max tile of repression domain from residues 1 to 80 (estimated 13.6% to 17.0% of cells repressed):
MELLDHDIYKGPVRERVTYTIPNHPYLSLTVHHSRELDVDLKDITEEMIIDSGTLTAEDLFMTRGLRFCDDSVLWAALAE

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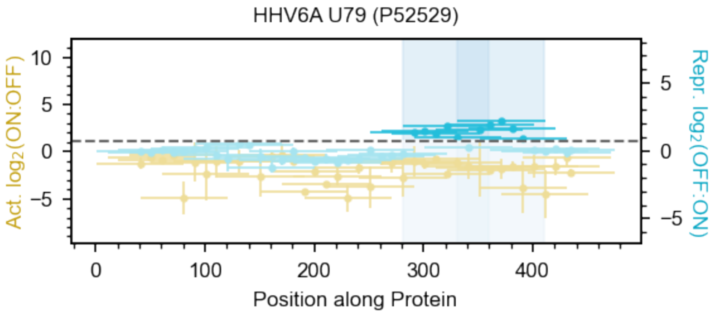
# HHV6A U79 (P52529)

Gene: U79/U80 ; Protein Family: U79



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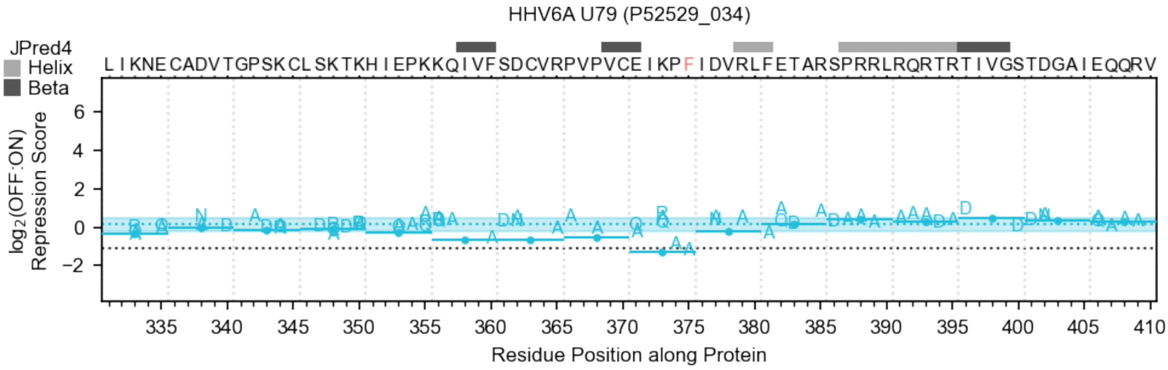
Extended repression domain from residues 251 to 370:
ALPPCISIDNHEDQQHDELDKRAYAQGTNREGLSNEDNYGNFRLNKSLEQLRAKLVASSGDIVERSLLKLKECLDNVKDNLIKNECADVTGPSKCLSKTKHIEPKKQIVFSDCVRPVPVC

Max tile of repression domain from residues 281 to 360 (estimated 36.5% to 43.5% of cells repressed):
EGLSNEDNYGNFRLNKSLEQLRAKLVASSGDIVERSLLKLKECLDNVKDNLIKNECADVTGPSKCLSKTKHIEPKKQIVF

---

Extended repression domain from residues 311 to 430:
DIVERSLLKLKECLDNVKDNLIKNECADVTGPSKCLSKTKHIEPKKQIVFSDCVRPVPVCEIKPFIDVRLFETARSPRRLRQRTRTIVGSTDGAIEQQRVISGQNRGRARGRGRGRAPRR

Max tile of repression domain from residues 331 to 410 (estimated 46.7% to 52.4% of cells repressed):
LIKNECADVTGPSKCLSKTKHIEPKKQIVFSDCVRPVPVCEIKPFIDVRLFETARSPRRLRQRTRTIVGSTDGAIEQQRV



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 332 | 335 | IKNE | No | - | - | |
| | - | - | | No | 371 | 375 | EIKPF |

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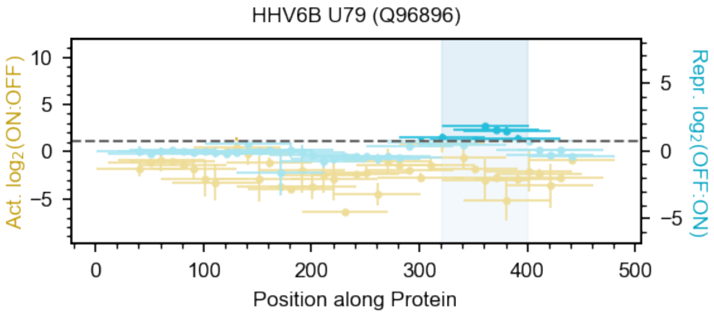
## HHV6B U79 (Q96896)

Gene: U79/U80 ; Protein Family: U79



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Extended repression domain from residues 311 to 430:
GEVVERSLSKLKERLDYVKDNLIKNVLECADVTVPSKCLSKTKHIEQKKQIVFSDCVRSVPVCEIKPFIDMRVFETETTQNARRVRQRTRTTVGSTDGAIGQQRVISGQNRGRARGRGRG

Max tile of repression domain from residues 321 to 400 (estimated 36.6% to 39.5% of cells repressed):
LKERLDYVKDNLIKNVLECADVTVPSKCLSKTKHIEQKKQIVFSDCVRSVPVCEIKPFIDMRVFETETTQNARRVRQRTR

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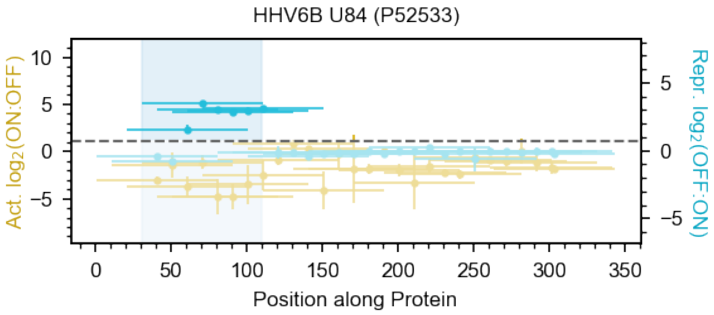
## HHV6B U84 (P52533)

Gene: U84 ; Protein Family: U84



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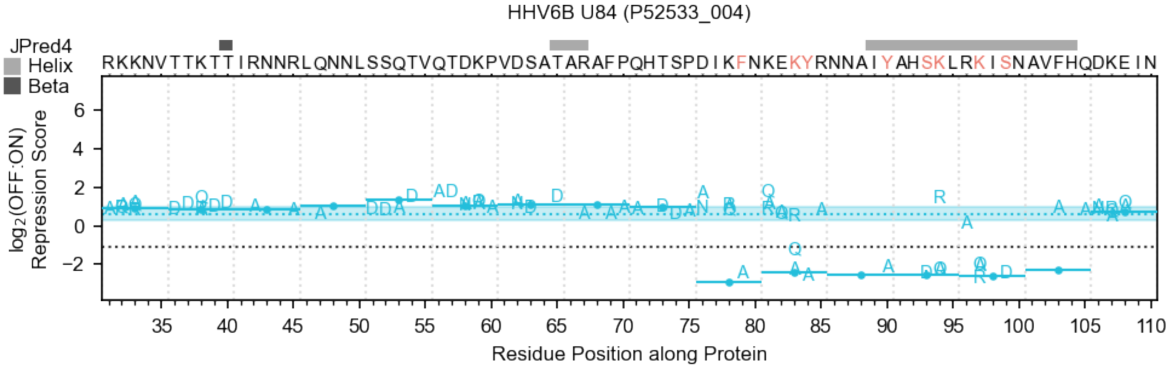
Extended repression domain from residues 21 to 150:
TRKTTKPSTERKKNVTTKTTIRNNRLQNNLSSQTVQTDKPVDSATARAFPQHTSPDIKFNKEKYRNNAIYAHSKLRKISNAVFHQDKEINRFSAFTDKPLADLSFNMPVKTSTTQKKEIVKSTECQRQDP

Max tile of repression domain from residues 31 to 110 (estimated 77.5% to 84.1% of cells repressed):
RKKNVTTKTTIRNNRLQNNLSSQTVQTDKPVDSATARAFPQHTSPDIKFNKEKYRNNAIYAHSKLRKISNAVFHQDKEIN



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_rev | 74 | 79 | SPDIKF | Yes | 76 | 105 | DIKFNKEKYRNNAIYAHSKLRKISNAVFHQ |

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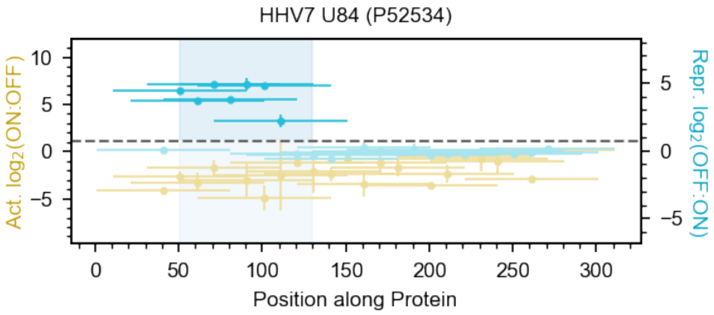
## HHV7 U84 (P52534)

Gene: U84 ; Protein Family: U84



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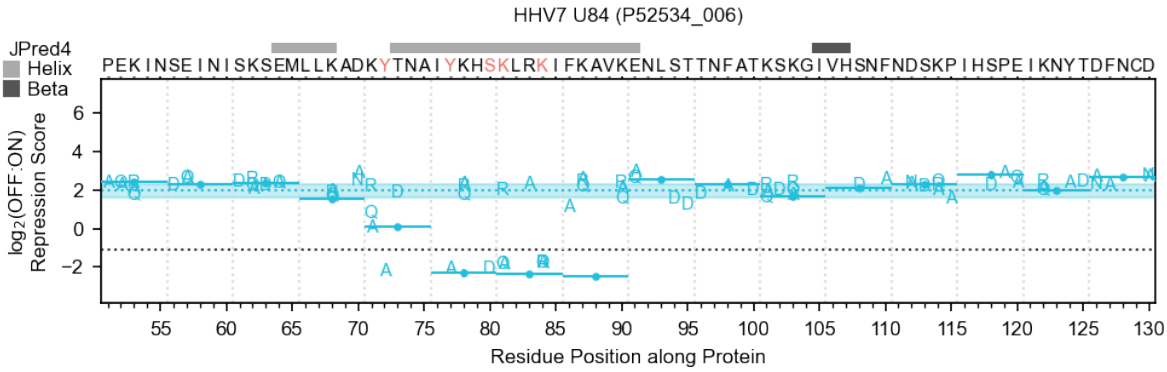
Extended repression domain from residues 11 to 150:
KAKGKLTSKSCMCTKANARYTCNCFSKTLPFNEKAIKCTIPEKINSEINISKSEMLLKADKYTNAIYKHSKLRKIFKAVKENLSTTNFATKSKGIVHSNFNDSKPIHSPEIKNYTDFNCDFMHPCGLCSPKNFLSEVYKL

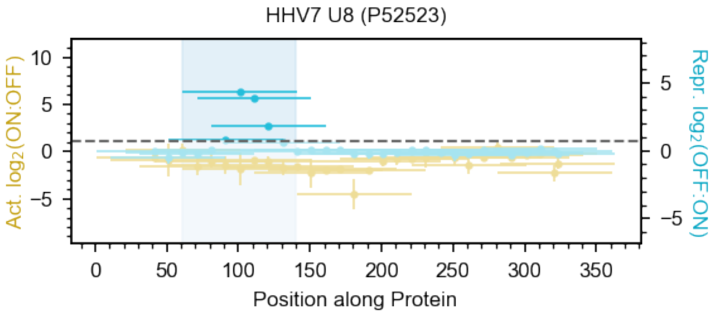
Max tile of repression domain from residues 51 to 130 (estimated 92.6% to 97.9% of cells repressed):
PEKINSEINISKSEMLLKADKYTNAIYKHSKLRKIFKAVKENLSTTNFATKSKGIVHSNFNDSKPIHSPEIKNYTDFNCD



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 81 | 87 | KLRKIFK | Yes | 76 | 90 | IYKHSKLRKIFKAVK |
| SUMO_rev | 108 | 116 | SNFNDSKPI | No | - | - | |

## HHV7 U8 (P52523)

Gene: U8 ; Protein Family: U8



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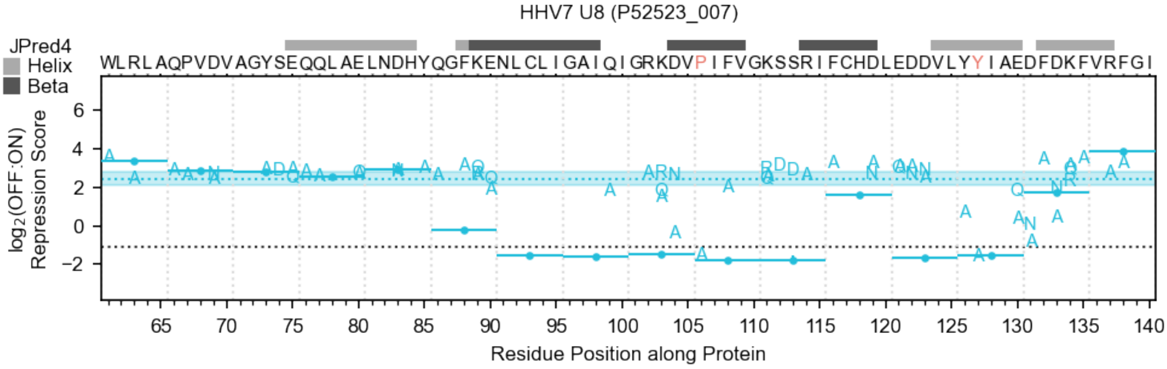
Extended repression domain from residues 51 to 160:
CLSLIWPKNLWLRLAQPVDVAGYSEQQLAELNDHYQGFKENLCLIGAIQIGRKDVPIFVGKSSRIFCHDLEDDVLYYIAEDFDKFVRFGILGTNVITCSEPVYTRFYYDG

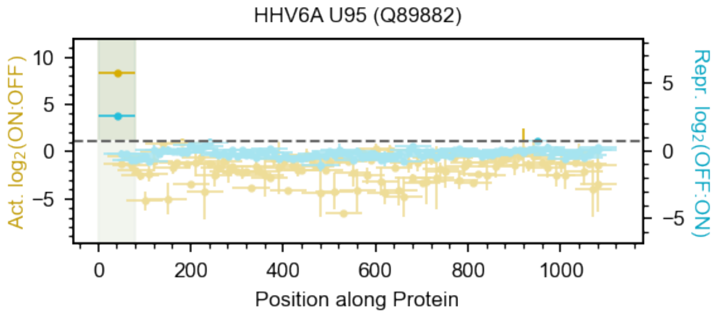
Max tile of repression domain from residues 61 to 140 (estimated 91.1% to 91.4% of cells repressed):
WLRLAQPVDVAGYSEQQLAELNDHYQGFKENLCLIGAIQIGRKDVPIFVGKSSRIFCHDLEDDVLYYIAEDFDKFVRFGI



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 91 | 115 | NLCLIGAIQIGRKDVPIFVGKSSRI |
| flexi_NRBOX | 123 | 129 | DVLYYIA | Yes | 121 | 130 | EDDVLYYIAE |
| flexi_NRBOX | 131 | 137 | DFDKFVR | No | - | - | |

## HHV6A U95 (Q89882)

Gene: U95 ; Protein Family: U95



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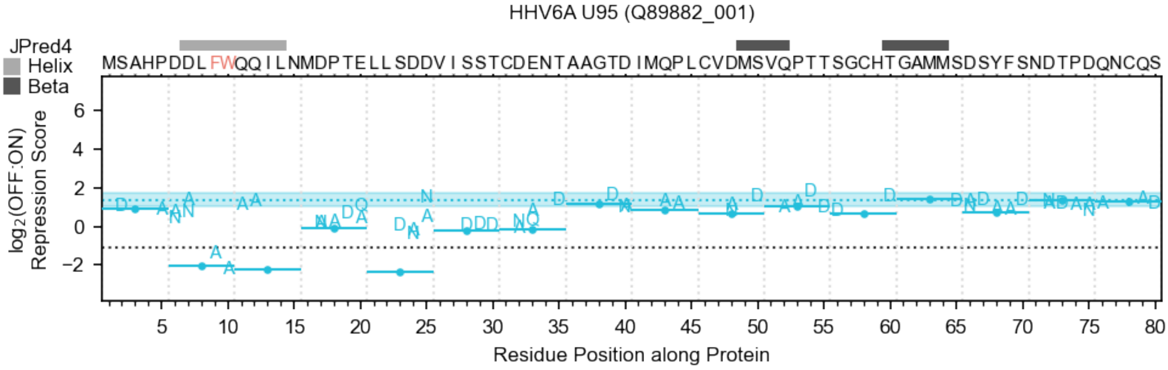
Extended repression domain from residues 1 to 80:
MSAHPDDLFWQQILNMDPTELLSDDVISSTCDENTAAGTDIMQPLCVDMSVQPTTSGCHTGAMMSDSYFSNDTPDQNCQS

Max tile of repression domain from residues 1 to 80 (estimated 58.2% to 60.7% of cells repressed):
MSAHPDDLFWQQILNMDPTELLSDDVISSTCDENTAAGTDIMQPLCVDMSVQPTTSGCHTGAMMSDSYFSNDTPDQNCQS



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| CtBP_expanded | 5 | 9 | PDDLF | Yes | 6 | 15 | DDLFWQQILN |
| flexi_NRBOX | 9 | 15 | FWQQILN | Yes | 6 | 15 | DDLFWQQILN |
| CtBP_expanded | 18 | 22 | PTELL | Yes | 21 | 25 | LLSDD |

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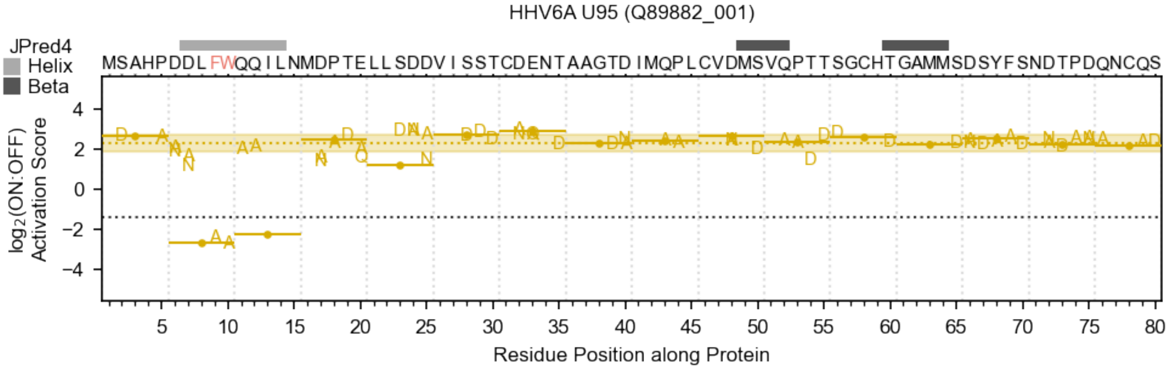
Extended activation domain from residues 1 to 80:
MSAHPDDLFWQQILNMDPTELLSDDVISSTCDENTAAGTDIMQPLCVDMSVQPTTSGCHTGAMMSDSYFSNDTPDQNCQS

Max tile of activation domain from residues 1 to 80 (estimated 87.9% to 91.4% of cells activated):
MSAHPDDLFWQQILNMDPTELLSDDVISSTCDENTAAGTDIMQPLCVDMSVQPTTSGCHTGAMMSDSYFSNDTPDQNCQS

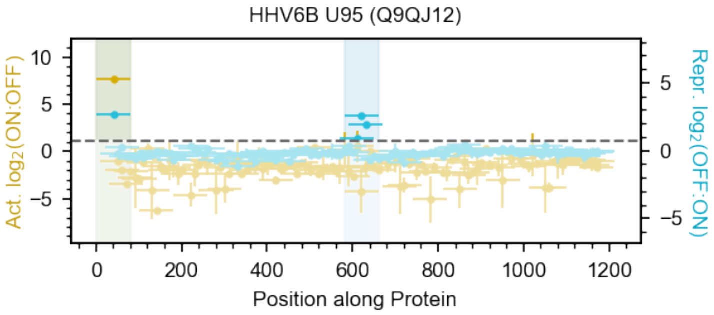


## Herpesvirus Tiling and Perturbation Screen Data from Ludwig, C.H. et al. 2023

| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| CtBP_expanded | 5 | 9 | PDDLF | Yes | 6 | 15 | DDLFWQQILN |
| flexi_NRBOX | 9 | 15 | FWQQILN | Yes | 6 | 15 | DDLFWQQILN |
| CtBP_expanded | 18 | 22 | PTELL | No | - | - | |

# HHV6B U95 (Q9QJ12)

Gene: U95 ; Protein Family: U95



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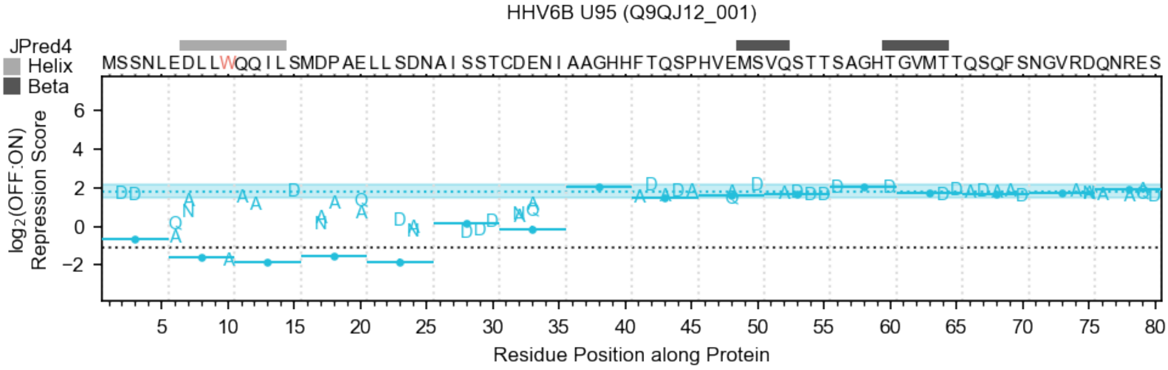
Extended repression domain from residues 1 to 80:
MSSNLEDLLWQQILSMDPAELLSDNAISSTCDENIAAGHHFTQSPHVEMSVQSTTSAGHTGVMTTQSQFSNGVRDQNRES

Max tile of repression domain from residues 1 to 80 (estimated 58.9% to 62.9% of cells repressed):
MSSNLEDLLWQQILSMDPAELLSDNAISSTCDENIAAGHHFTQSPHVEMSVQSTTSAGHTGVMTTQSQFSNGVRDQNRES



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| LIG_NRBOX | 4 | 10 | NLEDLLW | Yes | 6 | 25 | EDLLWQQILSMDPAELLSDN |
| CtBP_expanded | 18 | 22 | PAELL | Yes | 6 | 25 | EDLLWQQILSMDPAELLSDN |
| flexi_NRBOX | 9 | 15 | LWQQILS | Yes | 6 | 25 | EDLLWQQILSMDPAELLSDN |

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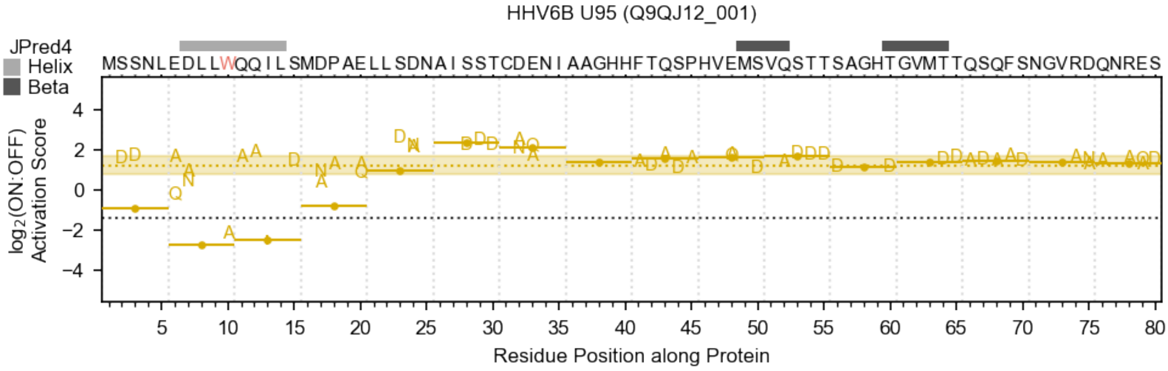
Extended activation domain from residues 1 to 80:
MSSNLEDLLWQQILSMDPAELLSDNAISSTCDENIAAGHHFTQSPHVEMSVQSTTSAGHTGVMTTQSQFSNGVRDQNRES

Max tile of activation domain from residues 1 to 80 (estimated 83.1% to 84.0% of cells activated):
MSSNLEDLLWQQILSMDPAELLSDNAISSTCDENIAAGHHFTQSPHVEMSVQSTTSAGHTGVMTTQSQFSNGVRDQNRES



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| LIG_NRBOX | 4 | 10 | NLEDLLW | Yes | 6 | 15 | EDLLWQQILS |
| flexi_NRBOX | 9 | 15 | LWQQILS | Yes | 6 | 15 | EDLLWQQILS |
| CtBP_expanded | 18 | 22 | PAELL | No | - | - | |

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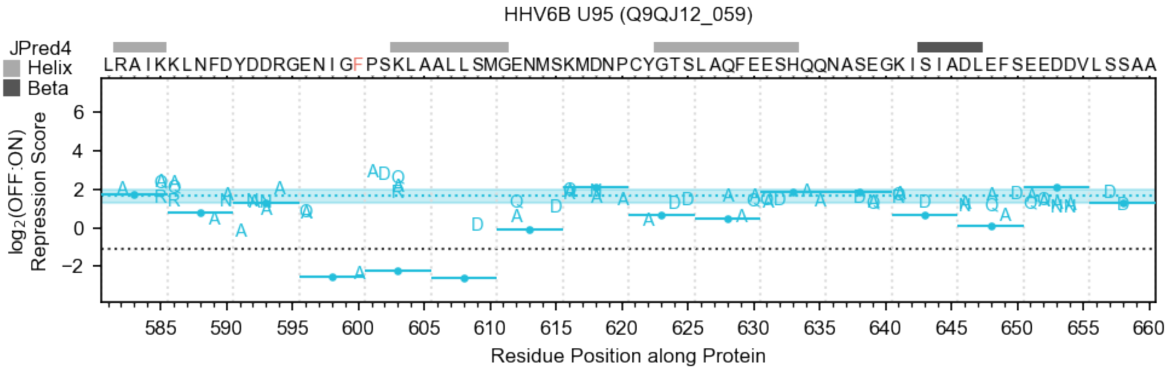
Extended repression domain from residues 571 to 670:
NKDVCKPTPSLRAIKKLNFDYDDRGENIGFPSKLAALLSMGENMSKMDNPCYGTSLAQFEESHQQNASEGKISIADLEFSEEDDVLSSAASVSCNDNCVM

Max tile of repression domain from residues 581 to 660 (estimated 55.7% to 61.2% of cells repressed):
LRAIKKLNFDYDDRGENIGFPSKLAALLSMGENMSKMDNPCYGTSLAQFEESHQQNASEGKISIADLEFSEEDDVLSSAA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| LIG_NRBOX | 603 | 609 | KLAALLS | Yes | 596 | 610 | ENIGFPSKLAALLSM |
| SUMO_rev | 638 | 643 | SEGKIS | No | - | - | |

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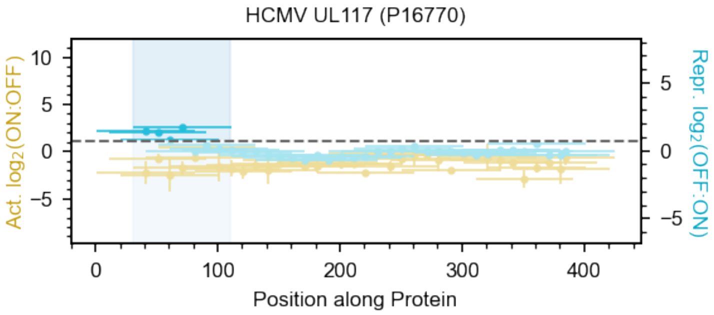
## HCMV UL117 (P16770)

Gene: UL117 ; Protein Family: UL117



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Extended repression domain from residues 1 to 110:
MVMFSQDHVQIVYGSTRICKSLAPANKRKTHRTIVVAPRRGFLRIPPDGQDVNHVKIVPTTSSSLAPPRDDERRPTPPLRPPLTVYPYGTSLIRRSARDAKLRSKLIVFH

Max tile of repression domain from residues 31 to 110 (estimated 34.3% to 38.0% of cells repressed):
HRTIVVAPRRGFLRIPPDGQDVNHVKIVPTTSSSLAPPRDDERRPTPPLRPPLTVYPYGTSLIRRSARDAKLRSKLIVFH

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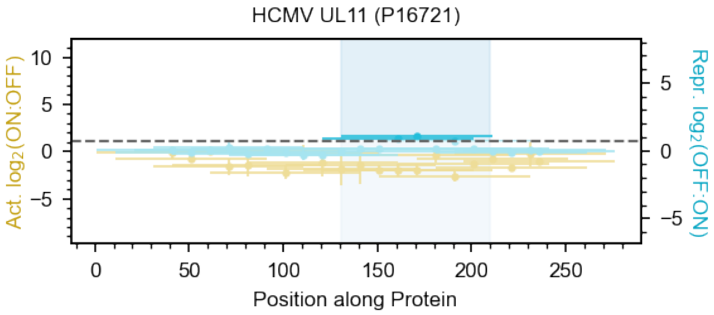
# HCMV UL11 (P16721)

Gene: UL11 ; Protein Family: UL11



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Extended repression domain from residues 121 to 210:
WHNHGNKWTLDTCYYVYVTQNGTLPTTTTKKPTTTTRTTTTTTTKKTTTTSTTTTTTTTKKTTTSTTHHRHSNPKESTTPKTHVELHVGL

Max tile of repression domain from residues 131 to 210 (estimated 19.3% to 23.8% of cells repressed):
DTCYYVYVTQNGTLPTTTTKKPTTTTRTTTTTTTKKTTTTSTTTTTTTTKKTTTSTTHHRHSNPKESTTPKTHVELHVGL

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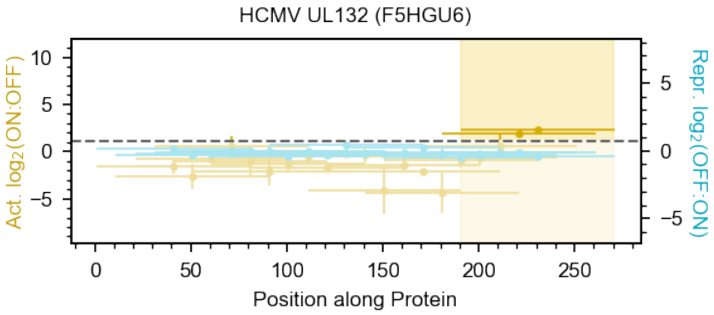
## HCMV UL132 (F5HGU6)

Gene: UL132 ; Protein Family: UL132

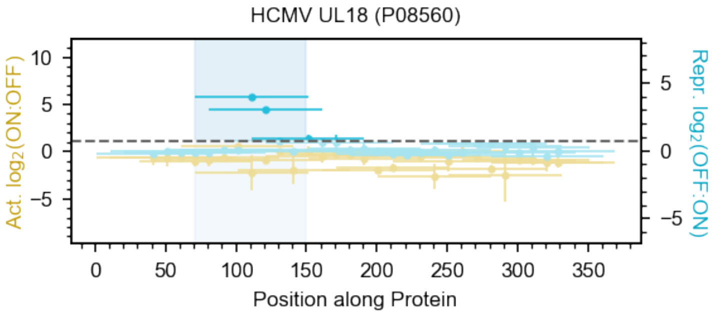


Extended activation domain from residues 181 to 270:
KHDPENVIYFRKDGNLDTSFVNPNYGRGSPLTIESHLSDNEEDPIRYYVSVYDELTASEMEEPSNSTSWQIPKLMKVAMQPVSLRDPEYD

Max tile of activation domain from residues 191 to 270 (estimated 4.7% to 6.0% of cells activated):
RKDGNLDTSFVNPNYGRGSPLTIESHLSDNEEDPIRYYVSVYDELTASEMEEPSNSTSWQIPKLMKVAMQPVSLRDPEYD

## HCMV UL18 (P08560)

Gene: UL18 ; Protein Family: UL18



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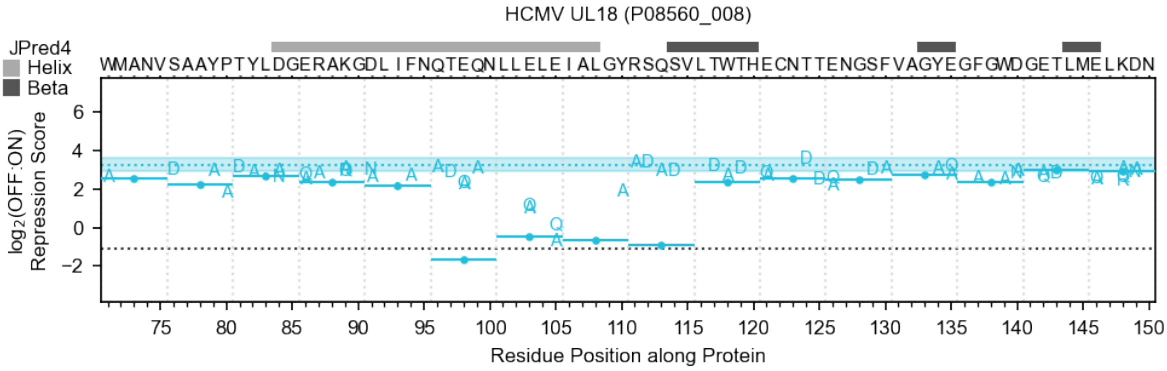
Extended repression domain from residues 71 to 170:
WMANVSAAYPTYLDGERAKGDLIFNQTEQNLLELEIALGYRSQSVLTWTHECNTTENGSFVAGYEGFGWDGETLMELKDNLTLWTGPNYEISWLKQNKTY

Max tile of repression domain from residues 71 to 150 (estimated 87.5% to 88.6% of cells repressed):
WMANVSAAYPTYLDGERAKGDLIFNQTEQNLLELEIALGYRSQSVLTWTHECNTTENGSFVAGYEGFGWDGETLMELKDN



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_par | 100 | 105 | NLLELE | Yes | 96 | 100 | QTEQN |

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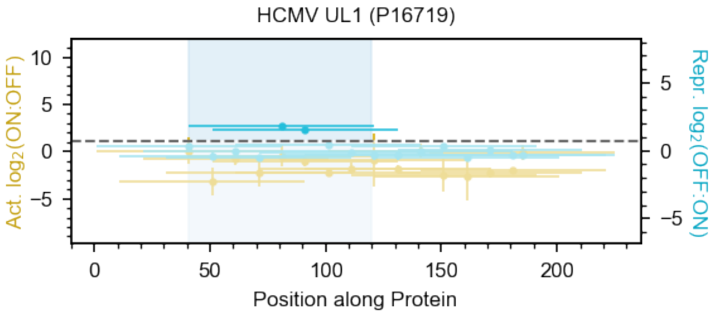
# HCMV UL1 (P16719)

Gene: UL1 ; Protein Family: UL1



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Extended repression domain from residues 41 to 130:
RLFLQSQHVEAPITVTQGDTVYLDASNNPCNYSSFWYHGNCELCGWNGYLRNVTHYYTNTSCSPQFMCINETKGLQLYNVTLNDSGAYTE

Max tile of repression domain from residues 41 to 120 (estimated 39.6% to 39.8% of cells repressed):
RLFLQSQHVEAPITVTQGDTVYLDASNNPCNYSSFWYHGNCELCGWNGYLRNVTHYYTNTSCSPQFMCINETKGLQLYNV

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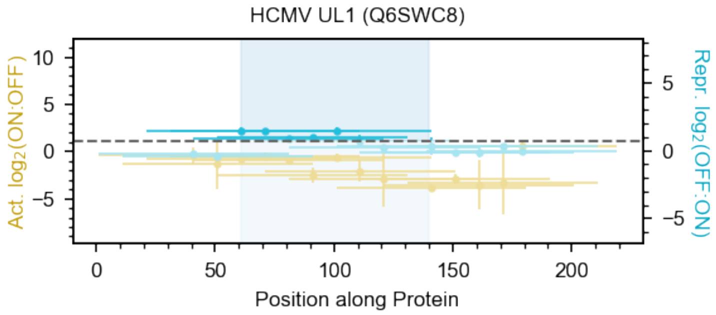
## HCMV UL1 (Q6SWC8)

Gene: UL1 ; Protein Family: UL1



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Extended repression domain from residues 21 to 150:
SSILVQAIPHKQKTSYQQLLLQSEHVQIPITVAEGDTICFNVSDNPCNFSSYWNHNNCELCGWTPFYSEYAGYSENKSCHPRFTCLHDTKGLKLHNVTTNDSGIYTRNVYYCDIPCNISDDHKHNVEDFD

Max tile of repression domain from residues 61 to 140 (estimated 24.5% to 36.3% of cells repressed):
NVSDNPCNFSSYWNHNNCELCGWTPFYSEYAGYSENKSCHPRFTCLHDTKGLKLHNVTTNDSGIYTRNVYYCDIPCNISD

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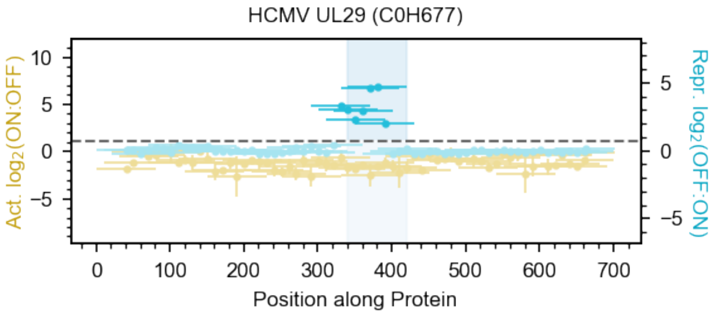
## HCMV UL29 (C0H677)

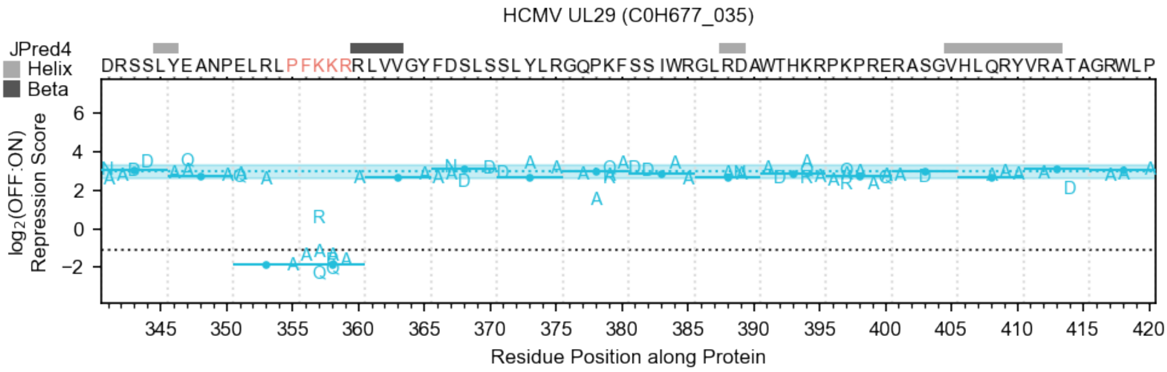
Gene: UL29 ; Protein Family: UL29



---

Extended repression domain from residues 291 to 430:
RILCGDTGTVYAALVGQDKLVRLARDLRGFVRVGLALLIDDFRYESIGPVDRSSLYEANPELRLPFKKRRLVVGYFDSLSSLYLRGQPKFSSIWRGLRDAWTHKRPKPRERASGVHLQRYVRATAGRWLPLCWPPLHGIM

Max tile of repression domain from residues 341 to 420 (estimated 94.1% to 95.2% of cells repressed):
DRSSLYEANPELRLPFKKRRLVVGYFDSLSSLYLRGQPKFSSIWRGLRDAWTHKRPKPRERASGVHLQRYVRATAGRWLP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| NCoR_SMRT_1 | 355 | 359 | PFKKR | Yes | 351 | 360 | ELRLPFKKRR |
| flexi_NRBOX | 361 | 367 | LVVGYFD | No | - | - | |
| flexi_NRBOX | 406 | 412 | HLQRYVR | No | - | - | |

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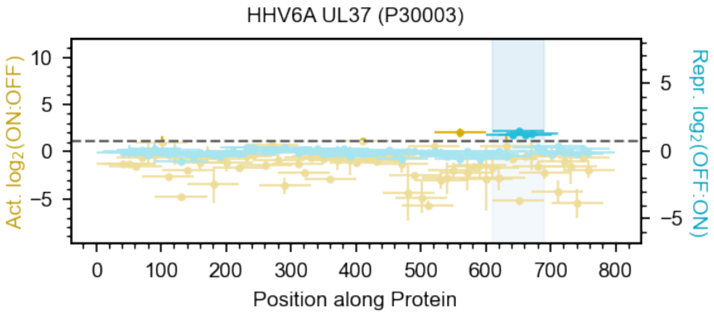
# HHV6A UL37 (P30003)

Gene: U30 ; Protein Family: UL37



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Extended repression domain from residues 601 to 710:
EKSLQTIQISETTLTGMLRNIITSVSSSKELLTNEALQKFIDTVQRISQHVNETYQSISMNLEKCKTSNDILIESLKKIIYIVDVLSSNAILNTSLASRCLEAANLAVSN

Max tile of repression domain from residues 611 to 690 (estimated 25.0% to 33.6% of cells repressed):
ETTLTGMLRNIITSVSSSKELLTNEALQKFIDTVQRISQHVNETYQSISMNLEKCKTSNDILIESLKKIIYIVDVLSSNA

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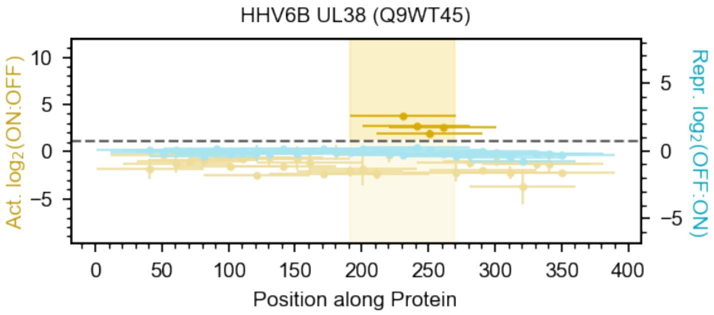
## HHV6B UL38 (Q9WT45)

Gene: U19 ; Protein Family: UL38



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Extended activation domain from residues 191 to 300:
DARASMRPIQSDSFGAKGPFCWPTEELLQPSAKKDVGGTVCMALSCQEDNSARHCTIYGLTKTPGIKIMLSRHTQTDRSEAMCDAATQTEDVVDNSSE
TLFLGGNLVHQS

Max tile of activation domain from residues 191 to 270 (estimated 12.3% to 17.9% of cells activated):
DARASMRPIQSDSFGAKGPFCWPTEELLQPSAKKDVGGTVCMALSCQEDNSARHCTIYGLTKTPGIKIMLSRHTQTDRSE

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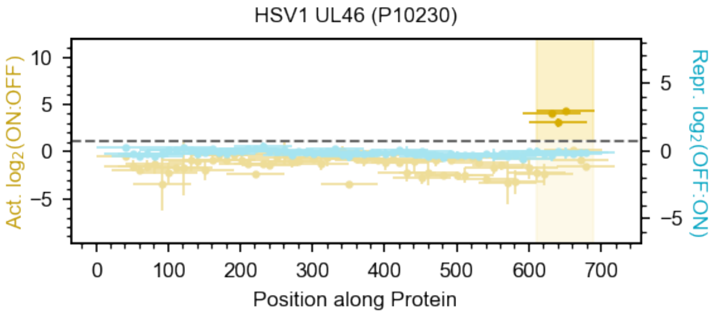
# HSV1 UL46 (P10230)

Gene: UL46 ; Protein Family: UL46



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Extended activation domain from residues 591 to 690:
RKATHAASARERHAPYEDDESIYETVSEDGGRVYEEIPWMRVYENVCVNTANAAPASPYIEAENPLYDWGGSALFSPPGRTGPPPPPLSPSPVLARHRAN

Max tile of activation domain from residues 611 to 690 (estimated 20.7% to 23.2% of cells activated):
SIYETVSEDGGRVYEEIPWMRVYENVCVNTANAAPASPYIEAENPLYDWGGSALFSPPGRTGPPPPPLSPSPVLARHRAN

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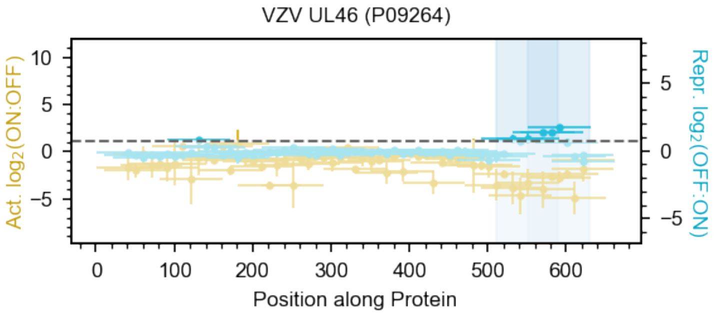
# VZV UL46 (P09264)

Gene: ORF12 ; Protein Family: UL46



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Extended repression domain from residues 491 to 590:
LSDDVNASSHVINTEAPLNSIAPDTNRQRTSRVLVRPDTGLDVTVRKNHCLDIGHTDGSPVDPTYPDHYTRIKAEYEGPVRDESNTMFDQRSDLRHIETQ

Max tile of repression domain from residues 511 to 590 (estimated 12.0% to 25.5% of cells repressed):
IAPDTNRQRTSRVLVRPDTGLDVTVRKNHCLDIGHTDGSPVDPTYPDHYTRIKAEYEGPVRDESNTMFDQRSDLRHIETQ

---

Extended repression domain from residues 531 to 630:
LDVTVRKNHCLDIGHTDGSPVDPTYPDHYTRIKAEYEGPVRDESNTMFDQRSDLRHIETQASLNDHVYENIPPKEVGFNSSSDLDVDSLNGYTSGDMHTD

Max tile of repression domain from residues 551 to 630 (estimated 33.7% to 39.5% of cells repressed):
VDPTYPDHYTRIKAEYEGPVRDESNTMFDQRSDLRHIETQASLNDHVYENIPPKEVGFNSSSDLDVDSLNGYTSGDMHTD

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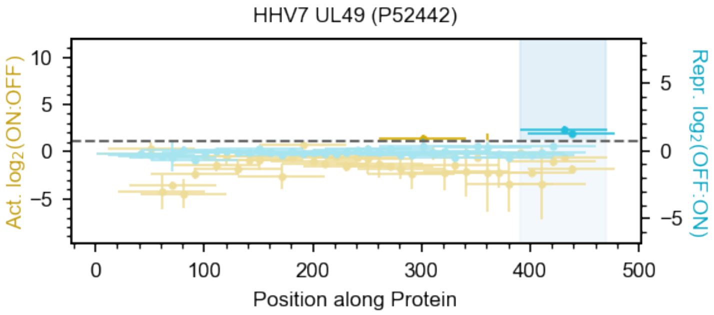
# HHV7 UL49 (P52442)

Gene: U33 ; Protein Family: UL49



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Extended repression domain from residues 391 to 477:
CTILNDSVKFDAIVACSCRTCYSMIHLQNLTINKLLKLISHSTEFQCQDCQNIYRETCLDLEDCGEICTGCKISQLAKCTQHGCDTW

Max tile of repression domain from residues 391 to 470 (estimated 25.3% to 38.2% of cells repressed):
CTILNDSVKFDAIVACSCRTCYSMIHLQNLTINKLLKLISHSTEFQCQDCQNIYRETCLDLEDCGEICTGCKISQLAKCT

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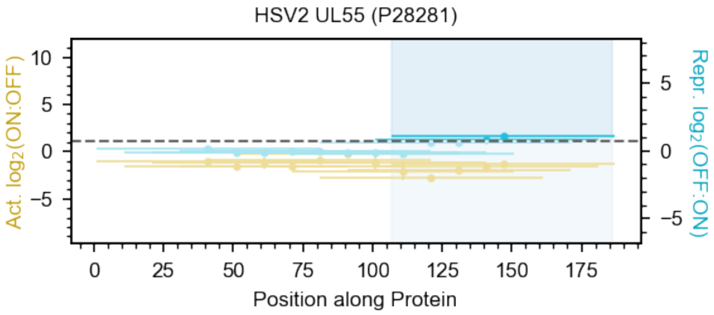
## HSV2 UL55 (P28281)

Gene: UL55 ; Protein Family: UL55



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Extended repression domain from residues 101 to 186:
DKRGGRLRCTGPFSCGTIKDVSGASPAGEYTINGIVYHCHCRYPFSKTCWLGASAALQHLRSISSSGTAARAAEQRRHKIKIKIKV

Max tile of repression domain from residues 107 to 186 (estimated 20.6% to 21.3% of cells repressed):
LRCTGPFSCGTIKDVSGASPAGEYTINGIVYHCHCRYPFSKTCWLGASAALQHLRSISSSGTAARAAEQRRHKIKIKIKV

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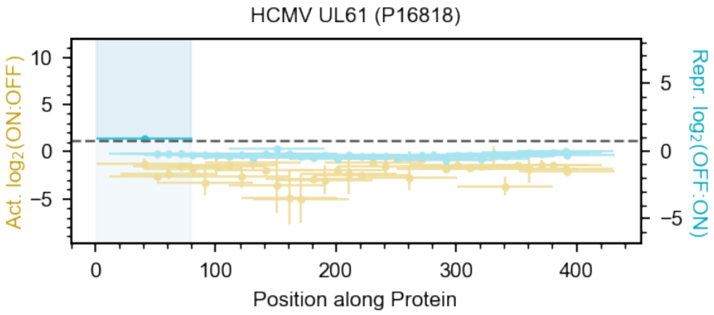
# HCMV UL61 (P16818)

Gene: UL61 ; Protein Family: UL61



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Extended repression domain from residues 1 to 80:
LWRGVLTTIEVSWRPTVDPERFRPHPTSPPHRPAHTPQPGGVRGADPGWAADGGRGVGDHAQGQQAATVRAEFFWGAAGE

Max tile of repression domain from residues 1 to 80 (estimated 16.5% to 16.9% of cells repressed):
LWRGVLTTIEVSWRPTVDPERFRPHPTSPPHRPAHTPQPGGVRGADPGWAADGGRGVGDHAQGQQAATVRAEFFWGAAGE

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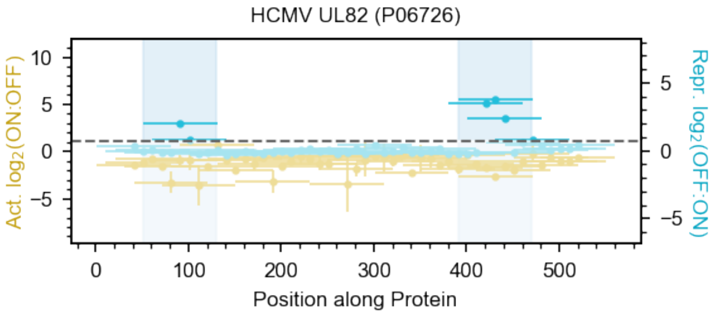
## HCMV UL82 (P06726)

Gene: UL82 ; Protein Family: UL82



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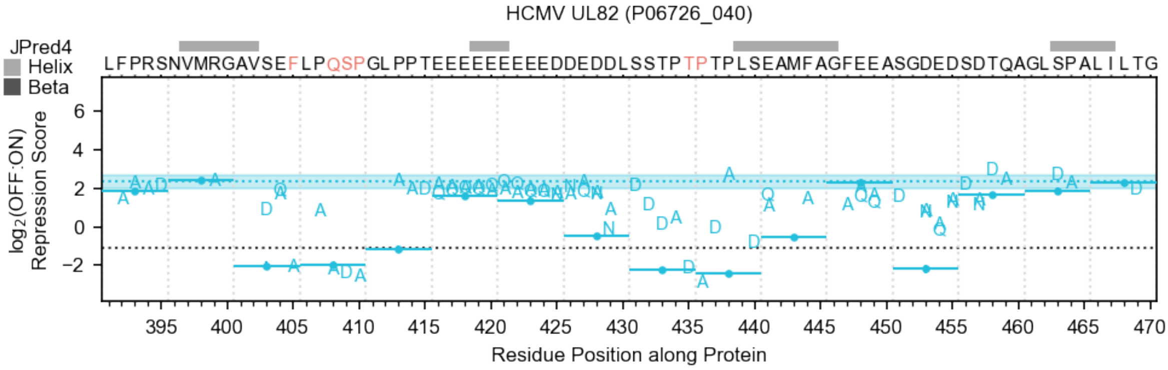
Extended repression domain from residues 51 to 140:
GRLRLLDLRTNIEVSRPSVLCCFQENKSPHDTVDLTDLNIKGRCVVGEQDRLLVDLNNFGPRRLTPGSENNTVSVLAFALPLDRVPVSGL

Max tile of repression domain from residues 51 to 130 (estimated 43.2% to 45.4% of cells repressed):
GRLRLLDLRTNIEVSRPSVLCCFQENKSPHDTVDLTDLNIKGRCVVGEQDRLLVDLNNFGPRRLTPGSENNTVSVLAFAL

---

Extended repression domain from residues 381 to 480:
KRPQVQLRAGLFPRSNVMRGAVSEFLPQSPGLPPTEEEEEEEEEEDDEDDLSSTPTPTPLSEAMFAGFEEASGDEDSDTQAGLSPALILTGQRRRSGNNGA

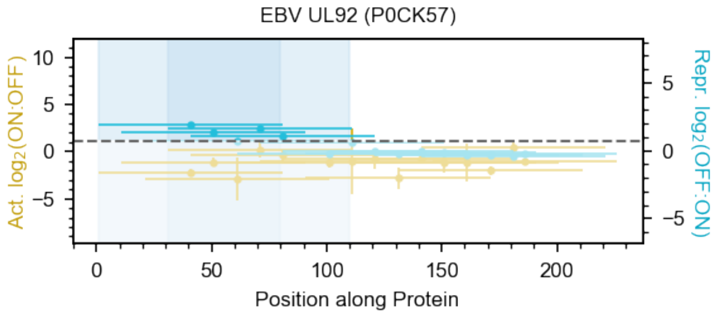
Max tile of repression domain from residues 391 to 470 (estimated 84.9% to 86.4% of cells repressed):
LFPRSNVMRGAVSEFLPQSPGLPPTEEEEEEEEEEDDEDDLSSTPTPTPLSEAMFAGFEEASGDEDSDTQAGLSPALILTG



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| MYND_1 | 410 | 414 | PGLPP | Yes | 401 | 415 | AVSEFLPQSPGLPPT |
|  | - | - |  | No | 431 | 440 | SSTPTPTPLS |
|  | - | - |  | No | 451 | 455 | SGDED |

## EBV UL92 (P0CK57)

Gene: BDLF4 ; Protein Family: UL92



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Extended repression domain from residues 1 to 90:
MSDQGRLSLPRGEGGTDEPNPRHLCSYSKLEFHLPLPESMASVFACWGCGEYHVCDGSSECTLIETHEGVVCALTGNYMGPHFQPALRPW

Max tile of repression domain from residues 1 to 80 (estimated 37.5% to 44.4% of cells repressed):
MSDQGRLSLPRGEGGTDEPNPRHLCSYSKLEFHLPLPESMASVFACWGCGEYHVCDGSSECTLIETHEGVVCALTGNYMG

---

Extended repression domain from residues 31 to 120:
EFHLPLPESMASVFACWGCGEYHVCDGSSECTLIETHEGVVCALTGNYMGPHFQPALRPWTEIRQDTQDQRDKWEPEQVQGLVKTVVNHL

Max tile of repression domain from residues 31 to 110 (estimated 29.5% to 38.2% of cells repressed):
EFHLPLPESMASVFACWGCGEYHVCDGSSECTLIETHEGVVCALTGNYMGPHFQPALRPWTEIRQDTQDQRDKWEPEQVQ

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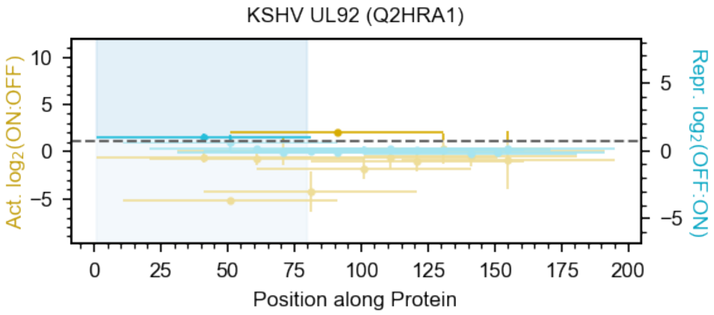
# KSHV UL92 (Q2HRA1)

Gene: ORF31 ; Protein Family: UL92



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Extended repression domain from residues 1 to 80:
MKSVASPLCQFHGVFCLYQCRQCLAYHVCDGGAECVLLHTPESVICELTGNCMLGNIQEGQFLGPVPYRTLDNQVDRDAY

Max tile of repression domain from residues 1 to 80 (estimated 15.6% to 24.9% of cells repressed):
MKSVASPLCQFHGVFCLYQCRQCLAYHVCDGGAECVLLHTPESVICELTGNCMLGNIQEGQFLGPVPYRTLDNQVDRDAY

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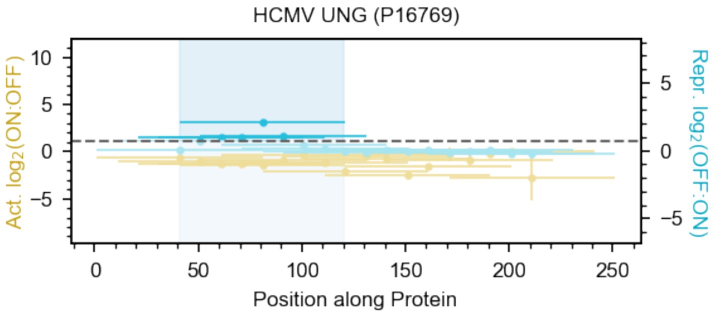
## HCMV UNG (P16769)

Gene: UL114 ; Protein Family: UNG



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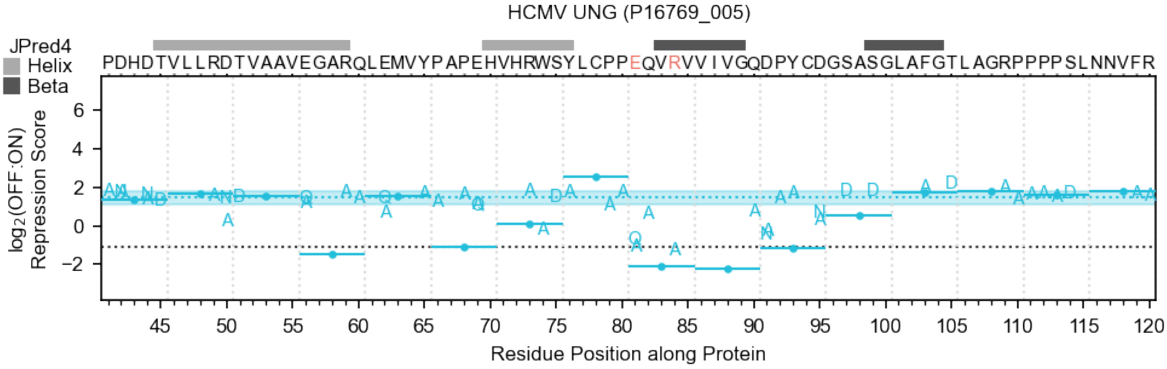
Extended repression domain from residues 11 to 130:
IADNKGSLLTPDEQARVFCLSADWIRFLSLPDHDTVLLRDTVAAVEGARQLEMVYPAPEHVHRWSYLCPPEQVRVVIVGQDPYCDGSASGLAFGTLAGRPPPPSLNNVFRELARTVDGFQ

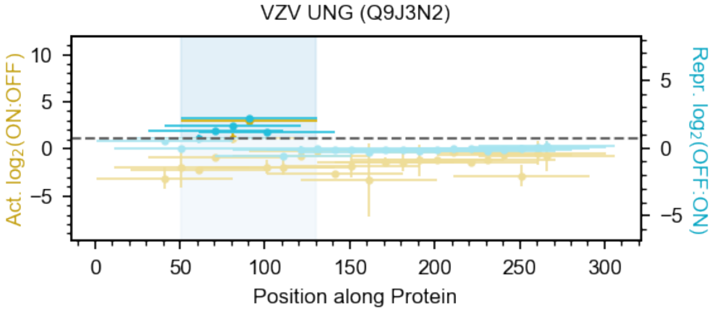
Max tile of repression domain from residues 41 to 120 (estimated 42.7% to 52.9% of cells repressed):
PDHDTVLLRDTVAAVEGARQLEMVYPAPEHVHRWSYLCPPEQVRVVIVGQDPYCDGSASGLAFGTLAGRPPPPSLNNVFR



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_par | 44 | 51 | DTVLLRDT | No | - | - | |
| | - | - | | No | 56 | 60 | EGARQ |
| | - | - | | No | 66 | 70 | PAPEH |
| flexi_NRBOX | 82 | 88 | QVRVVIV | Yes | 81 | 95 | EQVRVVIVGQDPYCD |
| CtBP_expanded | 112 | 116 | PPSLN | No | - | - | |
| flexi_NRBOX | 114 | 120 | SLNNVFR | No | - | - | |

# VZV UNG (Q9J3N2)

Gene: ORF59 ; Protein Family: UNG



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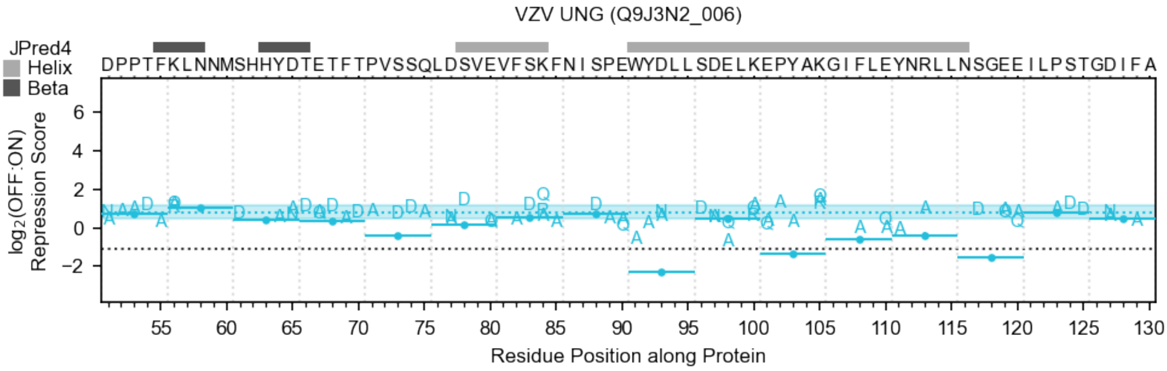
Extended repression domain from residues 21 to 140:
SDSKDIYVLAHPVTKKTRKRPRGPPLGVKLDPPTFKLNNMSHHYDTETFTPVSSQLDSVEVFSKFNISPEWYDLLSDELKEPYAKGIFLEYNRLLNSGEEILPSTGDIFAWTRFCGPQSI

Max tile of repression domain from residues 51 to 130 (estimated 46.4% to 51.2% of cells repressed):
DPPTFKLNNMSHHYDTETFTPVSSQLDSVEVFSKFNISPEWYDLLSDELKEPYAKGIFLEYNRLLNSGEEILPSTGDIFA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 90 | 96 | EWYDLLS | Yes | 91 | 95 | WYDLL |
| SUMO_rev | 93 | 102 | DLLSDELKEP | Yes | 91 | 95 | WYDLL |
| SUMO_rev | 93 | 102 | DLLSDELKEP | Yes | 101 | 105 | EPYAK |
|  | - | - |  | No | 116 | 120 | NSGEE |

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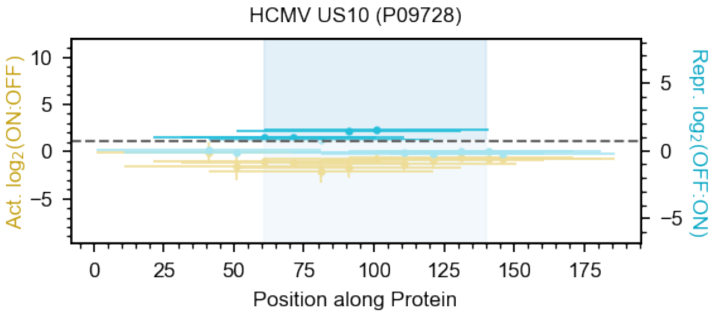
# HCMV US10 (P09728)

Gene: US10 ; Protein Family: US10



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Extended repression domain from residues 21 to 140:
VVAAATEETREPTYFTCGCVIQNHVLKGAVKLYGQFPSPKTLRASAWLHDGENHERHRQPILVEGTATATEALYILLPTELSSPEGNRPRNYSATLTLASRDCYERFVCPVYDSGTPMGV

Max tile of repression domain from residues 61 to 140 (estimated 30.7% to 32.3% of cells repressed):
TLRASAWLHDGENHERHRQPILVEGTATATEALYILLPTELSSPEGNRPRNYSATLTLASRDCYERFVCPVYDSGTPMGV

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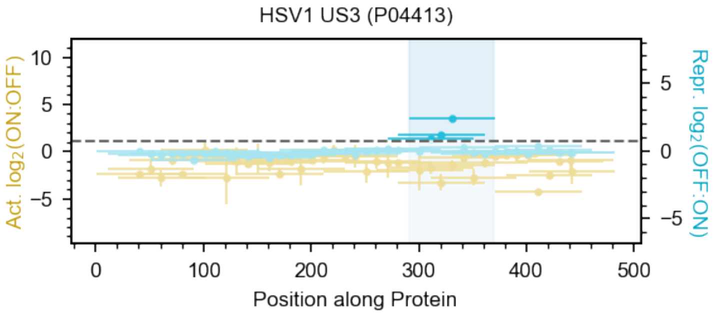
## HSV1 US3 (P04413)

Gene: US3 ; Protein Family: US3



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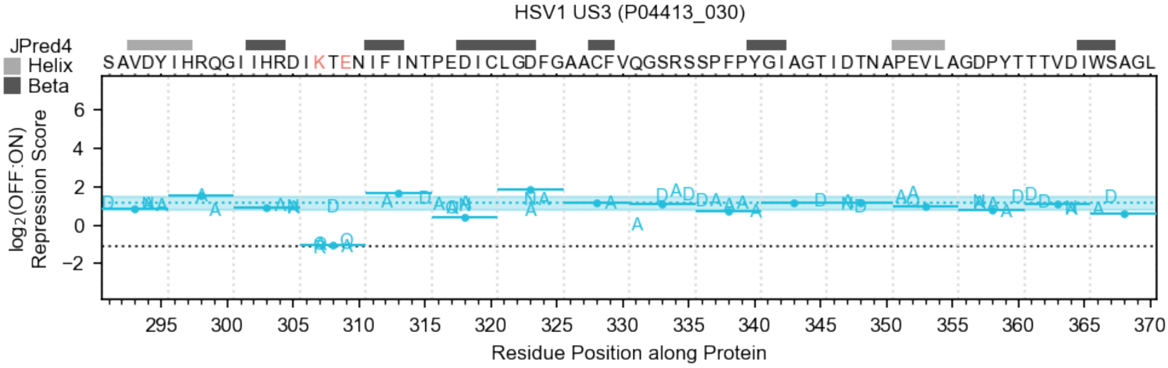
Extended repression domain from residues 271 to 370:
SRRLNPLGRPQIAAVSRQLLSAVDYIHRQGIIHRDIKTENIFINTPEDICLGDFGAACFVQGSRSSPFPYGIAGTIDTNAPEVLAGDPYTTTVDIWSAGL

Max tile of repression domain from residues 291 to 370 (estimated 53.1% to 55.4% of cells repressed):
SAVDYIHRQGIIHRDIKTENIFINTPEDICLGDFGAACFVQGSRSSPFPYGIAGTIDTNAPEVLAGDPYTTTVDIWSAGL



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_for | 306 | 309 | IKTE | No | - | - | |
| SUMO_SIM_par | 360 | 367 | TTTVDIWS | No | - | - | |

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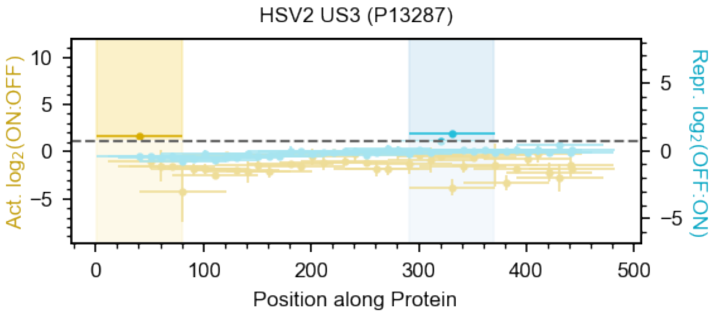
## HSV2 US3 (P13287)

Gene: US3 ; Protein Family: US3



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Extended activation domain from residues 1 to 80:
MACRKFCGVYRRPDKRQEASVPPETNTAPAFPASTFYTPAEDAYLAPGPPETIHPSRPPSPGEAARLCQLQEILAQMHSD

Max tile of activation domain from residues 1 to 80 (estimated 2.7% to 4.1% of cells activated):
MACRKFCGVYRRPDKRQEASVPPETNTAPAFPASTFYTPAEDAYLAPGPPETIHPSRPPSPGEAARLCQLQEILAQMHSD

---

Extended repression domain from residues 281 to 370:
QITAVSRQLLSAIDYVHCKGIIHRDIKTENIFINTPENICLGDFGAACFVRGCRSSPFHYGIAGTIDTNAPEVLAGDPYTQVIDIWSAGL

Max tile of repression domain from residues 291 to 370 (estimated 25.2% to 26.3% of cells repressed):
SAIDYVHCKGIIHRDIKTENIFINTPENICLGDFGAACFVRGCRSSPFHYGIAGTIDTNAPEVLAGDPYTQVIDIWSAGL

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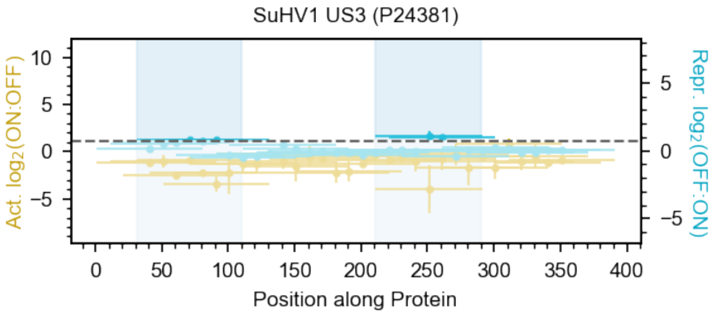
# SuHV1 US3 (P24381)

Gene: - ; Protein Family: US3



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Extended repression domain from residues 31 to 130:
CSLYLAGLSRGLSRVHAQRSHAATMADAGIPDEILYSDISDDEIIIDGDGDGDSSGDEDDDDGGLTRQAASRIATDLGFEVLQPLQSGSEGRVFVARRPG

Max tile of repression domain from residues 31 to 110 (estimated 15.9% to 16.7% of cells repressed):
CSLYLAGLSRGLSRVHAQRSHAATMADAGIPDEILYSDISDDEIIIDGDGDGDSSGDEDDDDGGLTRQAASRIATDLGFE

---

Extended repression domain from residues 211 to 300:
LAYLHGMRIMHRDVKAENIFLEDVDTVCLGDLGAARCNVAAPNFYGLAGTIETNAPEVLARDRYDTKVDVWGAGVVLFETLAYPKTIAGG

Max tile of repression domain from residues 211 to 290 (estimated 15.4% to 29.6% of cells repressed):
LAYLHGMRIMHRDVKAENIFLEDVDTVCLGDLGAARCNVAAPNFYGLAGTIETNAPEVLARDRYDTKVDVWGAGVVLFET

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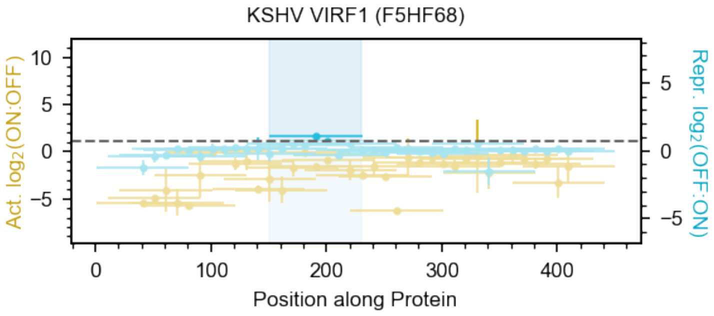
# KSHV VIRF1 (F5HF68)

Gene: K9 ; Protein Family: VIRF



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Extended repression domain from residues 151 to 240:
VDASFKGTRGRRRMLAALRRTRGLQEIGKGISQDGHHFLVFRVRKPEEEQCVECGVVAGAVHDFNNMARLLQEGFFSPGQCLPGEIVTPV

Max tile of repression domain from residues 151 to 230 (estimated 16.8% to 24.0% of cells repressed):
VDASFKGTRGRRRMLAALRRTRGLQEIGKGISQDGHHFLVFRVRKPEEEQCVECGVVAGAVHDFNNMARLLQEGFFSPGQ

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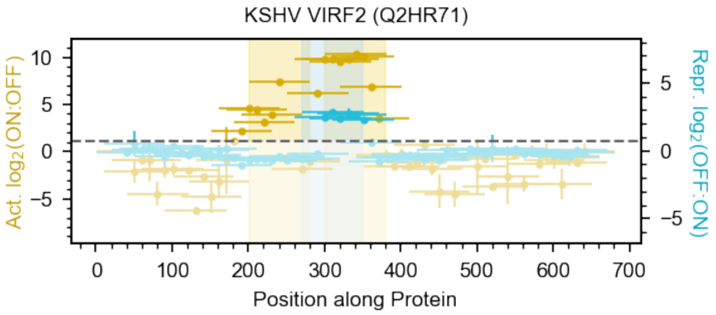
## KSHV VIRF2 (Q2HR71)

Gene: K11 ; Protein Family: VIRF



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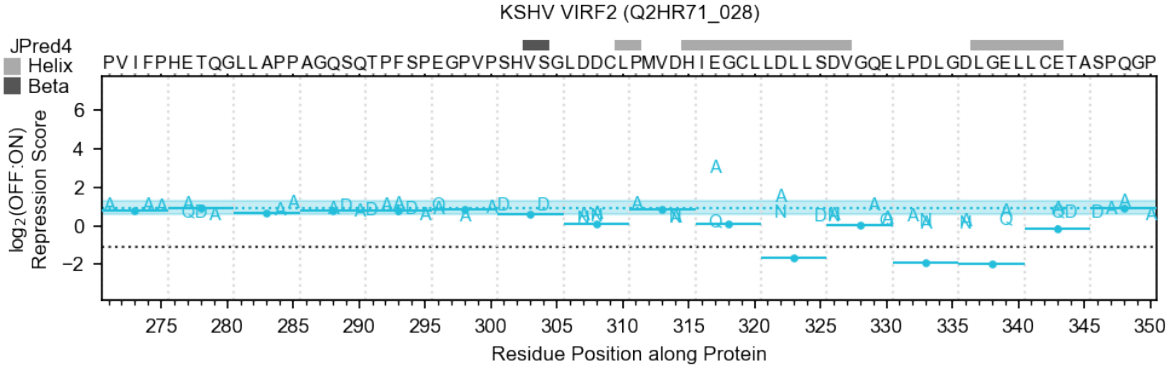
Extended activation domain from residues 141 to 280:
IYPHDDKHREKALRRSLRKKAQREAARKQAAAVATPTTSSAAEVSSRSQSEDTESSDSENELWVGAQGFVGRDMHSLFFEEPEPSGFGSSGQSSSLLAPDSPRPSTSQVQGPLHVHTPTDLCLPTGGLPSPVIFPHETQG

Max tile of activation domain from residues 201 to 280 (estimated 81.1% to 81.6% of cells activated):
ELWVGAQGFVGRDMHSLFFEEPEPSGFGSSGQSSSLLAPDSPRPSTSQVQGPLHVHTPTDLCLPTGGLPSPVIFPHETQG

---

Extended repression domain from residues 261 to 390:
LCLPTGGLPSPVIFPHETQGLLAPPAGQSQTPFSPEGPVPSHVSGLDDCLPMVDHIEGCLLDLLSDVGQELPDLGDLGELLCETASPQGPMQSEGGEEGSTESVSVLPATHPLESSAPGASVMGSGQELP

Max tile of repression domain from residues 271 to 350 (estimated 62.7% to 70.7% of cells repressed):
PVIFPHETQGLLAPPAGQSQTPFSPEGPVPSHVSGLDDCLPMVDHIEGCLLDLLSDVGQELPDLGDLGELLCETASPQGP

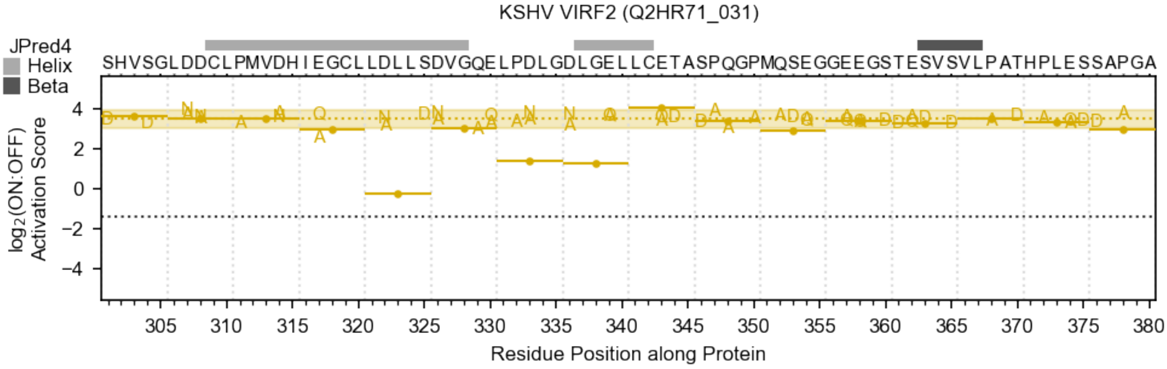


| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_par | 319 | 326 | CLLDLLSD | Yes | 321 | 325 | LDLLS |
| LIG_NRBOX | 319 | 325 | CLLDLLS | Yes | 321 | 325 | LDLLS |
| LIG_NRBOX | 336 | 342 | DLGELLC | Yes | 331 | 340 | LPDLGDLGEL |

---

Extended activation domain from residues 251 to 410:
GPLHVHTPTDLCLPTGGLPSPVIFPHETQGLLAPPAGQSQTPFSPEGPVPSHVSGLDDCLPMVDHIEGCLLDLLSDVGQELPDLGDLGELLCETASPQGPMQSEGGEEGSTESVSVLPATHPLESSAPGASVMGSGQELPDLGDLSELLCETASPQGPMQ

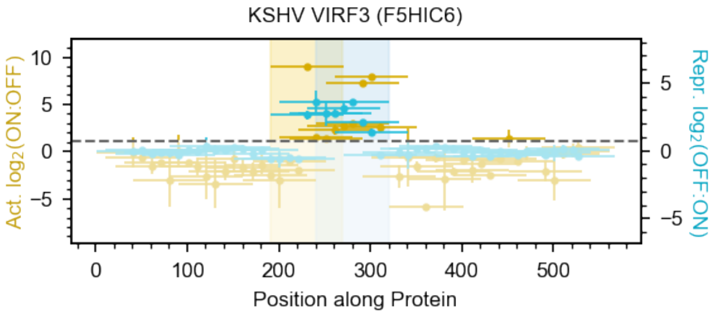
Max tile of activation domain from residues 301 to 380 (estimated 96.7% to 96.7% of cells activated):
SHVSGLDDCLPMVDHIEGCLLDLLSDVGQELPDLGDLGELLCETASPQGPMQSEGGEEGSTESVSVLPATHPLESSAPGA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| LIG_NRBOX | 319 | 325 | CLLDLLS | No | - | - | |
| SUMO_SIM_par | 319 | 326 | CLLDLLSD | No | - | - | |
| LIG_NRBOX | 336 | 342 | DLGELLC | No | - | - | |
| SUMO_SIM_anti | 360 | 368 | STESVSVLP | No | - | - | |

# KSHV VIRF3 (F5HIC6)

Gene: K10.5 ; Protein Family: VIRF



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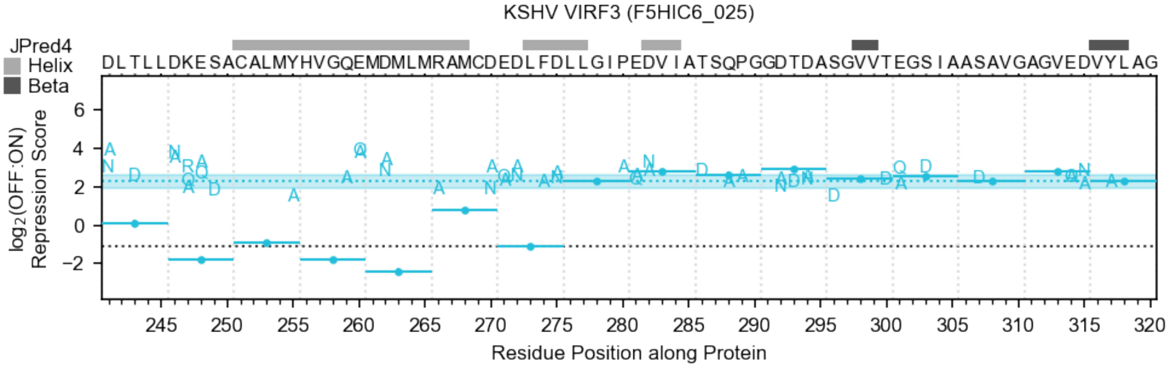
Extended activation domain from residues 191 to 350:
TRHSASGVQPVDDANADSPGSGDEGPSTRHSDSQPPPADETTVHTDNVEDDLTLLDKESACALMYHVGQEMDMLMRAMCDEDLFDLLGIPEDVIATSQPGGDTDASGVVTEGSIAASAVGAGVEDVYLAGALEAQNVAGEYVLEISDEEVDDGAGLPPAS

Max tile of activation domain from residues 191 to 270 (estimated 93.0% to 94.1% of cells activated):
TRHSASGVQPVDDANADSPGSGDEGPSTRHSDSQPPPADETTVHTDNVEDDLTLLDKESACALMYHVGQEMDMLMRAMCD

---

Extended repression domain from residues 191 to 340:
TRHSASGVQPVDDANADSPGSGDEGPSTRHSDSQPPPADETTVHTDNVEDDLTLLDKESACALMYHVGQEMDMLMRAMCDEDLFDLLGIPEDVIATSQPGGDTDASGVVTEGSIAASAVGAGVEDVYLAGALEAQNVAGEYVLEISDEEV

Max tile of repression domain from residues 241 to 320 (estimated 81.6% to 84.0% of cells repressed):
DLTLLDKESACALMYHVGQEMDMLMRAMCDEDLFDLLGIPEDVIATSQPGGDTDASGVVTEGSIAASAVGAGVEDVYLAG

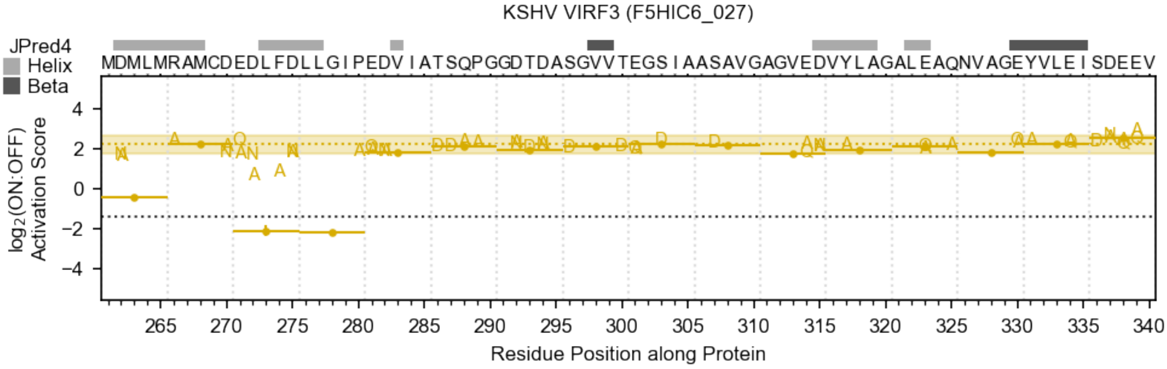


| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_anti | 241 | 246 | DLTLLD | Yes | 246 | 250 | DKESA |
|  | - | - |  | No | 256 | 265 | HVGQEMDMLM |
| LIG_NRBOX | 272 | 278 | DLFDLLG | Yes | 271 | 275 | EDLFD |

---

Extended activation domain from residues 191 to 340:
TRHSASGVQPVDDANADSPGSGDEGPSTRHSDSQPPPADETTVHTDNVEDDLTLLDKESACALMYHVGQEMDMLMRAMCDEDLFDLLGIPEDVIATSQPGGDTDASGVVTEGSIAASAVGAGVEDVYLAGALEAQNVAGEYVLEISDEEV

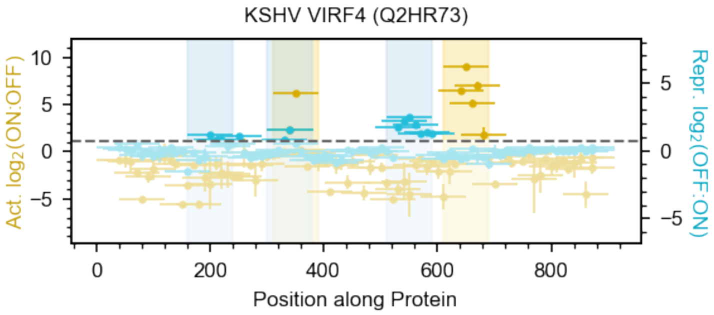
Max tile of activation domain from residues 261 to 340 (estimated 83.9% to 88.5% of cells activated):
MDMLMRAMCDEDLFDLLGIPEDVIATSQPGGDTDASGVVTEGSIAASAVGAGVEDVYLAGALEAQNVAGEYVLEISDEEV



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| LIG_NRBOX | 272 | 278 | DLFDLLG | Yes | 271 | 280 | EDLFDLLGIP |
| SUMO_SIM_par | 330 | 339 | EYVLEISDEE | No | - | - | |

## KSHV VIRF4 (Q2HR73)

Gene: K10 ; Protein Family: VIRF



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Extended repression domain from residues 161 to 260:
EEAGAAAPAPPKAPSGLRGRPRKSNRYYNVGDITTEQKAACSVWIPVNEGASTSGMGSSGTRQVTQASSFTWRVPGDPPAPSTLTGPSDPHSSGAGLPGT

Max tile of repression domain from residues 161 to 240 (estimated 21.4% to 25.0% of cells repressed):
EEAGAAAPAPPKAPSGLRGRPRKSNRYYNVGDITTEQKAACSVWIPVNEGASTSGMGSSGTRQVTQASSFTWRVPGDPPA

---

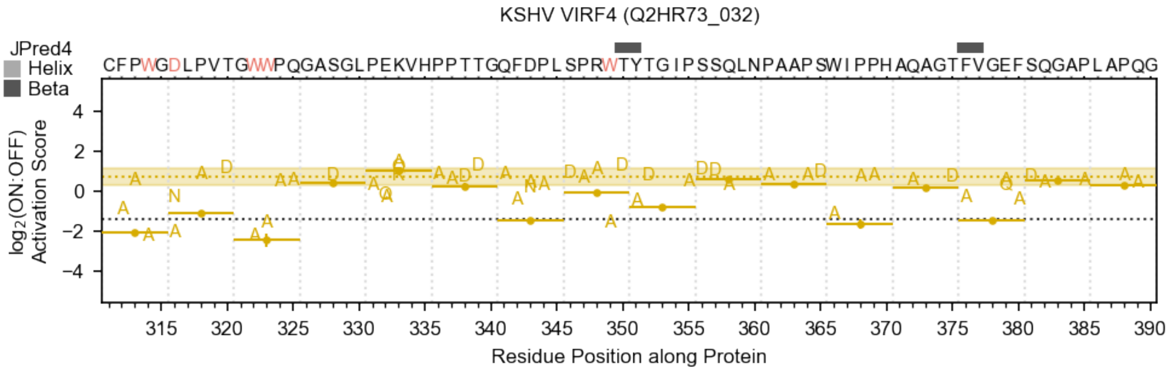
Extended repression domain from residues 291 to 380:
LAPPMRDGSRLPSTSPWIPACFPWGDLPVTGWWPQGASGLPEKVHPPTTGQFDPLSPRWTYTGIPSSQLNPAAPSWIPPHAQAGTFVGEF

Max tile of repression domain from residues 301 to 380 (estimated 28.5% to 34.7% of cells repressed):
LPSTSPWIPACFPWGDLPVTGWWPQGASGLPEKVHPPTTGQFDPLSPRWTYTGIPSSQLNPAAPSWIPPHAQAGTFVGEF

---

Extended activation domain from residues 301 to 390:
LPSTSPWIPACFPWGDLPVTGWWPQGASGLPEKVHPPTTGQFDPLSPRWTYTGIPSSQLNPAAPSWIPPHAQAGTFVGEFSQGAPLAPQG

Max tile of activation domain from residues 311 to 390 (estimated 58.1% to 62.1% of cells activated):
CFPWGDLPVTGWWPQGASGLPEKVHPPTTGQFDPLSPRWTYTGIPSSQLNPAAPSWIPPHAQAGTFVGEFSQGAPLAPQG

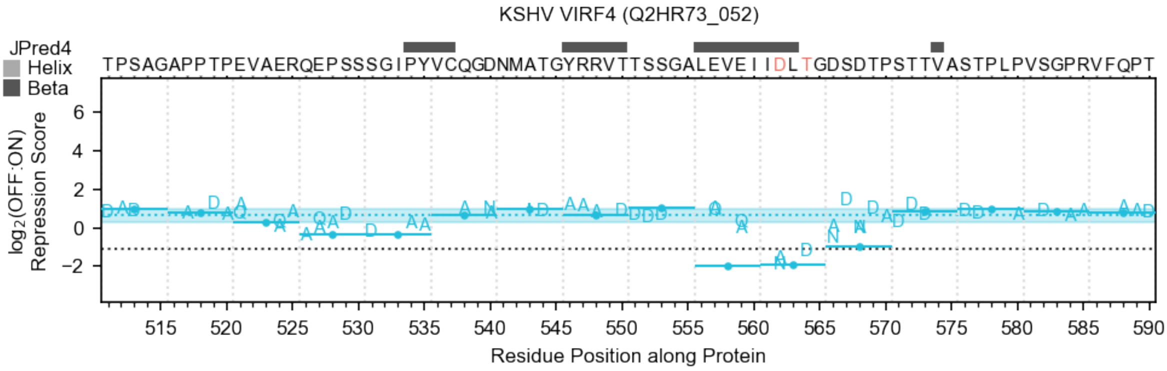


| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 311 | 315 | CFPWG |
| | - | - | | No | 321 | 325 | GWWPQ |
| | - | - | | No | 341 | 345 | QFDPL |
| | - | - | | No | 366 | 370 | WIPPH |
| | - | - | | No | 376 | 380 | FVGEF |

---

Extended repression domain from residues 491 to 630:
WSSGGAPNQGLSHTQGGASATPSAGAPPTPEVAERQEPSSSGIPYVCQGDNMATGYRRVTTSSGALEVEIIDLTGDSDTPSTTVASTPLPVSGPRVFQPTVLYSAPEPAVNPEVSHLPTELERRECVCPGSGERPRVPLV

Max tile of repression domain from residues 511 to 590 (estimated 54.2% to 58.2% of cells repressed):
TPSAGAPPTPEVAERQEPSSSGIPYVCQGDNMATGYRRVTTSSGALEVEIIDLTGDSDTPSTTVASTPLPVSGPRVFQPT

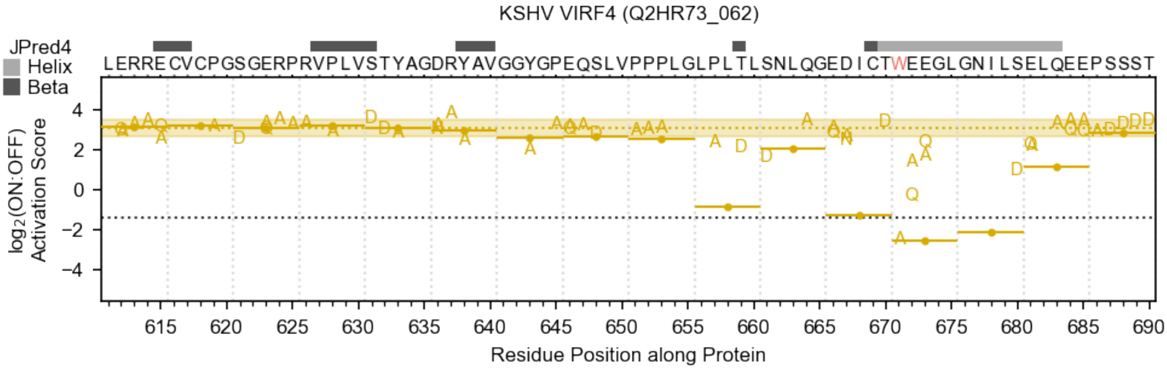


| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_anti | 557 | 562 | EVEIID | Yes | 556 | 565 | LEVEIIDLTG |
| SUMO_SIM_par | 559 | 564 | EIIDLT | Yes | 556 | 565 | LEVEIIDLTG |

---

Extended activation domain from residues 601 to 720:
NPEVSHLPTELERRECVCPGSGERPRVPLVSTYAGDRYAVGGYGPEQSLVPPPLGLPLTLSNLQGEDICTWEEGLGNILSELQEEPSSSTRQATDRRRPRSRSPHGRRTPVSHSGPEKPP

Max tile of activation domain from residues 611 to 690 (estimated 92.9% to 93.9% of cells activated):
LERRECVCPGSGERPRVPLVSTYAGDRYAVGGYGPEQSLVPPPLGLPLTLSNLQGEDICTWEEGLGNILSELQEEPSSST



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_SIM_par | 656 | 661 | LPLTLS | No | - | - | |
| flexi_NRBOX | 674 | 680 | GLGNILS | Yes | 671 | 680 | WEEGLGNILS |

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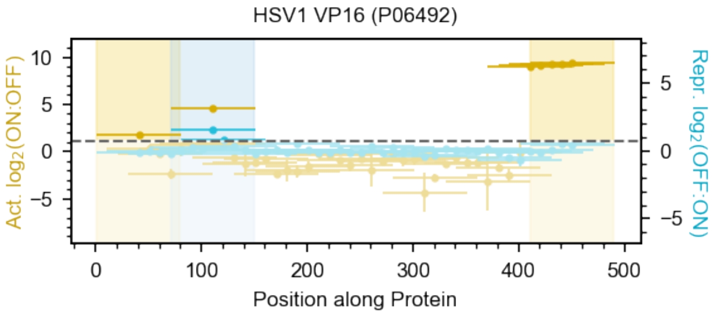
## HSV1 VP16 (P06492)

Gene: UL48 ; Protein Family: VP16



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Extended activation domain from residues 1 to 80:
MDLLVDELFADMNADGASPPPPRPAGGPKNTPAAPPLYATGRLSQAQLMPSPPMPVPPAALFNRLLDDLGFSAGPALCTM

Max tile of activation domain from residues 1 to 80 (estimated 3.3% to 4.2% of cells activated):
MDLLVDELFADMNADGASPPPPRPAGGPKNTPAAPPLYATGRLSQAQLMPSPPMPVPPAALFNRLLDDLGFSAGPALCTM

---

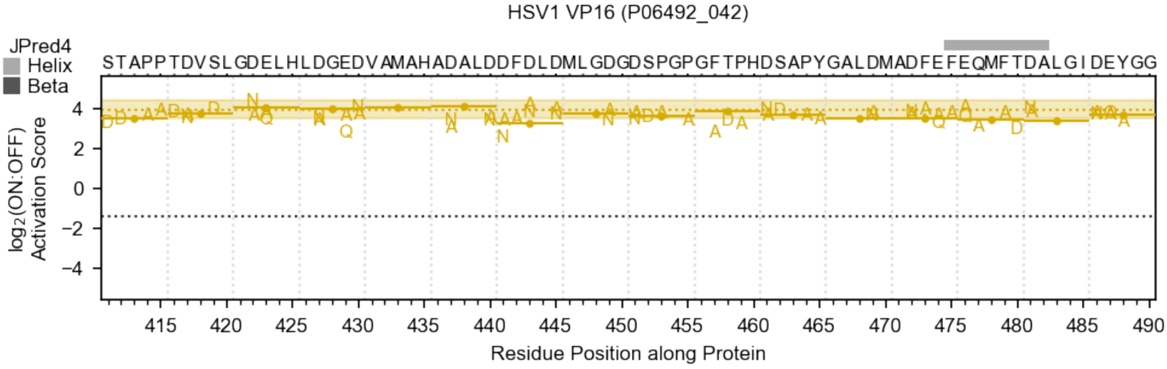
Extended repression domain from residues 71 to 160:
FSAGPALCTMLDTWNEDLFSALPTNADLYRECKFLSTLPSDVVEWGDAYVPERTQIDIRAHGDVAFPTLPATRDGLGLYYEALSRFFHAE

Max tile of repression domain from residues 71 to 150 (estimated 29.3% to 33.2% of cells repressed):
FSAGPALCTMLDTWNEDLFSALPTNADLYRECKFLSTLPSDVVEWGDAYVPERTQIDIRAHGDVAFPTLPATRDGLGLYY

---

Extended activation domain from residues 371 to 490:
NNYGSTIEGLLDLPDDDAPEEAGLAAPRLSFLPAGHTRRLSTAPPTDVSLGDELHLDGEDVAMAHADALDDFDLDMLGDGDSPGPGFTPHDSAPYGALDMADFEFEQMFTDALGIDEYGG

Max tile of activation domain from residues 411 to 490 (estimated 94.4% to 95.0% of cells activated):
STAPPTDVSLGDELHLDGEDVAMAHADALDDFDLDMLGDGDSPGPGFTPHDSAPYGALDMADFEFEQMFTDALGIDEYGG



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | - | - | |

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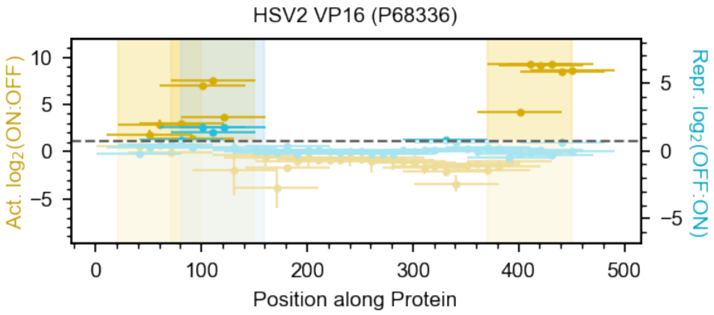
## HSV2 VP16 (P68336)

Gene: UL48 ; Protein Family: VP16



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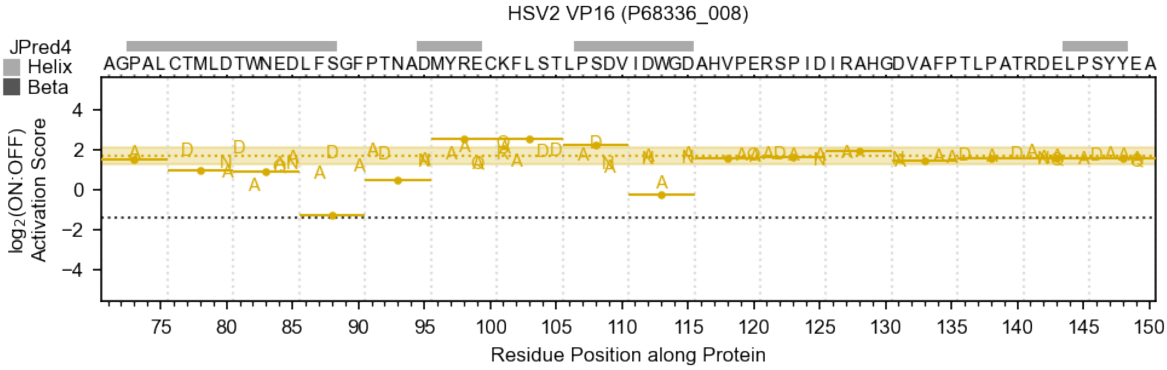
Extended activation domain from residues 11 to 100:
DADGVSPPPPRPAGGPKNTPAAPPLYATGRLSQAQLMPSPPMPVPPAALFNRLLDDLGFSAGPALCTMLDTWNEDLFSGFPTNADMYREC

Max tile of activation domain from residues 21 to 100 (estimated 5.6% to 11.3% of cells activated):
RPAGGPKNTPAAPPLYATGRLSQAQLMPSPPMPVPPAALFNRLLDDLGFSAGPALCTMLDTWNEDLFSGFPTNADMYREC

---

Extended activation domain from residues 41 to 160:
LSQAQLMPSPPMPVPPAALFNRLLDDLGFSAGPALCTMLDTWNEDLFSGFPTNADMYRECKFLSTLPSDVIDWGDAHVPERSPIDIRAHGDVAFPTLPATRDELPSYYEAMAQFFRGELR

Max tile of activation domain from residues 71 to 150 (estimated 83.3% to 83.4% of cells activated):
AGPALCTMLDTWNEDLFSGFPTNADMYRECKFLSTLPSDVIDWGDAHVPERSPIDIRAHGDVAFPTLPATRDELPSYYEA



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| SUMO_rev | 95 | 103 | DMYRECKFL | No | - | - | |

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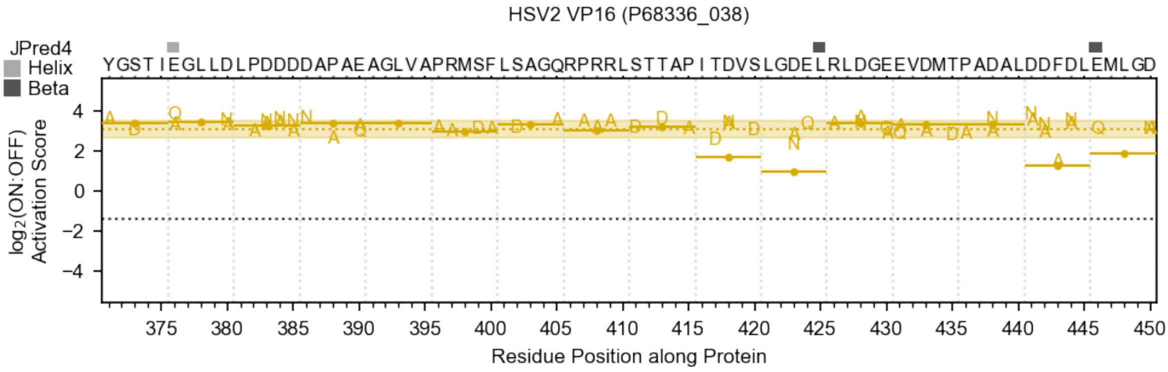
Extended repression domain from residues 61 to 160:
NRLLDDLGFSAGPALCTMLDTWNEDLFSGFPTNADMYRECKFLSTLPSDVIDWGDAHVPERSPIDIRAHGDVAFPTLPATRDELPSYYEAMAQFFRGELR

Max tile of repression domain from residues 81 to 160 (estimated 33.6% to 40.3% of cells repressed):
TWNEDLFSGFPTNADMYRECKFLSTLPSDVIDWGDAHVPERSPIDIRAHGDVAFPTLPATRDELPSYYEAMAQFFRGELR

---

Extended activation domain from residues 361 to 490:
AYSRGRTRNNYGSTIEGLLDLPDDDDAPAEAGLVAPRMSFLSAGQRPRRLSTTAPITDVSLGDELRLDGEEVDMTPADALDDFDLEMLGDVESPSPGMTHDPVSYGALDVDDFEFEQMFTDAMGIDDFGG

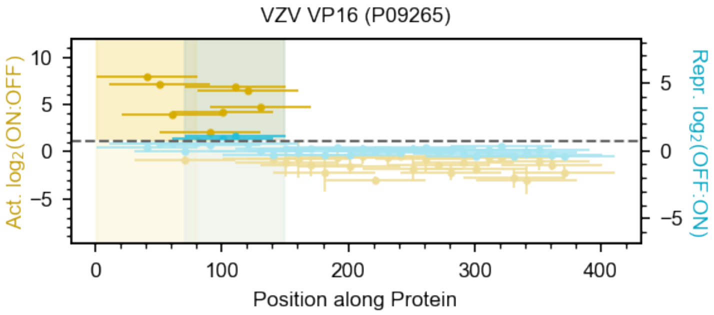
Max tile of activation domain from residues 371 to 450 (estimated 94.4% to 94.7% of cells activated):
YGSTIEGLLDLPDDDDAPAEAGLVAPRMSFLSAGQRPRRLSTTAPITDVSLGDELRLDGEEVDMTPADALDDFDLEMLGD



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| flexi_NRBOX | 374 | 380 | TIEGLLD | No | - | - | |
| SUMO_SIM_par | 376 | 386 | EGLLDLPDDDD | No | - | - | |

## VZV VP16 (P09265)

Gene: ORF10 ; Protein Family: VP16



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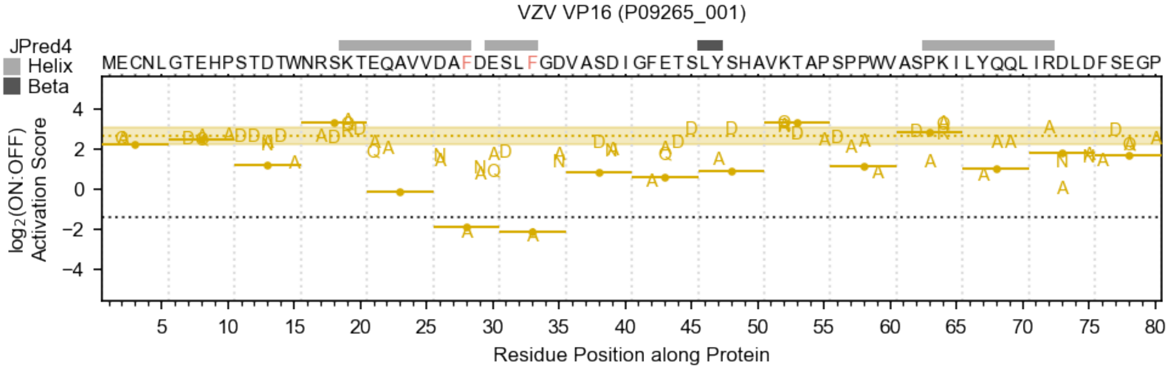
Extended activation domain from residues 1 to 100:
MECNLGTEHPSTDTWNRSKTEQAVVDAFDESLFGDVASDIGFETSLYSHAVKTAPSPPWVASPKILYQQLIRDLDFSEGPRLLSCLETWNEDLFSCFPIN

Max tile of activation domain from residues 1 to 80 (estimated 85.1% to 87.5% of cells activated):
MECNLGTEHPSTDTWNRSKTEQAVVDAFDESLFGDVASDIGFETSLYSHAVKTAPSPPWVASPKILYQQLIRDLDFSEGP



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 26 | 35 | DAFDESLFGD |

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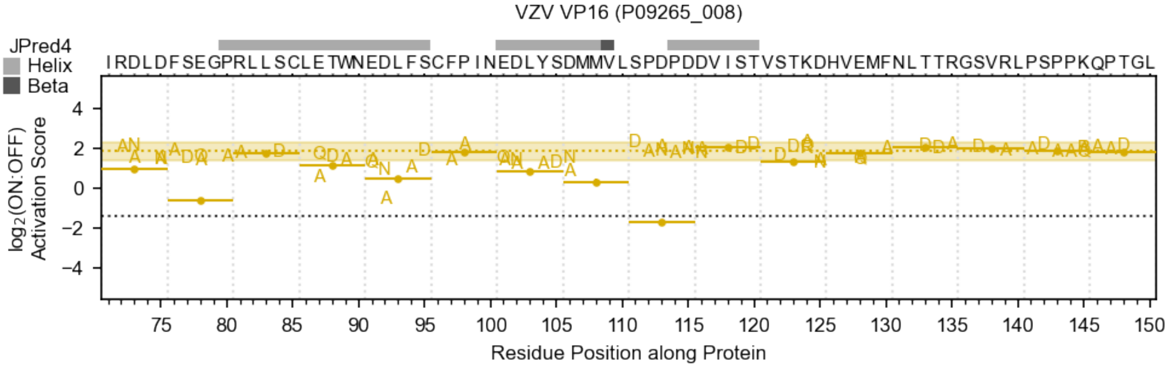
Extended activation domain from residues 51 to 170:
VKTAPSPPWVASPKILYQQLIRDLDFSEGPRLLSCLETWNEDLFSCFPINEDLYSDMMVLSPDPDDVISTVSTKDHVEMFNLTTRGSVRLPSPPKQPTGLPAYVQEVQDSFTVELRAREE

Max tile of activation domain from residues 71 to 150 (estimated 71.2% to 75.5% of cells activated):
IRDLDFSEGPRLLSCLETWNEDLFSCFPINEDLYSDMMVLSPDPDDVISTVSTKDHVEMFNLTTRGSVRLPSPPKQPTGL



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 111 | 115 | SPDPD |

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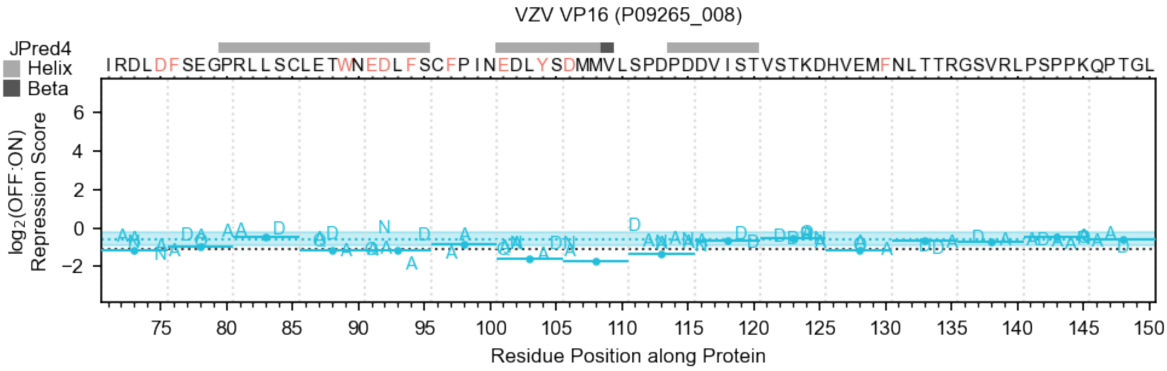
Extended repression domain from residues 61 to 150:
ASPKILYQQLIRDLDFSEGPRLLSCLETWNEDLFSCFPINEDLYSDMMVLSPDPDDVISTVSTKDHVEMFNLTTRGSVRLPSPPKQPTGL

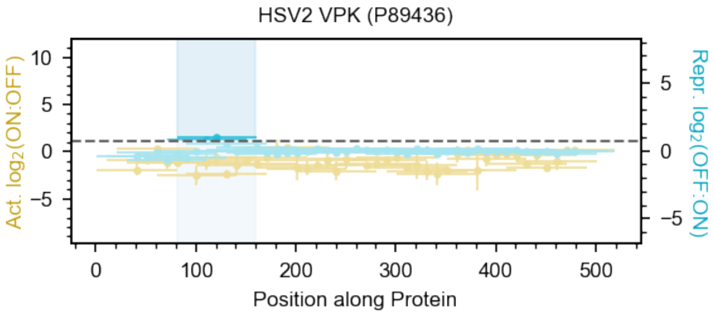
Max tile of repression domain from residues 71 to 150 (estimated 18.8% to 22.5% of cells repressed):
IRDLDFSEGPRLLSCLETWNEDLFSCFPINEDLYSDMMVLSPDPDDVISTVSTKDHVEMFNLTTRGSVRLPSPPKQPTGL



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| | - | - | | No | 71 | 75 | IRDLD |
| | - | - | | No | 86 | 95 | LETWNEDLFS |
| | - | - | | No | 101 | 115 | EDLYSDMMVLSPDPD |
| | - | - | | No | 126 | 130 | HVEMF |

## HSV2 VPK (P89436)

Gene: UL13 ; Protein Family: VPK



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Extended repression domain from residues 71 to 160:
ERLRAGLSRWRVSRSSRRRSSPEAPGPAAKLRRPPLRRSETAMTSPPSPPSHILSLARIHKLCIPVFAVNPALRYTTLEIPGARSFGGSG

Max tile of repression domain from residues 81 to 160 (estimated 18.4% to 20.2% of cells repressed):
RVSRSSRRRSSPEAPGPAAKLRRPPLRRSETAMTSPPSPPSHILSLARIHKLCIPVFAVNPALRYTTLEIPGARSFGGSG

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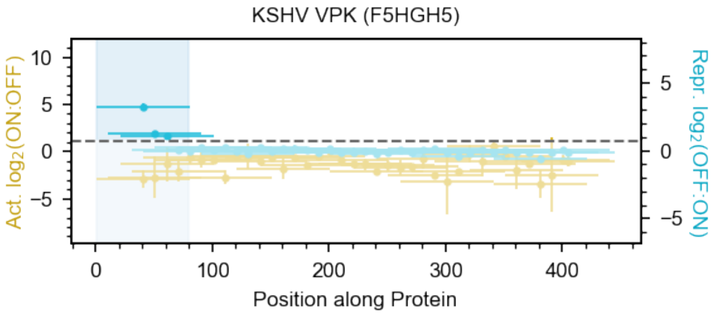
## KSHV VPK (F5HGH5)

Gene: ORF36 ; Protein Family: VPK



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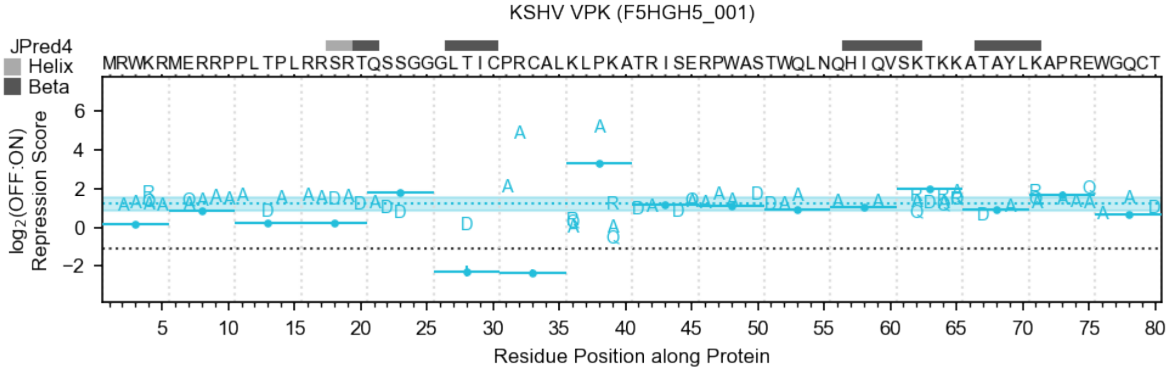
Extended repression domain from residues 1 to 100:
MRWKRMERRPPLTPLRRSRTQSSGGGLTICPRCALKLPKATRISERPWASTWQLNQHIQVSKTKKATAYLKAPREWGQCTHQDPDWSKRLGRGAFGII VP

Max tile of repression domain from residues 1 to 80 (estimated 70.4% to 80.6% of cells repressed):
MRWKRMERRPPLTPLRRSRTQSSGGGLTICPRCALKLPKATRISERPWASTWQLNQHIQVSKTKKATAYLKAPREWGQCT



| Motif Name | Motif Start | Motif End | Motif Sequence | Overlaps Essential? | Essential Start | Essential End | Essential Sequence |
|---|---|---|---|---|---|---|---|
| MYND_1 | 10 | 14 | PPLTP | No | - | - | |
| | - | - | | No | 26 | 35 | GLTICPRCAL |

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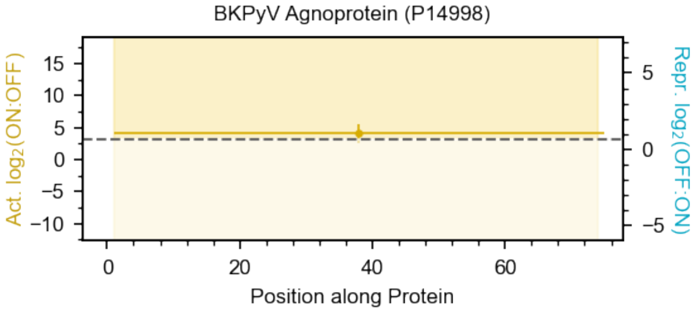
## BKPyV Agnoprotein (P14998)

Gene: Agnoprotein ; Protein Family: Agnoprotein



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Extended activation domain from residues 1 to 74:
MFCEPKNLVVLRQLSRQASVKVGKTWTGTKKRAQRIFIFILELLLEFCRGEDSVDGKNKSTTALPAVKDSVKDS

Max tile of activation domain from residues 1 to 74 (estimated 9.1% to 47.6% of cells activated):
MFCEPKNLVVLRQLSRQASVKVGKTWTGTKKRAQRIFIFILELLLEFCRGEDSVDGKNKSTTALPAVKDSVKDS

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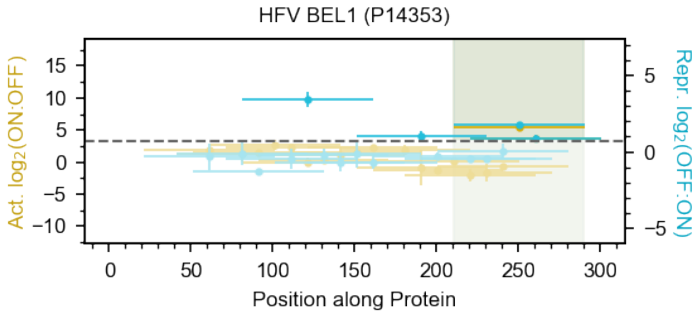
## HFV BEL1 (P14353)

Gene: BEL1 ; Protein Family: BEL1



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Extended activation domain from residues 211 to 300:
KHHKPRQKRPRRRSIDNESCASSSDTMANEPGSLCTNPLWNPGPLLSGLLEESSNLPNLEVHMSGGPFWEEVYGDSILGPPSGSGEHSVL

Max tile of activation domain from residues 211 to 290 (estimated 43.0% to 48.9% of cells activated):
KHHKPRQKRPRRRSIDNESCASSSDTMANEPGSLCTNPLWNPGPLLSGLLEESSNLPNLEVHMSGGPFWEEVYGDSILGP

---

Extended repression domain from residues 211 to 300:
KHHKPRQKRPRRRSIDNESCASSSDTMANEPGSLCTNPLWNPGPLLSGLLEESSNLPNLEVHMSGGPFWEEVYGDSILGPPSGSGEHSVL

Max tile of repression domain from residues 211 to 290 (estimated 32.4% to 34.1% of cells repressed):
KHHKPRQKRPRRRSIDNESCASSSDTMANEPGSLCTNPLWNPGPLLSGLLEESSNLPNLEVHMSGGPFWEEVYGDSILGP

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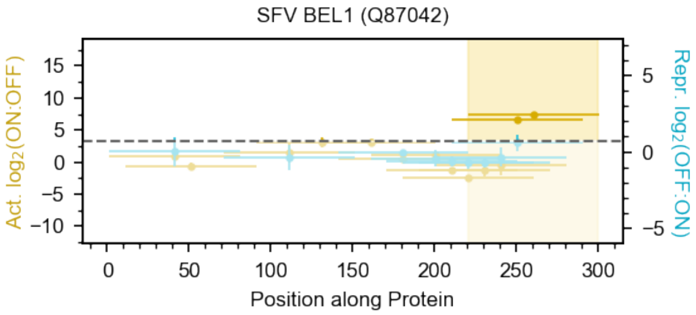
## SFV BEL1 (Q87042)

Gene: BEL1 ; Protein Family: BEL1



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Extended activation domain from residues 211 to 300:
KHHKPRPKRSRKRSIDHESCASSGDTVANESGPLCTNTFWTPGPVLQGLLGESSNLPDLEVHMSGGPFWKEVYGDSILGPPSGSGEHSVL

Max tile of activation domain from residues 221 to 300 (estimated 72.9% to 81.1% of cells activated):
RKRSIDHESCASSGDTVANESGPLCTNTFWTPGPVLQGLLGESSNLPDLEVHMSGGPFWKEVYGDSILGPPSGSGEHSVL

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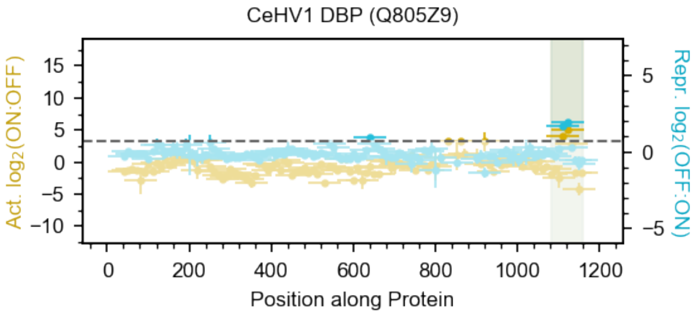
## CeHV1 DBP (Q805Z9)

Gene: UL29 ; Protein Family: DBP



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Extended activation domain from residues 1071 to 1160:
VAAVKSLGNRTPQLQIEDWLALLEDEYLSEEMMAFTARALERGGGEWAAEAALEVAHEAEALVTQTGGADGGEVFDFGAFGVDDDEVPSF

Max tile of activation domain from residues 1081 to 1160 (estimated 35.6% to 40.5% of cells activated):
TPQLQIEDWLALLEDEYLSEEMMAFTARALERGGGEWAAEAALEVAHEAEALVTQTGGADGGEVFDFGAFGVDDDEVPSF

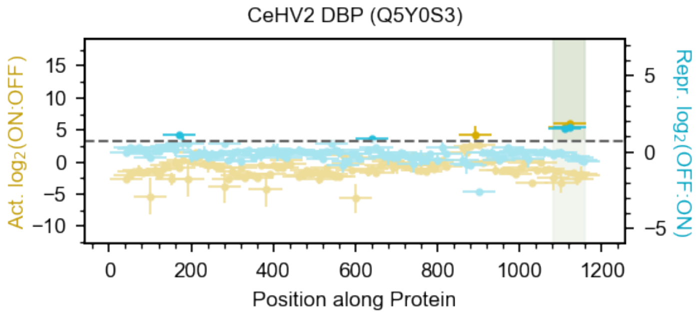
---

Extended repression domain from residues 1071 to 1160:
VAAVKSLGNRTPQLQIEDWLALLEDEYLSEEMMAFTARALERGGGEWAAEAALEVAHEAEALVTQTGGADGGEVFDFGAFGVDDDEVPSF

Max tile of repression domain from residues 1081 to 1160 (estimated 36.2% to 37.5% of cells repressed):
TPQLQIEDWLALLEDEYLSEEMMAFTARALERGGGEWAAEAALEVAHEAEALVTQTGGADGGEVFDFGAFGVDDDEVPSF

## CeHV2 DBP (Q5Y0S3)

Gene: UL29 ; Protein Family: DBP



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Extended activation domain from residues 1071 to 1160:
VAAVKSLGNRTPQLQIEDWLALLEDEYLGEEMMAFTARALERGGGEWTTEAALEVAHEAEALVTQTGGADVGEAFDFGAFGAEDDDAPTF

Max tile of activation domain from residues 1081 to 1160 (estimated 51.3% to 58.3% of cells activated):
TPQLQIEDWLALLEDEYLGEEMMAFTARALERGGGEWTTEAALEVAHEAEALVTQTGGADVGEAFDFGAFGAEDDDAPTF

---

Extended repression domain from residues 1071 to 1160:
VAAVKSLGNRTPQLQIEDWLALLEDEYLGEEMMAFTARALERGGGEWTTEAALEVAHEAEALVTQTGGADVGEAFDFGAFGAEDDDAPTF

Max tile of repression domain from residues 1081 to 1160 (estimated 29.2% to 29.6% of cells repressed):
TPQLQIEDWLALLEDEYLGEEMMAFTARALERGGGEWTTEAALEVAHEAEALVTQTGGADVGEAFDFGAFGAEDDDAPTF

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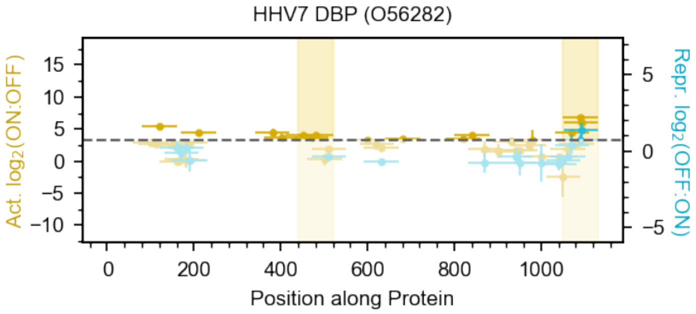
## HHV7 DBP (O56282)

Gene: U41 ; Protein Family: DBP



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Extended activation domain from residues 1051 to 1131:
DGREPLAKSVMNKIQHLTDLNVHDFSLSTLLSVFEEQVEDSAAIYDFSELLVEGNEQGFGILKCEETEHENEEPSLKKARL

Max tile of activation domain from residues 1051 to 1130 (estimated 65.9% to 73.2% of cells activated):
DGREPLAKSVMNKIQHLTDLNVHDFSLSTLLSVFEEQVEDSAAIYDFSELLVEGNEQGFGILKCEETEHENEEPSLKKAR

---

Extended activation domain from residues 431 to 520:
SHIIWNLNRMSIYNTNCGNSEIYNHIVNCSSNLCEFCEGKCCHSCIGTALIRINSRLPQISKTTKKEPIVMTMFSRFYADVDVLGSFGKK

Max tile of activation domain from residues 441 to 520 (estimated 21.0% to 24.3% of cells activated):
SIYNTNCGNSEIYNHIVNCSSNLCEFCEGKCCHSCIGTALIRINSRLPQISKTTKKEPIVMTMFSRFYADVDVLGSFGKK

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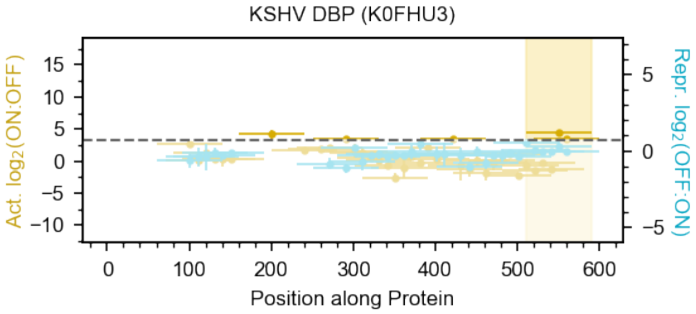
# KSHV DBP (K0FHU3)

Gene: ORF6 ; Protein Family: DBP



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Extended activation domain from residues 511 to 598:
GPYAVLGDEVLSLLSTVGQAGVPWTAEGVASVIQDIIDDCELQFVGPEEPCLIQGQSVVEELFPSPGVPSLTVGKKRKIASLLSDLDL

Max tile of activation domain from residues 511 to 590 (estimated 21.9% to 33.4% of cells activated):
GPYAVLGDEVLSLLSTVGQAGVPWTAEGVASVIQDIIDDCELQFVGPEEPCLIQGQSVVEELFPSPGVPSLTVGKKRKIA

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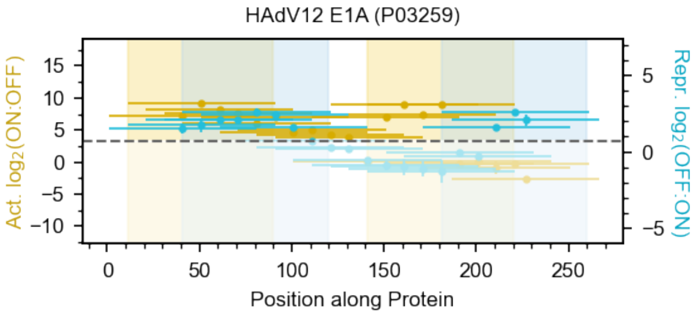
## HAdV12 E1A (P03259)

Gene: E1A ; Protein Family: E1A



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Extended activation domain from residues 1 to 170:
MRTEMTPLVLSYQEADDILEHLVDNFFNEVPSDDDLYVPSLYELYDLDVESAGEDNNEQAVNEFFPESLILAASEGLFLPEPPVLSPVCEPIGGECMPQLHPEDMDLLCYEMGFPCSDSEDEQDENGMAHVSASAAAAAADREREEFQLDHPELPGHNCKSCEHHRNSTG

Max tile of activation domain from residues 11 to 90 (estimated 90.9% to 92.0% of cells activated):
SYQEADDILEHLVDNFFNEVPSDDDLYVPSLYELYDLDVESAGEDNNEQAVNEFFPESLILAASEGLFLPEPPVLSPVCE

---

Extended activation domain from residues 111 to 220:
EMGFPCSDSEDEQDENGMAHVSASAAAAAADREREEFQLDHPELPGHNCKSCEHHRNSTGNTDLMCSLCYLRAYNMFIYSPVSDNEPEPNSTLDGDERPSPPKLGSAVPE

Max tile of activation domain from residues 141 to 220 (estimated 88.3% to 92.2% of cells activated):
DREREEFQLDHPELPGHNCKSCEHHRNSTGNTDLMCSLCYLRAYNMFIYSPVSDNEPEPNSTLDGDERPSPPKLGSAVPE

---

Extended repression domain from residues 1 to 150:
MRTEMTPLVLSYQEADDILEHLVDNFFNEVPSDDDLYVPSLYELYDLDVESAGEDNNEQAVNEFFPESLILAASEGLFLPEPPVLSPVCEPIGGECMPQLHPEDMDLLCYEMGFPCSDSEDEQDENGMAHVSASAAAAAADREREEFQLD

Max tile of repression domain from residues 41 to 120 (estimated 47.9% to 66.3% of cells repressed):
LYELYDLDVESAGEDNNEQAVNEFFPESLILAASEGLFLPEPPVLSPVCEPIGGECMPQLHPEDMDLLCYEMGFPCSDSE

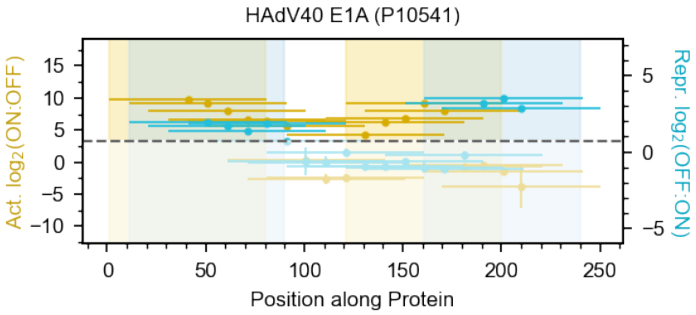
---

Extended repression domain from residues 171 to 266:
NTDLMCSLCYLRAYNMFIYSPVSDNEPEPNSTLDGDERPSPPKLGSAVPEGVIKPVPQRVTGRRRCAVESILDLIQEEEREQTVPVDLSVKRPRCN

Max tile of repression domain from residues 181 to 260 (estimated 52.8% to 61.0% of cells repressed):
LRAYNMFIYSPVSDNEPEPNSTLDGDERPSPPKLGSAVPEGVIKPVPQRVTGRRRCAVESILDLIQEEEREQTVPVDLSV

# HAdV40 E1A (P10541)

Gene: E1A ; Protein Family: E1A



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Extended activation domain from residues 1 to 130:
MRMLPDFFTGNWDDMFQGLLETEYVFDFPEPSEASEEMSLHDLFDVEVDGFEEDANQEAVDGMFPERLLSEAESAAESGSGDSGVGEELLPVDLDLKCYEDGLPPSDPETDEATEAEEEAAMPTYVNENE

Max tile of activation domain from residues 1 to 80 (estimated 93.3% to 93.7% of cells activated):
MRMLPDFFTGNWDDMFQGLLETEYVFDFPEPSEASEEMSLHDLFDVEVDGFEEDANQEAVDGMFPERLLSEAESAAESGS

---

Extended activation domain from residues 91 to 210:
PVDLDLKCYEDGLPPSDPETDEATEAEEEAAMPTYVNENENELVLDCPENPGRGCRACDFHRGTSGNPEAMCALCYMRLTGHCIYSPISDAEGESESGSPEDTDFPHPLTATPPHGIVRT

Max tile of activation domain from residues 121 to 200 (estimated 91.3% to 91.8% of cells activated):
AMPTYVNENENELVLDCPENPGRGCRACDFHRGTSGNPEAMCALCYMRLTGHCIYSPISDAEGESESGSPEDTDFPHPLT

---

Extended repression domain from residues 151 to 249:
HRGTSGNPEAMCALCYMRLTGHCIYSPISDAEGESESGSPEDTDFPHPLTATPPHGIVRTIPCRVSCRRRPAVECIEDLLEEDPTDEPLNLSLKRPKCS

Max tile of repression domain from residues 161 to 240 (estimated 81.9% to 86.1% of cells repressed):
MCALCYMRLTGHCIYSPISDAEGESESGSPEDTDFPHPLTATPPHGIVRTIPCRVSCRRRPAVECIEDLLEEDPTDEPLN

---

Extended repression domain from residues 11 to 120:
NWDDMFQGLLETEYVFDFPEPSEASEEMSLHDLFDVEVDGFEEDANQEAVDGMFPERLLSEAESAAESGSGDSGVGEELLPVDLDLKCYEDGLPPSDPETDEATEAEEEA

Max tile of repression domain from residues 11 to 90 (estimated 35.8% to 39.2% of cells repressed):
NWDDMFQGLLETEYVFDFPEPSEASEEMSLHDLFDVEVDGFEEDANQEAVDGMFPERLLSEAESAAESGSGDSGVGEELL

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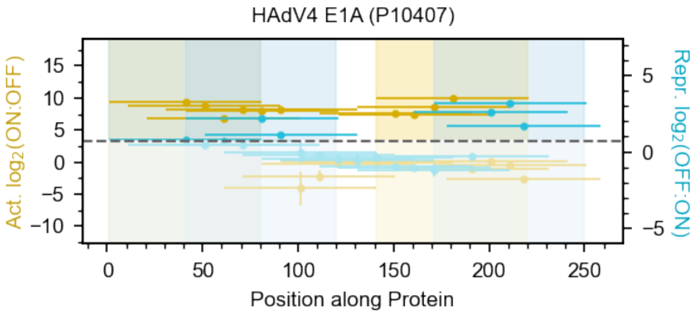
## HAdV4 E1A (P10407)

Gene: E1A ; Protein Family: E1A



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Extended activation domain from residues 111 to 220:
MDLRCYEECLPPSDDEDEQAIQNAASHGVQAVSESFALDCPPLPGHGCKSCEFHRINTGDKAVLCALCYMRAYNHCVYSPVSDADDETPTTESTLSPPEIGTSPSDNIVR

Max tile of activation domain from residues 141 to 220 (estimated 92.0% to 94.8% of cells activated):
AVSESFALDCPPLPGHGCKSCEFHRINTGDKAVLCALCYMRAYNHCVYSPVSDADDETPTTESTLSPPEIGTSPSDNIVR

---

Extended activation domain from residues 1 to 130:
MRHLRDLPDEEIIIASGSEILELVVNATMGDDHPEPPTPFGTPSLHDLYDLEVDVPEDDPNEKAVNDLFSDAALLAAEEASSPSSDSDSSLHTPRHDRGEKEIPGLKWEKMDLRCYEECLPPSDDEDEQA

Max tile of activation domain from residues 1 to 80 (estimated 91.8% to 92.5% of cells activated):
MRHLRDLPDEEIIIASGSEILELVVNATMGDDHPEPPTPFGTPSLHDLYDLEVDVPEDDPNEKAVNDLFSDAALLAAEEA

---

Extended repression domain from residues 161 to 257:
CEFHRINTGDKAVLCALCYMRAYNHCVYSPVSDADDETPTTESTLSPPEIGTSPSDNIVRPVPVRATGRRAAVECLDDLLQGGDEPLDLCTRKRPRH

Max tile of repression domain from residues 171 to 250 (estimated 71.1% to 79.1% of cells repressed):
KAVLCALCYMRAYNHCVYSPVSDADDETPTTESTLSPPEIGTSPSDNIVRPVPVRATGRRAAVECLDDLLQGGDEPLDLC

---

Extended repression domain from residues 41 to 130:
GTPSLHDLYDLEVDVPEDDPNEKAVNDLFSDAALLAAEEASSPSSDSDSSLHTPRHDRGEKEIPGLKWEKMDLRCYEECLPPSDDEDEQA

Max tile of repression domain from residues 41 to 120 (estimated 41.2% to 45.1% of cells repressed):
GTPSLHDLYDLEVDVPEDDPNEKAVNDLFSDAALLAAEEASSPSSDSDSSLHTPRHDRGEKEIPGLKWEKMDLRCYEECL

---

Extended repression domain from residues 1 to 80:
MRHLRDLPDEEIIIASGSEILELVVNATMGDDHPEPPTPFGTPSLHDLYDLEVDVPEDDPNEKAVNDLFSDAALLAAEEA

Max tile of repression domain from residues 1 to 80 (estimated 17.9% to 20.0% of cells repressed):
MRHLRDLPDEEIIIASGSEILELVVNATMGDDHPEPPTPFGTPSLHDLYDLEVDVPEDDPNEKAVNDLFSDAALLAAEEA

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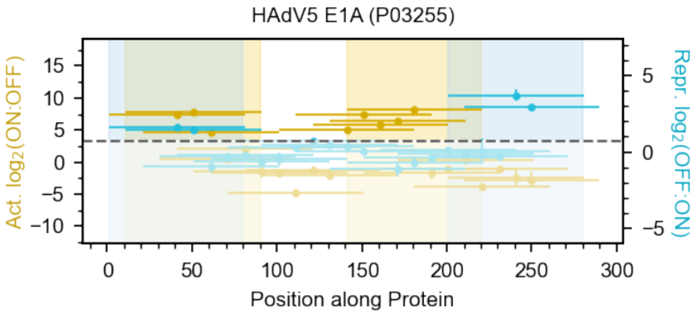
**Other Tiling Screen Data from Ludwig, C.H. et al. 2023**

## HAdV5 E1A (P03255)

Gene: E1A ; Protein Family: E1A



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Extended activation domain from residues 101 to 220:
QPEQRALGPVSMPNLVPEVIDLTCHEAGFPPSDDEDEEGEEFVLDYVEHPGHGCRSCHYHRRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPEPEPEPEPARPTRRPKMAPAILRRPTSP

Max tile of activation domain from residues 141 to 220 (estimated 85.9% to 86.5% of cells activated):
EFVLDYVEHPGHGCRSCHYHRRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPEPEPEPEPARPTRRPKMAPAILRRPTSP

---

Extended activation domain from residues 1 to 100:
MRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFEPPTLHELYDLDVTAPEDPNEEAVSQIFPDSVMLAVQEGIDLLTFPPAPGSPEPPHLSRQPE

Max tile of activation domain from residues 11 to 90 (estimated 81.3% to 84.4% of cells activated):
ITEEMAASLLDQLIEEVLADNLPPPSHFEPPTLHELYDLDVTAPEDPNEEAVSQIFPDSVMLAVQEGIDLLTFPPAPGSP

---

Extended repression domain from residues 201 to 289:
ARPTRRPKMAPAILRRPTSPVSRECNSSTDSCDSGPSNTPPEIHPVVPLCPIKPVAVRVGGRRQAVECIEDLLNEPGQPLDLSCKRPRP

Max tile of repression domain from residues 201 to 280 (estimated 78.9% to 92.7% of cells repressed):
ARPTRRPKMAPAILRRPTSPVSRECNSSTDSCDSGPSNTPPEIHPVVPLCPIKPVAVRVGGRRQAVECIEDLLNEPGQPL

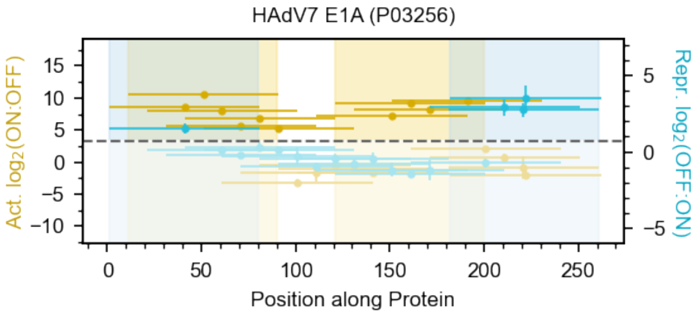
---

Extended repression domain from residues 1 to 90:
MRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFEPPTLHELYDLDVTAPEDPNEEAVSQIFPDSVMLAVQEGIDLLTFPPAPGSP

Max tile of repression domain from residues 1 to 80 (estimated 26.2% to 32.5% of cells repressed):
MRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFEPPTLHELYDLDVTAPEDPNEEAVSQIFPDSVMLAVQEGIDL

# HAdV7 E1A (P03256)

Gene: E1A ; Protein Family: E1A



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Extended activation domain from residues 1 to 130:
MRHLRFLPQEIISSETGIEILEFVVNTLMGDDPEPPVQPFDPPTLHDLYDLEVDGPEDPNEGAVNGFFTDSMLLAADEGLDINPPPETLVTPGVVVESGRGGKKLPDLGAAEMDLRCYEEGFPPSDDEDG

Max tile of activation domain from residues 11 to 90 (estimated 94.1% to 95.6% of cells activated):
IISSETGIEILEFVVNTLMGDDPEPPVQPFDPPTLHDLYDLEVDGPEDPNEGAVNGFFTDSMLLAADEGLDINPPPETLV

---

Extended activation domain from residues 111 to 210:
AEMDLRCYEEGFPPSDDEDGETEQSIHTAVNEGVKAASDVFKLDCPELPGHGCKSCEFHRNNTGMKELLCSLCYMRMHCHFIYSPVSDDESPSPDSTTSP

Max tile of activation domain from residues 121 to 200 (estimated 90.4% to 92.3% of cells activated):
GFPPSDDEDGETEQSIHTAVNEGVKAASDVFKLDCPELPGHGCKSCEFHRNNTGMKELLCSLCYMRMHCHFIYSPVSDDE

---

Extended repression domain from residues 171 to 261:
NNTGMKELLCSLCYMRMHCHFIYSPVSDDESPSPDSTTSPPEIQAPAPANVCKPIPVKPKPGKRPAVDKLEDLLEGGDGPLDLSTRKLPRQ

Max tile of repression domain from residues 182 to 261 (estimated 62.3% to 95.3% of cells repressed):
LCYMRMHCHFIYSPVSDDESPSPDSTTSPPEIQAPAPANVCKPIPVKPKPGKRPAVDKLEDLLEGGDGPLDLSTRKLPRQ

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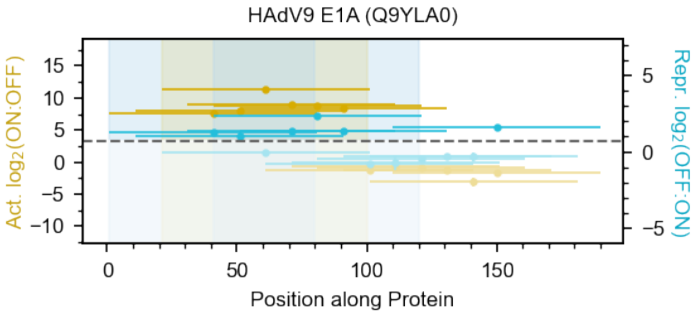
Extended repression domain from residues 1 to 80:
MRHLRFLPQEIISSETGIEILEFVVNTLMGDDPEPPVQPFDPPTLHDLYDLEVDGPEDPNEGAVNGFFTDSMLLAADEGL

Max tile of repression domain from residues 1 to 80 (estimated 22.6% to 35.6% of cells repressed):
MRHLRFLPQEIISSETGIEILEFVVNTLMGDDPEPPVQPFDPPTLHDLYDLEVDGPEDPNEGAVNGFFTDSMLLAADEGL

## HAdV9 E1A (Q9YLA0)

Gene: E1A ; Protein Family: E1A



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Extended activation domain from residues 1 to 130:
MRHLRLLPSTVPGELAVLMLEDFVDTVLEDELHPSPFELGPTLQDLYDLEVDAHDDDPNEEAVNLIFPESMILQADIANESTPLHTPTLSPIPELEEEDELDLRCYEEGFPPSDSEDERGPVSEDELSPS

Max tile of activation domain from residues 21 to 100 (estimated 95.4% to 96.0% of cells activated):
EDFVDTVLEDELHPSPFELGPTLQDLYDLEVDAHDDDPNEEAVNLIFPESMILQADIANESTPLHTPTLSPIPELEEEDE

---

Extended repression domain from residues 31 to 130:
ELHPSPFELGPTLQDLYDLEVDAHDDDPNEEAVNLIFPESMILQADIANESTPLHTPTLSPIPELEEEDELDLRCYEEGFPPSDSEDERGPVSEDELSPS

Max tile of repression domain from residues 41 to 120 (estimated 43.4% to 55.2% of cells repressed):
PTLQDLYDLEVDAHDDDPNEEAVNLIFPESMILQADIANESTPLHTPTLSPIPELEEEDELDLRCYEEGFPPSDSEDERG

---

Extended repression domain from residues 1 to 90:
MRHLRLLPSTVPGELAVLMLEDFVDTVLEDELHPSPFELGPTLQDLYDLEVDAHDDDPNEEAVNLIFPESMILQADIANESTPLHTPTLS

Max tile of repression domain from residues 1 to 80 (estimated 22.5% to 24.7% of cells repressed):
MRHLRLLPSTVPGELAVLMLEDFVDTVLEDELHPSPFELGPTLQDLYDLEVDAHDDDPNEEAVNLIFPESMILQADIANE

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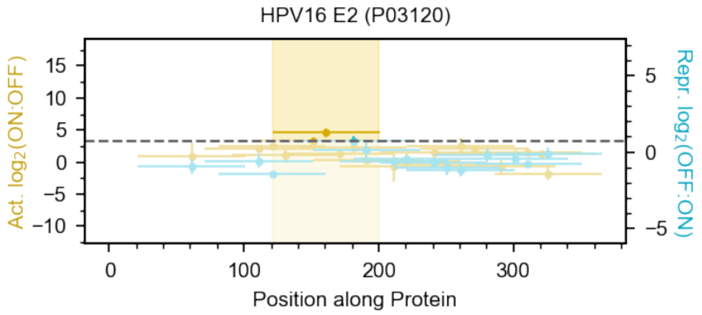
## HPV16 E2 (P03120)

Gene: E2 ; Protein Family: E2



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Extended activation domain from residues 111 to 200:
KKHGYTVEVQFDGDICNTMHYTNWTHIYICEEASVTVVEGQVDYYGLYYVHEGIRTYFVQFKDDAEKYSKNKVWEVHAGGQVILCPTSVF

Max tile of activation domain from residues 121 to 200 (estimated 21.0% to 43.5% of cells activated):
FDGDICNTMHYTNWTHIYICEEASVTVVEGQVDYYGLYYVHEGIRTYFVQFKDDAEKYSKNKVWEVHAGGQVILCPTSVF

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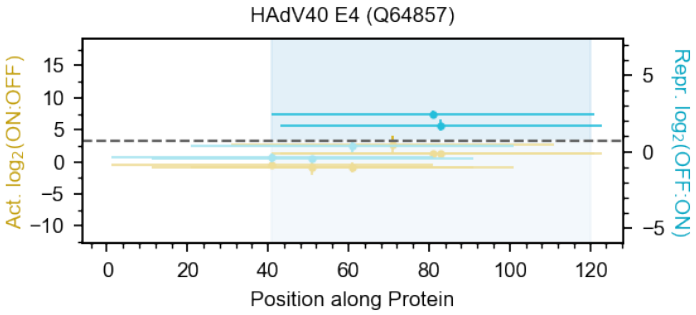
## HAdV40 E4 (Q64857)

Gene: E4 ; Protein Family: E4



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Extended repression domain from residues 41 to 122:
ECEHLNMHYSSALDSTVLLDDVSEGFISITDQRFASKEPVLILSQKNRCVNPKLQLFAVVQGEREVYKVKWKGGGRLTVRIL

Max tile of repression domain from residues 41 to 120 (estimated 44.1% to 59.8% of cells repressed):
ECEHLNMHYSSALDSTVLLDDVSEGFISITDQRFASKEPVLILSQKNRCVNPKLQLFAVVQGEREVYKVKWKGGGRLTVR

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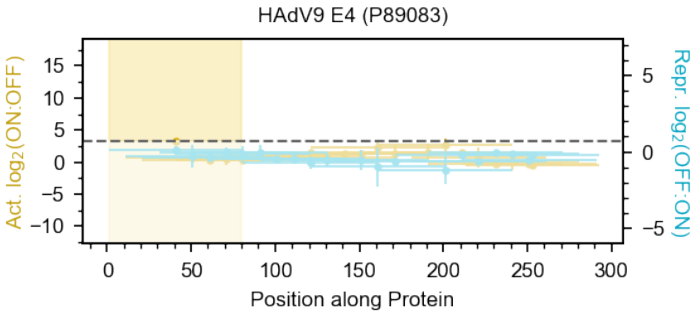
## HAdV9 E4 (P89083)

Gene: E4 ; Protein Family: E4



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Extended activation domain from residues 1 to 80:
MQTEIQSSSLRHHPYRRARLPRSDEETRASLTEQHPLLPDCDHADYHNVSSVRGLPCAAGFTLLQEFPVPWDMILTPEEI

Max tile of activation domain from residues 1 to 80 (estimated 13.9% to 15.8% of cells activated):
MQTEIQSSSLRHHPYRRARLPRSDEETRASLTEQHPLLPDCDHADYHNVSSVRGLPCAAGFTLLQEFPVPWDMILTPEEI

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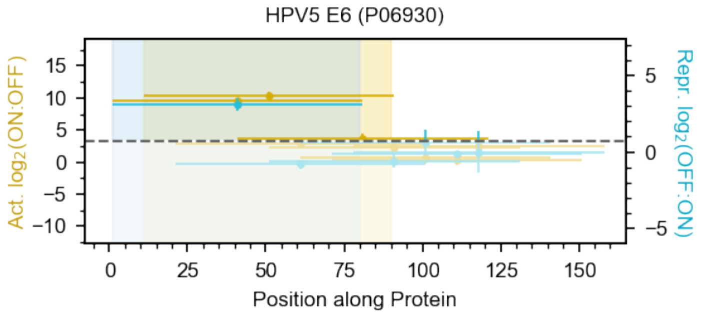
# HPV5 E6 (P06930)

Gene: E6 ; Protein Family: E6



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Extended activation domain from residues 1 to 90:
MAEGAEHQQKLTEKDKAELPLSIRDLAEALGIPVIDCLIPCNFCGNFLNYLEACEFDYKRLSLIWKDYCVFACCRVCCGATATYEFNQFY

Max tile of activation domain from residues 11 to 90 (estimated 93.4% to 95.6% of cells activated):
LTEKDKAELPLSIRDLAEALGIPVIDCLIPCNFCGNFLNYLEACEFDYKRLSLIWKDYCVFACCRVCCGATATYEFNQFY

---

Extended repression domain from residues 1 to 80:
MAEGAEHQQKLTEKDKAELPLSIRDLAEALGIPVIDCLIPCNFCGNFLNYLEACEFDYKRLSLIWKDYCVFACCRVCCGA

Max tile of repression domain from residues 1 to 80 (estimated 59.5% to 83.1% of cells repressed):
MAEGAEHQQKLTEKDKAELPLSIRDLAEALGIPVIDCLIPCNFCGNFLNYLEACEFDYKRLSLIWKDYCVFACCRVCCGA

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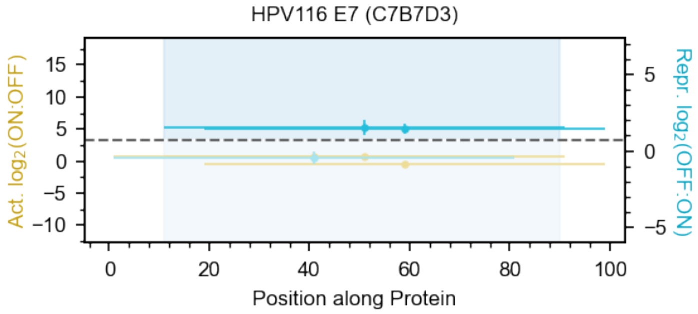
# HPV116 E7 (C7B7D3)

Gene: E7 ; Protein Family: E7



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Extended repression domain from residues 11 to 98:
VELHLEELVIPANLLSDESLSLDETPEEEQLSPYRVDSLCTRCNKCIRISVVCTTGAIYTLEQLLLSTELSFLCAGCSRTTVRNGRRF

Max tile of repression domain from residues 11 to 90 (estimated 21.1% to 38.3% of cells repressed):
VELHLEELVIPANLLSDESLSLDETPEEEQLSPYRVDSLCTRCNKCIRISVVCTTGAIYTLEQLLLSTELSFLCAGCSRT

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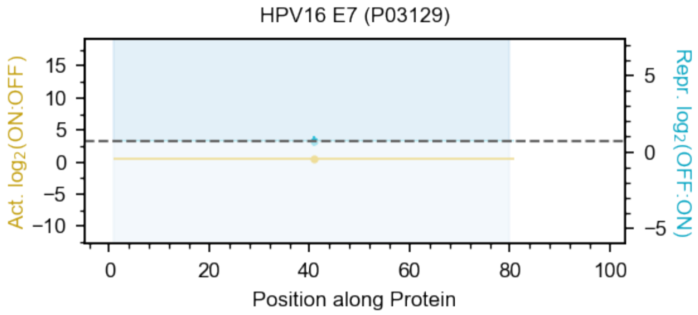
# HPV16 E7 (P03129)

Gene: E7 ; Protein Family: E7



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Extended repression domain from residues 1 to 80:
MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLE

Max tile of repression domain from residues 1 to 80 (estimated 16.4% to 21.0% of cells repressed):
MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLE

---

Extended repression domain from residues 1 to 80:
MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLE

Max tile of repression domain from residues 1 to 80 (estimated 16.4% to 21.0% of cells repressed):
MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLE

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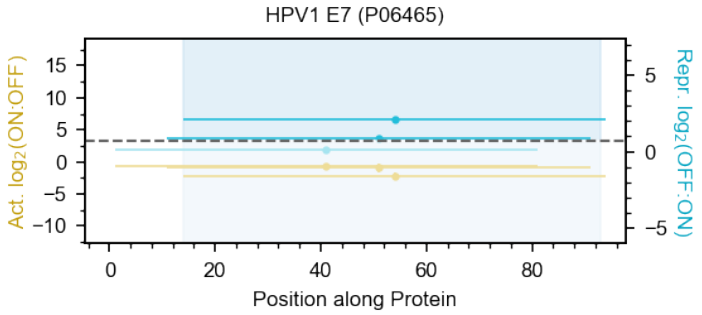
# HPV1 E7 (P06465)

Gene: E7 ; Protein Family: E7



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Extended repression domain from residues 11 to 93:
LVLQLEPSVLDLDLYCYEEVPPDDIEEELVSPQQPYAVVASCAYCEKLVRLTVLADHSAIRQLEELLLRSLNIVCPLCTLQRQ

Max tile of repression domain from residues 14 to 93 (estimated 39.2% to 42.5% of cells repressed):
QLEPSVLDLDLYCYEEVPPDDIEEELVSPQQPYAVVASCAYCEKLVRLTVLADHSAIRQLEELLLRSLNIVCPLCTLQRQ

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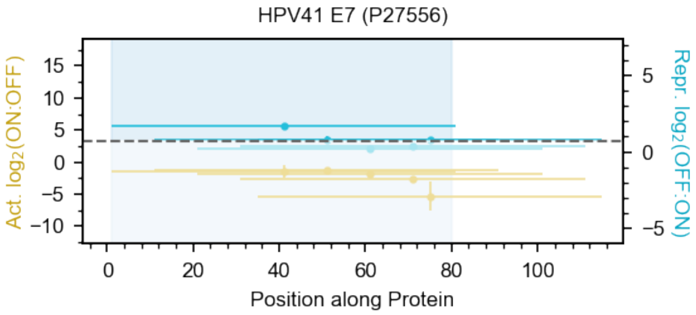
# HPV41 E7 (P27556)

Gene: E7 ; Protein Family: E7



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Extended repression domain from residues 1 to 90:
MRGNSVDLQEIVLVQQGEVPENAAVHSGEHSDDEGESEEEEREQVQQVPTPRRTLYLVESQCPFCQAIIRFVCVASNTGIRNLQALLVNS

Max tile of repression domain from residues 1 to 80 (estimated 28.5% to 35.2% of cells repressed):
MRGNSVDLQEIVLVQQGEVPENAAVHSGEHSDDEGESEEEEREQVQQVPTPRRTLYLVESQCPFCQAIIRFVCVASNTGI

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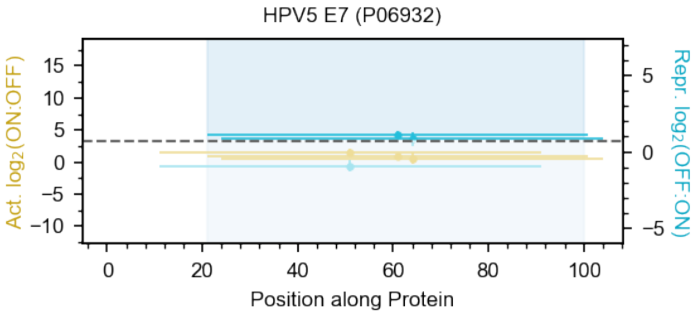
## HPV5 E7 (P06932)

Gene: E7 ; Protein Family: E7



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Extended repression domain from residues 21 to 103:
EVLPVDLFCEEELPNEQETEEEPDNERISYKVIAPCGCRNCEVKLRIFVHATEFGIRAFQQLLTGDLQLLCPDCRGNCKHDGS

Max tile of repression domain from residues 21 to 100 (estimated 20.2% to 24.5% of cells repressed):
EVLPVDLFCEEELPNEQETEEEPDNERISYKVIAPCGCRNCEVKLRIFVHATEFGIRAFQQLLTGDLQLLCPDCRGNCKH

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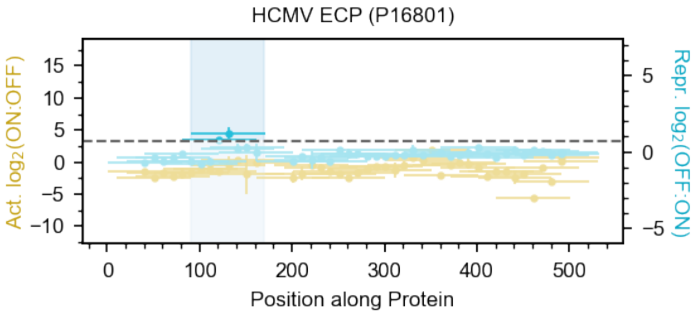
## HCMV ECP (P16801)

Gene: UL95 ; Protein Family: ECP



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Extended repression domain from residues 81 to 170:
PSTAVRSPGSAGVSTSLCSVERMVELSAQSPAADFSVSEAWRFEEAVNMALVACEAVSPYDRFRLIETPDENFLLVTNVIPRESAEVPVL

Max tile of repression domain from residues 91 to 170 (estimated 19.2% to 28.6% of cells repressed):
AGVSTSLCSVERMVELSAQSPAADFSVSEAWRFEEAVNMALVACEAVSPYDRFRLIETPDENFLLVTNVIPRESAEVPVL

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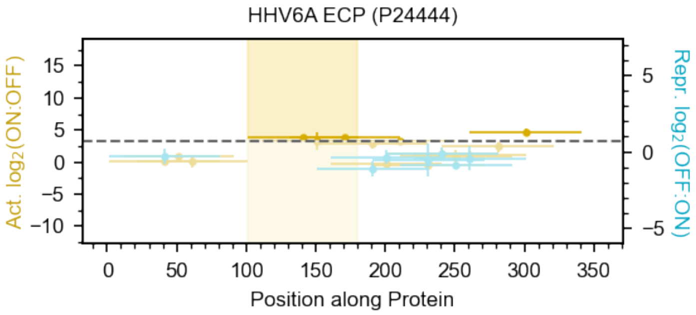
# HHV6A ECP (P24444)

Gene: U67 ; Protein Family: ECP



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Extended activation domain from residues 101 to 190:
KSKKMARTYLLQNVLRTQDQQVAISGKYILYTKKHIETSLMIDKTKLVKKILEYAETPNLLGYTDVRDLECLLWLVFCGPKSFCQSDSCF

Max tile of activation domain from residues 101 to 180 (estimated 17.3% to 22.0% of cells activated):
KSKKMARTYLLQNVLRTQDQQVAISGKYILYTKKHIETSLMIDKTKLVKKILEYAETPNLLGYTDVRDLECLLWLVFCGP

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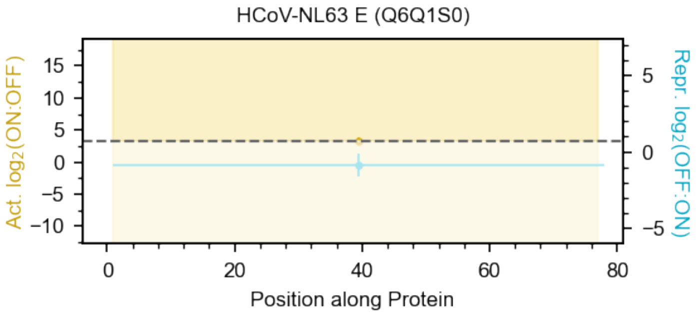
## HCoV-NL63 E (Q6Q1S0)

Gene: E ; Protein Family: E



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Extended activation domain from residues 1 to 77:
MFLRLIDDNGIVLNSILWLLVMIFFFVLAMTFIKLIQLCFTCHYFFSRTLYQPVYKIFLAYQDYMQIAPVPAEVLNV

Max tile of activation domain from residues 1 to 77 (estimated 9.2% to 21.4% of cells activated):
MFLRLIDDNGIVLNSILWLLVMIFFFVLAMTFIKLIQLCFTCHYFFSRTLYQPVYKIFLAYQDYMQIAPVPAEVLNV

---

Extended activation domain from residues 1 to 77:
MFLRLIDDNGIVLNSILWLLVMIFFFVLAMTFIKLIQLCFTCHYFFSRTLYQPVYKIFLAYQDYMQIAPVPAEVLNV

Max tile of activation domain from residues 1 to 77 (estimated 6.2% to 7.0% of cells activated):
MFLRLIDDNGIVLNSILWLLVMIFFFVLAMTFIKLIQLCFTCHYFFSRTLYQPVYKIFLAYQDYMQIAPVPAEVLNV

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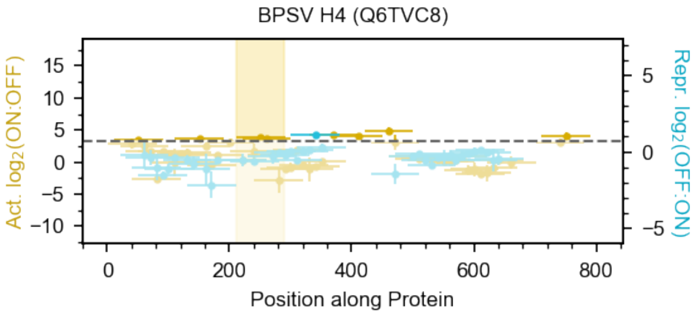
## BPSV H4 (Q6TVC8)

Gene: H4 ; Protein Family: H4



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Extended activation domain from residues 211 to 300:
VFMYDLDGVRIPIVIRDFLDVKKVFLEATGKVYLNNFADDHPGIVEWGRAFVDAMAHDERRLLYKYVFLSSRHLCDMFTDLLNPRNAKFR

Max tile of activation domain from residues 211 to 290 (estimated 16.6% to 22.3% of cells activated):
VFMYDLDGVRIPIVIRDFLDVKKVFLEATGKVYLNNFADDHPGIVEWGRAFVDAMAHDERRLLYKYVFLSSRHLCDMFTD

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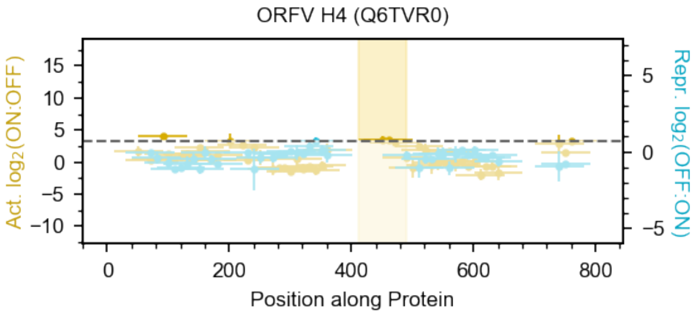
# ORFV H4 (Q6TVR0)

Gene: H4 ; Protein Family: H4



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Extended activation domain from residues 411 to 500:
NIVMSFDTIMKTQTWAVKYNINRLILNFLIAINARRQEYERRFAAEIKRGVFFLRLSANLLDVHASATELFQSAKTLNLNFIVALVIVLN

Max tile of activation domain from residues 411 to 490 (estimated 11.5% to 22.0% of cells activated):
NIVMSFDTIMKTQTWAVKYNINRLILNFLIAINARRQEYERRFAAEIKRGVFFLRLSANLLDVHASATELFQSAKTLNLN

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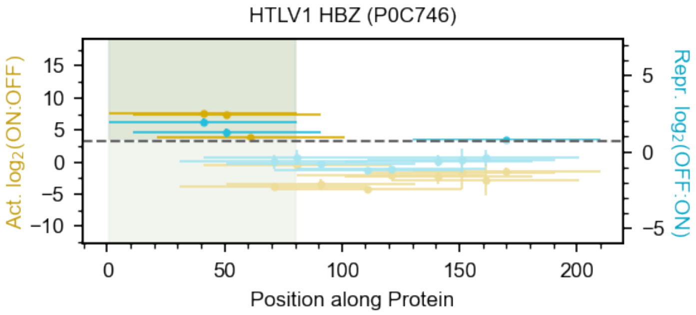
# HTLV1 HBZ (P0C746)

Gene: HBZ ; Protein Family: HBZ



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Extended activation domain from residues 1 to 100:
MVNFVSAGLFRCLPVSCPEDLLVEELVDGLLSLEEELKDKEEEEAVLDGLLSLEEESRGRLRRGPPGEKAPPRGETHRDRQRRAEEKRKRKKEREKEEEK

Max tile of activation domain from residues 1 to 80 (estimated 78.9% to 80.6% of cells activated):
MVNFVSAGLFRCLPVSCPEDLLVEELVDGLLSLEEELKDKEEEEAVLDGLLSLEEESRGRLRRGPPGEKAPPRGETHRDR

---

Extended repression domain from residues 1 to 90:
MVNFVSAGLFRCLPVSCPEDLLVEELVDGLLSLEEELKDKEEEEAVLDGLLSLEEESRGRLRRGPPGEKAPPRGETHRDRQRRAEEKRKR

Max tile of repression domain from residues 1 to 80 (estimated 31.3% to 44.1% of cells repressed):
MVNFVSAGLFRCLPVSCPEDLLVEELVDGLLSLEEELKDKEEEEAVLDGLLSLEEESRGRLRRGPPGEKAPPRGETHRDR

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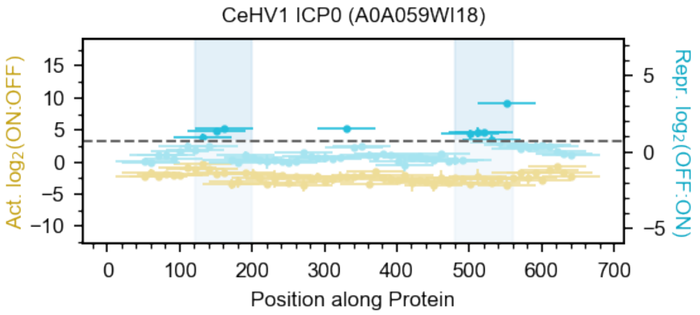
## CeHV1 ICP0 (A0A059WI18)

Gene: ICP0 ; Protein Family: ICP0



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Extended repression domain from residues 111 to 200:
LKTWLPMRNSCPLCNAAVAYLIVGVQPNGSYSTIPVVNDPRTRLEAEDAVRAGTAVDFIWVDRPGQPAPPSVTLGGRTVRALSPPARMGR

Max tile of repression domain from residues 121 to 200 (estimated 26.4% to 28.4% of cells repressed):
CPLCNAAVAYLIVGVQPNGSYSTIPVVNDPRTRLEAEDAVRAGTAVDFIWVDRPGQPAPPSVTLGGRTVRALSPPARMGR

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Extended repression domain from residues 461 to 570:
PHPRPAPARAPALAGAPPPPRPLAAPAAPPPPQAAPPPPAAPPPPVERRDRSSLGPRPAEQGPRKCVRKTRHVDAECAPAALGPTRYLPVSGVSSVVALAPYLNKTVTGD

Max tile of repression domain from residues 481 to 560 (estimated 22.7% to 25.9% of cells repressed):
RPLAAPAAPPPPQAAPPPPAAPPPPVERRDRSSLGPRPAEQGPRKCVRKTRHVDAECAPAALGPTRYLPVSGVSSVVALA

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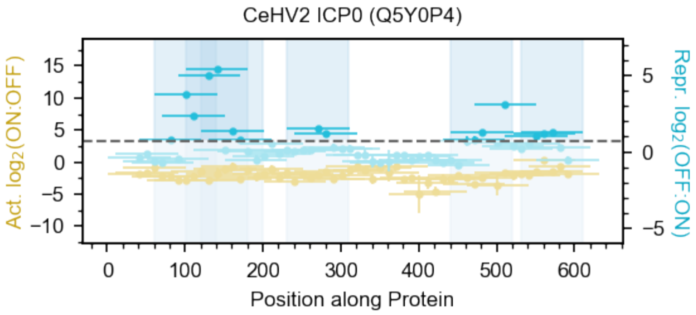
## CeHV2 ICP0 (Q5Y0P4)

Gene: RL2 ; Protein Family: ICP0



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Extended repression domain from residues 91 to 180:
VCTERIDETQLCAAFPCLHRFCIPCLKTWLPMRNSCPLCNAVVAYLIVGVKPDGSYSTIPVINDPRTRAEAEEAVRAGTAVDFIWTHRLP

Max tile of repression domain from residues 101 to 180 (estimated 99.9% to 100.1% of cells repressed):
LCAAFPCLHRFCIPCLKTWLPMRNSCPLCNAVVAYLIVGVKPDGSYSTIPVINDPRTRAEAEEAVRAGTAVDFIWTHRLP

---

Extended repression domain from residues 61 to 150:
DTDAELCEPGPASRGPRAPSPPPPPREVCAVCTERIDETQLCAAFPCLHRFCIPCLKTWLPMRNSCPLCNAVVAYLIVGVKPDGSYSTIP

Max tile of repression domain from residues 61 to 140 (estimated 85.5% to 90.1% of cells repressed):
DTDAELCEPGPASRGPRAPSPPPPPREVCAVCTERIDETQLCAAFPCLHRFCIPCLKTWLPMRNSCPLCNAVVAYLIVGV

---

Extended repression domain from residues 231 to 320:
DSPILIADSPPASPRRPPAVSGPPVAPVAPRPRAAMPRPPAQARPPALTQAQAQTQARSQARAQAALAQALAQALGRAPPRPAPPQHAHT

Max tile of repression domain from residues 231 to 310 (estimated 25.7% to 31.3% of cells repressed):
DSPILIADSPPASPRRPPAVSGPPVAPVAPRPRAAMPRPPAQARPPALTQAQAQTQARSQARAQAALAQALAQALGRAPP

---

Extended repression domain from residues 121 to 210:
PMRNSCPLCNAVVAYLIVGVKPDGSYSTIPVINDPRTRAEAEEAVRAGTAVDFIWTHRLPGEAAPASVTLGGRTVRALSPPARMGQPAPR

Max tile of repression domain from residues 121 to 200 (estimated 24.8% to 25.1% of cells repressed):
PMRNSCPLCNAVVAYLIVGVKPDGSYSTIPVINDPRTRAEAEEAVRAGTAVDFIWTHRLPGEAAPASVTLGGRTVRALSP

---

Extended repression domain from residues 511 to 610:
SGVSSVVAMAPYLNKTVTGDCLPVLDMETGAIGAYVVLVGRDCNLARCLADAEPQWARRSRLPEAAPGCVSPPEYPGDPAHGLWMTPVGGMLFEQGALLG

Max tile of repression domain from residues 531 to 610 (estimated 21.7% to 26.4% of cells repressed):
CLPVLDMETGAIGAYVVLVGRDCNLARCLADAEPQWARRSRLPEAAPGCVSPPEYPGDPAHGLWMTPVGGMLFEQGALLG

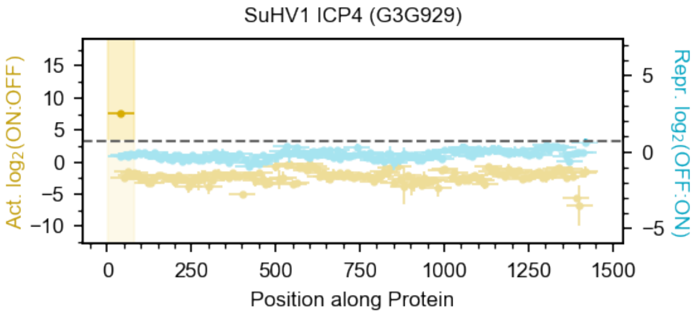
---

Extended repression domain from residues 421 to 520:
PARPAQLPPAPPLAAAAPPPAPPPPPASSAPRGSAAPPPPAAPPPAERAHGSSLGPRPAERGPRKCARKTHHVDADRAPAASGPTRYLPISGVSSVVAMA

Max tile of repression domain from residues 441 to 520 (estimated 22.0% to 24.9% of cells repressed):
APPPPPASSAPRGSAAPPPPAAPPPAERAHGSSLGPRPAERGPRKCARKTHHVDADRAPAASGPTRYLPISGVSSVVAMA

## SuHV1 ICP4 (G3G929)

Gene: ICP4 ; Protein Family: ICP4



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Extended activation domain from residues 1 to 80:
MADDLFDFIETEGNFSQLLAAAAAAAAEEEGIASGPDGGSQGSRRRGSSGEDLLFGPGGLFSDDAAEAEAEAAVLAAAAGA

Max tile of activation domain from residues 1 to 80 (estimated 77.7% to 83.1% of cells activated):
MADDLFDFIETEGNFSQLLAAAAAAAAEEEGIASGPDGGSQGSRRRGSSGEDLLFGPGGLFSDDAAEAEAEAAVLAAAAGA

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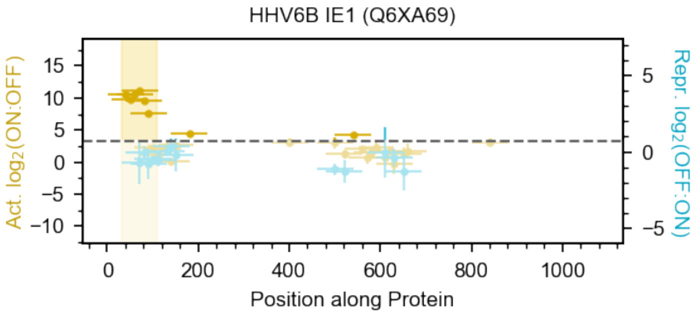
## HHV6B IE1 (Q6XA69)

Gene: U90 ; Protein Family: IE



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Extended activation domain from residues 1 to 130:
MESAKDTTSNSMFILGKPSGNNMESNEERMQNYHPDPVVEESIKEILEESLKCDVSFESLLFPELEAFDLFIPESSNDIASKNVSYSSNVEEGASEEFKALVAQSVGNCIQSIGASVKAAMKQEQSNMED

Max tile of activation domain from residues 31 to 110 (estimated 95.3% to 95.9% of cells activated):
QNYHPDPVVEESIKEILEESLKCDVSFESLLFPELEAFDLFIPESSNDIASKNVSYSSNVEEGASEEFKALVAQSVGNCI

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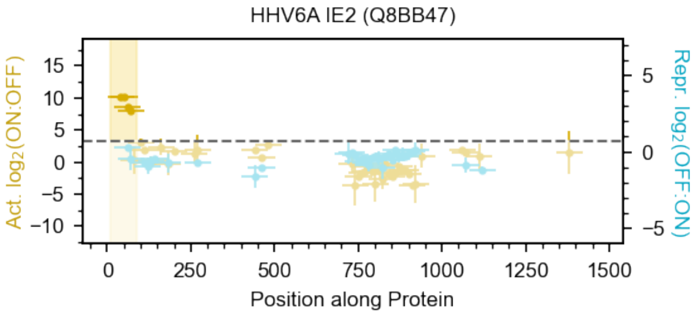
## HHV6A IE2 (Q8BB47)

Gene: U90/U86 ; Protein Family: IE



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Extended activation domain from residues 1 to 110:
MEPAKPSGNNMGSNDERMQDYRPDPMMEESIQQILEDSLMCDTSFDDLILPGLESFGLIIPESSNNIESNNVEEGSNEDLKTLAEHKCKQGNDNDVIQSAMKLSGLYCDA

Max tile of activation domain from residues 11 to 90 (estimated 94.2% to 94.3% of cells activated):
MGSNDERMQDYRPDPMMEESIQQILEDSLMCDTSFDDLILPGLESFGLIIPESSNNIESNNVEEGSNEDLKTLAEHKCKQ

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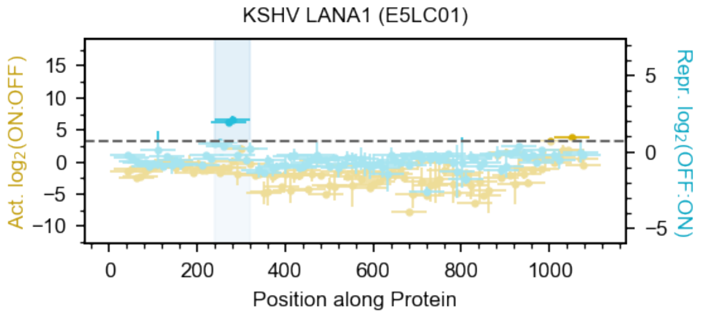
## KSHV LANA1 (E5LC01)

Gene: ORF73 ; Protein Family: LANA1



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Extended repression domain from residues 231 to 320:
NRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGSSSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGEDNGDNEISKESQ

Max tile of repression domain from residues 241 to 320 (estimated 36.2% to 48.7% of cells repressed):
ESPIYVGSSSDGDTPPRQPPTSPISIGSSSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGEDNGDNEISKESQ

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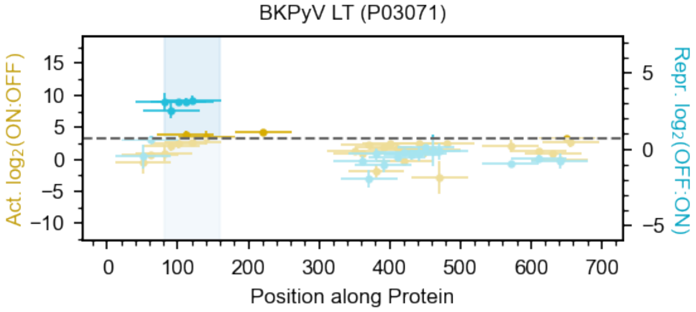
# BKPyV LT (P03071)

Gene: LT ; Protein Family: LT



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Extended repression domain from residues 41 to 160:
FHPDKGGDEDKMKRMNTLYKKMEQDVKVAHQPDFGTWSSSEVPTYGTEEWESWWSSFNEKWDEDLFCHEDMFASDEEATADSQHSTPPKKKRKVEDPKDFPSDLHQFLSQAVFSNRTLAC

Max tile of repression domain from residues 81 to 160 (estimated 68.0% to 83.2% of cells repressed):
EVPTYGTEEWESWWSSFNEKWDEDLFCHEDMFASDEEATADSQHSTPPKKKRKVEDPKDFPSDLHQFLSQAVFSNRTLAC

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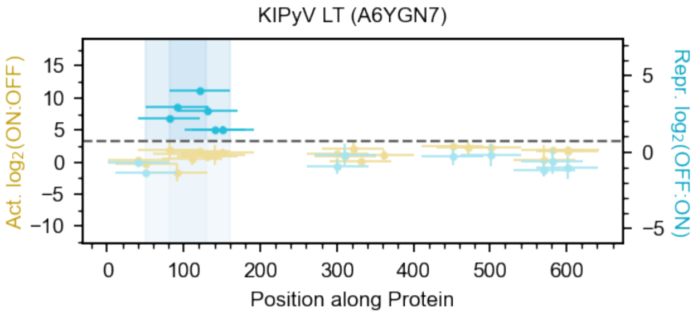
## KIPyV LT (A6YGN7)

Gene: LT ; Protein Family: LT



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Extended repression domain from residues 81 to 190:
QSSQIPTYGTPDWDEWWSQFNTYWEEELRCNESMPSSPKRSAPEEEPSCSQATPPKKKHAFDASLEFPKELLEFVSHAVFSNKCITCFVVHTTREKGE
VLYKKLLQKYQC

Max tile of repression domain from residues 81 to 160 (estimated 90.1% to 93.1% of cells repressed):
QSSQIPTYGTPDWDEWWSQFNTYWEEELRCNESMPSSPKRSAPEEEPSCSQATPPKKKHAFDASLEFPKELLEFVSHAVF

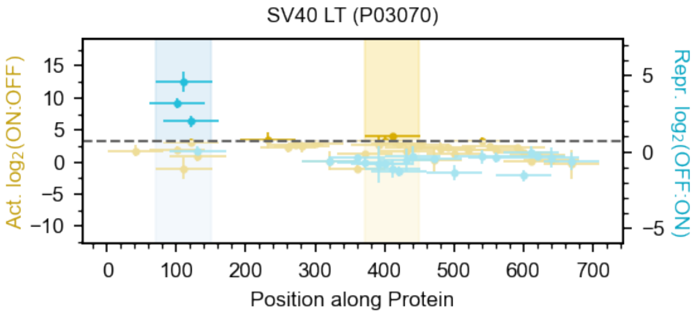
---

Extended repression domain from residues 41 to 130:
YHPDKGGNEESMKLLNSLYLKLQDSVSSVHDLNEEEDNIWQSSQIPTYGTPDWDEWWSQFNTYWEEELRCNESMPSSPKRSAPEEEPSCS

Max tile of repression domain from residues 51 to 130 (estimated 61.4% to 74.1% of cells repressed):
SMKLLNSLYLKLQDSVSSVHDLNEEEDNIWQSSQIPTYGTPDWDEWWSQFNTYWEEELRCNESMPSSPKRSAPEEEPSCS

## SV40 LT (P03070)

Gene: LT ; Protein Family: LT



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Extended activation domain from residues 361 to 450:
LTNRFNDLLDRMDIMFGSTGSADIEEWMAGVAWLHCLLPKMDSVVYDFLKCMVYNIPKKRYWLFKGPIDSGKTTLAAALLELCGGKALNV

Max tile of activation domain from residues 371 to 450 (estimated 16.8% to 29.1% of cells activated):
RMDIMFGSTGSADIEEWMAGVAWLHCLLPKMDSVVYDFLKCMVYNIPKKRYWLFKGPIDSGKTTLAAALLELCGGKALNV

---

Extended repression domain from residues 61 to 160:
KMEDGVKYAHQPDFGGFWDATEIPTYGTDEWEQWWNAFNEENLFCSEEMPSSDDEATADSQHSTPPKKKRKVEDPKDFPSELLSFLSHAVFSNRTLACFA

Max tile of repression domain from residues 71 to 150 (estimated 91.1% to 99.6% of cells repressed):
QPDFGGFWDATEIPTYGTDEWEQWWNAFNEENLFCSEEMPSSDDEATADSQHSTPPKKKRKVEDPKDFPSELLSFLSHAV

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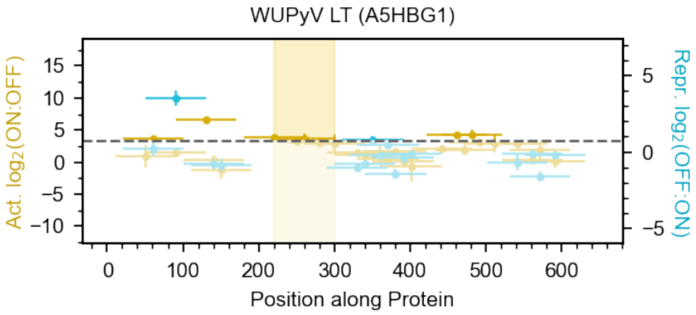
## WUPyV LT (A5HBG1)

Gene: LT ; Protein Family: LT



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Extended activation domain from residues 211 to 300:
LVFILTPFRHRVSAVNNFCKGYCTISFLFCKGVNNAYGLYSRMTRDPFTLCEENIPGGLKENDFKAEDLYGEFKDQLNWKALSEFALELG

Max tile of activation domain from residues 221 to 300 (estimated 11.1% to 28.6% of cells activated):
RVSAVNNFCKGYCTISFLFCKGVNNAYGLYSRMTRDPFTLCEENIPGGLKENDFKAEDLYGEFKDQLNWKALSEFALELG

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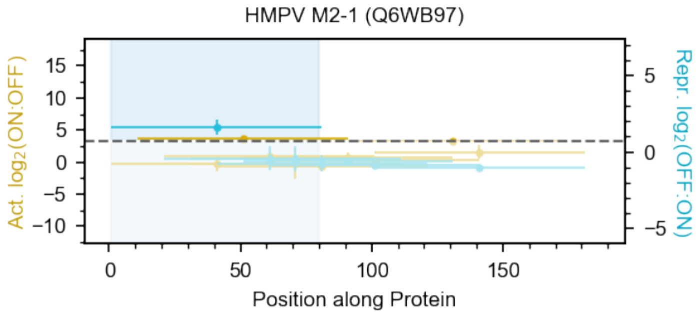
## HMPV M2-1 (Q6WB97)

Gene: M2-1 ; Protein Family: M2-1



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Extended repression domain from residues 1 to 80:
MSRKAPCKYEVRGKCNRGSECKFNHNYWSWPDRYLLIRSNYLLNQLLRNTDRADGLSIISGAGREDRTQDFVLGSTNVVQ

Max tile of repression domain from residues 1 to 80 (estimated 21.4% to 40.7% of cells repressed):
MSRKAPCKYEVRGKCNRGSECKFNHNYWSWPDRYLLIRSNYLLNQLLRNTDRADGLSIISGAGREDRTQDFVLGSTNVVQ

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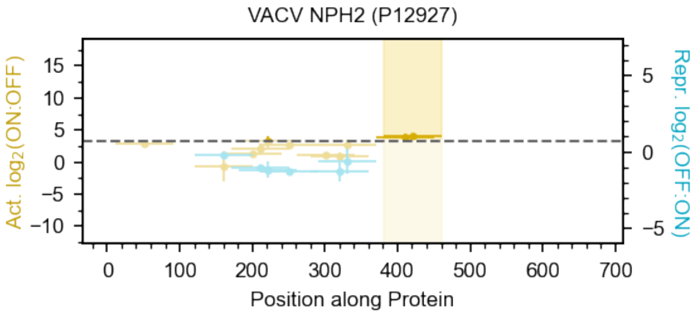
## VACV NPH2 (P12927)

Gene: NPH2 ; Protein Family: NPH2



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Extended activation domain from residues 371 to 460:
MAYIEEEKRNLVTAIQMYTPPDGSSGIVFVASVAQCHEYKSYLEKRLPYDMYIIHGKVLDIDEILEKVYSSPNVSIIISTPYLESSVTIR

Max tile of activation domain from residues 381 to 460 (estimated 17.0% to 27.8% of cells activated):
LVTAIQMYTPPDGSSGIVFVASVAQCHEYKSYLEKRLPYDMYIIHGKVLDIDEILEKVYSSPNVSIIISTPYLESSVTIR

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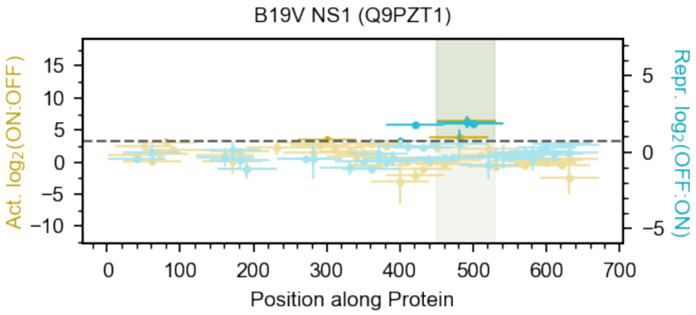
## B19V NS1 (Q9PZT1)

Gene: NS1 ; Protein Family: NS1



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Extended activation domain from residues 441 to 540:
KLNFTVRCSPDMGLLTEADVQQWLTWCNAQSWDHYENWAINYTFDFPGINADALHPDLQTTPIVTDTSISSSGGESSEELSESSFFNLITPGAWNTETPR

Max tile of activation domain from residues 451 to 530 (estimated 61.8% to 67.2% of cells activated):
DMGLLTEADVQQWLTWCNAQSWDHYENWAINYTFDFPGINADALHPDLQTTPIVTDTSISSSGGESSEELSESSFFNLIT

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Extended repression domain from residues 451 to 540:
DMGLLTEADVQQWLTWCNAQSWDHYENWAINYTFDFPGINADALHPDLQTTPIVTDTSISSSGGESSEELSESSFFNLITPGAWNTETPR

Max tile of repression domain from residues 451 to 530 (estimated 27.8% to 49.8% of cells repressed):
DMGLLTEADVQQWLTWCNAQSWDHYENWAINYTFDFPGINADALHPDLQTTPIVTDTSISSSGGESSEELSESSFFNLIT

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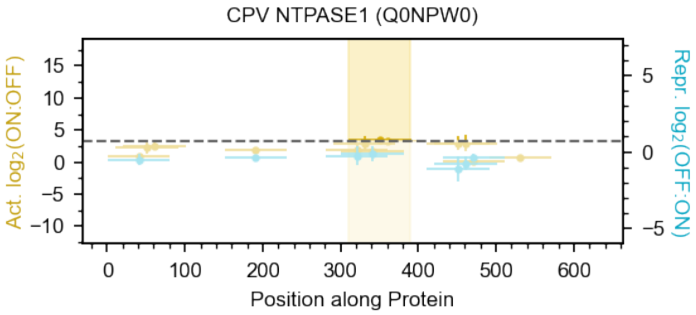
## CPV NTPASE1 (Q0NPW0)

Gene: NTPASE1 ; Protein Family: NTPASE1



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Extended activation domain from residues 311 to 400:
EYAQEIATLYNDFKNSLRDREFSKSALDTFKRGELLGGDASAADISLFTELKEKSVKFIDVCLGILASHGKCLVFEPFVNQSGIEILLLY

Max tile of activation domain from residues 311 to 390 (estimated 13.0% to 19.0% of cells activated):
EYAQEIATLYNDFKNSLRDREFSKSALDTFKRGELLGGDASAADISLFTELKEKSVKFIDVCLGILASHGKCLVFEPFVN

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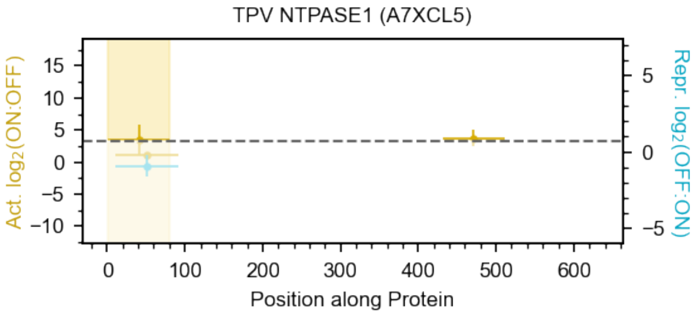
## TPV NTPASE1 (A7XCL5)

Gene: NTPASE1 ; Protein Family: NTPASE1



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Extended activation domain from residues 1 to 80:
MSTQHAAYIDYALNRMESMPIEMLGSDTITLKPYQHFVAKVFLGLDTMHSILLFHDTGVGKTITTVFILKHLKDIYTNWT

Max tile of activation domain from residues 1 to 80 (estimated 0.0% to 51.2% of cells activated):
MSTQHAAYIDYALNRMESMPIEMLGSDTITLKPYQHFVAKVFLGLDTMHSILLFHDTGVGKTITTVFILKHLKDIYTNWT

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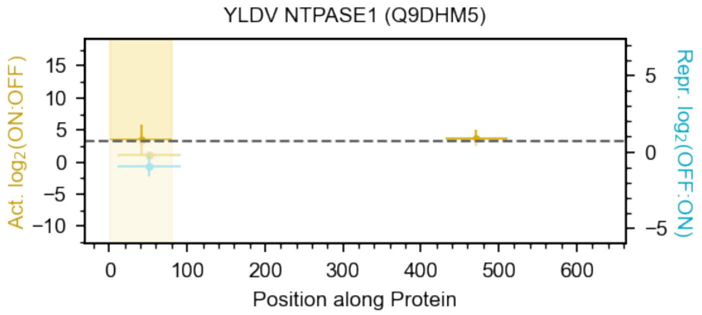
## YLDV NTPASE1 (Q9DHM5)

Gene: NTPASE1 ; Protein Family: NTPASE1



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Extended activation domain from residues 1 to 80:
MSTQHAAYIDYALNRMESMPIEMLGSDTITLKPYQHFVAKVFLGLDTMHSILLFHDTGVGKTITTVFILKHLKDIYTNWT

Max tile of activation domain from residues 1 to 80 (estimated 0.0% to 51.2% of cells activated):
MSTQHAAYIDYALNRMESMPIEMLGSDTITLKPYQHFVAKVFLGLDTMHSILLFHDTGVGKTITTVFILKHLKDIYTNWT

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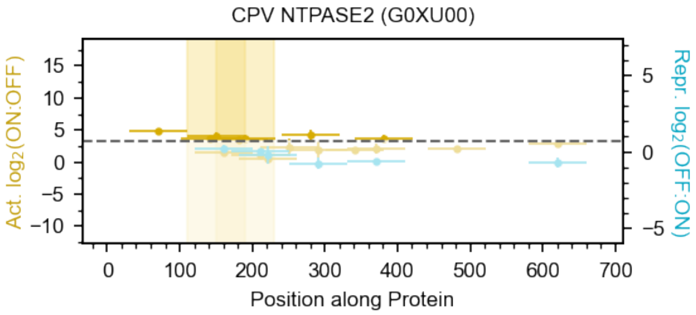
# CPV NTPASE2 (G0XU00)

Gene: NTPASE2 ; Protein Family: NTPASE2



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Extended activation domain from residues 101 to 190:
ECYSFLKCITNTEINSFDDYILRGLLEAGNSLQIFSNSVGKRTDTVGVLGNKYPFSKIPLASLTPKAQREIFSAWISHRPVVLTGGTGVG

Max tile of activation domain from residues 111 to 190 (estimated 16.9% to 31.8% of cells activated):
NTEINSFDDYILRGLLEAGNSLQIFSNSVGKRTDTVGVLGNKYPFSKIPLASLTPKAQREIFSAWISHRPVVLTGGTGVG

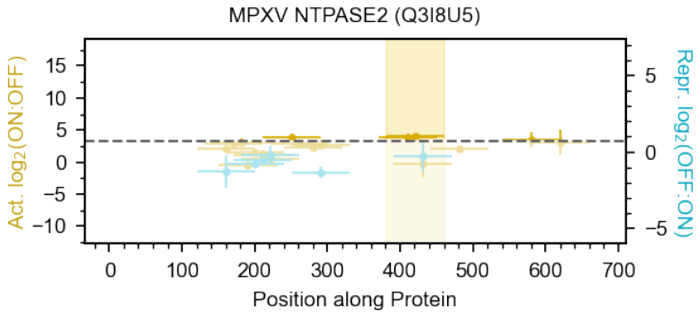
---

Extended activation domain from residues 141 to 230:
KRTDTVGVLGNKYPFSKIPLASLTPKAQREIFSAWISHRPVVLTGGTGVGKTSQVPKLLLWFNYLFGGFSTLDKITDFHERPVILSLPRI

Max tile of activation domain from residues 151 to 230 (estimated 12.7% to 25.2% of cells activated):
NKYPFSKIPLASLTPKAQREIFSAWISHRPVVLTGGTGVGKTSQVPKLLLWFNYLFGGFSTLDKITDFHERPVILSLPRI

# MPXV NTPASE2 (Q3I8U5)

Gene: NTPASE2 ; Protein Family: NTPASE2



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Extended activation domain from residues 371 to 460:
MAYIEEEKRNLVTAIQMYTPPDGSSGIVFVASVAQCHEYKSYLEKRLPYDMYIIHGKVLDIDEILEKVYSSPNVSIIISTPYLESSVTIR

Max tile of activation domain from residues 381 to 460 (estimated 17.0% to 27.8% of cells activated):
LVTAIQMYTPPDGSSGIVFVASVAQCHEYKSYLEKRLPYDMYIIHGKVLDIDEILEKVYSSPNVSIIISTPYLESSVTIR

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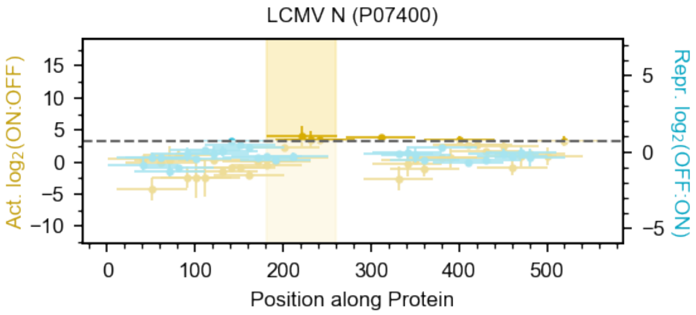
## LCMV N (P07400)

Gene: N ; Protein Family: N



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Extended activation domain from residues 181 to 280:
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGYNFSLGAAVKAGAALLHGGNMLESILIKPSNSEDLLKAVLG

Max tile of activation domain from residues 181 to 260 (estimated 7.6% to 48.8% of cells activated):
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDKHPVLGVITEQQSSINISGYNFSLGAAVKAGAALLHGGNM

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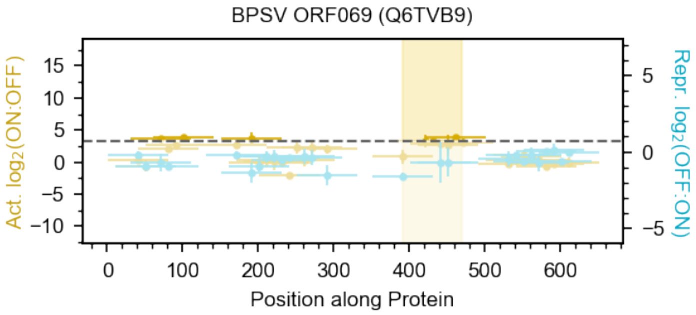
## BPSV ORF069 (Q6TVB9)

Gene: ORF069 ; Protein Family: ORF069



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Extended activation domain from residues 381 to 470:
SEYNGSHSNNPHTIDGRPKTFAIVTSKMKASLEELLEAYNSPENDDGSRLMFLFSSNIMSESYTLKEVRNIWFMTIPDTFSQFNQILGRA

Max tile of activation domain from residues 391 to 470 (estimated 11.8% to 17.5% of cells activated):
PHTIDGRPKTFAIVTSKMKASLEELLEAYNSPENDDGSRLMFLFSSNIMSESYTLKEVRNIWFMTIPDTFSQFNQILGRA

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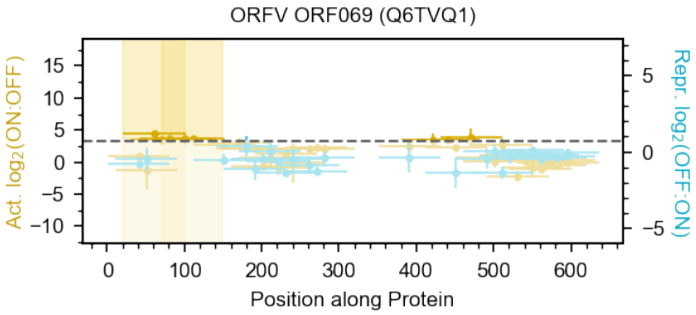
## ORFV ORF069 (Q6TVQ1)

Gene: ORF069 ; Protein Family: ORF069



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Extended activation domain from residues 21 to 120:
PHQLATVDFLIRRVLDDNVSVLLFHIMGSGKTVIALLFAMVASRTKKVYILVPNVNVMNIFNYSMVMVANLFNAPFVAENIFVYSTTSFYSLNCNDGVVN

Max tile of activation domain from residues 21 to 100 (estimated 21.5% to 33.2% of cells activated):
PHQLATVDFLIRRVLDDNVSVLLFHIMGSGKTVIALLFAMVASRTKKVYILVPNVNVMNIFNYSMVMVANLFNAPFVAEN

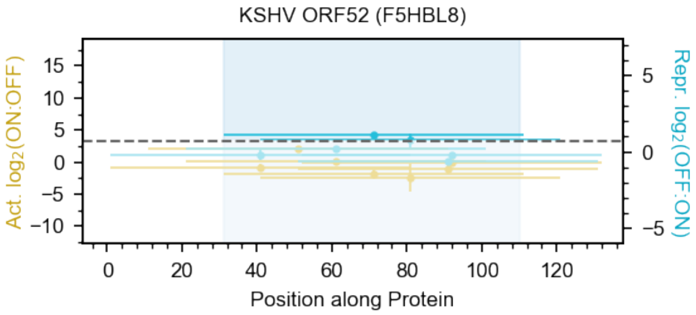
---

Extended activation domain from residues 61 to 150:
VASRTKKVYILVPNVNVMNIFNYSMVMVANLFNAPFVAENIFVYSTTSFYSLNCNDGVVNYNGLSKYENSVFVVDEAHNIFGNNTGELMM

Max tile of activation domain from residues 71 to 150 (estimated 18.0% to 19.0% of cells activated):
LVPNVNVMNIFNYSMVMVANLFNAPFVAENIFVYSTTSFYSLNCNDGVVNYNGLSKYENSVFVVDEAHNIFGNNTGELMM

# KSHV ORF52 (F5HBL8)

Gene: ORF52 ; Protein Family: ORF52



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Extended repression domain from residues 31 to 120:
LRKALGSTADPRDRPLTATEKEAQLTATVGALSAAAAKKIEARVRTIFSKVVTQKQVDDALKGLSLRIDVCMSDGGTAKPPPGANNRRRR

Max tile of repression domain from residues 31 to 110 (estimated 21.5% to 21.7% of cells repressed):
LRKALGSTADPRDRPLTATEKEAQLTATVGALSAAAAKKIEARVRTIFSKVVTQKQVDDALKGLSLRIDVCMSDGGTAKP

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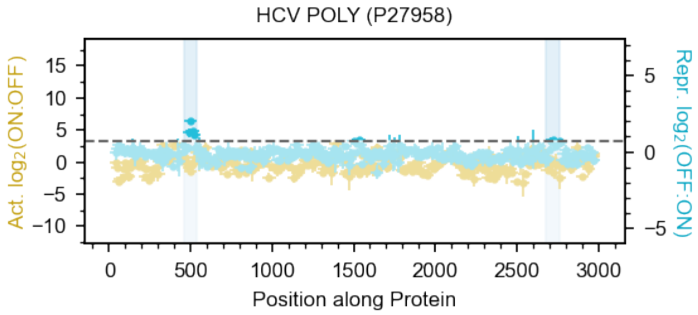
## HCV POLY (P27958)

Gene: POLY ; Protein Family: POLY



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Extended repression domain from residues 451 to 560:
GCPERLASCRRLTDFAQGWGPISYANGSGLDERPYCWHYPPRPCGIVPAKSVCGPVYCFTPSPVVVGTTDRSGAPTYSWGANDTDVFVLNNTRPPLGNWFGCTWMNSTGF

Max tile of repression domain from residues 461 to 540 (estimated 35.7% to 41.1% of cells repressed):
RLTDFAQGWGPISYANGSGLDERPYCWHYPPRPCGIVPAKSVCGPVYCFTPSPVVVGTTDRSGAPTYSWGANDTDVFVLN

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Extended repression domain from residues 2671 to 2760:
VAIKSLTERLYVGGPLTNSRGENCGYRRCRASRVLTTSCGNTLTRYIKARAACRAAGLQDCTMLVCGDDLVVICESAGVQEDAASLRAFT

Max tile of repression domain from residues 2681 to 2760 (estimated 17.9% to 20.2% of cells repressed):
YVGGPLTNSRGENCGYRRCRASRVLTTSCGNTLTRYIKARAACRAAGLQDCTMLVCGDDLVVICESAGVQEDAASLRAFT

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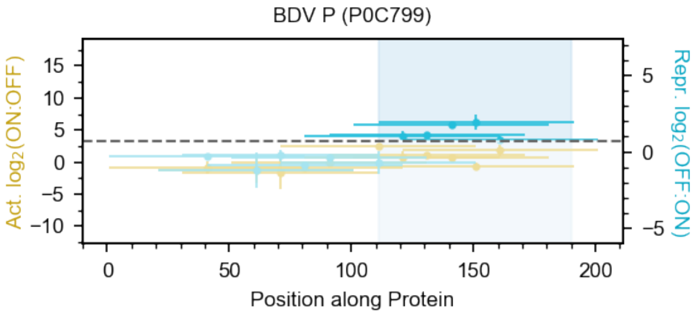
## BDV P (P0C799)

Gene: P ; Protein Family: P



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Extended repression domain from residues 81 to 200:
ELAENSMIEAEEVRGTLGDISARIEAGFESLSALQVETIQTAQRCDHSDSIRILGENIKILDRSMKTMMETMKLMMEKVDLLYASTAVGTSAPMLPSHPAPPRIYPQLPSAPTTDEWDII

Max tile of repression domain from residues 111 to 190 (estimated 26.6% to 50.7% of cells repressed):
LSALQVETIQTAQRCDHSDSIRILGENIKILDRSMKTMMETMKLMMEKVDLLYASTAVGTSAPMLPSHPAPPRIYPQLPS

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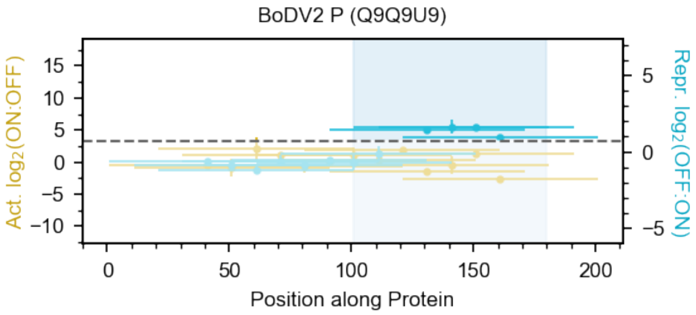
## BoDV2 P (Q9Q9U9)

Gene: P ; Protein Family: P



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Extended repression domain from residues 91 to 200:
EEVRGTLGDISARLEAGFESLSALQVETIQTAQRCDHSDSIRVLGENIKILDRSMKTMMETMKLMMEKVDLLYASTAVGTSAPMLPSHPAPPRIYPQLPSAPTADEWDII

Max tile of repression domain from residues 101 to 180 (estimated 22.4% to 41.6% of cells repressed):
SARLEAGFESLSALQVETIQTAQRCDHSDSIRVLGENIKILDRSMKTMMETMKLMMEKVDLLYASTAVGTSAPMLPSHPA

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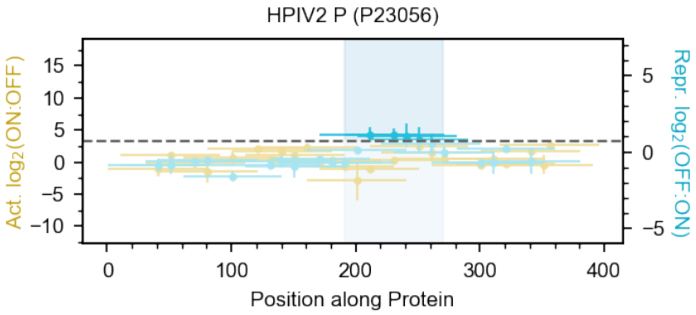
# HPIV2 P (P23056)

Gene: P ; Protein Family: P



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Extended repression domain from residues 191 to 290:
SSGVIPGVPQSRPQLASSPAHADPAPASAENVKEIIELLKGLDLRLQTVEGKVDKILATSATIINLKNEMTSLKASVATMEGMITTIKIMDPSTPTNVPV

Max tile of repression domain from residues 191 to 270 (estimated 18.4% to 27.1% of cells repressed):
SSGVIPGVPQSRPQLASSPAHADPAPASAENVKEIIELLKGLDLRLQTVEGKVDKILATSATIINLKNEMTSLKASVATM

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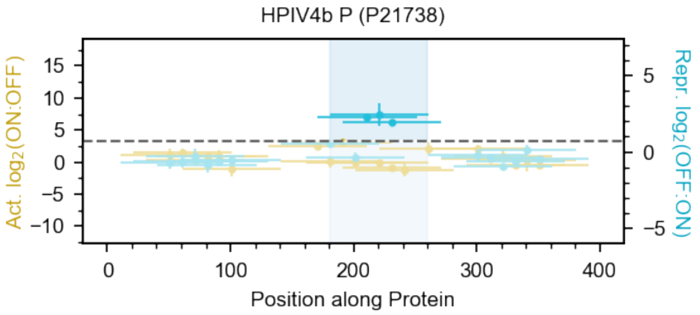
# HPIV4b P (P21738)

Gene: P ; Protein Family: P



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Extended repression domain from residues 171 to 270:
KIQSSFQDIEESTRFHGSMEEPQYQSGAIHVAHQSNQLPPSKNVHVEDVPKFANYALEILDAIKALEVRLDRIEGKVDKIMLTQNTIQQTKNDTQQIKGS

Max tile of repression domain from residues 181 to 260 (estimated 31.6% to 76.2% of cells repressed):
ESTRFHGSMEEPQYQSGAIHVAHQSNQLPPSKNVHVEDVPKFANYALEILDAIKALEVRLDRIEGKVDKIMLTQNTIQQT

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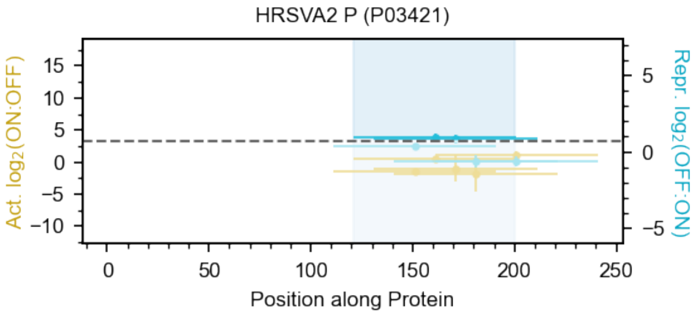
## HRSVA2 P (P03421)

Gene: P ; Protein Family: P



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Extended repression domain from residues 121 to 210:
EEINDQTNDNITARLDRIDEKLSEILGMLHTLVVASAGPTSARDGIRDAMIGLREEMIEKIRTEALMTNDRLEAMARLRNEESEKMAKDT

Max tile of repression domain from residues 121 to 200 (estimated 17.6% to 23.1% of cells repressed):
EEINDQTNDNITARLDRIDEKLSEILGMLHTLVVASAGPTSARDGIRDAMIGLREEMIEKIRTEALMTNDRLEAMARLRN

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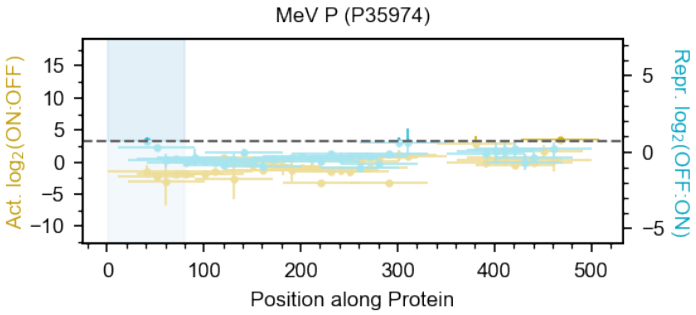
## MeV P (P35974)

Gene: P ; Protein Family: P



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Extended repression domain from residues 1 to 80:
MAEEQARHVKNGLECIRALKAEPIGSLAIEEAMAAWSEISDNPGQERATCREEKAGSSGLSKPCLSAIGSTEGGAPRIRG

Max tile of repression domain from residues 1 to 80 (estimated 17.2% to 19.7% of cells repressed):
MAEEQARHVKNGLECIRALKAEPIGSLAIEEAMAAWSEISDNPGQERATCREEKAGSSGLSKPCLSAIGSTEGGAPRIRG

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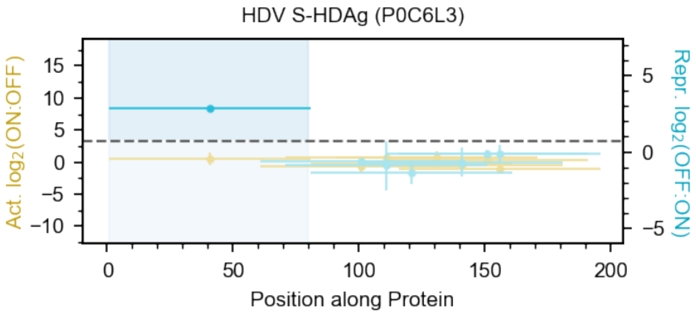
# HDV S-HDAg (P0C6L3)

Gene: S-HDAg ; Protein Family: S-HDAg



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Extended repression domain from residues 1 to 80:
MSRPEGRKNRGGREEVLEQWVSGRKKLEELERDLRKVKKKIKKLEDEHPWLGNIKGILGKKDKDGEGAPPAKRARTDQME

Max tile of repression domain from residues 1 to 80 (estimated 56.1% to 71.8% of cells repressed):
MSRPEGRKNRGGREEVLEQWVSGRKKLEELERDLRKVKKKIKKLEDEHPWLGNIKGILGKKDKDGEGAPPAKRARTDQME

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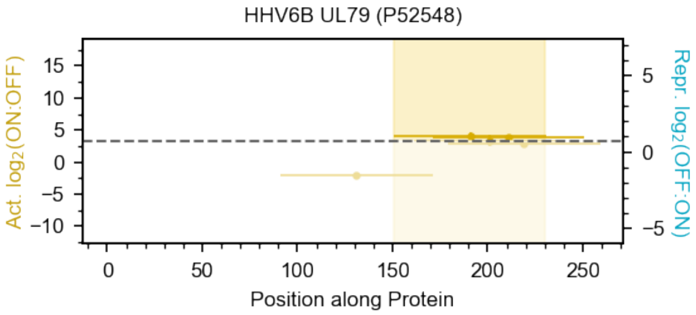
## HHV6B UL79 (P52548)

Gene: U52 ; Protein Family: UL79



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Extended activation domain from residues 151 to 250:
FSVGAIYNHRLLKICRFFNRFWGDQEREPAVRLICKHLWFAYLIMFGKFEISTLAYNQQRAEHKAGLFSFLQNDFKVFCGMSENPQLLDSSAIFDLTGIS

Max tile of activation domain from residues 151 to 230 (estimated 18.8% to 30.2% of cells activated):
FSVGAIYNHRLLKICRFFNRFWGDQEREPAVRLICKHLWFAYLIMFGKFEISTLAYNQQRAEHKAGLFSFLQNDFKVFCG

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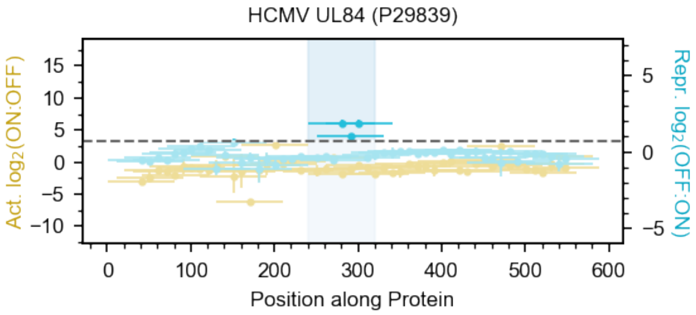
## HCMV UL84 (P29839)

Gene: UL84 ; Protein Family: UL84



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Extended repression domain from residues 241 to 340:
PPLKRVPLRRKAAHHTALHDCMALHLPELTFESTLDINNVTENAASVADAAESTDADLTPTLTVRVRHAVCWHRVEGGISGPRGLTSRISARLSETTAKT

Max tile of repression domain from residues 241 to 320 (estimated 30.7% to 40.9% of cells repressed):
PPLKRVPLRRKAAHHTALHDCMALHLPELTFESTLDINNVTENAASVADAAESTDADLTPTLTVRVRHAVCWHRVEGGIS

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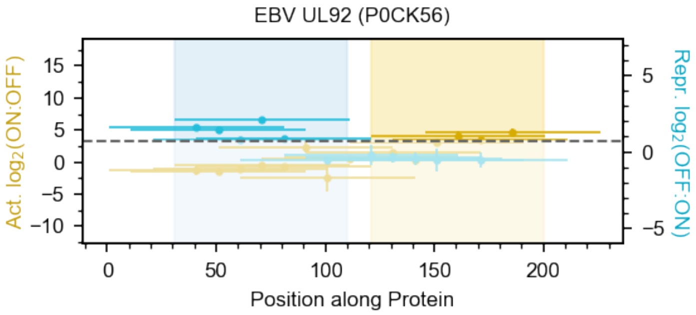
## EBV UL92 (P0CK56)

Gene: BDLF4 ; Protein Family: UL92



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Extended activation domain from residues 121 to 210:
YHYFLNENVISGVSEALFDQEGALRPHIPALVSFVFPCCLMLFRGASSEKVVDVVLSLYIHVIISIYSQKTVYGALLFKSTRNKRYDAVA

Max tile of activation domain from residues 121 to 200 (estimated 15.1% to 35.6% of cells activated):
YHYFLNENVISGVSEALFDQEGALRPHIPALVSFVFPCCLMLFRGASSEKVVDVVLSLYIHVIISIYSQKTVYGALLFKS

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Extended repression domain from residues 1 to 120:
MSDQGRLSLPRGEGGTDEPNPRHLCSYSKLEFHLPLPESMASVFACWGCGEYHVCDGSSECTLIETHEGVVCALTGNYMGPHFQPALRPWTEIRQDTQDQRDKWEPEQVQGLVKTVVNHL

Max tile of repression domain from residues 31 to 110 (estimated 39.1% to 42.9% of cells repressed):
EFHLPLPESMASVFACWGCGEYHVCDGSSECTLIETHEGVVCALTGNYMGPHFQPALRPWTEIRQDTQDQRDKWEPEQVQ

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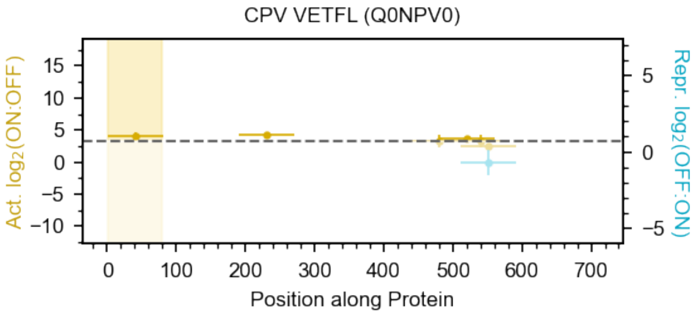
## CPV VETFL (Q0NPV0)

Gene: VETFL ; Protein Family: VETFL



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Extended activation domain from residues 1 to 80:
MRYIVSPQLVLQVGKGQEVERALYLTPYDYIDEKSPIYYFLRSHLNIQQPEIVKRHILLTLRMTQLKGYLGNLLDIKDDI

Max tile of activation domain from residues 1 to 80 (estimated 14.3% to 30.9% of cells activated):
MRYIVSPQLVLQVGKGQEVERALYLTPYDYIDEKSPIYYFLRSHLNIQQPEIVKRHILLTLRMTQLKGYLGNLLDIKDDI

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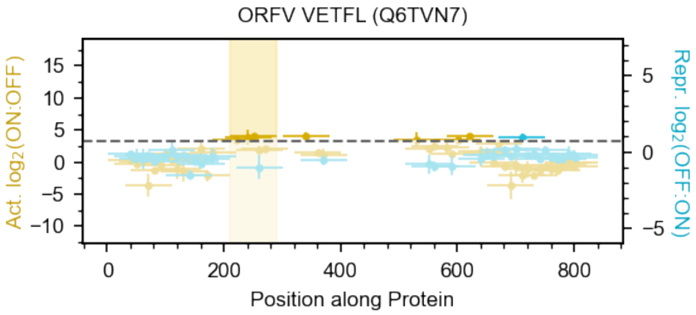
## ORFV VETFL (Q6TVN7)

Gene: VETFL ; Protein Family: VETFL



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Extended activation domain from residues 201 to 290:
KGYLGSLLGLQDEIIVYSHKNNLEYSYVDNTIFNPFSPTQKKTLIRTDGILYNAYADACNFLVVWVARAADTSAPEFGSFEEPNDSILKF

Max tile of activation domain from residues 211 to 290 (estimated 19.1% to 27.7% of cells activated):
QDEIIVYSHKNNLEYSYVDNTIFNPFSPTQKKTLIRTDGILYNAYADACNFLVVWVARAADTSAPEFGSFEEPNDSILKF

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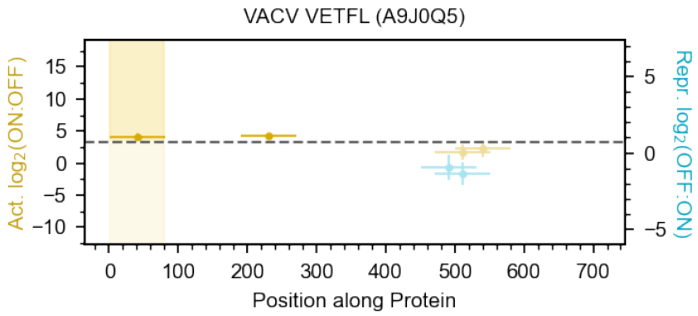
## VACV VETFL (A9J0Q5)

Gene: VETFL ; Protein Family: VETFL



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Extended activation domain from residues 1 to 80:
MRYIVSPQLVLQVGKGQEVERALYLTPYDYIDEKSPIYYFLRSHLNIQQPEIVKRHILLTLRMTQLKGYLGNLLDIKDDI

Max tile of activation domain from residues 1 to 80 (estimated 14.3% to 30.9% of cells activated):
MRYIVSPQLVLQVGKGQEVERALYLTPYDYIDEKSPIYYFLRSHLNIQQPEIVKRHILLTLRMTQLKGYLGNLLDIKDDI

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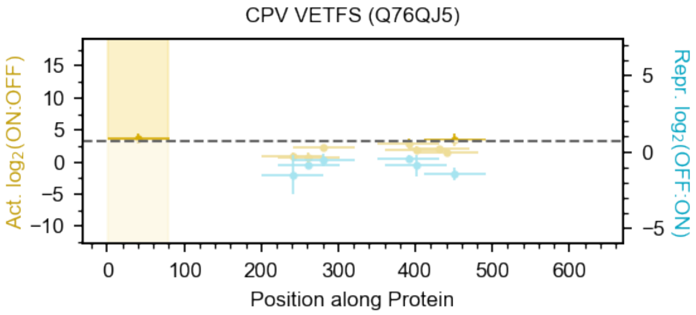
## CPV VETFS (Q76QJ5)

Gene: VETFS ; Protein Family: VETFS

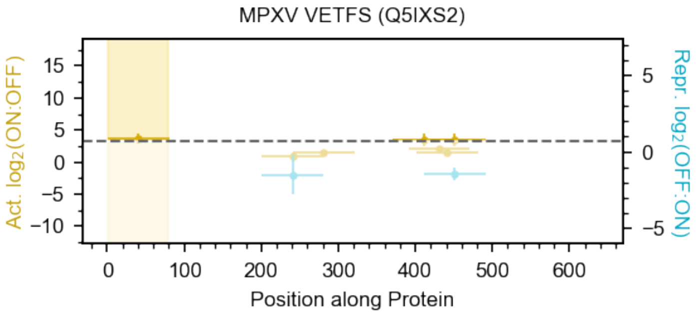


Extended activation domain from residues 1 to 80:
MNTGIIDLFDNHVDSIPTILPHQLATLDYLVRTIIDENRSVLLFHIMGSGKTIIALLFALVASRFKKVYILVPNINILKI

Max tile of activation domain from residues 1 to 80 (estimated 11.3% to 28.1% of cells activated):
MNTGIIDLFDNHVDSIPTILPHQLATLDYLVRTIIDENRSVLLFHIMGSGKTIIALLFALVASRFKKVYILVPNINILKI

## MPXV VETFS (Q5IXS2)

Gene: VETFS ; Protein Family: VETFS



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Extended activation domain from residues 1 to 80:
MNTGIIDLFDNHVDSIPTILPHQLATLDYLVRTIIDENRSVLLFHIMGSGKTIIALLFALVASRFKKVYILVPNINILKI

Max tile of activation domain from residues 1 to 80 (estimated 11.3% to 28.1% of cells activated):
MNTGIIDLFDNHVDSIPTILPHQLATLDYLVRTIIDENRSVLLFHIMGSGKTIIALLFALVASRFKKVYILVPNINILKI

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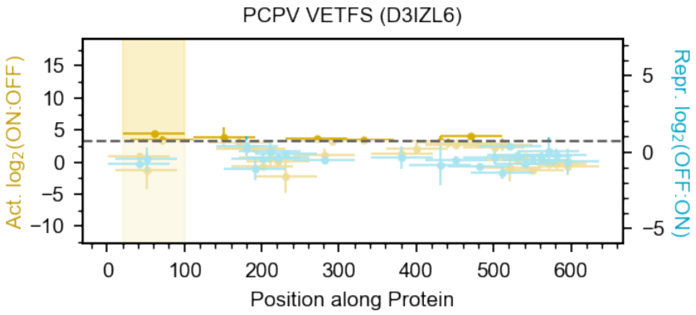
## PCPV VETFS (D3IZL6)

Gene: VETFS ; Protein Family: VETFS



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Extended activation domain from residues 21 to 110:
PHQLATVDFLIRRVLDDNVSVLLFHIMGSGKTVIALLFAMVASRTKKVYILVPNVNVMNIFNYSMVMVANLFNAPFVAENIFVYSTTSFY

Max tile of activation domain from residues 21 to 100 (estimated 21.5% to 33.2% of cells activated):
PHQLATVDFLIRRVLDDNVSVLLFHIMGSGKTVIALLFAMVASRTKKVYILVPNVNVMNIFNYSMVMVANLFNAPFVAEN

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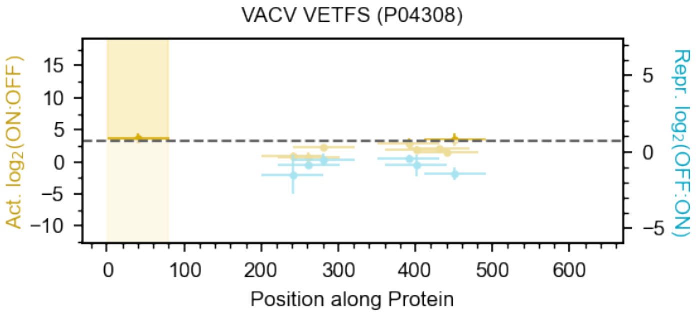
# VACV VETFS (P04308)

Gene: VETFS ; Protein Family: VETFS



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Extended activation domain from residues 1 to 80:
MNTGIIDLFDNHVDSIPTILPHQLATLDYLVRTIIDENRSVLLFHIMGSGKTIIALLFALVASRFKKVYILVPNINILKI

Max tile of activation domain from residues 1 to 80 (estimated 11.3% to 28.1% of cells activated):
MNTGIIDLFDNHVDSIPTILPHQLATLDYLVRTIIDENRSVLLFHIMGSGKTIIALLFALVASRFKKVYILVPNINILKI

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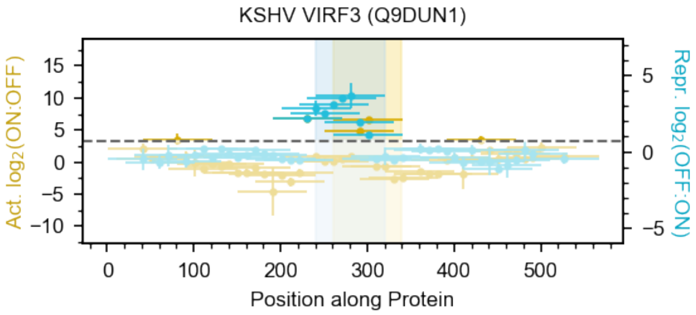
## KSHV VIRF3 (Q9DUN1)

Gene: K10.5 ; Protein Family: VIRF



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Extended activation domain from residues 251 to 340:
CALMYHVGQEMDMLMRAMCDEDLFDLLGIPEDVIATSQPGGDTDASGVVTEGSIAASAVGAGVEDVYLAGALEAQNVAGEYVLEISDEEV

Max tile of activation domain from residues 261 to 340 (estimated 66.7% to 67.9% of cells activated):
MDMLMRAMCDEDLFDLLGIPEDVIATSQPGGDTDASGVVTEGSIAASAVGAGVEDVYLAGALEAQNVAGEYVLEISDEEV

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Extended repression domain from residues 191 to 340:
TRHSASGVQPVDDANADSPGSGDEGPSTRHSDSQPPPADETTVHTDNVEDDLTLLDKESACALMYHVGQEMDMLMRAMCDEDLFDLLGIPEDVIATSQPGGDTDASGVVTEGSIAASAVGAGVEDVYLAGALEAQNVAGEYVLEISDEEV

Max tile of repression domain from residues 241 to 320 (estimated 66.6% to 96.9% of cells repressed):
DLTLLDKESACALMYHVGQEMDMLMRAMCDEDLFDLLGIPEDVIATSQPGGDTDASGVVTEGSIAASAVGAGVEDVYLAG

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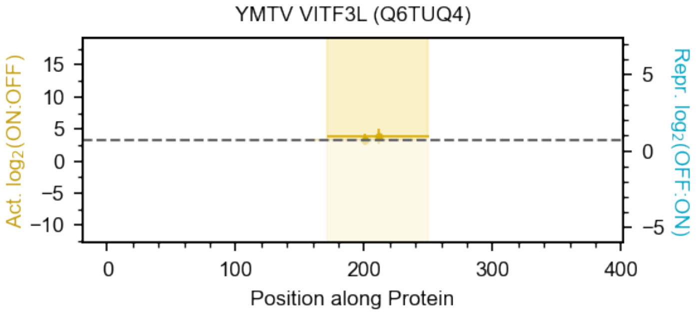
## YMTV VITF3L (Q6TUQ4)

Gene: VITF3L ; Protein Family: VITF3L



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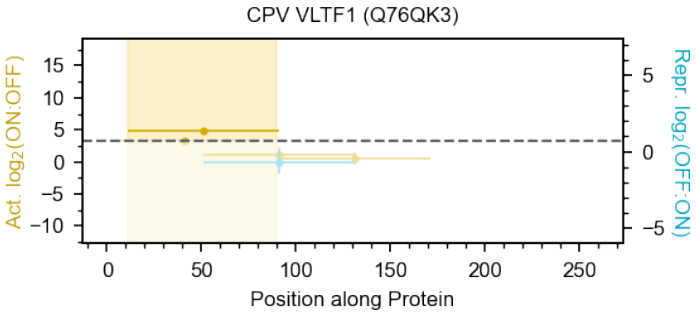
Extended activation domain from residues 161 to 250:
YMSTTVRYDNTNPWIKSVSKRMRVDIVNNAIITKGKSSILQTIEIVFLNRTCVKIFKDSTMHIILSKERRELGCVGLIDKLFSVYKILFL

Max tile of activation domain from residues 171 to 250 (estimated 9.0% to 37.0% of cells activated):
TNPWIKSVSKRMRVDIVNNAIITKGKSSILQTIEIVFLNRTCVKIFKDSTMHIILSKERRELGCVGLIDKLFSVYKILFL

---

## CPV VLTF1 (Q76QK3)

Gene: VLTF1 ; Protein Family: VLTF1



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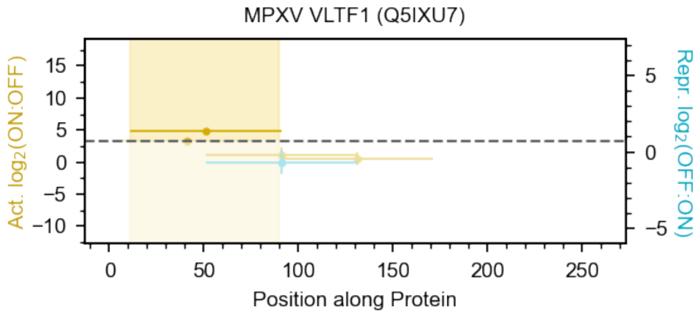
Extended activation domain from residues 1 to 90:
MSIRIKIDKLRQIVAYFSEFSEEVSINVDSTDELMYIFAALGGSVNIWAIIPLSASVFYRGAENIVFNLPVSKVKSCLCSFHNDAIIDIE

Max tile of activation domain from residues 11 to 90 (estimated 32.2% to 39.3% of cells activated):
RQIVAYFSEFSEEVSINVDSTDELMYIFAALGGSVNIWAIIPLSASVFYRGAENIVFNLPVSKVKSCLCSFHNDAIIDIE

---

# MPXV VLTF1 (Q5IXU7)

Gene: VLTF1 ; Protein Family: VLTF1



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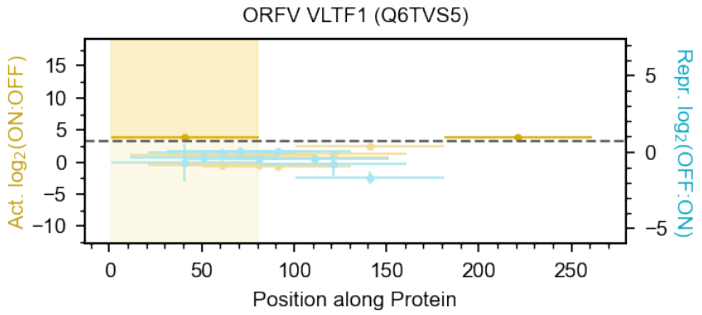
Extended activation domain from residues 1 to 90:
MSIRIKIDKLRQIVAYFSEFSEEVSINVDSTDELMYIFAALGGSVNIWAIIPLSASVFYRGAENIVFNLPVSKVKSCLCSFHNDAIIDIE

Max tile of activation domain from residues 11 to 90 (estimated 32.2% to 39.3% of cells activated):
RQIVAYFSEFSEEVSINVDSTDELMYIFAALGGSVNIWAIIPLSASVFYRGAENIVFNLPVSKVKSCLCSFHNDAIIDIE

---

# ORFV VLTF1 (Q6TVS5)

Gene: VLTF1 ; Protein Family: VLTF1



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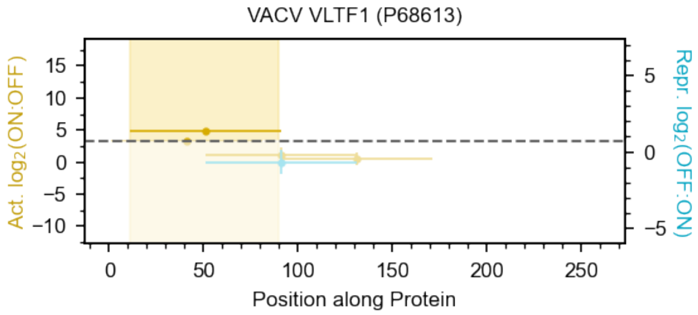
Extended activation domain from residues 1 to 80:
MTLRIKLEKLKQIVTYFSEFSEEVSVNVDVGDGLMYIFAALGGSVNIWTIVPLSASVVYDGDVSRVFNLPVLKVKACLCS

Max tile of activation domain from residues 1 to 80 (estimated 16.2% to 24.1% of cells activated):
MTLRIKLEKLKQIVTYFSEFSEEVSVNVDVGDGLMYIFAALGGSVNIWTIVPLSASVVYDGDVSRVFNLPVLKVKACLCS

---

# VACV VLTF1 (P68613)

Gene: VLTF1 ; Protein Family: VLTF1



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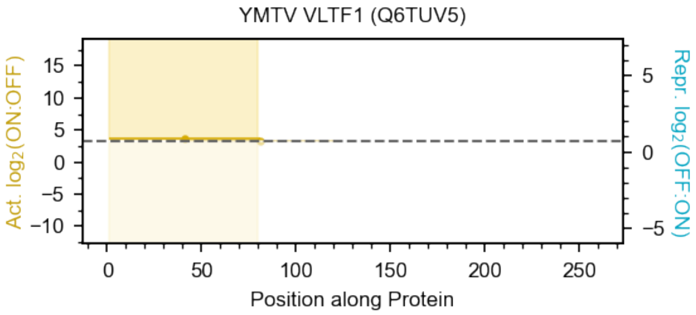
Extended activation domain from residues 1 to 90:
MSIRIKIDKLRQIVAYFSEFSEEVSINVDSTDELMYIFAALGGSVNIWAIIPLSASVFYRGAENIVFNLPVSKVKSCLCSFHNDAIIDIE

Max tile of activation domain from residues 11 to 90 (estimated 32.2% to 39.3% of cells activated):
RQIVAYFSEFSEEVSINVDSTDELMYIFAALGGSVNIWAIIPLSASVFYRGAENIVFNLPVSKVKSCLCSFHNDAIIDIE

---

# YMTV VLTF1 (Q6TUV5)

Gene: VLTF1 ; Protein Family: VLTF1



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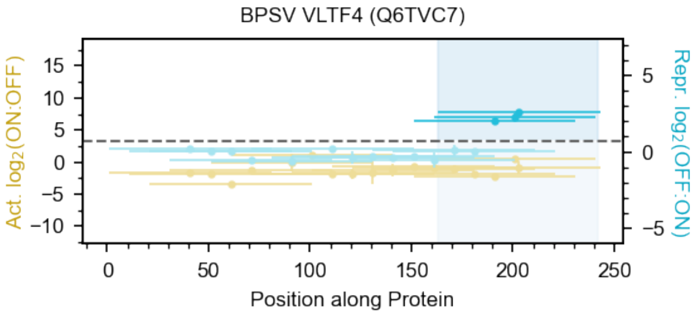
Extended activation domain from residues 1 to 80:
MSLRIKIDKLRQIVAYFSEFSEEVSINVDASSNIMYIFAALGGSVNIWAMVPLSSSVFYEGENNKVFNLPVSKVKSCLCS

Max tile of activation domain from residues 1 to 80 (estimated 17.0% to 20.2% of cells activated):
MSLRIKIDKLRQIVAYFSEFSEEVSINVDASSNIMYIFAALGGSVNIWAMVPLSSSVFYEGENNKVFNLPVSKVKSCLCS

---

## BPSV VLTF4 (Q6TVC7)

Gene: VLTF4 ; Protein Family: VLTF4



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Extended repression domain from residues 151 to 242:
VASGGAAAGDDELDELGESDLDLAFAAILADFKHLTGRVKALSSVLTDVQASGVRRSFAGLSKALTEAAAIAAGGSKVPVAPRKKKAAAGKK

Max tile of repression domain from residues 163 to 242 (estimated 56.9% to 60.4% of cells repressed):
LDELGESDLDLAFAAILADFKHLTGRVKALSSVLTDVQASGVRRSFAGLSKALTEAAAIAAGGSKVPVAPRKKKAAAGKK

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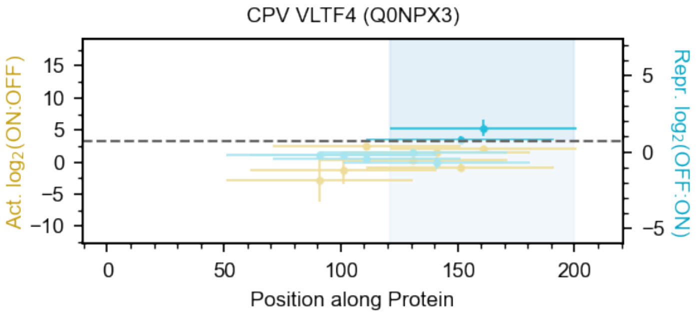
## CPV VLTF4 (Q0NPX3)

Gene: VLTF4 ; Protein Family: VLTF4



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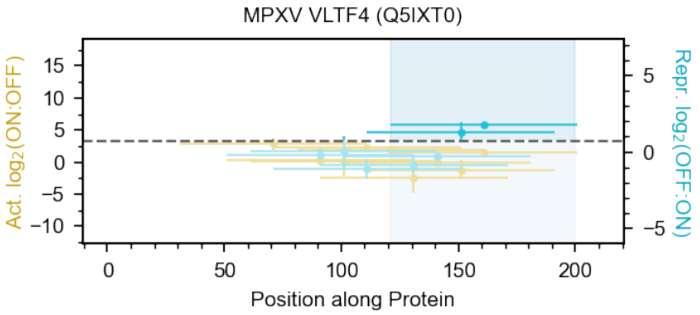
Extended repression domain from residues 111 to 200:
AVELDDSDGDDEPMAQAGAKVNHSARSDLSDLKVATDNIVKDLKKIITRISAVSTVLEDVQAAGISRQFTSMTKAITTLSDLVTEGKSKV

Max tile of repression domain from residues 121 to 200 (estimated 20.8% to 41.4% of cells repressed):
DEPMAQAGAKVNHSARSDLSDLKVATDNIVKDLKKIITRISAVSTVLEDVQAAGISRQFTSMTKAITTLSDLVTEGKSKV

---

## MPXV VLTF4 (Q5IXT0)

Gene: VLTF4 ; Protein Family: VLTF4



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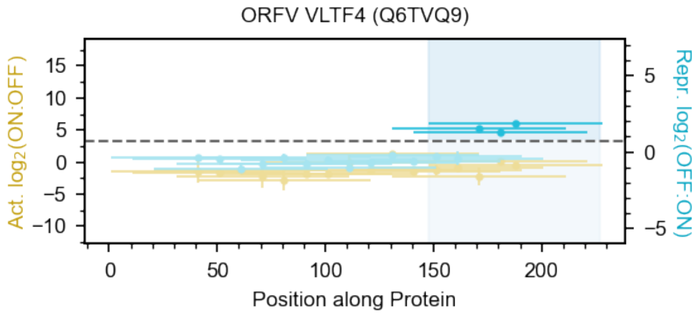
Extended repression domain from residues 111 to 200:
VELDDSDGDDEPMVQVEAGKVNHSTRSDLSDLKVATDNIVKDLKKIITRISAVSTVLEDVQAAGISRQFTSMTKAITTLSDLVTEGKSKV

Max tile of repression domain from residues 121 to 200 (estimated 30.0% to 35.0% of cells repressed):
EPMVQVEAGKVNHSTRSDLSDLKVATDNIVKDLKKIITRISAVSTVLEDVQAAGISRQFTSMTKAITTLSDLVTEGKSKV

---

# ORFV VLTF4 (Q6TVQ9)

Gene: VLTF4 ; Protein Family: VLTF4



---

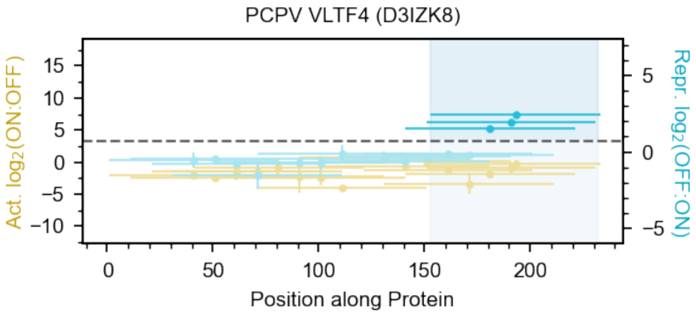
Extended repression domain from residues 131 to 227:
GDAEGGASARSPSDIDNVDEMDDSDLMVAFSAILADFKDLTQRVKALSSVLTDVQATGIRRSFSTLGKALTEAAHIANTGAKPVTAPRKKKAATCKK

Max tile of repression domain from residues 148 to 227 (estimated 32.2% to 37.5% of cells repressed):
VDEMDDSDLMVAFSAILADFKDLTQRVKALSSVLTDVQATGIRRSFSTLGKALTEAAHIANTGAKPVTAPRKKKAATCKK

---

# PCPV VLTF4 (D3IZK8)

Gene: VLTF4 ; Protein Family: VLTF4



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Extended repression domain from residues 141 to 232:
GASGRSPSDLDNLDEMDDSDLMLAFSTILADFKDLTHRVKCLSTVLTDVQAAGVRRSFSALGKALNEAAAIASTGAKPAAAPRKKKAAASKK

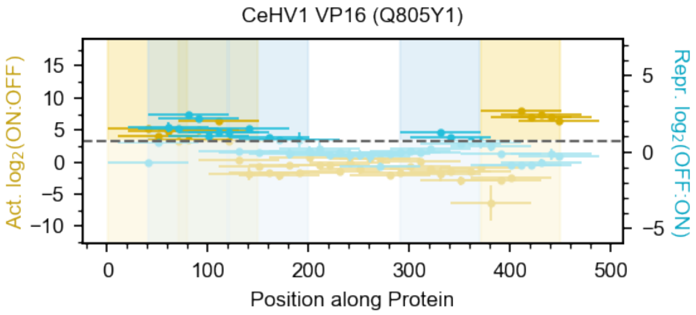
Max tile of repression domain from residues 153 to 232 (estimated 51.8% to 52.8% of cells repressed):
LDEMDDSDLMLAFSTILADFKDLTHRVKCLSTVLTDVQAAGVRRSFSALGKALNEAAAIASTGAKPAAAPRKKKAAASKK

---

**Other Tiling Screen Data from Ludwig, C.H. et al. 2023**

## CeHV1 VP16 (Q805Y1)

Gene: UL48 ; Protein Family: VP16



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Extended activation domain from residues 371 to 487:
RTNYGSSIEGLLELPDDTDYDPDAPPPPPRLSFAAAPPRRRSAAPRTDVSLGDELRFDGDVSMTPSEALDDFDLTLLGDDDHAGGLDDAAAYASLDMADFEFEQMFTDALGIDDIGG

Max tile of activation domain from residues 371 to 450 (estimated 82.6% to 84.2% of cells activated):
RTNYGSSIEGLLELPDDTDYDPDAPPPPPRLSFAAAPPRRRSAAPRTDVSLGDELRFDGDVSMTPSEALDDFDLTLLGDD

---

Extended activation domain from residues 41 to 160:
TGRLSQAQIMPQPPVPVPPAALYNRLLEDLGFGDGPALCTILDSWNEDLFSGLPANPDLYRECQFLSTLPSDVVAWGDGHTPDRGPIDIRAHGSAPFPSLPARREDLPAYCEALTRFFRA

Max tile of activation domain from residues 71 to 150 (estimated 59.4% to 65.9% of cells activated):
GFGDGPALCTILDSWNEDLFSGLPANPDLYRECQFLSTLPSDVVAWGDGHTPDRGPIDIRAHGSAPFPSLPARREDLPAY

---

Extended activation domain from residues 1 to 100:
MESLFDELFADMDTDGDSPPRRPTGTAELPDAATAPRPYATGRLSQAQIMPQPPVPVPPAALYNRLLEDLGFGDGPALCTILDSWNEDLFSGLPANPDLY

Max tile of activation domain from residues 1 to 80 (estimated 40.5% to 40.9% of cells activated):
MESLFDELFADMDTDGDSPPRRPTGTAELPDAATAPRPYATGRLSQAQIMPQPPVPVPPAALYNRLLEDLGFGDGPALCT

---

Extended repression domain from residues 21 to 160:
RRPTGTAELPDAATAPRPYATGRLSQAQIMPQPPVPVPPAALYNRLLEDLGFGDGPALCTILDSWNEDLFSGLPANPDLYRECQFLSTLPSDVVAWGDGHTPDRGPIDIRAHGSAPFPSLPARREDLPAYCEALTRFFRA

Max tile of repression domain from residues 41 to 120 (estimated 50.4% to 50.5% of cells repressed):
TGRLSQAQIMPQPPVPVPPAALYNRLLEDLGFGDGPALCTILDSWNEDLFSGLPANPDLYRECQFLSTLPSDVVAWGDGH

---

Extended repression domain from residues 291 to 380:
ARLREINYVRERLNLPLVRSAATEEPGAALTAAPALQTQRARSSGYFMTLIRVKLDAYSEGSGSEGAEVLREHAYSRRRERTNYGSSIEG

Max tile of repression domain from residues 291 to 370 (estimated 21.7% to 26.8% of cells repressed):
ARLREINYVRERLNLPLVRSAATEEPGAALTAAPALQTQRARSSGYFMTLIRVKLDAYSEGSGSEGAEVLREHAYSRRRE

---

Extended repression domain from residues 121 to 210:
TPDRGPIDIRAHGSAPFPSLPARREDLPAYCEALTRFFRAELRAREESYRRVLANFCSALYRYLRASTRQLHRQAALKGRPRDLQEMLRA

Max tile of repression domain from residues 121 to 200 (estimated 18.4% to 22.1% of cells repressed):
TPDRGPIDIRAHGSAPFPSLPARREDLPAYCEALTRFFRAELRAREESYRRVLANFCSALYRYLRASTRQLHRQAALKGR

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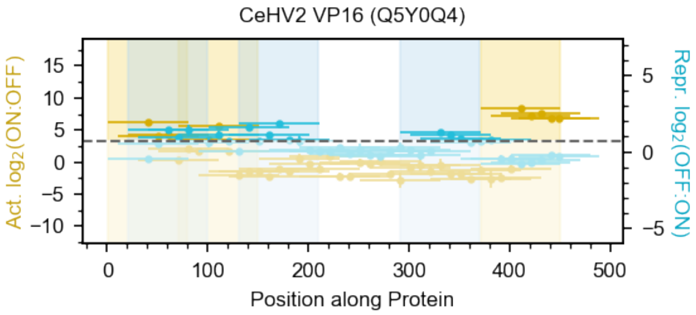
## CeHV2 VP16 (Q5Y0Q4)

Gene: UL48 ; Protein Family: VP16



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Extended activation domain from residues 371 to 488:
ERTNYGSSIEGLLELPDDADYDPDAPPPPPRLSFATGSPRRRRSTVPRTDVSLGDELCLDASPSMTPSEALDDFDLTLLGDDDHAGTLDAAAYASLDMADFEFEQMFTDALGIDEFGG

Max tile of activation domain from residues 371 to 450 (estimated 85.4% to 87.6% of cells activated):
ERTNYGSSIEGLLELPDDADYDPDAPPPPPRLSFATGSPRRRRSTVPRTDVSLGDELCLDASPSMTPSEALDDFDLTLLG

---

Extended activation domain from residues 1 to 100:
MESLFDELFADMDTDGASPPRRPTGGAELPDAATAPRPYATTRLSQAQIMPPPPVPIPPAALYNRLLEDLGFGDGPALCTILDSWNEDLFSGLPANPDLY

Max tile of activation domain from residues 1 to 80 (estimated 59.6% to 60.1% of cells activated):
MESLFDELFADMDTDGASPPRRPTGGAELPDAATAPRPYATTRLSQAQIMPPPPVPIPPAALYNRLLEDLGFGDGPALCT

---

Extended activation domain from residues 61 to 150:
ALYNRLLEDLGFGDGPALCTILDSWNEDLFSGLPANPDLYRECRFLSTLPGDVVAWGDAHAPDRAPIDIRAHGSAPFPSLPARREGLPAY

Max tile of activation domain from residues 71 to 150 (estimated 44.5% to 51.3% of cells activated):
GFGDGPALCTILDSWNEDLFSGLPANPDLYRECRFLSTLPGDVVAWGDAHAPDRAPIDIRAHGSAPFPSLPARREGLPAY

---

Extended repression domain from residues 121 to 230:
APDRAPIDIRAHGSAPFPSLPARREGLPAYCAALTRFFESELRAREESYRRVLANFCSALYRYLRASTRQLHRQAALKGRPRDLQEMLRASVAERYYRETARLARVMFLH

Max tile of repression domain from residues 131 to 210 (estimated 33.6% to 37.9% of cells repressed):
AHGSAPFPSLPARREGLPAYCAALTRFFESELRAREESYRRVLANFCSALYRYLRASTRQLHRQAALKGRPRDLQEMLRA

---

Extended repression domain from residues 21 to 120:
RRPTGGAELPDAATAPRPYATTRLSQAQIMPPPPVPIPPAALYNRLLEDLGFGDGPALCTILDSWNEDLFSGLPANPDLYRECRFLSTLPGDVVAWGDAH

Max tile of repression domain from residues 21 to 100 (estimated 23.8% to 28.1% of cells repressed):
RRPTGGAELPDAATAPRPYATTRLSQAQIMPPPPVPIPPAALYNRLLEDLGFGDGPALCTILDSWNEDLFSGLPANPDLY

---

Extended repression domain from residues 291 to 390:
ARLRELNHVRERLNLPLIRSAATEEPGAALTAAPALQTQQARSSGYFMTLIRVKLDAYSEGSAGSEGAEVLREHAYSRRRERTNYGSSIEGLLELPDDAD

Max tile of repression domain from residues 291 to 370 (estimated 23.7% to 25.0% of cells repressed):
ARLRELNHVRERLNLPLIRSAATEEPGAALTAAPALQTQQARSSGYFMTLIRVKLDAYSEGSAGSEGAEVLREHAYSRRR

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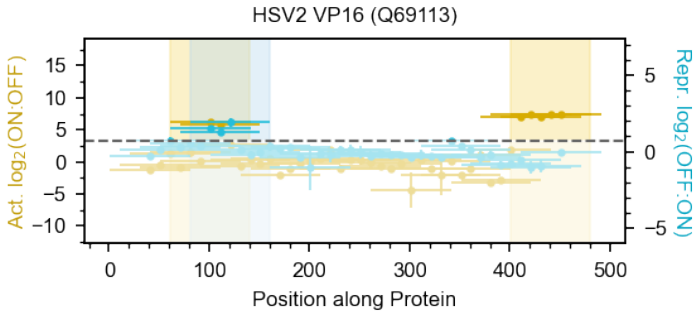
## HSV2 VP16 (Q69113)

Gene: UL48 ; Protein Family: VP16



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Extended activation domain from residues 371 to 490:
YGSTIEGLLDLPDDDDAPAEAGLVAPRMSFLSAGQRPRRLSTTAPITDVSLGDELRLDGEEVDMTPADALDDFDLEMLGDVESPSPGMTHDPVSYGALDVDDFEFEQMFTDALGIDDFGG

Max tile of activation domain from residues 401 to 480 (estimated 75.1% to 81.6% of cells activated):
LSAGQRPRRLSTTAPITDVSLGDELRLDGEEVDMTPADALDDFDLEMLGDVESPSPGMTHDPVSYGALDVDDFEFEQMFT

---

Extended activation domain from residues 61 to 150:
NRLLDDLGFSAGPALCTMLDTWNEDLFSGFPTNADMYRECKFLSTLPSDVIDWGDAHVPERSPIDIRAHGDVAFPTLPATRDELPSYYEA

Max tile of activation domain from residues 61 to 140 (estimated 59.6% to 61.4% of cells activated):
NRLLDDLGFSAGPALCTMLDTWNEDLFSGFPTNADMYRECKFLSTLPSDVIDWGDAHVPERSPIDIRAHGDVAFPTLPAT

---

Extended repression domain from residues 61 to 160:
NRLLDDLGFSAGPALCTMLDTWNEDLFSGFPTNADMYRECKFLSTLPSDVIDWGDAHVPERSPIDIRAHGDVAFPTLPATRDELPSYYEAMAQFFRGELR

Max tile of repression domain from residues 81 to 160 (estimated 29.4% to 44.7% of cells repressed):
TWNEDLFSGFPTNADMYRECKFLSTLPSDVIDWGDAHVPERSPIDIRAHGDVAFPTLPATRDELPSYYEAMAQFFRGELR

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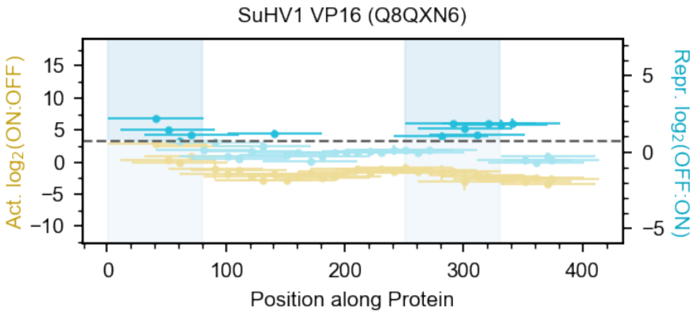
## SuHV1 VP16 (Q8QXN6)

Gene: UL48 ; Protein Family: VP16



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Extended repression domain from residues 1 to 110:
MRDEECVVAFDEALLGGAAPGRPPVVAVPRAASPDALYQRLISDLAFDEGPALLGAMERWNEDLFSCLPGNEDLYARLVMLSASADEVAAQVRAPTADASVDLGVPGAEP

Max tile of repression domain from residues 1 to 80 (estimated 40.0% to 46.1% of cells repressed):
MRDEECVVAFDEALLGGAAPGRPPVVAVPRAASPDALYQRLISDLAFDEGPALLGAMERWNEDLFSCLPGNEDLYARLVM

---

Extended repression domain from residues 241 to 380:
VVLLSGAPVPAAQLRAVNHRRRELGLPLVRAGLIEEDGADLVEEPPFSAALPRAAGYLSHQVRIKMEAYSREYRDHTYCRPPSPVASYGSTAEALLPPPSPSAVLPCDPTPPARVSAAPLITTVTLAEAEEDGALTTAAP

Max tile of repression domain from residues 251 to 330 (estimated 35.7% to 35.9% of cells repressed):
AAQLRAVNHRRRELGLPLVRAGLIEEDGADLVEEPPFSAALPRAAGYLSHQVRIKMEAYSREYRDHTYCRPPSPVASYGS

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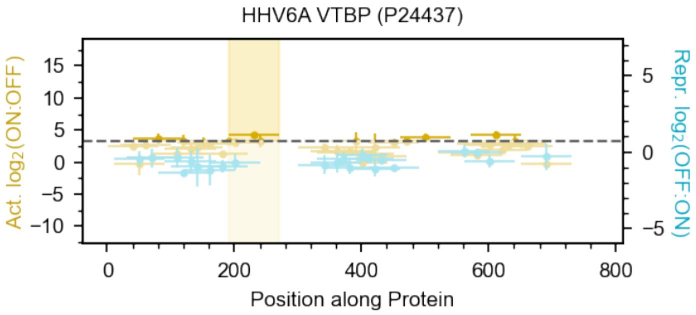
## HHV6A VTBP (P24437)

Gene: U58 ; Protein Family: VTBP



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Extended activation domain from residues 191 to 280:
PYFLCYLCRHLTVIEIEQCTNDLISLLGPKVAQRVIIHFKLLFGFRHKPHIGTVDSWFWENFFMLELHKLWLTVVKHNRVTTDFFNVVYE

Max tile of activation domain from residues 191 to 270 (estimated 20.5% to 30.0% of cells activated):
PYFLCYLCRHLTVIEIEQCTNDLISLLGPKVAQRVIIHFKLLFGFRHKPHIGTVDSWFWENFFMLELHKLWLTVVKHNRV

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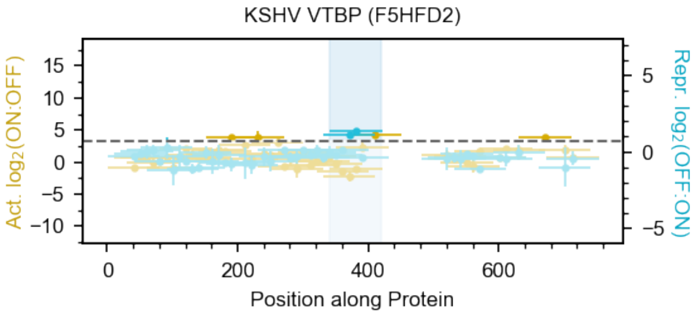
## KSHV VTBP (F5HFD2)

Gene: ORF24 ; Protein Family: VTBP



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Extended repression domain from residues 331 to 420:
MCMAVADCIGHSCSGLHPCANFLGTHETPRLLAATLSRIRYAPKDRRAAMKGNLQACFQRYAATDARTLGSSTVSDMLEPTKHVSLENFK

Max tile of repression domain from residues 341 to 420 (estimated 24.2% to 25.3% of cells repressed):
HSCSGLHPCANFLGTHETPRLLAATLSRIRYAPKDRRAAMKGNLQACFQRYAATDARTLGSSTVSDMLEPTKHVSLENFK

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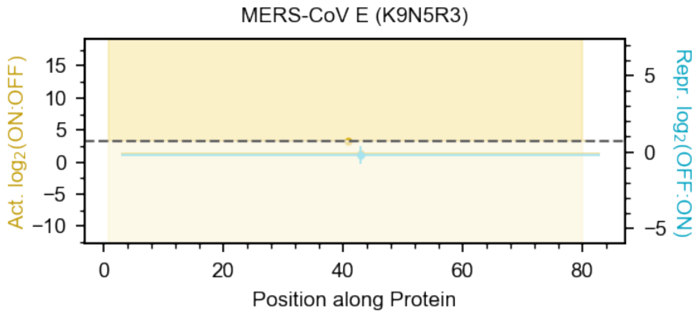
## MERS-CoV E (K9N5R3)

Gene: E ; Protein Family: E



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Extended activation domain from residues 1 to 80:
MLPFVQERIGLFIVNFFIFTVVCAITLLVCMAFLTATRLCVQCMTGFNTLLVQPALYLYNTGRSVYVKFQDSKPPLPPDE

Max tile of activation domain from residues 1 to 80 (estimated 12.7% to 16.0% of cells activated):
MLPFVQERIGLFIVNFFIFTVVCAITLLVCMAFLTATRLCVQCMTGFNTLLVQPALYLYNTGRSVYVKFQDSKPPLPPDE

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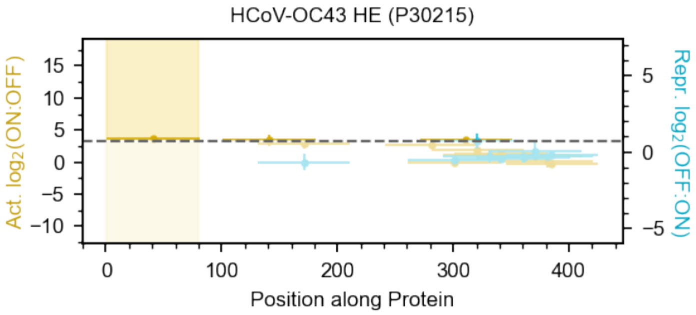
## HCoV-OC43 HE (P30215)

Gene: HE ; Protein Family: HE



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Extended activation domain from residues 1 to 80:
MFLLPRFILVSCIIGSLGFYNPPTNVVSHVNGDWFLFGDSRSDCNHIVNINPHNYSYMDLNPVLCDSGKISSKAGNSIFR

Max tile of activation domain from residues 1 to 80 (estimated 14.0% to 20.6% of cells activated):
MFLLPRFILVSCIIGSLGFYNPPTNVVSHVNGDWFLFGDSRSDCNHIVNINPHNYSYMDLNPVLCDSGKISSKAGNSIFR

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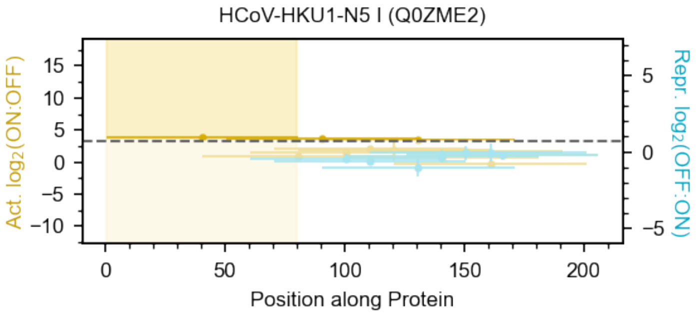
# HCoV-HKU1-N5 I (Q0ZME2)

Gene: I ; Protein Family: I



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Extended activation domain from residues 1 to 80:
MLEVEAPLEIVQESSRKLLGLTNLSEAIKPIIEAENPNQNSLCLLNHKETLSHIIPGSLGLPNFKKVETLNFQMVKEYPL

Max tile of activation domain from residues 1 to 80 (estimated 20.5% to 21.4% of cells activated):
MLEVEAPLEIVQESSRKLLGLTNLSEAIKPIIEAENPNQNSLCLLNHKETLSHIIPGSLGLPNFKKVETLNFQMVKEYPL

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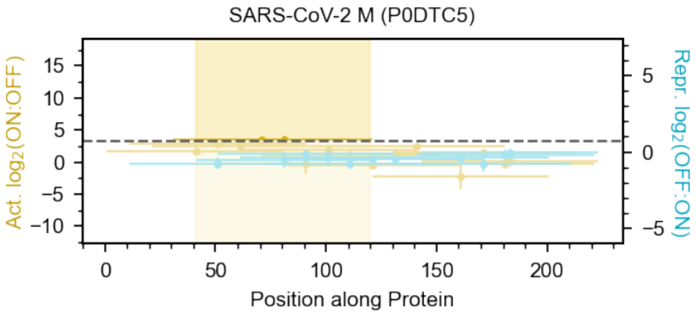
## SARS-CoV-2 M (P0DTC5)

Gene: M ; Protein Family: M



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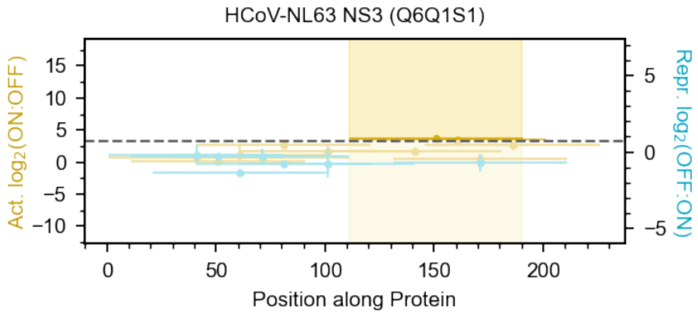
Extended activation domain from residues 31 to 120:
WICLLQFAYANRNRFLYIIKLIFLWLLWPVTLACFVLAAVYRINWITGGIAIAMACLVGLMWLSYFIASFRLFARTRSMWSFNPETNILL

Max tile of activation domain from residues 41 to 120 (estimated 11.4% to 21.7% of cells activated):
NRNRFLYIIKLIFLWLLWPVTLACFVLAAVYRINWITGGIAIAMACLVGLMWLSYFIASFRLFARTRSMWSFNPETNILL

---

# HCoV-NL63 NS3 (Q6Q1S1)

Gene: NS3 ; Protein Family: NS3



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Extended activation domain from residues 111 to 200:
GYYAYLYKNFSFVLFNVTKLCFVSGKCWYLEQSFYENRFAAIYGGDHYVVLGGETITFVSFDDLYVAIRGSCEKNLQLMRKVDLYNGAVI

Max tile of activation domain from residues 111 to 190 (estimated 11.9% to 26.0% of cells activated):
GYYAYLYKNFSFVLFNVTKLCFVSGKCWYLEQSFYENRFAAIYGGDHYVVLGGETITFVSFDDLYVAIRGSCEKNLQLMR

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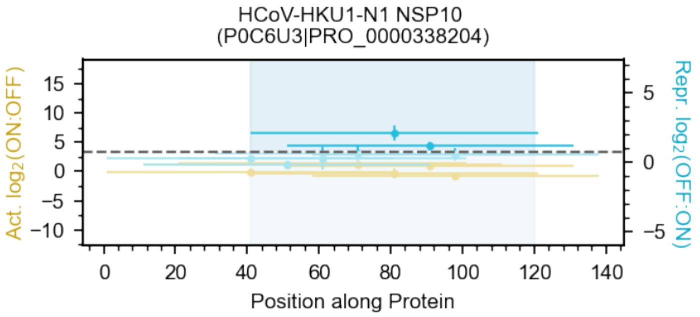
# HCoV-HKU1-N1 NSP10 (P0C6U3|PRO_0000338204)

Gene: NSP10 ; Protein Family: NSP10



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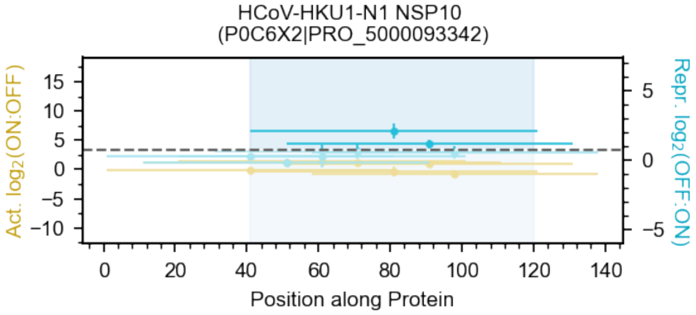
Extended repression domain from residues 31 to 137:
IQQGGVPIINCVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGICKLRGKFVQVPLGIKDPILYVLTHDVCQVCGFWRDGSCSCVGSSVAVQ

Max tile of repression domain from residues 41 to 120 (estimated 27.4% to 59.6% of cells repressed):
CVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGICKLRGKFVQVPLGIKDPILYVLTHDVCQVCG

---

## HCoV-HKU1-N1 NSP10 (P0C6X2|PRO_5000093342)

Gene: NSP10 ; Protein Family: NSP10



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Extended repression domain from residues 31 to 137:
IQQGGVPIINCVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGICKLRGKFVQVPLGIKDPILYVLTHDVCQVCGFWRDGSCSCVGSSVAVQ

Max tile of repression domain from residues 41 to 120 (estimated 27.4% to 59.6% of cells repressed):
CVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGICKLRGKFVQVPLGIKDPILYVLTHDVCQVCG

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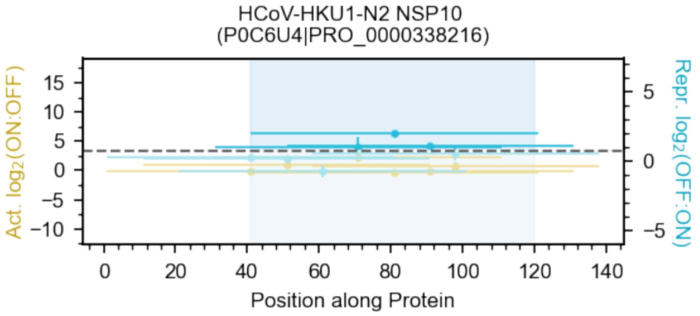
## HCoV-HKU1-N2 NSP10 (P0C6U4|PRO_0000338216)

Gene: NSP10 ; Protein Family: NSP10



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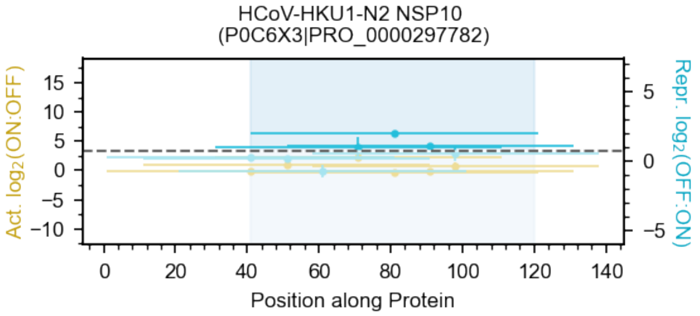
Extended repression domain from residues 31 to 130:
IQQGGVPIINCVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGLCKLRGKFVQVPLGIKDPILYVLTHDVCQVCGFWRDGSCSCV

Max tile of repression domain from residues 41 to 120 (estimated 35.6% to 41.3% of cells repressed):
CVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGLCKLRGKFVQVPLGIKDPILYVLTHDVCQVCG

---

# HCoV-HKU1-N2 NSP10 (P0C6X3|PRO_0000297782)

Gene: NSP10 ; Protein Family: NSP10



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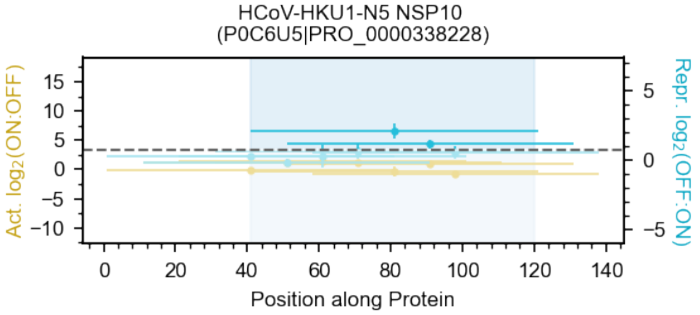
Extended repression domain from residues 31 to 130:
IQQGGVPIINCVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGLCKLRGKFVQVPLGIKDPILYVLTHDVCQVCGFWRDGSCSCV

Max tile of repression domain from residues 41 to 120 (estimated 35.6% to 41.3% of cells repressed):
CVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGLCKLRGKFVQVPLGIKDPILYVLTHDVCQVCG

---

# HCoV-HKU1-N5 NSP10 (P0C6U5|PRO_0000338228)

Gene: NSP10 ; Protein Family: NSP10



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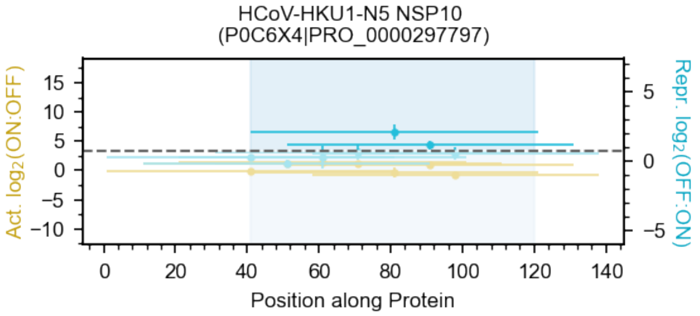
Extended repression domain from residues 31 to 137:
IQQGGVPIINCVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGICKLRGKFVQVPLGIKDPILYVLTHDVCQVCGFWRDGSCSCVGSSVAVQ

Max tile of repression domain from residues 41 to 120 (estimated 27.4% to 59.6% of cells repressed):
CVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGICKLRGKFVQVPLGIKDPILYVLTHDVCQVCG

---

# HCoV-HKU1-N5 NSP10 (P0C6X4|PRO_0000297797)

Gene: NSP10 ; Protein Family: NSP10



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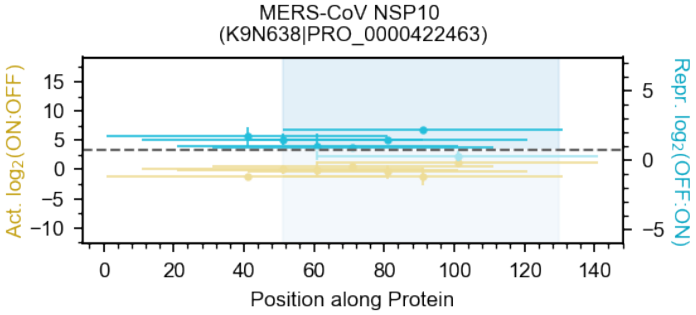
Extended repression domain from residues 31 to 137:
IQQGGVPIINCVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGICKLRGKFVQVPLGIKDPILYVLTHDVCQVCGFWRDGSCSCVGSSVAVQ

Max tile of repression domain from residues 41 to 120 (estimated 27.4% to 59.6% of cells repressed):
CVKMLCDHAGTGMAITIKPEATINQDSYGGASVCIYCRARVEHPDVDGICKLRGKFVQVPLGIKDPILYVLTHDVCQVCG

---

# MERS-CoV NSP10 (K9N638|PRO_0000422463)

Gene: NSP10 ; Protein Family: NSP10



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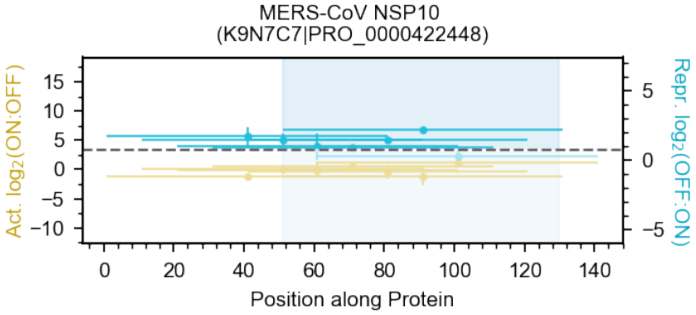
Extended repression domain from residues 1 to 130:
AGSNTEFASNSSVLSLVNFTVDPQKAYLDFVNAGGAPLTNCVKMLTPKTGTGIAISVKPESTADQETYGGASVCLYCRAHIEHPDVSGVCKYKGKFVQIPAQCVRDPVGFCLSNTPCNVCQYWIGYGCNC

Max tile of repression domain from residues 51 to 130 (estimated 38.0% to 47.8% of cells repressed):
TGIAISVKPESTADQETYGGASVCLYCRAHIEHPDVSGVCKYKGKFVQIPAQCVRDPVGFCLSNTPCNVCQYWIGYGCNC

---

## MERS-CoV NSP10 (K9N7C7|PRO_0000422448)

Gene: NSP10 ; Protein Family: NSP10



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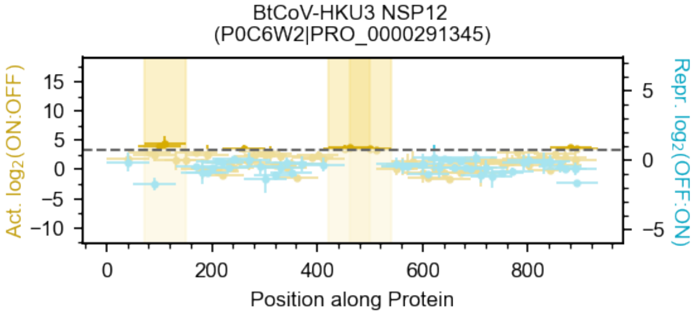
Extended repression domain from residues 1 to 130:
AGSNTEFASNSSVLSLVNFTVDPQKAYLDFVNAGGAPLTNCVKMLTPKTGTGIAISVKPESTADQETYGGASVCLYCRAHIEHPDVSGVCKYKGKFVQIPAQCVRDPVGFCLSNTPCNVCQYWIGYGCNC

Max tile of repression domain from residues 51 to 130 (estimated 38.0% to 47.8% of cells repressed):
TGIAISVKPESTADQETYGGASVCLYCRAHIEHPDVSGVCKYKGKFVQIPAQCVRDPVGFCLSNTPCNVCQYWIGYGCNC

---

# BtCoV-HKU3 NSP12 (P0C6W2|PRO_0000291345)

Gene: NSP12 ; Protein Family: NSP12



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Extended activation domain from residues 61 to 150:
EEGNLLDSYFVVKRHTMSNYQHEETIYNLIKECPAVAVHDFFKFRVDGDMVPHISRQRLTKYTMADLVYALRHFDEGNCDTLKEILVTYN

Max tile of activation domain from residues 71 to 150 (estimated 12.7% to 50.6% of cells activated):
VVKRHTMSNYQHEETIYNLIKECPAVAVHDFFKFRVDGDMVPHISRQRLTKYTMADLVYALRHFDEGNCDTLKEILVTYN

---

Extended activation domain from residues 411 to 500:
KPGNFNKDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDK

Max tile of activation domain from residues 421 to 500 (estimated 15.1% to 22.9% of cells activated):
DFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDK

---

Extended activation domain from residues 461 to 550:
PTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALFAYTKRNVIPTITQMNLKYAISA

Max tile of activation domain from residues 461 to 540 (estimated 15.5% to 17.7% of cells activated):
PTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALFAYTKRNVIPTIT

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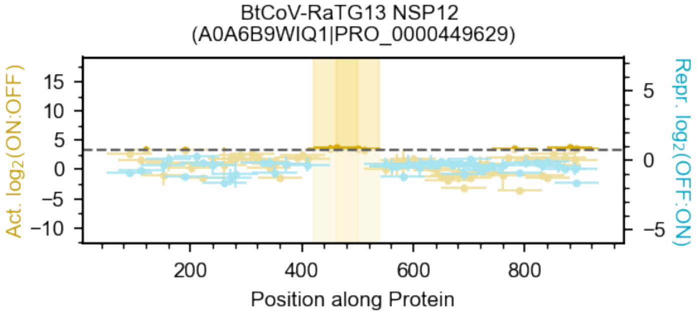
# BtCoV-RaTG13 NSP12 (A0A6B9WIQ1|PRO_0000449629)

Gene: NSP12 ; Protein Family: NSP12



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Extended activation domain from residues 411 to 500:
KPGNFNKDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDK

Max tile of activation domain from residues 421 to 500 (estimated 15.1% to 22.9% of cells activated):
DFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDK

---

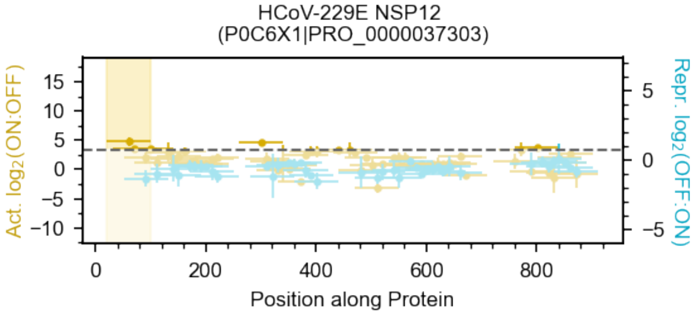
Extended activation domain from residues 461 to 550:
PTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALFAYTKRNVIPTITQMNLKYAISA

Max tile of activation domain from residues 461 to 540 (estimated 15.5% to 17.7% of cells activated):
PTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALFAYTKRNVIPTIT

---

# HCoV-229E NSP12 (P0C6X1|PRO_0000037303)

Gene: NSP12 ; Protein Family: NSP12



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Extended activation domain from residues 21 to 110:
CNGTDIDYCVRAFDVYNKDASFIGKNLKSNCVRFKNVDKDDAFYIVKRCIKSVMDHEQSMYNLLKGCNAVAKHDFFTWHEGRTIYGNVSR

Max tile of activation domain from residues 21 to 100 (estimated 21.8% to 48.8% of cells activated):
CNGTDIDYCVRAFDVYNKDASFIGKNLKSNCVRFKNVDKDDAFYIVKRCIKSVMDHEQSMYNLLKGCNAVAKHDFFTWHE

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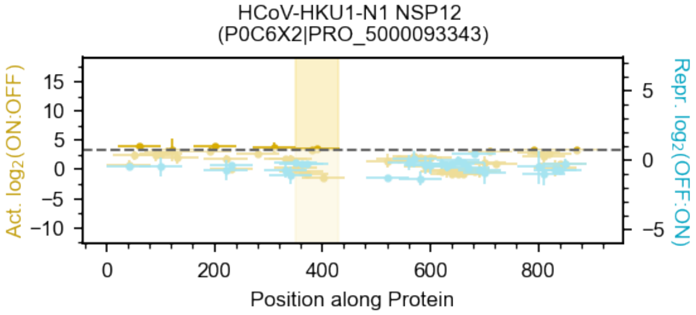
## HCoV-HKU1-N1 NSP12 (P0C6X2|PRO_5000093343)

Gene: NSP12 ; Protein Family: NSP12



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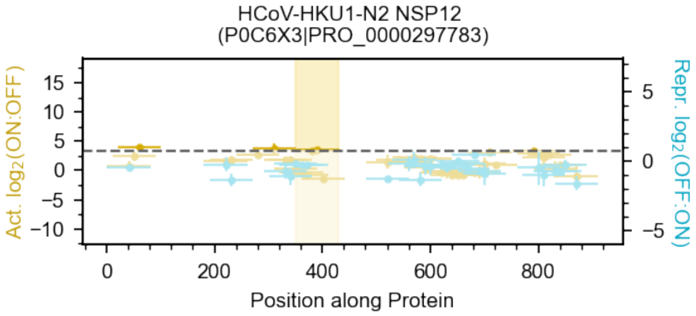
Extended activation domain from residues 341 to 430:
GYHYKELGVVMNLDVDTHRYRLSLKDLLLYAADPAMHVASASALLDLRTCCFSVAAITSGIKFQTVKPGNFNQDFYEFVKSKGLFKEGST

Max tile of activation domain from residues 351 to 430 (estimated 13.9% to 21.5% of cells activated):
MNLDVDTHRYRLSLKDLLLYAADPAMHVASASALLDLRTCCFSVAAITSGIKFQTVKPGNFNQDFYEFVKSKGLFKEGST

---

## HCoV-HKU1-N2 NSP12 (P0C6X3|PRO_0000297783)

Gene: NSP12 ; Protein Family: NSP12



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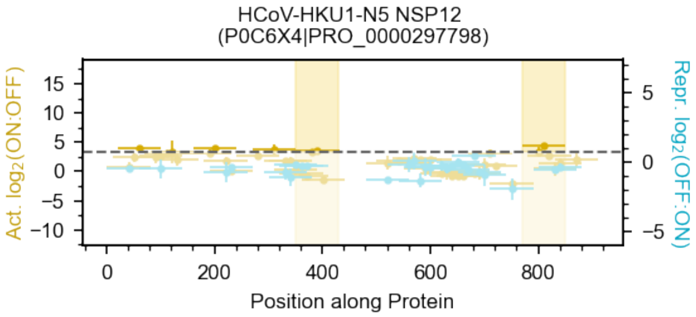
Extended activation domain from residues 341 to 430:
GYHYKELGVVMNLDVDTHRYRLSLKDLLLYAADPAMHVASASALLDLRTCCFSVAAITSGIKFQTVKPGNFNQDFYEFVKSKGLFKEGST

Max tile of activation domain from residues 351 to 430 (estimated 13.9% to 21.5% of cells activated):
MNLDVDTHRYRLSLKDLLLYAADPAMHVASASALLDLRTCCFSVAAITSGIKFQTVKPGNFNQDFYEFVKSKGLFKEGST

---

## HCoV-HKU1-N5 NSP12 (P0C6X4|PRO_0000297798)

Gene: NSP12 ; Protein Family: NSP12



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Extended activation domain from residues 761 to 850:
CYNSDYANKGYIANISAFQQVLYYQNNVFMSESKCWVENDITNGPHEFCSQHTMLVKIDGDYVYLPYPDPSRILGAGCFVDDLLKTDSVL

Max tile of activation domain from residues 771 to 850 (estimated 26.0% to 29.6% of cells activated):
YIANISAFQQVLYYQNNVFMSESKCWVENDITNGPHEFCSQHTMLVKIDGDYVYLPYPDPSRILGAGCFVDDLLKTDSVL

---

Extended activation domain from residues 341 to 430:
GYHYKELGVVMNLDVDTHRYRLSLKDLLLYAADPAMHVASASALLDLRTCCFSVAAITSGIKFQTVKPGNFNQDFYEFVKSKGLFKEGST

Max tile of activation domain from residues 351 to 430 (estimated 13.9% to 21.5% of cells activated):
MNLDVDTHRYRLSLKDLLLYAADPAMHVASASALLDLRTCCFSVAAITSGIKFQTVKPGNFNQDFYEFVKSKGLFKEGST

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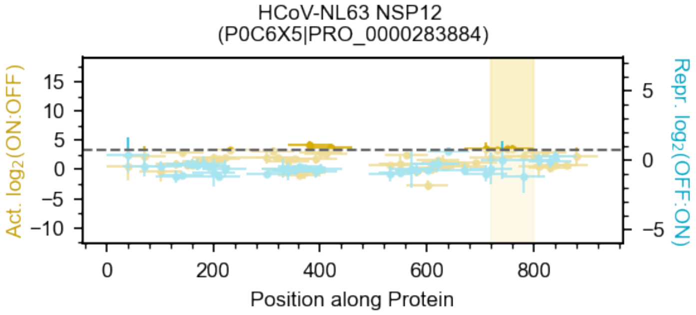
## HCoV-NL63 NSP12 (P0C6X5|PRO_0000283884)

Gene: NSP12 ; Protein Family: NSP12



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Extended activation domain from residues 711 to 800:
NNVNVRDLQRRLYDNCYRLTSVEESFIDDYYGYLRKHFSMMILSDDGVVCYNKDYAELGYIADISAFKATLYYQNNVFMSTSKCWVEEDL

Max tile of activation domain from residues 721 to 800 (estimated 13.0% to 23.9% of cells activated):
RLYDNCYRLTSVEESFIDDYYGYLRKHFSMMILSDDGVVCYNKDYAELGYIADISAFKATLYYQNNVFMSTSKCWVEEDL

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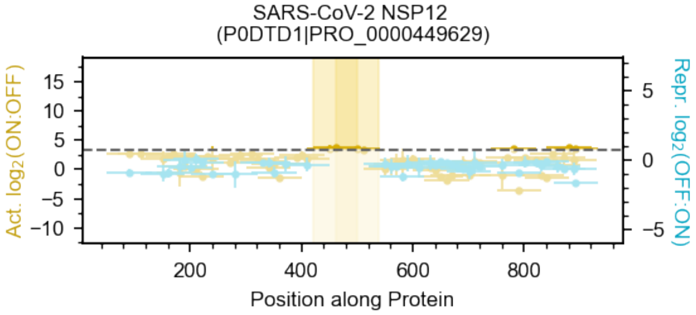
## SARS-CoV-2 NSP12 (P0DTD1|PRO_0000449629)

Gene: NSP12 ; Protein Family: NSP12



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Extended activation domain from residues 411 to 500:
KPGNFNKDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDK

Max tile of activation domain from residues 421 to 500 (estimated 15.1% to 22.9% of cells activated):
DFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDK

---

Extended activation domain from residues 461 to 550:
PTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALFAYTKRNVIPTITQMNLKYAISA

Max tile of activation domain from residues 461 to 540 (estimated 15.5% to 17.7% of cells activated):
PTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALFAYTKRNVIPTIT

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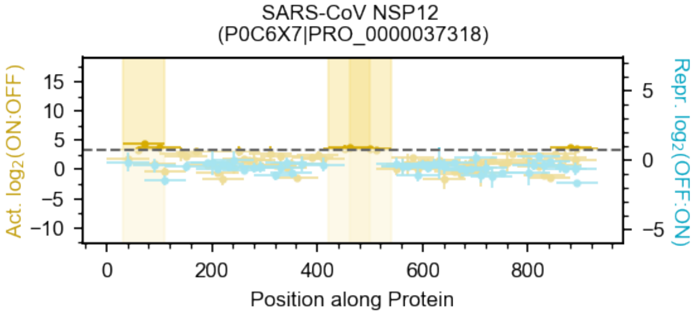
## SARS-CoV NSP12 (P0C6X7|PRO_0000037318)

Gene: NSP12 ; Protein Family: NSP12



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Extended activation domain from residues 21 to 110:
PCGTGTSTDVVYRAFDIYNEKVAGFAKFLKTNCCRFQEKDEEGNLLDSYFVVKRHTMSNYQHEETIYNLVKDCPAVAVHDFFKFRVDGDM

Max tile of activation domain from residues 31 to 110 (estimated 21.9% to 34.0% of cells activated):
VYRAFDIYNEKVAGFAKFLKTNCCRFQEKDEEGNLLDSYFVVKRHTMSNYQHEETIYNLVKDCPAVAVHDFFKFRVDGDM

---

Extended activation domain from residues 411 to 500:
KPGNFNKDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDK

Max tile of activation domain from residues 421 to 500 (estimated 15.1% to 22.9% of cells activated):
DFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDK

---

Extended activation domain from residues 461 to 550:
PTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALFAYTKRNVIPTITQMNLKYAISA

Max tile of activation domain from residues 461 to 540 (estimated 15.5% to 17.7% of cells activated):
PTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNKWGKARLYYDSMSYEDQDALFAYTKRNVIPTIT

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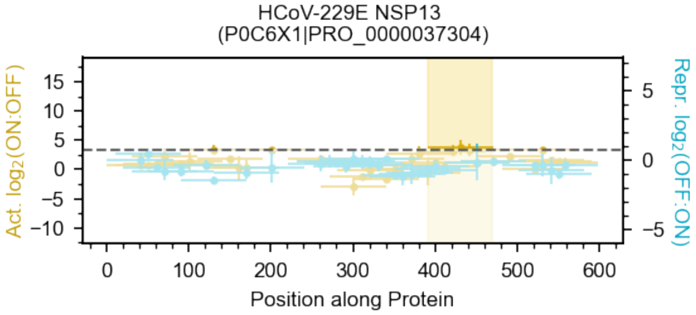
# HCoV-229E NSP13 (P0C6X1|PRO_0000037304)

Gene: NSP13 ; Protein Family: NSP13



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Extended activation domain from residues 391 to 480:
RISYKHIVYVGDPQQLPAPRVLISKGVMEPIDYNVVTQRMCAIGPDVFLHKCYRCPAEIVNTVSELVYENKFVPVKEASKQCFKIFERGS

Max tile of activation domain from residues 391 to 470 (estimated 8.0% to 37.3% of cells activated):
RISYKHIVYVGDPQQLPAPRVLISKGVMEPIDYNVVTQRMCAIGPDVFLHKCYRCPAEIVNTVSELVYENKFVPVKEASK

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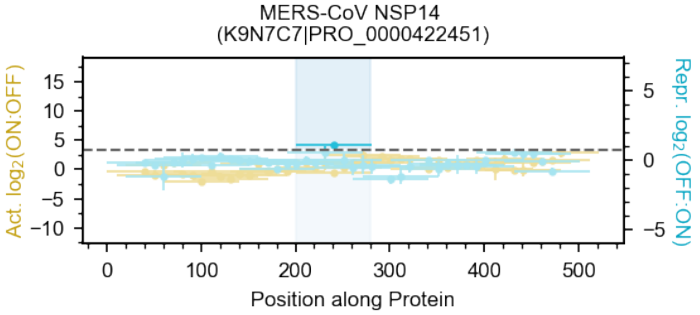
## MERS-CoV NSP14 (K9N7C7|PRO_0000422451)

Gene: NSP14 ; Protein Family: NSP14



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Extended repression domain from residues 191 to 280:
ELTSASYFCKIGKEQKCCMCNRRAAAYSSPLQSYACWTHSCGYDYVYNPFFVDVQQWGYVGNLATNHDRYCSVHQGAHVASNDAIMTRCL

Max tile of repression domain from residues 201 to 280 (estimated 19.7% to 23.6% of cells repressed):
IGKEQKCCMCNRRAAAYSSPLQSYACWTHSCGYDYVYNPFFVDVQQWGYVGNLATNHDRYCSVHQGAHVASNDAIMTRCL

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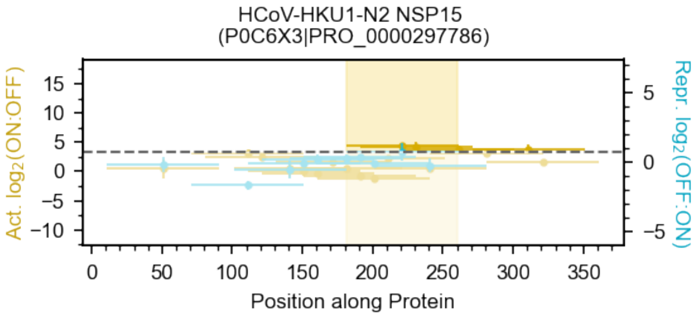
## HCoV-HKU1-N2 NSP15 (P0C6X3|PRO_0000297786)

Gene: NSP15 ; Protein Family: NSP15



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Extended activation domain from residues 181 to 270:
DVIFSRADSLSPSHYWSPQGNLGGNCAGNASGNDALARFTIFTQSRVLSTFEPRSDLERDFIDMEDSLFIAKYGLEDYAFDHIVYGSFNY

Max tile of activation domain from residues 181 to 260 (estimated 28.6% to 30.2% of cells activated):
DVIFSRADSLSPSHYWSPQGNLGGNCAGNASGNDALARFTIFTQSRVLSTFEPRSDLERDFIDMEDSLFIAKYGLEDYAF

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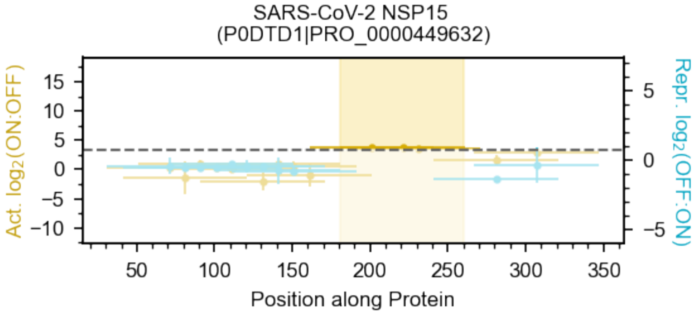
## SARS-CoV-2 NSP15 (P0DTD1|PRO_0000449632)

Gene: NSP15 ; Protein Family: NSP15



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Extended activation domain from residues 181 to 270:
KVDGVVQQLPETYFTQSRNLQEFKPRSQMEIDFLELAMDEFIERYKLEGYAFEHIVYGDFSHSQLGGLHLLIGLAKRFKESPFELEDFIP

Max tile of activation domain from residues 181 to 260 (estimated 16.2% to 21.0% of cells activated):
KVDGVVQQLPETYFTQSRNLQEFKPRSQMEIDFLELAMDEFIERYKLEGYAFEHIVYGDFSHSQLGGLHLLIGLAKRFKE

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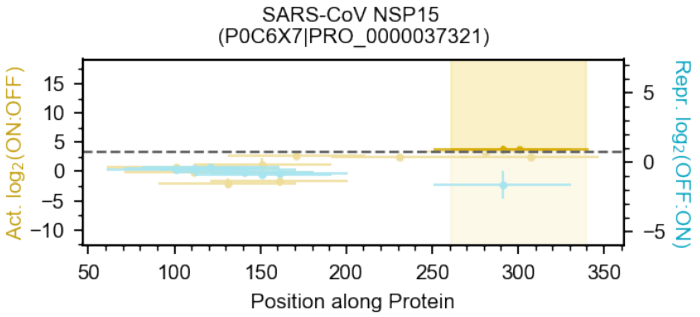
## SARS-CoV NSP15 (P0C6X7|PRO_0000037321)

Gene: NSP15 ; Protein Family: NSP15



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Extended activation domain from residues 241 to 340:
SHGQLGGLHLMIGLAKRSQDSPLKLEDFIPMDSTVKNYFITDAQTGSSKCVCSVIDLLLDDFVEIIKSQDLSVISKVVKVTIDYAEISFMLWCKDGHVET

Max tile of activation domain from residues 261 to 340 (estimated 14.9% to 23.2% of cells activated):
SPLKLEDFIPMDSTVKNYFITDAQTGSSKCVCSVIDLLLDDFVEIIKSQDLSVISKVVKVTIDYAEISFMLWCKDGHVET

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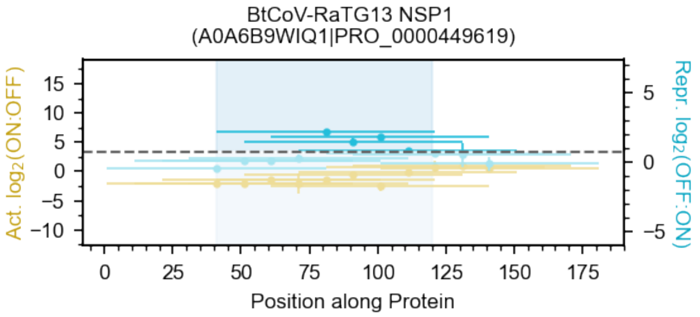
## BtCoV-RaTG13 NSP1 (A0A6B9WIQ1|PRO_0000449619)

Gene: NSP1 ; Protein Family: NSP1



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Extended repression domain from residues 41 to 160:
EARQHLKDGTCGLVEVEKGVLPQLEQPYVFIKRSDARTAPHGHVMVELVAELNGIQYGRSGETLGVLVPYVGETPVVYRKVLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQEN

Max tile of repression domain from residues 41 to 120 (estimated 42.3% to 46.4% of cells repressed):
EARQHLKDGTCGLVEVEKGVLPQLEQPYVFIKRSDARTAPHGHVMVELVAELNGIQYGRSGETLGVLVPYVGETPVVYRK

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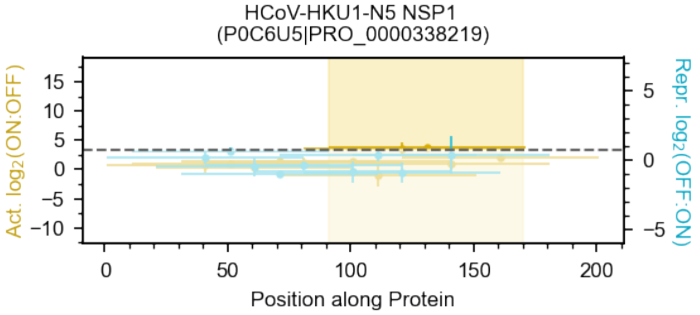
## HCoV-HKU1-N5 NSP1 (P0C6U5|PRO_0000338219)

Gene: NSP1 ; Protein Family: NSP1



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Extended activation domain from residues 81 to 170:
FVHEDLHVVEVLTKTAVKSGTAILIKSPLHSLGGFPKGYVMGLFRSYKTKRYVVHHLSMTTSTTNFGEDFFGWIVPFGFMPSYVHKWFQF

Max tile of activation domain from residues 91 to 170 (estimated 17.0% to 20.3% of cells activated):
VLTKTAVKSGTAILIKSPLHSLGGFPKGYVMGLFRSYKTKRYVVHHLSMTTSTTNFGEDFFGWIVPFGFMPSYVHKWFQF

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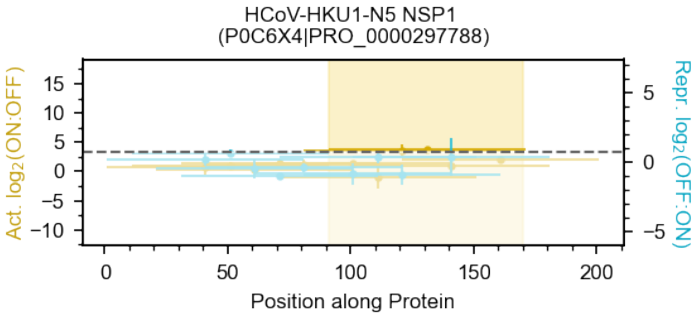
## HCoV-HKU1-N5 NSP1 (P0C6X4|PRO_0000297788)

Gene: NSP1 ; Protein Family: NSP1



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Extended activation domain from residues 81 to 170:
FVHEDLHVVEVLTKTAVKSGTAILIKSPLHSLGGFPKGYVMGLFRSYKTKRYVVHHLSMTTSTTNFGEDFFGWIVPFGFMPSYVHKWFQF

Max tile of activation domain from residues 91 to 170 (estimated 17.0% to 20.3% of cells activated):
VLTKTAVKSGTAILIKSPLHSLGGFPKGYVMGLFRSYKTKRYVVHHLSMTTSTTNFGEDFFGWIVPFGFMPSYVHKWFQF

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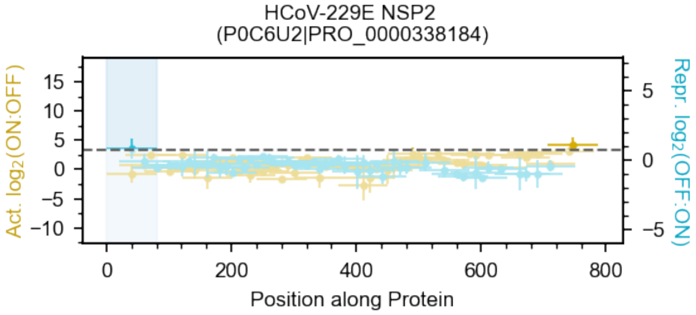
## HCoV-229E NSP2 (P0C6U2|PRO_0000338184)

Gene: NSP2 ; Protein Family: NSP2



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Extended repression domain from residues 1 to 80:
NVTYTDQYLCGADGKPVMSEDLWQFVDHFGENEEIIINGHTYVCAWLTKRKPLDYKRQNNLAIEEIEYVHGDALHTLRNG

Max tile of repression domain from residues 1 to 80 (estimated 15.4% to 28.2% of cells repressed):
NVTYTDQYLCGADGKPVMSEDLWQFVDHFGENEEIIINGHTYVCAWLTKRKPLDYKRQNNLAIEEIEYVHGDALHTLRNG

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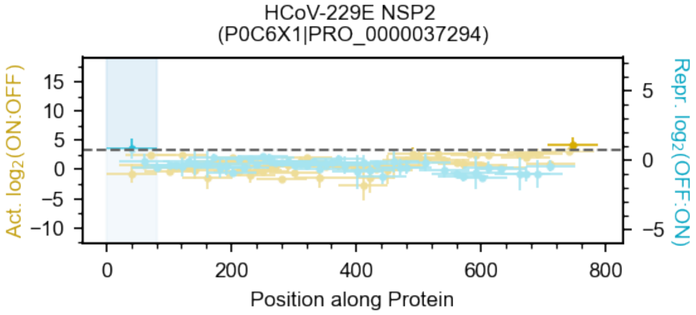
## HCoV-229E NSP2 (P0C6X1|PRO_0000037294)

Gene: NSP2 ; Protein Family: NSP2



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Extended repression domain from residues 1 to 80:
NVTYTDQYLCGADGKPVMSEDLWQFVDHFGENEEIIINGHTYVCAWLTKRKPLDYKRQNNLAIEEIEYVHGDALHTLRNG

Max tile of repression domain from residues 1 to 80 (estimated 15.4% to 28.2% of cells repressed):
NVTYTDQYLCGADGKPVMSEDLWQFVDHFGENEEIIINGHTYVCAWLTKRKPLDYKRQNNLAIEEIEYVHGDALHTLRNG

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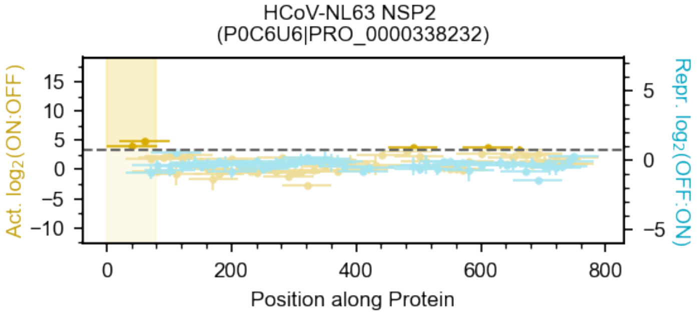
## HCoV-NL63 NSP2 (P0C6U6|PRO_0000338232)

Gene: NSP2 ; Protein Family: NSP2



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Extended activation domain from residues 1 to 80:
SVVFVDKYMCGFDGKPVLPKNMWEFRDYFNNNTDSIVIGGVTYQLAWDVIRKDLSYEQQNVLAIESIHYLGTTGHTLKSG

Max tile of activation domain from residues 1 to 80 (estimated 16.9% to 30.9% of cells activated):
SVVFVDKYMCGFDGKPVLPKNMWEFRDYFNNNTDSIVIGGVTYQLAWDVIRKDLSYEQQNVLAIESIHYLGTTGHTLKSG

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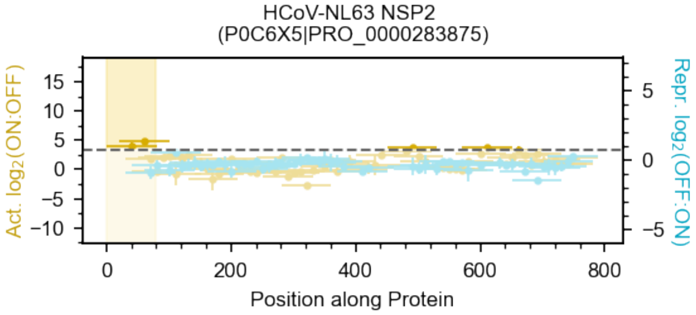
## HCoV-NL63 NSP2 (P0C6X5|PRO_0000283875)

Gene: NSP2 ; Protein Family: NSP2



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Extended activation domain from residues 1 to 80:
SVVFVDKYMCGFDGKPVLPKNMWEFRDYFNNNTDSIVIGGVTYQLAWDVIRKDLSYEQQNVLAIESIHYLGTTGHTLKSG

Max tile of activation domain from residues 1 to 80 (estimated 16.9% to 30.9% of cells activated):
SVVFVDKYMCGFDGKPVLPKNMWEFRDYFNNNTDSIVIGGVTYQLAWDVIRKDLSYEQQNVLAIESIHYLGTTGHTLKSG

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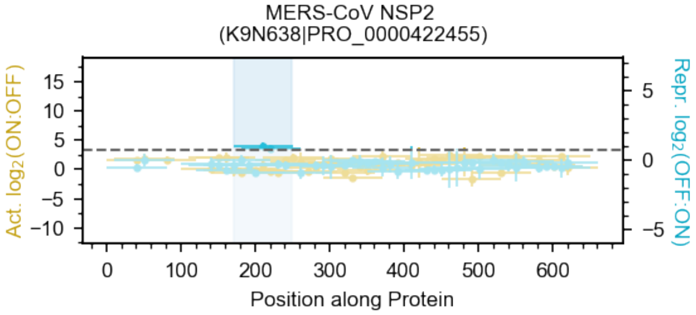
## MERS-CoV NSP2 (K9N638|PRO_0000422455)

Gene: NSP2 ; Protein Family: NSP2



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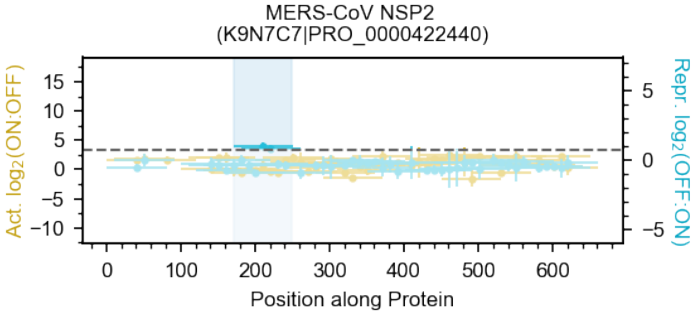
Extended repression domain from residues 171 to 260:
TANDVEVQSSGMIKPNALLCATCPFAKGDSCSSNCKHSVAQLVSYLSERCNVIADSKSFTLIFGGVAYAYFGCEEGTMYFVPRAKSVVSR

Max tile of repression domain from residues 171 to 250 (estimated 18.0% to 23.6% of cells repressed):
TANDVEVQSSGMIKPNALLCATCPFAKGDSCSSNCKHSVAQLVSYLSERCNVIADSKSFTLIFGGVAYAYFGCEEGTMYF

## MERS-CoV NSP2 (K9N7C7|PRO_0000422440)

Gene: NSP2 ; Protein Family: NSP2



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Extended repression domain from residues 171 to 260:
TANDVEVQSSGMIKPNALLCATCPFAKGDSCSSNCKHSVAQLVSYLSERCNVIADSKSFTLIFGGVAYAYFGCEEGTMYFVPRAKSVVSR

Max tile of repression domain from residues 171 to 250 (estimated 18.0% to 23.6% of cells repressed):
TANDVEVQSSGMIKPNALLCATCPFAKGDSCSSNCKHSVAQLVSYLSERCNVIADSKSFTLIFGGVAYAYFGCEEGTMYF

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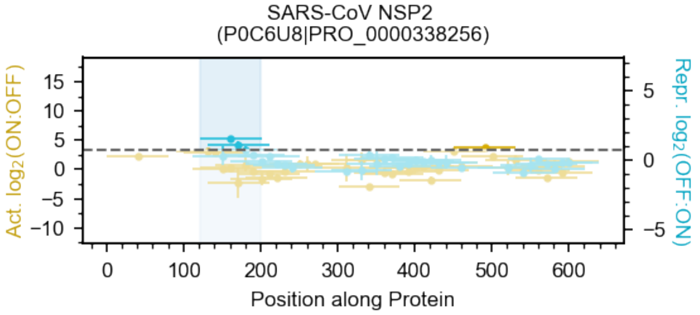
## SARS-CoV NSP2 (P0C6U8|PRO_0000338256)

Gene: NSP2 ; Protein Family: NSP2



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Extended repression domain from residues 121 to 220:
RSVYPVASPQECNNMHLSTLMKCNHCDEVSWQTCDFLKATCEHCGTENLVIEGPTTCGYLPTNAVVKMPCPACQDPEIGPEHSVADYHNHSNIETRLRKG

Max tile of repression domain from residues 121 to 200 (estimated 27.8% to 28.6% of cells repressed):
RSVYPVASPQECNNMHLSTLMKCNHCDEVSWQTCDFLKATCEHCGTENLVIEGPTTCGYLPTNAVVKMPCPACQDPEIGP

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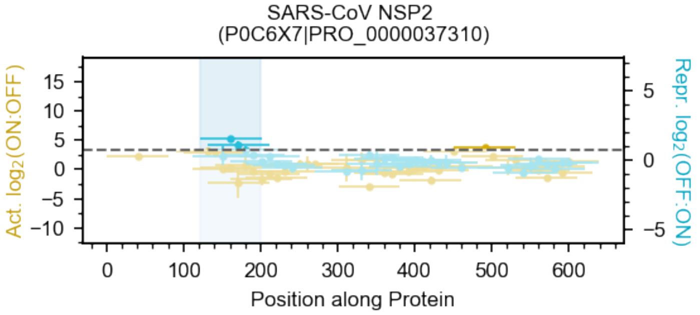
## SARS-CoV NSP2 (P0C6X7|PRO_0000037310)

Gene: NSP2 ; Protein Family: NSP2



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Extended repression domain from residues 121 to 220:
RSVYPVASPQECNNMHLSTLMKCNHCDEVSWQTCDFLKATCEHCGTENLVIEGPTTCGYLPTNAVVKMPCPACQDPEIGPEHSVADYHNHSNIETRLRKG

Max tile of repression domain from residues 121 to 200 (estimated 27.8% to 28.6% of cells repressed):
RSVYPVASPQECNNMHLSTLMKCNHCDEVSWQTCDFLKATCEHCGTENLVIEGPTTCGYLPTNAVVKMPCPACQDPEIGP

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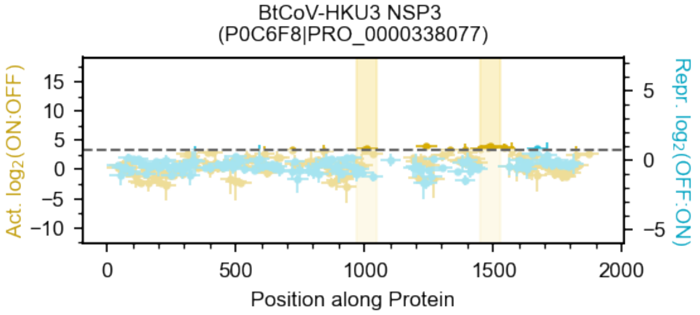
## BtCoV-HKU3 NSP3 (P0C6F8|PRO_0000338077)

Gene: NSP3 ; Protein Family: NSP3



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Extended activation domain from residues 1441 to 1530:
CSVCLSGLDSLDSYPALETIQVTISSYKLDLTFLGLAAEWLLAYMLFTKFFYLLGLSAIMQAFFGYFASHFISNSWLMWFIISIVQMAPV

Max tile of activation domain from residues 1451 to 1530 (estimated 17.7% to 25.2% of cells activated):
LDSYPALETIQVTISSYKLDLTFLGLAAEWLLAYMLFTKFFYLLGLSAIMQAFFGYFASHFISNSWLMWFIISIVQMAPV

---

Extended activation domain from residues 961 to 1050:
SAPPAEYKLQQGAFLCANEYTGNYQCGHYTHITAKETLYRVDGAHLTKMSEYKGPVTDVFYKETSYTTAIKPVSYKLDGVTYTEIEPKLD

Max tile of activation domain from residues 971 to 1050 (estimated 15.4% to 18.5% of cells activated):
QGAFLCANEYTGNYQCGHYTHITAKETLYRVDGAHLTKMSEYKGPVTDVFYKETSYTTAIKPVSYKLDGVTYTEIEPKLD

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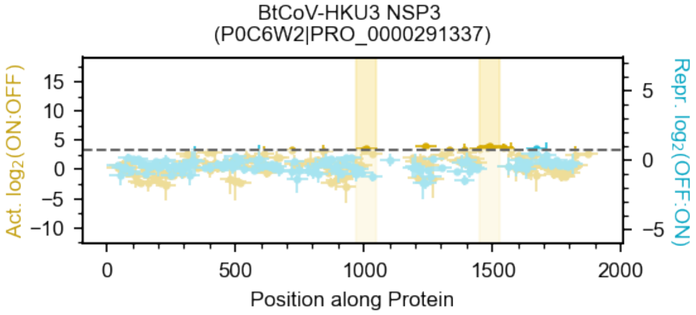
## BtCoV-HKU3 NSP3 (P0C6W2|PRO_0000291337)

Gene: NSP3 ; Protein Family: NSP3



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Extended activation domain from residues 1441 to 1530:
CSVCLSGLDSLDSYPALETIQVTISSYKLDLTFLGLAAEWLLAYMLFTKFFYLLGLSAIMQAFFGYFASHFISNSWLMWFIISIVQMAPV

Max tile of activation domain from residues 1451 to 1530 (estimated 17.7% to 25.2% of cells activated):
LDSYPALETIQVTISSYKLDLTFLGLAAEWLLAYMLFTKFFYLLGLSAIMQAFFGYFASHFISNSWLMWFIISIVQMAPV

---

Extended activation domain from residues 961 to 1050:
SAPPAEYKLQQGAFLCANEYTGNYQCGHYTHITAKETLYRVDGAHLTKMSEYKGPVTDVFYKETSYTTAIKPVSYKLDGVTYTEIEPKLD

Max tile of activation domain from residues 971 to 1050 (estimated 15.4% to 18.5% of cells activated):
QGAFLCANEYTGNYQCGHYTHITAKETLYRVDGAHLTKMSEYKGPVTDVFYKETSYTTAIKPVSYKLDGVTYTEIEPKLD

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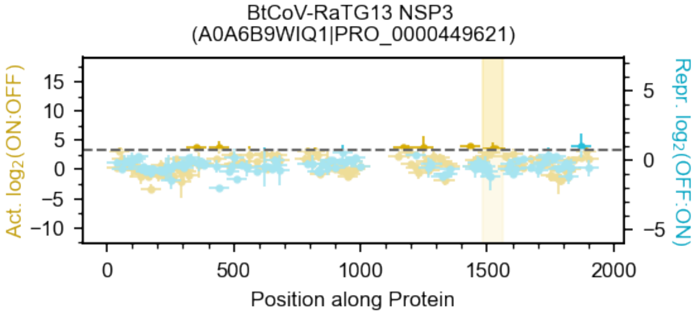
## BtCoV-RaTG13 NSP3 (A0A6B9WIQ1|PRO_0000449621)

Gene: NSP3 ; Protein Family: NSP3



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Extended activation domain from residues 1481 to 1570:
TYPSLETIQITISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIINLVQMAPISAMVRMYIFFAS

Max tile of activation domain from residues 1481 to 1560 (estimated 8.3% to 30.0% of cells activated):
TYPSLETIQITISSFKWDLTAFGLVAEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIINLVQMAPISA

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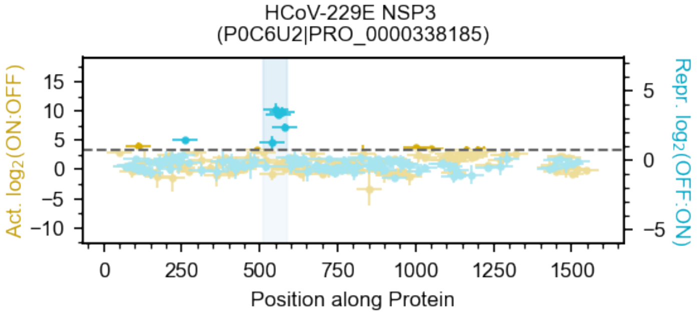
## HCoV-229E NSP3 (P0C6U2|PRO_0000338185)

Gene: NSP3 ; Protein Family: NSP3



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Extended repression domain from residues 501 to 620:
KLETSLEVLLDVCNTKEVKVFVYTDTEVCKVKDFVSGLVNVQKVEQPKIEPKPVSVIKVAPKPYRVDGKFSYFTEDLLCVADDKPIVLFTDSMLTLDDRGLALDNALSGVLSAAIKDCVD

Max tile of repression domain from residues 511 to 590 (estimated 72.3% to 93.4% of cells repressed):
DVCNTKEVKVFVYTDTEVCKVKDFVSGLVNVQKVEQPKIEPKPVSVIKVAPKPYRVDGKFSYFTEDLLCVADDKPIVLFT

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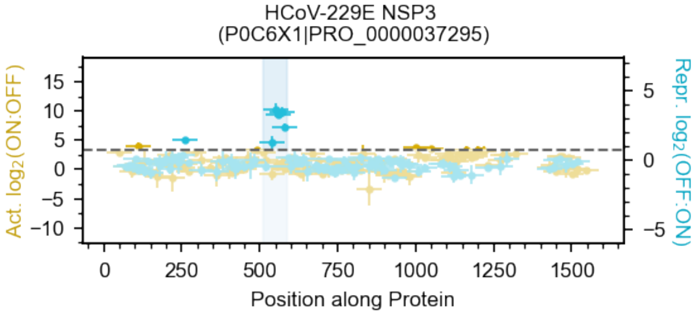
**Other Tiling Screen Data from Ludwig, C.H. et al. 2023**

## HCoV-229E NSP3 (P0C6X1|PRO_0000037295)

Gene: NSP3 ; Protein Family: NSP3



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Extended repression domain from residues 501 to 620:
KLETSLEVLLDVCNTKEVKVFVYTDTEVCKVKDFVSGLVNVQKVEQPKIEPKPVSVIKVAPKPYRVDGKFSYFTEDLLCVADDKPIVLFTDSMLTLDDRGLALDNALSGVLSAAIKDCVD

Max tile of repression domain from residues 511 to 590 (estimated 72.3% to 93.4% of cells repressed):
DVCNTKEVKVFVYTDTEVCKVKDFVSGLVNVQKVEQPKIEPKPVSVIKVAPKPYRVDGKFSYFTEDLLCVADDKPIVLFT

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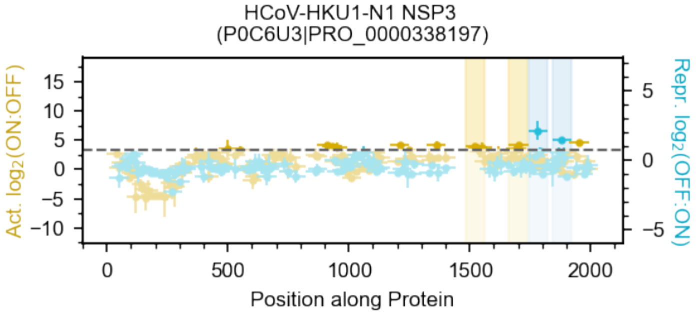
## HCoV-HKU1-N1 NSP3 (P0C6U3|PRO_0000338197)

Gene: NSP3 ; Protein Family: NSP3



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Extended activation domain from residues 1651 to 1740:
YIVVTAMYKVVGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

Max tile of activation domain from residues 1661 to 1740 (estimated 18.3% to 32.1% of cells activated):
VGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

---

Extended activation domain from residues 1481 to 1570:
VATVFLFWFNFLYINVIFSDFYLPNISVFPIFVGRIVMWIKATFGLVTICDFYSKLGVGFTSHFCNGSFICELCHSGFDMLDTYAAIDFV

Max tile of activation domain from residues 1481 to 1560 (estimated 21.5% to 21.5% of cells activated):
VATVFLFWFNFLYINVIFSDFYLPNISVFPIFVGRIVMWIKATFGLVTICDFYSKLGVGFTSHFCNGSFICELCHSGFDM

---

Extended repression domain from residues 1741 to 1830:
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFLNAVVFYAQSL

Max tile of repression domain from residues 1741 to 1820 (estimated 26.0% to 63.7% of cells repressed):
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFL

---

Extended repression domain from residues 1831 to 1920:
YRPILLVDKKLITTACNGISVTQTMFDVYVDTFMSHFDVDRKSFNNFVNIAHASLREGVQLEKVLDTFVGCVRKCCSIDSDVETRFITKS

Max tile of repression domain from residues 1841 to 1920 (estimated 26.2% to 27.1% of cells repressed):
LITTACNGISVTQTMFDVYVDTFMSHFDVDRKSFNNFVNIAHASLREGVQLEKVLDTFVGCVRKCCSIDSDVETRFITKS

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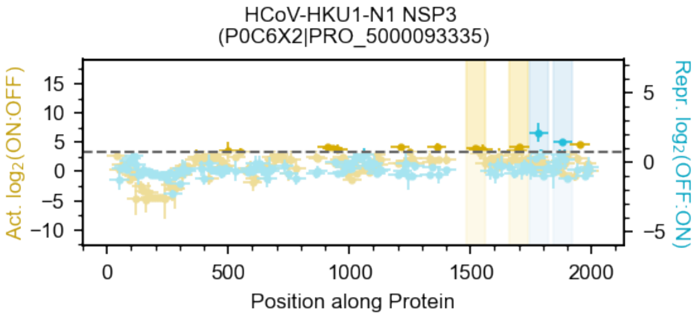
## HCoV-HKU1-N1 NSP3 (P0C6X2|PRO_5000093335)

Gene: NSP3 ; Protein Family: NSP3



Extended activation domain from residues 1651 to 1740:
YIVVTAMYKVVGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

Max tile of activation domain from residues 1661 to 1740 (estimated 18.3% to 32.1% of cells activated):
VGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

Extended activation domain from residues 1481 to 1570:
VATVFLFWFNFLYINVIFSDFYLPNISVFPIFVGRIVMWIKATFGLVTICDFYSKLGVGFTSHFCNGSFICELCHSGFDMLDTYAAIDFV

Max tile of activation domain from residues 1481 to 1560 (estimated 21.5% to 21.5% of cells activated):
VATVFLFWFNFLYINVIFSDFYLPNISVFPIFVGRIVMWIKATFGLVTICDFYSKLGVGFTSHFCNGSFICELCHSGFDM

Extended repression domain from residues 1741 to 1830:
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFLNAVVFYAQSL

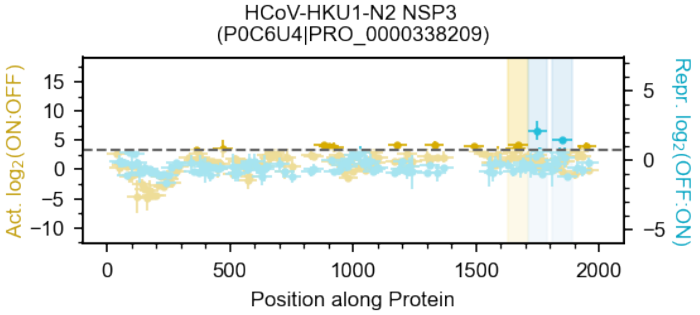
Max tile of repression domain from residues 1741 to 1820 (estimated 26.0% to 63.7% of cells repressed):
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFL

Extended repression domain from residues 1831 to 1920:
YRPILLVDKKLITTACNGISVTQTMFDVYVDTFMSHFDVDRKSFNNFVNIAHASLREGVQLEKVLDTFVGCVRKCCSIDSDVETRFITKS

Max tile of repression domain from residues 1841 to 1920 (estimated 26.2% to 27.1% of cells repressed):
LITTACNGISVTQTMFDVYVDTFMSHFDVDRKSFNNFVNIAHASLREGVQLEKVLDTFVGCVRKCCSIDSDVETRFITKS

## HCoV-HKU1-N2 NSP3 (P0C6U4|PRO_0000338209)

Gene: NSP3 ; Protein Family: NSP3



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Extended activation domain from residues 1621 to 1710:
YIVVTAMYKVVGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

Max tile of activation domain from residues 1631 to 1710 (estimated 18.3% to 32.1% of cells activated):
VGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

---

Extended repression domain from residues 1711 to 1800:
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFLNAVVFYAQSL

Max tile of repression domain from residues 1711 to 1790 (estimated 26.0% to 63.7% of cells repressed):
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFL

---

Extended repression domain from residues 1801 to 1890:
YRPILLVDKKLITTACNGISVTQTMFDVYVDTFMSHFDVDRKSFNNFVNIAHASLREGVQLEKVLDTFVGCVRKCCSIDSDVETRFITKS

Max tile of repression domain from residues 1811 to 1890 (estimated 26.2% to 27.1% of cells repressed):
LITTACNGISVTQTMFDVYVDTFMSHFDVDRKSFNNFVNIAHASLREGVQLEKVLDTFVGCVRKCCSIDSDVETRFITKS

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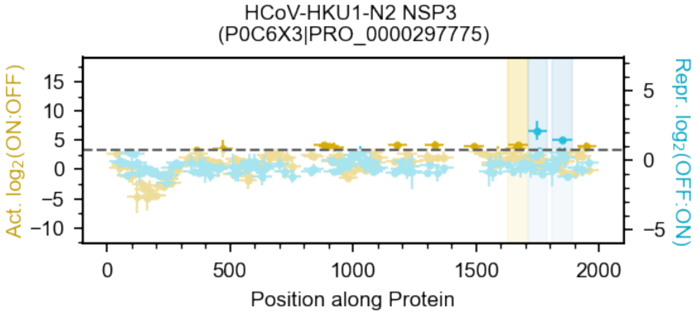
## HCoV-HKU1-N2 NSP3 (P0C6X3|PRO_0000297775)

Gene: NSP3 ; Protein Family: NSP3



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Extended activation domain from residues 1621 to 1710:
YIVVTAMYKVVGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

Max tile of activation domain from residues 1631 to 1710 (estimated 18.3% to 32.1% of cells activated):
VGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

---

Extended repression domain from residues 1711 to 1800:
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFLNAVVFYAQSL

Max tile of repression domain from residues 1711 to 1790 (estimated 26.0% to 63.7% of cells repressed):
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFL

---

Extended repression domain from residues 1801 to 1890:
YRPILLVDKKLITTACNGISVTQTMFDVYVDTFMSHFDVDRKSFNNFVNIAHASLREGVQLEKVLDTFVGCVRKCCSIDSDVETRFITKS

Max tile of repression domain from residues 1811 to 1890 (estimated 26.2% to 27.1% of cells repressed):
LITTACNGISVTQTMFDVYVDTFMSHFDVDRKSFNNFVNIAHASLREGVQLEKVLDTFVGCVRKCCSIDSDVETRFITKS

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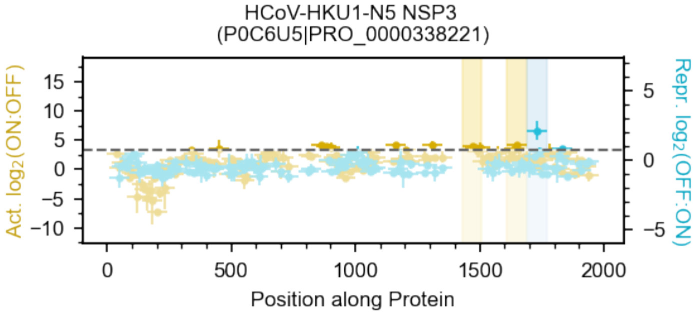
**Other Tiling Screen Data from Ludwig, C.H. et al. 2023**

## HCoV-HKU1-N5 NSP3 (P0C6U5|PRO_0000338221)

Gene: NSP3 ; Protein Family: NSP3



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Extended activation domain from residues 1601 to 1690:
YIVVTAMYKVVGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

Max tile of activation domain from residues 1611 to 1690 (estimated 18.3% to 32.1% of cells activated):
VGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

---

Extended activation domain from residues 1431 to 1520:
VATVFLFWFNFLYINVIFSDFYLPNISVFPIFVGRIVMWIKATFGLVTICDFYSKLGVGFTSHFCNGSFICELCHSGFDMLDTYAAIDFV

Max tile of activation domain from residues 1431 to 1510 (estimated 21.5% to 21.5% of cells activated):
VATVFLFWFNFLYINVIFSDFYLPNISVFPIFVGRIVMWIKATFGLVTICDFYSKLGVGFTSHFCNGSFICELCHSGFDM

---

Extended repression domain from residues 1691 to 1780:
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFLNAVVFYAQSL

Max tile of repression domain from residues 1691 to 1770 (estimated 26.0% to 63.7% of cells repressed):
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFL

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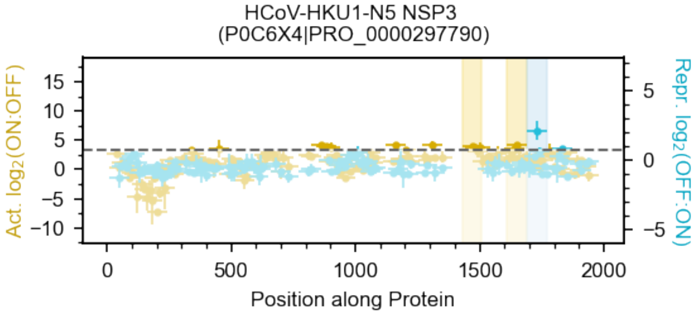
## HCoV-HKU1-N5 NSP3 (P0C6X4|PRO_0000297790)

Gene: NSP3 ; Protein Family: NSP3



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Extended activation domain from residues 1601 to 1690:
YIVVTAMYKVVGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

Max tile of activation domain from residues 1611 to 1690 (estimated 18.3% to 32.1% of cells activated):
VGFIRHIVYGCNKAGCLFCYKRNCSVRVKCSTIVGGVIRYYDITANGGTGFCVKHQWNCFNCHSFKPGNTFITVEAAIEL

---

Extended activation domain from residues 1431 to 1520:
VATVFLFWFNFLYINVIFSDFYLPNISVFPIFVGRIVMWIKATFGLVTICDFYSKLGVGFTSHFCNGSFICELCHSGFDMLDTYAAIDFV

Max tile of activation domain from residues 1431 to 1510 (estimated 21.5% to 21.5% of cells activated):
VATVFLFWFNFLYINVIFSDFYLPNISVFPIFVGRIVMWIKATFGLVTICDFYSKLGVGFTSHFCNGSFICELCHSGFDM

---

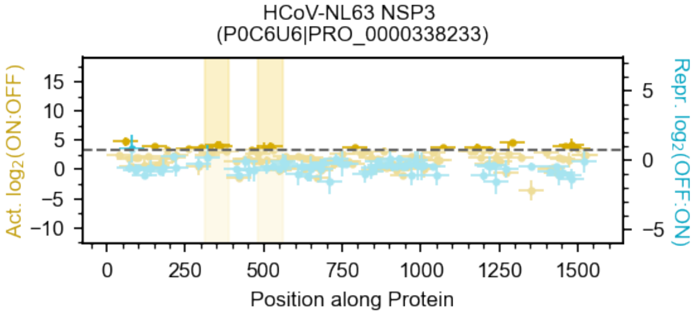
Extended repression domain from residues 1691 to 1780:
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFLNAVVFYAQSL

Max tile of repression domain from residues 1691 to 1770 (estimated 26.0% to 63.7% of cells repressed):
SKELKRPVNPTDASHYVVTDIKQVGCMMRLFYDRDGQRVYDDVDASLFVDINNLLHSKVKVVPNLYVVVVESDADRANFL

---

## HCoV-NL63 NSP3 (P0C6U6|PRO_0000338233)

Gene: NSP3 ; Protein Family: NSP3



---

Extended activation domain from residues 311 to 400:
GSGHYQTNLYSFNKAIDGFGVFDIKNSSVNTVCFVDVDFHSVEIEAGEVKPFAVYKNVKFYLGDISHLVNCVSFDFVVNAANENLLHGGG

Max tile of activation domain from residues 311 to 390 (estimated 17.3% to 35.0% of cells activated):
GSGHYQTNLYSFNKAIDGFGVFDIKNSSVNTVCFVDVDFHSVEIEAGEVKPFAVYKNVKFYLGDISHLVNCVSFDFVVNA

---

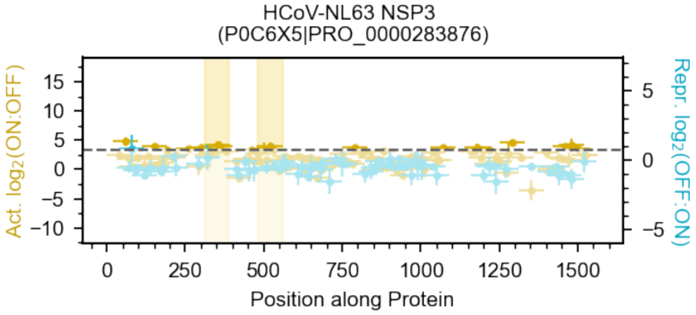
Extended activation domain from residues 481 to 570:
IFGVRIENSLKALFSCDINKPLQVFVYSSNEEQAVLKFLDGLDLTPVIDDVDVVKPFRVEGNFSFFDCGVNALDGDIYLLFTNSILMLDK

Max tile of activation domain from residues 481 to 560 (estimated 13.5% to 31.3% of cells activated):
IFGVRIENSLKALFSCDINKPLQVFVYSSNEEQAVLKFLDGLDLTPVIDDVDVVKPFRVEGNFSFFDCGVNALDGDIYLL

---

## HCoV-NL63 NSP3 (P0C6X5|PRO_0000283876)

Gene: NSP3 ; Protein Family: NSP3



---

Extended activation domain from residues 311 to 400:
GSGHYQTNLYSFNKAIDGFGVFDIKNSSVNTVCFVDVDFHSVEIEAGEVKPFAVYKNVKFYLGDISHLVNCVSFDFVVNAANENLLHGGG

Max tile of activation domain from residues 311 to 390 (estimated 17.3% to 35.0% of cells activated):
GSGHYQTNLYSFNKAIDGFGVFDIKNSSVNTVCFVDVDFHSVEIEAGEVKPFAVYKNVKFYLGDISHLVNCVSFDFVVNA

---

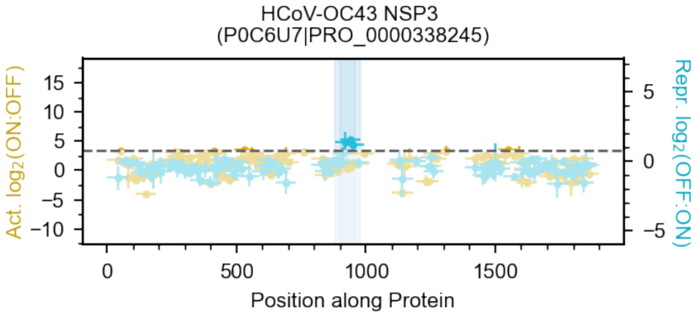
Extended activation domain from residues 481 to 570:
IFGVRIENSLKALFSCDINKPLQVFVYSSNEEQAVLKFLDGLDLTPVIDDVDVVKPFRVEGNFSFFDCGVNALDGDIYLLFTNSILMLDK

Max tile of activation domain from residues 481 to 560 (estimated 13.5% to 31.3% of cells activated):
IFGVRIENSLKALFSCDINKPLQVFVYSSNEEQAVLKFLDGLDLTPVIDDVDVVKPFRVEGNFSFFDCGVNALDGDIYLL

---

# HCoV-OC43 NSP3 (P0C6U7|PRO_0000338245)

Gene: NSP3 ; Protein Family: NSP3



---

Extended repression domain from residues 901 to 990:
GVKQEQRTGLDAVMHFGTLSREDLEIGYTVDCSCGKKLIHCVRFDVPFLICSNTPASVKLPKGVGSANIFIGDNVGHYVHVKCEQSYQLY

Max tile of repression domain from residues 901 to 980 (estimated 24.0% to 32.4% of cells repressed):
GVKQEQRTGLDAVMHFGTLSREDLEIGYTVDCSCGKKLIHCVRFDVPFLICSNTPASVKLPKGVGSANIFIGDNVGHYVH

---

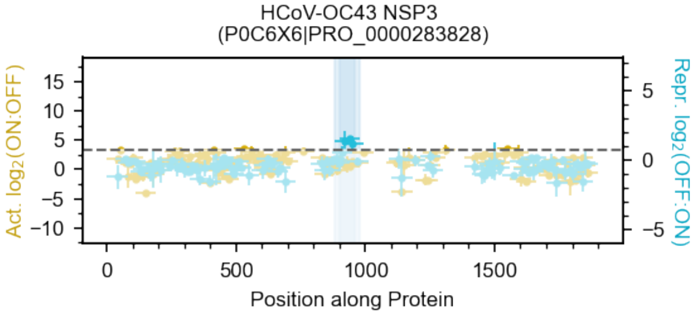
Extended repression domain from residues 871 to 960:
PADSRDFLRVVFSQVDLTGAICDFEIACKCGVKQEQRTGLDAVMHFGTLSREDLEIGYTVDCSCGKKLIHCVRFDVPFLICSNTPASVKL

Max tile of repression domain from residues 881 to 960 (estimated 18.1% to 40.2% of cells repressed):
VFSQVDLTGAICDFEIACKCGVKQEQRTGLDAVMHFGTLSREDLEIGYTVDCSCGKKLIHCVRFDVPFLICSNTPASVKL

---

# HCoV-OC43 NSP3 (P0C6X6|PRO_0000283828)

Gene: NSP3 ; Protein Family: NSP3



---

Extended repression domain from residues 901 to 990:
GVKQEQRTGLDAVMHFGTLSREDLEIGYTVDCSCGKKLIHCVRFDVPFLICSNTPASVKLPKGVGSANIFIGDNVGHYVHVKCEQSYQLY

Max tile of repression domain from residues 901 to 980 (estimated 24.0% to 32.4% of cells repressed):
GVKQEQRTGLDAVMHFGTLSREDLEIGYTVDCSCGKKLIHCVRFDVPFLICSNTPASVKLPKGVGSANIFIGDNVGHYVH

---

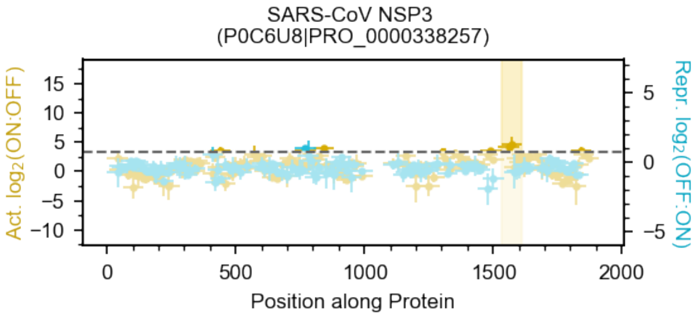
Extended repression domain from residues 871 to 960:
PADSRDFLRVVFSQVDLTGAICDFEIACKCGVKQEQRTGLDAVMHFGTLSREDLEIGYTVDCSCGKKLIHCVRFDVPFLICSNTPASVKL

Max tile of repression domain from residues 881 to 960 (estimated 18.1% to 40.2% of cells repressed):
VFSQVDLTGAICDFEIACKCGVKQEQRTGLDAVMHFGTLSREDLEIGYTVDCSCGKKLIHCVRFDVPFLICSNTPASVKL

---

## SARS-CoV NSP3 (P0C6U8|PRO_0000338257)

Gene: NSP3 ; Protein Family: NSP3



---

Extended activation domain from residues 1521 to 1610:
SWLMWFIISIVQMAPVSAMVRMYIFFASFYYIWKSYVHIMDGCTSSTCMMCYKRNRATRVECTTIVNGMKRSFYVYANGGRGFCKTHNWN

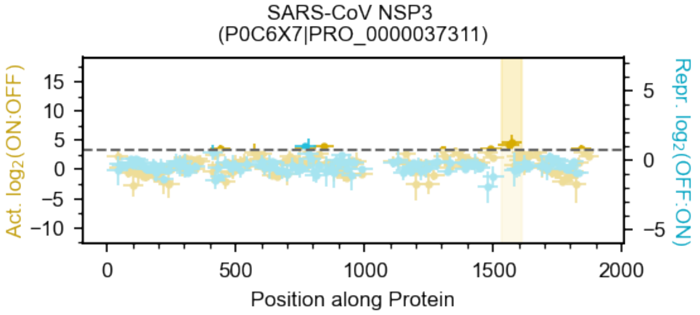
Max tile of activation domain from residues 1531 to 1610 (estimated 12.6% to 56.1% of cells activated):
VQMAPVSAMVRMYIFFASFYYIWKSYVHIMDGCTSSTCMMCYKRNRATRVECTTIVNGMKRSFYVYANGGRGFCKTHNWN

---

**Other Tiling Screen Data from Ludwig, C.H. et al. 2023**

## SARS-CoV NSP3 (P0C6X7|PRO_0000037311)

Gene: NSP3 ; Protein Family: NSP3



---

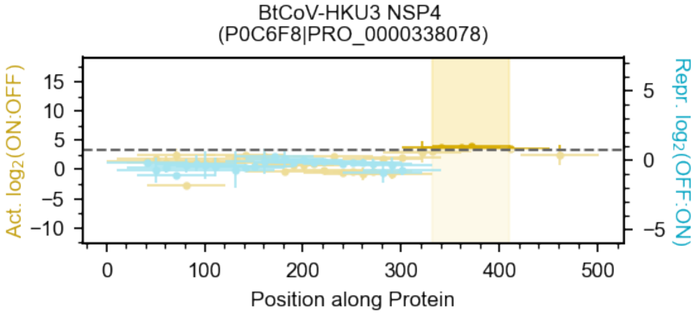
Extended activation domain from residues 1521 to 1610:
SWLMWFIISIVQMAPVSAMVRMYIFFASFYYIWKSYVHIMDGCTSSTCMMCYKRNRATRVECTTIVNGMKRSFYVYANGGRGFCKTHNWN

Max tile of activation domain from residues 1531 to 1610 (estimated 12.6% to 56.1% of cells activated):
VQMAPVSAMVRMYIFFASFYYIWKSYVHIMDGCTSSTCMMCYKRNRATRVECTTIVNGMKRSFYVYANGGRGFCKTHNWN

---

## BtCoV-HKU3 NSP4 (P0C6F8|PRO_0000338078)

Gene: NSP4 ; Protein Family: NSP4



---

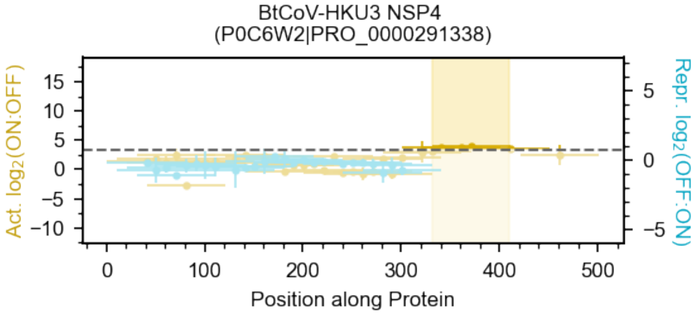
Extended activation domain from residues 321 to 410:
LFLMSFTILCLAPAYSFLPGVYSIFYLYLTFYFTNDVSFLAHLQWFAMFSPIVPFWITAIYVFCISLKHFHWFFSNYLKKRVMFNGVTFS

Max tile of activation domain from residues 331 to 410 (estimated 18.6% to 24.8% of cells activated):
LAPAYSFLPGVYSIFYLYLTFYFTNDVSFLAHLQWFAMFSPIVPFWITAIYVFCISLKHFHWFFSNYLKKRVMFNGVTFS

---

## BtCoV-HKU3 NSP4 (P0C6W2|PRO_0000291338)

Gene: NSP4 ; Protein Family: NSP4



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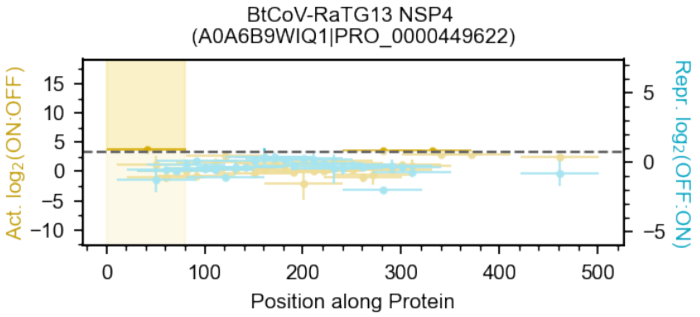
Extended activation domain from residues 321 to 410:
LFLMSFTILCLAPAYSFLPGVYSIFYLYLTFYFTNDVSFLAHLQWFAMFSPIVPFWITAIYVFCISLKHFHWFFSNYLKKRVMFNGVTFS

Max tile of activation domain from residues 331 to 410 (estimated 18.6% to 24.8% of cells activated):
LAPAYSFLPGVYSIFYLYLTFYFTNDVSFLAHLQWFAMFSPIVPFWITAIYVFCISLKHFHWFFSNYLKKRVMFNGVTFS

---

## BtCoV-RaTG13 NSP4 (A0A6B9WIQ1|PRO_0000449622)

Gene: NSP4 ; Protein Family: NSP4



---

Extended activation domain from residues 1 to 80:
KIVNNWLKQLIKVTLVFLFVAAIFYLITPVHVMSKHTDFSSEIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGG

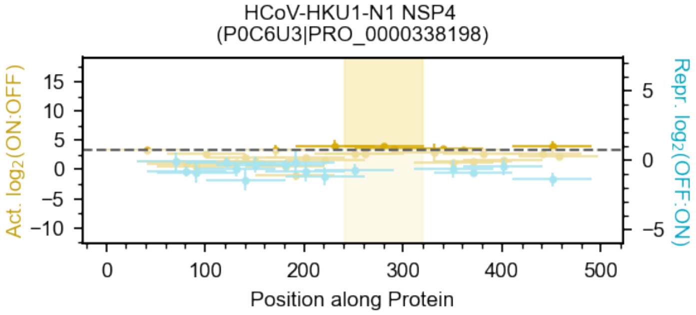
Max tile of activation domain from residues 1 to 80 (estimated 14.0% to 22.9% of cells activated):
KIVNNWLKQLIKVTLVFLFVAAIFYLITPVHVMSKHTDFSSEIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGG

---

**Other Tiling Screen Data from Ludwig, C.H. et al. 2023**

## HCoV-HKU1-N1 NSP4 (P0C6U3|PRO_0000338198)

Gene: NSP4 ; Protein Family: NSP4



---

Extended activation domain from residues 241 to 330:
VLNNDYYRSMPGTFCGRDLFDLFYQFFSSLIRPIDFFSLTASSIFGAILAIVVVLVFYYLIKLKRAFGDYTSVVVINVVVWCINFLMLFV

Max tile of activation domain from residues 241 to 320 (estimated 17.7% to 25.6% of cells activated):
VLNNDYYRSMPGTFCGRDLFDLFYQFFSSLIRPIDFFSLTASSIFGAILAIVVVLVFYYLIKLKRAFGDYTSVVVINVVV

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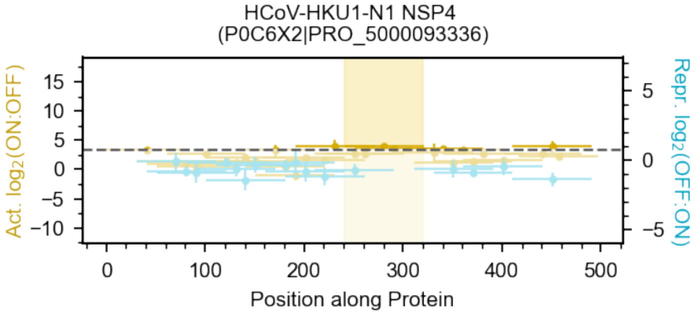
# HCoV-HKU1-N1 NSP4 (P0C6X2|PRO_5000093336)

Gene: NSP4 ; Protein Family: NSP4



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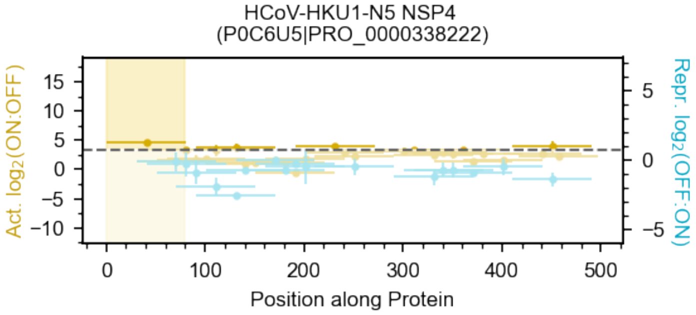
Extended activation domain from residues 241 to 330:
VLNNDYYRSMPGTFCGRDLFDLFYQFFSSLIRPIDFFSLTASSIFGAILAIVVVLVFYYLIKLKRAFGDYTSVVVINVVVWCINFLMLFV

Max tile of activation domain from residues 241 to 320 (estimated 17.7% to 25.6% of cells activated):
VLNNDYYRSMPGTFCGRDLFDLFYQFFSSLIRPIDFFSLTASSIFGAILAIVVVLVFYYLIKLKRAFGDYTSVVVINVVV

---

## HCoV-HKU1-N5 NSP4 (P0C6U5|PRO_0000338222)

Gene: NSP4 ; Protein Family: NSP4



---

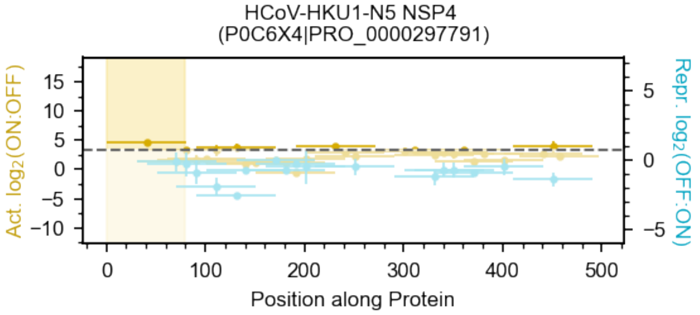
Extended activation domain from residues 1 to 80:
VVLSNLLYILFFISLICFILLWALLPTYSVYKSDIHLPAYASFKVIDNGVVRDISVNDLCFANKFFQFDQWYESTFGSVY

Max tile of activation domain from residues 1 to 80 (estimated 31.3% to 34.3% of cells activated):
VVLSNLLYILFFISLICFILLWALLPTYSVYKSDIHLPAYASFKVIDNGVVRDISVNDLCFANKFFQFDQWYESTFGSVY

---

## HCoV-HKU1-N5 NSP4 (P0C6X4|PRO_0000297791)

Gene: NSP4 ; Protein Family: NSP4



---

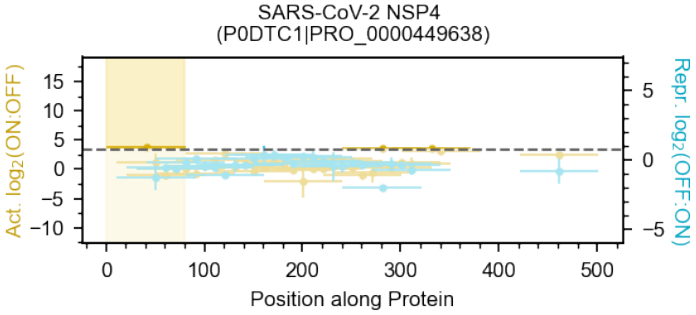
Extended activation domain from residues 1 to 80:
VVLSNLLYILFFISLICFILLWALLPTYSVYKSDIHLPAYASFKVIDNGVVRDISVNDLCFANKFFQFDQWYESTFGSVY

Max tile of activation domain from residues 1 to 80 (estimated 31.3% to 34.3% of cells activated):
VVLSNLLYILFFISLICFILLWALLPTYSVYKSDIHLPAYASFKVIDNGVVRDISVNDLCFANKFFQFDQWYESTFGSVY

---

## SARS-CoV-2 NSP4 (P0DTC1|PRO_0000449638)

Gene: NSP4 ; Protein Family: NSP4



---

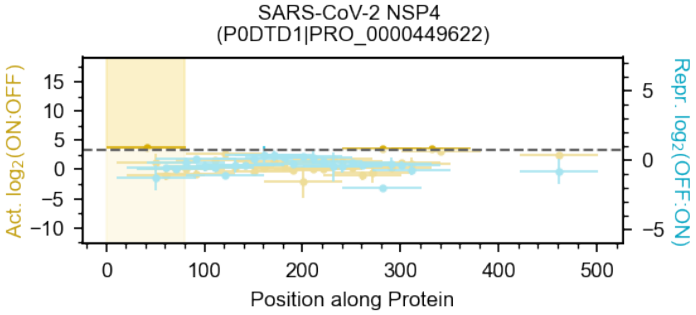
Extended activation domain from residues 1 to 80:
KIVNNWLKQLIKVTLVFLFVAAIFYLITPVHVMSKHTDFSSEIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGG

Max tile of activation domain from residues 1 to 80 (estimated 14.0% to 22.9% of cells activated):
KIVNNWLKQLIKVTLVFLFVAAIFYLITPVHVMSKHTDFSSEIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGG

---

## SARS-CoV-2 NSP4 (P0DTD1|PRO_0000449622)

Gene: NSP4 ; Protein Family: NSP4



---

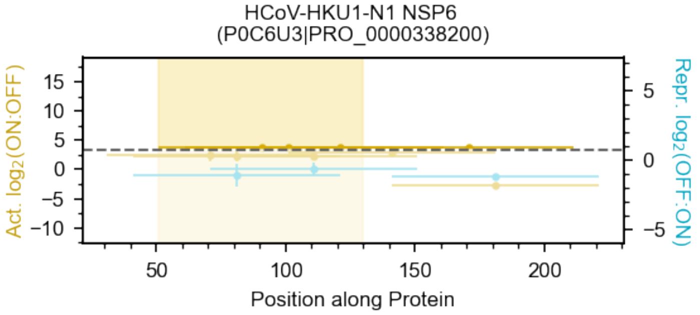
Extended activation domain from residues 1 to 80:
KIVNNWLKQLIKVTLVFLFVAAIFYLITPVHVMSKHTDFSSEIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGG

Max tile of activation domain from residues 1 to 80 (estimated 14.0% to 22.9% of cells activated):
KIVNNWLKQLIKVTLVFLFVAAIFYLITPVHVMSKHTDFSSEIIGYKAIDGGVTRDIASTDTCFANKHADFDTWFSQRGG

---

# HCoV-HKU1-N1 NSP6 (P0C6U3|PRO_0000338200)

Gene: NSP6 ; Protein Family: NSP6



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Extended activation domain from residues 51 to 140:
FVSFMMLLVKHKHFYLTMYIIPVLCTLFYVNYLVVYKEGFRGFTYVWLSYFVPAVNFTYVYEVFYGCILCVFAIFITMHSINHDIFSLMF

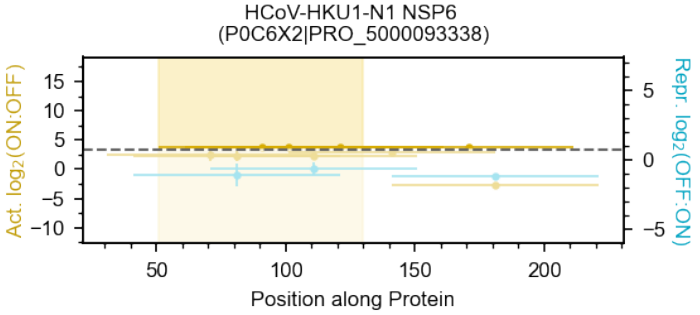
Max tile of activation domain from residues 51 to 130 (estimated 18.4% to 22.4% of cells activated):
FVSFMMLLVKHKHFYLTMYIIPVLCTLFYVNYLVVYKEGFRGFTYVWLSYFVPAVNFTYVYEVFYGCILCVFAIFITMHS

---

**Other Tiling Screen Data from Ludwig, C.H. et al. 2023**

## HCoV-HKU1-N1 NSP6 (P0C6X2|PRO_5000093338)

Gene: NSP6 ; Protein Family: NSP6



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Extended activation domain from residues 51 to 140:
FVSFMMLLVKHKHFYLTMYIIPVLCTLFYVNYLVVYKEGFRGFTYVWLSYFVPAVNFTYVYEVFYGCILCVFAIFITMHSINHDIFSLMF

Max tile of activation domain from residues 51 to 130 (estimated 18.4% to 22.4% of cells activated):
FVSFMMLLVKHKHFYLTMYIIPVLCTLFYVNYLVVYKEGFRGFTYVWLSYFVPAVNFTYVYEVFYGCILCVFAIFITMHS

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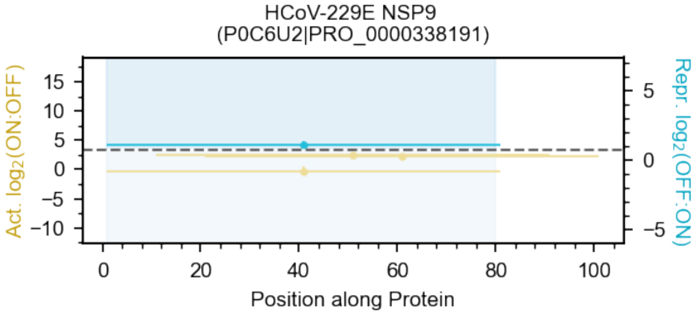
## HCoV-229E NSP9 (P0C6U2|PRO_0000338191)

Gene: NSP9 ; Protein Family: NSP9



---

Extended repression domain from residues 1 to 80:
NNEIMPGKMKVKATKGEGDGGITSEGNALYNNEGGRAFMYAYVTTKPGMKYVKWEHDSGVVTVELEPPCRFVIDTPTGPQ

Max tile of repression domain from residues 1 to 80 (estimated 19.6% to 24.7% of cells repressed):
NNEIMPGKMKVKATKGEGDGGITSEGNALYNNEGGRAFMYAYVTTKPGMKYVKWEHDSGVVTVELEPPCRFVIDTPTGPQ

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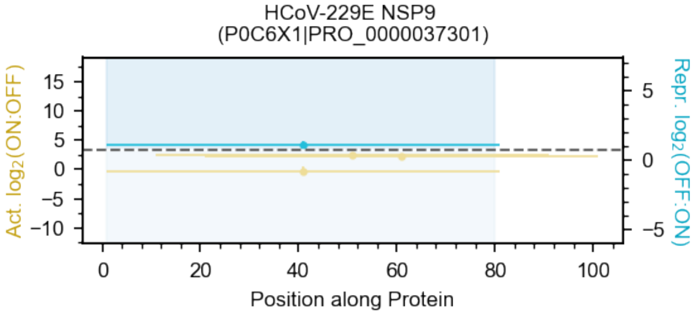
## HCoV-229E NSP9 (P0C6X1|PRO_0000037301)

Gene: NSP9 ; Protein Family: NSP9



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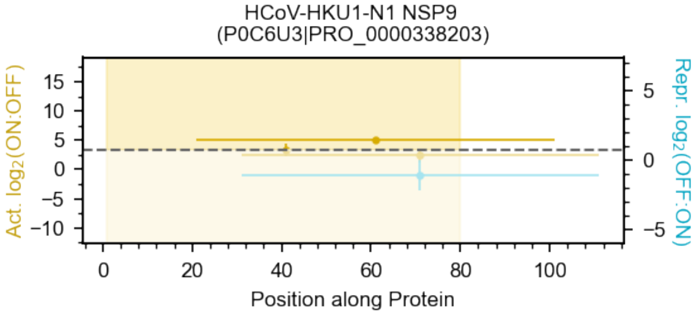
Extended repression domain from residues 1 to 80:
NNEIMPGKMKVKATKGEGDGGITSEGNALYNNEGGRAFMYAYVTTKPGMKYVKWEHDSGVVTVELEPPCRFVIDTPTGPQ

Max tile of repression domain from residues 1 to 80 (estimated 19.6% to 24.7% of cells repressed):
NNEIMPGKMKVKATKGEGDGGITSEGNALYNNEGGRAFMYAYVTTKPGMKYVKWEHDSGVVTVELEPPCRFVIDTPTGPQ

---

## HCoV-HKU1-N1 NSP9 (P0C6U3|PRO_0000338203)

Gene: NSP9 ; Protein Family: NSP9



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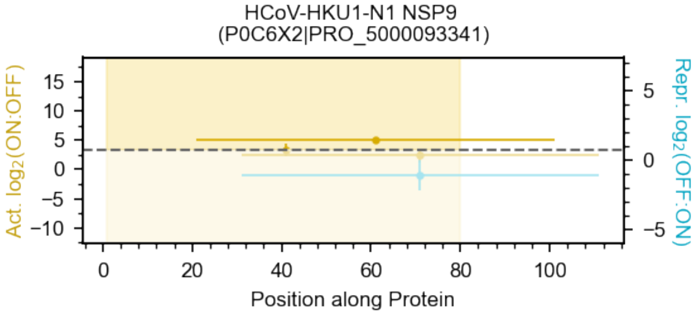
Extended activation domain from residues 1 to 80:
NNELMPHKLKIQVVNSGSDMNCNIPTQCYYNNGSSGRIVYAVLSDVDGLKYTKIMKDDGNCVVLELDPPCKFSIQDVKGL

Max tile of activation domain from residues 1 to 80 (estimated 7.3% to 29.1% of cells activated):
NNELMPHKLKIQVVNSGSDMNCNIPTQCYYNNGSSGRIVYAVLSDVDGLKYTKIMKDDGNCVVLELDPPCKFSIQDVKGL

---

# HCoV-HKU1-N1 NSP9 (P0C6X2|PRO_5000093341)

Gene: NSP9 ; Protein Family: NSP9



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Extended activation domain from residues 1 to 80:
NNELMPHKLKIQVVNSGSDMNCNIPTQCYYNNGSSGRIVYAVLSDVDGLKYTKIMKDDGNCVVLELDPPCKFSIQDVKGL

Max tile of activation domain from residues 1 to 80 (estimated 7.3% to 29.1% of cells activated):
NNELMPHKLKIQVVNSGSDMNCNIPTQCYYNNGSSGRIVYAVLSDVDGLKYTKIMKDDGNCVVLELDPPCKFSIQDVKGL

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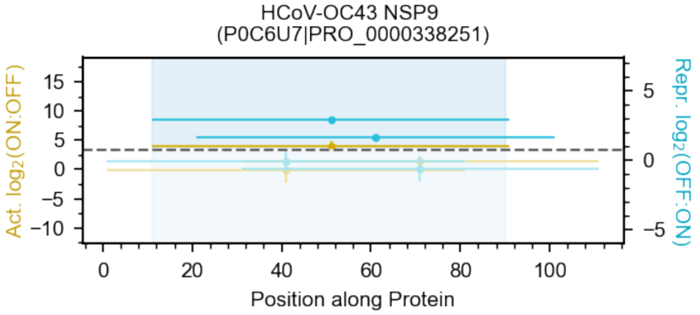
## HCoV-OC43 NSP9 (P0C6U7|PRO_0000338251)

Gene: NSP9 ; Protein Family: NSP9



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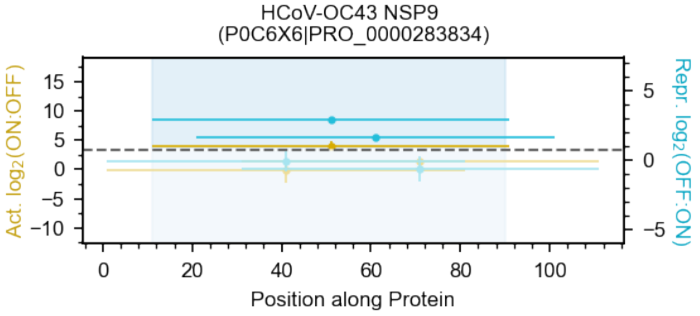
Extended repression domain from residues 11 to 100:
IQVVNSGPDQTCNTPTQCYYNNSNNGKIVYAILSDVDGLKYTKILKDDGNFVVLELDPPCKFTVQDAKGLKIKYLYFVKGCNTLARGWVV

Max tile of repression domain from residues 11 to 90 (estimated 62.3% to 70.7% of cells repressed):
IQVVNSGPDQTCNTPTQCYYNNSNNGKIVYAILSDVDGLKYTKILKDDGNFVVLELDPPCKFTVQDAKGLKIKYLYFVKG

---

# HCoV-OC43 NSP9 (P0C6X6|PRO_0000283834)

Gene: NSP9 ; Protein Family: NSP9



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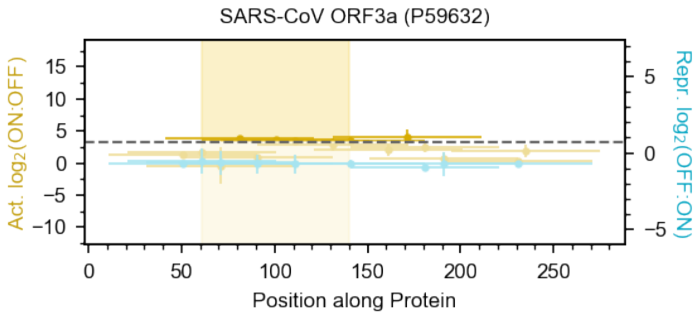
Extended repression domain from residues 11 to 100:
IQVVNSGPDQTCNTPTQCYYNNSNNGKIVYAILSDVDGLKYTKILKDDGNFVVLELDPPCKFTVQDAKGLKIKYLYFVKGCNTLARGWVV

Max tile of repression domain from residues 11 to 90 (estimated 62.3% to 70.7% of cells repressed):
IQVVNSGPDQTCNTPTQCYYNNSNNGKIVYAILSDVDGLKYTKILKDDGNFVVLELDPPCKFTVQDAKGLKIKYLYFVKG

---

## SARS-CoV ORF3a (P59632)

Gene: ORF3a ; Protein Family: ORF3a



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Extended activation domain from residues 61 to 150:
KIIALNKRWQLALYKGFQFICNLLLLFVTIYSHLLLVAAGMEAQFLYLYALIYFLQCINACRIIMRCWLCWKCKSKNPLLYDANYFVCWH

Max tile of activation domain from residues 61 to 140 (estimated 11.9% to 23.4% of cells activated):
KIIALNKRWQLALYKGFQFICNLLLLFVTIYSHLLLVAAGMEAQFLYLYALIYFLQCINACRIIMRCWLCWKCKSKNPLL

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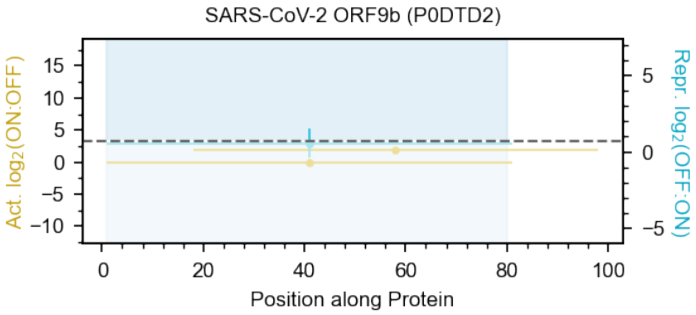
## SARS-CoV-2 ORF9b (P0DTD2)

Gene: ORF9b ; Protein Family: ORF9b



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Extended repression domain from residues 1 to 80:
MDPKISEMHPALRLVDPQIQLAVTRMENAVGRDQNNVGPKVYPIILRLGSPLSLNMARKTLNSLEDKAFQLTPIAVQMTK

Max tile of repression domain from residues 1 to 80 (estimated 14.5% to 27.1% of cells repressed):
MDPKISEMHPALRLVDPQIQLAVTRMENAVGRDQNNVGPKVYPIILRLGSPLSLNMARKTLNSLEDKAFQLTPIAVQMTK

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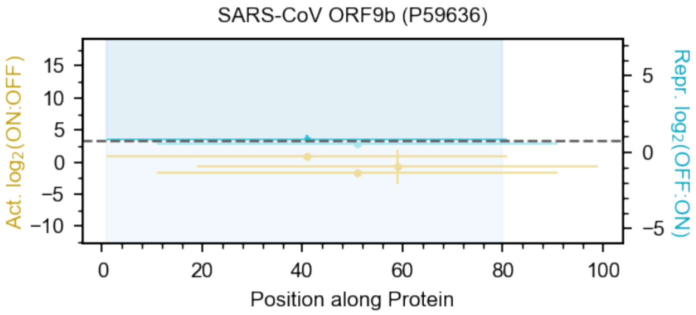
## SARS-CoV ORF9b (P59636)

Gene: ORF9b ; Protein Family: ORF9b



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Extended repression domain from residues 1 to 90:
MDPNQTNVVPPALHLVDPQIQLTITRMEDAMGQGQNSADPKVYPIILRLGSQLSLSMARRNLDSLEARAFQSTPIVVQMTKLATTEELPD

Max tile of repression domain from residues 1 to 80 (estimated 17.3% to 21.5% of cells repressed):
MDPNQTNVVPPALHLVDPQIQLTITRMEDAMGQGQNSADPKVYPIILRLGSQLSLSMARRNLDSLEARAFQSTPIVVQMT

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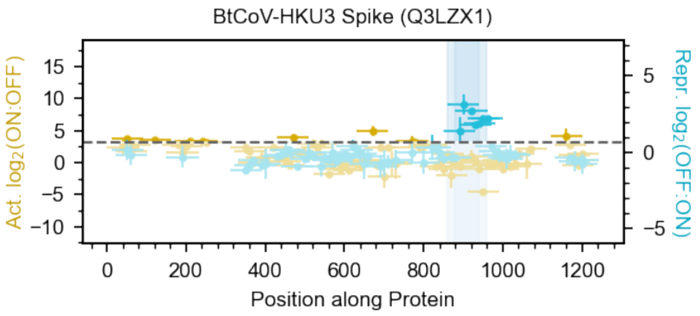
## BtCoV-HKU3 Spike (Q3LZX1)

Gene: Spike ; Protein Family: Spike



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Extended repression domain from residues 851 to 940:
ATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQESLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFG

Max tile of repression domain from residues 861 to 940 (estimated 53.9% to 88.6% of cells repressed):
AALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQESLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFG

---

Extended repression domain from residues 881 to 1000:
TQNVLYENQKLIANQFNSAIGKIQESLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSE

Max tile of repression domain from residues 881 to 960 (estimated 59.8% to 62.9% of cells repressed):
TQNVLYENQKLIANQFNSAIGKIQESLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEV

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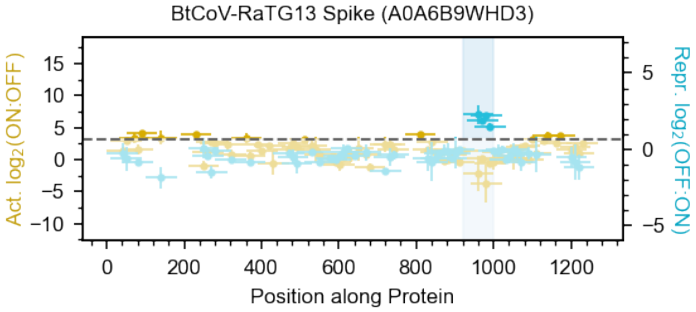
## BtCoV-RaTG13 Spike (A0A6B9WHD3)

Gene: Spike ; Protein Family: Spike



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Extended repression domain from residues 921 to 1030:
NQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVL

Max tile of repression domain from residues 921 to 1000 (estimated 30.2% to 68.0% of cells repressed):
NQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSL

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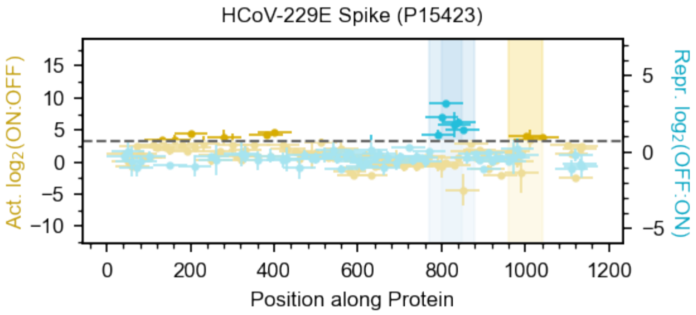
## HCoV-229E Spike (P15423)

Gene: Spike ; Protein Family: Spike



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Extended activation domain from residues 961 to 1050:
EAWSGLCVDGTNGYVLRQPNLALYKEGNYYRITSRIMFEPRIPTMADFVQIENCNVTFVNISRSELQTIVPEYIDVNKTLQELSYKLPNY

Max tile of activation domain from residues 961 to 1040 (estimated 23.1% to 24.6% of cells activated):
EAWSGLCVDGTNGYVLRQPNLALYKEGNYYRITSRIMFEPRIPTMADFVQIENCNVTFVNISRSELQTIVPEYIDVNKTL

---

Extended repression domain from residues 751 to 850:
SLIGGIALGGLTSAVSIPFSLAIQARLNYVALQTDVLQENQKILAASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNSLNHLTSQ

Max tile of repression domain from residues 771 to 850 (estimated 75.5% to 75.6% of cells repressed):
LAIQARLNYVALQTDVLQENQKILAASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNSLNHLTSQ

---

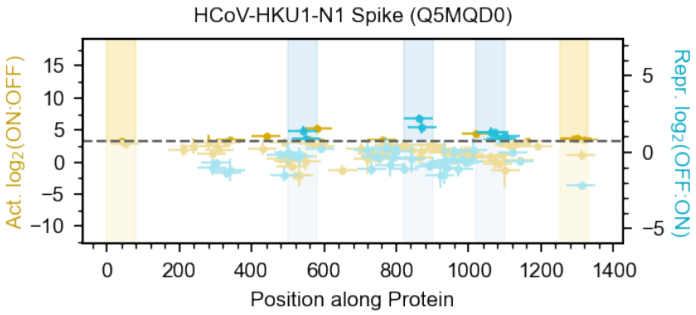
Extended repression domain from residues 791 to 890:
QKILAASFNKAMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNSLNHLTSQLRQNFQAISSSIQAIYDRLDTIQADQQVDRLITGRLAALN

Max tile of repression domain from residues 801 to 880 (estimated 29.7% to 44.4% of cells repressed):
AMTNIVDAFTGVNDAITQTSQALQTVATALNKIQDVVNQQGNSLNHLTSQLRQNFQAISSSIQAIYDRLDTIQADQQVDR

---

## HCoV-HKU1-N1 Spike (Q5MQD0)

Gene: Spike ; Protein Family: Spike



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Extended activation domain from residues 1251 to 1340:
NLTLNLHTINATFLDLYYEMNLIQESIKSLNNSYINLKDIGTYEMYVKWPWYVWLLISFSFIIFLVLLFFICCCTGCGSACFSKCHNCCD

Max tile of activation domain from residues 1251 to 1330 (estimated 17.2% to 19.5% of cells activated):
NLTLNLHTINATFLDLYYEMNLIQESIKSLNNSYINLKDIGTYEMYVKWPWYVWLLISFSFIIFLVLLFFICCCTGCGSA

---

Extended activation domain from residues 1 to 80:
MLLIIFILPTTLAVIGDFNCTNFAINDLNTTVPRISEYVVDVSYGLGTYYILDRVYLNTTILFTGYFPKSGANFRDLSLK

Max tile of activation domain from residues 1 to 80 (estimated 13.4% to 14.3% of cells activated):
MLLIIFILPTTLAVIGDFNCTNFAINDLNTTVPRISEYVVDVSYGLGTYYILDRVYLNTTILFTGYFPKSGANFRDLSLK

---

Extended repression domain from residues 821 to 910:
FVCSNYAACHDLLSEYGTFCDNINSILDEVNGLLDTTQLHVADTLMQGVTLSSNLNTNLHFDVDNINFKSLVGCLGPHCGSSSRSFFEDL

Max tile of repression domain from residues 821 to 900 (estimated 39.0% to 50.5% of cells repressed):
FVCSNYAACHDLLSEYGTFCDNINSILDEVNGLLDTTQLHVADTLMQGVTLSSNLNTNLHFDVDNINFKSLVGCLGPHCG

---

Extended repression domain from residues 501 to 590:
YRSCESTTVLDHTDWCRCSCLPDPITAYDPRSCSQKKSLVGVGEHCAGFGVDEEKCGVLDGSYNVSCLCSTDAFLGWSYDTCVSNNRCNI

Max tile of repression domain from residues 501 to 580 (estimated 21.6% to 30.5% of cells repressed):
YRSCESTTVLDHTDWCRCSCLPDPITAYDPRSCSQKKSLVGVGEHCAGFGVDEEKCGVLDGSYNVSCLCSTDAFLGWSYD

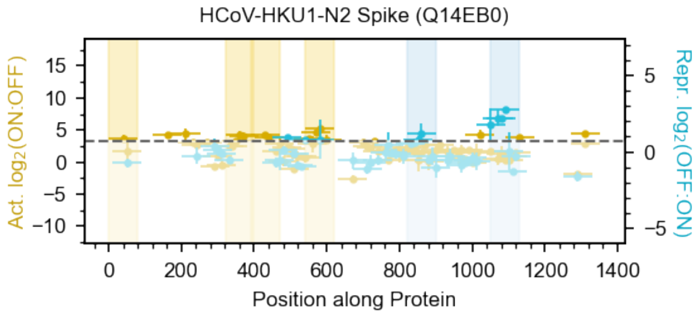
---

Extended repression domain from residues 1021 to 1140:
NGFSATNSALAKIQSVVNSNAQALNSLLQQLFNKFGAISSSLQEILSRLDALEAQVQIDRLINGRLTALNAYVSQQLSDISLVKFGAALAMEKVNECVKSQSPRINFCGNGNHILSLVQN

Max tile of repression domain from residues 1021 to 1100 (estimated 20.8% to 28.8% of cells repressed):
NGFSATNSALAKIQSVVNSNAQALNSLLQQLFNKFGAISSSLQEILSRLDALEAQVQIDRLINGRLTALNAYVSQQLSDI

## HCoV-HKU1-N2 Spike (Q14EB0)

Gene: Spike ; Protein Family: Spike



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Extended activation domain from residues 531 to 620:
NTCPQKKVVVGIGEHCPGLGINEEKCGTQLNHSSCSCSPDAFLGWSFDSCISNNRCNIFSNFIFNGINSGTTCSNDLLYSNTEVSTGVCV

Max tile of activation domain from residues 541 to 620 (estimated 33.4% to 51.0% of cells activated):
GIGEHCPGLGINEEKCGTQLNHSSCSCSPDAFLGWSFDSCISNNRCNIFSNFIFNGINSGTTCSNDLLYSNTEVSTGVCV

---

Extended activation domain from residues 391 to 480:
FAIPNRRRDDLQLGSSGFLQSSNYKIDISSSSCQLYYSLPLVNVTINNFNPSSWNRRYGFGSFNVSSYDVVYSDHCFSVNSDFCPCADPS

Max tile of activation domain from residues 391 to 470 (estimated 20.9% to 31.9% of cells activated):
FAIPNRRRDDLQLGSSGFLQSSNYKIDISSSSCQLYYSLPLVNVTINNFNPSSWNRRYGFGSFNVSSYDVVYSDHCFSVN

---

Extended activation domain from residues 311 to 410:
VKPVATVYRRIPNLPDCDIDNWLNNVSVPSPLNWERRIFSNCNFNLSTLLRLVHVDSFSCNNLDKSKIFGSCFNSITVDKFAIPNRRRDDLQLGSSGFLQ

Max tile of activation domain from residues 321 to 400 (estimated 15.5% to 35.9% of cells activated):
IPNLPDCDIDNWLNNVSVPSPLNWERRIFSNCNFNLSTLLRLVHVDSFSCNNLDKSKIFGSCFNSITVDKFAIPNRRRDD

---

Extended activation domain from residues 1 to 80:
MFLIIFILPTTLAVIGDFNCTNSFINDYNKTIPRISEDVVDVSLGLGTYYVLNRVYLNTTLLFTGYFPKSGANFRDLALK

Max tile of activation domain from residues 1 to 80 (estimated 12.7% to 26.9% of cells activated):
MFLIIFILPTTLAVIGDFNCTNSFINDYNKTIPRISEDVVDVSLGLGTYYVLNRVYLNTTLLFTGYFPKSGANFRDLALK

---

Extended repression domain from residues 1031 to 1130:
SVVNANAQALNSLLQQLFNKFGAISSSLQEILSRLDNLEAQVQIDRLINGRLTALNAYVSQQLSDITLIKAGASRAIEKVNECVKSQSPRINFCGNGNHI

Max tile of repression domain from residues 1051 to 1130 (estimated 60.3% to 66.4% of cells repressed):
FGAISSSLQEILSRLDNLEAQVQIDRLINGRLTALNAYVSQQLSDITLIKAGASRAIEKVNECVKSQSPRINFCGNGNHI

---

Extended repression domain from residues 791 to 900:
PTNFTIAGHEEFIQTSSPKVTIDCSAFVCSNYAACHDLLSEYGTFCDNINSILNEVNDLLDITQLQVANALMQGVTLSSNLNTNLHSDVDNIDFKSLLGCLGSQCGSSSR

Max tile of repression domain from residues 821 to 900 (estimated 16.8% to 34.8% of cells repressed):
NYAACHDLLSEYGTFCDNINSILNEVNDLLDITQLQVANALMQGVTLSSNLNTNLHSDVDNIDFKSLLGCLGSQCGSSSR

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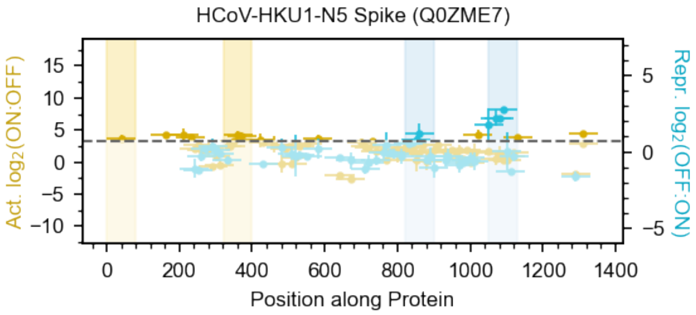
## HCoV-HKU1-N5 Spike (Q0ZME7)

Gene: Spike ; Protein Family: Spike



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Extended activation domain from residues 311 to 410:
VKPVATVYRRIPNLPDCDIDNWLNNVSVPSPLNWERRIFSNCNFNLSTLLRLVHVDSFSCNNLDKSKIFGSCFNSITVDKFAIPNRRRDDLQLGSSGFLQ

Max tile of activation domain from residues 321 to 400 (estimated 15.5% to 35.9% of cells activated):
IPNLPDCDIDNWLNNVSVPSPLNWERRIFSNCNFNLSTLLRLVHVDSFSCNNLDKSKIFGSCFNSITVDKFAIPNRRRDD

---

Extended activation domain from residues 1 to 80:
MFLIIFILPTTLAVIGDFNCTNSFINDYNKTIPRISEDVVDVSLGLGTYYVLNRVYLNTTLLFTGYFPKSGANFRDLALK

Max tile of activation domain from residues 1 to 80 (estimated 12.7% to 26.9% of cells activated):
MFLIIFILPTTLAVIGDFNCTNSFINDYNKTIPRISEDVVDVSLGLGTYYVLNRVYLNTTLLFTGYFPKSGANFRDLALK

---

Extended repression domain from residues 1031 to 1130:
SVVNANAQALNSLLQQLFNKFGAISSSLQEILSRLDNLEAQVQIDRLINGRLTALNAYVSQQLSDITLIKAGASRAIEKVNECVKSQSPRINFCGNGNHI

Max tile of repression domain from residues 1051 to 1130 (estimated 60.3% to 66.4% of cells repressed):
FGAISSSLQEILSRLDNLEAQVQIDRLINGRLTALNAYVSQQLSDITLIKAGASRAIEKVNECVKSQSPRINFCGNGNHI

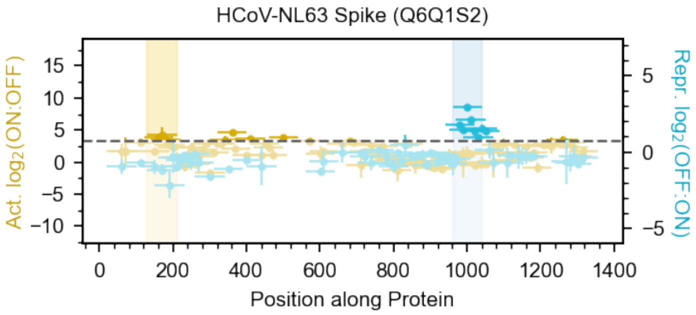
---

Extended repression domain from residues 791 to 900:
PTNFTIAGHEEFIQTSSPKVTIDCSAFVCSNYAACHDLLSEYGTFCDNINSILNEVNDLLDITQLQVANALMQGVTLSSNLNTNLHSDVDNIDFKSLLGCLGSQCGSSSR

Max tile of repression domain from residues 821 to 900 (estimated 16.8% to 34.8% of cells repressed):
NYAACHDLLSEYGTFCDNINSILNEVNDLLDITQLQVANALMQGVTLSSNLNTNLHSDVDNIDFKSLLGCLGSQCGSSSR

## HCoV-NL63 Spike (Q6Q1S2)

Gene: Spike ; Protein Family: Spike



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Extended activation domain from residues 121 to 220:
SSSFDCIVNLLFTEQLGAPLGITISGETVRLHLYNVTRTFYVPAAYKLTKLSVKCYFNYSCVFSVVNATVTVNVTTHNGRVVNYTVCDDCNGYTDNIFSV

Max tile of activation domain from residues 131 to 210 (estimated 12.1% to 44.1% of cells activated):
LFTEQLGAPLGITISGETVRLHLYNVTRTFYVPAAYKLTKLSVKCYFNYSCVFSVVNATVTVNVTTHNGRVVNYTVCDDC

---

Extended repression domain from residues 941 to 1090:
GLTSAAAIPFSLALQARLNYVALQTDVLQENQKILAASFNKAINNIVASFSSVNDAITQTAEAIHTVTIALNKIQDVVNQQGSALNHLTSQLRHNFQAISNSIQAIYDRLDSIQADQQVDRLITGRLAALNAFVSQVLNKYTEVRGSRRL

Max tile of repression domain from residues 961 to 1040 (estimated 66.9% to 71.1% of cells repressed):
VALQTDVLQENQKILAASFNKAINNIVASFSSVNDAITQTAEAIHTVTIALNKIQDVVNQQGSALNHLTSQLRHNFQAIS

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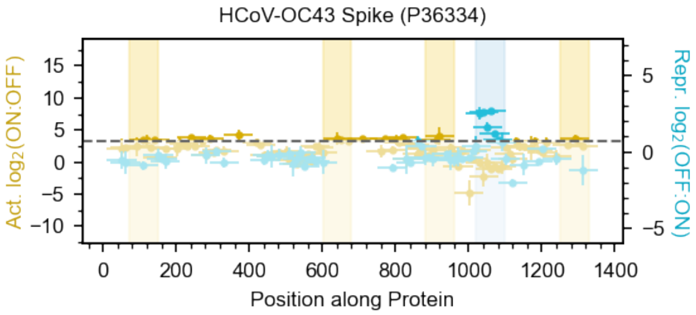
## HCoV-OC43 Spike (P36334)

Gene: Spike ; Protein Family: Spike



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Extended activation domain from residues 871 to 960:
TKLKDGVNFNVDDINFSPVLGCLGSECSKASSRSAIEDLLFDKVKLSDVGFVEAYNNCTGGAEIRDLICVQSYKGIKVLPPLLSENQISG

Max tile of activation domain from residues 881 to 960 (estimated 9.1% to 47.4% of cells activated):
VDDINFSPVLGCLGSECSKASSRSAIEDLLFDKVKLSDVGFVEAYNNCTGGAEIRDLICVQSYKGIKVLPPLLSENQISG

---

Extended activation domain from residues 601 to 690:
SGLTCSTDLQKANTDIILGVCVNYDLYGILGQGIFVEVNATYYNSWQNLLYDSNGNLYGFRDYIINRTFMIRSCYSGRVSAAFHANSSEP

Max tile of activation domain from residues 601 to 680 (estimated 9.7% to 32.1% of cells activated):
SGLTCSTDLQKANTDIILGVCVNYDLYGILGQGIFVEVNATYYNSWQNLLYDSNGNLYGFRDYIINRTFMIRSCYSGRVS

---

Extended activation domain from residues 1251 to 1340:
LSLDYINVTFLDLQVEMNRLQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLICLAGVAMLVLLFFICCCTGCGTSCFKKCGGCCDDYT

Max tile of activation domain from residues 1251 to 1330 (estimated 11.4% to 26.2% of cells activated):
LSLDYINVTFLDLQVEMNRLQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLICLAGVAMLVLLFFICCCTGCGTSCFK

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Extended activation domain from residues 71 to 160:
SGSTYRNMALKGSVLLSRLWFKPPFLSDFINGIFAKVKNTKVIKDRVMYSEFPAITIGSTFVNTSYSVVVQPRTINSTQDGDNKLQGLLE

Max tile of activation domain from residues 71 to 150 (estimated 14.2% to 15.8% of cells activated):
SGSTYRNMALKGSVLLSRLWFKPPFLSDFINGIFAKVKNTKVIKDRVMYSEFPAITIGSTFVNTSYSVVVQPRTINSTQD

---

Extended repression domain from residues 991 to 1130:
NGLGVTMDVLSQNQKLIANAFNNALYAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISASLQEILSRLDALEAEAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSQSSRINFCGNG

Max tile of repression domain from residues 1021 to 1100 (estimated 54.9% to 65.6% of cells repressed):
GFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISASLQEILSRLDALEAEAQIDRLINGRLTALNAYVSQQLSDST

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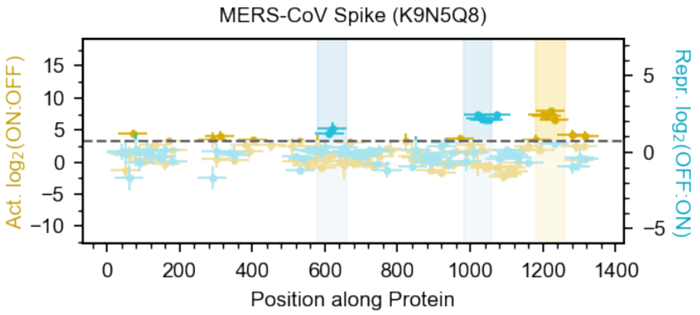
## MERS-CoV Spike (K9N5Q8)

Gene: Spike ; Protein Family: Spike



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Extended activation domain from residues 1161 to 1270:
PTNCIAPVNGYFIKTNNTRIVDEWSYTGSSFYAPEPITSLNTKYVAPQVTYQNISTNLPPPLLGNSTGIDFQDELDEFFKNVSTSIPNFGSLTQINTTLLDLTYEMLSLQ

Max tile of activation domain from residues 1181 to 1260 (estimated 81.3% to 85.0% of cells activated):
VDEWSYTGSSFYAPEPITSLNTKYVAPQVTYQNISTNLPPPLLGNSTGIDFQDELDEFFKNVSTSIPNFGSLTQINTTLL

---

Extended repression domain from residues 981 to 1090:
NGVGITQQVLSENQKLIANKFNQALGAMQTGFTTTNEAFHKVQDAVNNNAQALSKLASELSNTFGAISASIGDIIQRLDVLEQDAQIDRLINGRLTTLNAFVAQQLVRSE

Max tile of repression domain from residues 981 to 1060 (estimated 45.7% to 58.5% of cells repressed):
NGVGITQQVLSENQKLIANKFNQALGAMQTGFTTTNEAFHKVQDAVNNNAQALSKLASELSNTFGAISASIGDIIQRLDV

---

Extended repression domain from residues 571 to 660:
FGITVQYGTDTNSVCPKLEFANDTKIASQLGNCVEYSLYGVSGRGVFQNCTAVGVRQQRFVYDAYQNLVGYYSDDGNYYCLRACVSVPVS

Max tile of repression domain from residues 581 to 660 (estimated 22.1% to 37.2% of cells repressed):
TNSVCPKLEFANDTKIASQLGNCVEYSLYGVSGRGVFQNCTAVGVRQQRFVYDAYQNLVGYYSDDGNYYCLRACVSVPVS

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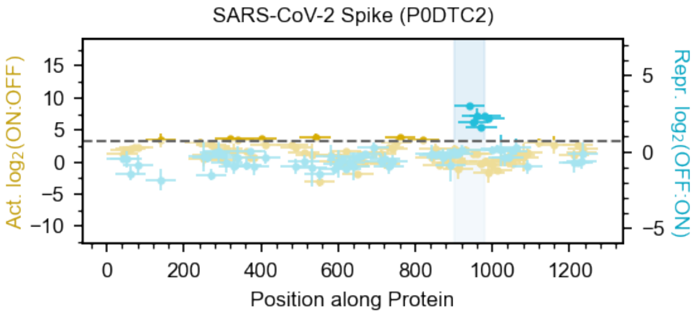
## SARS-CoV-2 Spike (P0DTC2)

Gene: Spike ; Protein Family: Spike



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Extended repression domain from residues 901 to 1030:
QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMS

Max tile of repression domain from residues 901 to 980 (estimated 67.7% to 72.2% of cells repressed):
QMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDI

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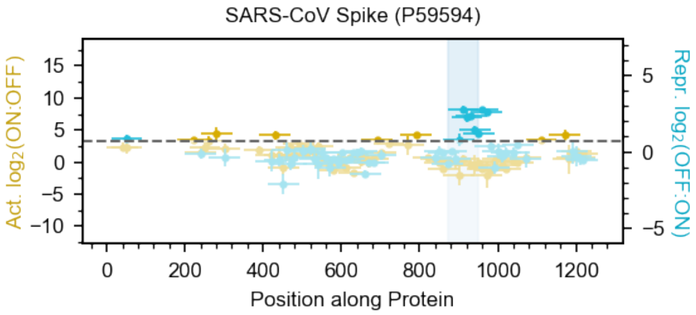
**Other Tiling Screen Data from Ludwig, C.H. et al. 2023**

## SARS-CoV Spike (P59594)

Gene: Spike ; Protein Family: Spike



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Extended repression domain from residues 861 to 1010:
SGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK

Max tile of repression domain from residues 871 to 950 (estimated 55.9% to 71.0% of cells repressed):
GAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS

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