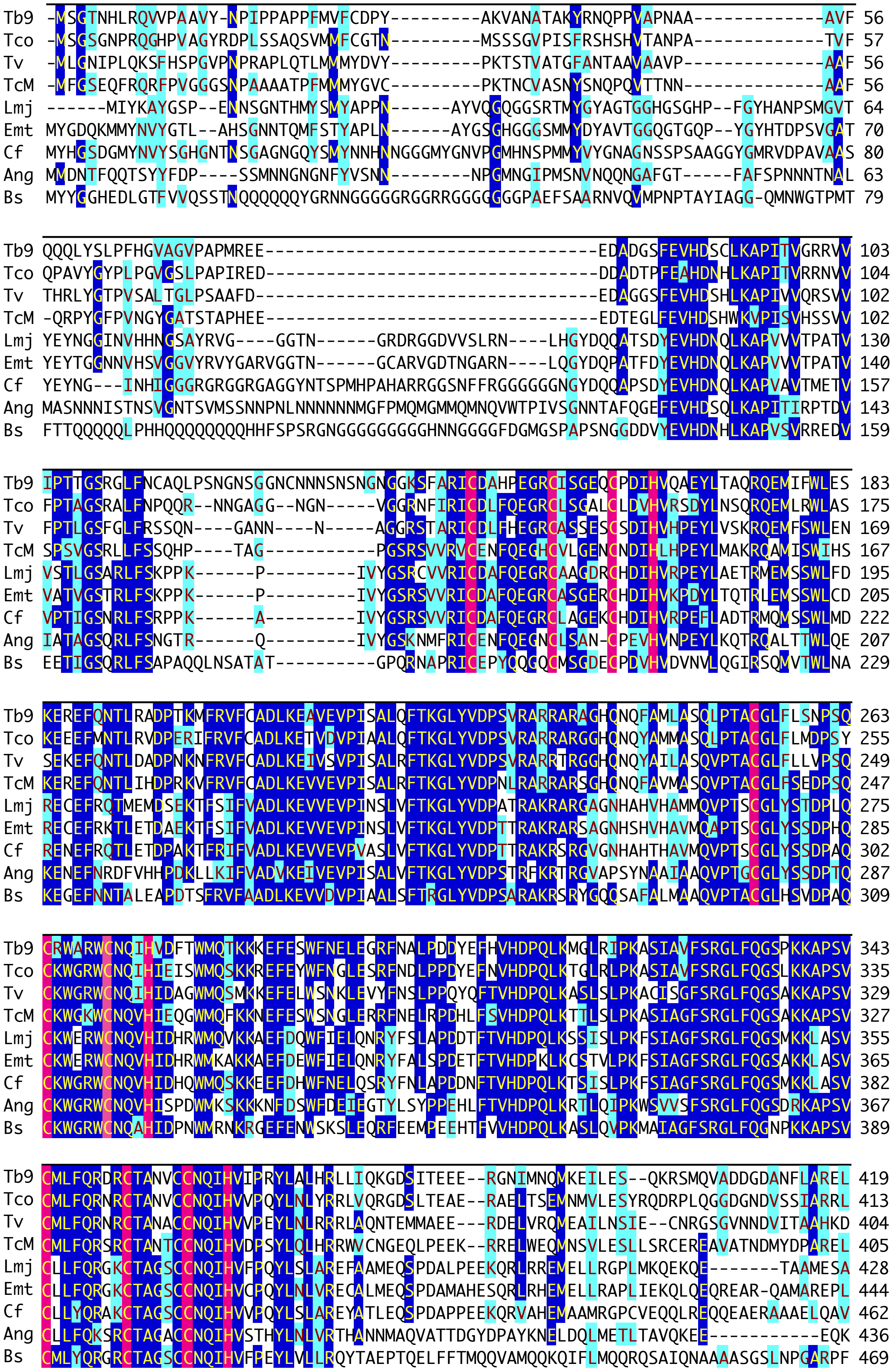
A. Alignment



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Tb9 -MSGTNHLRQVVPAAVY-NPIPPAPPFMVFCDPY---------AKVANATAKYRNQPPVAPNAA-------------AVF 56
Tco -MSGSGNPRQGHPVAGYRDPLSSAQSVMMFCGTN---------MSSSGVPISFRSHSHVTANPA-------------TVF 57
Tv  -MLGNIPLQKSFHSPGVPNPRAPLQTLMMMYDVY---------PKTSTVATGFANTAAVAAVP--------------AAF 56
TcM -MFGSEQFRQRFPVGGGSNPAAAATPFMMMYGVC---------PKTNCVASNYSNQPQVTTNN--------------AAF 56
Lmj ------MIYKAYGSP--ENNSGNTHMYSMYAPPN------AYVQGQGGSRTMYGYAGTGGHGSGHP--FGYHANPSMGVT 64
Emt MYGDQKMMYNVYGTL--AHSGNNTQMFSTYAPLN------AYGSGHGGGSMMYDYAVTGGQGTGQP--YGYHTDPSVGAT 70
Cf  MYHGSDGMYNVYSGHGNTNSGAGNGQYSMYNNHNNGGGMYGNVPGMHNSPMMYVYGNAGNSSPSAAGGYGMRVDPAVAAS 80
Ang MMDNTFQQTSYYFDP----SSMNNGNGNFYVSNN--------NPGMNGIPMSNVNQQNGAFGT-----FAFSPNNNTNAL 63
Bs  MYYGGHEDLGTFVVQSSTNQQQQQQYGRNNGGGGGRGGRRGGGGGGGPAEFSAARNVQVMPNPTAYIAGG-QMNWGTPMT 79

Tb9 QQQLYSLPFHGVAGVPAPMREE---------------------------------EDADGSFEVHDSCLKAPITVGRRVV 103
Tco QPAVYGYPLPGVGSLPAPIRED---------------------------------DDADTPFEAHDNHLKAPITVRRNVV 104
Tv  THRLYGTPVSALTGLPSAAFD----------------------------------EDAGGSFEVHDSHLKAPIVVQRSVV 102
TcM -QRPYGFPVNGYGATSTAPHEE---------------------------------EDTEGLFEVHDSHWKVPISVHSSVV 102
Lmj YEYNGGINVHHNGSAYRVG----GGTN------GRDRGGDVVSLRN----LHGYDQQATSDYEVHDNQLKAPVVVTPATV 130
Emt YEYTGGNNVHSVGGVYRVYGARVGGTN------GCARVGDTNGARN----LQGYDQPATFDYEVHDNQLKAPVVVTPATV 140
Cf  YEYNG---INHIGGGRGRGGRGAGGYNTSPMHPAHARRGGSNFFRGGGGGGNGYDQQAPSDYEVHDNQLKAPVAVTMETV 157
Ang MASNNNISTNSVGNTSVMSSNNPNLNNNNNNMGFPMQMGMMQMNQVWTPIVSGNNTAFQGEFEVHDSQLKAPITIRPTDV 143
Bs  FTTQQQQQLPHHQQQQQQQQHHFSPSRGNGGGGGGGGGHNNGGGGFDGMGSPAPSNGGDDVYEVHDNHLKAPVSVRREDV 159

Tb9 IPTTGSRGLFNCAQLPSNGNSGGNCNNNSNSNGNGGKSFARICDAHPEGRCISGEQCPDIHVQAEYLTAQRQEMIFWLES 183
Tco FPTAGSRALFNPQQR--NNGAGG--NGN-----VGGRNFIRICDLFQEGRCLSGALCLDVHVRSDYLNSQRQEMLRWLAS 175
Tv  FPTLGSFGLFRSSQN----GANN----N-----AGGRSTARICDLFHEGRCASSESCSDIHVHPEYLVSKRQEMFSWLEN 169
TcM SPSVGSRLLFSSQHP----TAG-----------PGSRSVVRVCENFQEGHCVLGENCNDIHLHPEYLMAKRQAMISWIHS 167
Lmj VSTLGSARLFSKPPK------P---------IVYGSRCVVRICDAFQEGRCAAGDRCHDIHVRPEYLAETRMEMSSWLFD 195
Emt VATVGSTRLFSKPPK------P---------IVYGSRSVVRICDAFQEGRCASGERCHDIHVKPDYLTQTRLEMSSWLCD 205
Cf  VPTIGSNRLFSRPPK------A---------IVYGSRSVVRICDAFQEGRCLAGEKCHDIHVRPEFLADTRMQMSSWLMD 222
Ang IATAGSQRLFSNGTR------Q---------IVYGSKNMFRICENFQEGNCLSAN-CPEVHVNPEYLKQTRQALTTWLQE 207
Bs  EETIGSQRLFSAPAQQLNSATAT----------GPQRNAPRICEPYQQGQCMSGDECPDVHVDVNVLQGIRSQMVTWLNA 229

Tb9 KEREFQNTLRADPTKMFRVFCADLKEAVEVPISALQFTKGLYVDPSVRARRARAGHQNQFAMLASQLPTACGLFLSNPSQ 263
Tco KEEEFMNTLRVDPERIFRVFCADLKETVDVPIAALQFTKGLYVDPSVRARRARGGHQNQYAMMASQLPTACGLFLMDPSY 255
Tv  SEKEFQNTLDADPNKNFRVFCADLKEIVSVPISALRFTKGLYVDPSVRARRTRGGHQNQYAILASQVPTACGLFLLVPSQ 249
TcM KEREFQNTLIHDPRKVFRVFCADLKEVVEVPISALRFTKGLYVDPNLRARRARSGHQNQFAVMASQVPTACGLFSEDPSQ 247
Lmj RECEFRQTMEMDSEKTFSIFVADLKEVVEVPINSLVFTKGLYVDPATRAKRARGAGNHAHVHAMMQVPTSCGLYSTDPLQ 275
Emt RECEFRKTLETDAEKTFSIFVADLKEVVEVPINSLVFTKGLYVDPTTRAKRARSAGNHSHVHAVMQAPTSCGLYSSDPHQ 285
Cf  RENEFRQTLETDPAKTFRIFVADLKEVVEVPVASLVFTKGLYVDPTTRAKRSRGVGNHAHTHAVMQVPTSCGLYSSDPAQ 302
Ang KENEFNRDFVHHPDKLLKIFVADVKEIVEVPISALVFTKGLYVDPSTRFKRTRGVAPSYNAAIAAQVPTGCGLYSSDPTQ 287
Bs  KEGEFNNTALEAPDTSFRVFAADLKEVVDVPIAALSFTRGLYVDPSARAKRSRYGQQSAFALMAAQVPTACGLHSVDPAQ 309

Tb9 CRWARWCNQIHVDFTWMQTKKKEFESWFNELEGRFNALPDDYEFHVHDPQLKMGLRIPKASIAVFSRGLFQGSPKKAPSV 343
Tco CKWGRWCNQIHIEISWMQSKKREFEYWFNGLESRFNDLPPDYEFNVHDPQLKTGLRLPKASIAVFSRGLFQGSLKKAPSV 335
Tv  CKWGRWCNQIHIDAGWMQSMKKEFELWSNKLEVYFNSLPPQYQFTVHDPQLKASLSLPKACISGFSRGLFQGSAKKAPSV 329
TcM CKWGKWCNQVHIEQGWMQFKKNEFESWSNGLERRFNELRPDHLFSVHDPQLKTTLSLPKASIAGFSRGLFQGSAKKAPSV 327
Lmj CKWERWCNQVHIDHRWMQVKKAEFDQWFIELQNRYFSLAPDDTFTVHDPQLKSSISLPKFSIAGFSRGLFQGSMKKLASV 355
Emt CKWERWCNQVHIDHRWMKAKKAEFDEWFIELQNRYFALSPDETFTVHDPKLKCSTVLPKFSIAGFSRGLFQGSAKKLASV 365
Cf  CKWGRWCNQVHIDHQWMQSKKEEFDHWFNELQSRYFNLAPDDNFTVHDPQLKTSISLPKFSIAGFSRGLFQGSMKKLASV 382
Ang CKWGRWCNQVHISPDWMKSKKKNFDSWFDEIEGTYLSYPPEHLFTVHDPQLKRTLQIPKWSVVSFSRGLFQGSDRKAPSV 367
Bs  CKWGRWCNQAHIDPNWMRNKRGEFENWSKSLEQRFEEMPEEHTFVVHDPQLKASLQVPKMAIAGFSRGLFQGNPKKAPSV 389

Tb9 CMLFQRDRCTANVCCNQIHVIPRYLALHRLLIQKGDSITEEE--RGNIMNQMKEILES--QKRSMQVADDGDANFLAREL 419
Tco CMLFQRNRCTANVCCNQIHVVPQYLNLYRRLVQRGDSLTEAE--RAELTSEMNMVLESYRQDRPLQGGDGNDVSSIARRL 413
Tv  CMLFQRNRCTANACCNQIHVVPEYLNLRRRLAQNTEMMAEE---RDELVRQMEAILNSIE--CNRGSGVNNDVITAAHKD 404
TcM CMLFQRSRCTANTCCNQIHVDPSYLQLHRRWVCNGEQLPEEK--RRELWEQMNSVLESLLSRCEREAVATNDMYDPAREL 405
Lmj CLLFQRGKCTAGSCCNQIHVFPQYLSLAREFAAMEQSPDALPEEKQRLRREMELLRGPLMKQEKQE-------TAAMESA 428
Emt CLLFQRGKCTAGSCCNQIHVCPQYLNLVRECALMEQSPDAMAHESQRLRHEMELLRAPLIEKQLQEQREAR-QAMAREPL 444
Cf  CLLYQRAKCTAGSCCNQIHVVPQYLSLAREYATLEQSPDAPPEEKQRVAHEMAAMRGPCVEQQLREQQEAERAAAELQAV 462
Ang CLLFQKSRCTAGACCNQIHVSTHYLNLVRTHANNMAQVATTDGYDPAYKNELDQLMETLTAVQKEE-----------EQK 436
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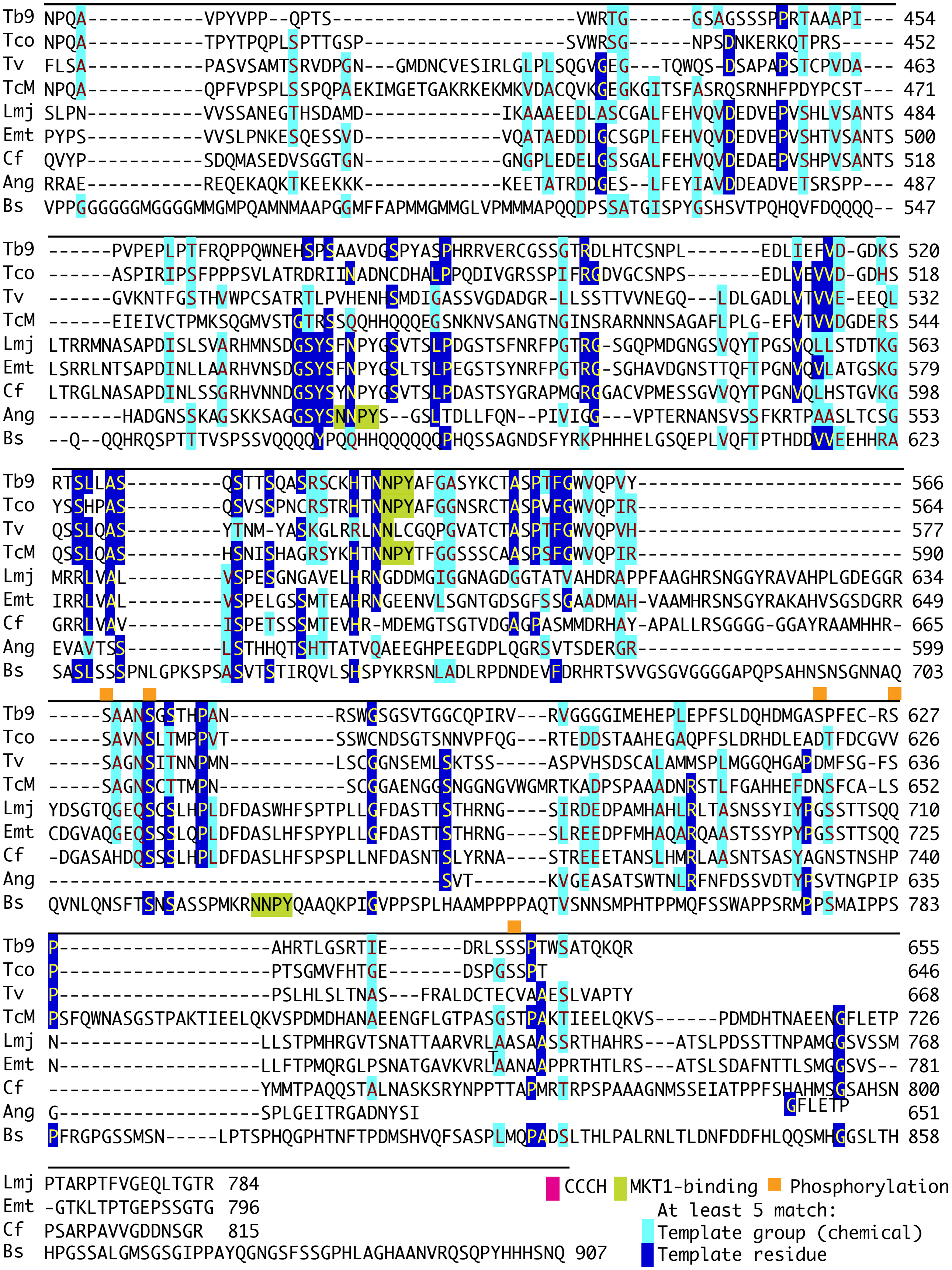

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Tco NPQA-----------TPYTPQPLSPTTGSP-------------------SVWRSG------NPSDNKERKQTPRS----- 452
Tv  FLSA-----------PASVSAMTSRVDPGN---GMDNCVESIRLGLPLSQGVGEG---TQWQS-DSAPAPSTCPVDA--- 463
TcM NPQA-----------QPFVPSPLSSPQPAEKIMGETGAKRKEKMKVDACQVKGEGKGITSFASRQSRNHFPDYPCST--- 471
Lmj SLPN-----------VVSSANEGTHSDAMD-------------IKAAAEEDLASCGALFEHVQVDEDVEPVSHLVSANTS 484
Emt PYPS-----------VVSLPNKESQESSVD-------------VQATAEDDLGCSGPLFEHVQVDEDVEPVSHTVSANTS 500
Cf  QVYP-----------SDQMASEDVSGGTGN-------------GNGPLEDELGSSGALFEHVQVDEDAEPVSHPVSANTS 518
Ang RRAE-----------REQEKAQKTKEEKKK-------------KEETATRDDGES--LFEYIAVDDEADVETSRSPP--- 487
Bs  VPPGGGGGGMGGGGMMGMPQAMNMAAPGGMFFAPMMGMMGLVPMMMAPQQDPSSATGISPYGSHSVTPQHQVFDQQQQ-- 547

Tb9 ------PVPEPLPTFRQPPQWNEHSPSAAVDGSPYASPHRRVERCGSSGTRDLHTCSNPL-------EDLIEFVD-GDKS 520
Tco ------ASPIRIPSFPPPSVLATRDRIINADNCDHALPPQDIVGRSSPIFRGDVGCSNPS-------EDLVEVVD-GDHS 518
Tv  ------GVKNTFGSTHVWPCSATRTLPVHENHSMDIGASSVGDADGR-LLSSTTVVNEGQ---LDLGADLVTVVE-EEQL 532
TcM ------EIEIVCTPMKSQGMVSTGTRSSQQHHQQQEGSNKNVSANGTNGINSRARNNNSAGAFLPLG-EFVTVVDGDERS 544
Lmj LTRRMNASAPDISLSVARHMNSDGSYSFNPYGSVTSLPDGSTSFNRFPGTRG-SGQPMDGNGSVQYTPGSVQLLSTDTKG 563
Emt LSRRLNTSAPDINLLAARHVNSDGSYSFNPYGSLTSLPEGSTSYNRFPGTRG-SGHAVDGNSTTQFTPGNVQVLATGSKG 579
Cf  LTRGLNASAPDINLSSGRHVNNDGSYSYNPYGSVTSLPDASTSYGRAPMGRGGACVPMESSGVVQYTPGNVQLHSTGVKG 598
Ang -------HADGNSSKAGSKKSAGGSYSNNPYS--GSLTDLLFQN--PIVIGG---VPTERNANSVSSFKRTPAASLTCSG 553
Bs  --Q--QQHRQSPTTTVSPSSVQQQQYPQQHHQQQQQQPHQSSAGNDSFYRKPHHHELGSQEPLVQFTPTHDDVVEEHHRA 623

Tb9 RTSLLAS---------QSTTSQASRSCKHTNNPYAFGASYKCTASPTFGWVQPVY------------------------- 566
Tco YSSHPAS---------QSVSSPNCRSTRHTNNPYAFGGNSRCTASPVFGWVQPIR------------------------- 564
Tv  QSSLQAS---------YTNM-YASKGLRRLNNLCGQPGVATCTASPTFGWVQPVH------------------------- 577
TcM QSSLQAS---------HSNISHAGRSYKHTNNPYTFGGSSSCAASPSFGWVQPIR------------------------- 590
Lmj MRRLVAL---------VSPESGNGAVELHRNGDDMGIGGNAGDGGTATVAHDRAPPFAAGHRSNGGYRAVAHPLGDEGGR 634
Emt IRRLVAL---------VSPELGSSMTEAHRNGEENVLSGNTGDSGFSSGAADMAH-VAAMHRSNSGYRAKAHVSGSDGRR 649
Cf  GRRLVAV---------ISPETSSSMTEVHR-MDEMGTSGTVDGAGPASMMDRHAY-APALLRSGGGG-GGAYRAAMHHR- 665
Ang EVAVTSS---------LSTHHQTSHTTATVQAEEGHPEEGDPLQGRSVTSDERGR------------------------- 599
Bs  SASLSSSPNLGPKSPSASVTSTIRQVLSHSPYKRSNLADLRPDNDEVFDRHRTSVVGSGVGGGGAPQPSAHNSNSGNNAQ 703

Tb9 -----SAANSGSTHPAN----------RSWGSGSVTGGCQPIRV---RVGGGGIMEHEPLEPFSLDQHDMGASPFEC-RS 627
Tco -----SAVNSLTMPPVT----------SSWCNDSGTSNNVPFQG---RTEDDSTAAHEGAQPFSLDRHDLEADTFDCGVV 626
Tv  -----SAGNSITNNPMN----------LSCGGNSEMLSKTSS-----ASPVHSDSCALAMMSPLMGGQHGAPDMFSG-FS 636
TcM -----SAGNSCTTMPN------------SCGGAENGGSNGGNGVWGMRTKADPSPAAADNRSTLFGAHHEFDNSFCA-LS 652
Lmj YDSGTQGEQSCSLHPLDFDASWHFSPTPLLGFDASTTSTHRNG----SIRDEDPAMHAHLRLTASNSSYIYPGSSTTSQQ 710
Emt CDGVAQGEQSSSLQPLDFDASLHFSPYPLLGFDASTTSTHRNG----SLREEDPFMHAQARQAASTSSYPYPGSSTTSQQ 725
Cf  -DGASAHDQSSSLHPLDFDASLHFSPSPLLNFDASNTSLYRNA----STREEETANSLHMRLAASNTSASYAGNSTNSHP 740
Ang -----------------------------------SVT-------KVGEASATSWTNLRFNFDSSVDTYPSVTNGPIP 635
Bs  QVNLQNSFTSNSASSPMKRNNPYQAAQKPIGVPPSPLHAAMPPPPAQTVSNNSMPHTPPMQFSSWAPPSRMPPSMAIPPS 783

Tb9 P--------------------AHRTLGSRTIE-------DRLSSSPTWSATQKQR                          655
Tco P--------------------PTSGMVFHTGE-------DSPGSSPT                                  646
Tv  P--------------------PSLHLSLTNAS---FRALDCTECVAAESLVAPTY                          668
TcM PSFQWNASGSTPAKTIEELQKVSPDMDHANAEENGFLGTPASGSTPAKTIEELQKVS------PDMDHTNAEENGFLETP 726
Lmj N-------------------LLSTPMHRGVTSNATTAARVRLAASAASSRTHAHRS---ATSLPDSSTTNPAMGGSVSSM 768
                                              T
Emt N-------------------LLFTPMQRGLPSNATGAVKVRLAANAAPPRTHTLRS---ATSLSDAFNTTLSMGGSVS-- 781
Cf  --------------------YMMTPAQQSTALNASKSRYNPPTTAPMRTRPSPAAAGNMSSEIATPPFSHAHMSGSAHSN 800
                                                                         GFLETP
Ang G-------------------SPLGEITRGADNYSI                                              651
Bs  PFRGPGSSMSN-----LPTSPHQGPHTNFTPDMSHVQFSASPLMQPADSLTHLPALRNLTLDNFDDFHLQQSMHGGSLTH 858

Lmj PTARPTFVGEQLTGTR  784
Emt -GTKLTPTGEPSSGTG  796
Cf  PSARPAVVGDDNSGR   815
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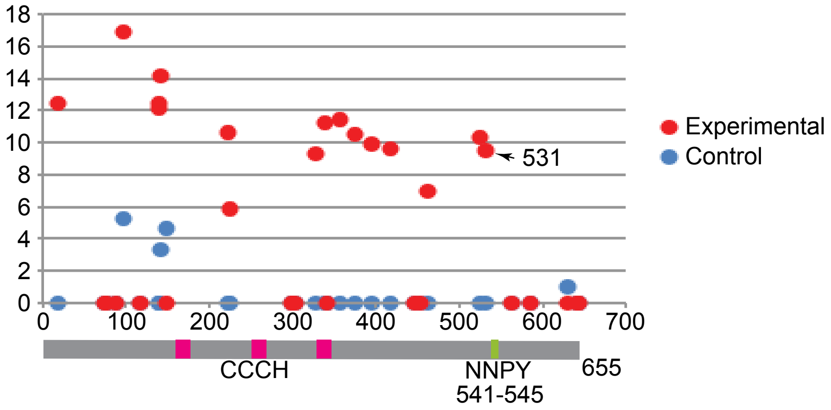
B. Tethering screen results



C. Structural predictions