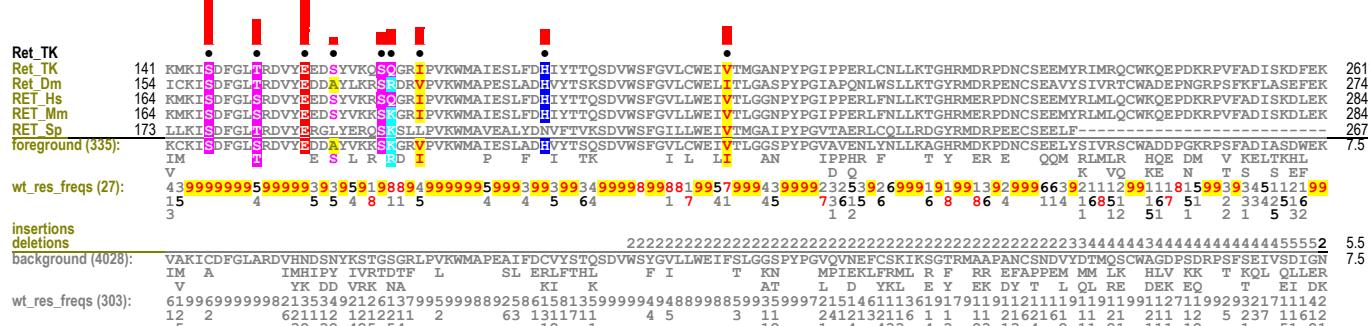
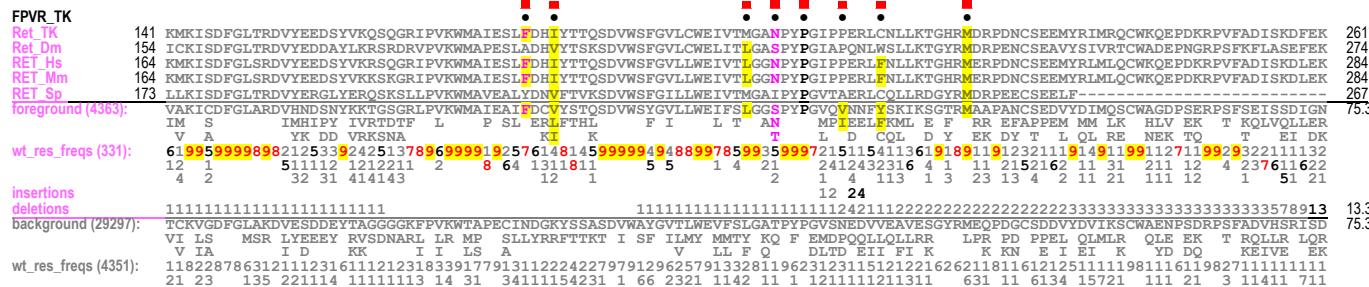
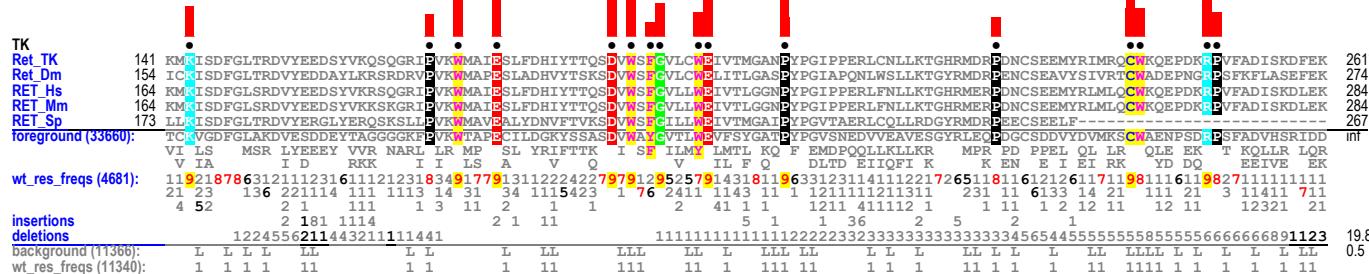
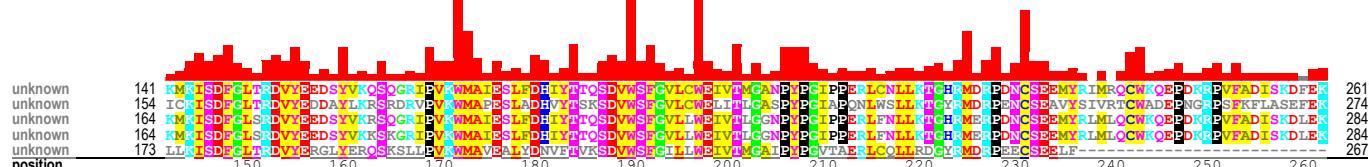
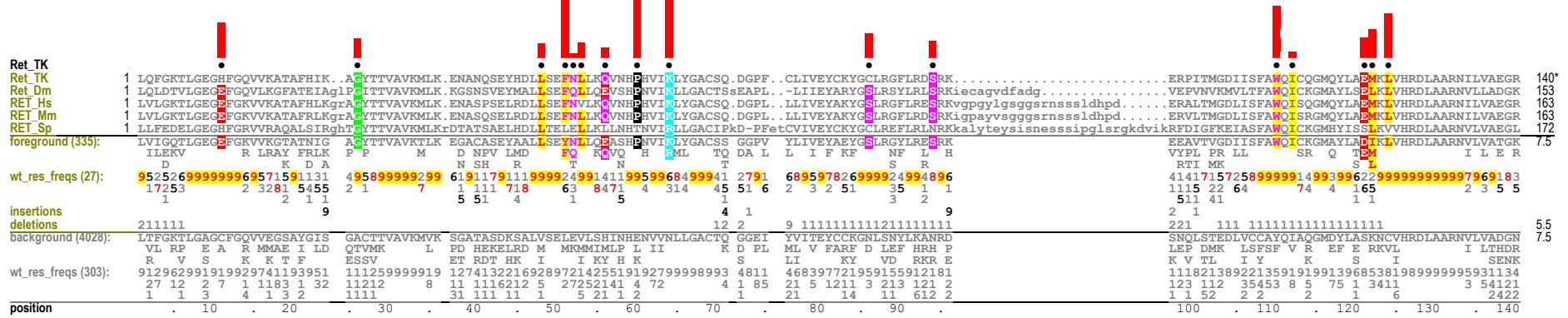
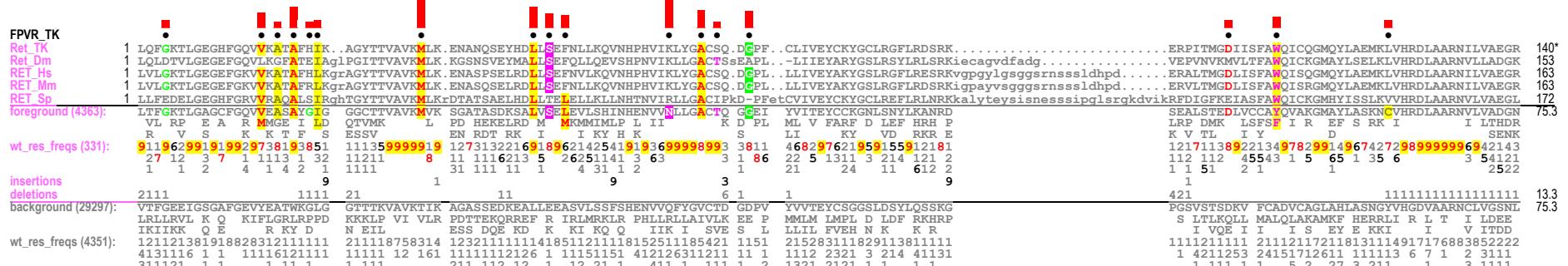
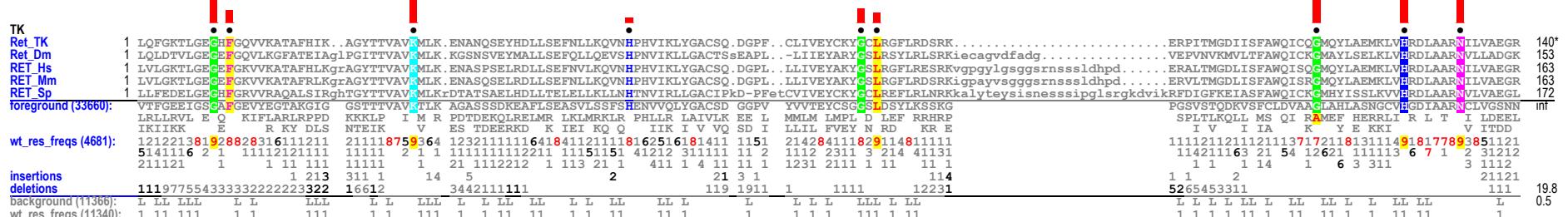
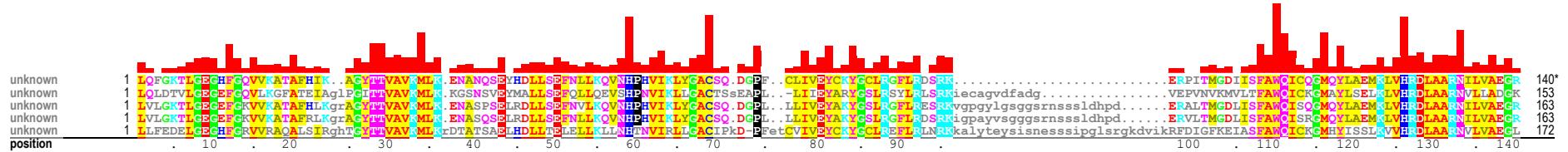
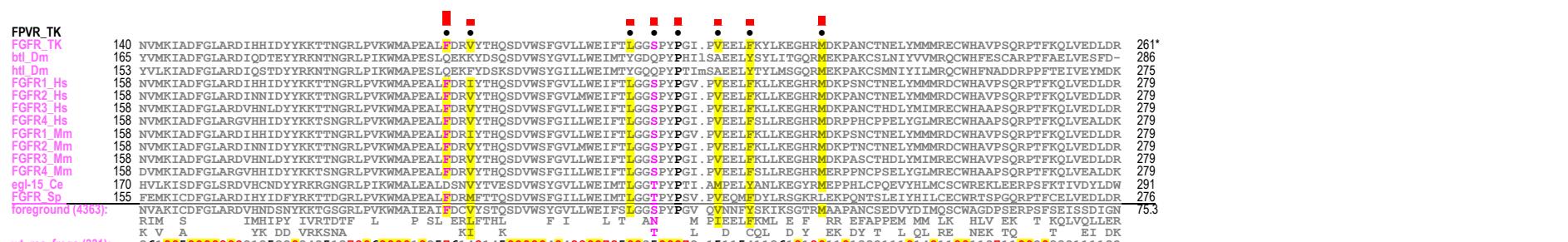
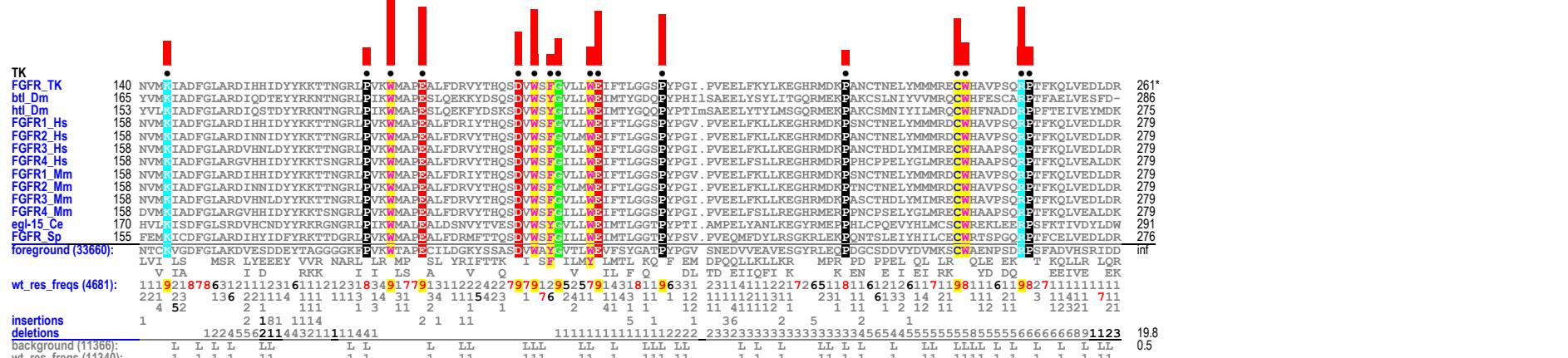
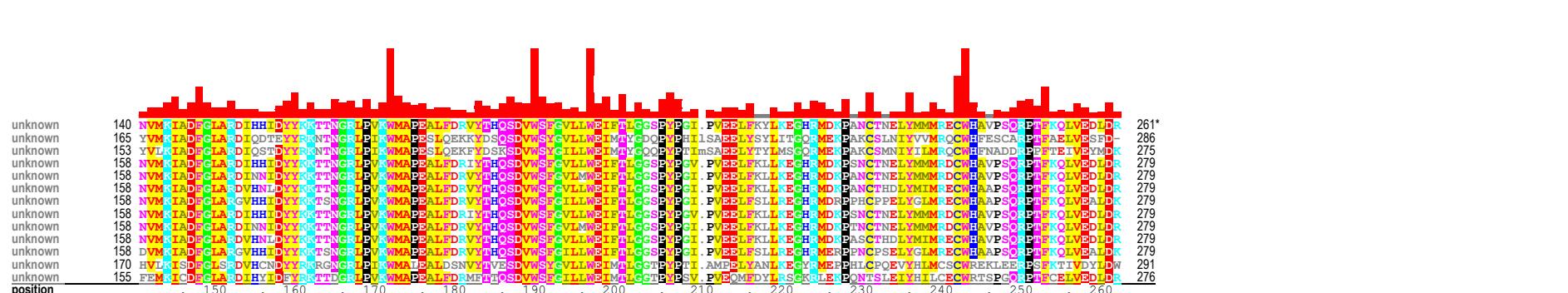
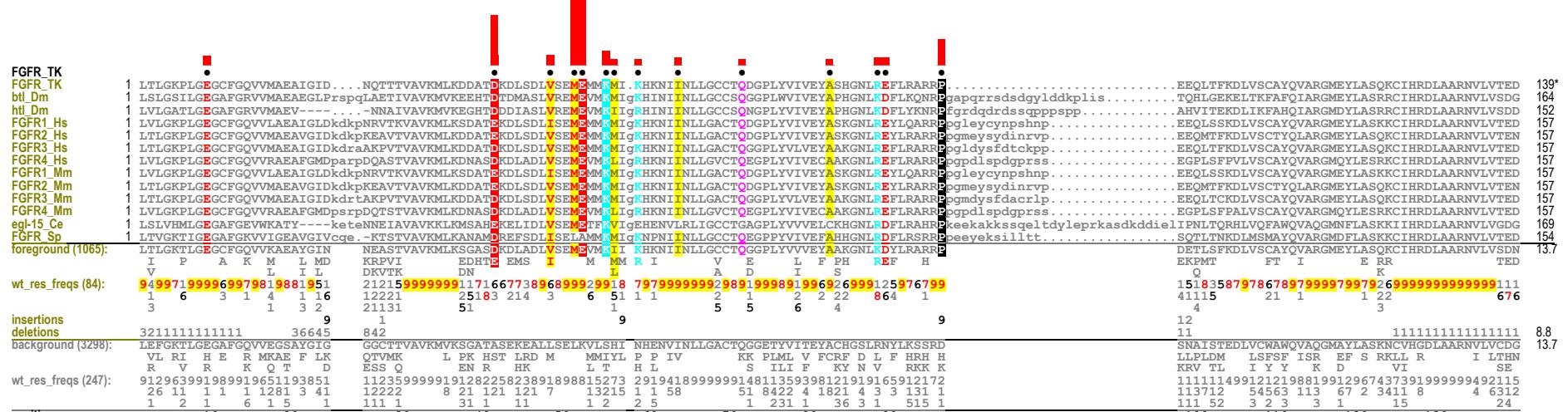
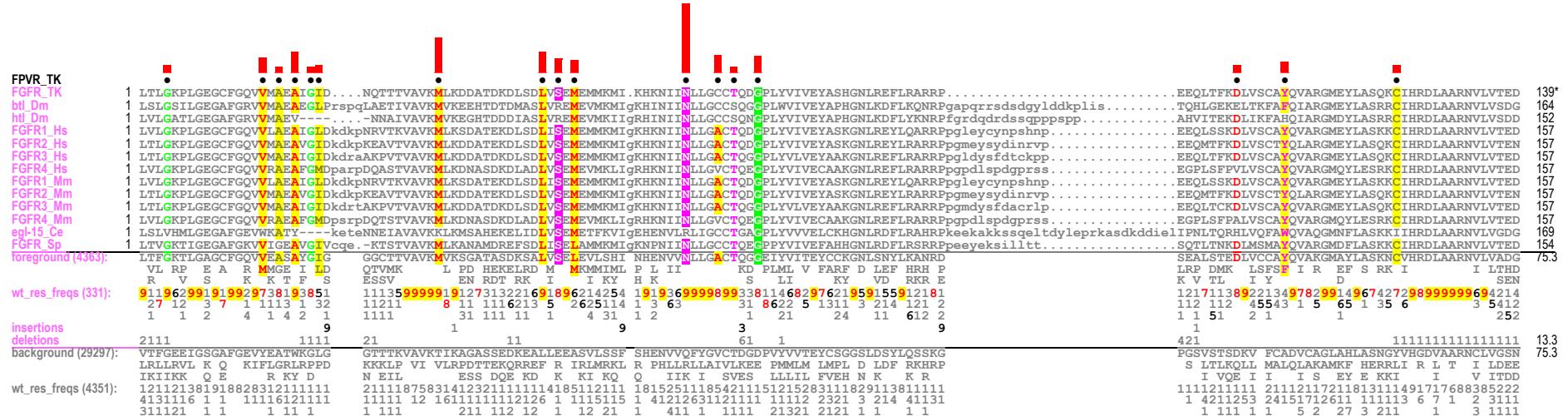
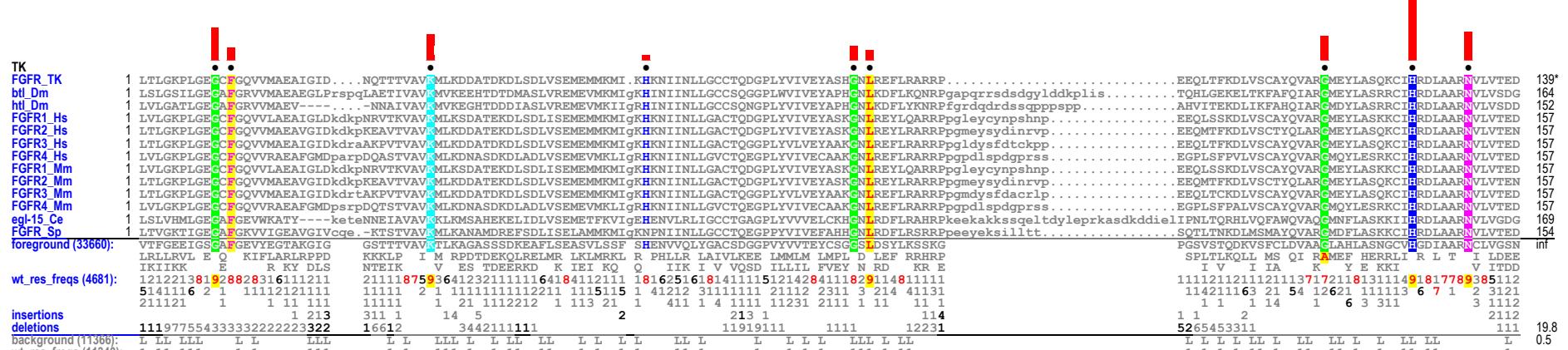
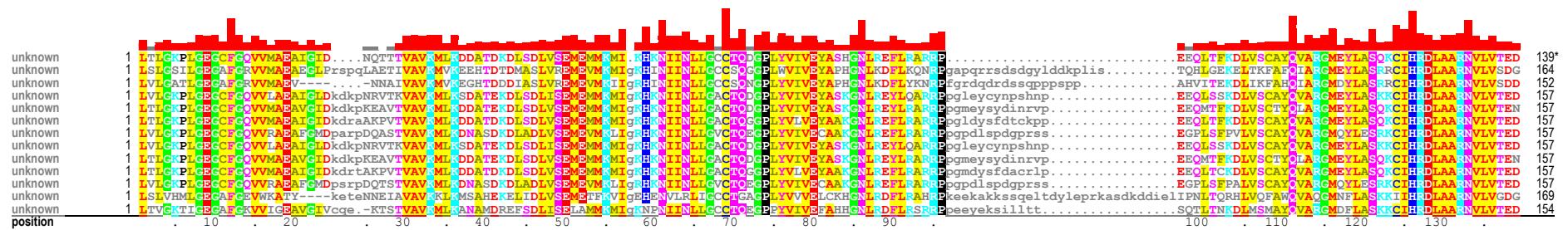


Ret_TK

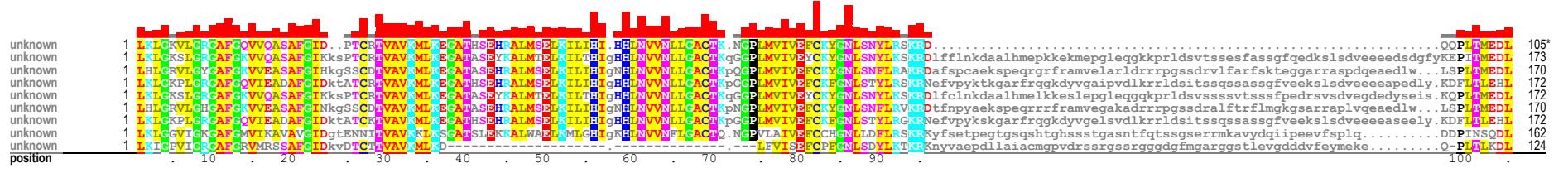


FGFR_TK

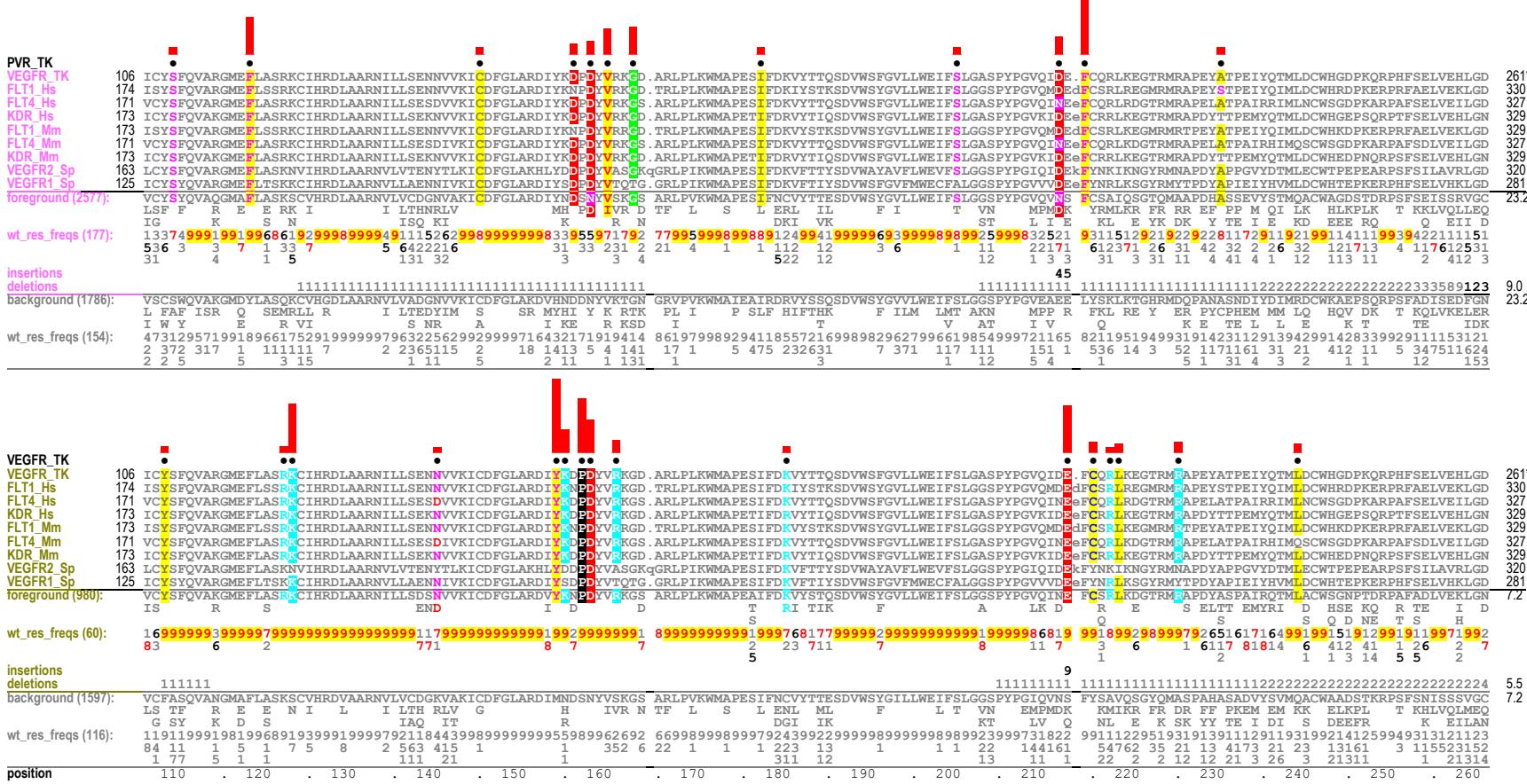


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2	4	32	31	414143			12	1				2	1	4	113	1	3	23	13	4	2	11	111	1	51	21
<i>insertions</i>																										
<i>deletions</i>																										
background (29297):																										
LTCKVGDGFGLAKDVEESDDETYAGGGKFKPVWTAPECINDGKYSSADSVWAYGVTLWEVFSLGATPGYPGV SNEDVVEAVESQRYMRQEDPQGCSDDVVDYKCSWAENPSDRSPFADVHSRISD																										
VI	LSD	MSR	LYEEVE	RVSNDARL	LR	MP	SLLYRRFTKT	I	SF	ILMY	MMTY	KQ	F	EM	DPOQLQLLRR	LPR	PD	PPEL	QMLR	OLE	EK	T	ROLLER	LOR		
V	IA	I	D	KK	I	LS	A	V	L	F	O	DL	TD	EII	FT	K	KN	E	EI	K	YD	DO	KEIVE	EK		
wt_res_freqs (4351):	2118228786312111236111212131833917791311222422797912962579133281196231																									
21	23	135	221114	11111113	14	31	3411154231	1	66	2321	1142	11	12	1111211311	631	11	6134	15721	111	21	3	11441	711			
4	52		1	1	1	4	11	2		2	11	1	1	12	11	412	12	1	1	11	1	12	1	12311	21	

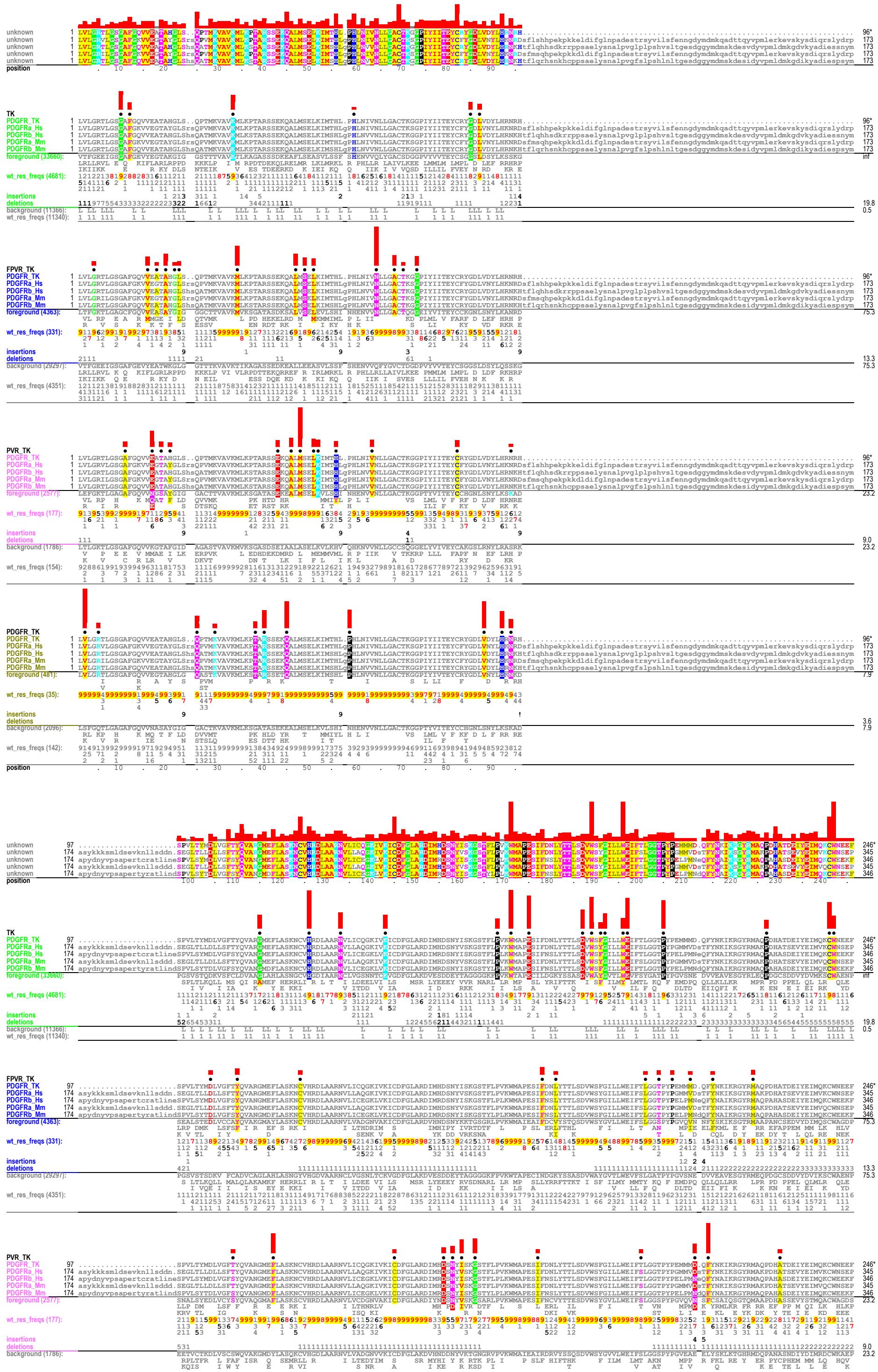
VEGFR_TK



FPVR_TK	1	LKLKGKVLGRGAFGVQVQS AF G ID..PTCRTVAVKMLKEGATHSEHRAI N S E K I L I H I H HHLN V NNLLGACT K .N	CPLMVIVEFCKYGNLSNLRSKRDKRd l f l n kdalhme p kk e kmegp l gleggkprldsvtssesfassgfqedkslsdv ee edsdgf y KEPITMEDL	QQPLTMEDL	105*
FLT1_Hs	1	LKLKGKSLGRGAFGVQVQS AF G IKksPTCRTVAVKMLKEGATA S E K I L I H I H HHLN V NNLLGACT K q	CPLMVIVEFCKYGNLSNLRSKRDKRd l f l n kdalhme p kk e kmegp l gleggkprldsvtssesfassgfqedkslsdv ee edsdgf y KEPITMEDL	QQPLTMEDL	173
FLT4_Hs	1	LHLKGKPLGRGAFGVQVIEAD A F G ID..tACTRCVAVKMLKEGATHSEHRAI N S E K I L I H I H HHLN V NNLLGACT K q	CPLMVIVEFCKYGNLSNLRSKRDKRd l f l n kdalhme p kk e kmegp l gleggkprldsvtssesfassgfqedkslsdv ee edsdgf y KEPITMEDL	QQPLTMEDL	170
KDR_Hs	1	LKLKGKPLGRGAFGVQVIEAD A F G ID..tACTRCVAVKMLKEGATHSEHRAI N S E K I L I H I H HHLN V NNLLGACT K q	CPLMVIVEFCKYGNLSNLRSKRDKRd l f l n kdalhme p kk e kmegp l gleggkprldsvtssesfassgfqedkslsdv ee edsdgf y KEPITMEDL	QQPLTMEDL	172
FLT1_Mm	1	LKLKGKPLGRGAFGVQVIEAD A F G ID..tACTRCVAVKMLKEGATA S E K I L I H I H HHLN V NNLLGACT K q	CPLMVIVEFCKYGNLSNLRSKRDKRd l f l n kdalhme p kk e kmegp l gleggkprldsvtssesfassgfqedkslsdv ee edsdgf y KEPITMEDL	QQPLTMEDL	172
FLT4_Mm	1	LHLKGKPLGRGAFGVQVIEAD A F G ID..tACTRCVAVKMLKEGATA S E K I L I H I H HHLN V NNLLGACT K q	CPLMVIVEFCKYGNLSNLRSKRDKRd l f l n kdalhme p kk e kmegp l gleggkprldsvtssesfassgfqedkslsdv ee edsdgf y KEPITMEDL	QQPLTMEDL	170
KDR_Mm	1	LKLKGKPLGRGAFGVQVIEAD A F G ID..tACTRCVAVKMLKEGATHSEHRAI N S E K I L I H I H HHLN V NNLLGACT K q	CPLMVIVEFCKYGNLSNLRSKRDKRd l f l n kdalhme p kk e kmegp l gleggkprldsvtssesfassgfqedkslsdv ee edsdgf y KEPITMEDL	QQPLTMEDL	172
VEGFR2_Sp	1	LKLGGVIGKGFAGMVKRAV A GID..tENNTIVAVKLLKGATSELEKKAL N AEKILIHIHGHKLNNVNNLLGACTKq	CPLVLAIEFCCHGNLFLDRSKRYKfsetpegtgshtgssstgatqfqtgserrmkavdygiipeefvslpq..	DSDPINSQL	162
VEGFR1_Sp	1	LKLGGVIGRGRGAFGRV M RSSA F G Idkv T CTTVAVKMLKD..	..-L V FE S CFPGNLSLDLYT K TKR N kyvaepdllaicmgpvdrrssrgssrggdgfmarggstlevgdddfeimeke..	Q-PLTLDK	124
foreground (4363):		LTFGKT L GAGCFCGVQV E S A G ICGCCTT V AVK N S KGATASD K SA I S E V L H I N HN V NNLLGACT K Q	C E I V Y I VTE C CKGNLSNL Y AN K RD	SEALSTEDL	75.3
		VL RP E A R M G E L D Q T VMK L P D HEKELRD M KMMMKM L P L II	K D P L ML V F A RF D L E F H R H P	LRP DMK	
		R S V K K T F E S SSV EN RDT RK I I KY H K K S LI KY VD R K E	K V T VL		
wt_res_freqs (331):		9 ¹ 19 ⁶² 99 ¹⁹ 19 ²⁹ 27 ³⁸ 19 ⁸³ 51 1113 ⁵⁹⁹⁹⁹⁹¹⁹ 19 ¹²⁷³ 13221 ⁶⁹ 1896 ¹⁴²⁵⁴ 19 ⁹³⁶ 99998993 3811468 ⁹⁷ 621 ⁹⁵⁹ 559 ¹²¹ 81		121 ⁷ 113 ⁸⁹	
		2 ⁷ 12 ³ 7 ¹ 113 ¹ 32 112111 ⁸ 11 1116213 ⁵ 2625114 ¹ 3 ⁶³ 3 ¹ 8 ⁶²² 5 1311 ³ 214 ¹²² 2 1 ¹ 21 ²⁴ 11 ⁶¹² 2		112 ¹¹²	
insertions		9	1	9	9
deletions		1111	21	11	3
		9	1	9	9
		1111	21	6 1 1	421
background (29297):		VTFGE E IGSGAFGEVYEATW R GLG	GTTKVAVKT I AKGASSEDE K ALLEEAV V LSS F SHENVVQFYGV C TD GP V Y V TE C CGGS L DSY L Q S KG	PGS V TS D K	75.3
		LRLLRLV K Q KLFGLRLR P KKLP V VL R PD T TE Q RF R I T RLMRKL R PH L RL L AI V LK EE PMML I LMPL D LDF R K RP	S LTLKQL		
		IKIIK Q E R K Y D EIL ESS DQE KD K K QO Q I I K I SVE S L L L I I V EE N K K R	I VQE		
wt_res_freqs (4351):		121121381918828312111111 21111875831412331111114185112111 18152511185421 1151215283111291131811111		1111211111	
		431116 1 ¹ 1116121111 11111 12 16111111112126 1 ¹ 115115 4121263112111 112321 3 214 41131		1 421125	
		311121 1 ¹ 11 1 1 1 111 211 122 12 1 21 411 1 111 21321 2121 1 1 1 1		1 111	



PDGFR_TK



TK
 unknown 247 EKRPPFYQLVEIVEN 261*
 unknown 346 EKRPPFYHLSEIVEN 360
 unknown 347 EIRPPFSQLVLLLE- 360
 unknown 346 EKRPPFYHLSEIVEN 360
 unknown 347 ECRPPFSQLVLLLE- 360
 position 250 . 260

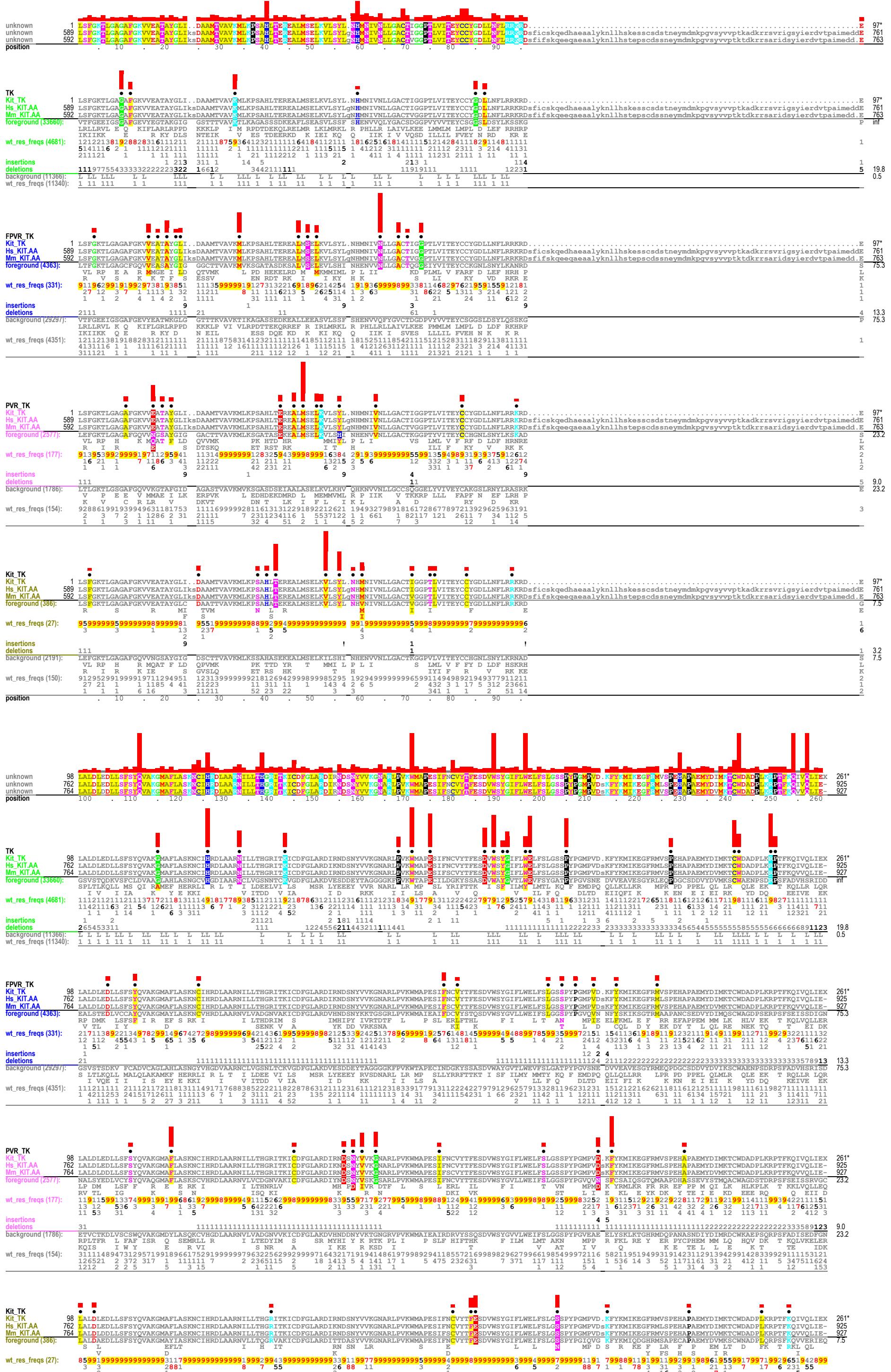
TK
 TK
 PDGFR_TK 247 EKRPPFYQLVEIVEN 261*
 PDGFRa_Hs 346 EKRPPFYHLSEIVEN 360
 PDGFRb_Hs 347 EIRPPFSQLVLLLE- 360
 PDGFRa_Mm 346 EKRPPFYHLSEIVEN 360
 PDGFRb_Mm 347 ETRPPFSQLVLLLE- 360
 foreground (33660): SDRPSFADVHSRIDD int
 EK T KQLLR LQR
 DQ EETIVE EK
 wt_res_freqs (4681): 11 9827 111111111
 21 3 11411 711
 11 12321 21
 insertions 556666666891123 19.8
 deletions background (11366): L L L L LL 0.5
 wt_res_freqs (11340): 1 1 1 1 11

PVPR_TK
 PDGFR_TK 247 EKRPPFYQLVEIVEN 261*
 PDGFRa_Hs 346 EKRPPFYHLSEIVEN 360
 PDGFRb_Hs 347 EIRPPFSQLVLLLE- 360
 PDGFRa_Mm 346 EKRPPFYHLSEIVEN 360
 PDGFRb_Mm 347 ETRPPFSQLVLLLE- 360
 foreground (4363): SDRPSFSEISSLSDGN 75.3
 EK T KQLVOLLER
 TO T EI DK
 wt_res_freqs (331): 11 9929 322111132
 12 4 237611622
 12 1 51 21
 insertions 333333333578913 13.3
 deletions background (29297): SDRPSFADVHSRID 75.3
 EK T ROLLER LQR
 DQ KEIVE EK
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 21 3 11411 711
 11 12311 21

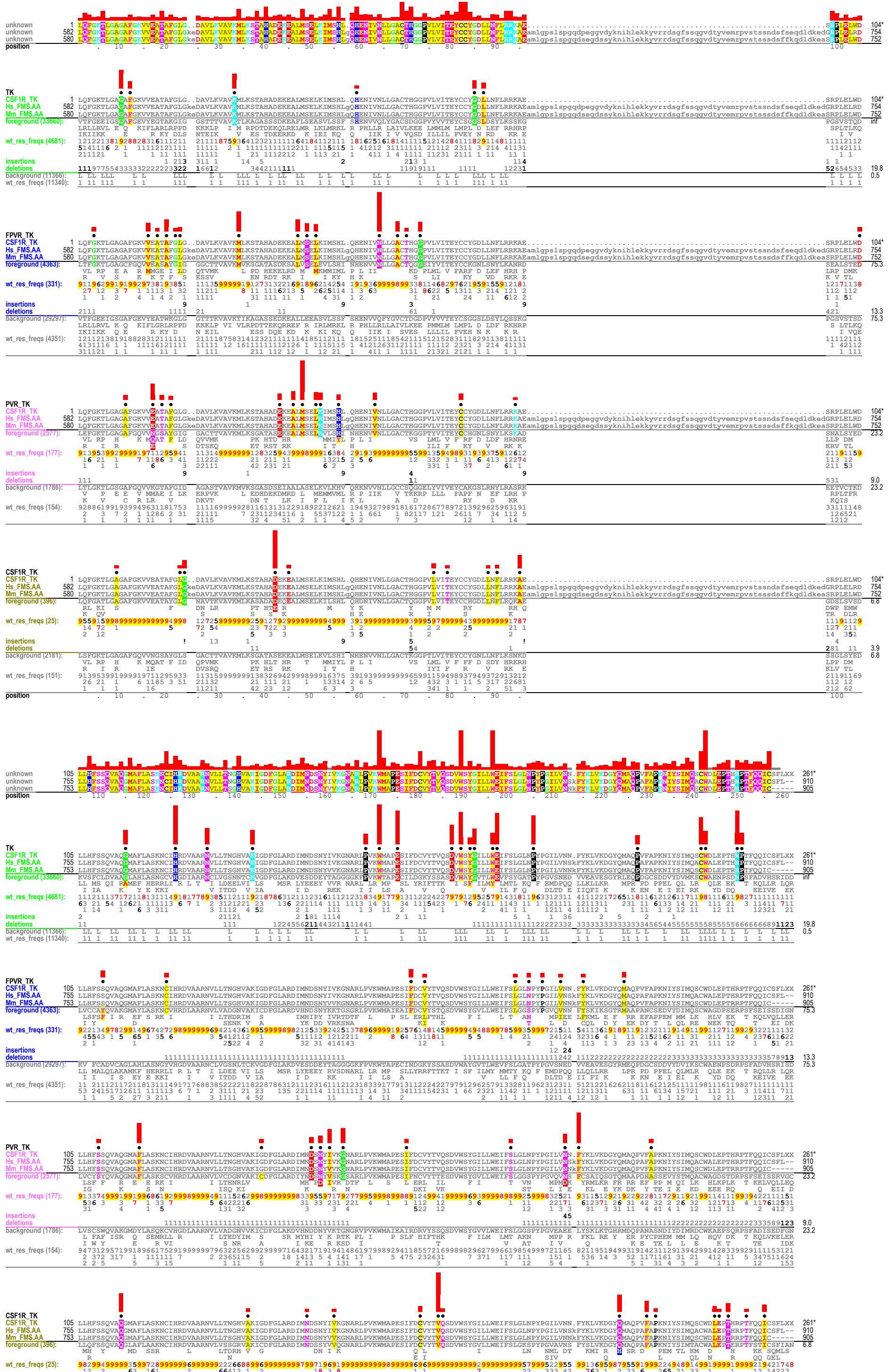
PVPR_TK
 PDGFR_TK 247 EKRPPFYQLVEIVEN 261*
 PDGFRa_Hs 346 EKRPPFYHLSEIVEN 360
 PDGFRb_Hs 347 EIRPPFSQLVLLLE- 360
 PDGFRa_Mm 346 EKRPPFYHLSEIVEN 360
 PDGFRb_Mm 347 ETRPPFSQLVLLLE- 360
 foreground (2577): TDRPSFSEISSRVGC 23.2
 LK T KKLVQLLEQ
 RQ Q EII D
 wt_res_freqs (177): 11 9939 422111151
 13 4 11 7612531
 11 2 412 3
 insertions 222222333589123 9.0
 deletions background (1786): SQRPSFADISEDFGN 23.2
 DR T KQLVRELER
 T TS IDK
 wt_res_freqs (154): 3399291111153121
 11 5 347511624
 1 12 153

PDGFR_TK
 TK
 PDGFR_TK 247 EKRPPFYQLVEIVEN 261*
 PDGFRa_Hs 346 EKRPPFYHLSEIVEN 360
 PDGFRb_Hs 347 EIRPPFSQLVLLLE- 360
 PDGFRa_Mm 346 EKRPPFYHLSEIVEN 360
 PDGFRb_Mm 347 ETRPPFSQLVLLLE- 360
 foreground (481): EKRPSFSQLSETVGN 7.9
 I E YL VLLME
 E H VIL
 wt_res_freqs (35): 96999539441539
 2 1 31 51325
 1 3 132
 insertions 444444444444415 3.6
 deletions background (2096): TDRPSFSEISSRVGC 7.9
 LK T KKLQLEQ
 RQ TO D
 219929422721262
 12 5 116 22621
 11 12 41 4
 position 250 . 260

Kit_TK

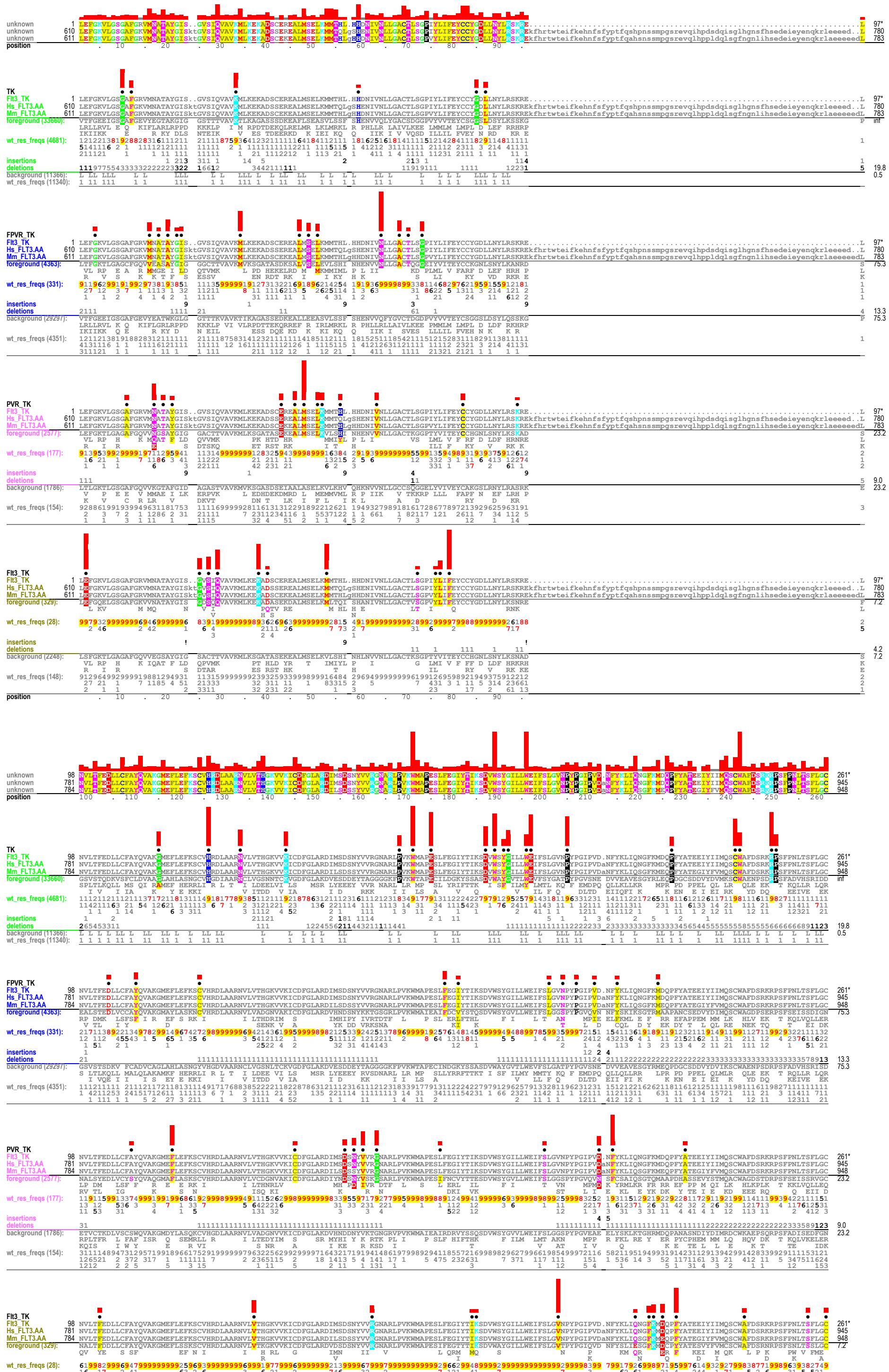


CSF1R_TK

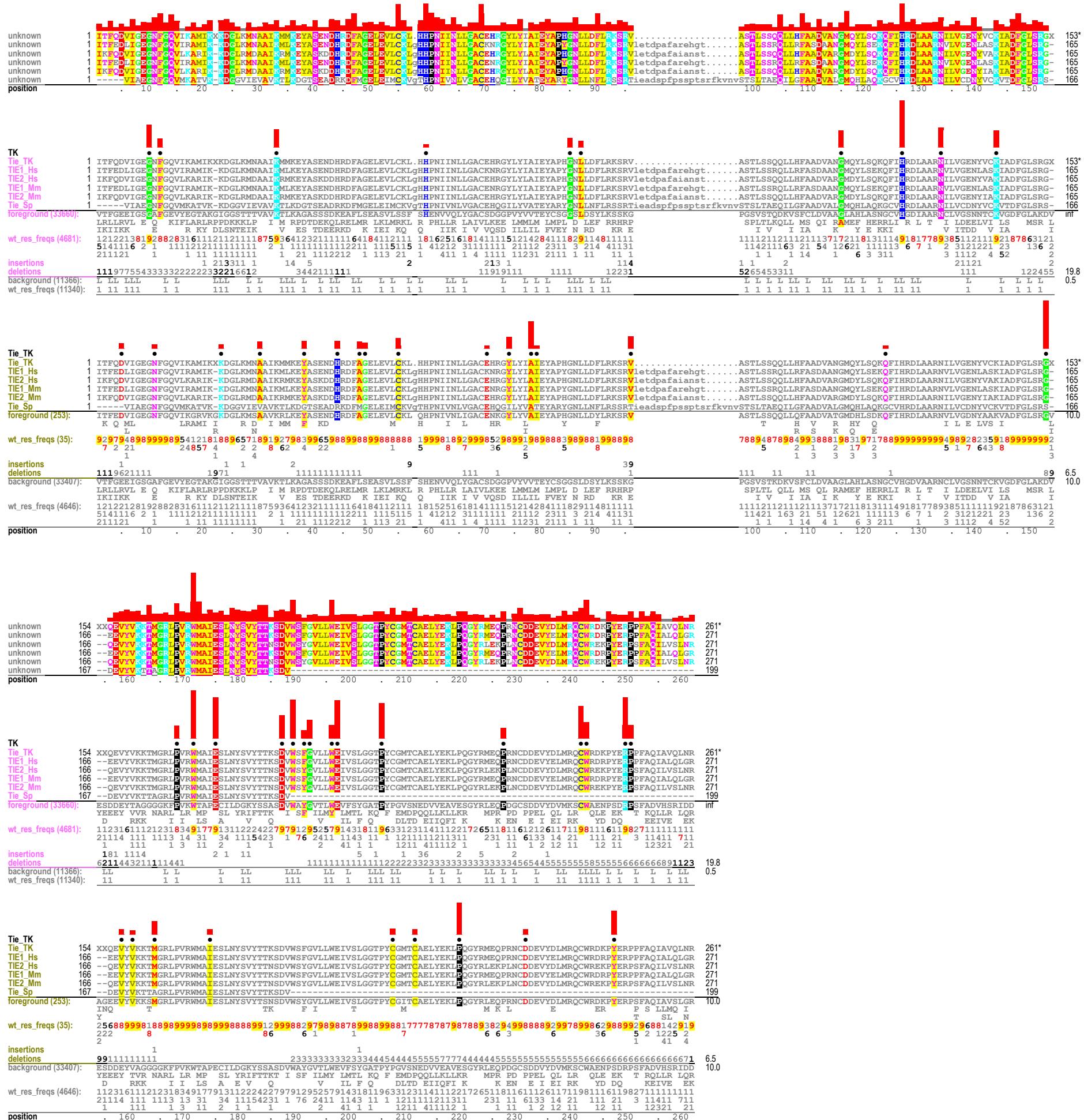


insertions 3 . 1 . 142 . 1 . 2 . 51 . 2 . 1 . 25 . 116
 deletions
 background (2181): LVCYSYQVAKGMEFLASKSCVHRDLAARNVLVCEGNVTKICDFGLARDVYNDNSNYVVKGSARLPVKWMAPEISFNCSVYTTQSDVWSYGVLLWEIFSLGGSPYPGVQVNFCASAIQSGTKMAAPDHAPSVDYDQMOSCWALESEDRTFSEIISRVGC 3.9
 LSFTF R E RE I I LTHNRLV IME PD SR DTF L S TL ERL IL F I T VN MPMK YRALKK FR RE YY SPEQ QL HGKPLK S TSVQLEQ 6.8
 IGS S N ISQ KI K B N DKI FK ST LKI E KL E Y QO E TE I AV KD EHQO TO EII D
 wt_res_freqs (151): 91337599959989968519299999994911453519999999991429559827926799499989989925999833421 931151293191391282112911922991121219939421111151
 44614 3 1 33 6 5 6322217 831 34 122 222 5 1 11 112 12 3 6 1 11 23171 51 177 27 31 14 1272 25 42 121614 3 118711531
 31 1 4 141 32 3 3 3 522 12 113 3 31 4 3 11 4 51 5 21 12 114111 12 411 3
 position . 110 . 120 . 130 . 140 . 150 . 160 . 170 . 180 . 190 . 200 . 210 . 220 . 230 . 240 . 250 . 260

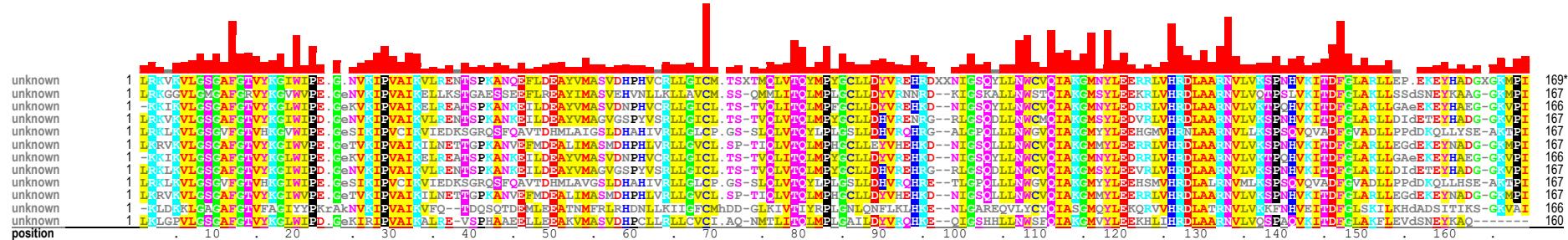
Flt3_TK



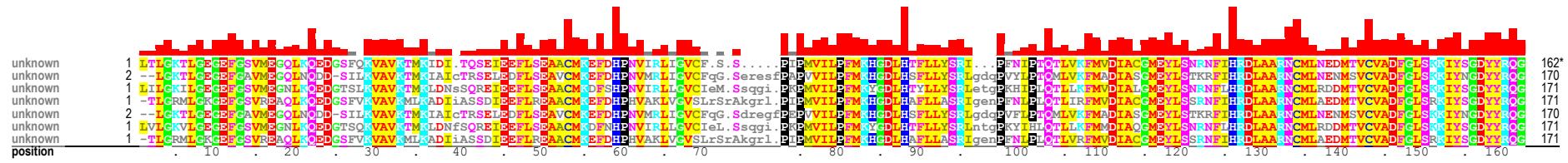
Tie_TK



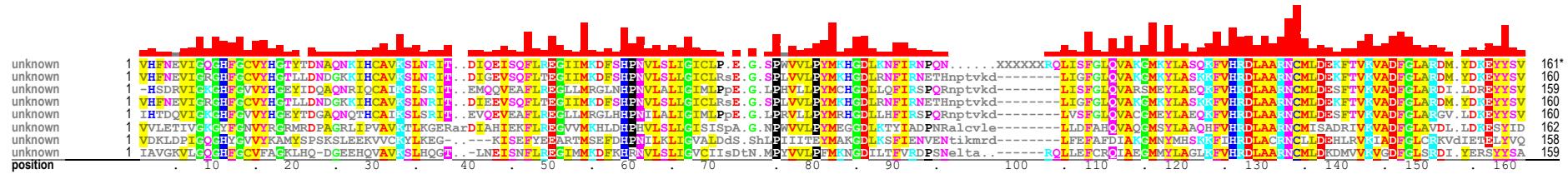
EGFR_TK



AxI_TK

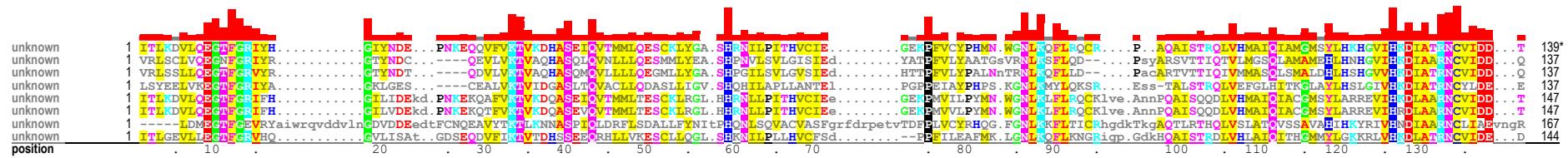


Met_TK

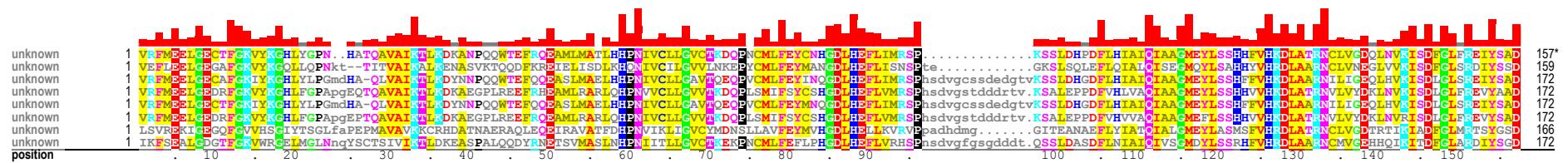


The sequence logo displays the probability of each amino acid (A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y) at each position of the protein sequence. The x-axis represents the positions, and the y-axis represents the amino acids. The height of each bar indicates the probability of that amino acid at that position.

Ryk_TK

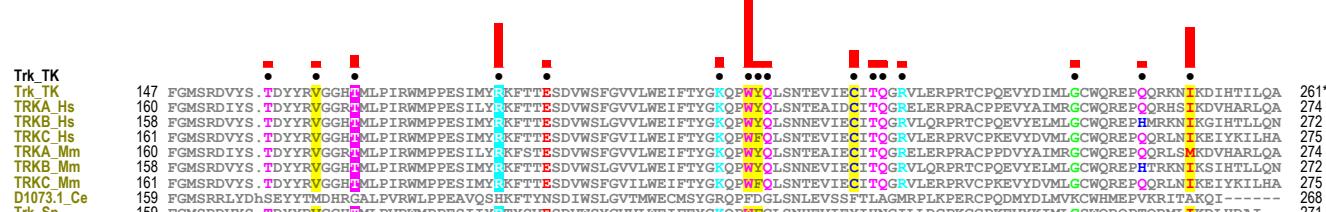
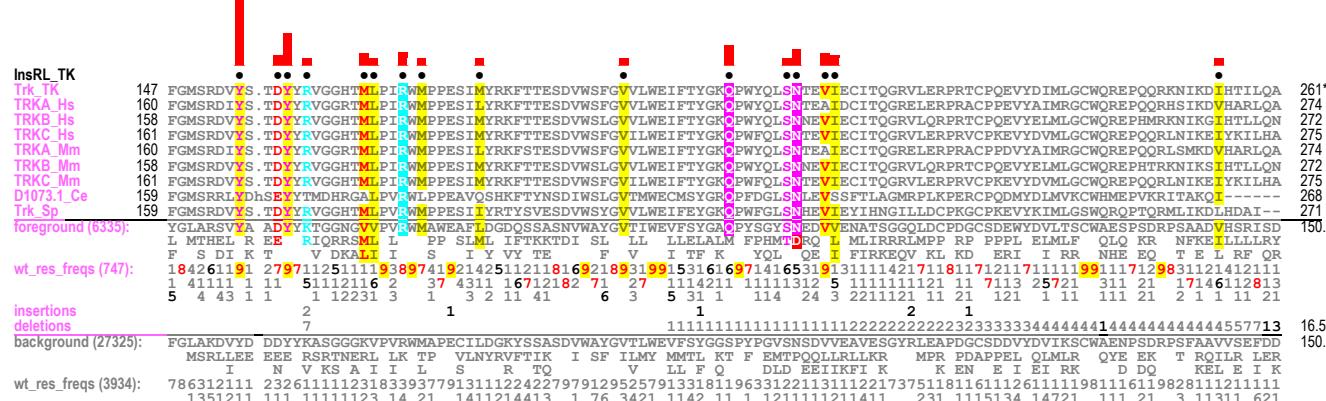
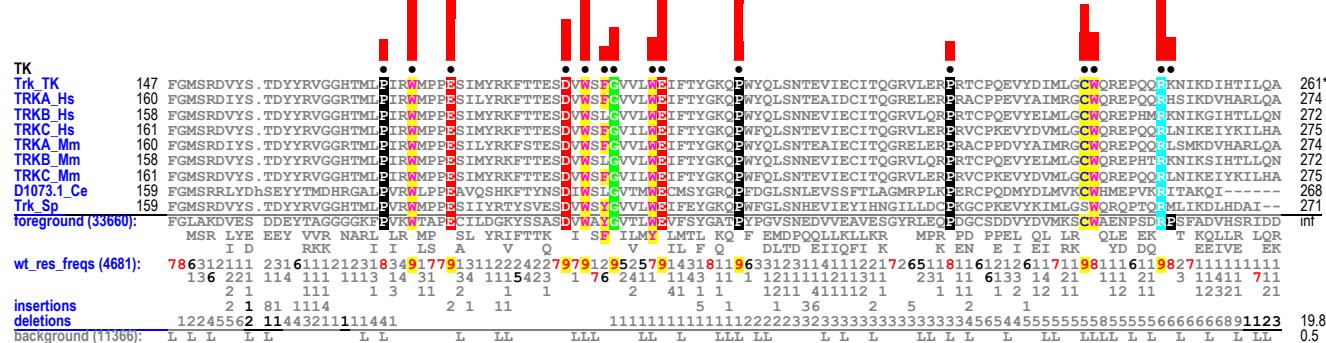
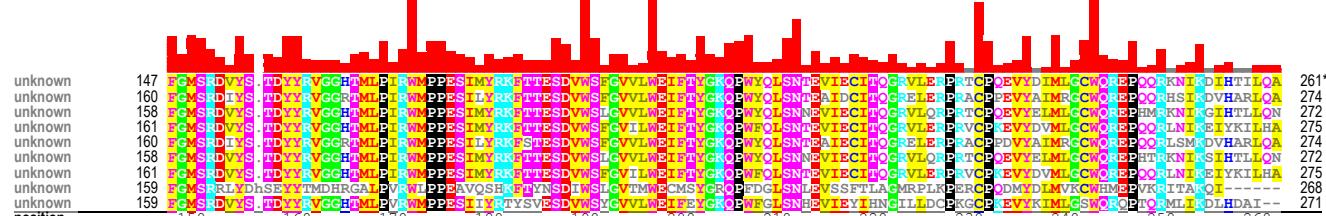
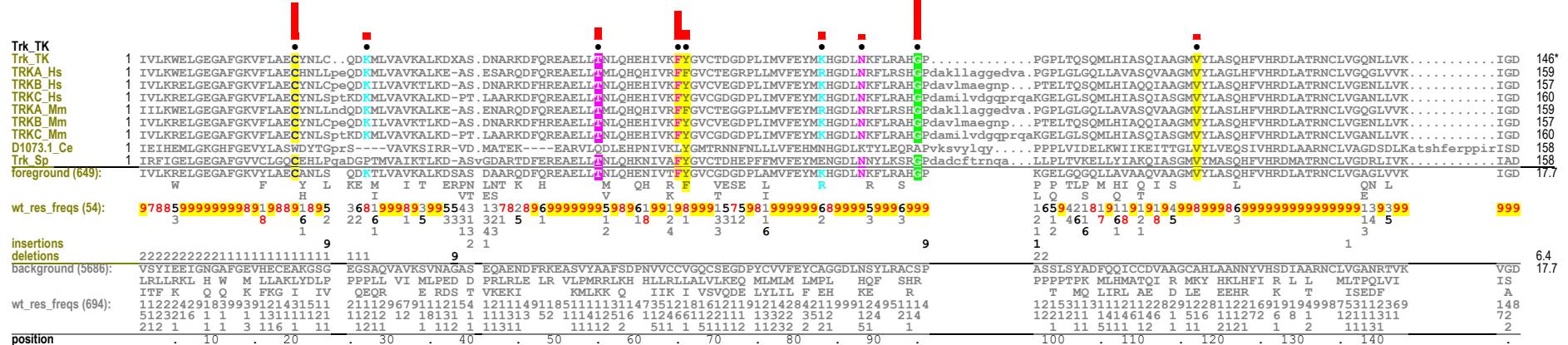
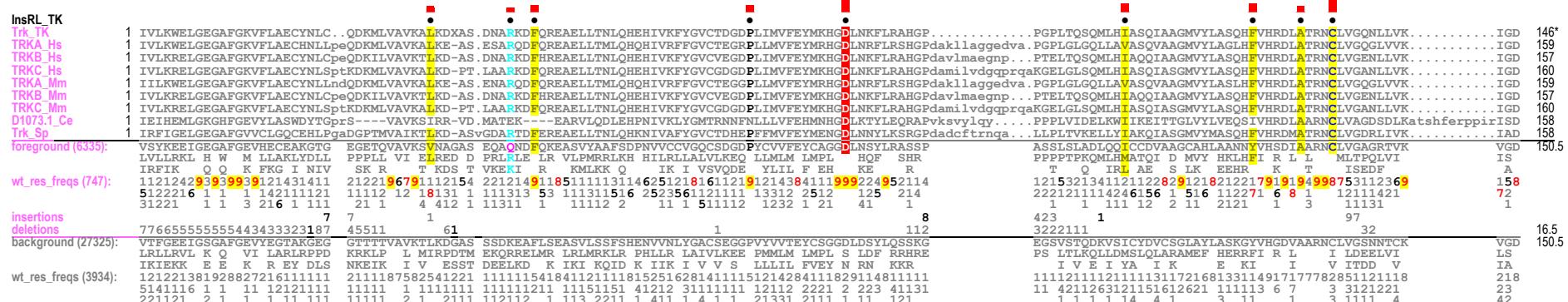
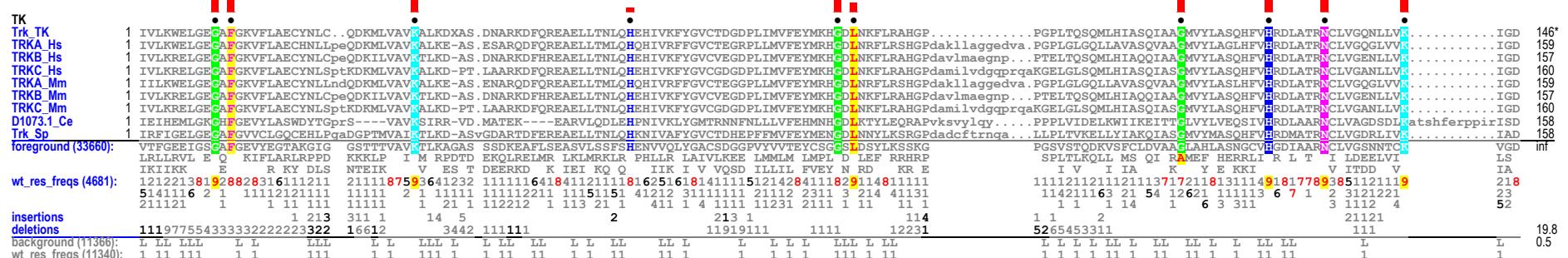
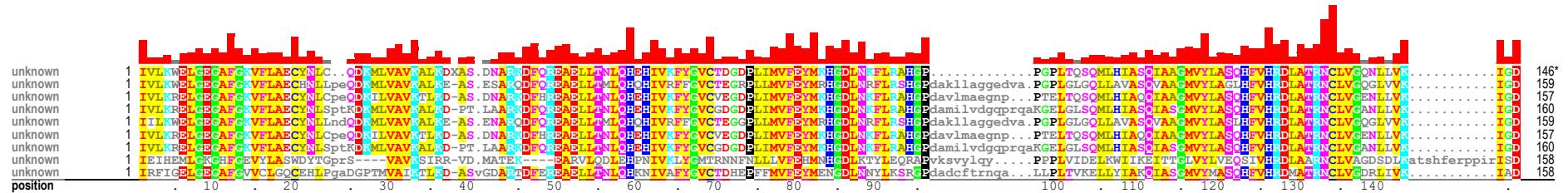


Ror_TK



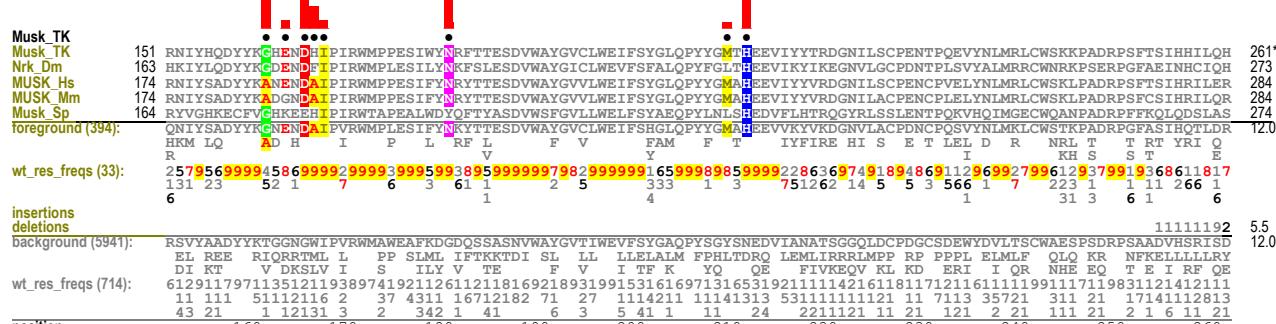
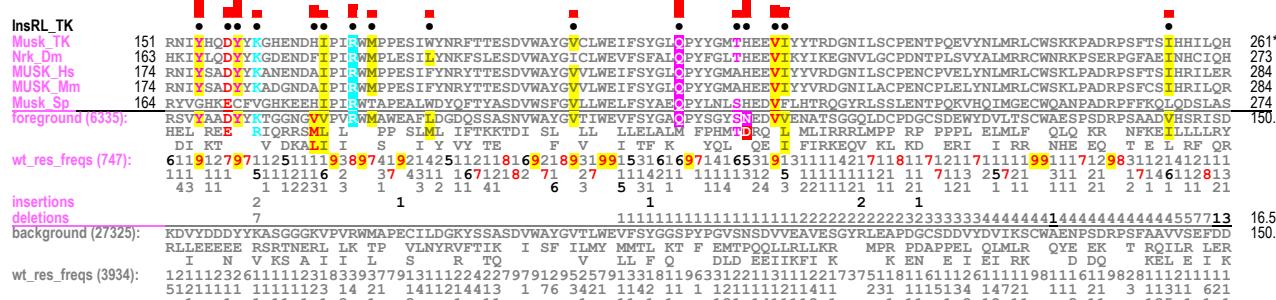
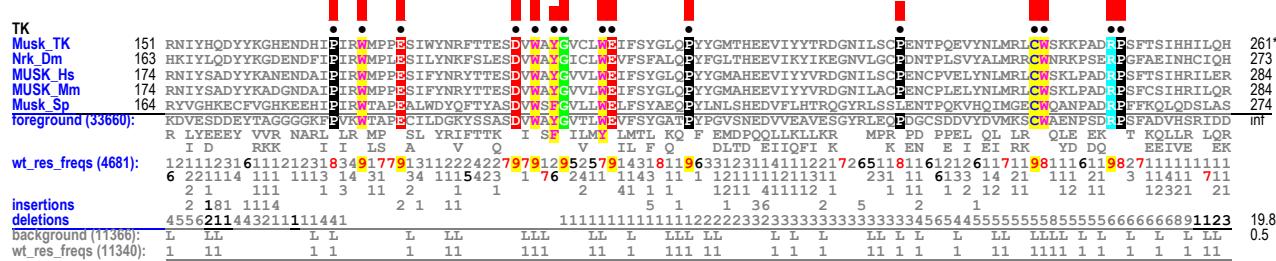
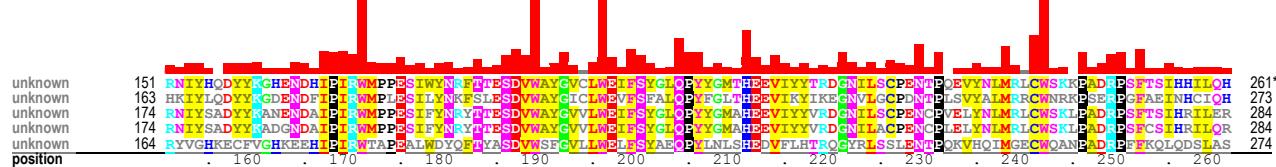
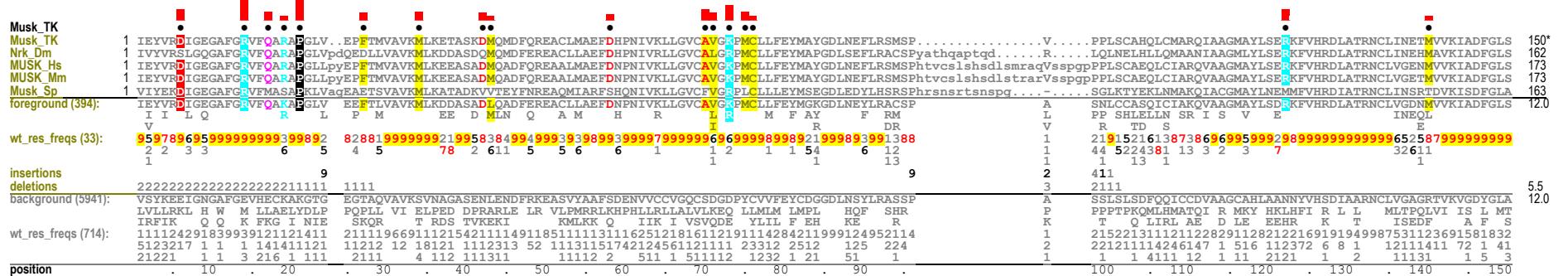
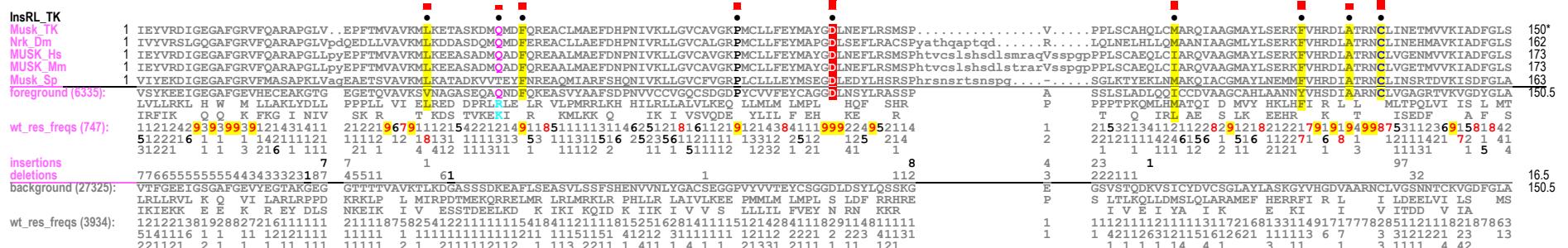
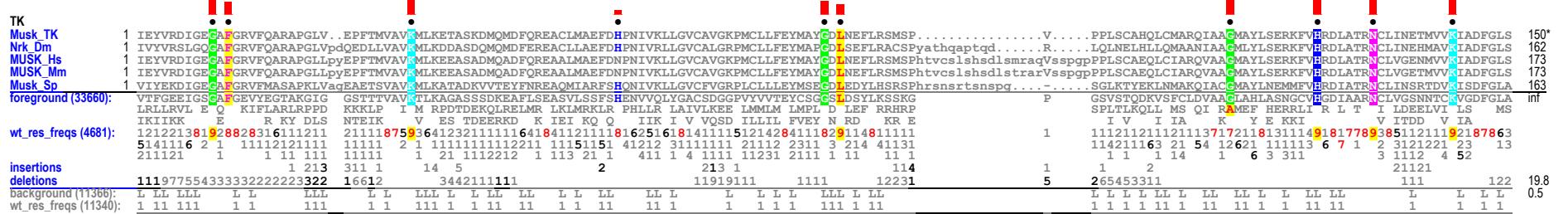
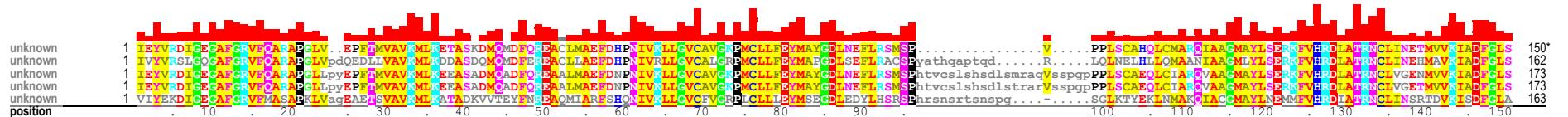
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160 . 170 . 180 . 190 . 200 . 210 . 220 . 230 . 240 . 250 . 260
1 12 31 3 1 242 11 41 6 2 5 41 3 11 4 111111 12 22 121 2 11 311 22 3 1 6 11 11

Trk_TK

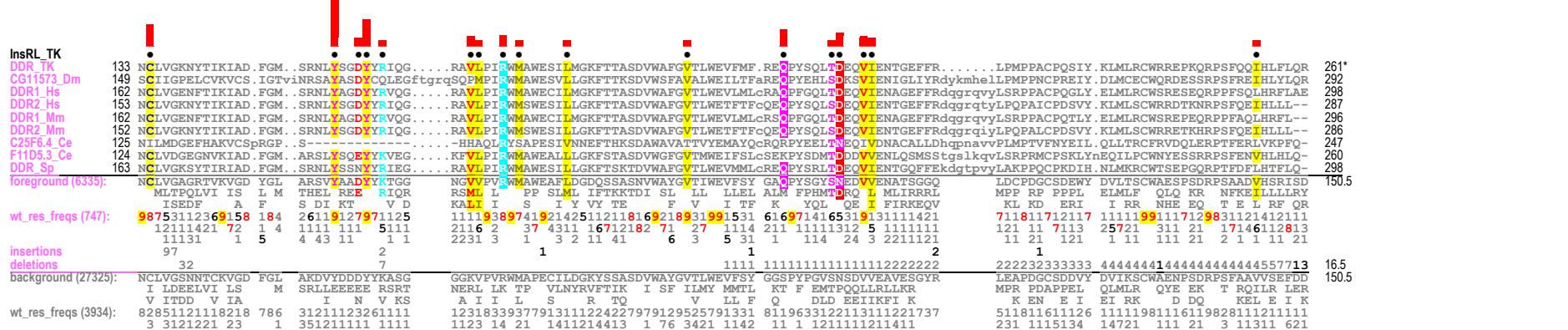
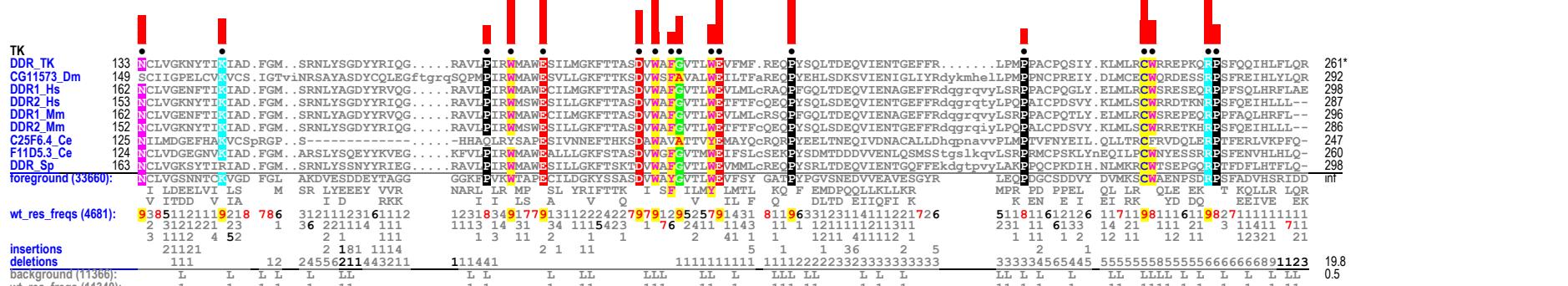
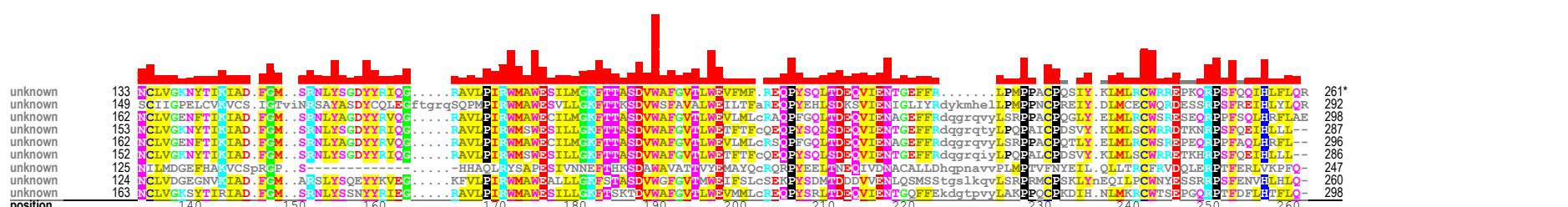
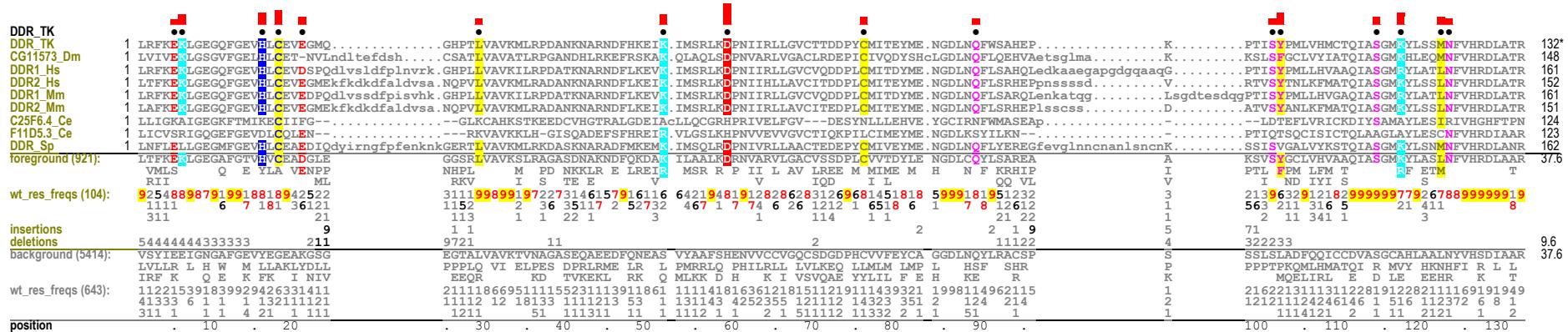
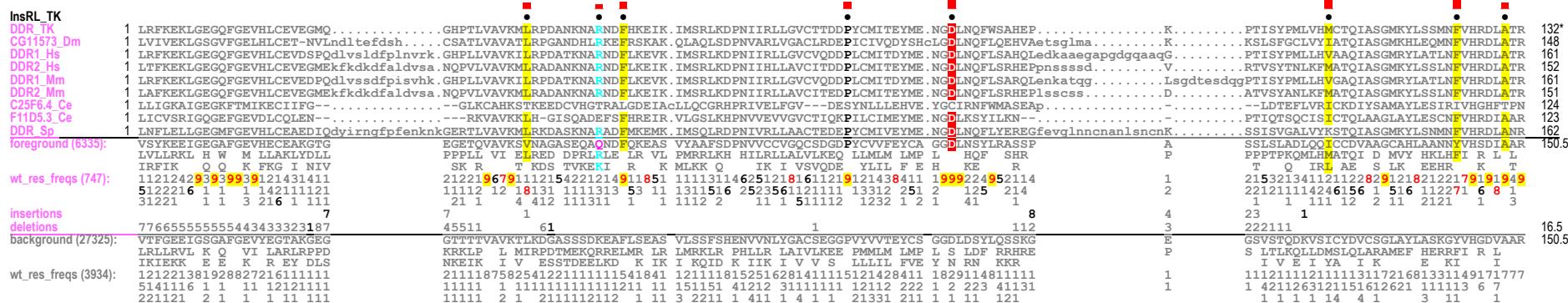
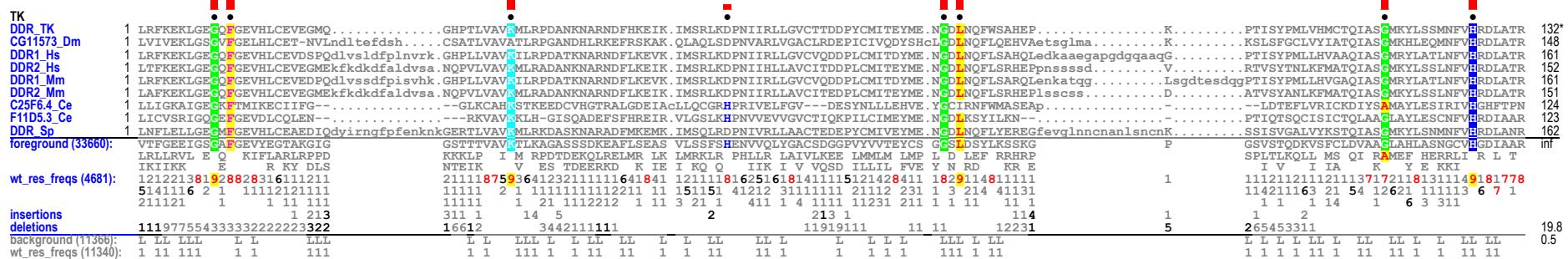
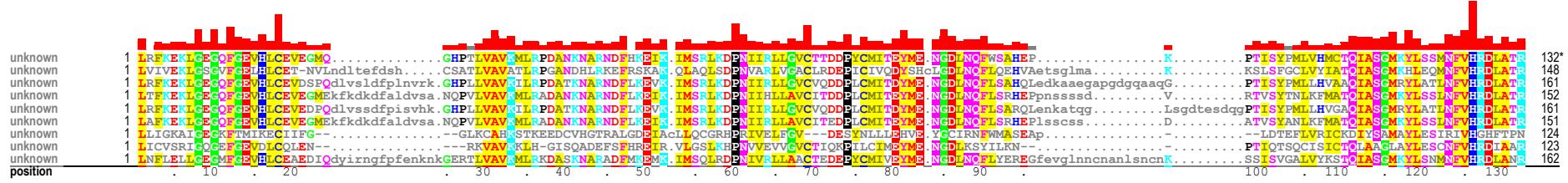


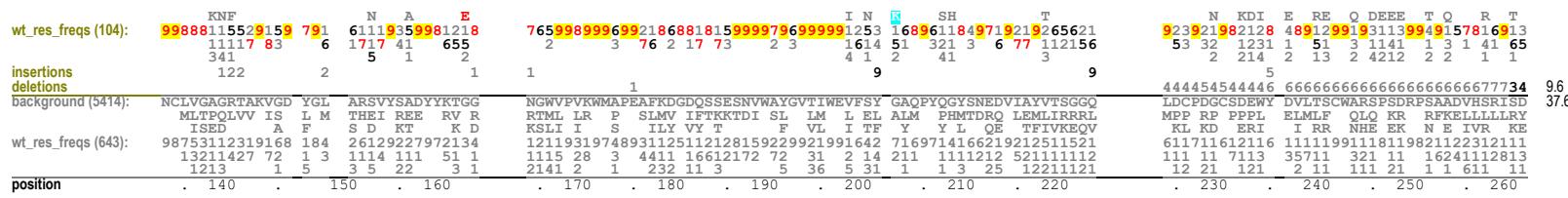
I H I M I L I E N V V Q V P DL LS HM LV E I Y K L LN
 wt_res_freqs (54): 999999489 999999993 99991 99999993 998888997 997996 9999998 9999968 98949 988998983 999199699911 92899888966 91189 9113957
 5 5 8 6 2 2 2 2 3 6 3 6 5 2 2 1 5 6 1 11 5 58 31 11
 insertions 2
 deletions
 background (5686): YCLARSVVA TDYYKVGGNGWV/PVKWMAWEAFKDGDSSSENVWAYGVIIWEVFSYGAQPYGYSNEDVANARSGGCOLSPDGCSDRNYDVLTSCWAESPSDRPSAADVHSRISD 6.4
 L MTHEL R EE RIQRSSML LR PP SMLM IPTKKTDI SL LL LLELALM FPHMTDRO LEMLIRFOLMP KP PPPP ELMLE QLO KR NFKELLRLRY 17.7
 F S DI K A T DKALI I S ILX VY TA F V I TFE S L QO I FIVKR R KL ED E I I RR NHD ER T E I RF QR
 184261191 1797212412119319741931126112118169218931991531516981415531911111142161181161221611111199111712993111412111
 1 31111 1 11 41112116 28 27 4311 16712182 61 37 1114211 11112413 531111122121 21 7113 36711 211 21 17141112813
 5 3 43 2 2 1 12231 3 2 341 11 31 6 3 5 31 2 1 4 24 2 21111 2 12 11 1 1 1 11 111 21 3 1 6 11 21
 position 150 . 160 . 170 . 180 . 190 . 200 . 210 . 220 . 230 . 240 . 250 . 260

MusK_TK

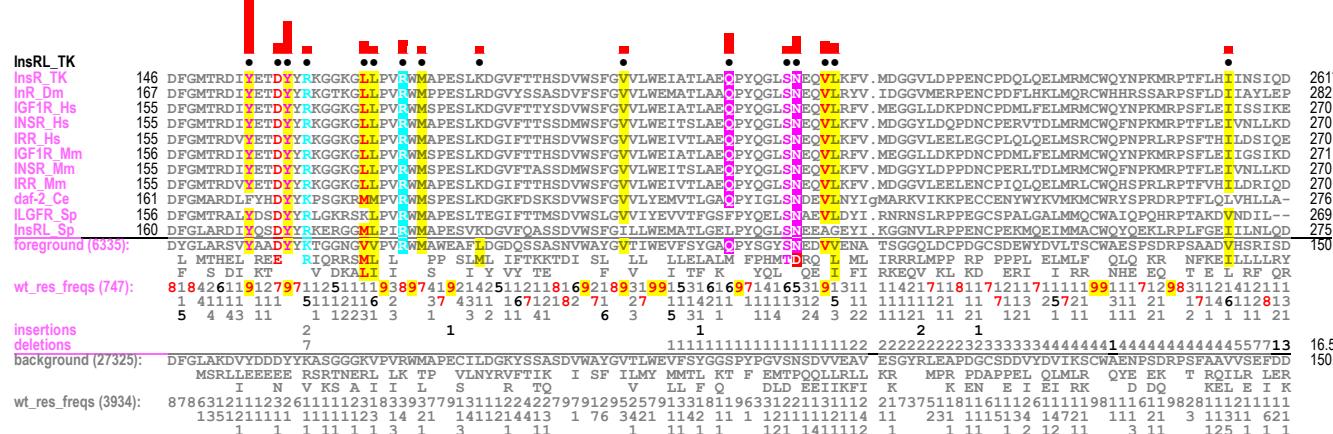
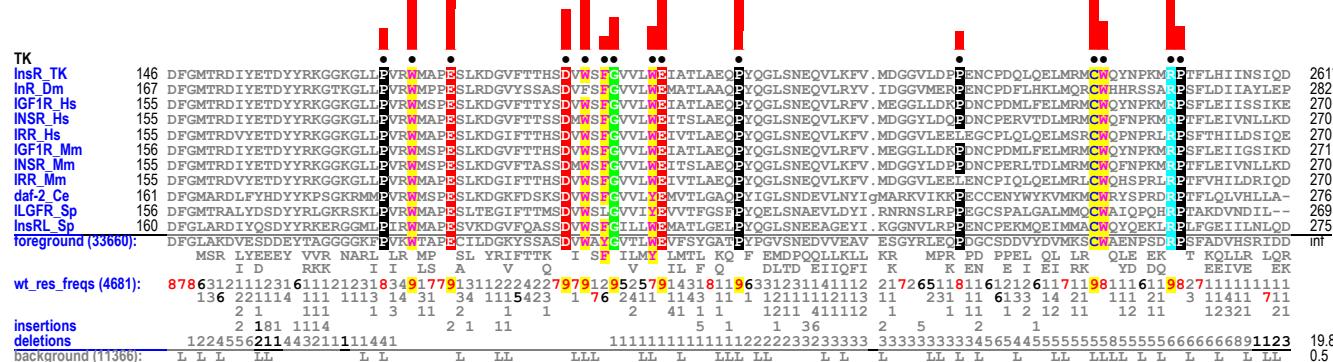
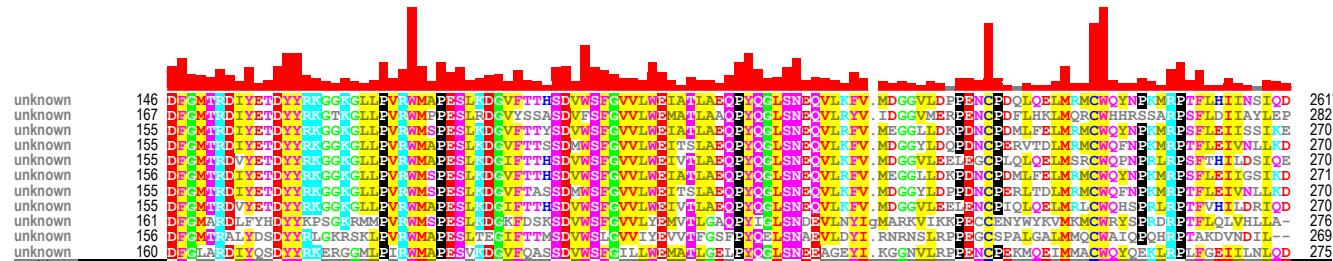
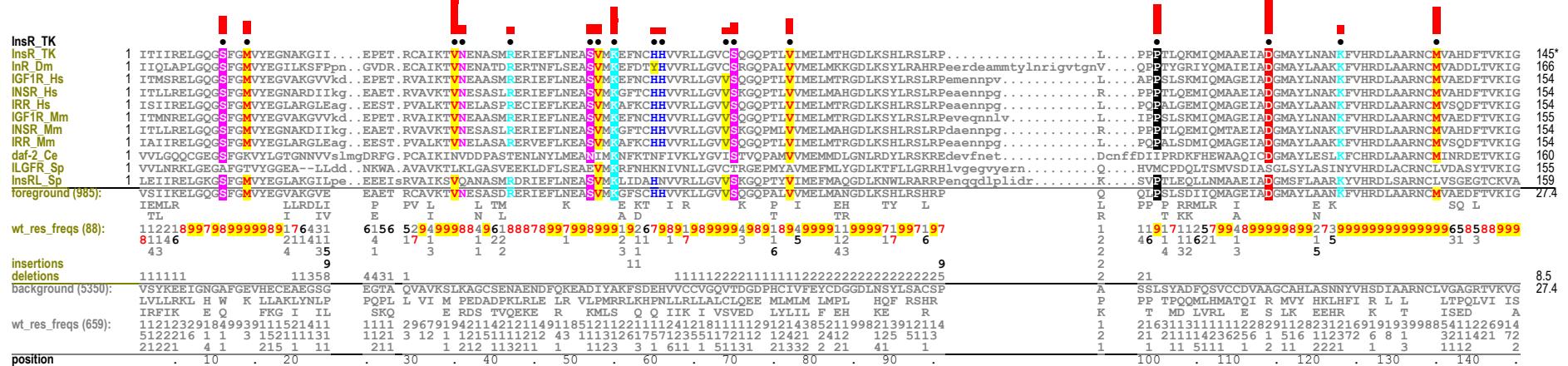
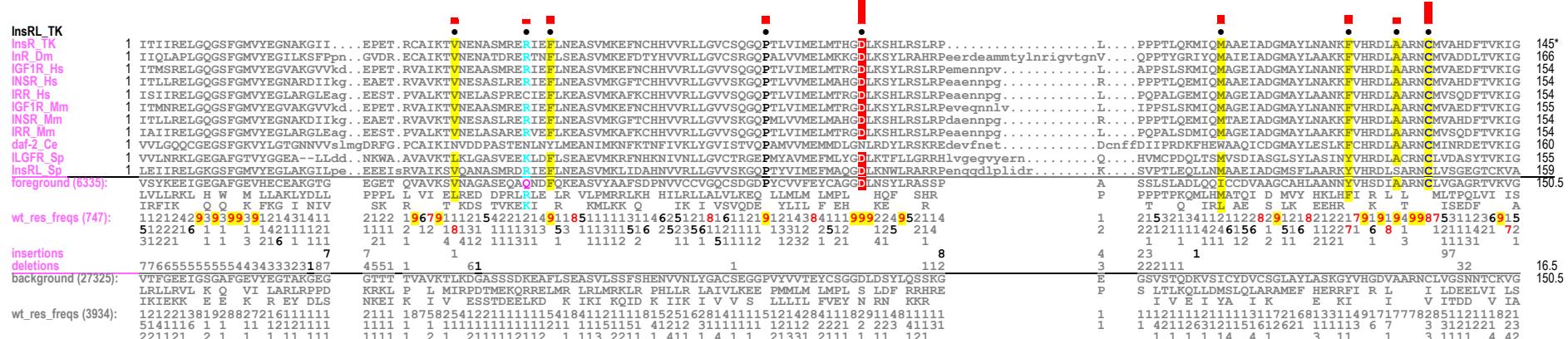
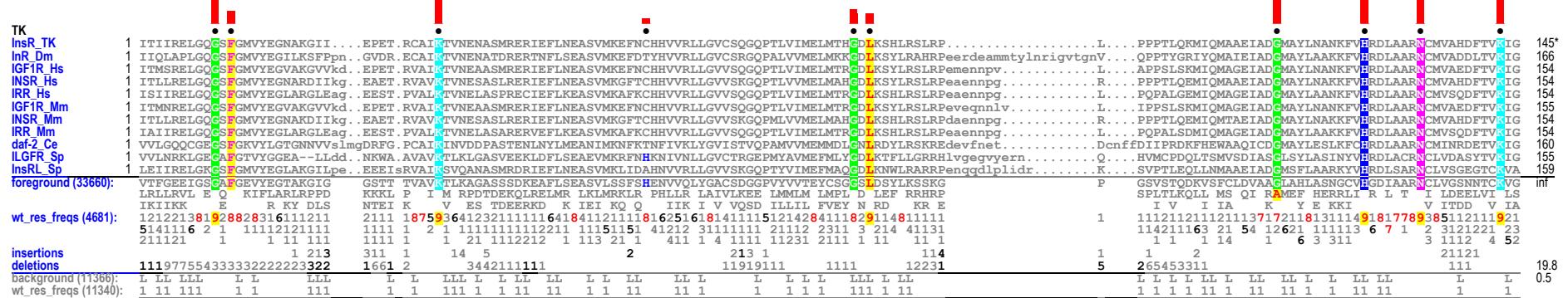
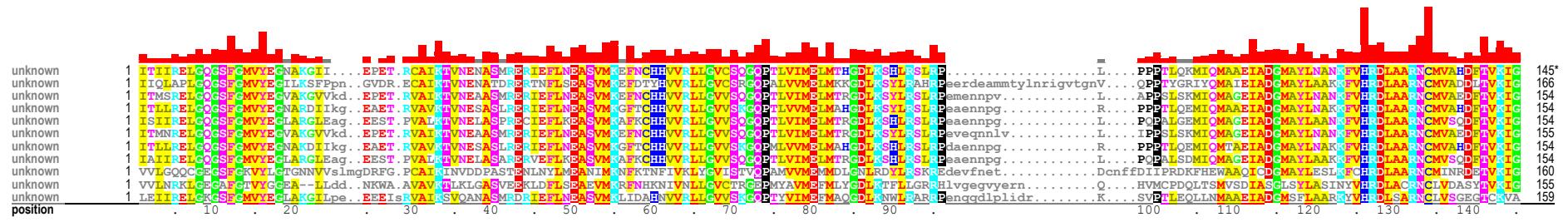


DDR_TK

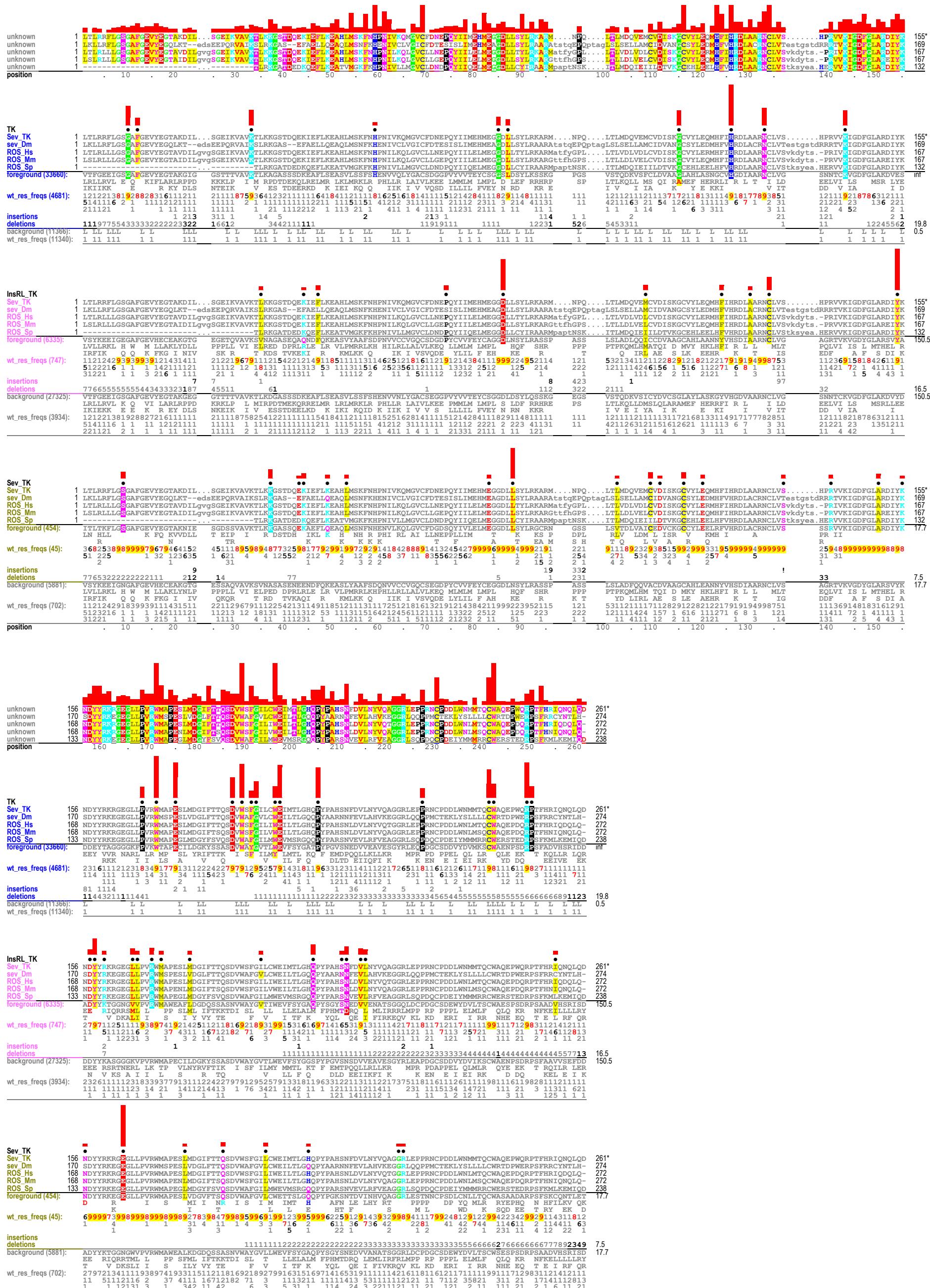




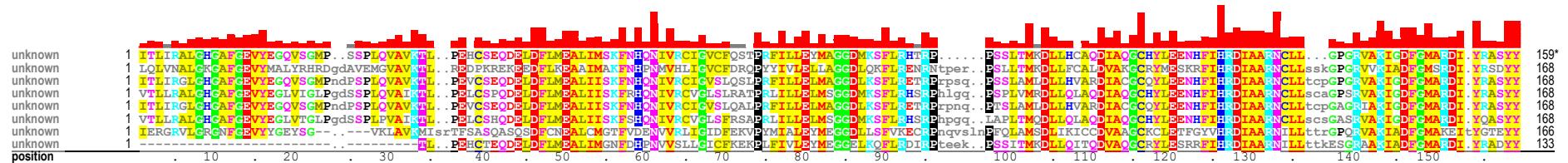
InsR_TK



Sev_TK

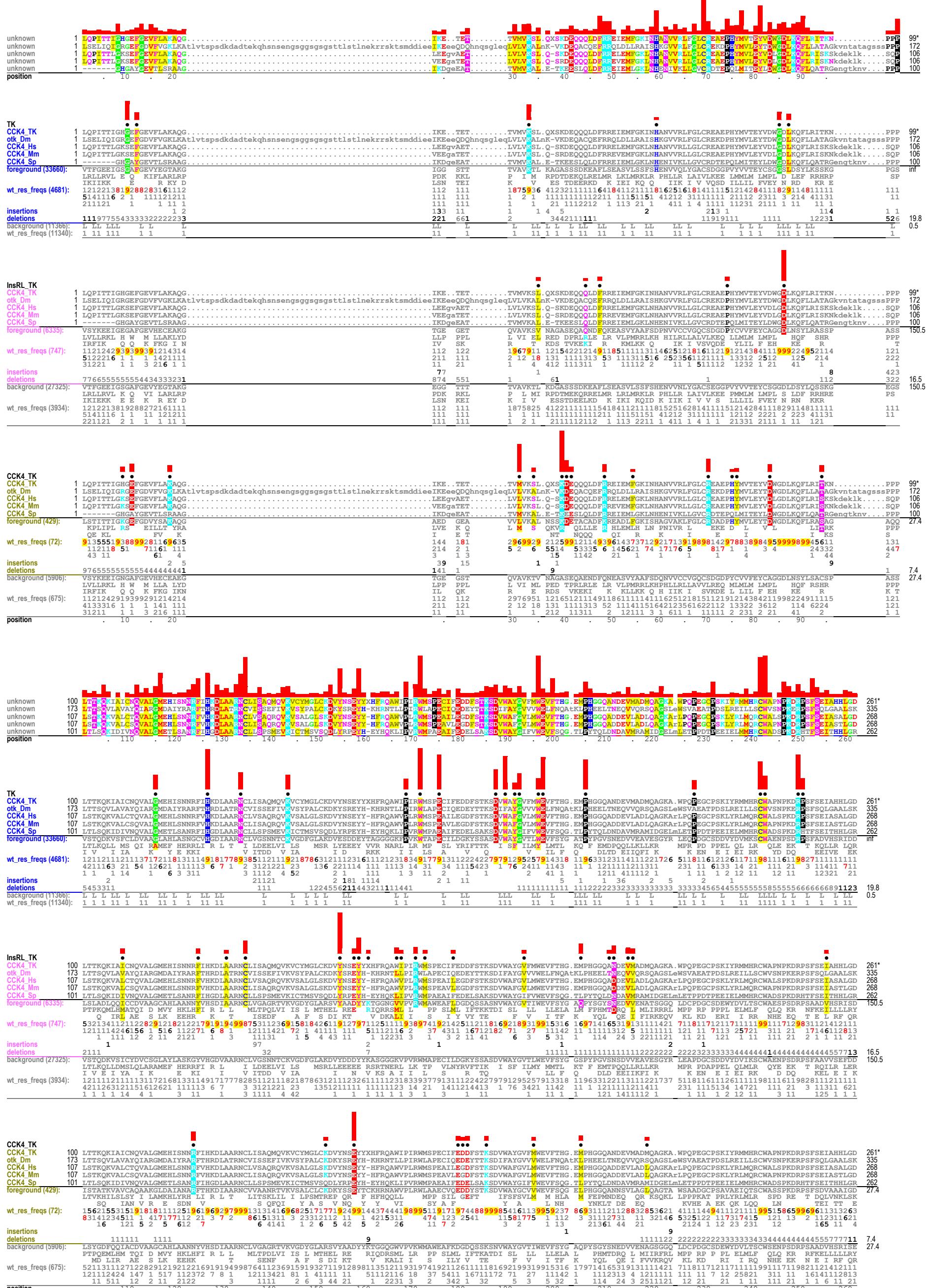


ALK_TK

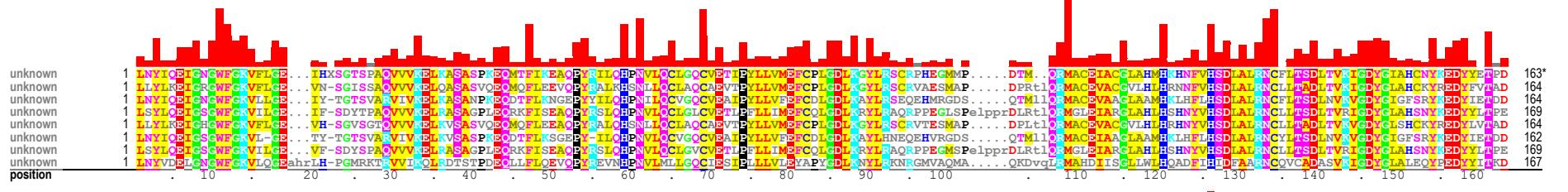


wt_res_freqs (672): 21241211939974192112511211917931893199152251797141653191111141171181161311611121991117119831122411811
51111116 2 27 5411 16612 72 61 21 211321 11111413 43111112 22 11 7123 36721 211 21 16151 12 12
1 12131 3 2 332 31 42 5 36 5 42 1 114 14 3 1221121 11 11 1 1 1 11 121 11 1 1 6 11 21
position . 170 . 180 . 190 . 200 . 210 . 220 . 230 . 240 . 250 . 260

CCK4_TK



Lmr_TK



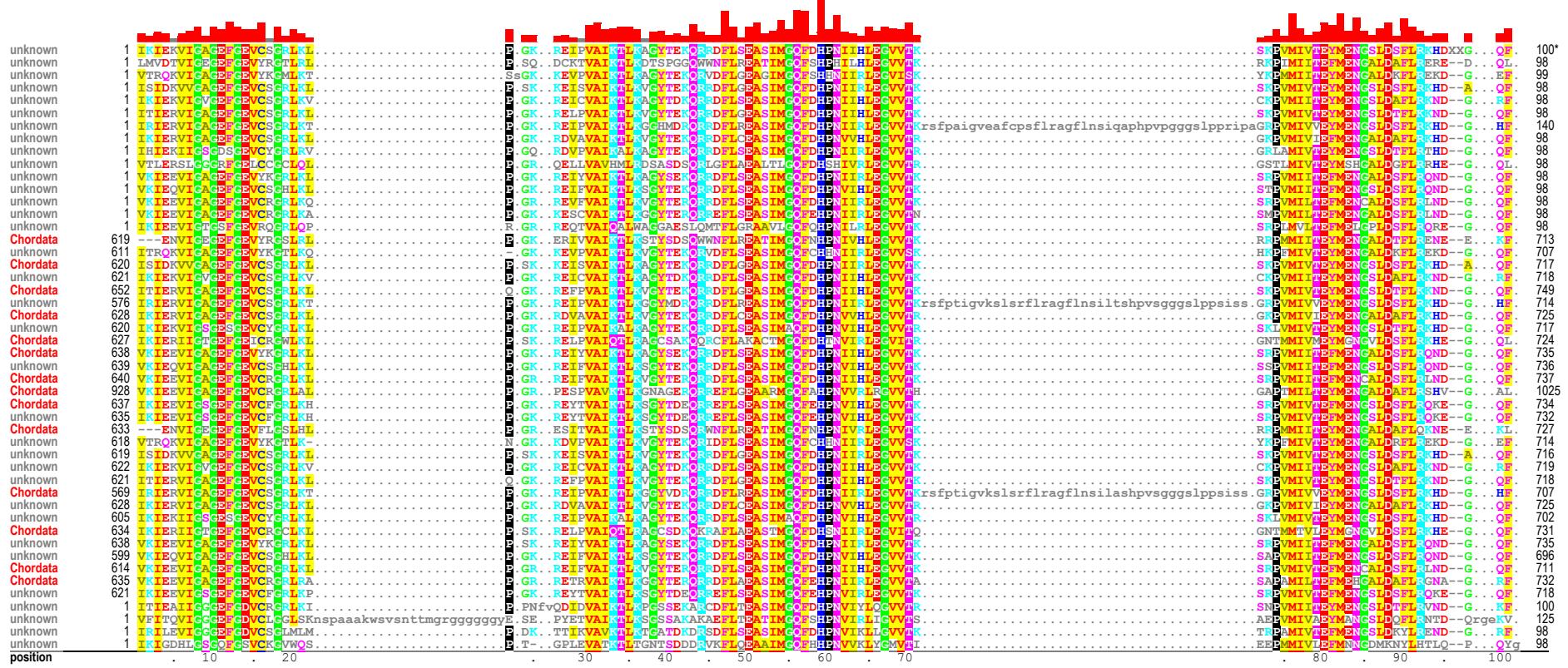
Sequence logo showing the conservation of amino acids at positions 164-168 across 100 homologous proteins. The x-axis shows positions 170 to 260. The y-axis shows amino acid probabilities for K, R, P, L, D, E, V, M, I, T, S, N, F, Y, C, W, G, H, Q, and G.

Position	Amino Acid	Probability (approx.)
164	K	0.95
164	R	0.05
165	Q	0.95
165	K	0.05
165	V	0.95
165	P	0.05
165	T	0.95
165	E	0.05
165	I	0.95
165	L	0.05
165	D	0.95
165	S	0.05
165	M	0.95
165	C	0.05
165	H	0.95
165	F	0.05
165	Y	0.95
165	G	0.05
166	Q	0.95
166	R	0.05
166	P	0.95
166	T	0.05
166	E	0.95
166	I	0.05
166	V	0.95
166	M	0.05
166	N	0.95
166	S	0.05
166	F	0.95
166	Y	0.05
166	G	0.95
167	Q	0.95
167	R	0.05
167	P	0.95
167	T	0.05
167	E	0.95
167	I	0.05
167	V	0.95
167	M	0.05
167	N	0.95
167	S	0.05
167	F	0.95
167	Y	0.05
167	G	0.95
168	Q	0.95
168	R	0.05
168	P	0.95
168	T	0.05
168	E	0.95
168	I	0.05
168	V	0.95
168	M	0.05
168	N	0.95
168	S	0.05
168	F	0.95
168	Y	0.05
168	G	0.95

wt_res_freqs (622):
1 21194198319
2 127 18 47
2 14 4 2
position . 170 . 180 . 190 . 200 . 210 . 220 . 230 . 240 . 250 . 260

311273122189693289179915426369714156319141411532711811
5211 177531 1 671 31 6144111 11112222 411121112121 11
432 1 1 3 1 1 1 4 5 3 22111 1 22 23
113 17 21 311 21 1 241121811
112 11 121 11 1 1 1 11

Eph_TK

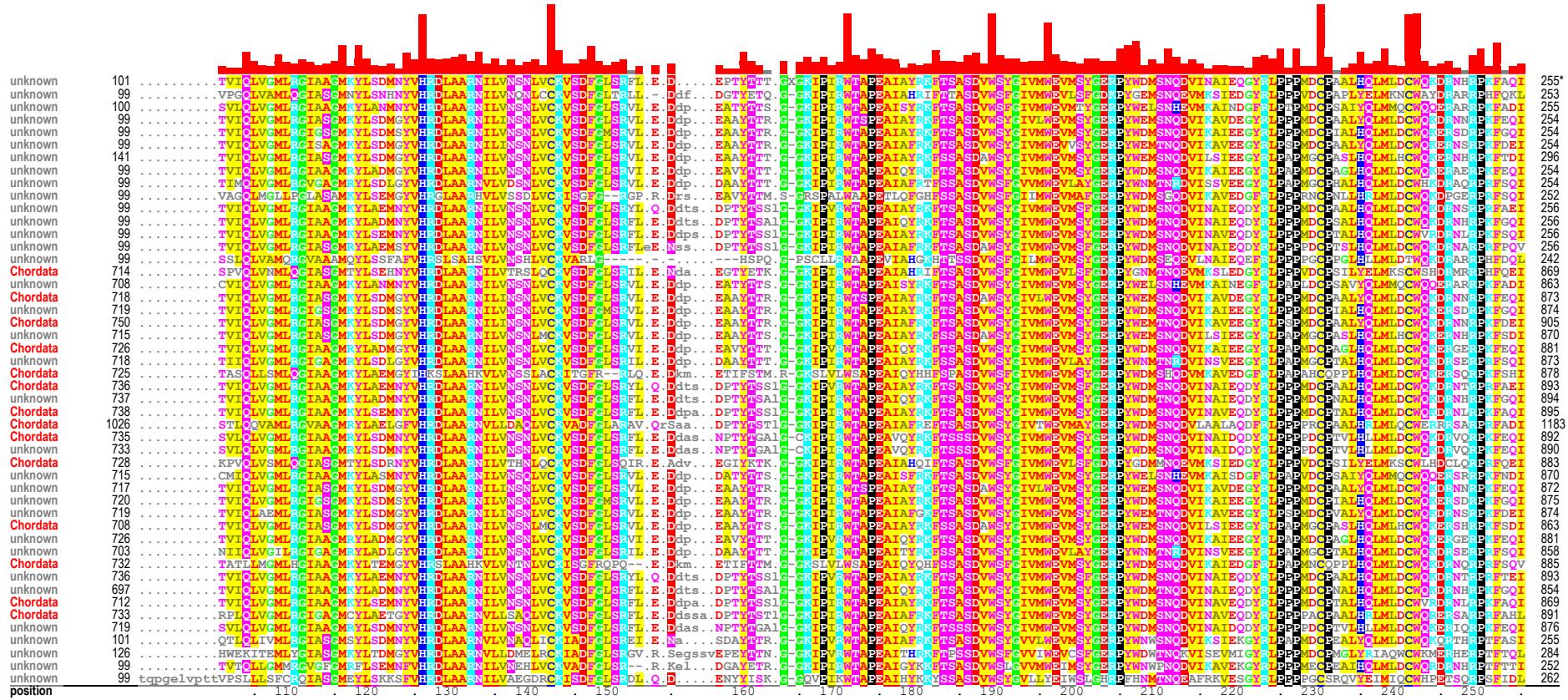


Legend:

- Insertions: Red dot
- Deletions: Blue dot
- wt_res_freqs (238): Red numbers (e.g., 31, 78, 78, 59, 99, 88, 62, 91, 81, 14, 5, 21)
- wt_res_freqs (443): Red numbers (e.g., 7, 75, 111, 99, 111, 97, 19, 1331, 7, 51, 99, 1996, 12, 9996, 91, 19, 31, 69, 99, 97, 95)

Nodes and Labels:

- Eph TK**: Root node.
- Eph_A1_Hs**, **Eph_A2_Hs**, **Eph_A3_Hs**, **Eph_A4_Hs**, **Eph_A5_Hs**, **Eph_A6_Hs**, **Eph_A7_Hs**, **Eph_A8_Hs**, **Eph_A10_Hs**, **Eph_B1_Hs**, **Eph_B2_Hs**, **Eph_B3_Hs**, **Eph_B4_Hs**, **Eph_B6_Hs**, **NP_989691.1**, **A0A1D5PX5_CHI**, **XP_015151343.1**, **XP_015131628.1**, **F1NUJP4_CHICK**, **NP_990414.1**, **F1HNC6_CHICK**, **XP_425778.2**, **XP_015132631.1**, **EPHB2_CHICK**, **XP_004943488.2**, **XP_015129488.1**, **NP_001004387.1**, **F1NAX7_CHICK**, **XP_014464720.1**, **EphA2**, **EphA3**, **EphA4**, **EphA5**, **XP_006262317.1**, **XP_006264943.1**, **EphB1**, **EphB2**, **XP_006260832.1**, **XP_014464024.1**, **EphB5**, **Eph_Dm**, **vab-1_Ce**, **Eph_Sp**, **An_AqueK315**: Various Eph TK orthologs across different species.
- foreground (2906):** A large clade containing many mutations.
- background (30754):** A large clade containing mutations.
- wt_res_freqs (443):** Specific mutations highlighted with red numbers.



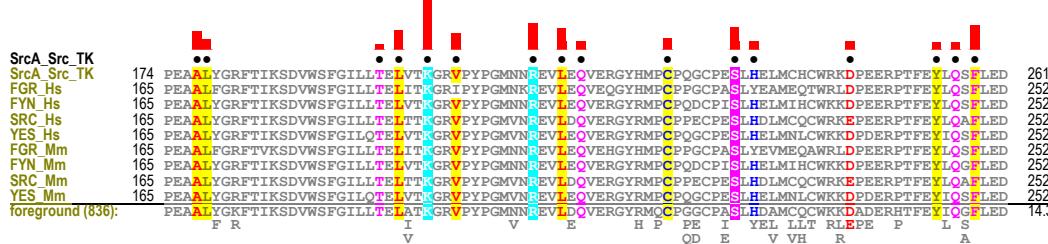
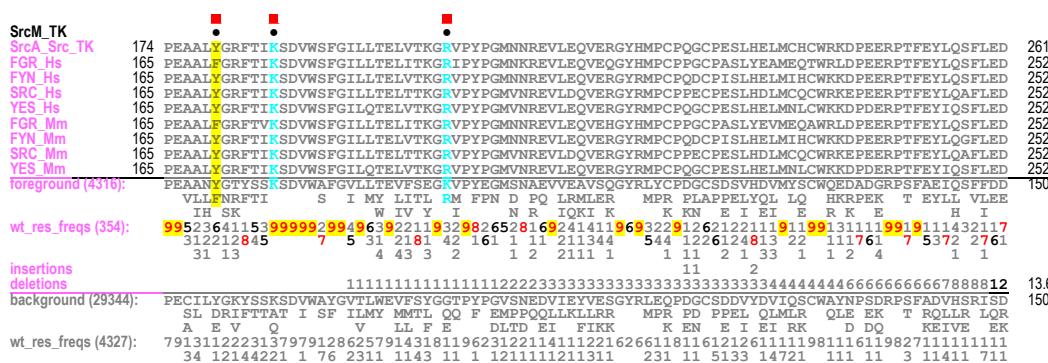
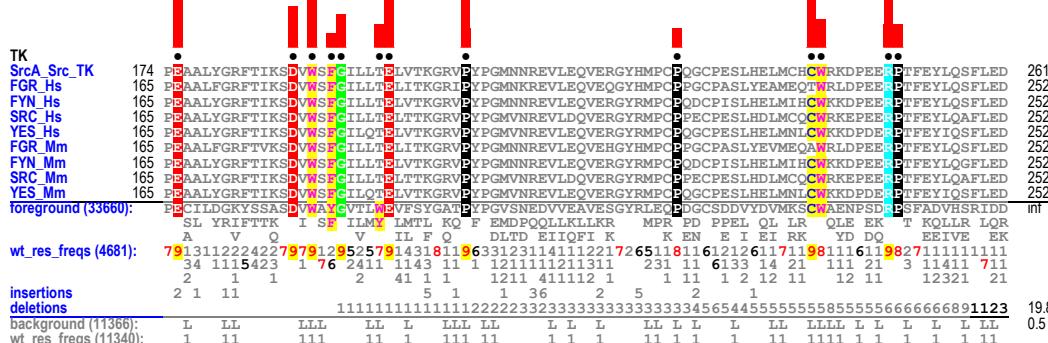
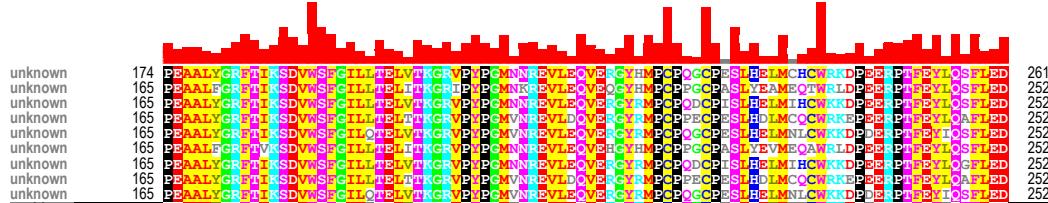
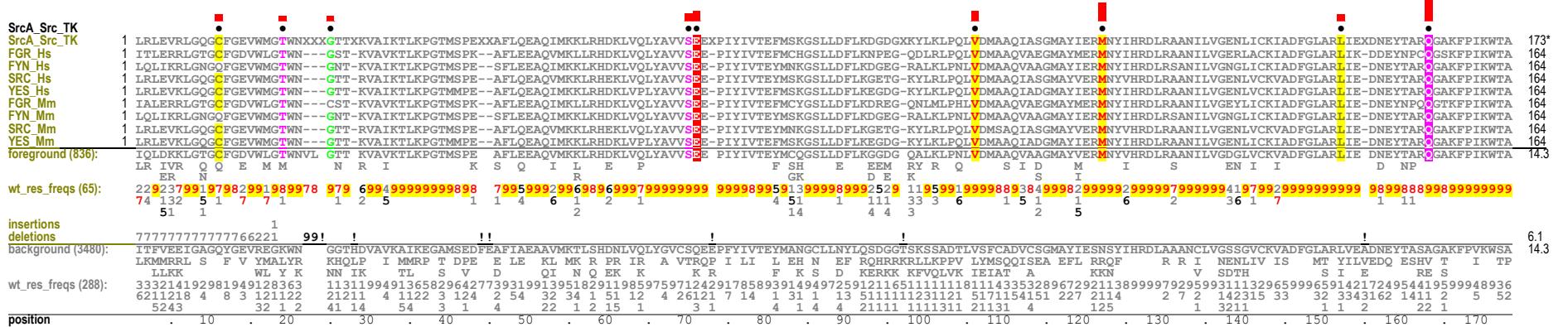
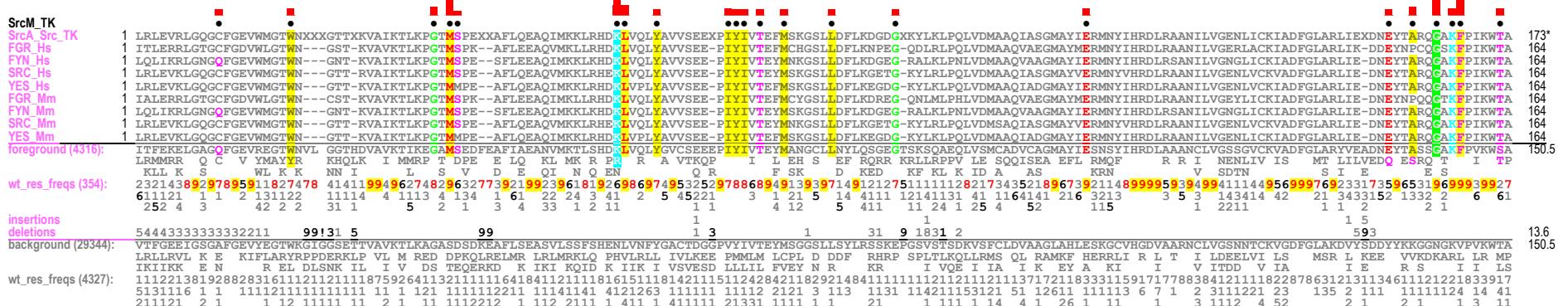
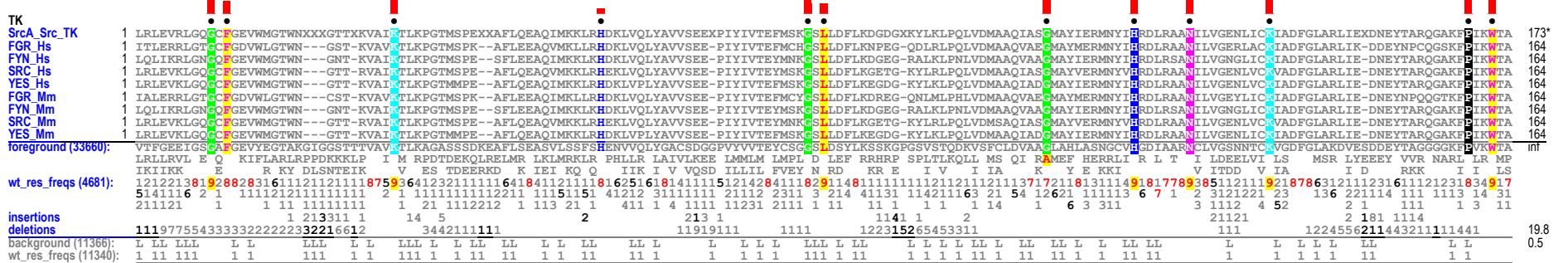
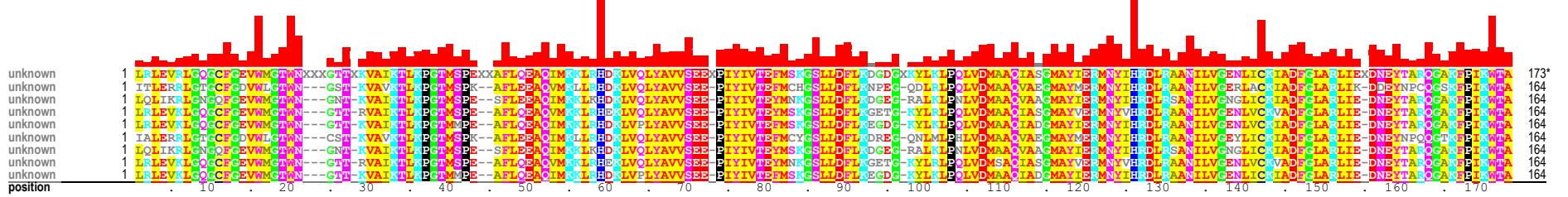
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unknown	254	QAHLEQ	259
unknown	256	VSILDK	261
unknown	256	VSILDK	260
unknown	256	VNMLDK	260
unknown	256	VNMLDK	260
unknown	297	VSFLDK	302
unknown	256	VGILDK	260
unknown	256	VSVDL-	259
unknown	253	HSILSK	258
unknown	257	VNTLDK	262
unknown	257	VNTLDK	262
unknown	257	VNTLDK	262
unknown	257	VSALDK	262
Chordata	243	VAAFDK	248
Chordata	870	RAQL--	873
unknown	864	VSILDK	869
Chordata	874	VSILDK	879
unknown	875	VNMLDK	880
Chordata	906	VSMLDK	911
unknown	871	VSFLDK	876
Chordata	882	VGILDK	887
unknown	874	VGILDK	878
Chordata	879	HDVLSK	884
Chordata	894	VNTLDK	899
unknown	895	VNTLDK	900
Chordata	896	VNTLDK	901
Chordata	1184	VRALDR	1189
Chordata	893	VSALDK	898
unknown	891	VSALDK	896
Chordata	884	QAQLE-	888
unknown	871	VSILDK	876
unknown	873	VSILDK	878
unknown	876	VNMLDK	881
unknown	875	VSMLDK	880
Chordata	864	VSFLDK	869
unknown	882	VGILDK	887
unknown	855	VSILDK	863
Chordata	886	HSILSK	891
unknown	894	VNTLDK	899
unknown	855	VNTLDK	860
Chordata	870	VNTLDK	875
Chordata	892	VRALDR	897
unknown	877	VSALDK	882
unknown	256	VSTLDN	261
unknown	285	LATFKH	290
unknown	253	YSTTDR	258
unknown	263	VTRLSQ	268

position
260

TK	256	VNTLDK	261*
Eph_A1_Hs	254	QAHLEQ	259
Eph_A2_Hs	256	VSILDK	261
Eph_A3_Hs	255	VSILDK	260
Eph_A4_Hs	255	VNMLDK	260
Eph_A5_Hs	255	VNMLDK	260
Eph_A6_Hs	297	VSFLDK	302
Eph_A7_Hs	256	VGILDK	260
Eph_A8_Hs	255	VSVDL-	259
Eph_A10_Hs	253	HSILSK	258
Eph_B1_Hs	257	VNTLDK	262
Eph_B2_Hs	257	VNTLDK	262
Eph_B3_Hs	257	VNTLDK	262
Eph_B4_Hs	257	VSALDK	262
Eph_B5_Hs	243	VAAFDK	248
NP_989691.1	870	RAQL--	873
A0A1D5PXE5_CH	864	VSILDK	869
XP_015151343.1	874	VSILDK	879
EPHA4_CHICK	875	VNMLDK	880
XP_015131628.1	906	VSMLDK	911
F1NUP4_CHICK	871	VSFLDK	876
NP_990414.1	882	VGILDK	887
F1NHG6_CHICK	874	VGILDK	878
XP_425778.2	879	HDVLSK	884
XP_015132631.1	894	VNTLDK	899
EPHB2_CHICK	895	VNTLDK	900
XP_004943488.2	896	VNTLDK	901
XP_015129488.1	1184	VRALDR	1189
NP_001004387.1	893	VSALDK	898
F1NAX7_CHICK	891	VSALDK	896
XP_014464720.1	884	QAQLE-	888
Eph_A2	871	VSILDK	876
Eph_A3	873	VSILDK	878
Eph_A4	876	VNMLDK	881
Eph_A5	875	VSMLDK	880
XP_006262317.1	864	VSFLDK	869
Eph_A7	882	VGILDK	887
Eph_A8	859	VSILD-	863
XP_006264943.1	886	HSILSK	891
Eph_B1	894	VNTLDK	899
Eph_B2	895	VNTLDK	890
XP_006260832.1	870	VNTLDK	875
XP_014464024.1	894	VRALDK	897
Eph_B5	877	VSALDK	882
Eph_Dm	256	VSTLDN	261
vab-1_Ce	285	LATFKH	290
Eph_Sp	253	VSTLDR	258
Ag_AqueK315	263	VTRLSQ	268
foreground (33660):		HSRIDD	inf
		LB_LQR	
		VE_EK	
wt_res_freqs (4681):	111111		
	11 711		
	21 21		
insertions			
deletions	891123	19.8	
background (11366):	L LL	0.5	
wt_res_freqs (11340):	1 11		

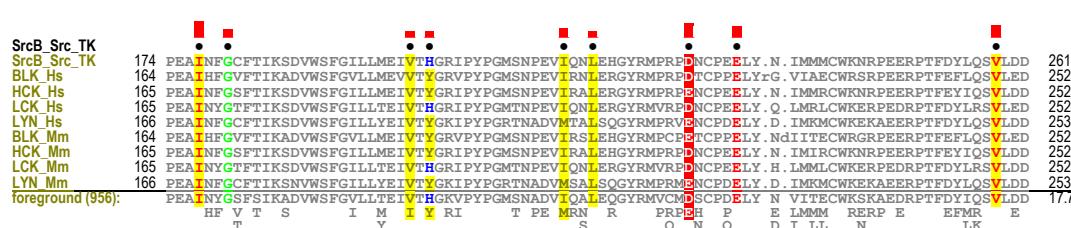
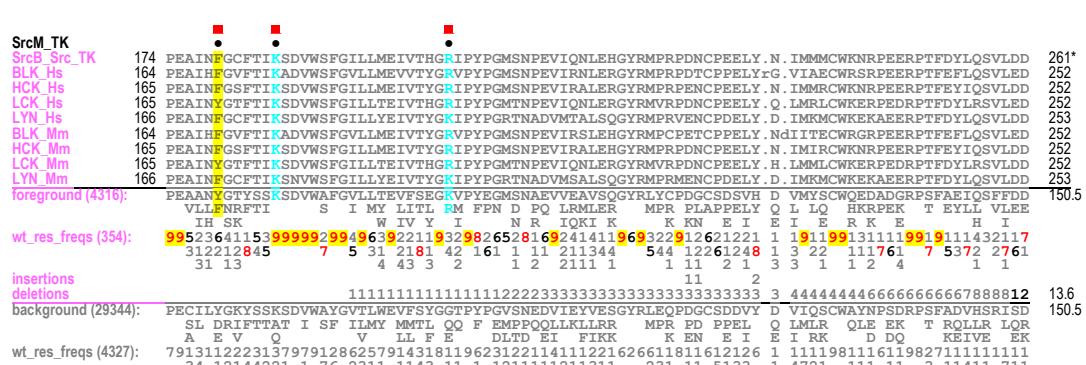
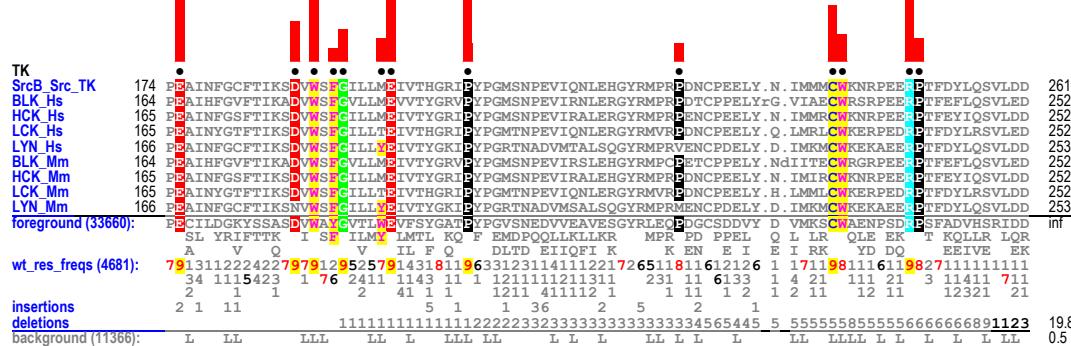
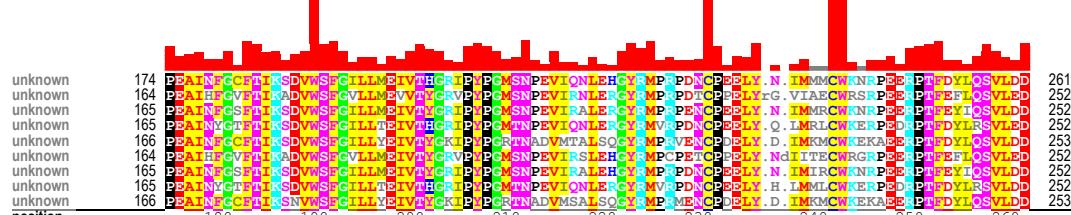
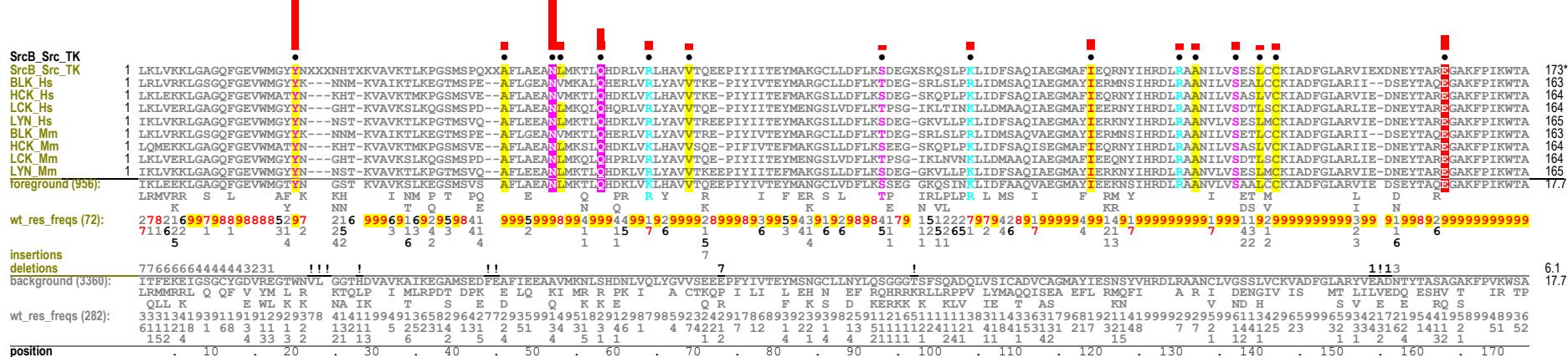
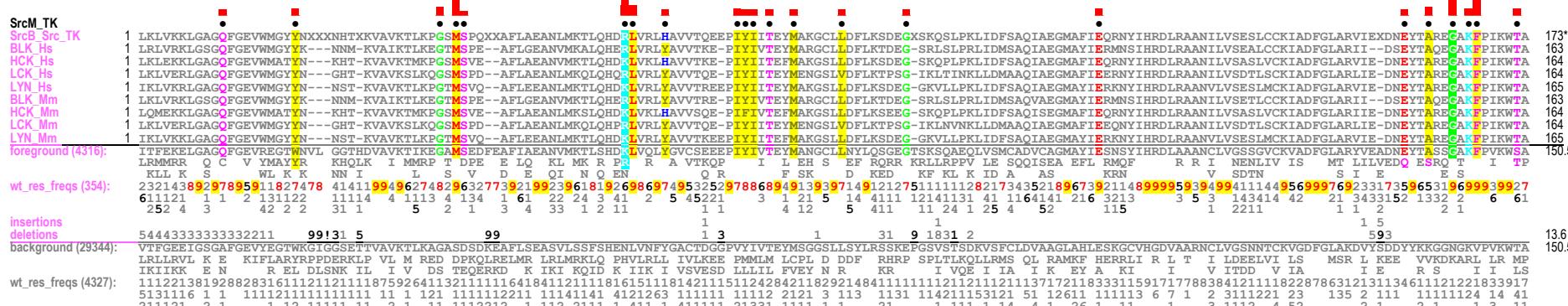
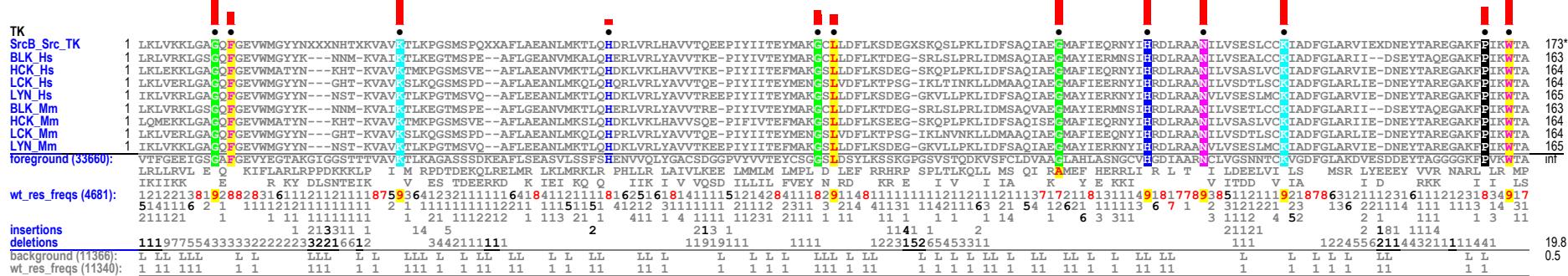
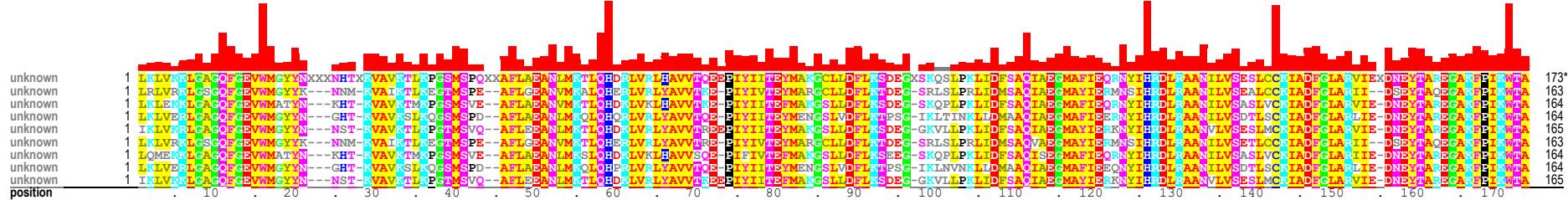
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Eph_A1_Hs	254	QAHLEQ	259
Eph_A2_Hs	256	VSILDK	261
Eph_A3_Hs	256	VSILDK	260
Eph_A4_Hs	257	VNMLDK	260
Eph_A5_Hs	257	VNMLDK	260
Eph_A6_Hs	297	VSFLDK	302
Eph_A7_Hs	256	VGILDK	260
Eph_A8_Hs	255	VSVDL-	259
Eph_A10_Hs	253	HSILSK	258
Eph_B1_Hs	257	VNTLDK	262
Eph_B2_Hs	257	VNTLDK	262
Eph_B3_Hs	257	VNTLDK	262
Eph_B4_Hs	257	VSALDK	262
Eph_B6_Hs	243	VAAFDK	248
NP_989691.1	870	RAQL--	873
A0A1D5PXE5_CH	864	VSILDK	869
XP_015151343.1	874	VSILDK	879
EPHA4_CHICK	875	VNMLDK	880
XP_015131628.1	906	VSMLDK	911
F1NUP4_CHICK	871	VSFLDK	876
NP_990414.1	882	VGILDK	887
F1NHG6_CHICK	874	VGILDK	878
XP_425778.2	879	HDVLSK	884
XP_015132631.1	894	VNTLDK	899
EPHB2_CHICK	895	VNTLDK	900
XP_004943488.2	896	VNTLDK	901
XP_015129488.1	1184	VRALDR	1189
NP_001004387.1	893	VSALDK	898
F1NAX7_CHICK	891	VSALDK	896
XP_014464720.1	884	QAQLE-	888
Eph_A2	871	VSILDK	876
Eph_A3	873	VSILDK	878
Eph_A4	876	VNMLDK	881
Eph_A5	875	VSMLDK	880
XP_006262317.1	864	VSFLDK	869
Eph_A7	882	VGILDK	887
Eph_A8	859	VSILD-	863
XP_006264943.1	886	HSILSK	891
Eph_B1	894	VNTLDK	899
Eph_B2	855	VNTLDK	860
XP_006260832.1	870	VNTLDK	875
XP_014464024.1	892	VRALDK	897
Eph_B5	877	VSALDK	882
Eph_Dm	256	VSTLDN	261
vab-1_Ce	285	LATFKH	290
Eph_Sp	253	VSTLDR	258
Ag_AqueK315	263	VTRLSQ	268
foreground (2906):	HAALSK	100.3	
	VNI_D		
	ST		
wt_res_freqs (238):	111918		
	7227		
	41		
insertions			
deletions	444471	11.2	
background (30754):	HSRIED	100.3	
	LB_LQR		
	VE_E		
wt_res_freqs (4443):	111121		
	11 711		
	11 111		
position	260		

SrcA_Src_TK

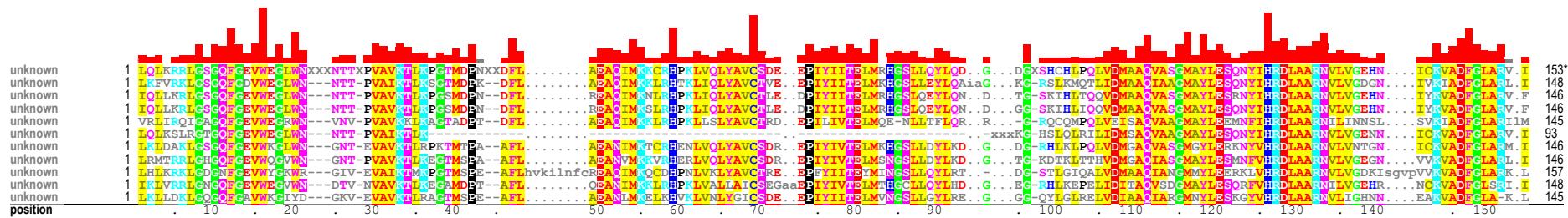


insertions
 deletions
 background (3480): PEAALYGTYSKSDVWAYGVLLTEVFSEGKVPMGRSSNAEVLEQVSQCHRLCPDGGSDEVNVMSGSCWQEKADGRPSFAYIOSQFDD 6.1
 VLNFRFTI SF I MY IITL RM FPNMD PQ YRMLER Y MPR KLAPP L QL MR H RPEK T ETLLWVLEE 14.3
 IH SK W V Y I T S TOKI K YK QN K I EI LO K E DE HH I
 994116311639999921949529331294198351271681313229194119115212391291199143111992912123116
 423222734 78 5 41 5171 32 15141 12 111433 5 545 13361 3 12 11 2 1751 6 417212651
 31 24 5 2 4 2 3 2 3111 1 31 12 1 2 34 21 2 3 11 11 1
 position . 180 . 190 . 200 . 210 . 220 . 230 . 240 . 250 . 260

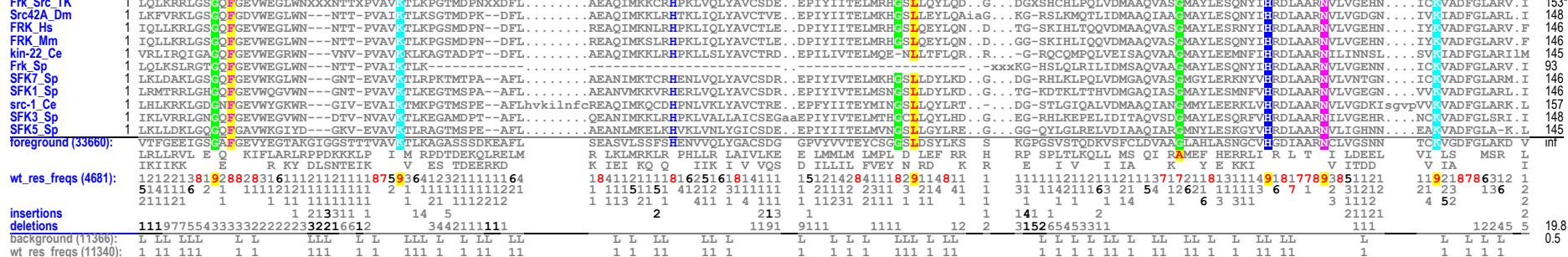
SrcB_Src_TK



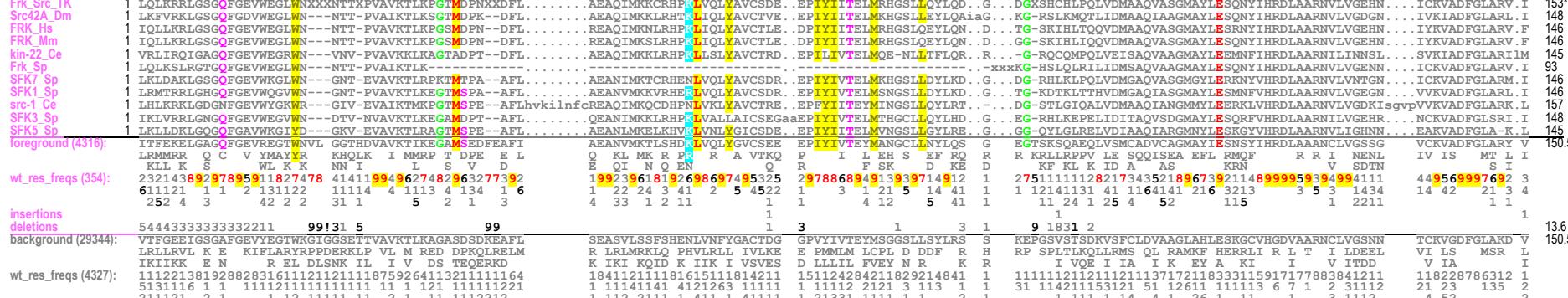
Frk_Src_TK



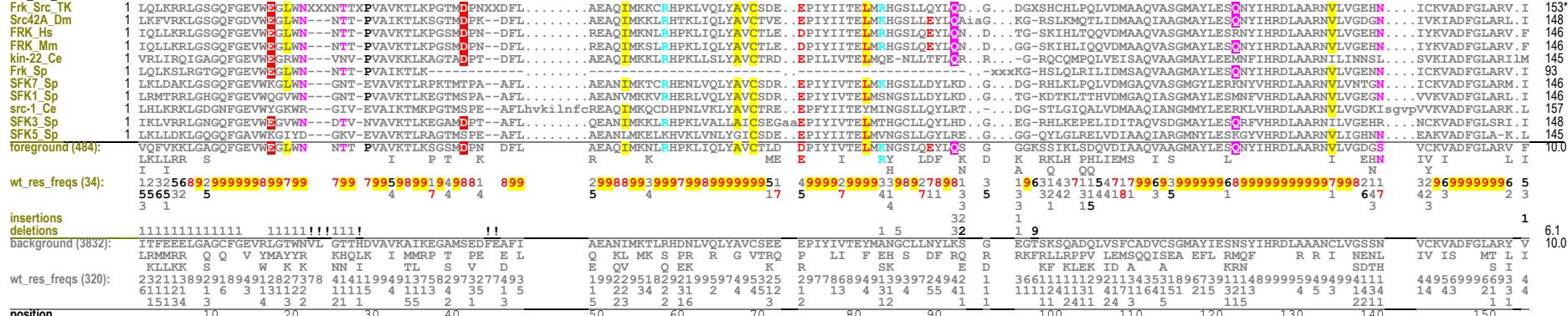
TK



SrcM_TK



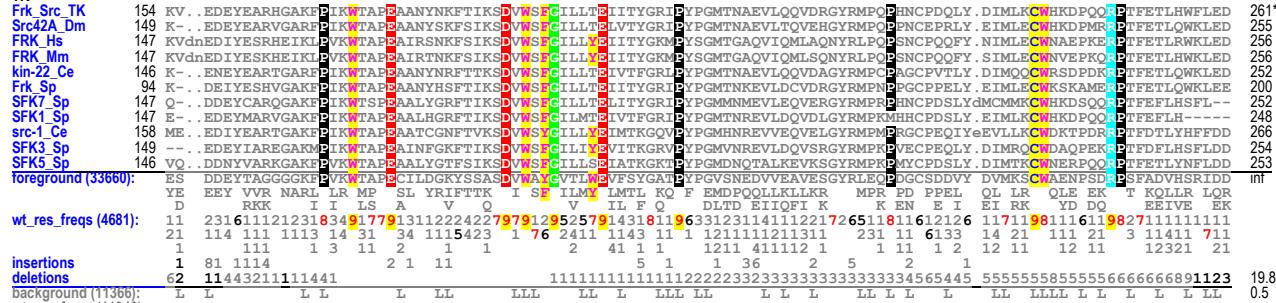
Frk_Src_TK



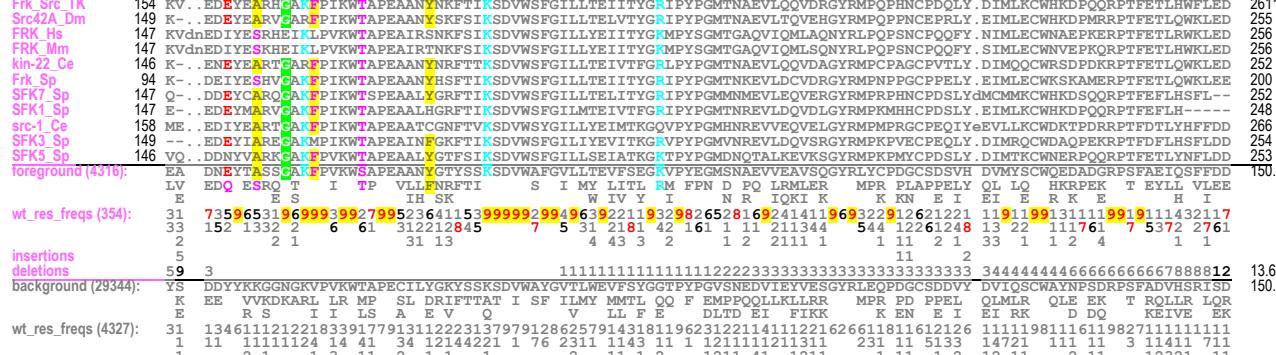
TK



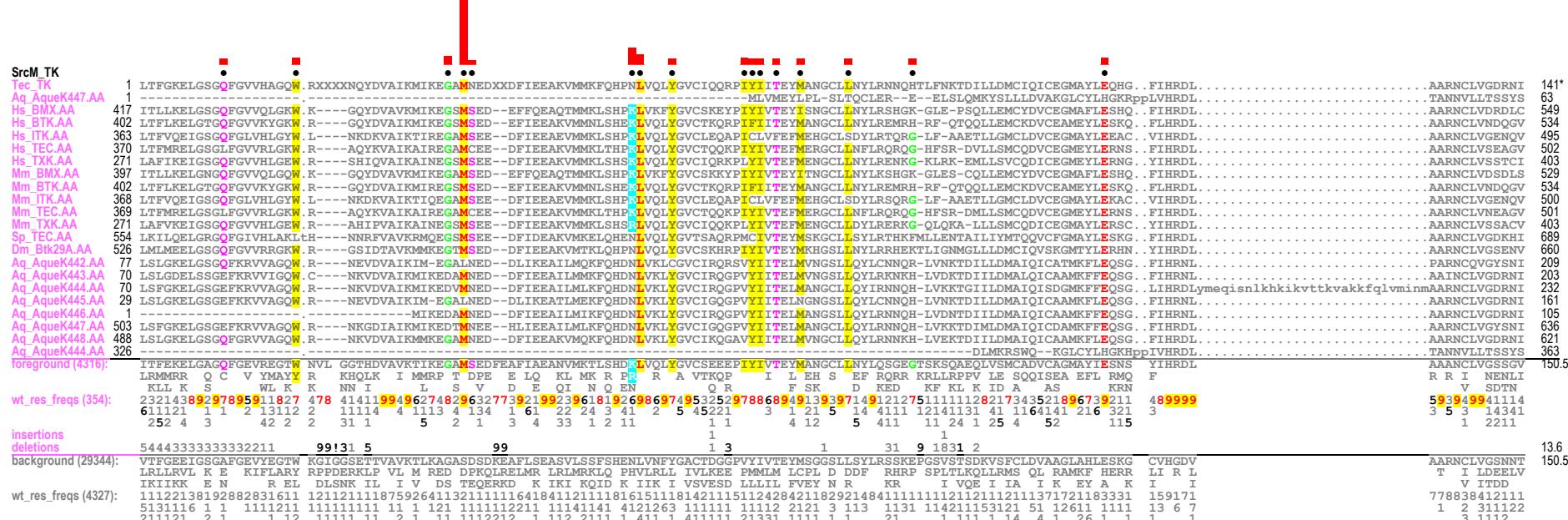
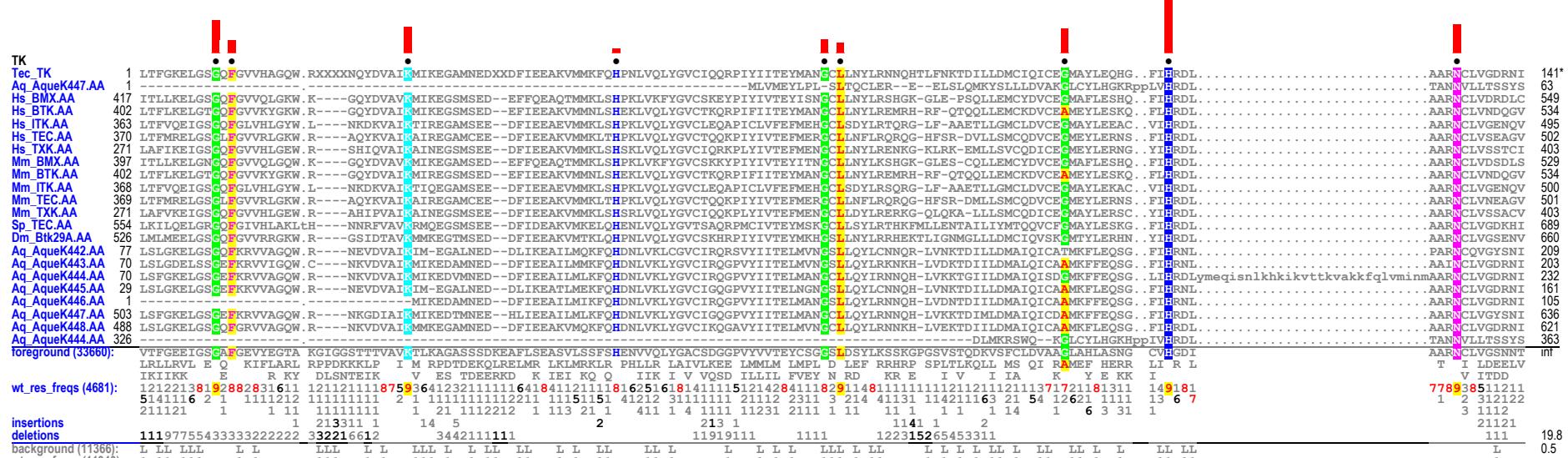
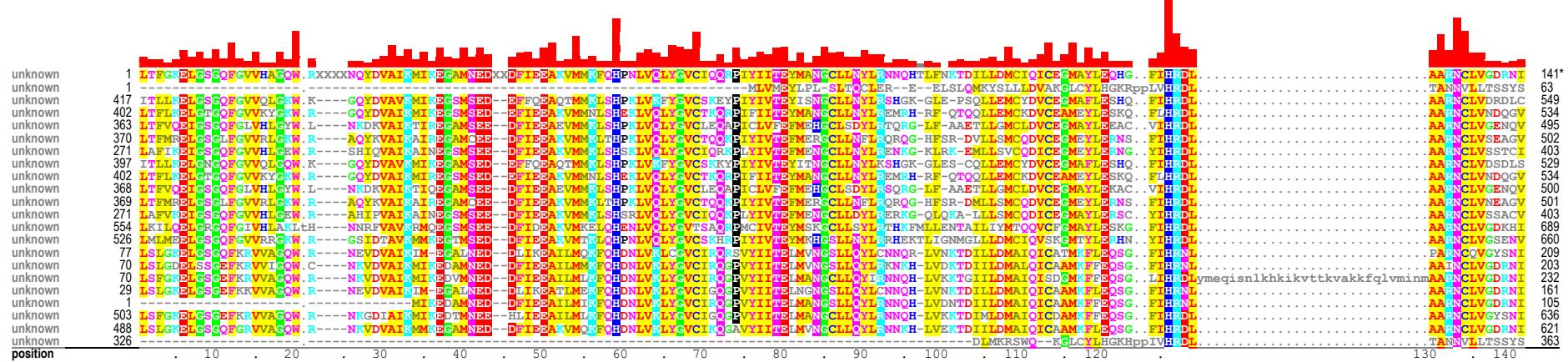
SrcM_TK



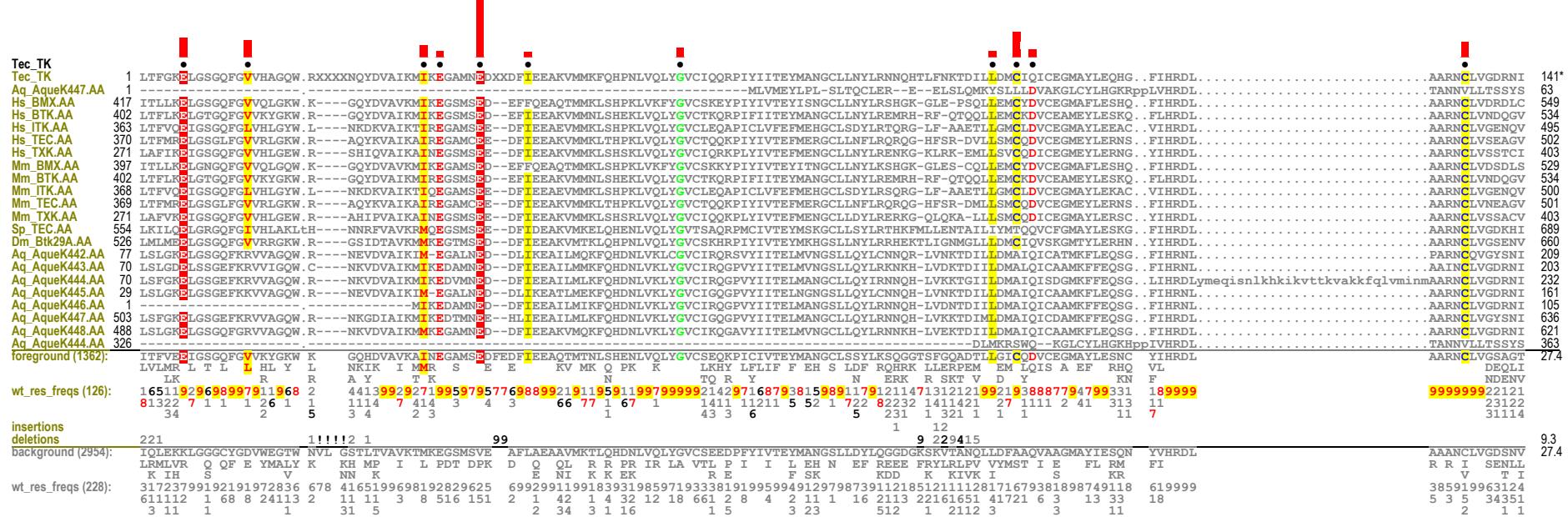
Frk_Src_TK

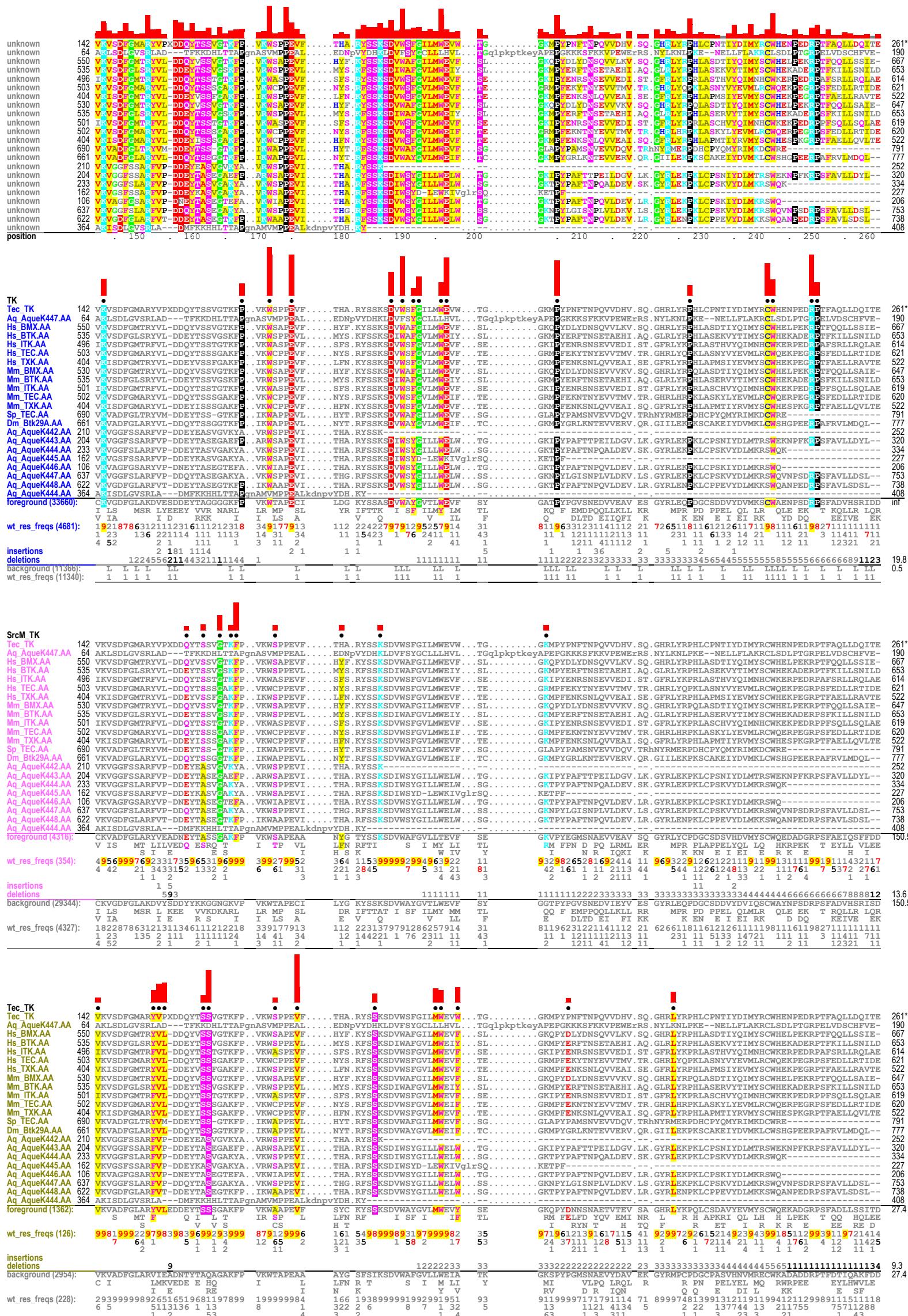


Tec_TK

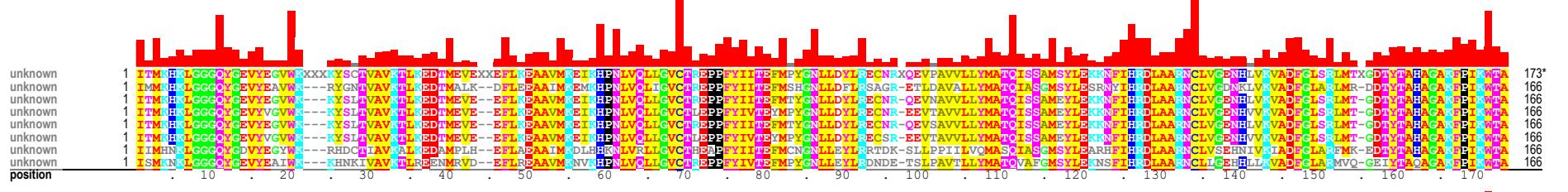


~~211121 2 1 1 12 111111 11 2 1 11 1112212 1 112 2111 1 411 1 411111 21531 1111 1 1 21 1 1 111 1 14 4 1 26 1 1 1 1~~ 3 1112



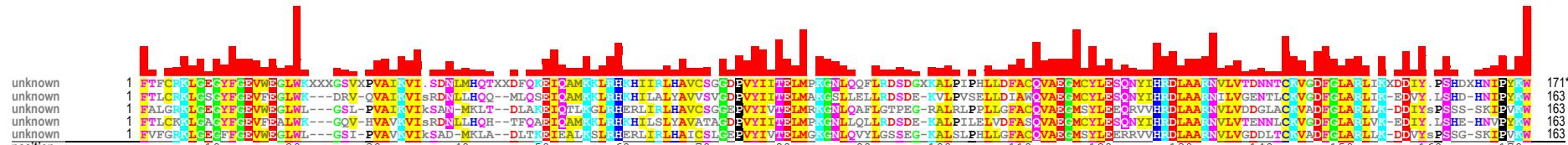


Abl_TK

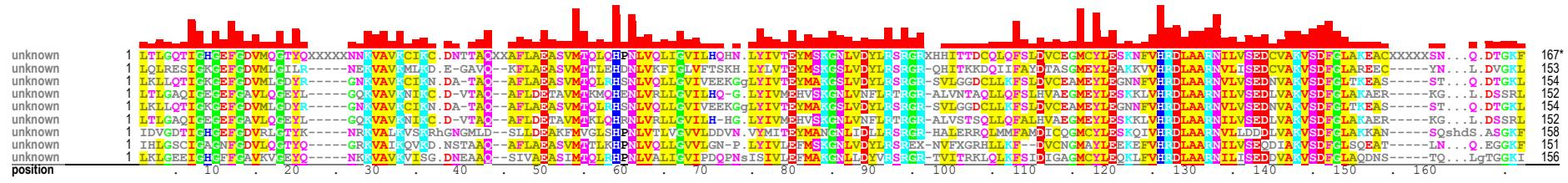


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312213845 8 6 31 2181 52 15151 11 211244 554 1226225712 12 211761 7 5 2 2761
31 1 3 33 3 2 5 2 2121 1 12 1 34 21 1 2 4
position . 180 . 190 . 200 . 210 . 220 . 230 . 240 . 250 . 260

SRM_Src_TK



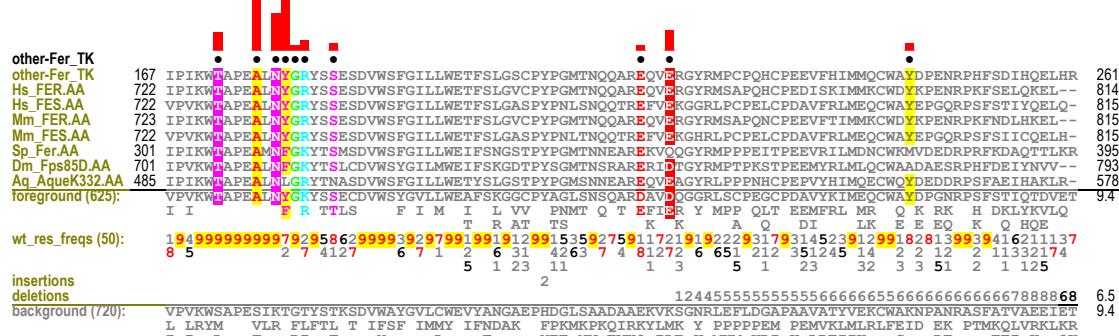
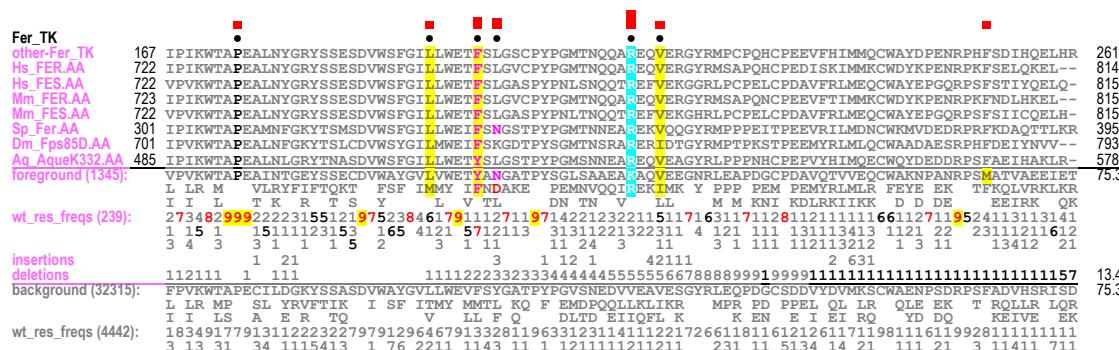
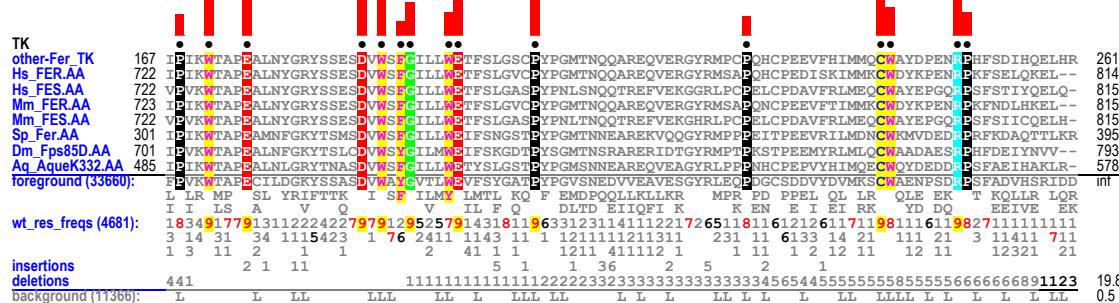
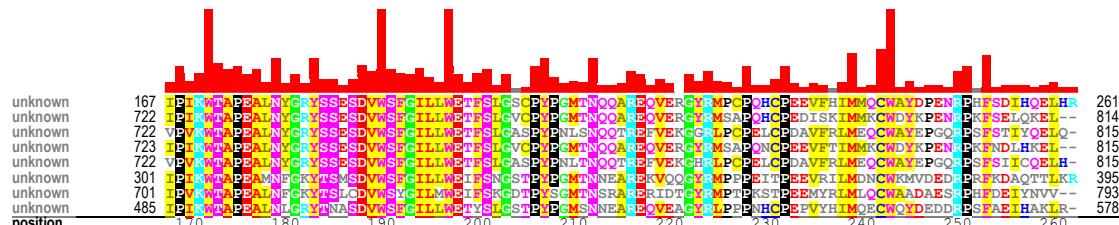
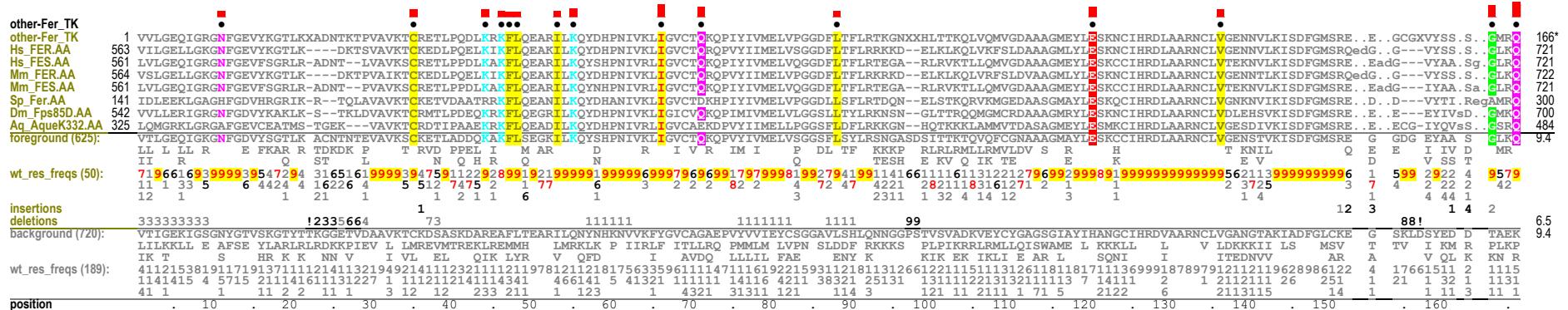
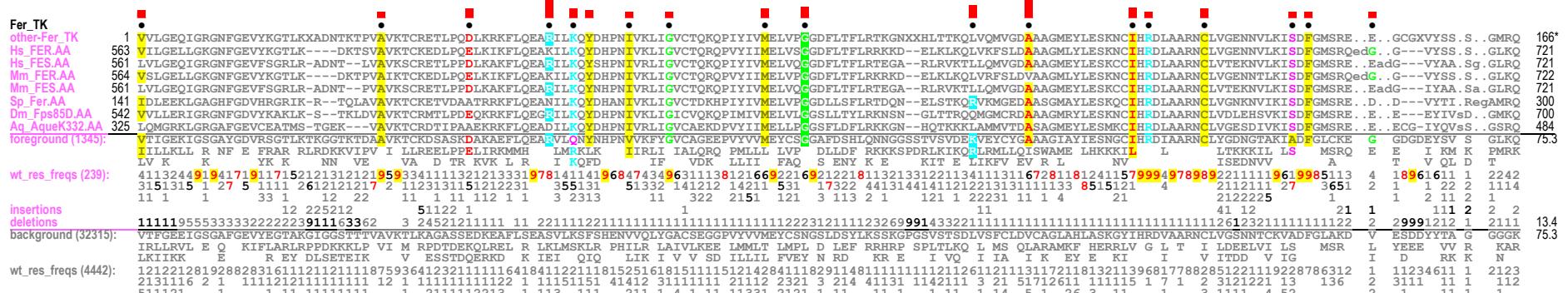
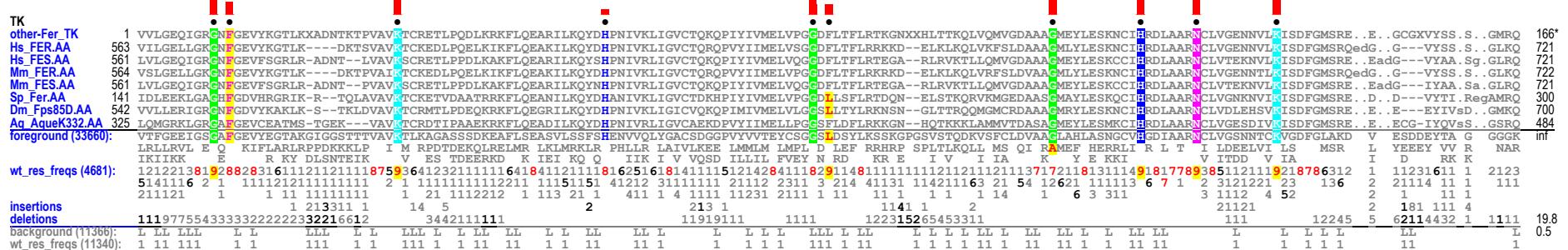
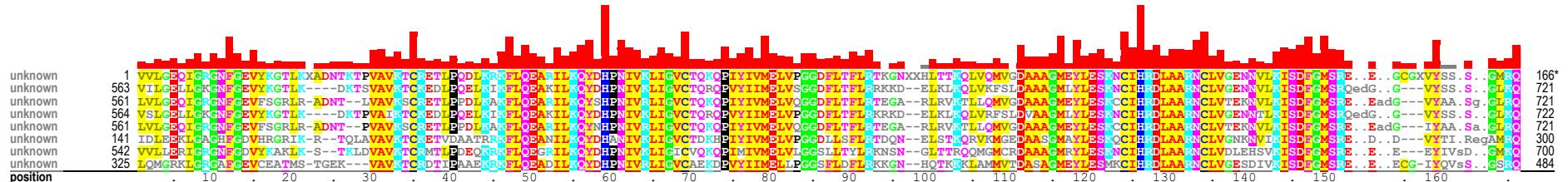
Csk_TK



Sequence logo showing the conservation of amino acids at each position of the protein sequence. The x-axis represents positions 168 to 261, and the y-axis represents amino acids (P, S, T, C, I, L, V, M, D, E, G, R, K, H, N, Q, Y, F).

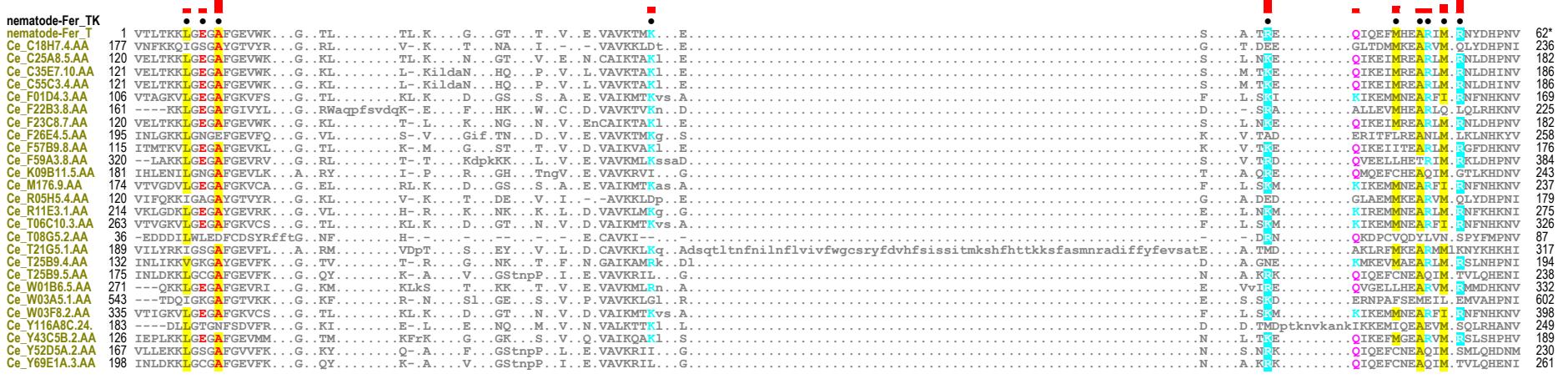
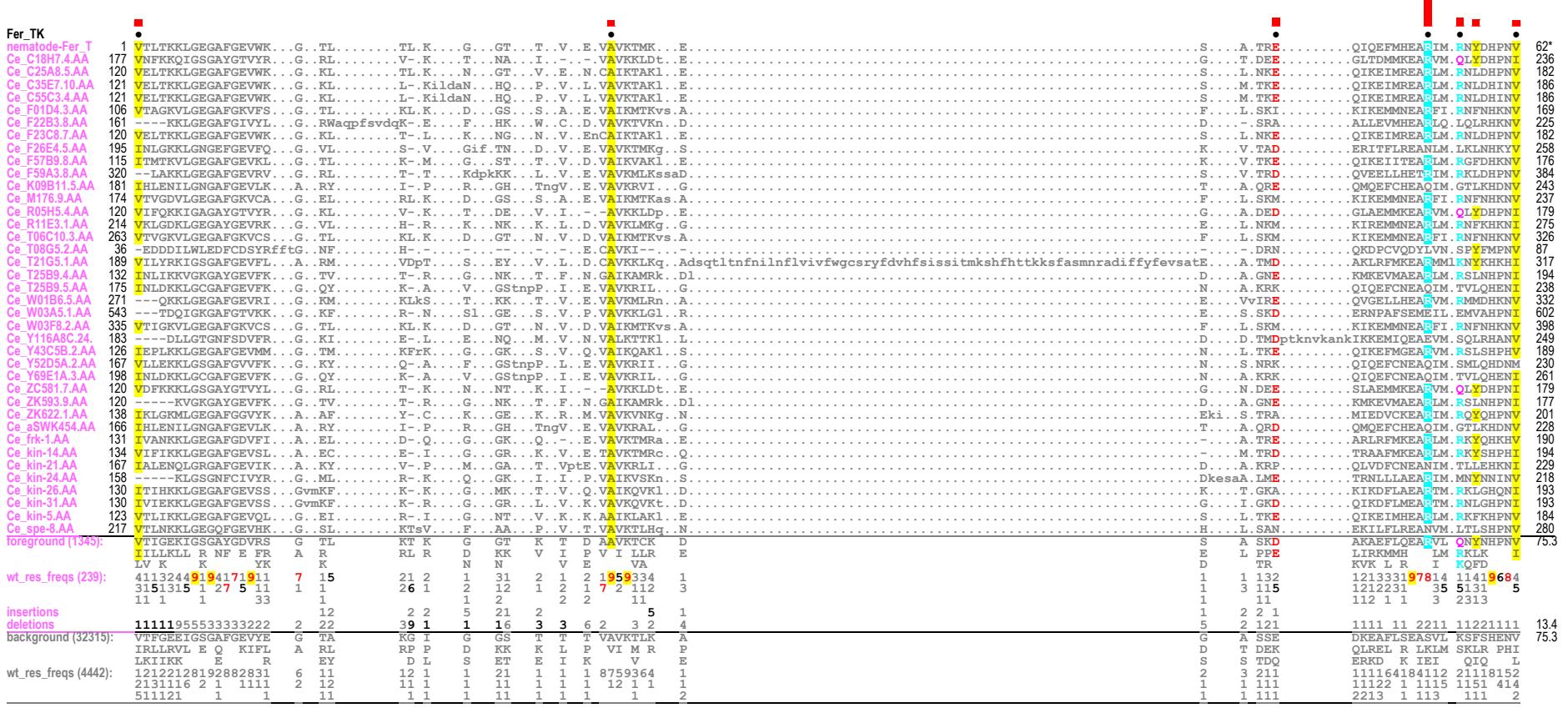
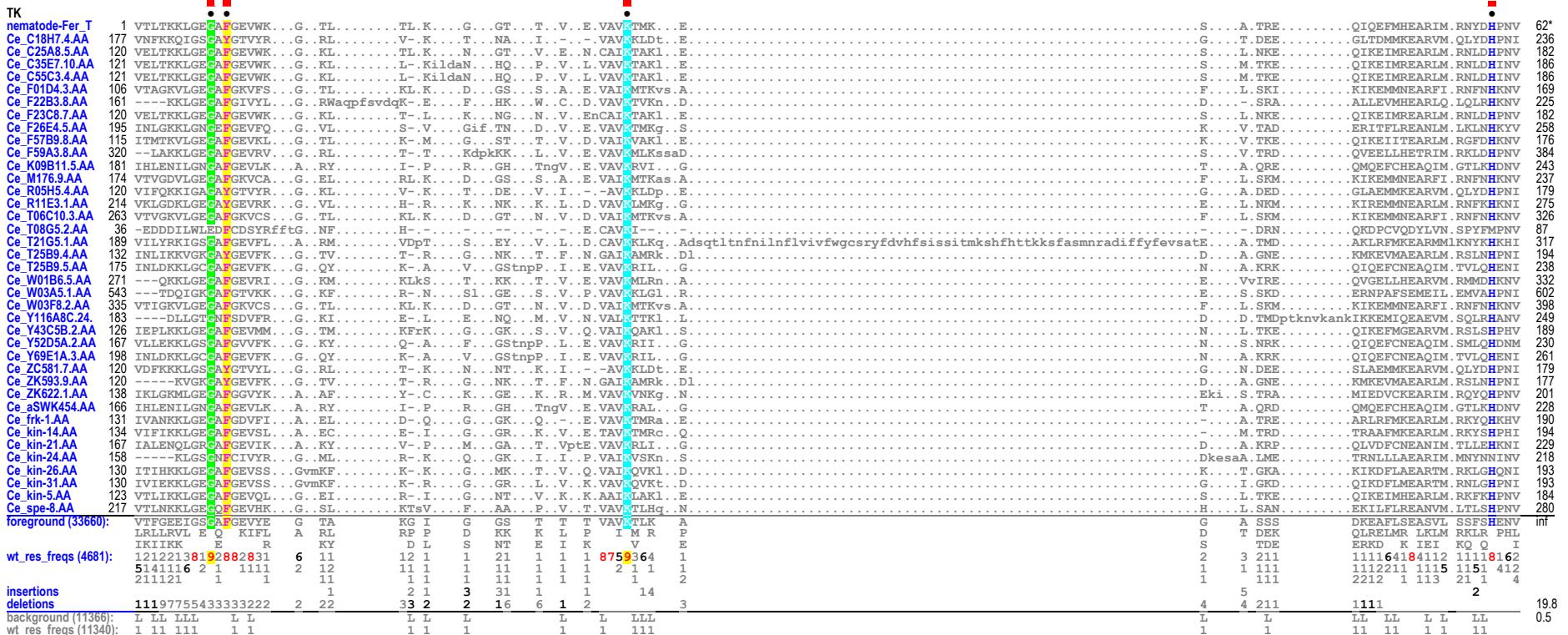
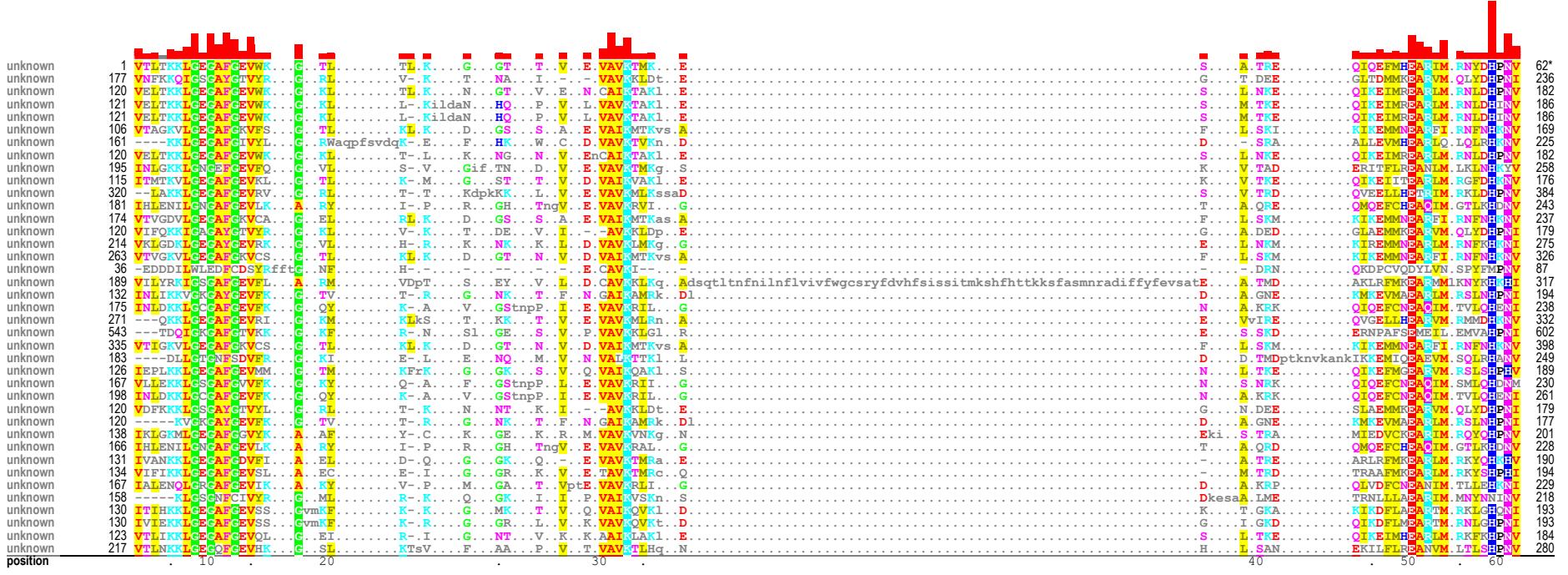
position	168	170	172	174	176	178	180	182	184	186	188	190	192	194	196	198	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
unknown	P	S	T	C	I	L	V	M	D	E	G	R	K	H	N	Q	
position	170	172	174	176	178	180	182	184	186	188	190	192	194	196	198	200	

other-Fer_TK

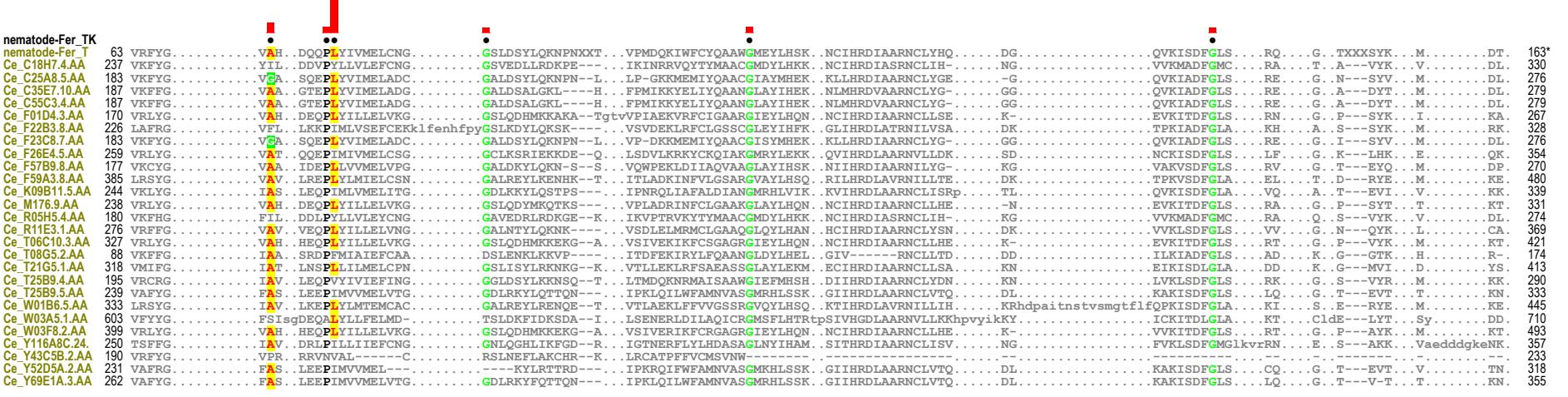
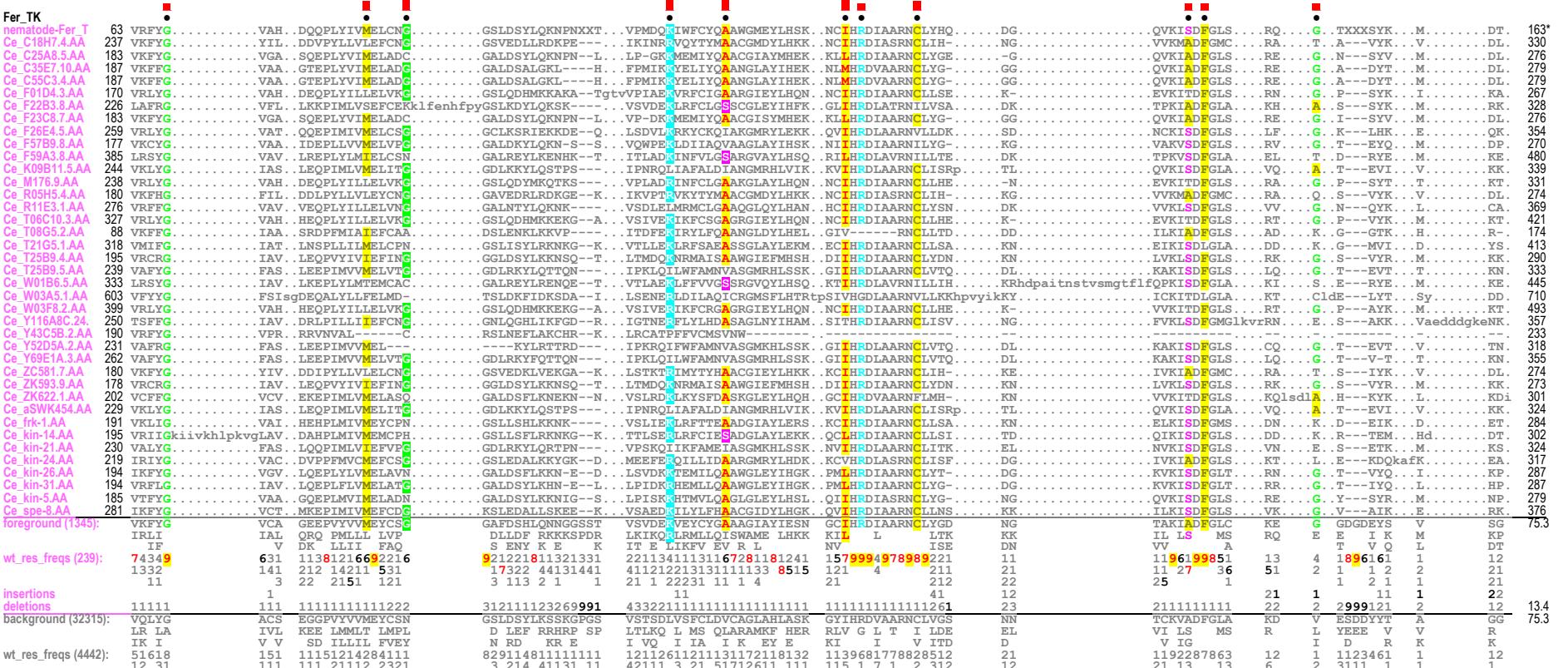
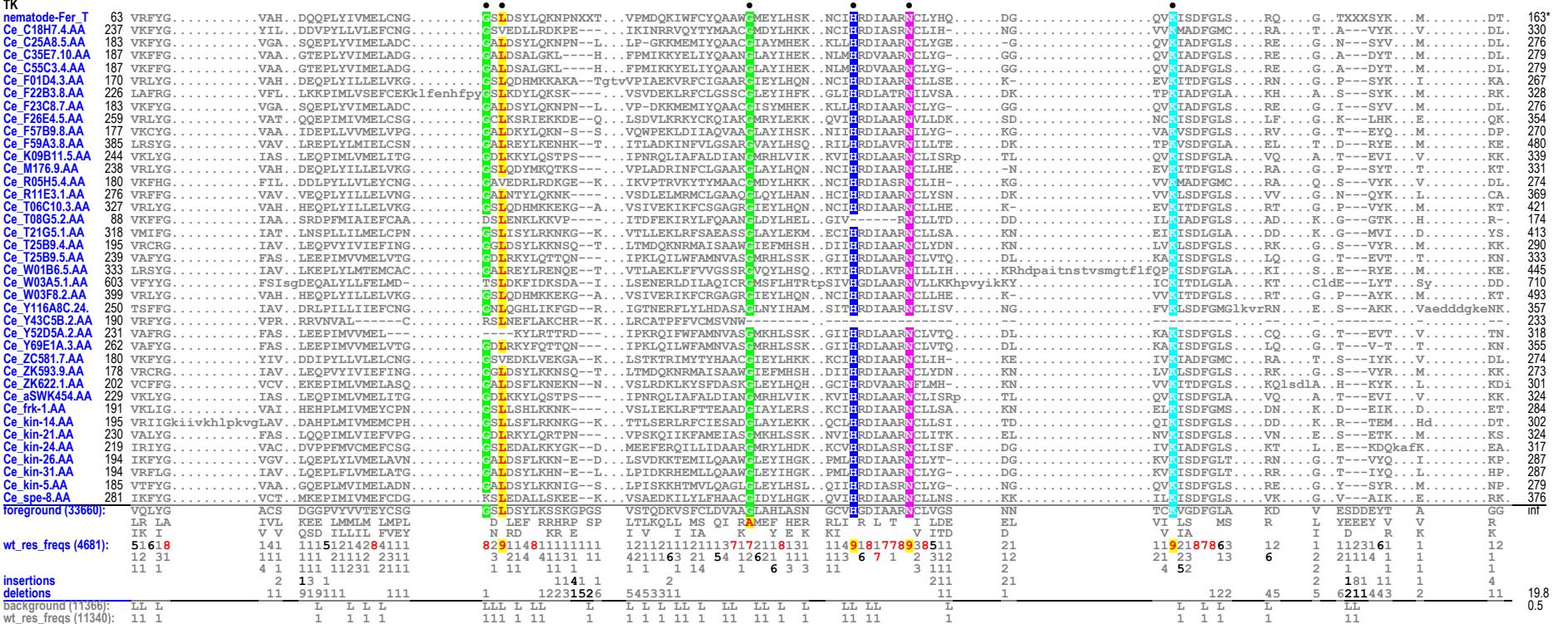
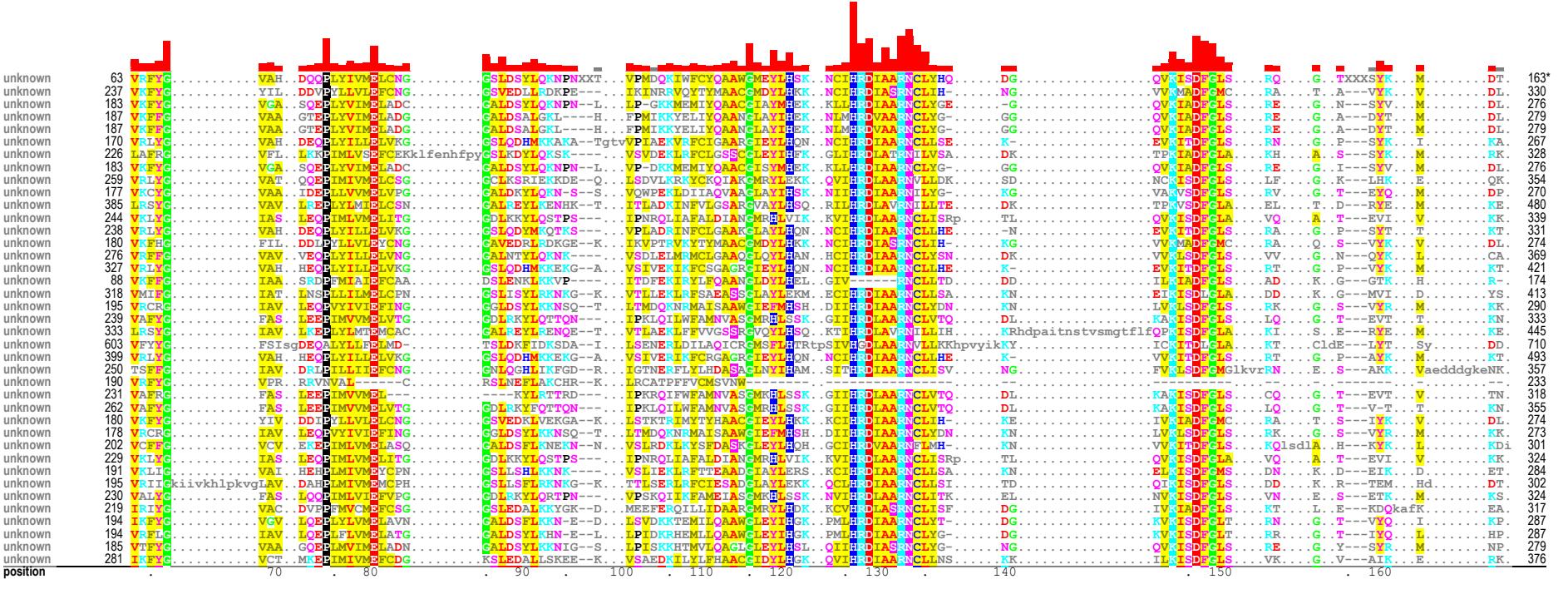


wt_res_freqs (189):
position 27338189922132145164974238451691213614911411311124116153211118112111212551137119122114112141
1 1611 241 11331 4 1155 4222 661311 12121111211111 3 1216212 12111331211113 13 435111211612
2 4 4 11 1 3 1 2 611 11 4431 311 1 312 111 1 211321 1 11 133 2 11
170 . 180 . 190 . 200 . 210 . 220 . 230 . 240 . 250 . 260

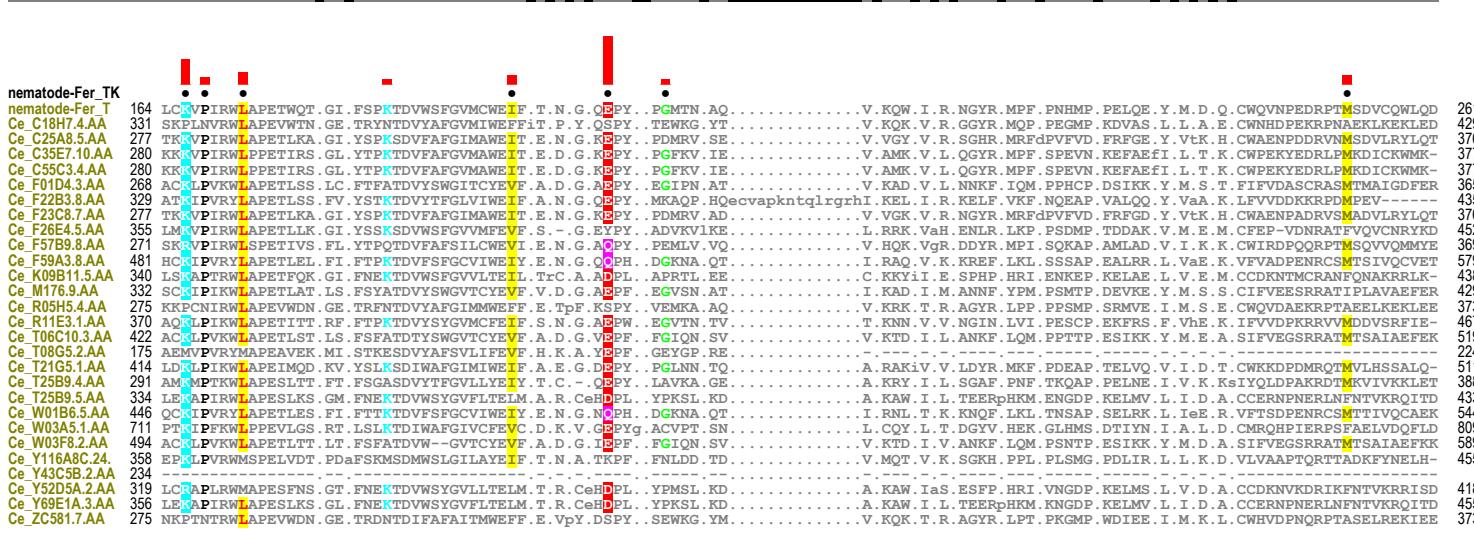
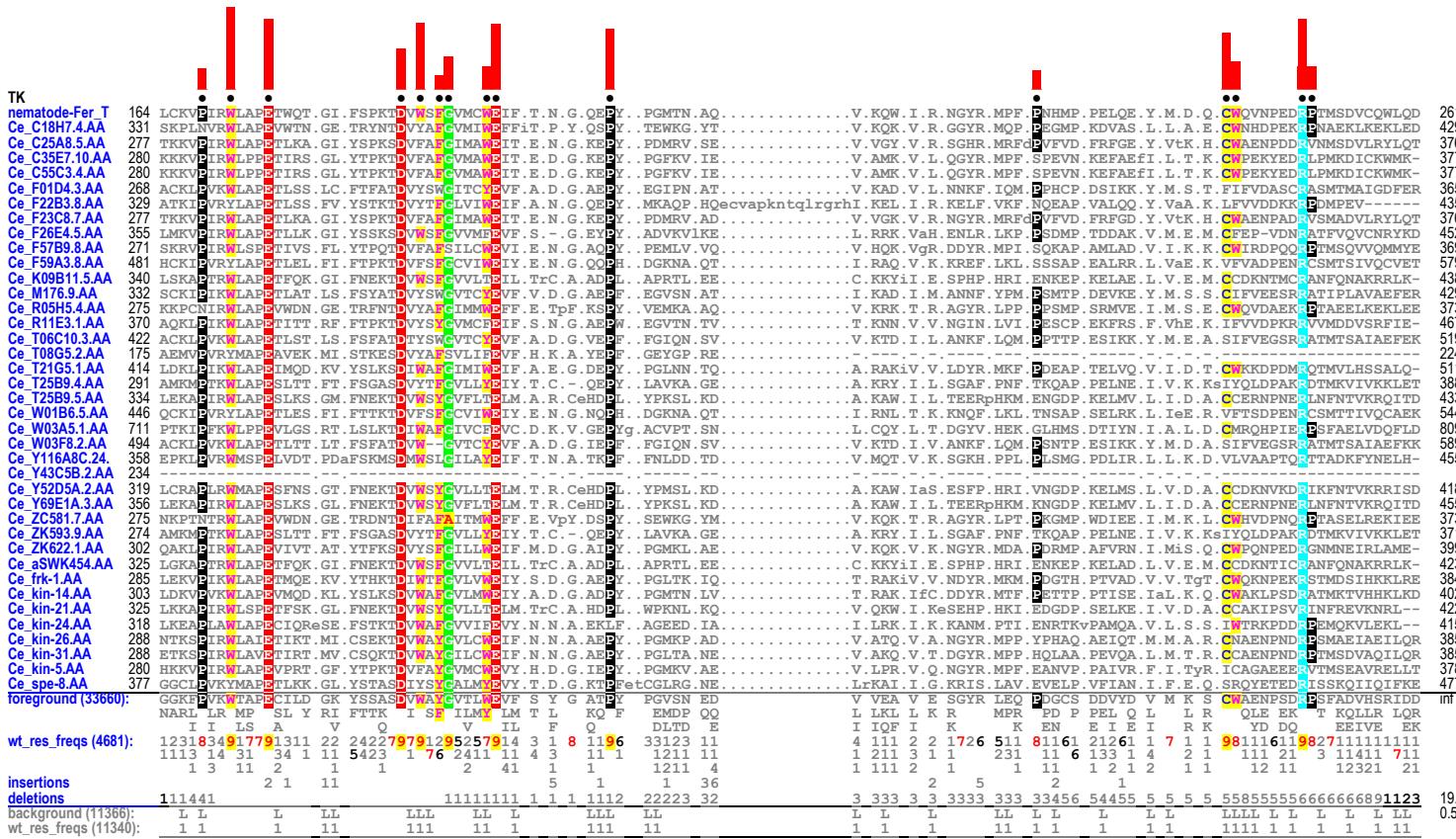
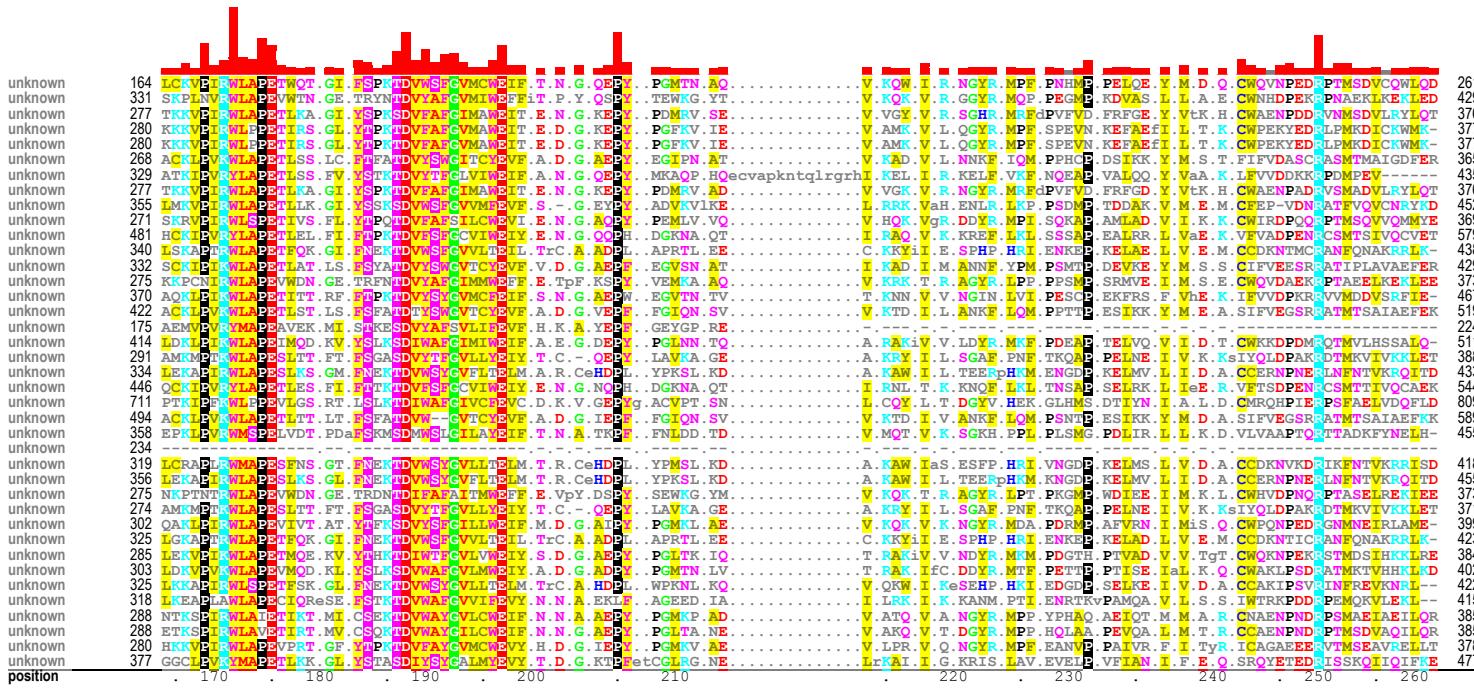
nematode-Fer_TK



Ce_ZC581.7.AA	120	VDFKKKLGSQAYGTVYL...G..RL.....T..K....N..NT..K..I..-.AVKKLDt..E.....	G...N.DEE.....SLAEMKEARVM.QLYDHPNI 179
Ce_ZK593.9.AA	120	----KVGGKAYGEVFK...G..TV.....T..R....G...NK..T..F..N.GAIKAMRK..DL.	D...A.GNE.....RMKEVMAERLM.RSLNHPNI 177
Ce_ZK622.1.AA	138	IKLGMRLCEGAFGGVYK...A..AF.....Y..C..K..GE..K..R..M.VAVVKVNKG..N.	EKI..S.TRA.....MIEDVCKEARIM.RQYQHPNV 201
Ce_aSWK454.AA	166	IHLENILGNGAFGEVLIK...A..RY.....I..P..R..GH..TngV..E.VAVVKRAL..G.	T...A.QRD.....MQEFCHEAQIM.GTLKHDNV 228
Ce_frk1.AA	131	IVANKKLCEGAFGDVF1...A..EL.....D..Q..G..GK..Q..-..E.VAVKTMRA..E.	..A.TRE.....ARLRFMEARLM.RKYQKHV 190
Ce_kin-14.AA	134	VIFIKKLCEGAFGEVSL...A..EC.....E..I..G..GR..K..V..E.TAVKTMRC..Q.	..M.TRD.....TRAFFMEARLM.RKYSRPHI 194
Ce_kin-21.AA	167	IALENQKLGSQAFGEVIK...A..KY.....V..P..M..GA..T..VptE.VAVKRLLI..G.	..A.KRP.....QLVDFCNEANIM.TLLEHKNI 229
Ce_kin-24.AA	158	-----KLGSGNFCIVYR...G..ML.....R..K..Q..GK..I..I..P.VAIKVSRA..S.	DkesaA.LME.....TRNLILLAEARIM.MNYNNINV 218
Ce_kin-26.AA	138	ITIHKKLCEGAFGEVSS...GvMKF...K..K..G..MK..T..V..Q.VAIKQVK1..D.	K...T.CRA.....KIKDFLAERTM.RKLGHQNI 193
Ce_kin-31.AA	136	IVIEKKLCEGAFGEVSS...GvMKF...K..R..G..GR..L..V..K.VAVVKQVK1..D.	G...I.CRD.....QIKDFLMEARIM.RNLGHQNI 193
Ce_kin-5.AA	123	VTLIHKKLCEGAFGEVQL...G..EI.....R..I..G..NT..V..K..K.AAIKLAQ1..E.	S...L.TRE.....QIKEIIMEARLM.RKFKHPNV 184
Ce_spe-8.AA	217	VTLNKKLCEGAFGEVHK...G..SL.....KTSV...F..AA..P..V..T.VAVKTLLHg..N.	H...L.SAN.....EKILFLREANVM.LTLSHPNV 280
foreground (323):			
			A...A.SKA.....QRKEFMEARIM.RNYNHNKV 11.1
			K...M.TRE.....KILMHLRLKPHI
			E...L.D.....AVIR.R.KFD
wt_res_freqs (72):		4212678979889921 7 11 11 3 2 51 1 5 2 1959148 1 4151 11 12 1 11 17 1 11 1 1 1 7 4 111 3 1 1 11 25 4 1 1 3 2 2 21 1	1 1 171 416727399918 93219286 1 1 425 361 2 2 6 121 513 1 3 1 11 2 1 243 3 4 2 2
insertions	2		1 1
deletions	996644332222222222 1 11 26 2 2 22 2 3 2 2 11		
position	10	20	30
background (1022):			9.2
			S...L.SKD.....OKAAFMTEARVM.RQYDHPNV 11.1
			D...PPE.....LLIMMRCCLLQ.LK.I
			T...D.....AIRKLKGIIK
wt_res_freqs (167):		51131338192171911 7 16 25 1 1 22 2 1 1 1969143 3 1251225 2 4714 11 1 1 11 1 3 12 1 3 2 7 1 112 31113 1 1 1 44 1 2 1 1 31 1 1 2 2 411	1 3 112 131141196713 34538773 1 214 1111211 1 25 1 41 6 1 1 1112241 1 4 3
			40 50 60

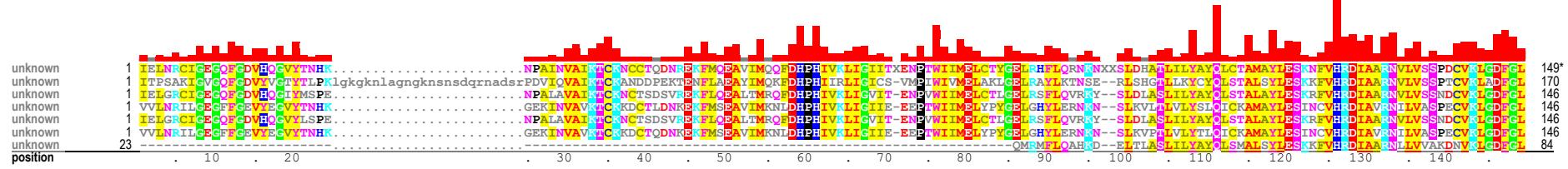


Ce_ZC581.7.AA	180	VKFYG.....YIV..DDIPIYLLVLELCNG.....GSVEDKLVEKGAA--K...LSTKTRIMTYHAACGIEYLHKK..KCIHRDIAARNCLIH-.....KE.....IVKIADFGMC...RA...T..S---IYK...V...DL...274												
Ce_ZK593.9.AA	178	VRCRG.....IAV..LEQPVYIVIEFING.....GGLDSYLKNSQ--T...LTMDQKNRMAISAAWGIEFMISH..DIHLDIAARNCLYDN...KN.....LVKLSDFGLS...RK...G...S---VYR...M...KK...273												
Ce_ZK622.1.AA	202	VCFFG.....VCV..EKEPIMLVMELASQ.....GALDSYLKNEKN--N...VSLRDKLKYSDASKGLEYLHQH..GCIHRDVAARNFLMH...KN.....VVKITDFGLS...KQ1sd1A..H---KYK...L...KK...301												
Ce_aSWK454.AA	229	VKLYG.....IAS..LEQPIMLVMELETG.....GDLLKYLQSTS--...IPNRQLIAFALDIANGMRHLVIK..KVIHRDIAARNCLISR...TL...QVKISDFGLA...VQ...A...T---EVI...V...KK...324												
Ce_frk-1.AA	191	VKLIG.....VAI..HEHPIMIVMEYCPN.....GSLLSHLKKNK---...VSLIEKLRFTTEAADGIAAYLERS..KCIHRDIAARNCLLSA...KN.....ELKISDFGMS...DN...K..D---EIK...D...ET...284												
Ce_kin-14.AA	195	VRIIGkiivkhlpkvgAV...DAHPIMIVMEMCPH.....GSLLSFLRKNGK--K...TTLSELRFCIESADGLAYLEKK..QCLHRDIAARNCLLSI...TD...QIKISDFGLS...DD...K..R---TEM...Hd...DT...302												
Ce_kin-21.AA	230	VALYG.....FAS..LQQPIMLVIEFVPG.....GDLRKYLQRTPN--...VPSKQIIKFAIMEIASGMKHLSSK..NVHRDIAARNCLITK...EL...NVKISDFGLS...VN...E..S---ETK...M...KS...324												
Ce_kin-24.AA	219	IRIYG.....VAC..DPPEPMVCMFCSG.....GSLEDALKYVGK--D...MEEFERQILLIDAARKCMRYLHDK..KCVHRDIAARNCLISF...DG...IVKIAIDFGLS...KT...L..E---KDQkaFK...EA...317												
Ce_kin-26.AA	194	IKFYG.....GV...LQEPLFLVMELAVN.....GALDSFLKKN-E--D...LSVDKKTTEMILQAANGLEYIHKG..PMLHRDIAARNCLYT...DG...KVKISDFGLT...RN...G..T---VYQ...I...KP...287												
Ce_kin-31.AA	194	VRFLG.....IAV..LQEPLFLVMELATG.....GALDSYLKHN-E--L...LPIDKRHEMLLQAANGLEYIHKG..PMLHRDIAARNCLYG...DG...KVKISDFGLT...RR...G..T---IYQ...L...HP...287												
Ce_kin-5.AA	185	VTFYG.....VAI..GOEPIMIVMELEN.....GALDSYLKNIIG--S...LPISKKHTMVLQAQIGLEYLHSI..QTIHRDIAARNCLYG...NG...QVKISDFGLS...RE...G..Y---SYR...M...NP...279												
Ce_spe-8.AA	281	IKFYG.....VCT..MKEDPIMIVMFCGDG.....KSLEDALLSKEE--K...VSAEDKILYLPHAACGIDYLEHK...QVIHRDIAARNCLLNS...KK...ILKISDFGLS...VK...G..V---AIK...E...RK...376												
foreground (323):														
VRKFYG		V A G E E P Y V V L E I C S G	G A L N S Y L O K N G G T	V S V A D K N N F C L G A A R G V A Y I E A N	N C I H R D V A A R N C L Y G E	GG	EAKISDFGLA	D E	G	T	S Y E	D	D T	11.1
RLF		I V L R Q M L L M I P N	S L E F R K K K T	L P M E K R M R M I Q S W L E L H K K	P I M L L T E	KK	V I L M T	R	P	I	R	M	R P	
I		D Q I L I I V R K	DD K E N	I D L D E L K V E I	I S Q K V L I	SK	K V S		V	K	L		KK	
wt_res_freqs (72):	83379	883 23698314297214	59156916612 1	32111711234377191291111	3469991989975532	12	1197899971	13	7	3	171	1	22	
511	1 4	111 4226 112	2 111 2 21 1	3111211161 2113 55 8814	121 2 221	11	21 1	21	6	1	1 1	4	12	
2		41 3 1 1	4123 31 1 1	21123 31 1 1	2 31 112 6	11	16	7		1	2	2	21	
insertions		1		1	54		1	1	14		4	2		
deletions		1	111 1 111111222	222222322211!2	744221211111	11111 111122233	35	4222223333	33	2	2!!!222	2	22	9.2
background (1022):														11.1
VQFYG		VAT DAEFYIYVILEYCSG	GAFDSHLKTNGGST	VSTKTKVQCYDAGAGLAYTESK	GCIHRDIAARNCLVGD	NG	TAKIADFGLC	KE	G	G D G D E Y S	A	SG		
IRLI		ITL QRQ PMMIM LVE	DLLDF RKKKDPP	LKURLLRMLLQIARAMZ	KLL L LDK	KK	IL LS MS	VQ	E	I	I	M	K	
K F		CV K ILL FAQ	SVENY NE S R	ITV QRILV EV S E	NI	ITE	DN	VV A	R	T	V K	I	D	
wt_res_freqs (167):	61339	522 21271247192217	812111821221331	12131311121361283181346	1579994878989321	11	1196289842	23	2	1896261	1	13		
1243	211 213 1317 442	26422 44131441	421 1221312117141 84	111 4	211 21	21	22 26	45	11	2 2	1 1	1	2	
4 1	42 2 412 121	41112 11 1 1	211 22311 11 1 2	22	313	12	24	1	5	1	1 2	2 2	1	1
position		70	80	90	100	110	120	130	140				150	160

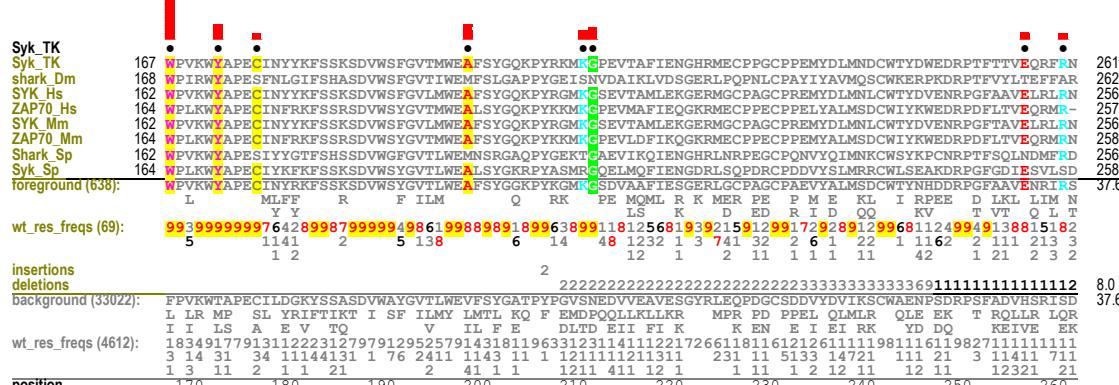
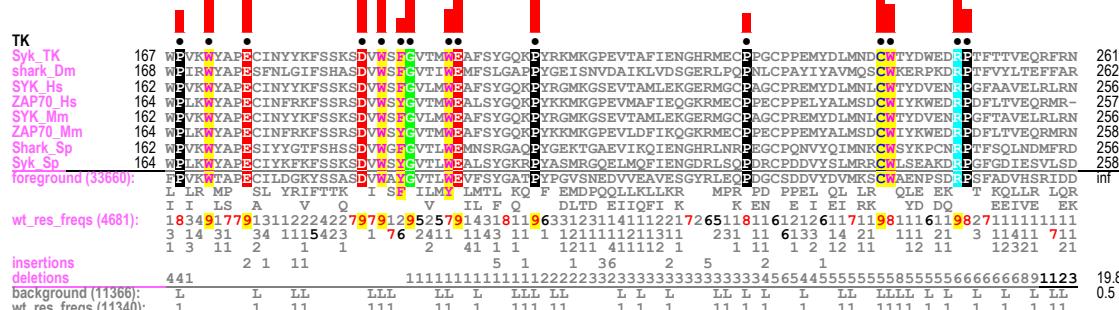
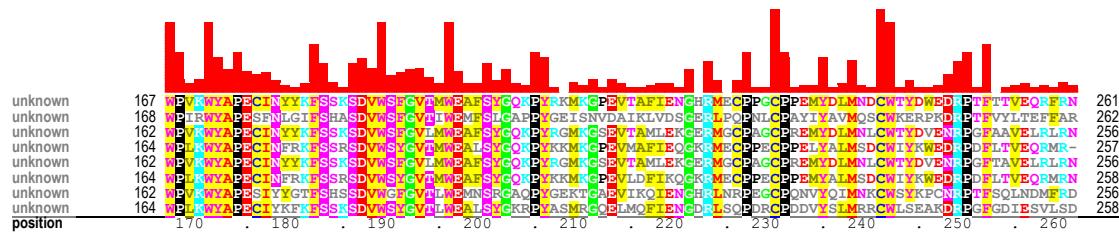
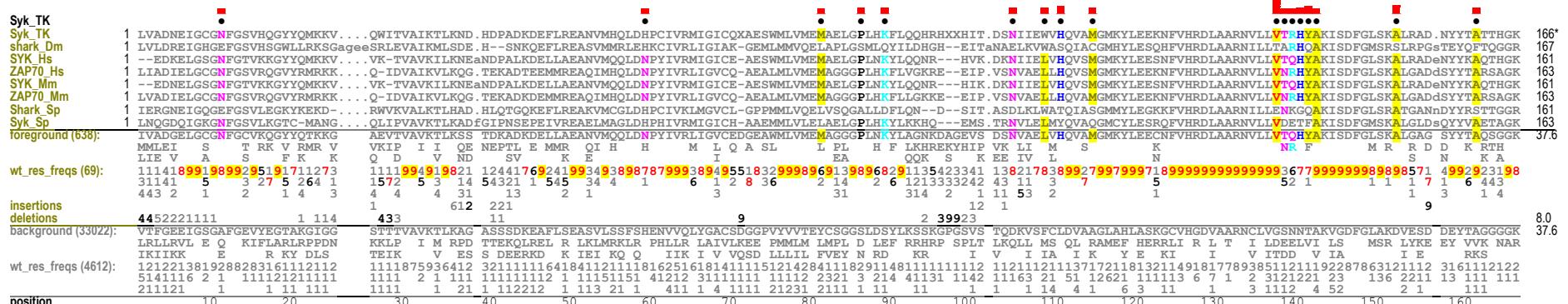
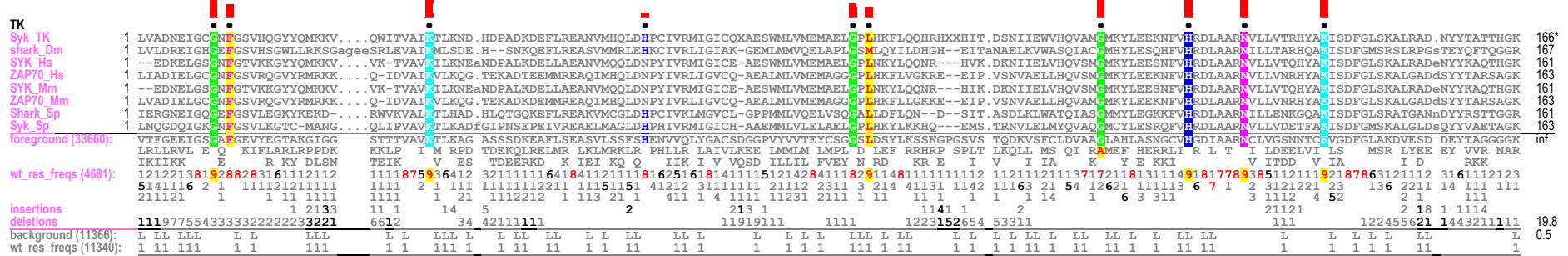
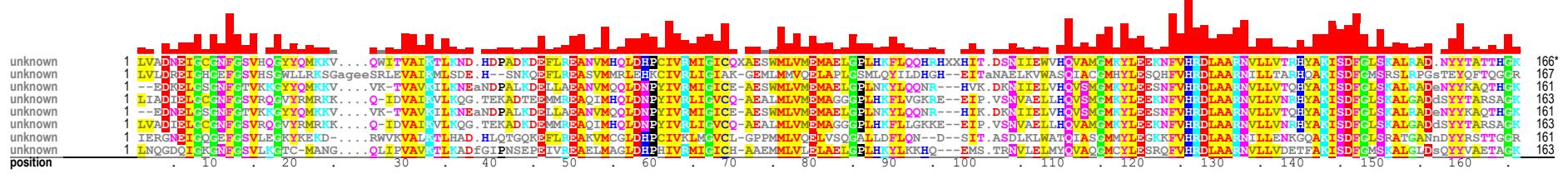


Ce_ZK593.9AA	274	AM KPKVW LAPESLIT_TT_FSGASDVYTFGVLLYEY_T.C.-C_EPEY..LAVKA.GE.	A_KRY_I.L.SGAF_PNF.TKQAP_PELNE_I.V.K.KsIYQLDPAKRDTMKVIVKKLET
Ce_ZK622.1AA	302	QANR KPKVW LAPAEPIVTT_AT_YTFKSDVSYFGILLWEI.F.M.D.G.A_EPEY..PGMLK.AE.	V_KQK_V.K.NGRY.MDA.PDRPM_AFVRN_I.MiS_Q.CWFQNPEDRGNMNEIRLAME
Ce_aSWK454-AA	326	LGKAPTRFLAPETFGI.K.FNEDTWDVWSFGVVLTEELTR.C.A.DPL_APRTL_EE.	C_KKYYI_E.SPHR.HRI.ENKEP.KELAD_L.V.E.M.CDDKNTICRANFQNAKRRLK
Ce_fkr-1AA	285	LeR KPKVW LAPETFMQE_KR.YTHRTDITWFGVLUWEY_S.D.G.A_EPEY..PGLTK.IQ.	T_RAKIV_V.NDVR.MKMK.PDGTB_PTVDW_V.TgT_CWQKPLNSDRATTSIHKKLR
Ce_kin-14AA	303	LDL KPKVW LAPAEVMDL_KR.YLSKLSDWVAFGVLWMEY_A.D.G.A_EPEY..PGMTN.LV.	T.RAK_I.fCDYR.MTF_PETTP_PTSE_IaL_K.Q.CWAKLPLSDRATVTKVHHLKD
Ce_kin-21AA	325	LNK KPKVW LAPESTFSK.GL.FNEKTDVWSTGYVLLTEL.M.TRC_A.DPL_WPKNL.KQ.	V_QKWI_K.eSEHP.HKI.EDGDP._I.V.D.A.CCAK1PSVSRINPREVKNRLL
Ce_kin-24AA	318	KEIAKPLANLAPECIQRSe_EFST_KDVTWVAFFGVLFIVEY_N.N.A.EKFL_AEGED_IA.	I.LRK_I.K.KANM.PTI.ENTRKPVAMQOA_V.L.S.S.USWTRKDRPDRPEQVKLELL
Ce_kin-26AA	288	NTKPSKIRNLAPETIKT.MI.CSEKTDVWAGYVGLCWEI.F.N.N.A.EPEY..PGMPK.AD.	V_ATQ_V.A.NGRY.MPF.VPHQAO_AEQTQ_M.M.A.R.CNAENPNDRPSMAETAEIQLQ
Ce_kin-31AA	288	ETKPSKIRNLAPETITK.TM.VN.CSQKTDVWAGYLCLWEI.F.N.N.G.A_EPEY..PGLTA.NE.	V_AKQ_V.T.DCYR.MPF.HQLAPEA_VQVA_L.M.T.R.CCAENPNDRPTMSDVAQIQLQ
Ce_kin-5AA	280	HK KPKVW LAPAEVPR.T.FG.YTPKTDFVAGYVCMWCWEY_H.D.G.EPEY..PGMKV.AE.	V_LPR_V.Q.NGRY.MPF.EAANPV_PAIVR_F.T.YTR_ICAGAEERVVTRMSAEVRELLT
Ce_spe-8AA	377	GCG EVKVMAYTEL KL.GL.YSTASDISTSYALGMYVEV_T.D.G.KTPFetCGLRNG.E	LKEAI_I.G.KRIS_LAV_EVELP_VFIAN_I.F.E.Q.SROYETDETRISSQKQIQIFKE
foreground (323):			
		ACK KPKVW LAPESIST_FTYSQSKDVGWAGYVGLCWEVY_A.N.G.A_EPEY..DGVSAA_EE	A_AAQ_V.E.K.SGRK.LEF_PSGCP_AFAAN_V.E.K.CWAANPADRAS_MADVAQEFT
		LKRLR I IL F FT S IMLY Y PF D A K Y P MKV Q	V_RKK_I.L.K.YF PF PEV PLV K.M.K FR E PT KK1VRLRKK
		H_V T TLK I Y I N Q LNN	T_KQ_V.E.KL_KNT_KDIRE_I.I_V.Q_D O DE T Q_K.Q
wt_res_freqs (72):			
	1171924988991314	11_541829833483427913_1 4 8 2791 18111 55	1_121 7_2 1716_222 71117_11111 2 2 3 552147129138_114212141
	1312 65	112_11 341 6_465 5411 85_1 4 1 1 7_4 412 1	6_212 2_2 21 51_621_112 22211_31 1 2 12123 21 23 114311614
	1 4	641_22 2 2 1_1 1 213	1_31 1_1 12 112 12212_2 3 1 12 1 21 22 1 21 2 22
insertions			
deletions			
	2211111_111111_1	112211_1_3_4_1111_11111_11	1_122_2 3_4444_444_447455555_5_5_5_6_666666666777891111125
background (1022):			
	LEKVPFWNLAPEAINT_G	WSSKCDVYAGYVGLCWEVY_A.N.G.A_EPEY..SGLSN_AE	A_KQS_V.E.AGNR_LDGCPP.DAVOT_V.E.Q.CWANPANRPSMSTVKEELET
	MPPL_LR_VYL_VLRR	RTFELTYIMF_I.MY.IF.LA_V.S.F.PKMT_KQ	I_Ref_L.M.R.Y.PPP_PPEM.PEMYR_L.M.L.R.E.IE.KPFLQVVLK
	ROI_I_S_T_K	K.Y.KES_S.L.T.D.KT_DE.Q	V_Y.I.L.K.M.M.KDI_K.D.L.I.I.K.Q.D.D.D.N.EEYKQ.QB
wt_res_freqs (167):			
	3121734829993122_41	152319761394717911_2 2 6 1196 13234 12	2_211_4 2_1716_411128_11211_1 1 1 1 6713271192221211312
	1111_14 1_1612_12_22112_1216_4_21_48_1_2 1_11_1 2132_13	1_431_1 1 1 3_131_7111_13111_4 5 2 3 1_111_23_15112121711	
	134_3_1_2 1_15_136_6_3_2 2_2_11_11_2	2_1_3 1_2 2_1_111_1 3_1 1_2_1 2_1_124111_22	
position			
	.170 .180 .190 .200 .210 .220 .230 .240 .250 .260		

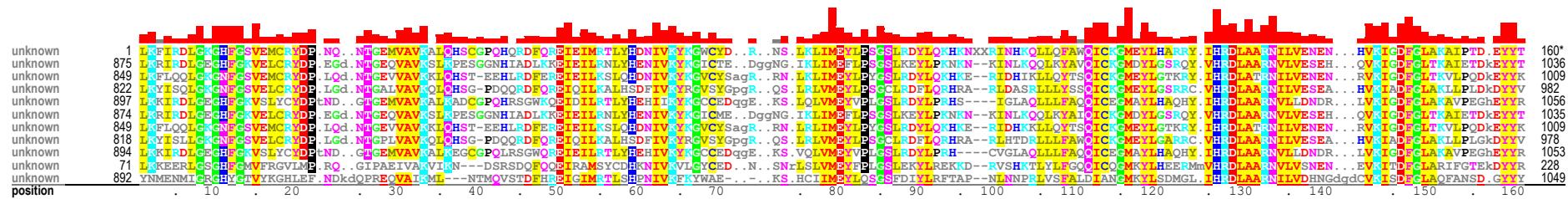
FAK_TK



Syk_TK

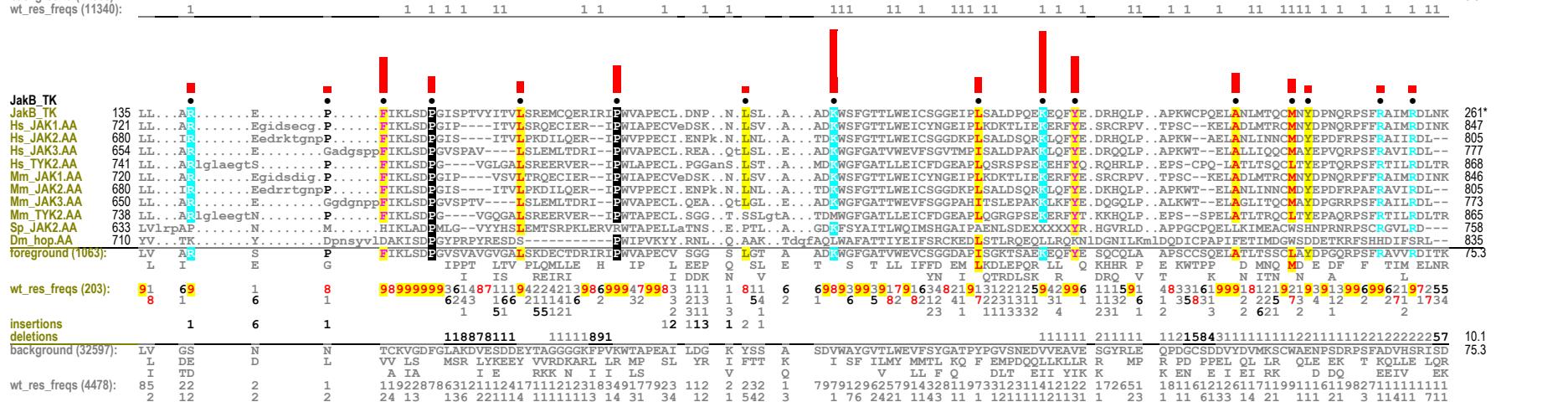
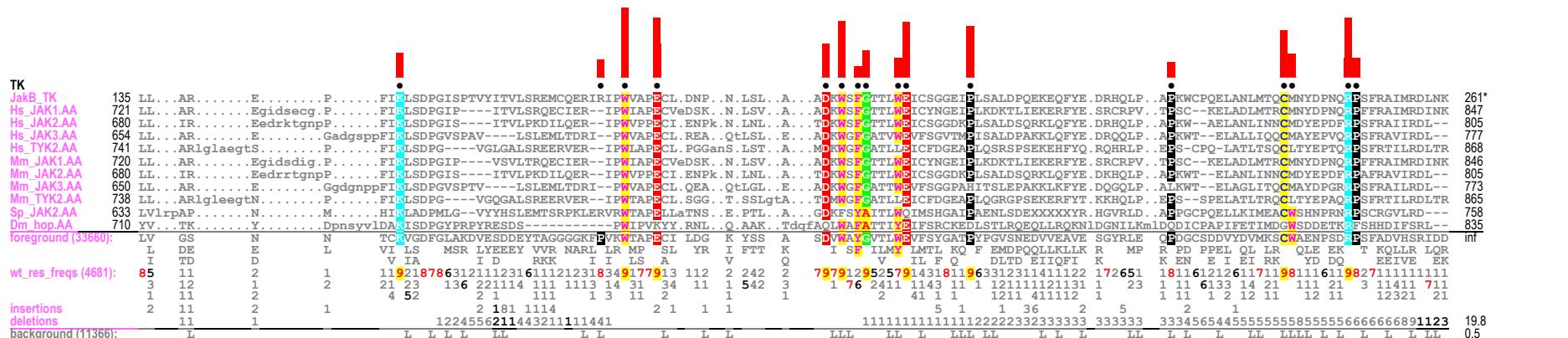
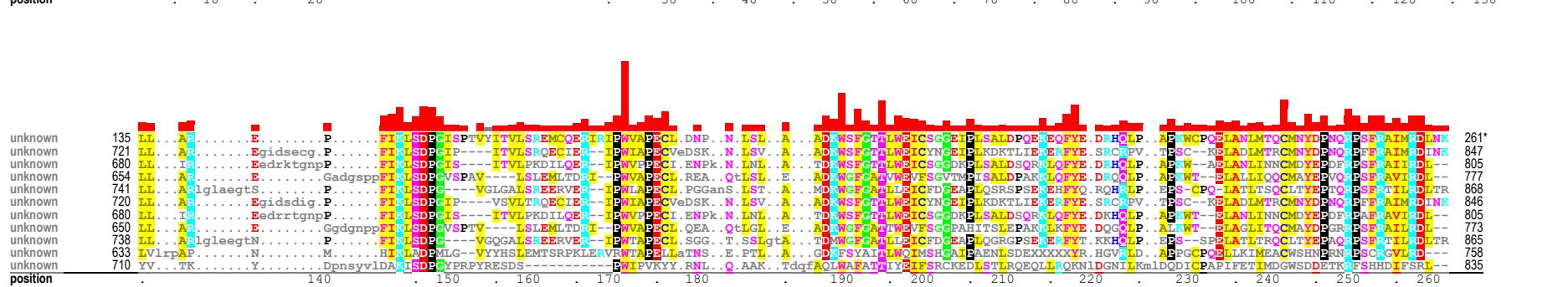
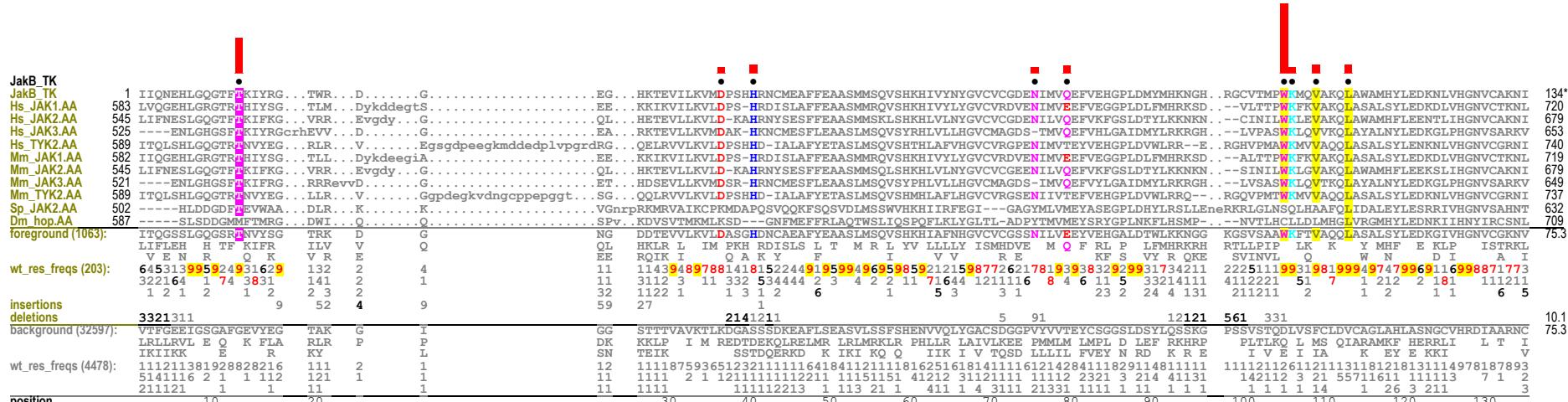
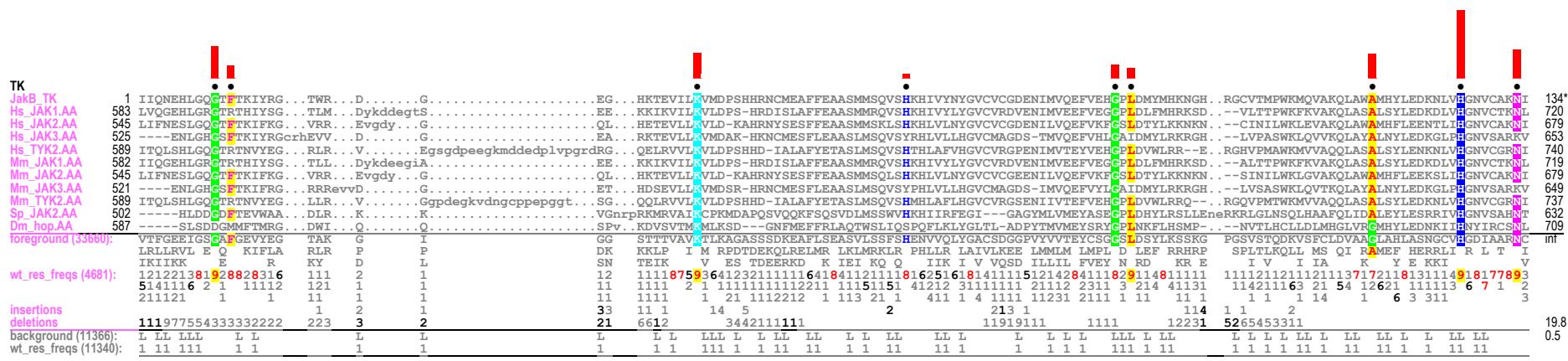
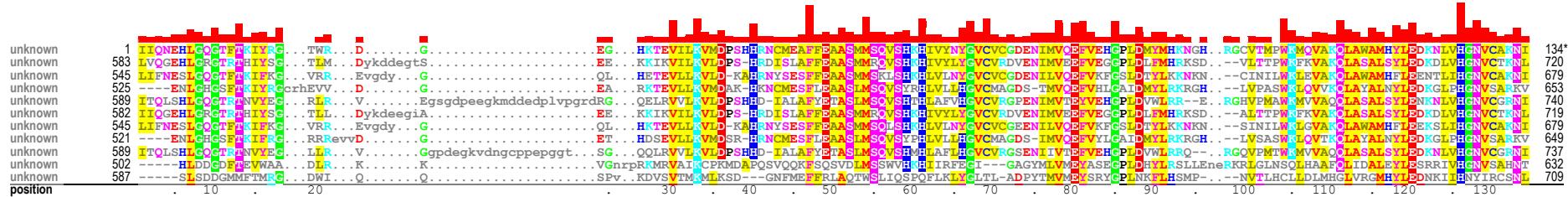


Jak_TK

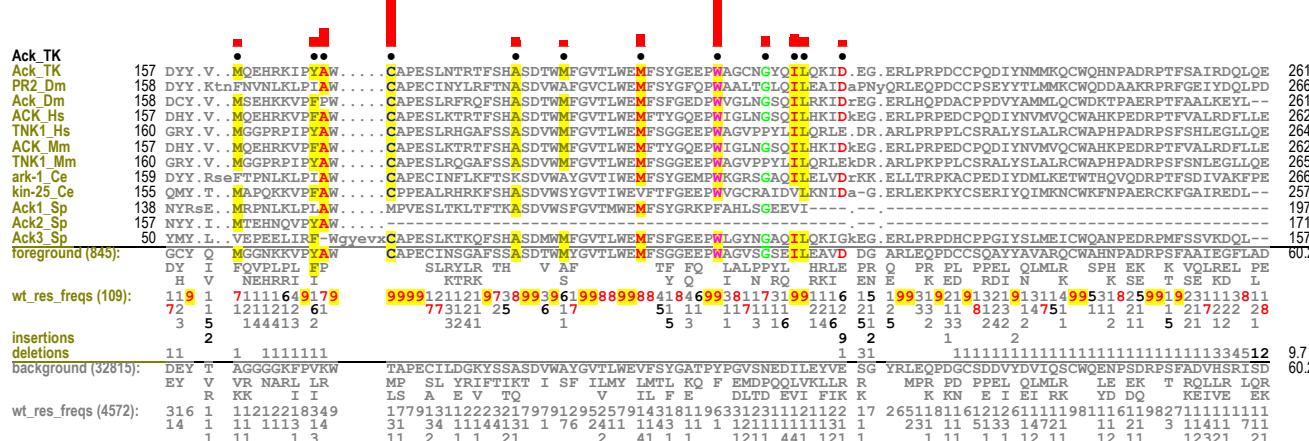
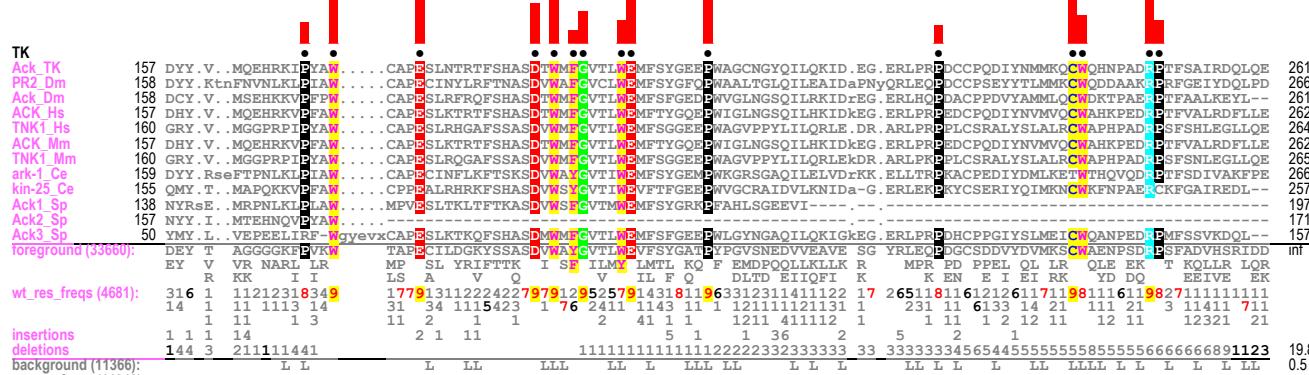
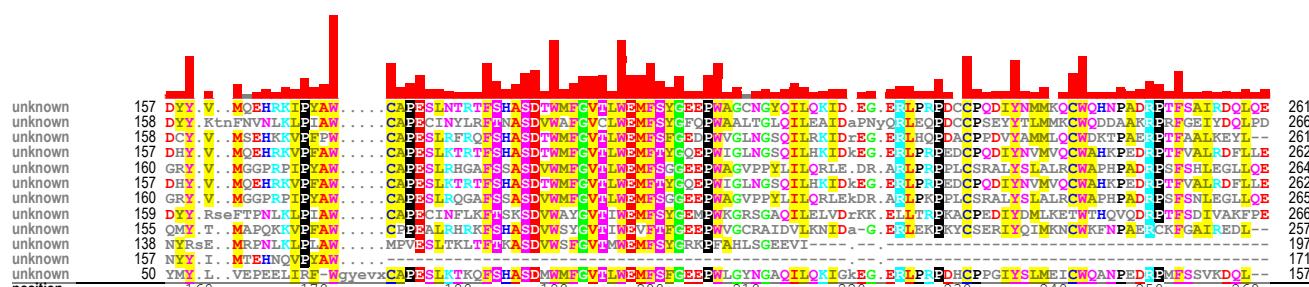
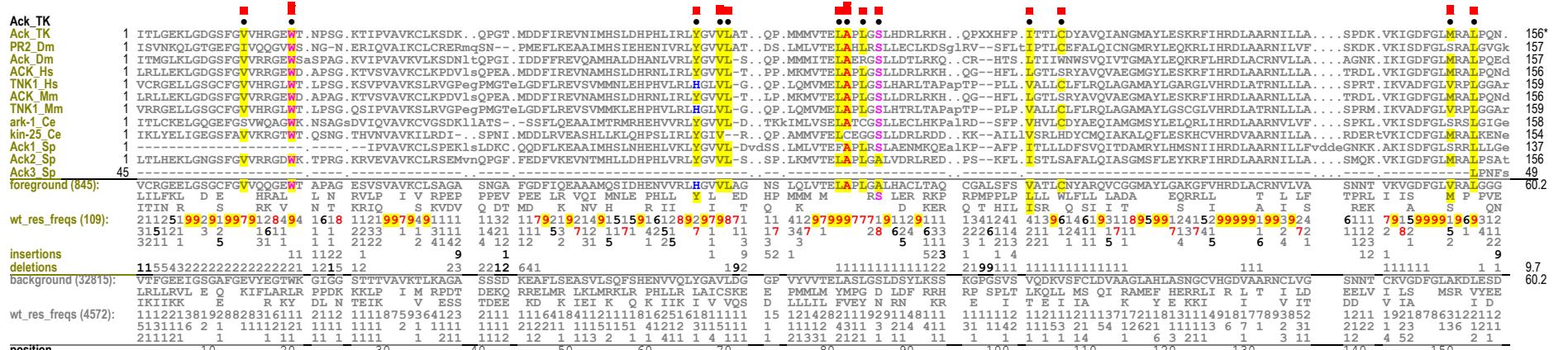
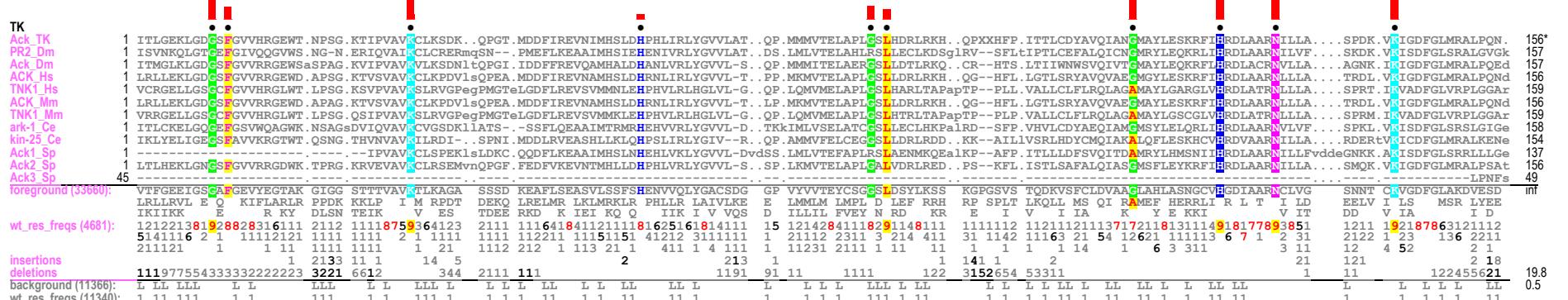
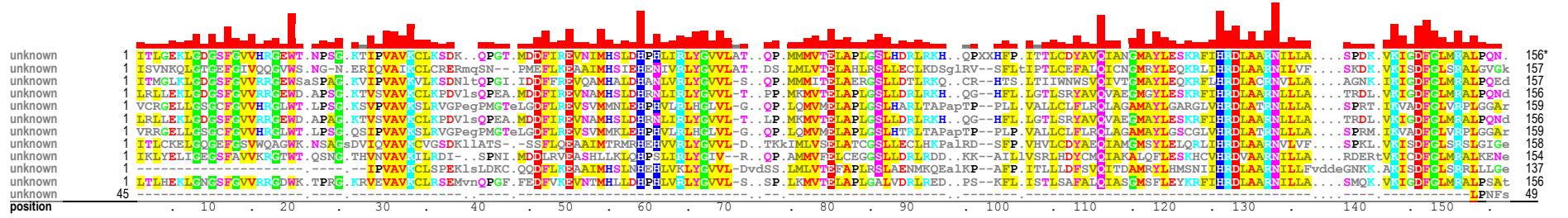


Sequence logo showing the conservation of amino acids at each position of the protein sequence. The x-axis represents positions 161 to 1153. The y-axis lists amino acids: V, I, F, P, G, D, E, R, C, M, T, S, N, Q, H, K, Y, W, L, A, D, S, F, I, V, M, R, G, and H. Red indicates high conservation, while blue indicates low conservation.

JakB_TK



Ack_TK

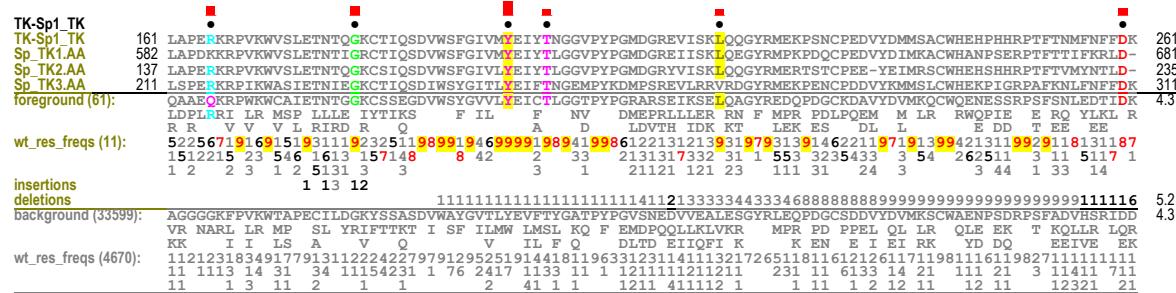
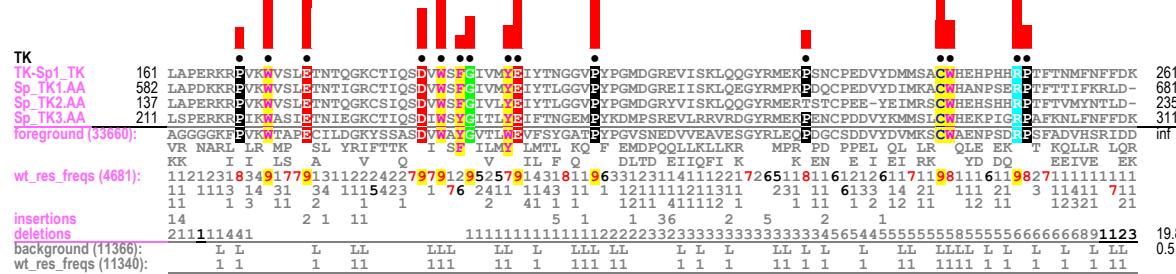
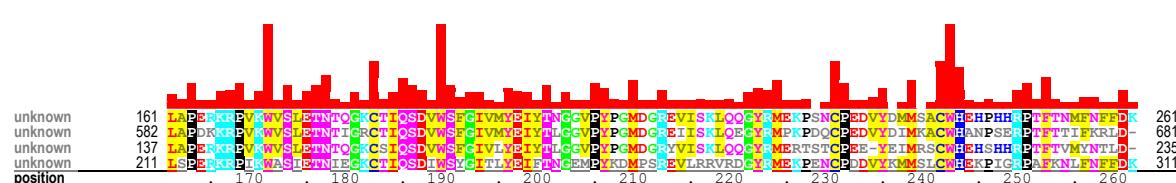
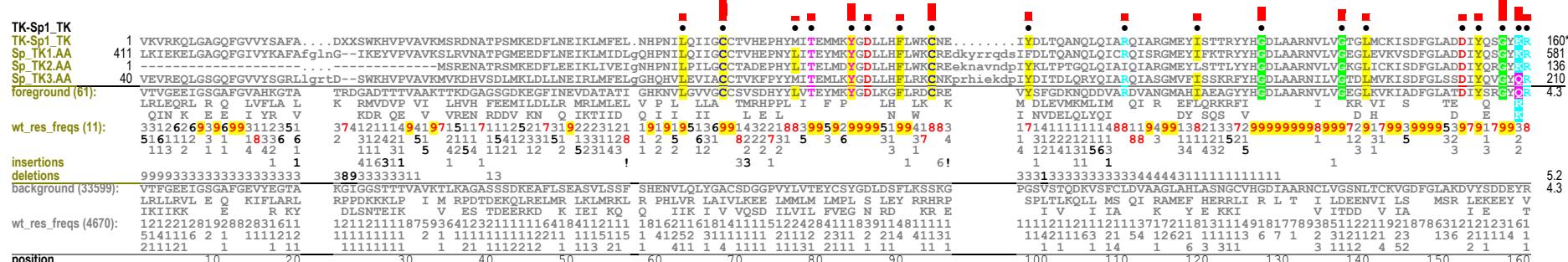
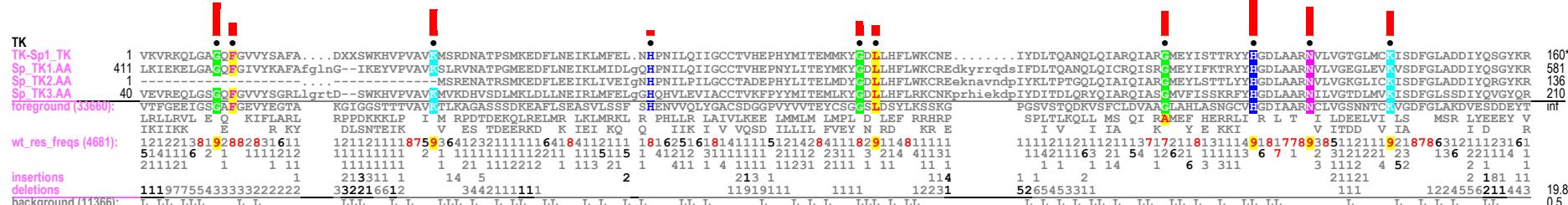
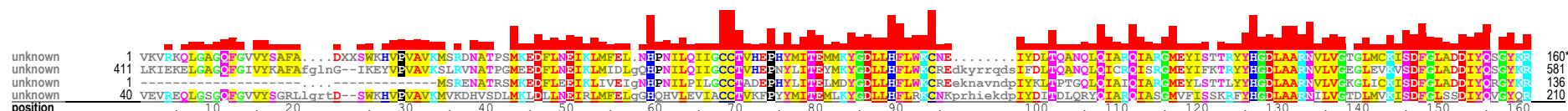


Position 156*: SPDK VKIGDFGLMRA LPQN

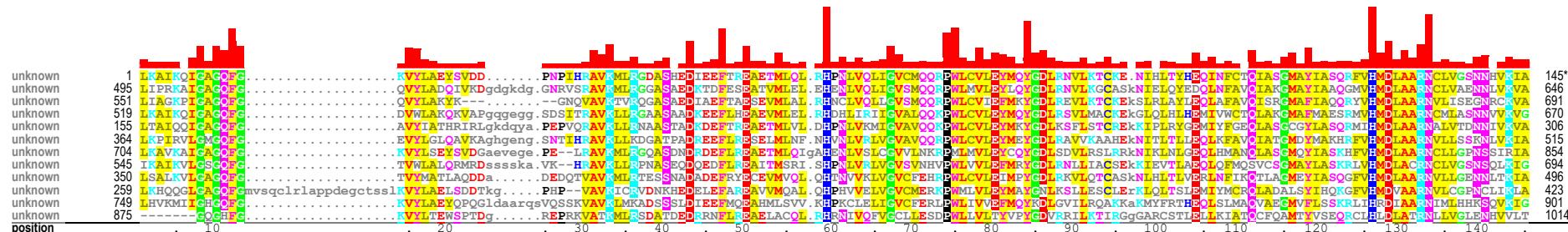
STYK1 TK



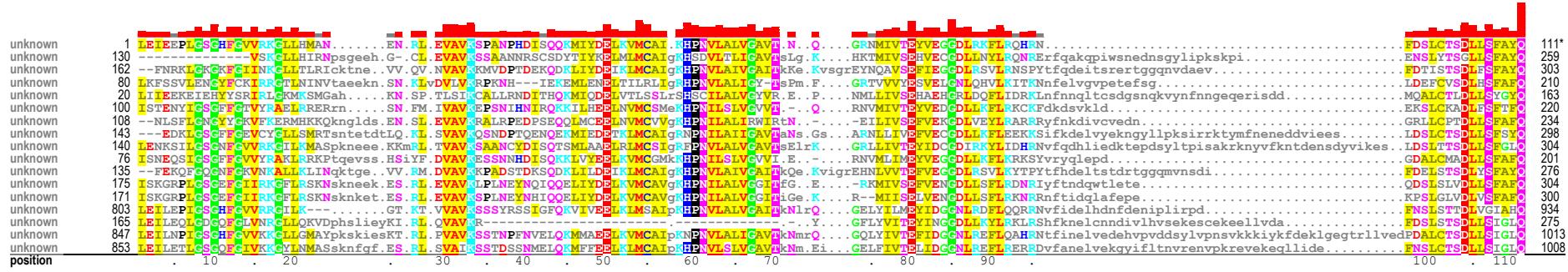
TK-Sp1_TK

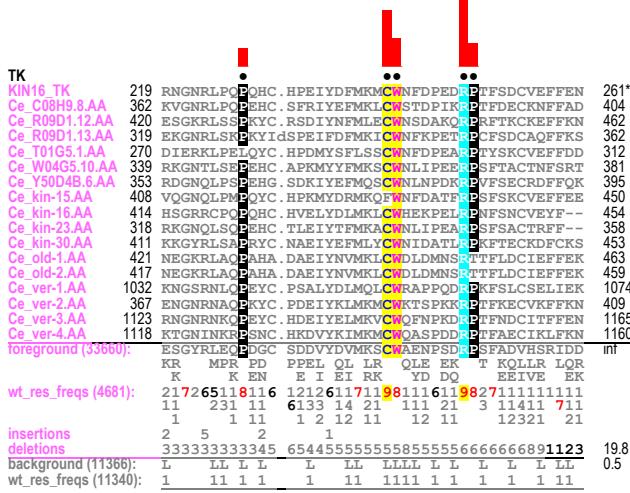
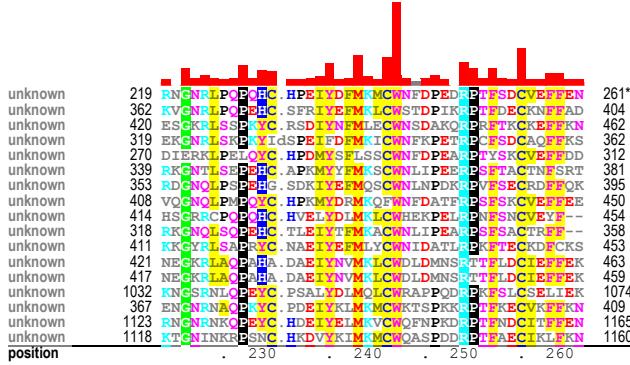


HMTK_TK

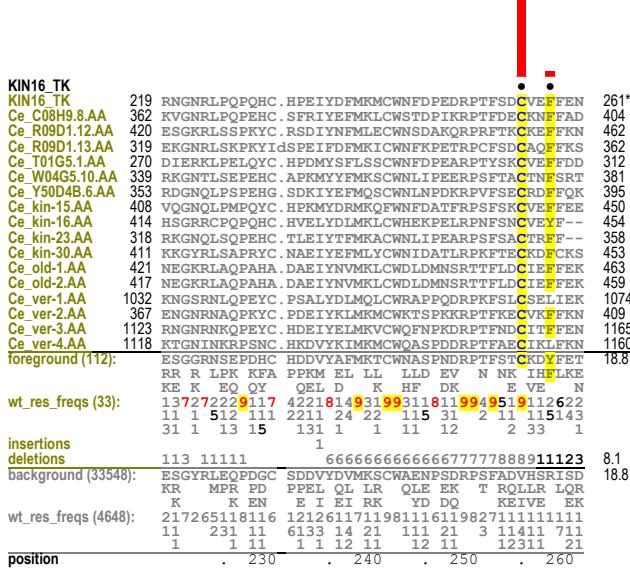


KIN16_TK





W_100_W_000 (11010).pdf



KIN6_TK

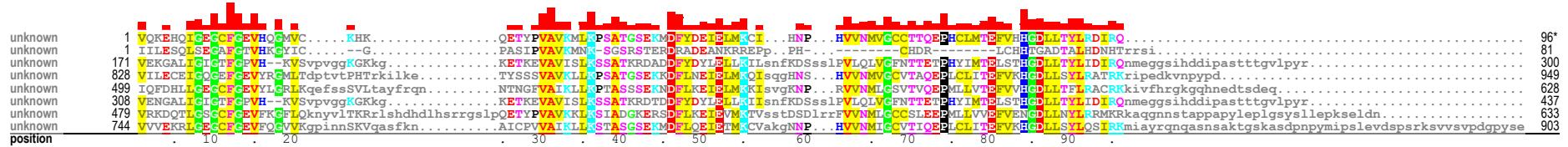


unknown	254	QT <u>R</u> MQ <u>FAT</u>	261
unknown	705	QL <u>KNAFH</u> V	712
unknown	836	DVR <u>MOLAT</u>	843
unknown	777	EMR <u>GEITV</u>	784
unknown	808	ELSK <u>FLAT</u>	815
unknown	577	QT <u>CAVLAQ</u>	584
position			260

TK				
KING_1K	254	QTRMFQAT	261	
Ce_B0251.2.AA	705	QLKNKAHF	712	
Ce_C24G6.2.AA	836	RNMQLAT	843	
Ce_F09A5.2.AA	777	EMRGEITV	784	
Ce_F09G2.1.AA	808	ELSKLKFAT	815	
Ce_kin-9-AA	577	OCTAVLAQD	584	
foreground (33860):		DVHSRRIDD		inf
		QLLSE_LQR		
		EIVE_EK		
wt_res_freqs (4681):		111111111		
		14111_711		
		2321121		
insertions				
deletions		66891123		19.8
background (433661):		7_737373		

KING6_TK				
KING6_TK				
Ce_B0521.1.AA	254	QTRMQLPAT		261
Ce_C24G6.2.AA	705	QLKNAFHV		712
Ce_F049A5.2.AA	836	DVRMQLAT		843
Ce_F09G2.1.AA	777	EMRGEITV		784
Ce_kin-9.AA	808	ELSKLPLAT		815
foreground (105):	577	OITCAVLAQ		584
		EICGFEGAT		7.0
		QLRQLTY		
		SER Q		
wt_res_freqs (17):				
	54111174			
	134111613			
	211 1			
insertions				
deletions				
background (33555):	55688836			6.1
	DVHSRIDD			
	QLLR LQR			
	EIVE EK			
wt_res_freqs (4664):				
	11111111			
	1411 711			

REF_TK



The sequence logo displays the probability of each amino acid (A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y) at each position in the protein sequence. The x-axis represents the position from 100 to 250. The y-axis represents the probability scale from 0.0 to 1.0. A color key indicates the likelihood of each amino acid: black (0.0), dark gray (0.1), medium gray (0.2), light gray (0.3), yellow (0.4), orange (0.5), red (0.6), magenta (0.7), cyan (0.8), green (0.9), and blue (1.0).

unknown	258	KEDN	261*
unknown	191	---	
unknown	407	---	
unknown	1111	KVD-	1113
unknown	790	NED-	792
unknown	599	TITN	602
unknown	795	LFD-	797
unknown	1065	KED-	1067

TK
 REF_TK 258 KFDN 261*
 Aq_AqueK392.AA 191 ----
 Aq_AqueK393.AA 407 ----
 Aq_AqueK394.AA 1111 KVD- 1113
 Aq_AqueK395.AA 790 NFD- 792
 Aq_AqueK396.AA 599 TILN 602
 Aq_AqueK397.AA 795 LFD- 797
 Aq_AqueK398.AA 1065 KFD- 1067
 foreground (33660): RIDD Inf
 LQR
 EK
 wt_res_freqs (4681): 1111
 711
 21
 insertions 19.8
 deletions 1123
 background (11366): LL 0.5

REF_TK	REF_TK	258	KFDN	261*
Aq_AqueK392_AA	191	----		
Aq_AqueK393_AA	407	----		
Aq_AqueK394_AA	1111	KVD-	1113	
Aq_AqueK395_AA	790	NED-	792	
Aq_AqueK396_AA	599	TILM	602	
Aq_AqueK397_AA	795	LED-	797	

foreground (720):	QLDD	23.2
	R EW	
	K R	
wt_res_freqs (92):	1831	
	1 31	
	1 2	
insertions		
deletions	2247	11.6
background (32940):	RIDD	23.2
	LQR	
	EK	
wt_res_freqs (4589):	1111	
	711	
	21	
position	260	

RTKC_TK

