



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 03:45 AM UTC

PDB ID : 5UOT / pdb_00005uot
EMDB ID : EMD-8577
Title : CryoEM structure of the helical assembly of full length MxB
Authors : Perilla, J.R.; Alvarez, F.J.D.; Zhang, P.; Schulten, K.
Deposited on : 2017-02-01
Resolution : 4.60 Å (reported)
Based on initial model : 4WHJ

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

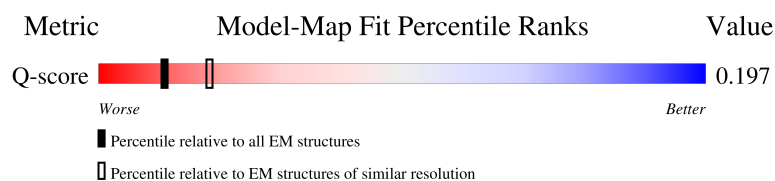
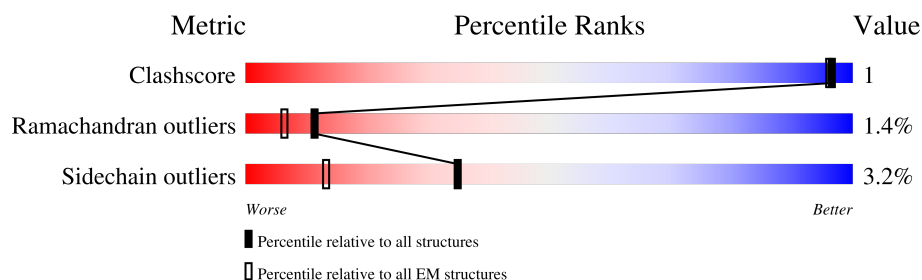
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2407 (4.10 - 5.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	619	96% 43% 49% • •
1	1	619	96% 42% 49% 5% •
1	2	619	96% 45% 47% • • •
1	3	619	96% 42% 48% 5% •

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Mol	Chain	Length	Quality of chain		
1	4	619	96%	41%	49% 6% .
1	5	619	96%	38%	53% 6% .
1	6	619	96%	43%	49% . .
1	7	619	96%	43%	48% 5% .
1	8	619	96%	42%	49% 5% .
1	9	619	96%	44%	47% 5% .
1	A	619	96%	44%	46% 6% .
1	B	619	96%	42%	49% 6% .
1	C	619	96%	42%	48% 6% . .
1	D	619	96%	43%	48% 5% .
1	E	619	96%	41%	49% 6% .
1	F	619	96%	40%	49% 6% . .
1	G	619	96%	38%	53% 5% .
1	H	619	96%	40%	51% . .
1	I	619	96%	39%	54% . .
1	J	619	96%	41%	51% . . .
1	K	619	96%	37%	53% 5% .
1	L	619	96%	43%	47% 5% .
1	M	619	96%	41%	50% 5% .
1	N	619	96%	41%	50% 6% .
1	O	619	96%	43%	49% . .
1	P	619	96%	39%	52% 5% .
1	Q	619	96%	42%	49% 5% .
1	R	619	96%	42%	50% . .
1	S	619	96%	42%	49% 5% .

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Mol	Chain	Length	Quality of chain		
1	T	619	96%	41%	50%
1	U	619	96%	38%	53%
1	V	619	96%	41%	50%
1	W	619	96%	44%	48%
1	X	619	96%	42%	50%
1	Y	619	96%	44%	48%
1	Z	619	96%	39%	52%
1	a	619	96%	42%	49%
1	b	619	96%	45%	45%
1	c	619	96%	45%	47%
1	d	619	96%	42%	47%
1	e	619	96%	39%	52%
1	f	619	96%	42%	49%
1	g	619	96%	40%	50%
1	h	619	96%	42%	48%
1	i	619	96%	42%	50%
1	j	619	96%	41%	50%
1	k	619	96%	43%	48%
1	l	619	96%	41%	50%
1	m	619	96%	43%	48%
1	n	619	96%	38%	53%
1	o	619	96%	42%	50%
1	p	619	96%	38%	53%
1	q	619	96%	42%	48%
1	r	619	96%	42%	49%

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Mol	Chain	Length	Quality of chain
1	s	619	96% 45% 47% . .
1	t	619	96% 41% 49% 5% .
1	u	619	96% 41% 50% 5% . .
1	v	619	96% 41% 50% 5% .
1	w	619	96% 40% 52% . .
1	x	619	96% 41% 49% 6% . .
1	y	619	96% 42% 49% 5% .
1	z	619	96% 39% 51% 6% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 298034 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Interferon-induced GTP-binding protein Mx2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	1	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	2	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	3	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	4	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	5	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	6	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	7	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	8	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	9	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	a	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	b	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	c	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	d	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	e	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	f	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	g	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	h	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	i	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	j	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	k	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	l	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	m	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	n	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	o	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	p	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	q	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	r	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	s	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	t	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	u	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	v	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	w	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	x	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	y	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	z	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	A	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	B	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	D	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	E	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	F	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	G	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	H	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	I	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	J	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	K	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	L	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	M	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	N	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	O	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	P	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	Q	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	R	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	S	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	T	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	U	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	V	596	Total 4807	C 3046	N 841	O 896	S 24	0	0
1	W	596	Total 4807	C 3046	N 841	O 896	S 24	0	0

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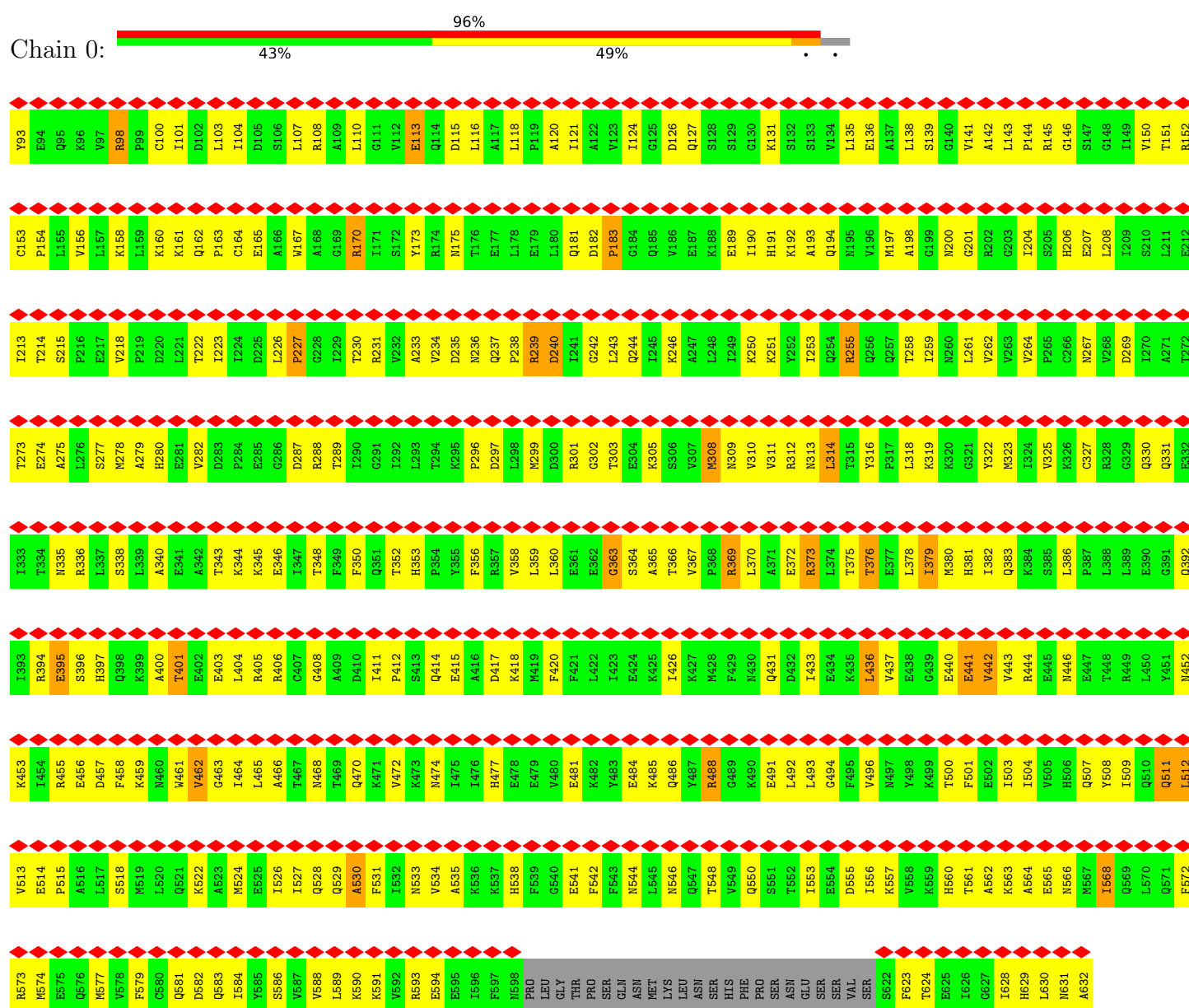
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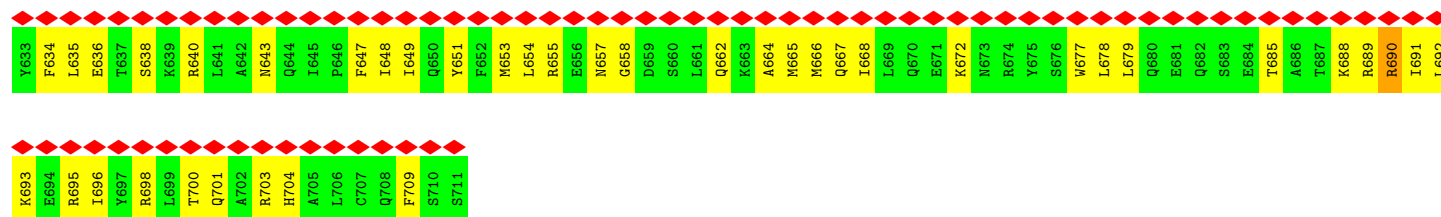
Mol	Chain	Residues	Atoms					AltConf	Trace
1	X	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	Y	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		
1	Z	596	Total	C	N	O	S	0	0
			4807	3046	841	896	24		

3 Residue-property plots

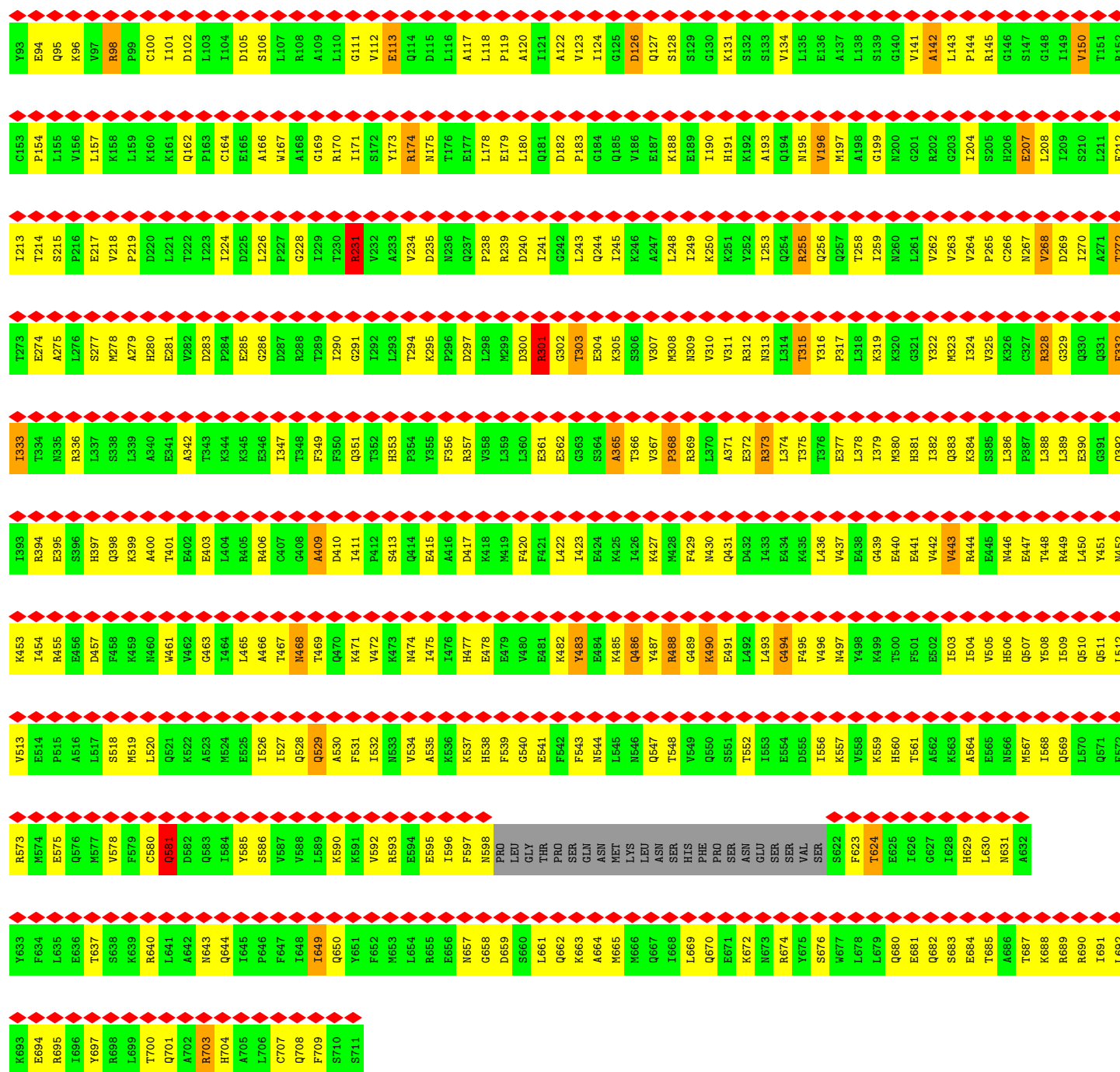
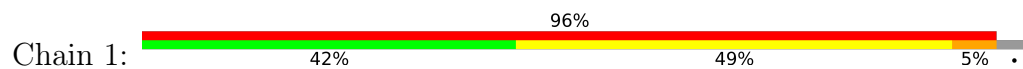
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Interferon-induced GTP-binding protein Mx2

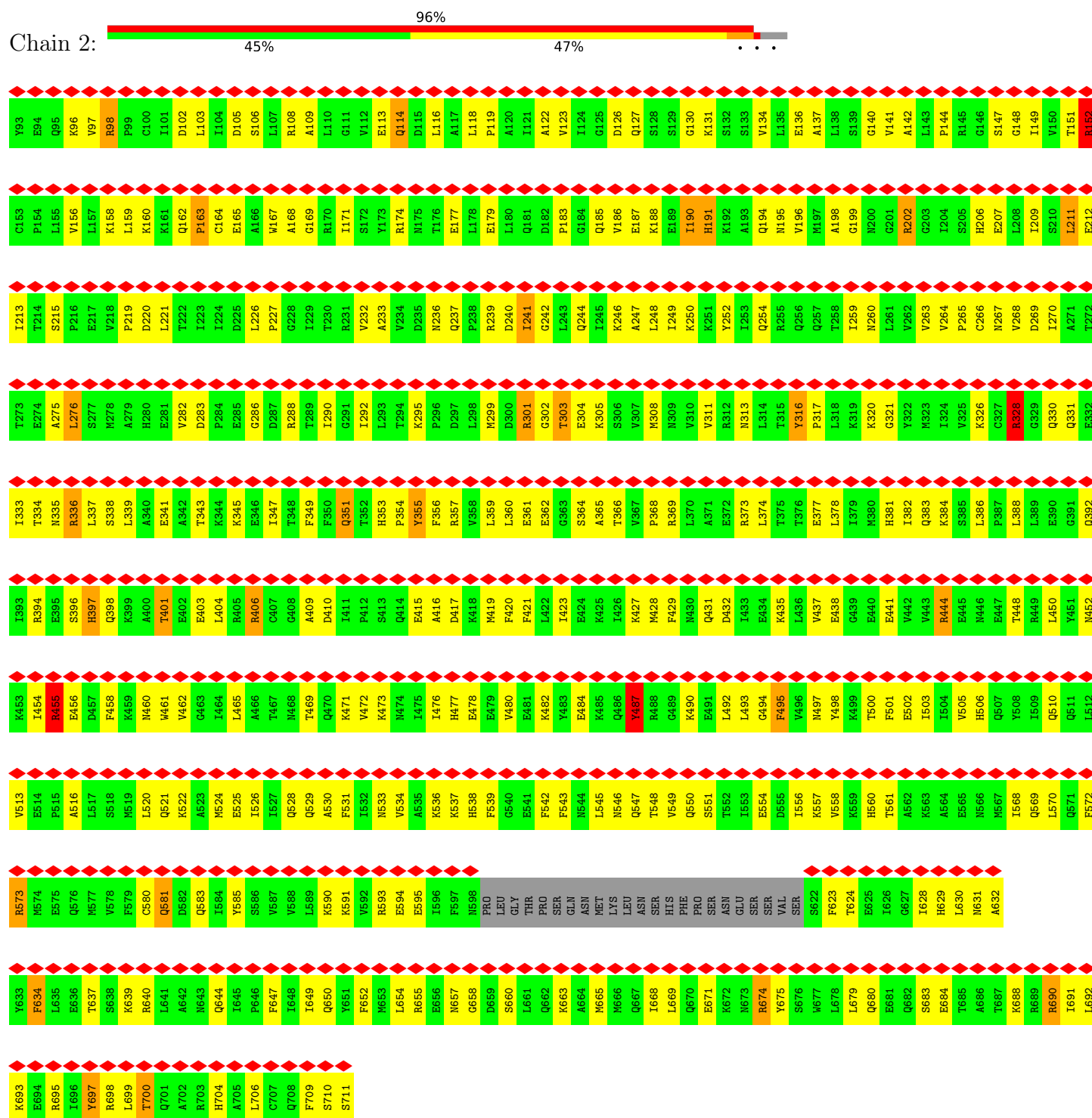




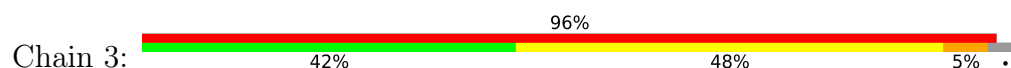
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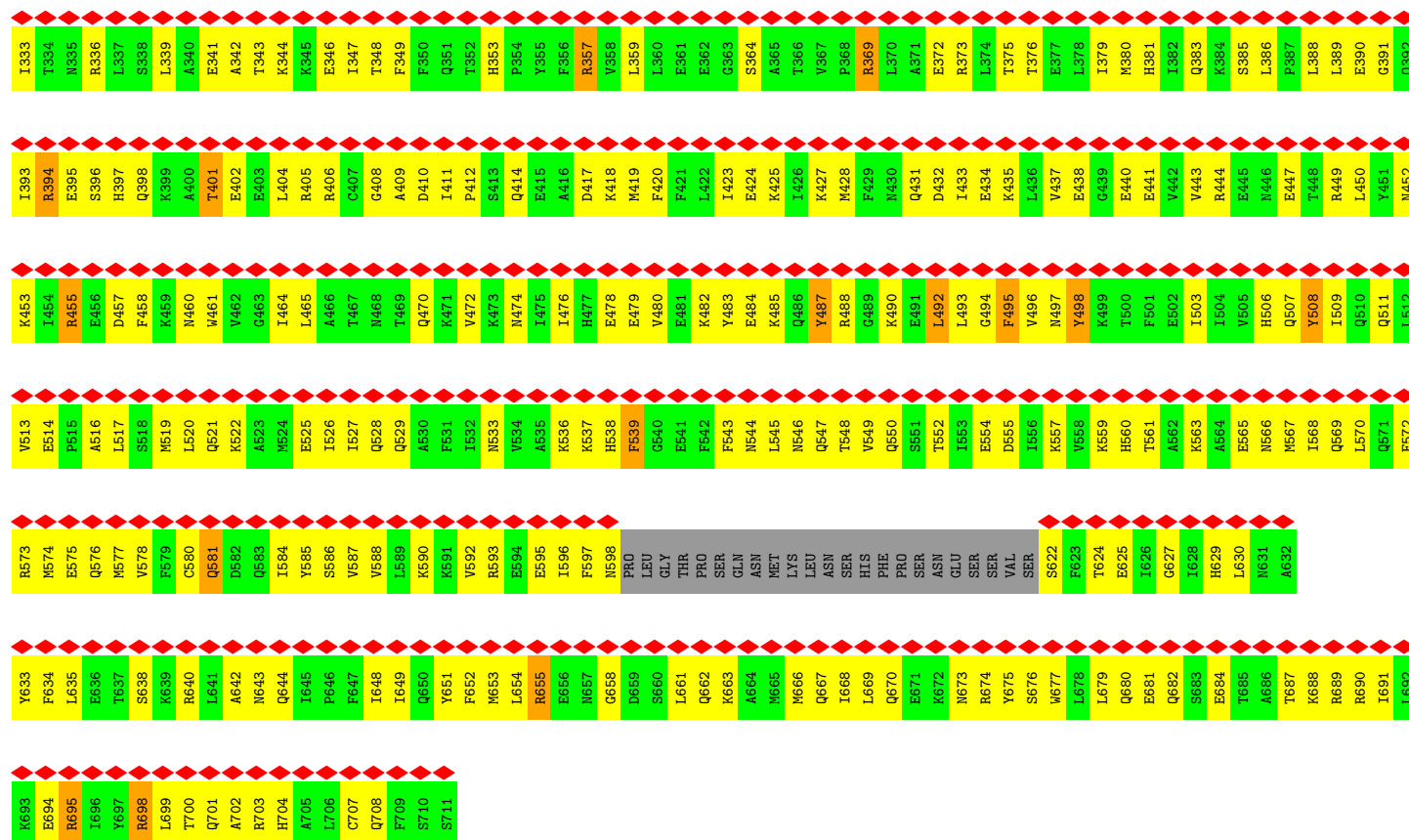


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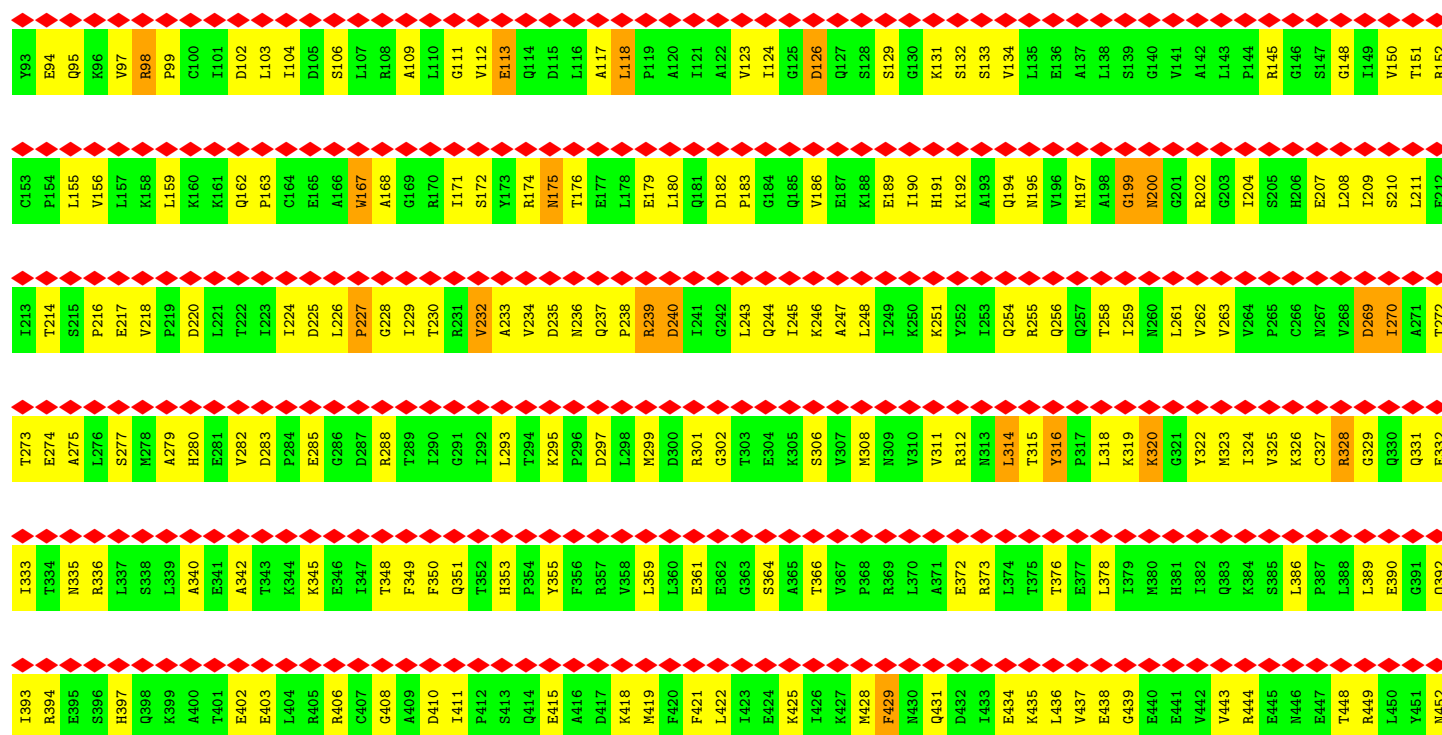


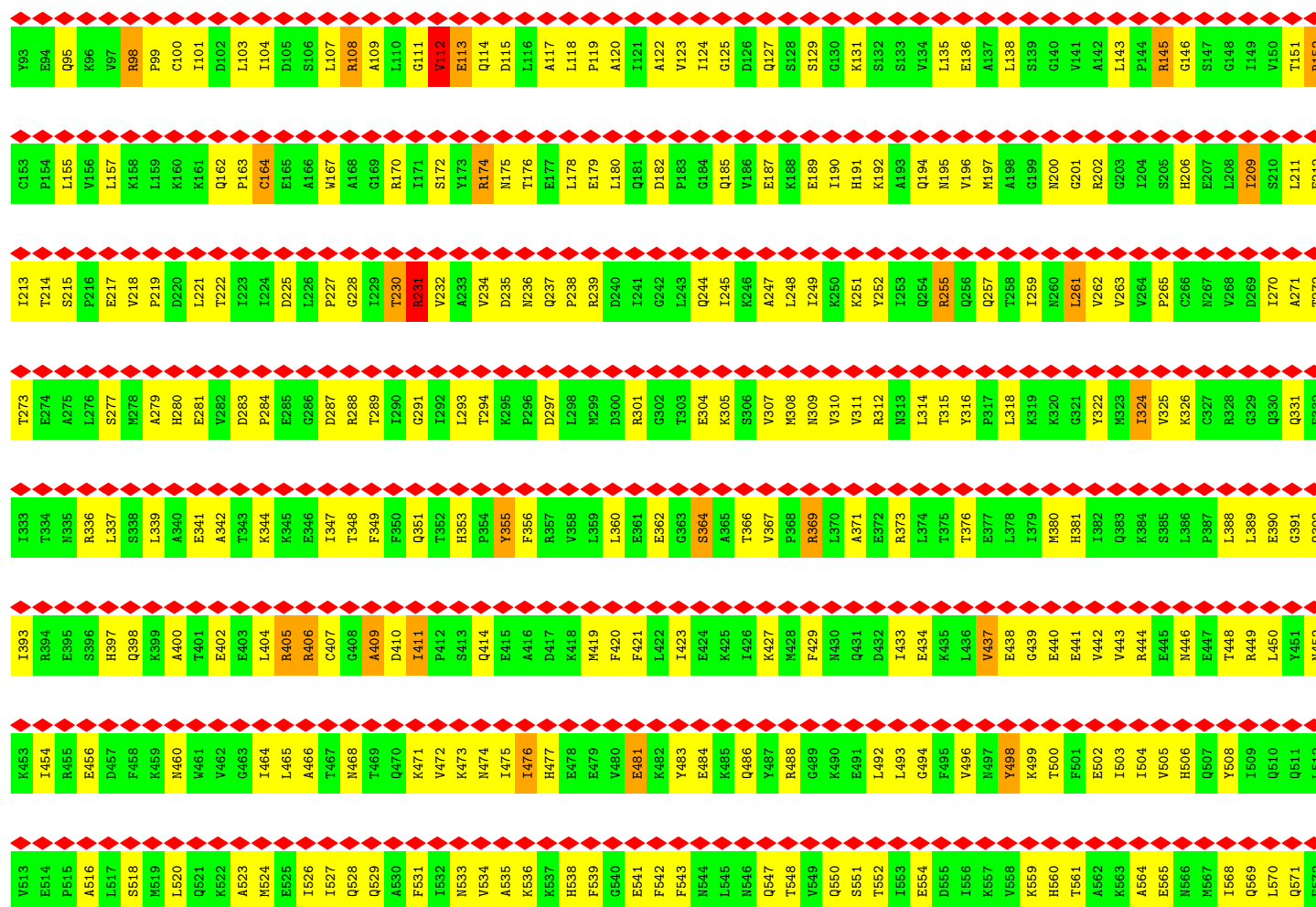
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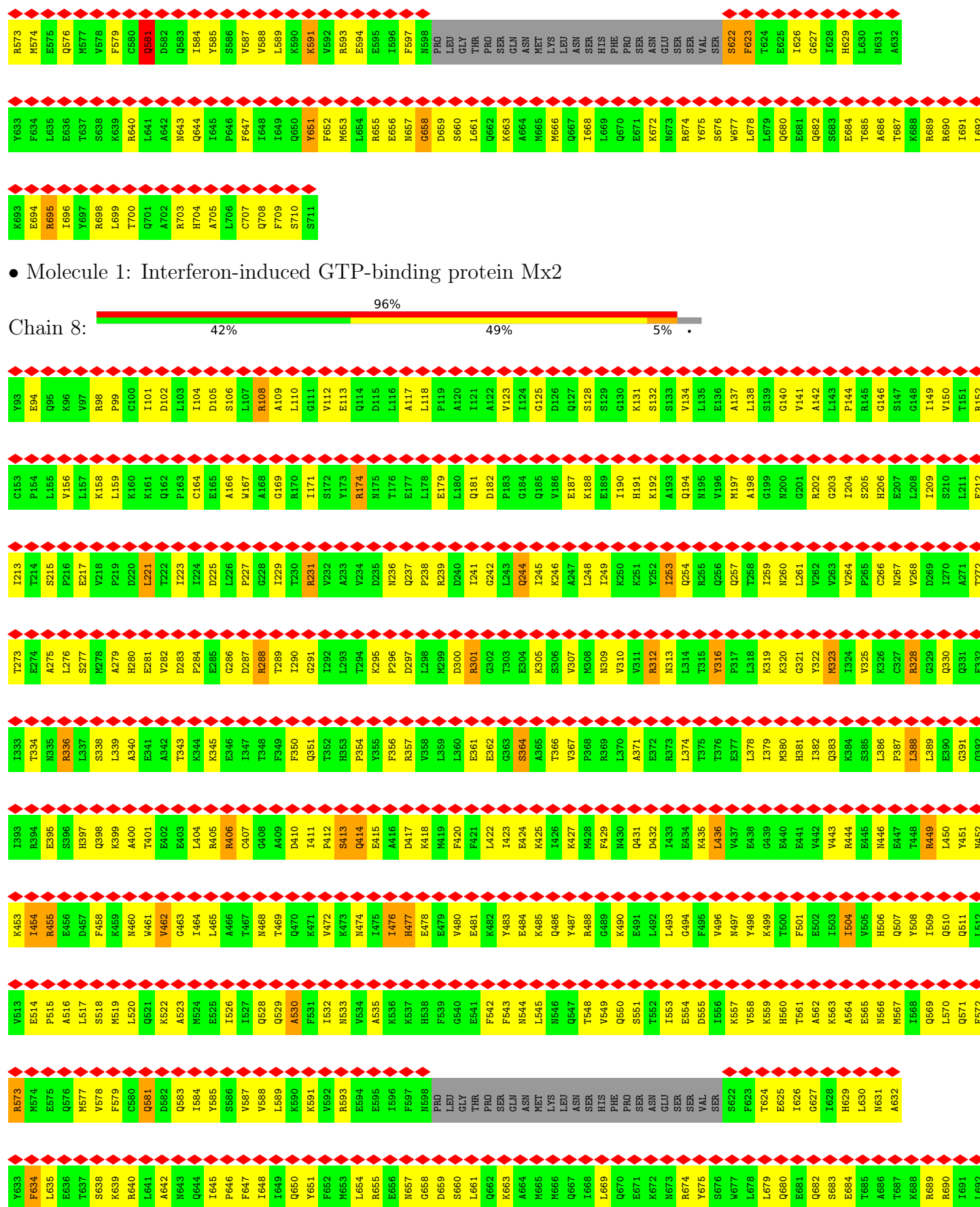




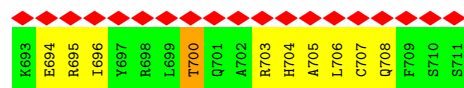
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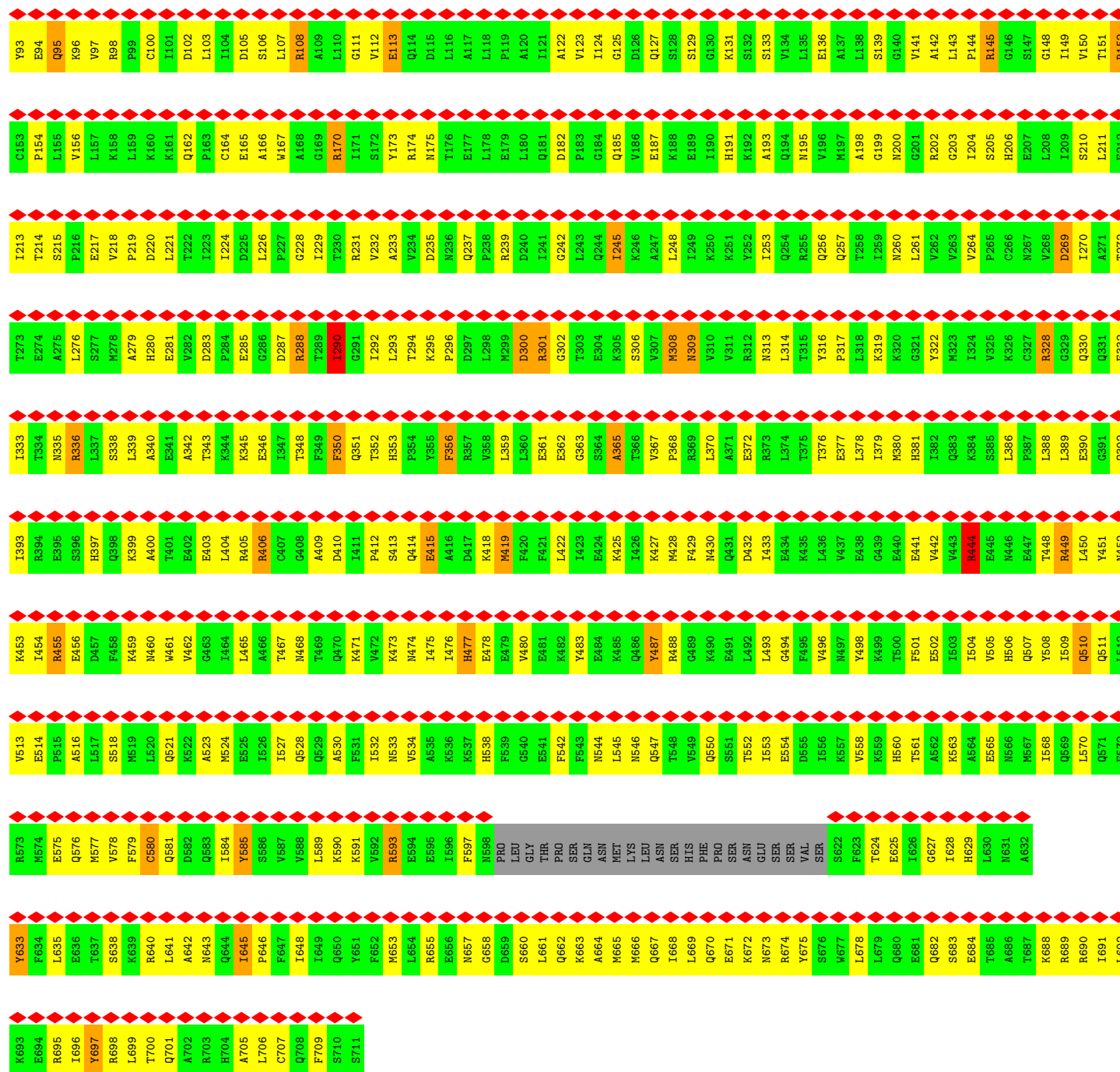




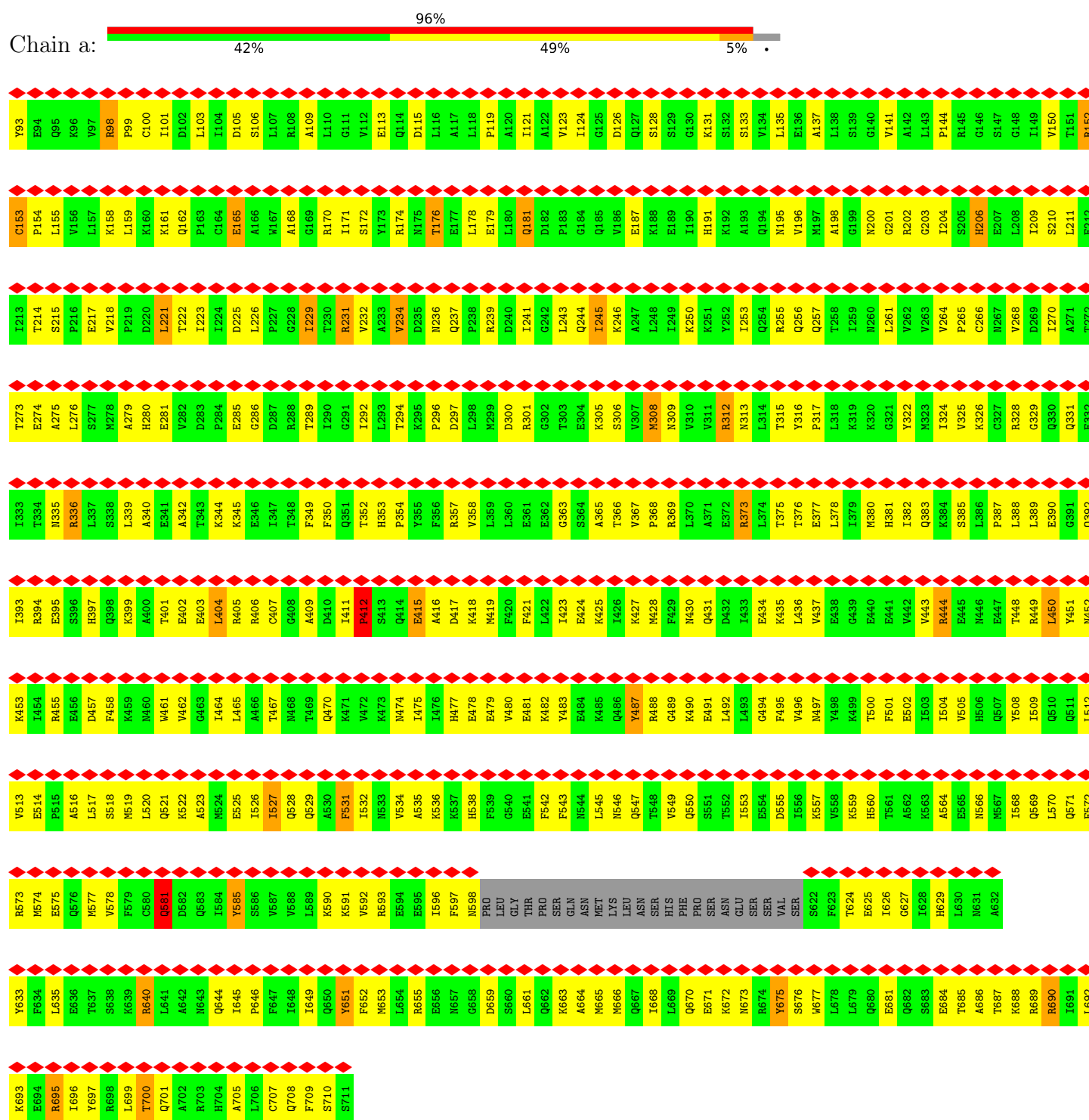
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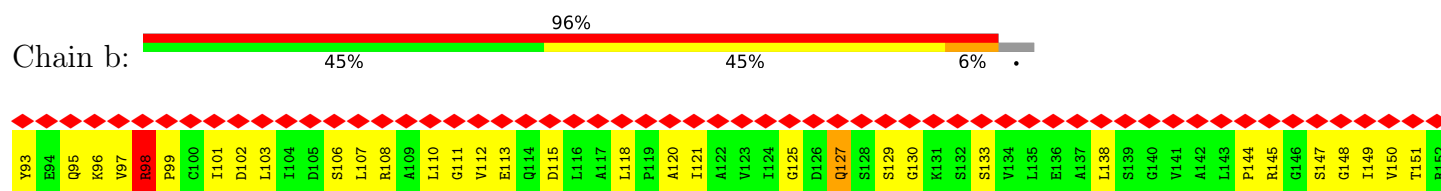
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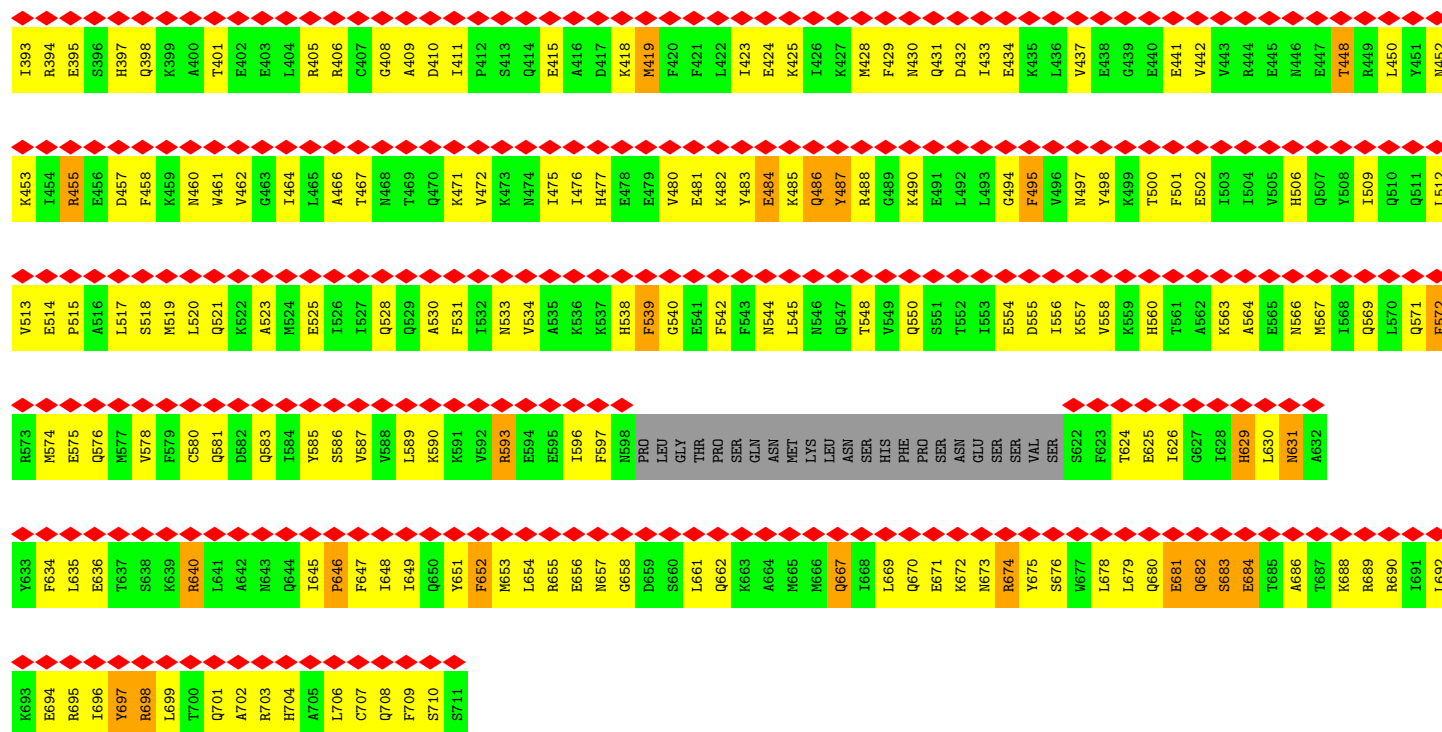
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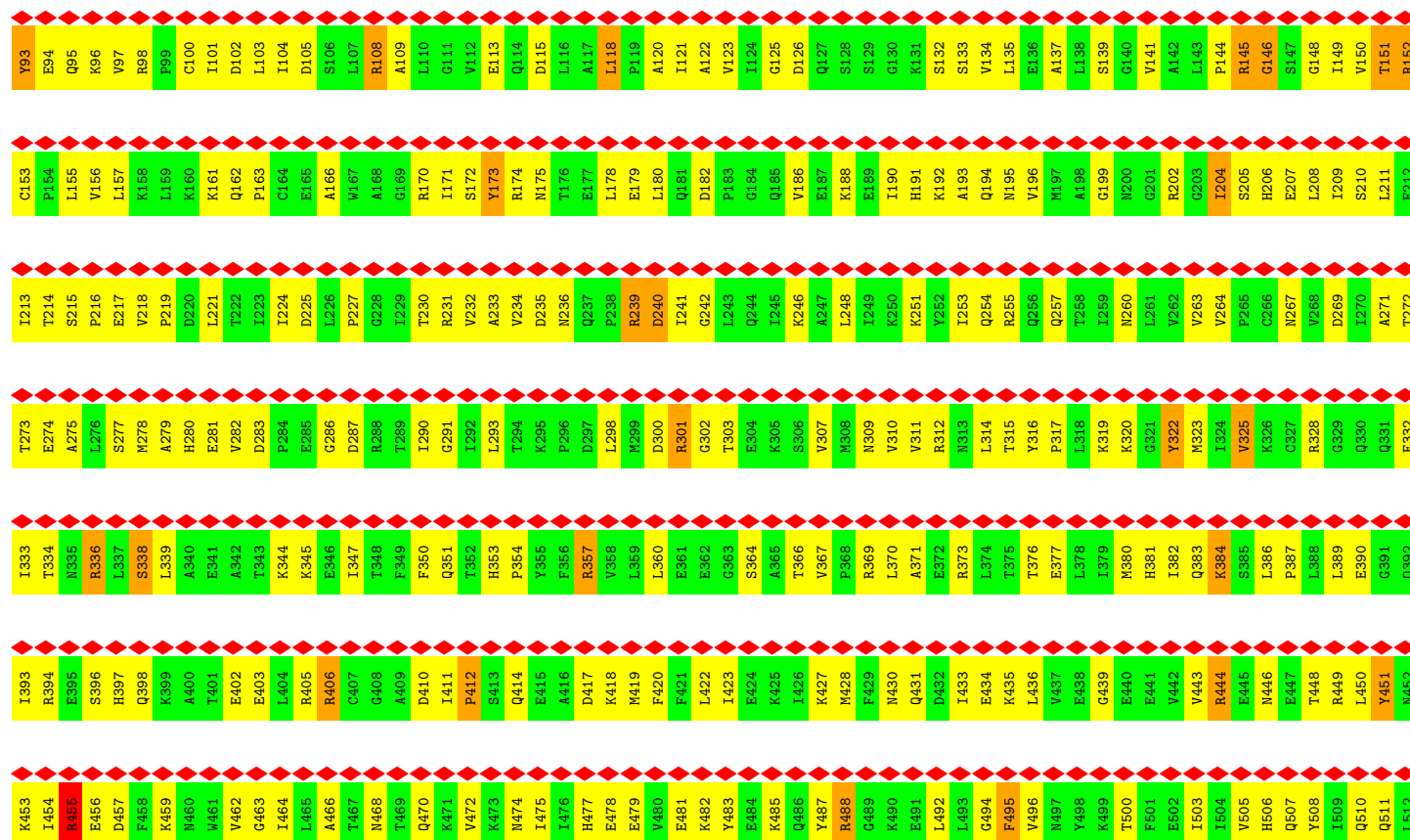
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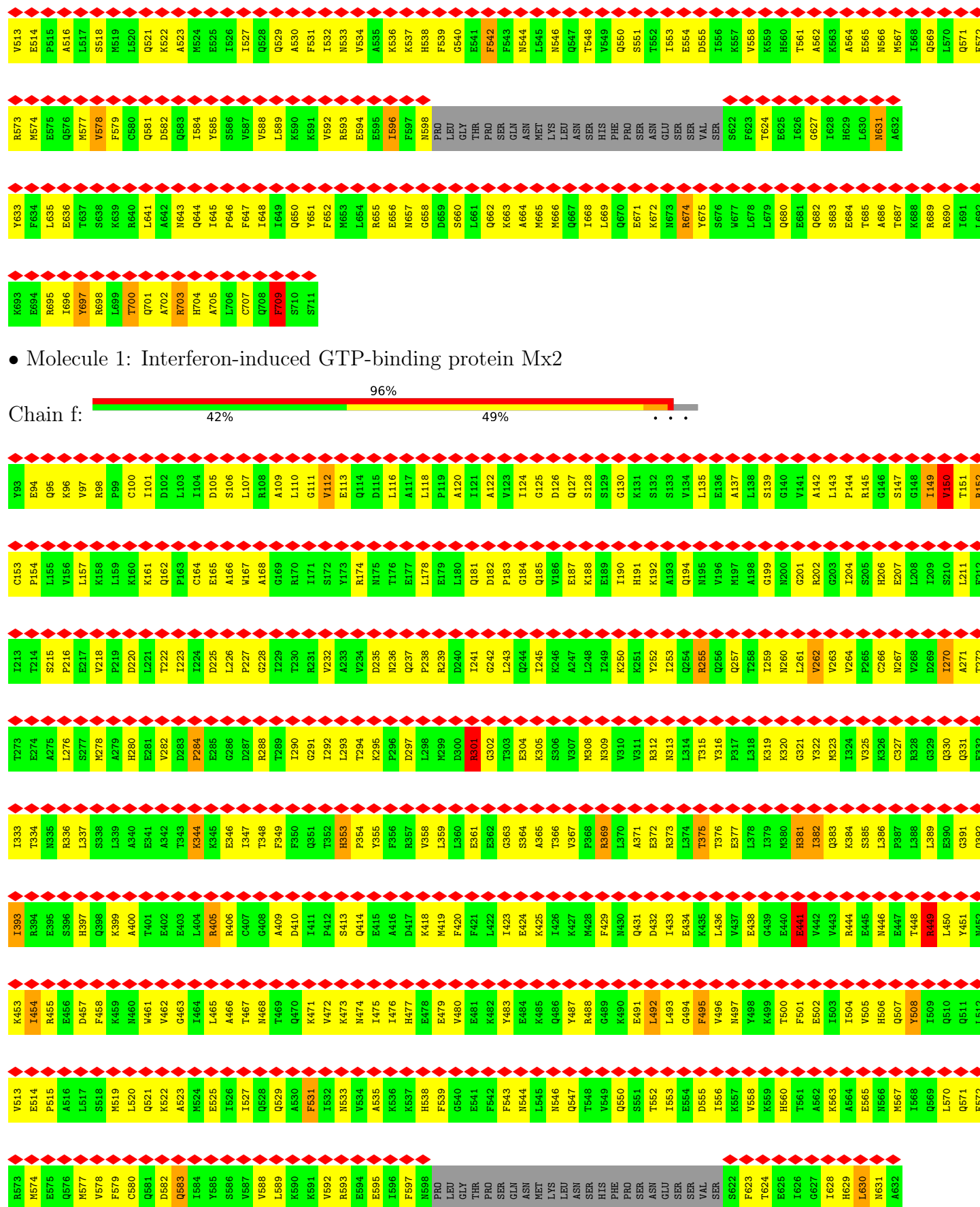






• Molecule 1: Interferon-induced GTP-binding protein Mx2





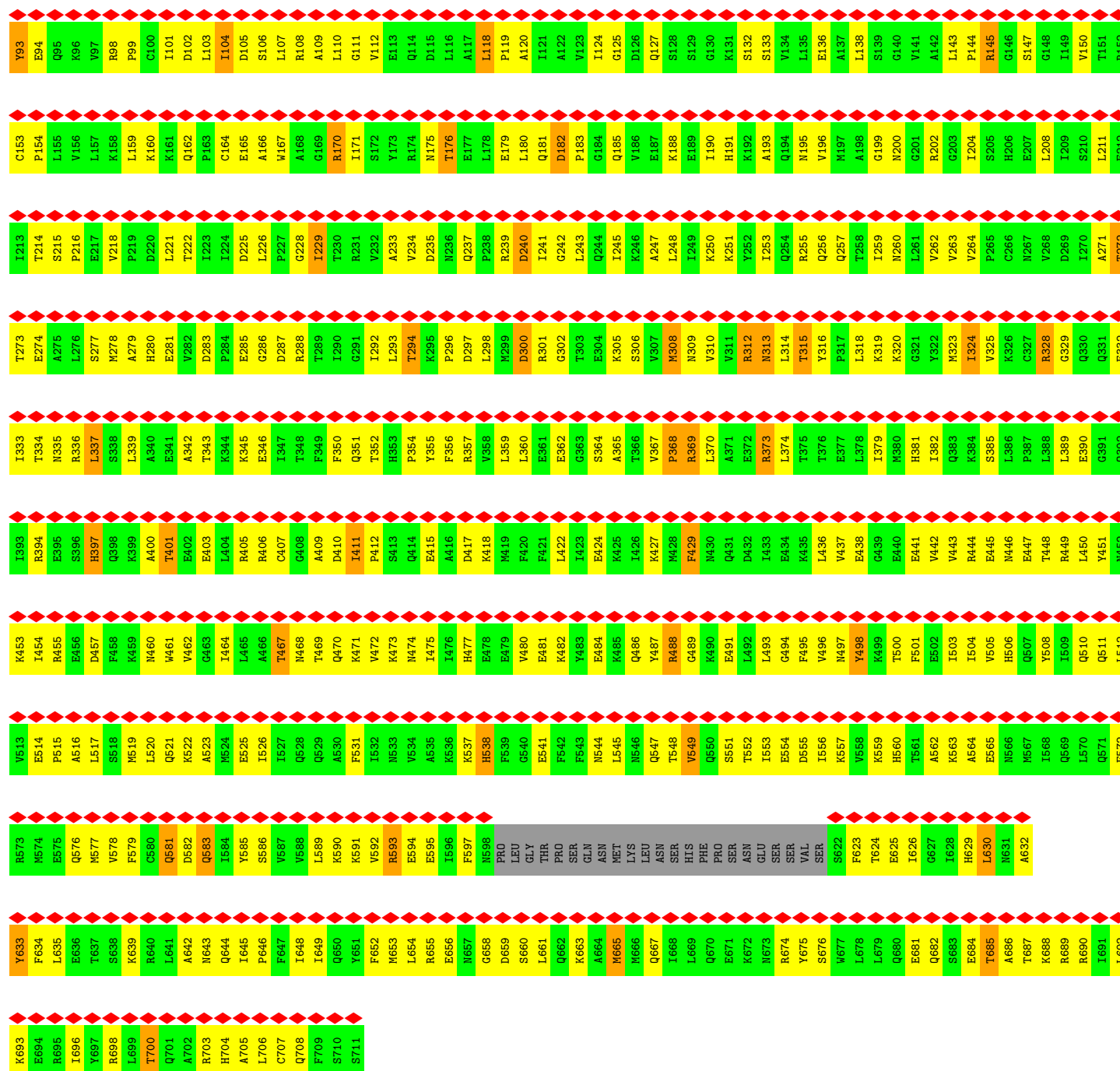
• Molecule 1: Interferon-induced GTP-binding protein Mx2

96%

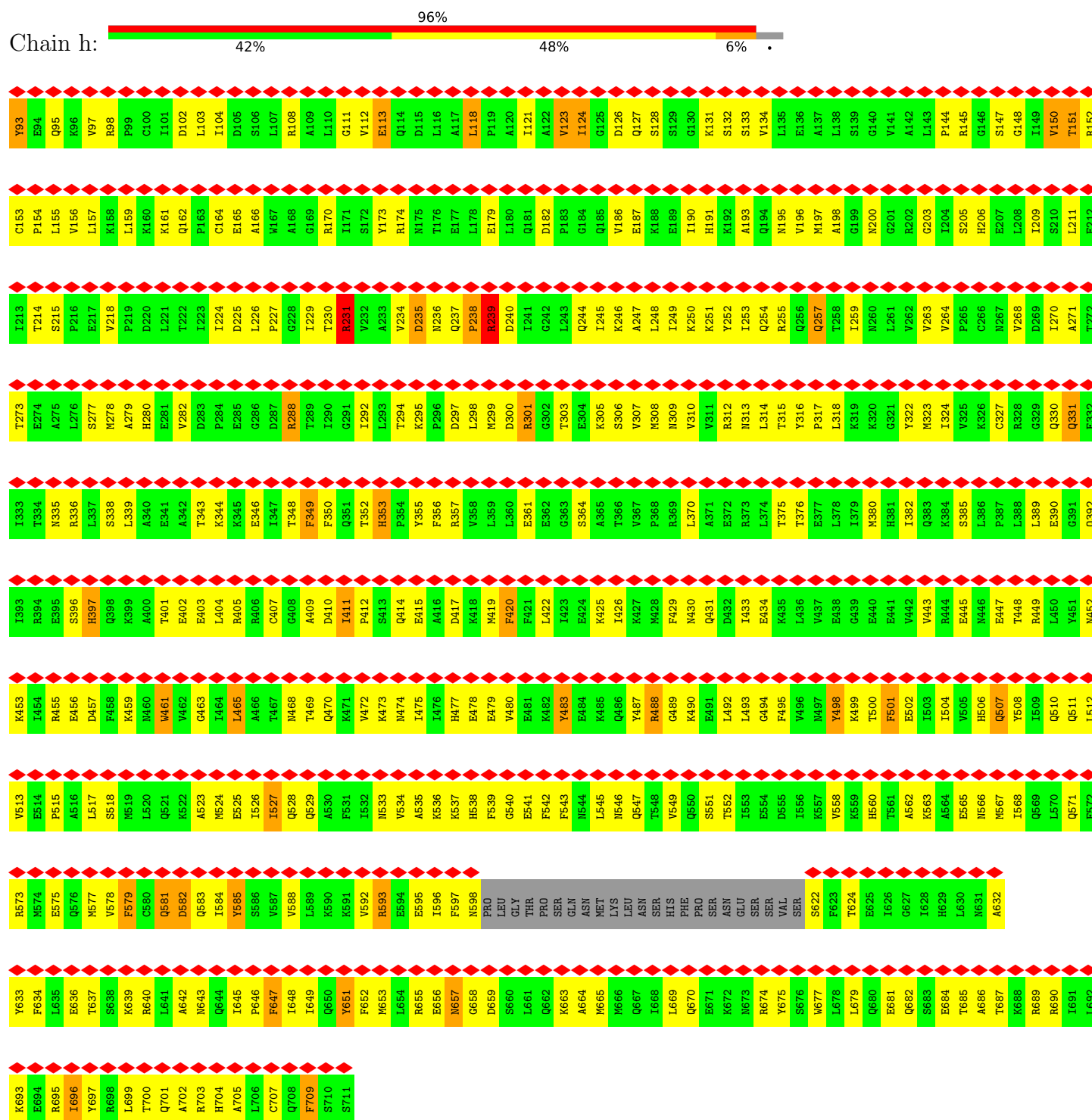
Chain f:

42%

49%

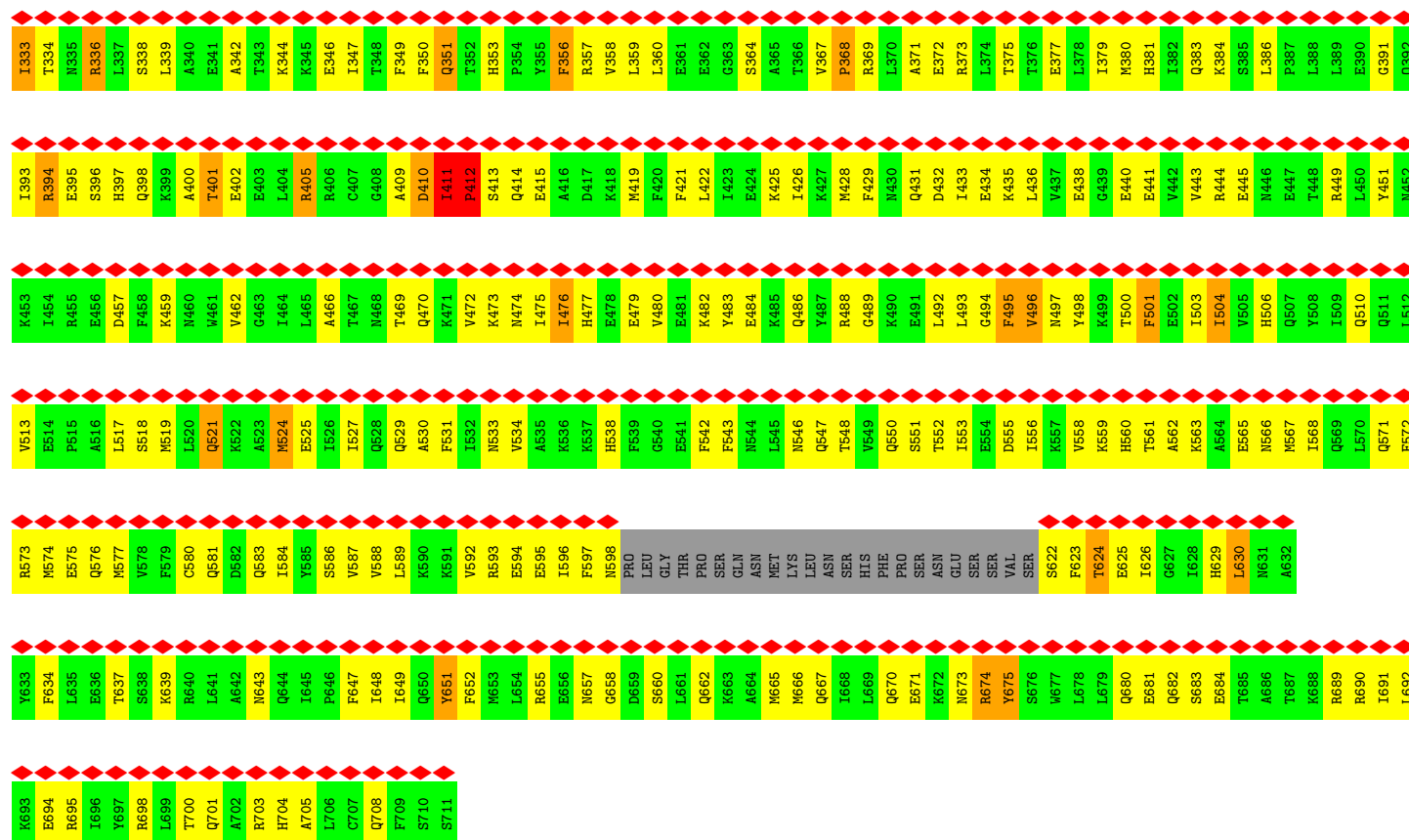


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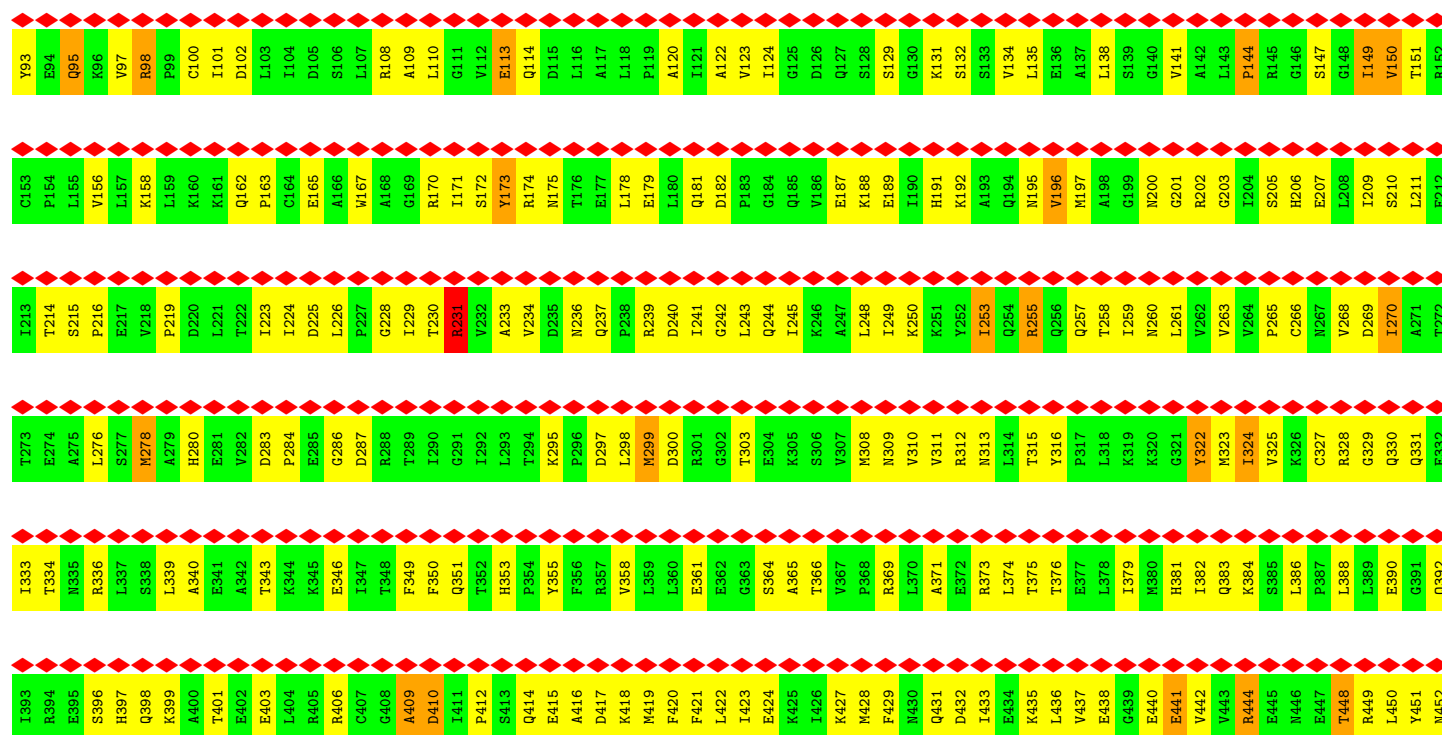


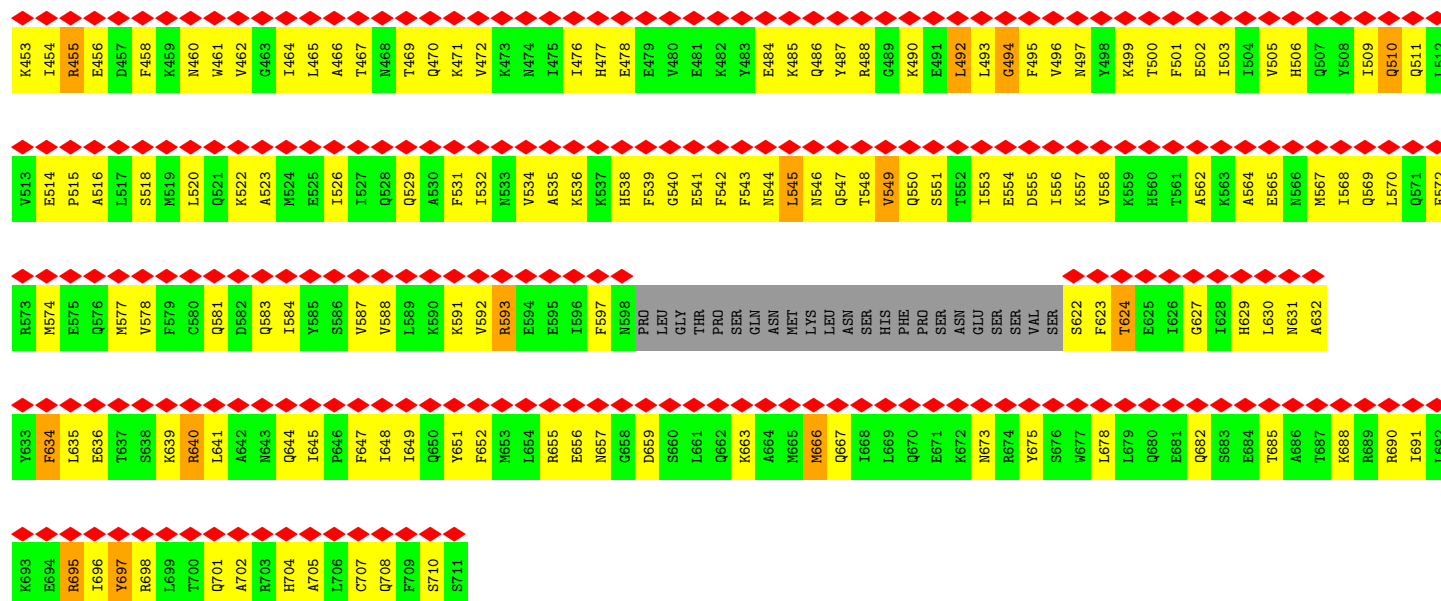
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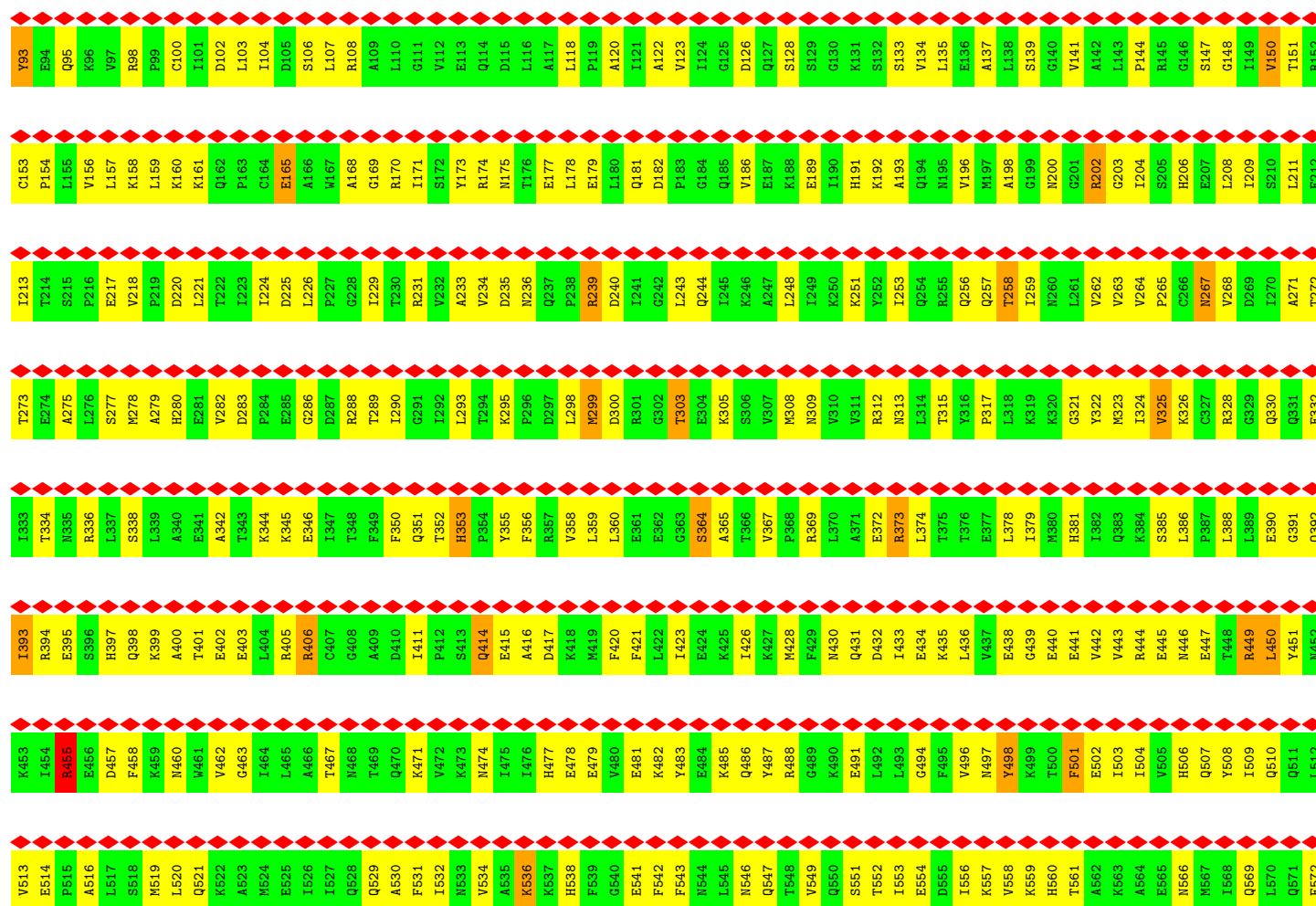


• Molecule 1: Interferon-induced GTP-binding protein Mx2



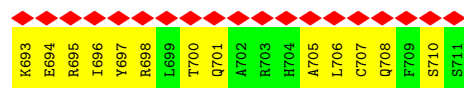


• Molecule 1: Interferon-induced GTP-binding protein Mx2

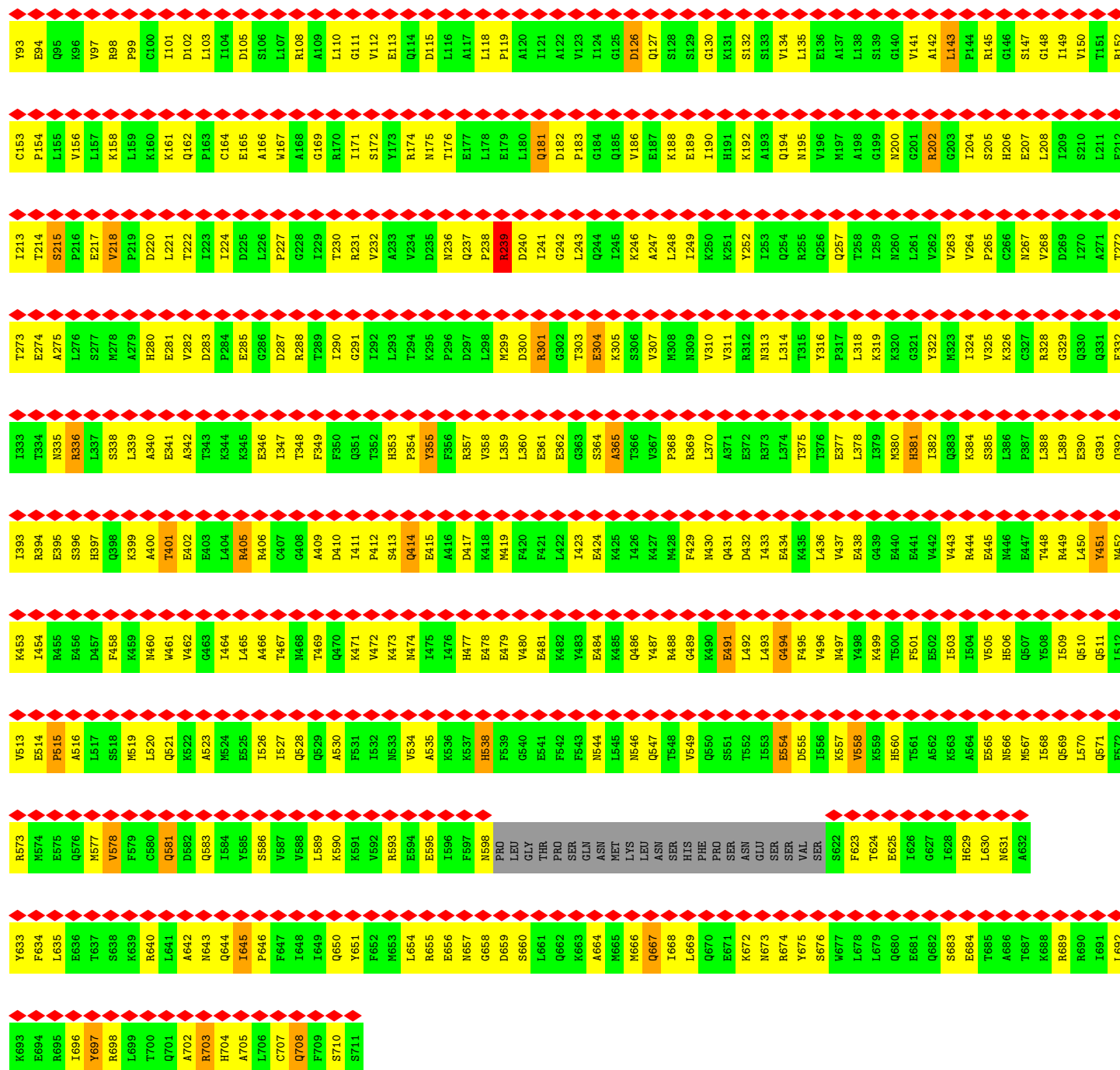
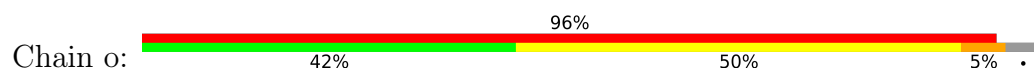




• Molecule 1: Interferon-induced GTP-binding protein Mx2

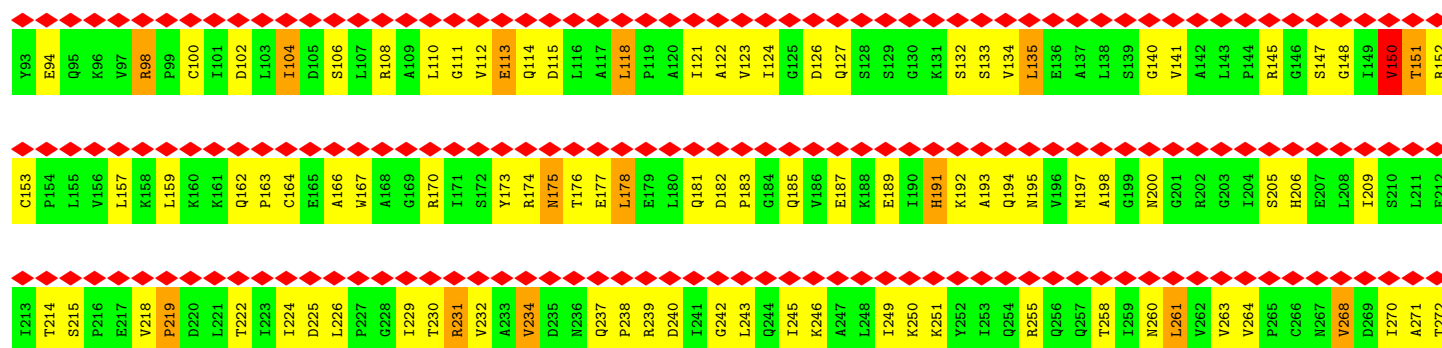


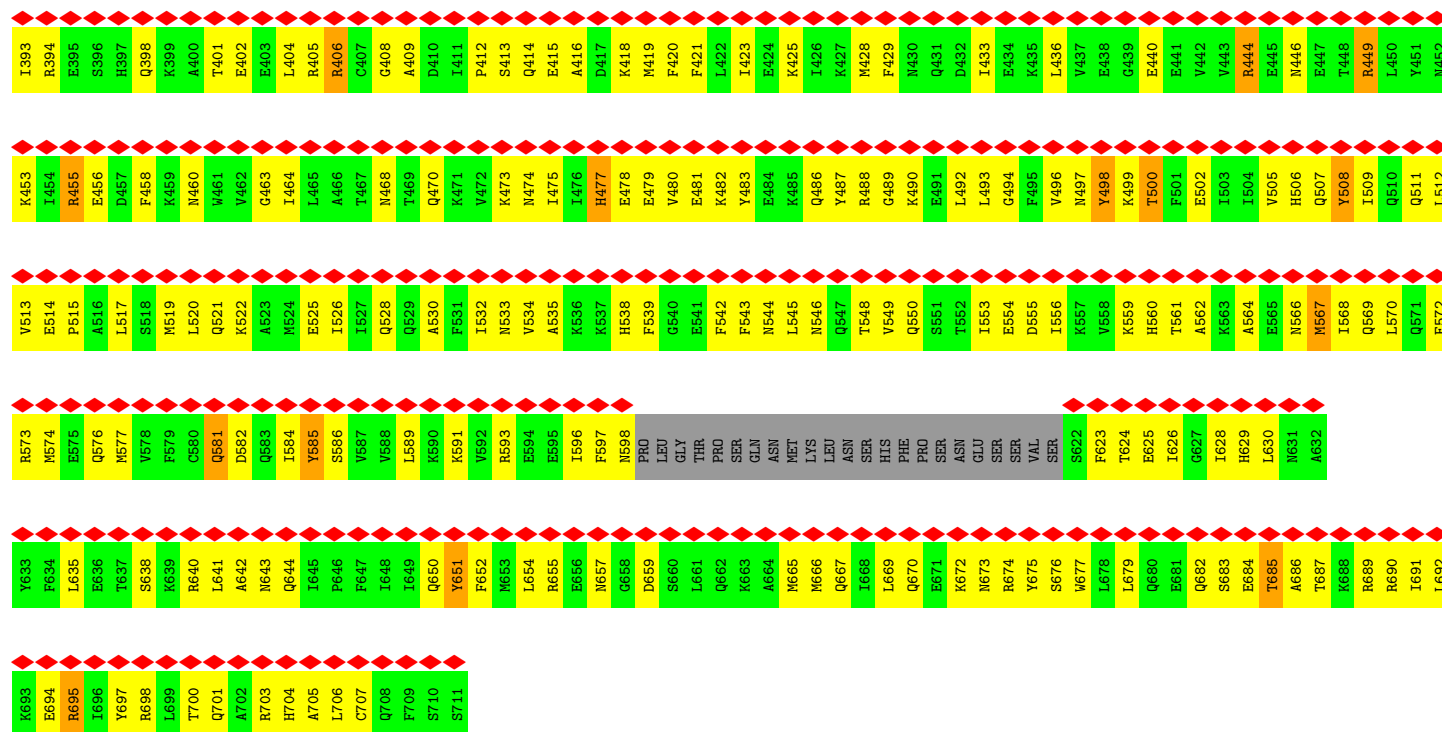
• Molecule 1: Interferon-induced GTP-binding protein Mx2



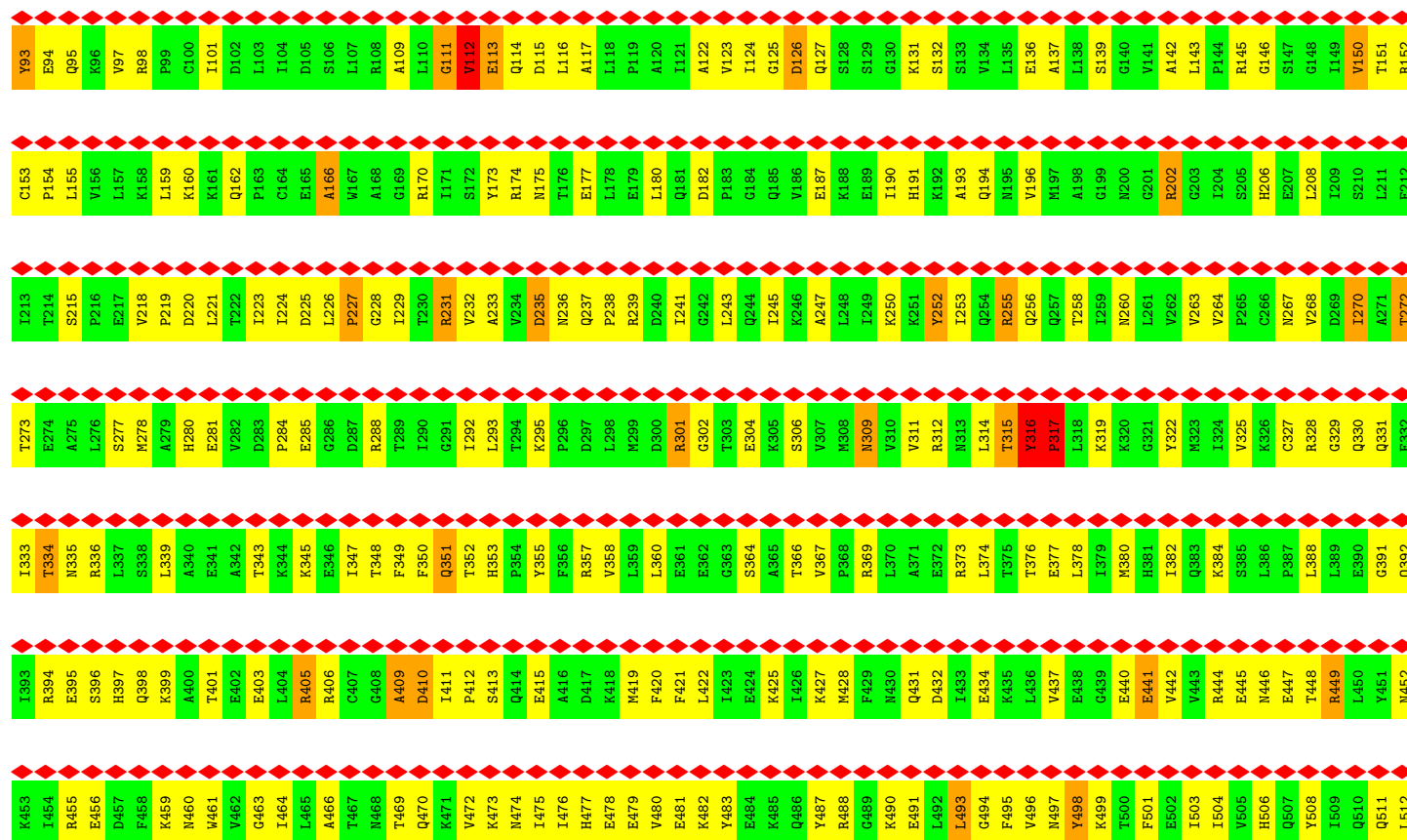
• Molecule 1: Interferon-induced GTP-binding protein Mx2

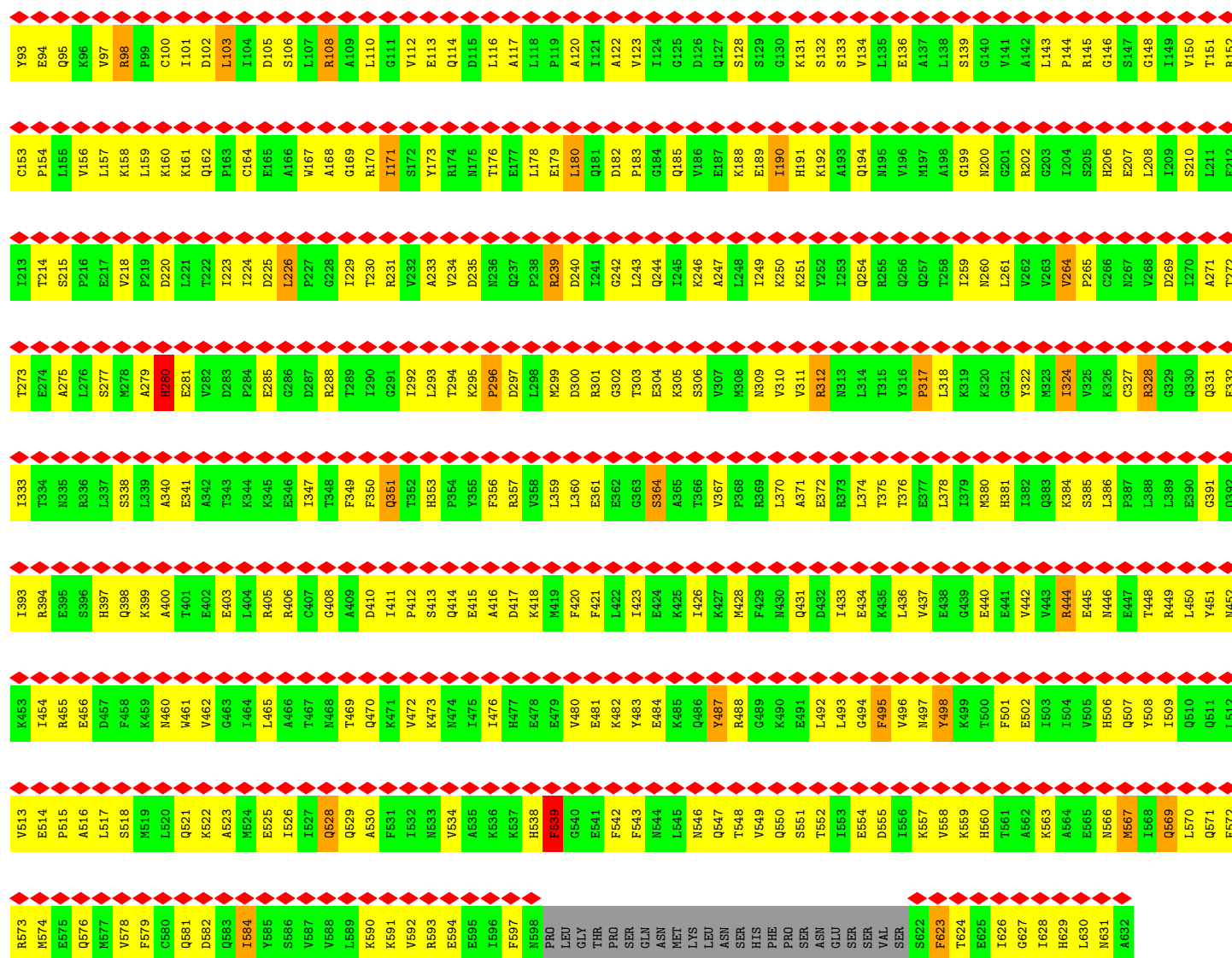


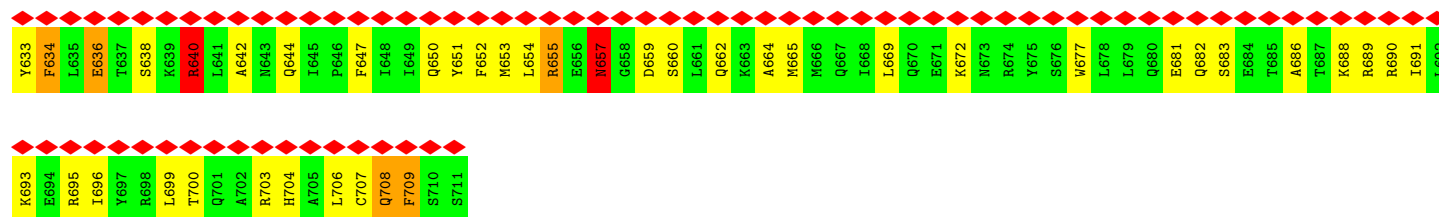




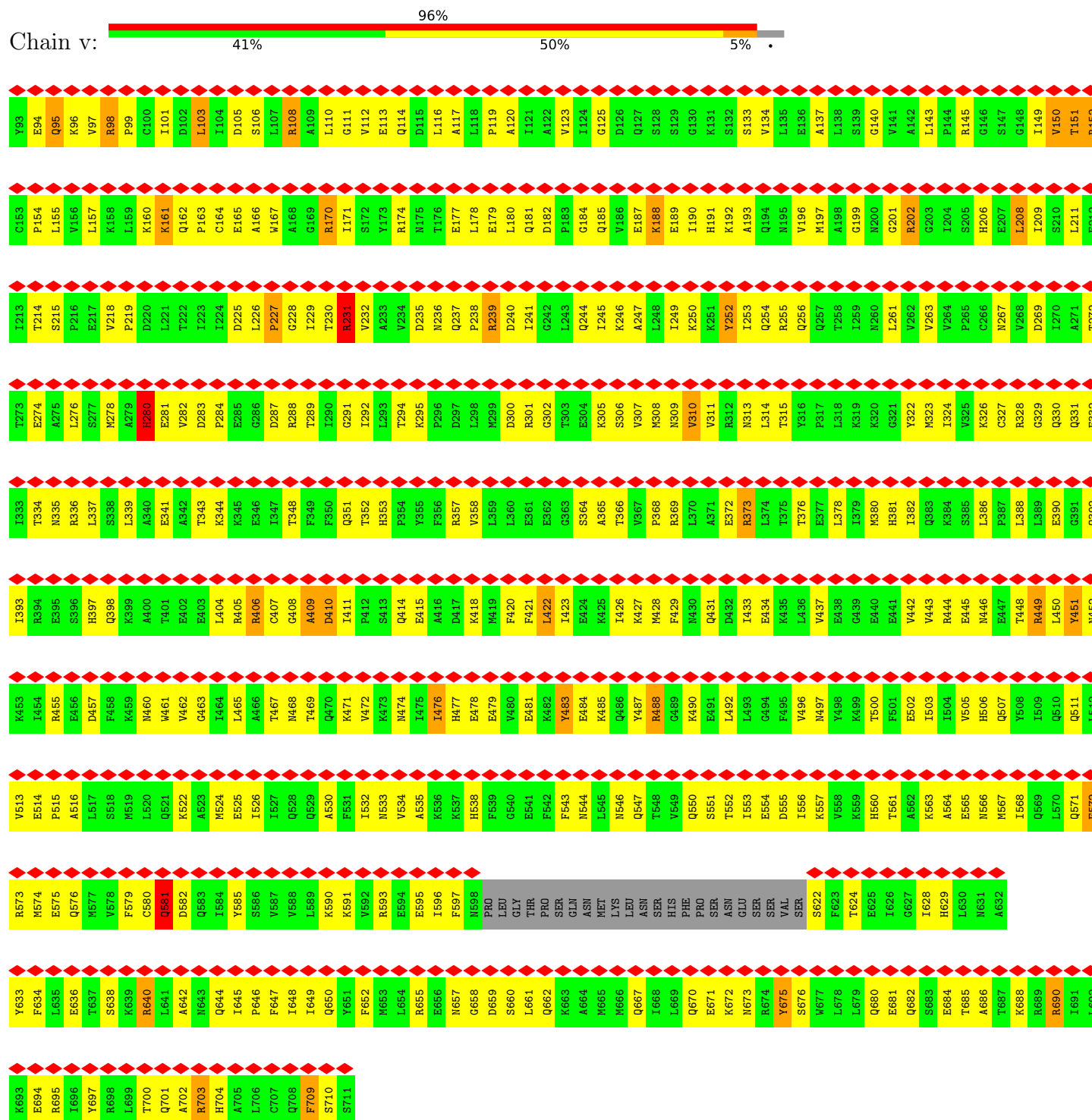
• Molecule 1: Interferon-induced GTP-binding protein Mx2



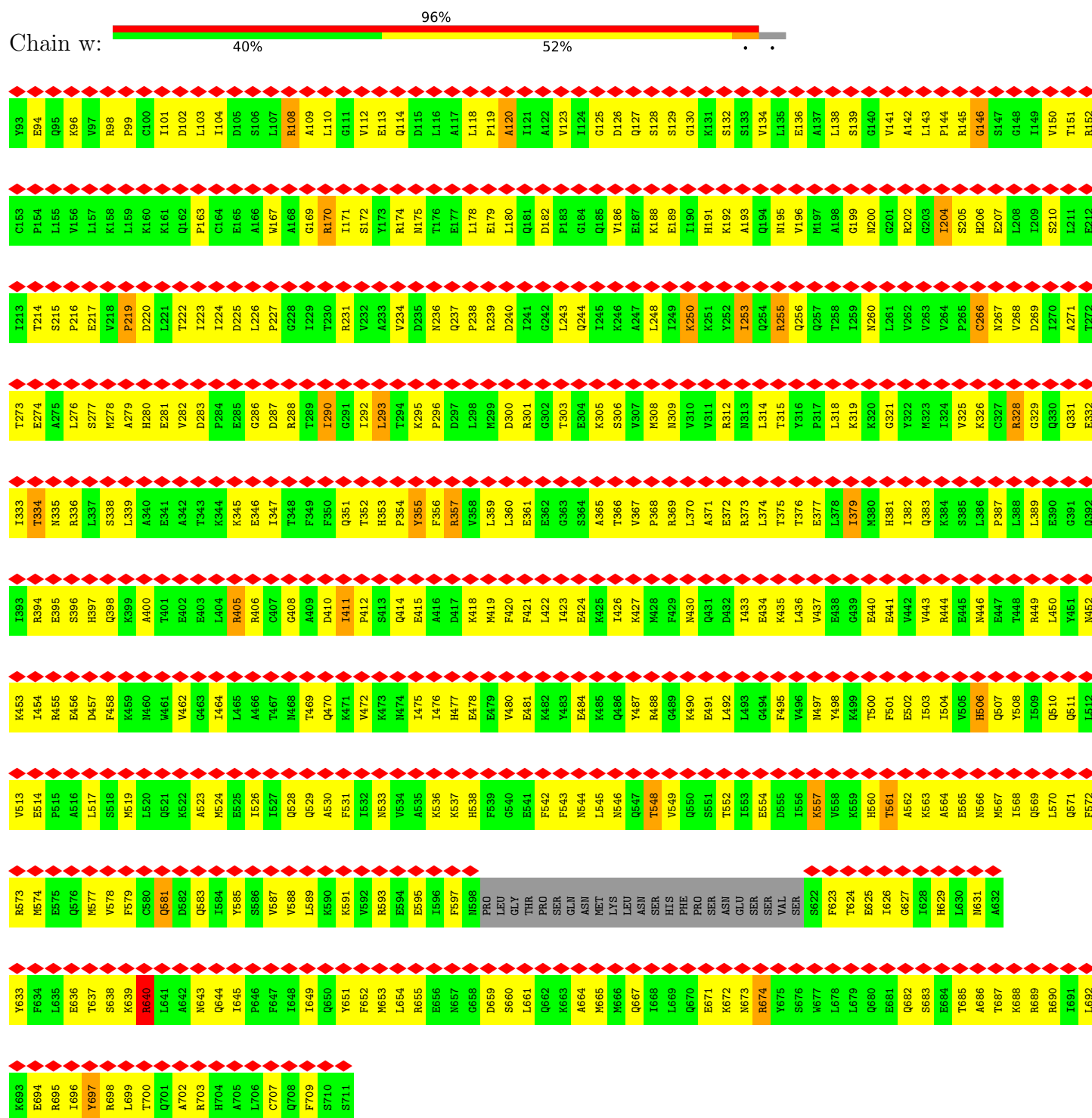




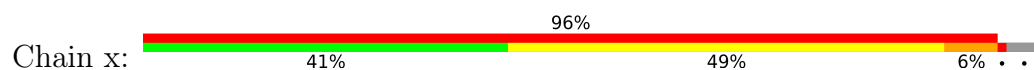
• Molecule 1: Interferon-induced GTP-binding protein Mx2



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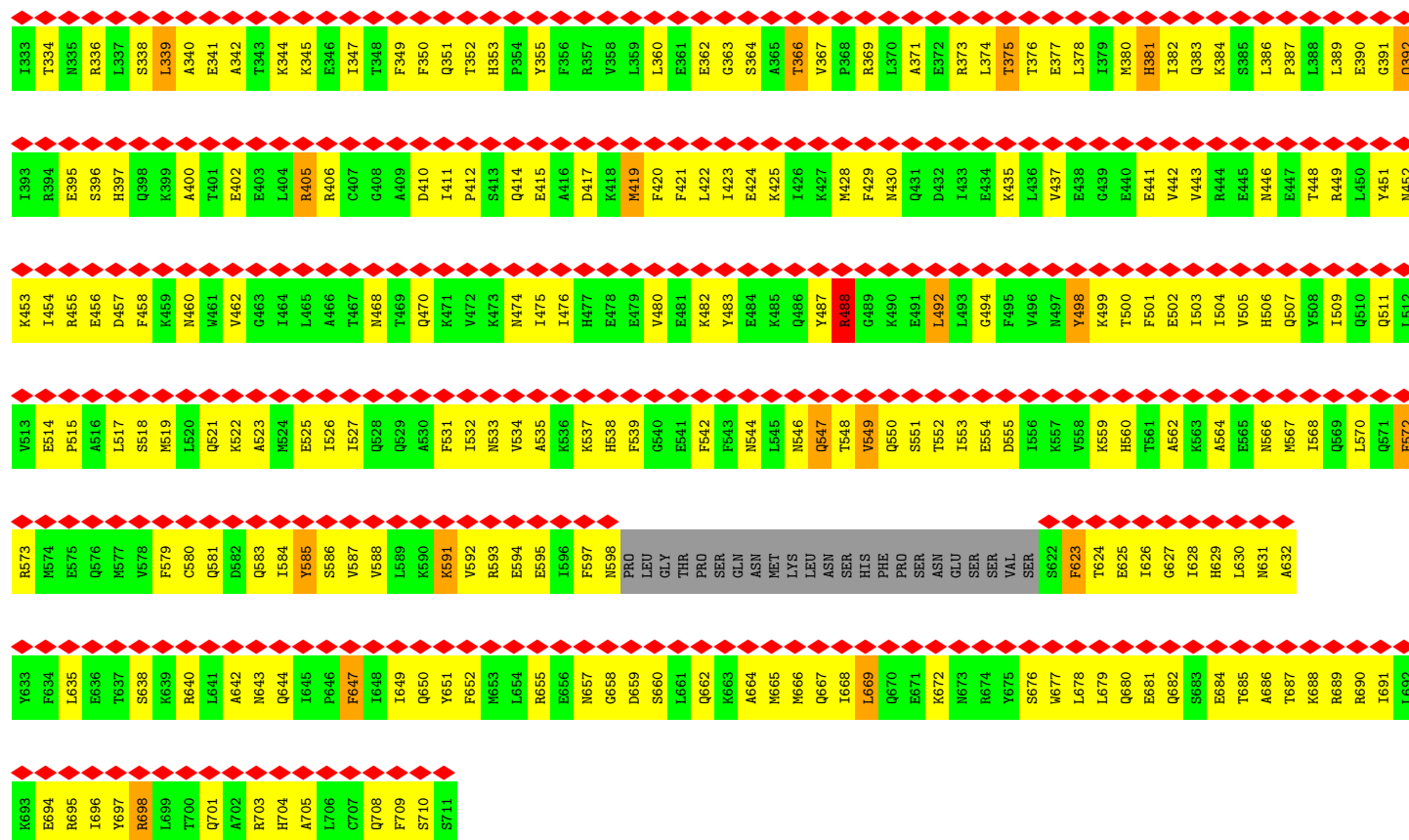


I213	T273	I333	I393	K453	V513	R573	G633	K693
T214	E274	T334	R394	I454	E514	M574	F634	E694
S215	A275	N335	E395	R455	P515	E575	L635	R695
P216	L276	R336	S396	E456	A516	Q576	E636	L696
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V218	M278	S338	Q398	F458	S518	V578	S638	R698
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G242	G302	E362	L422	K482	F542	THR	Q662	
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I270	Q330	E390	L450	Q510	L570		R690	
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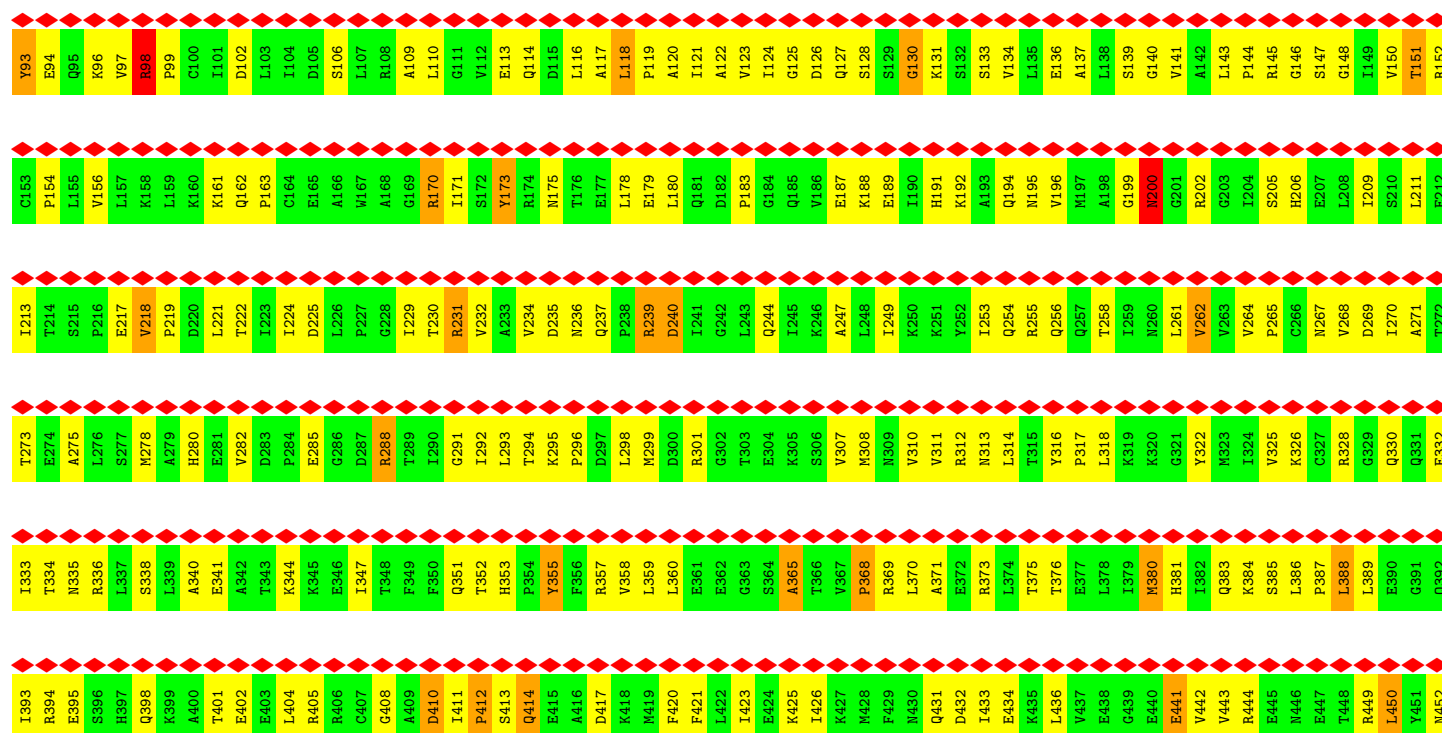
• Molecule 1: Interferon-induced GTP-binding protein Mx2

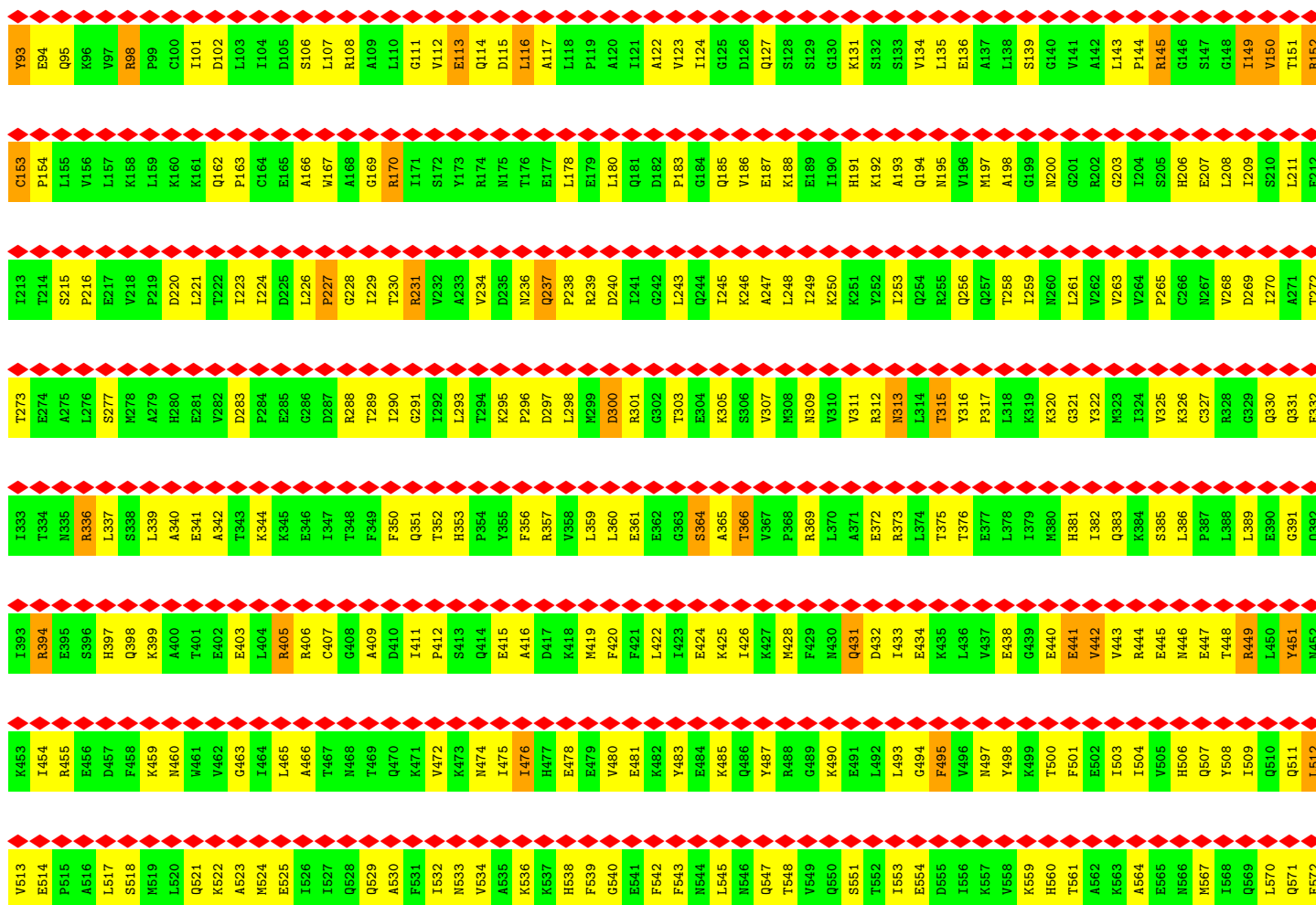


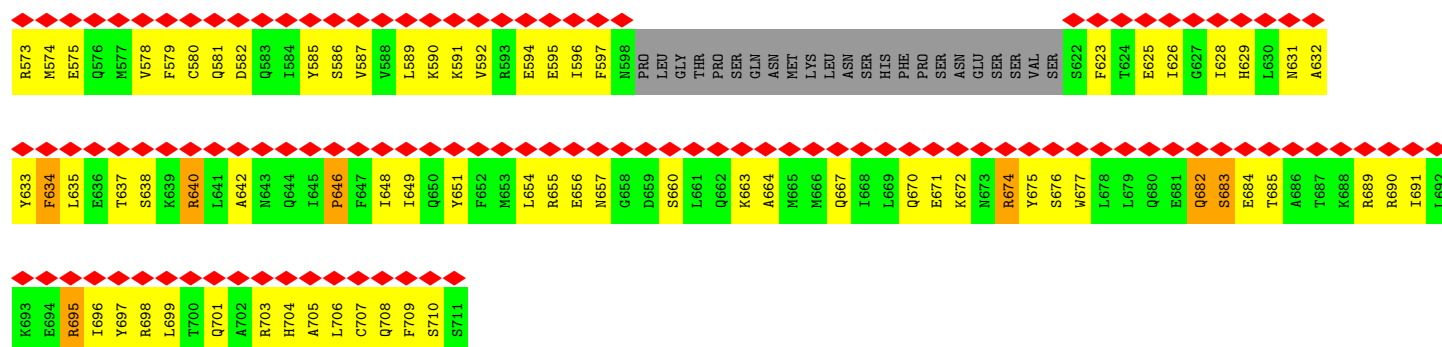
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I101	K161	L221	E281
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L103	P163	I223	D283
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D105	E165	D225	E285
L106	A166	L226	G286
S107	W167	P227	D287
R108	A168	G228	R288
A109	G169	I229	T289
L110	R170	T230	I290
G111	I171	R231	G291
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E113	Y173	A233	L293
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G125	Q185	I245	K305
D126	V186	K246	S306
Q127	E187	A247	V307
S128	L188	L248	M308
I129	E189	I249	N309
K130	I190	K250	V310
X131	H191	K251	V311
S132	K192	Y252	R312
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V134	Q194	Q254	L314
L135	N195	R255	T315
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A137	M197	Q257	P317
L138	A198	T258	L318
S139	G199	I259	K319
G140	N200	N260	K320
V141	G201	L261	G321
A142	R202	V262	Y322
L143	G203	V263	M323
P144	I204	V264	I324
R145	S205	P265	V325
G146	H206	C266	K326
S147	E207	N267	C327
G148	L208	V268	R328
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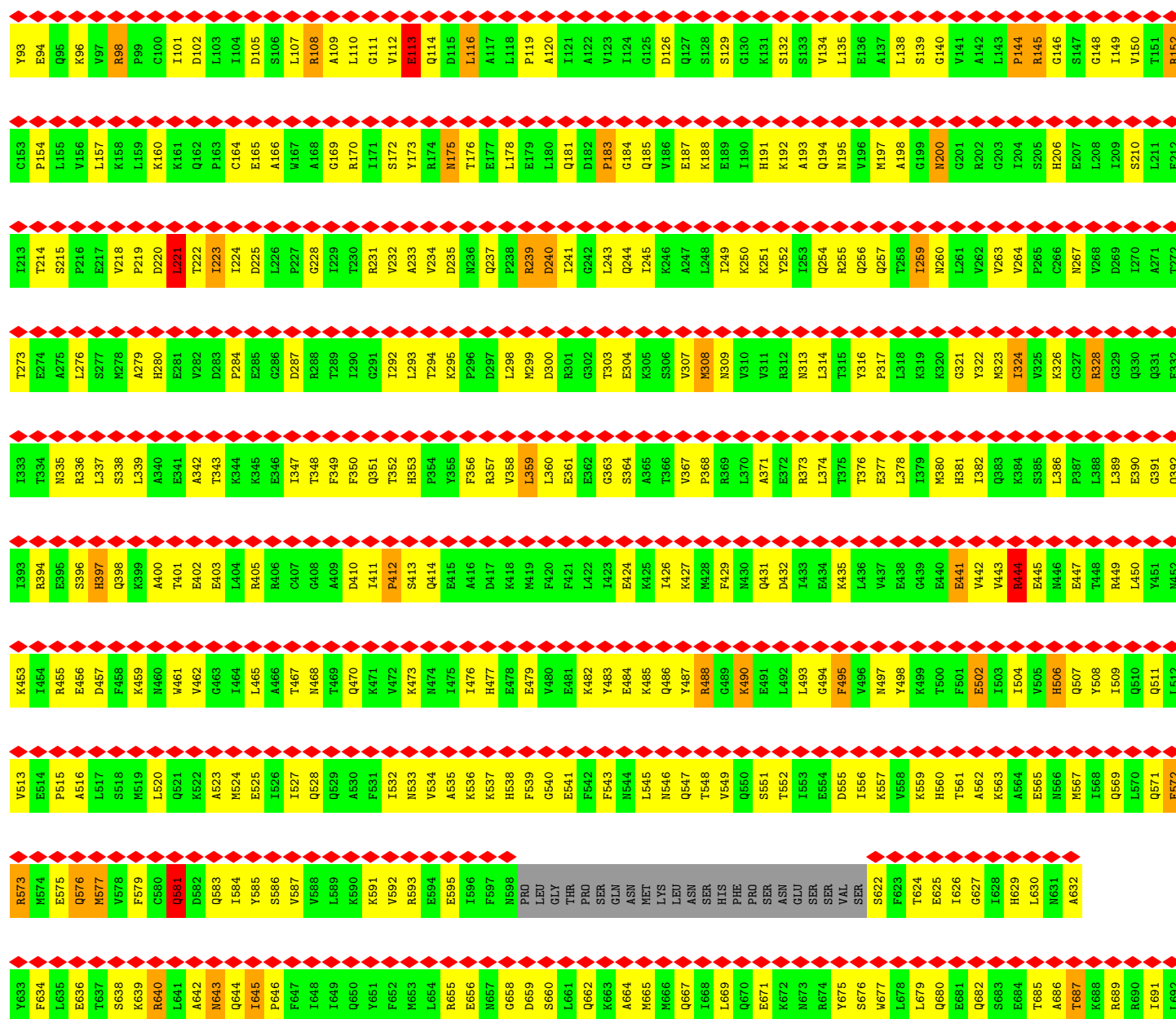
• Molecule 1: Interferon-induced GTP-binding protein Mx2

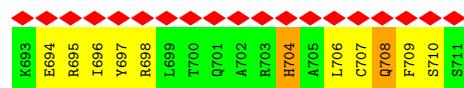




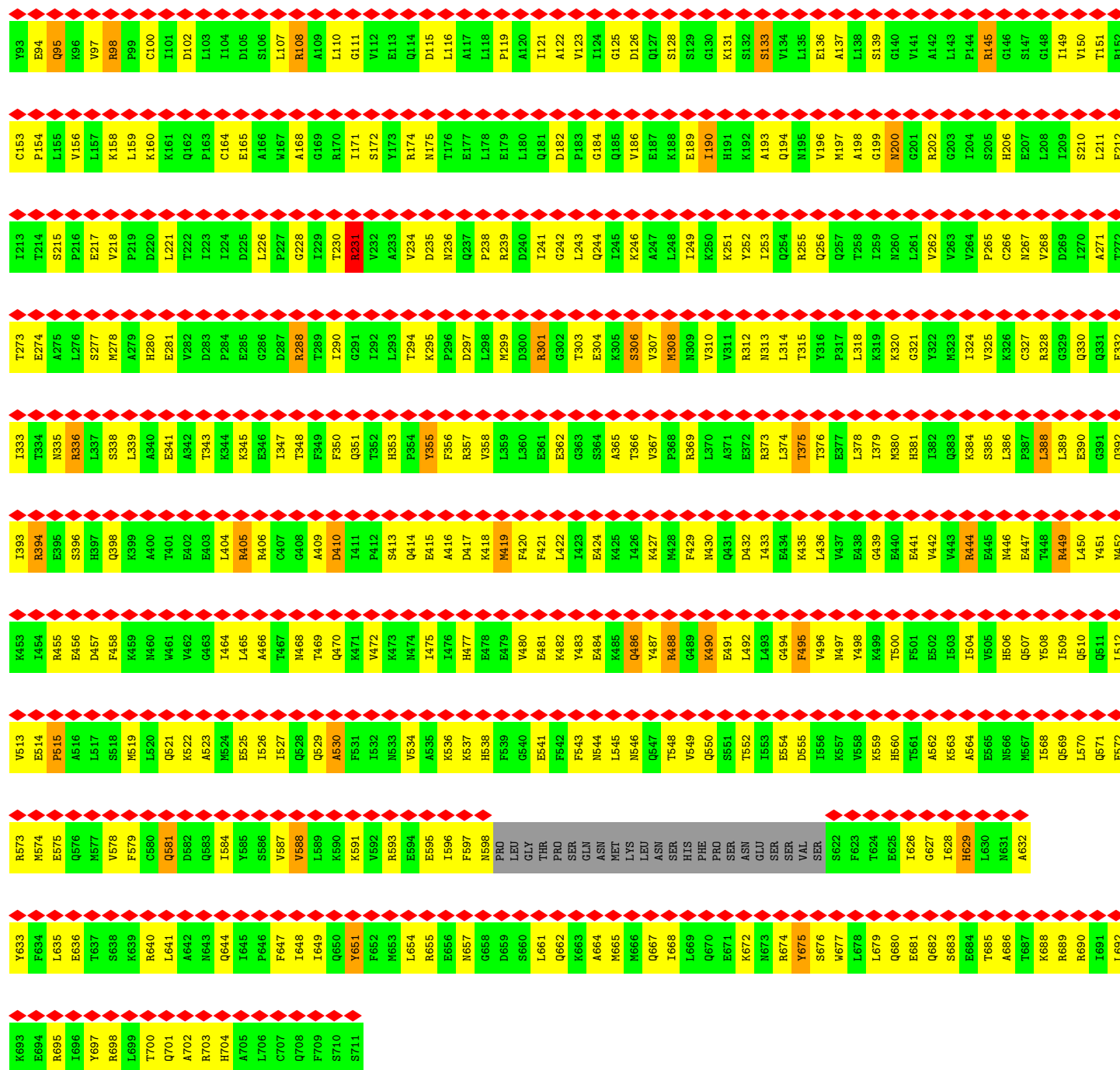


• Molecule 1: Interferon-induced GTP-binding protein Mx2

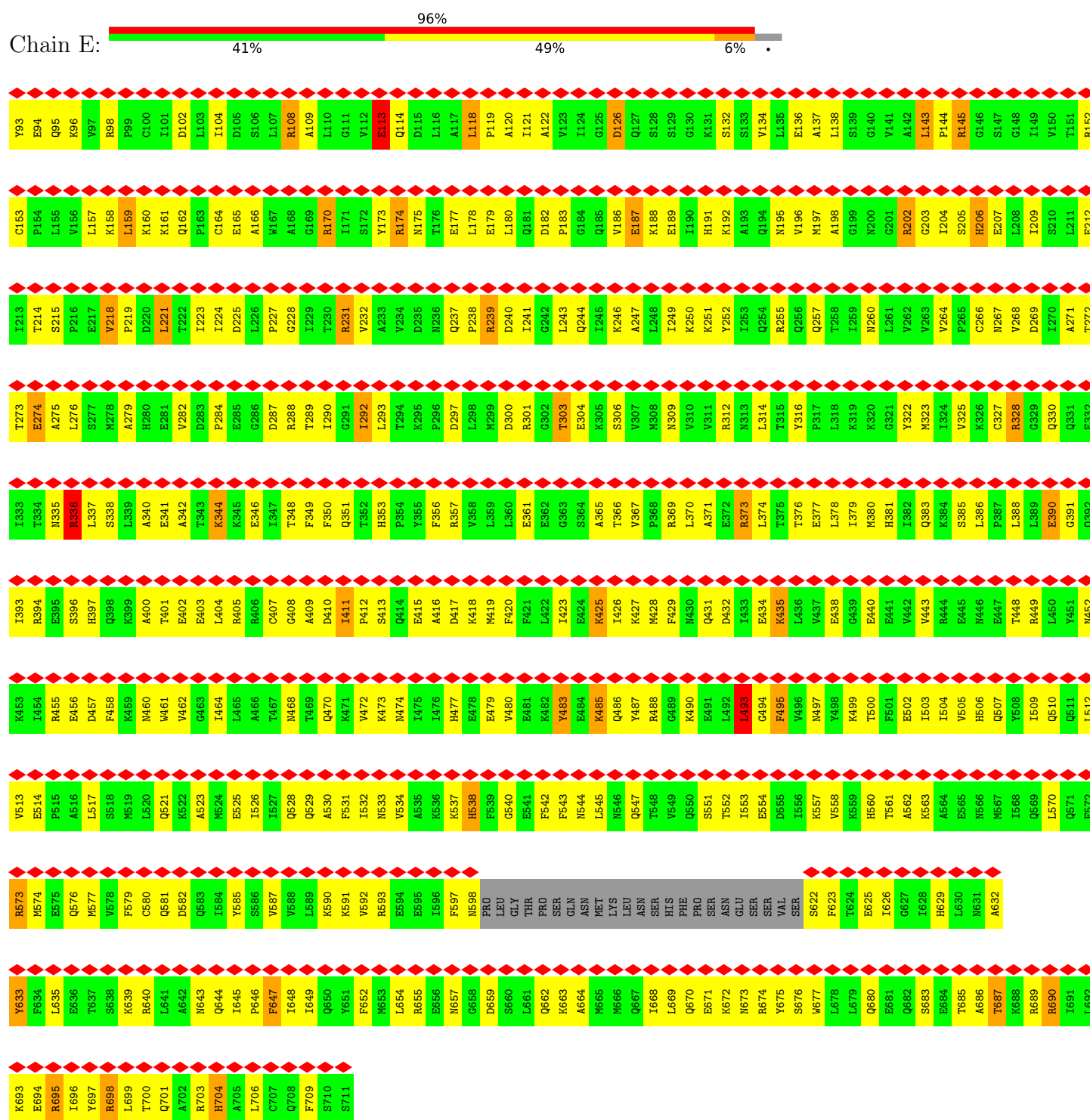




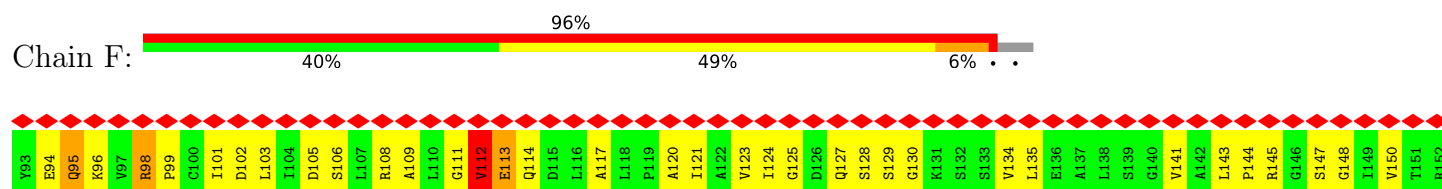
• Molecule 1: Interferon-induced GTP-binding protein Mx2



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- Molecule 1: Interferon-induced GTP-binding protein Mx2





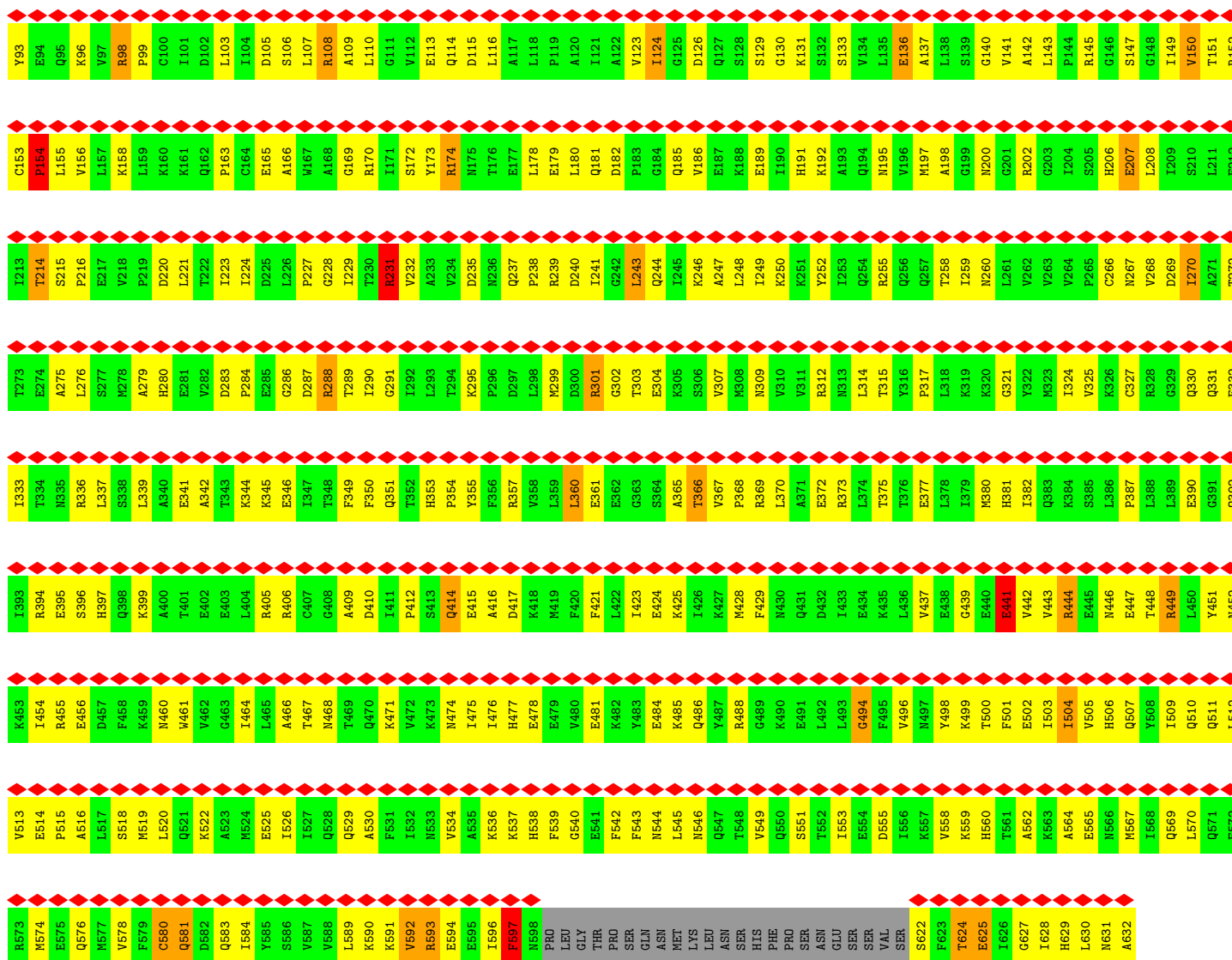
K693	E694	R695	I696	Y697	R698	L699	T700	Q701	A702	R703	H704	A705	L706	C707	Q708	F709	S710	S711																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
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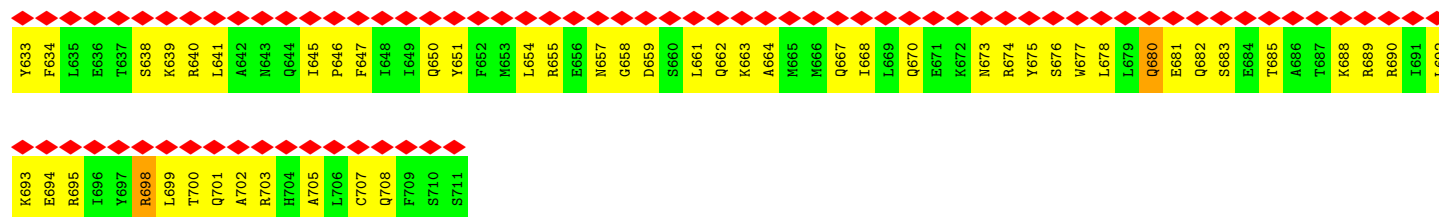
• Molecule 1: Interferon-induced GTP-binding protein Mx2



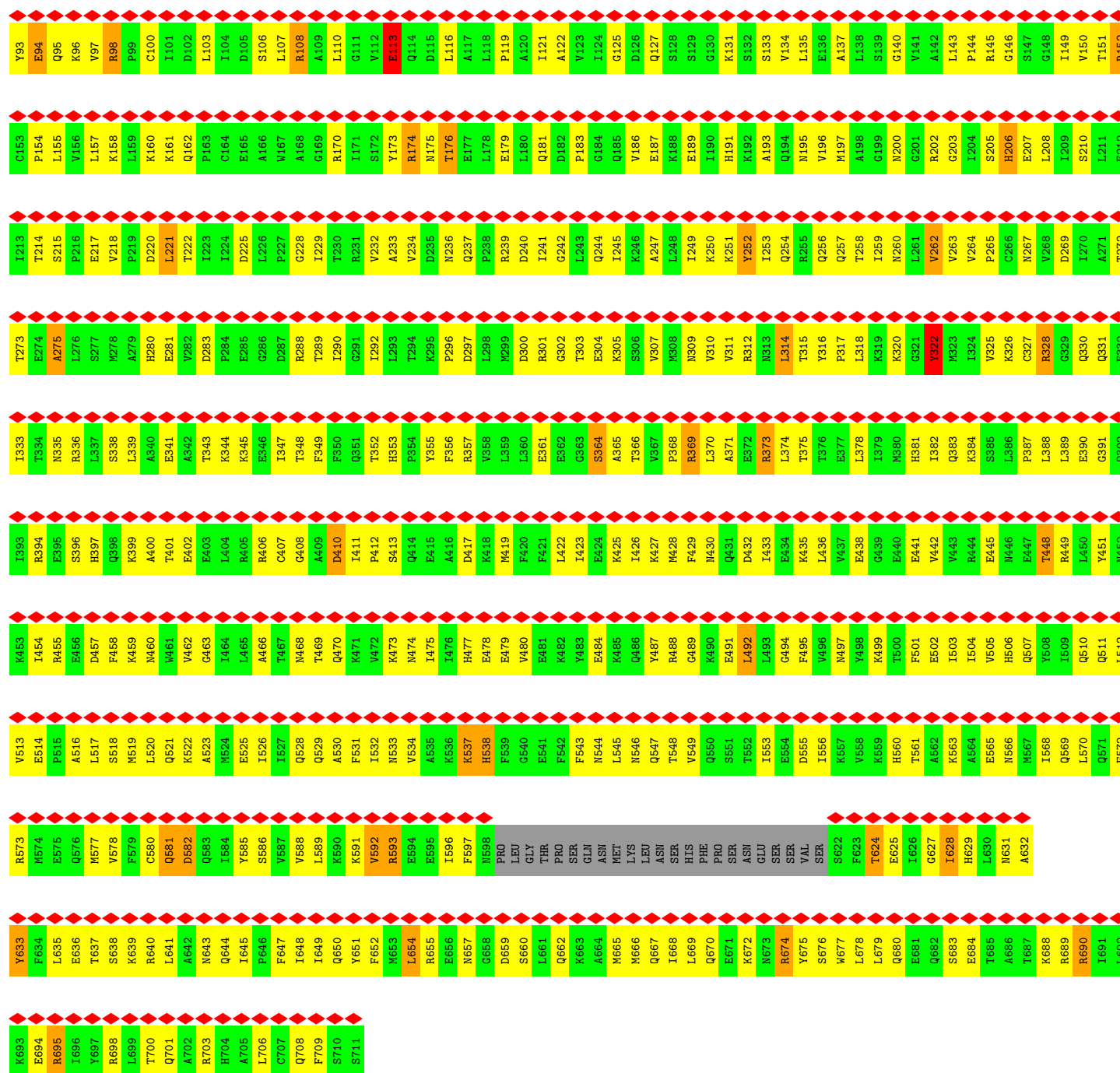
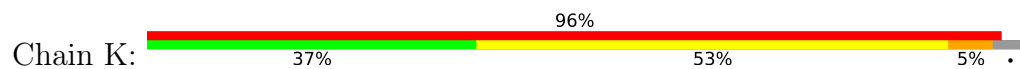
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K346	G286	L226	A166	S106
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G362	G302	G242	D182	A122
G363	T303	L243	P183	V123
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V367	V307	A247	E187	Q127
P368	M308	L248	K188	S128
R369	N309	I249	E189	S129
L370	V310	K250	I190	G130
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E372	R312	Y252	K192	S132
R373	N313	I253	A193	S133
L374	L314	Q254	Q194	V134
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- Molecule 1: Interferon-induced GTP-binding protein Mx2

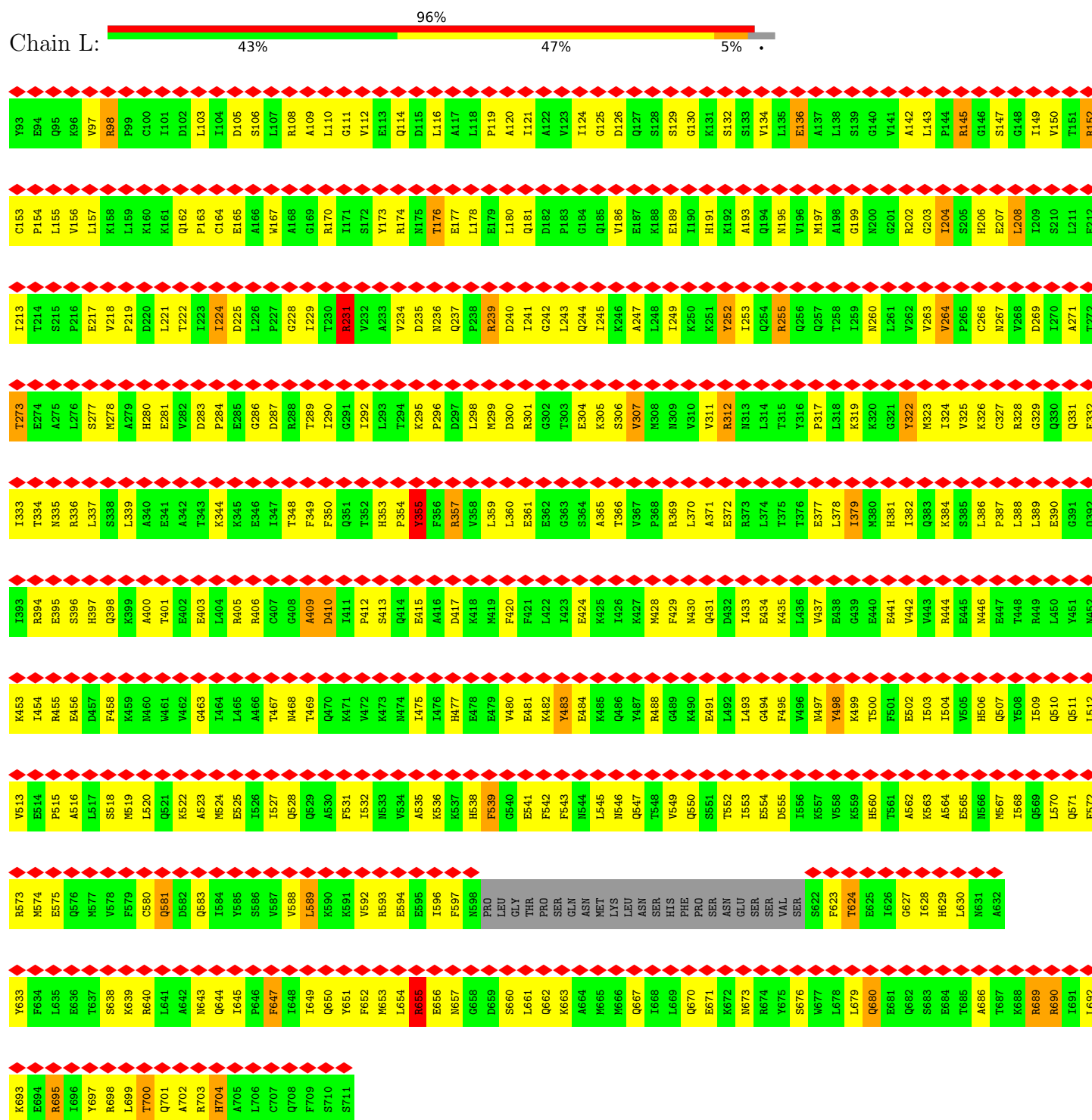




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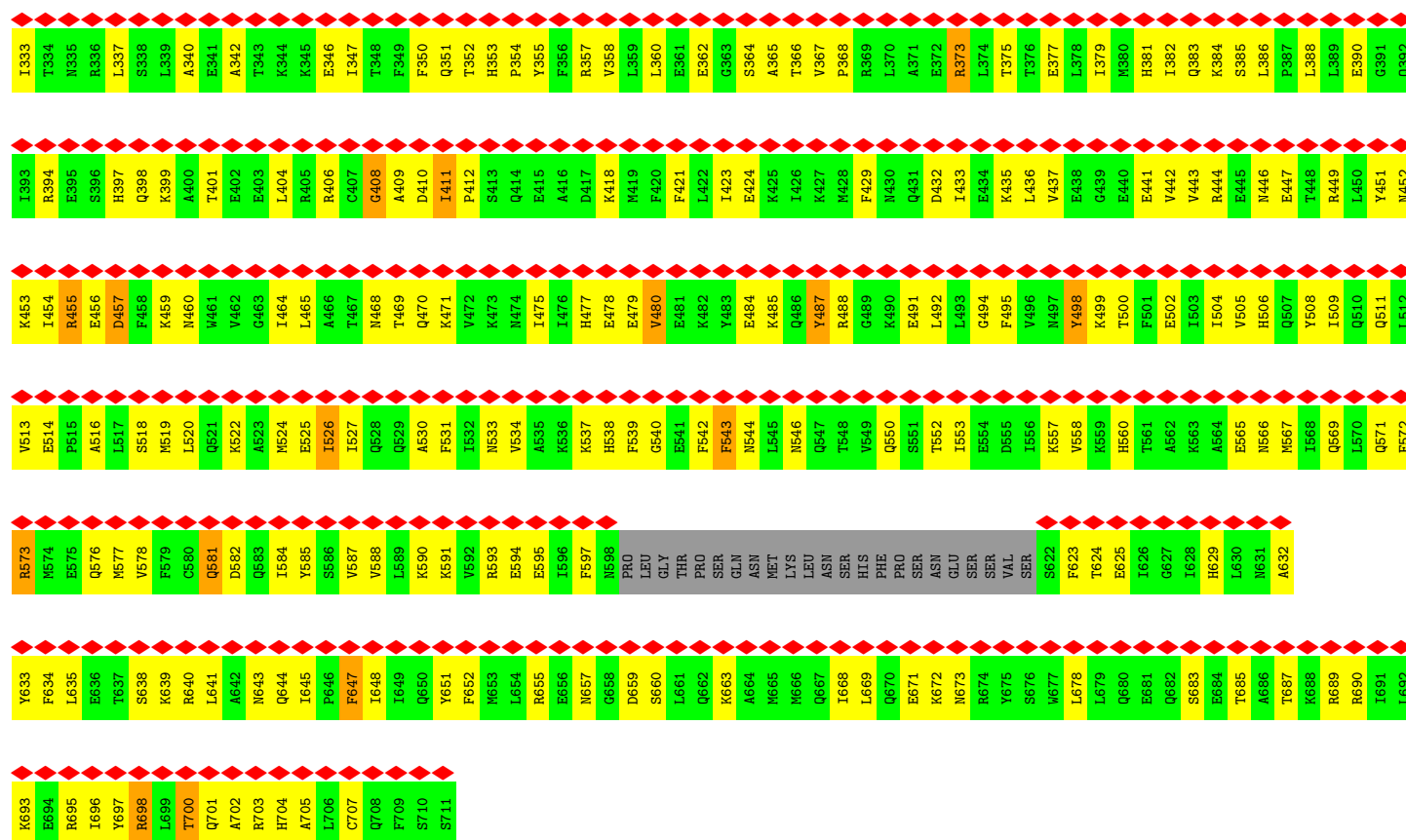


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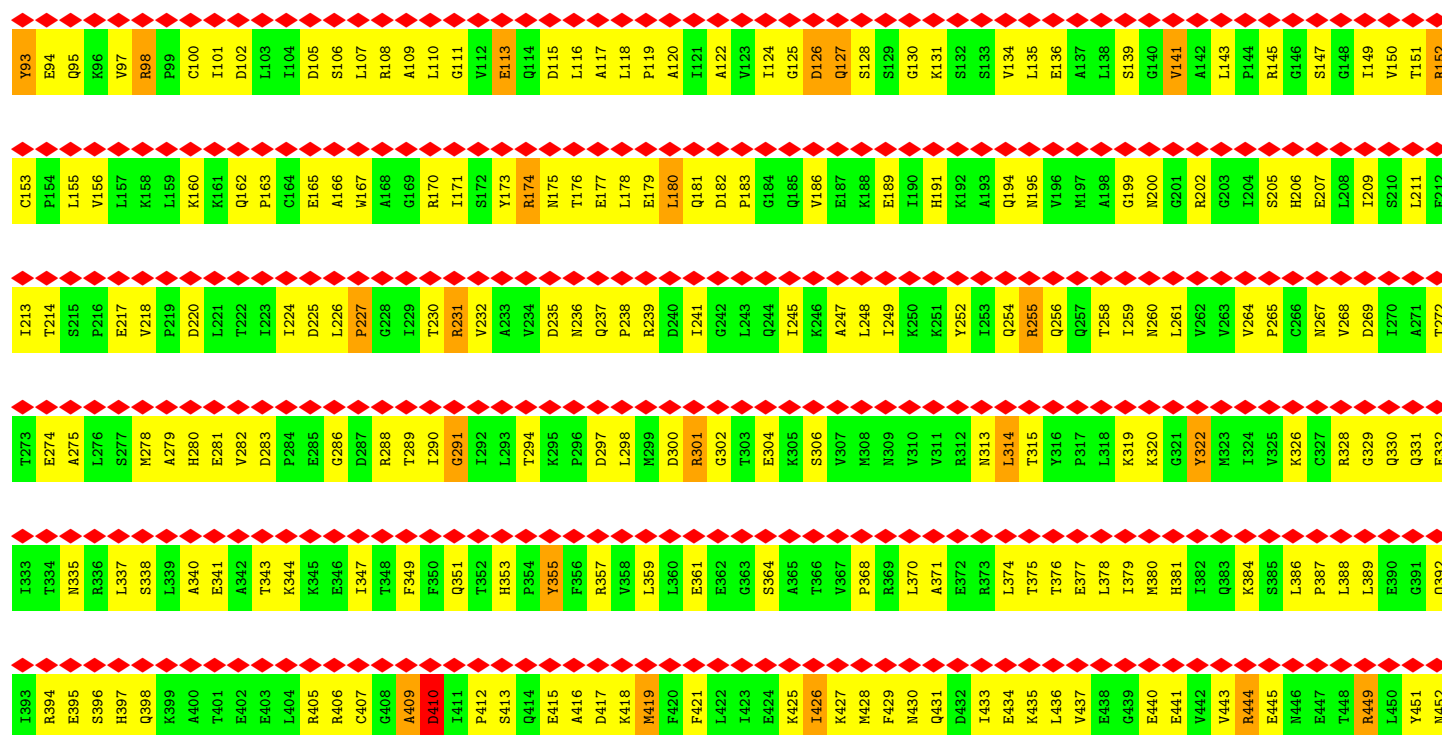


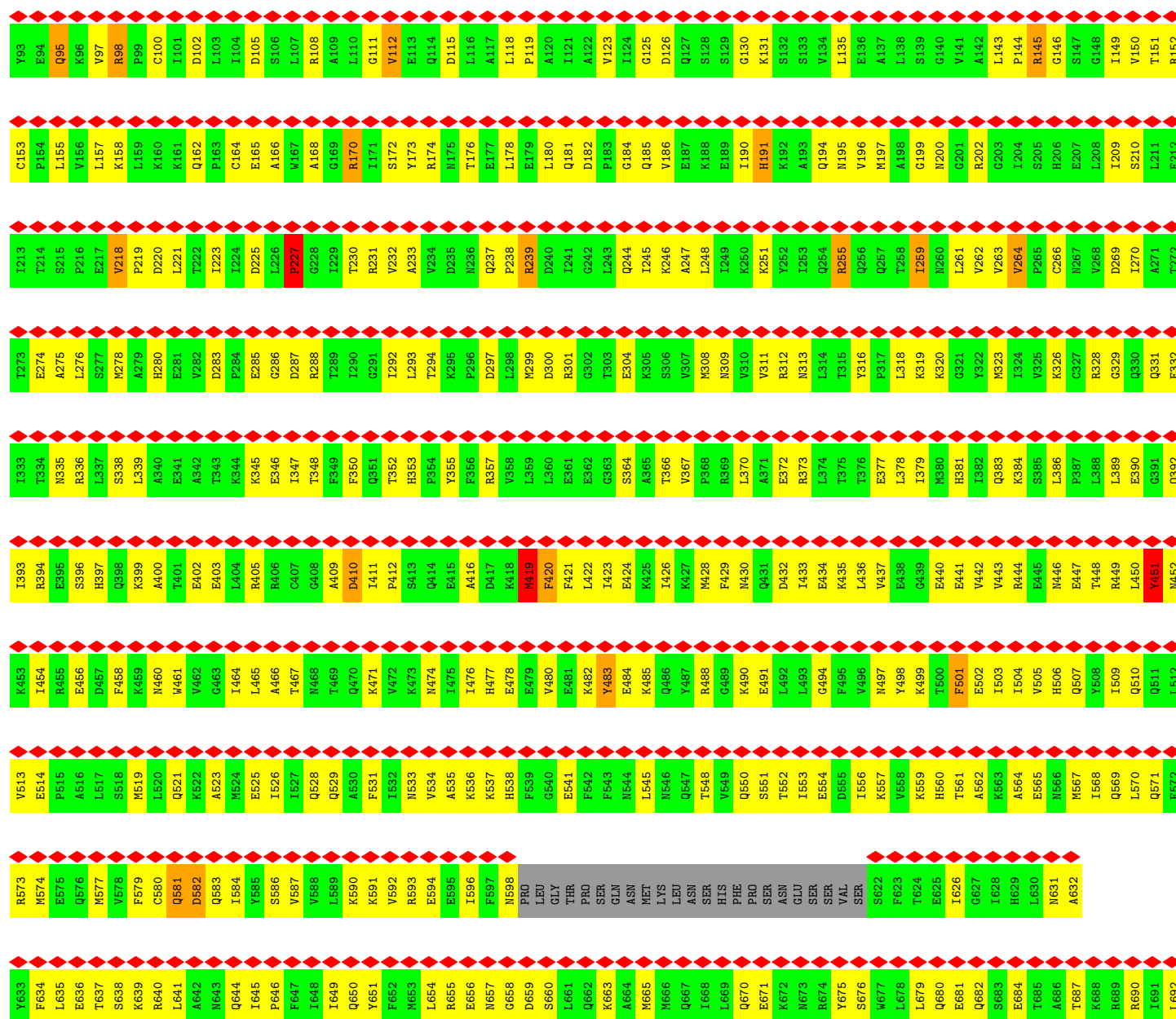
• Molecule 1: Interferon-induced GTP-binding protein Mx2





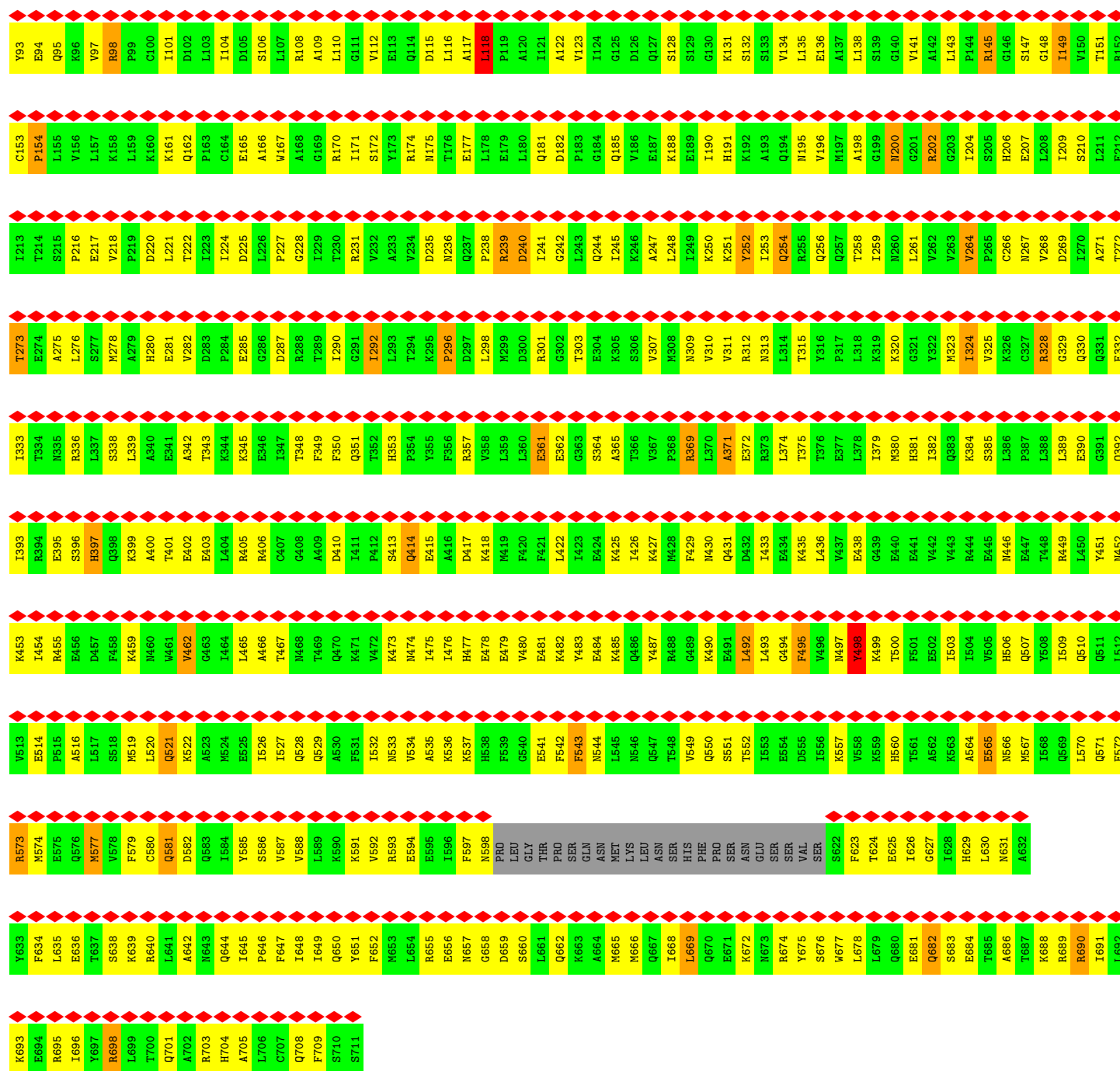
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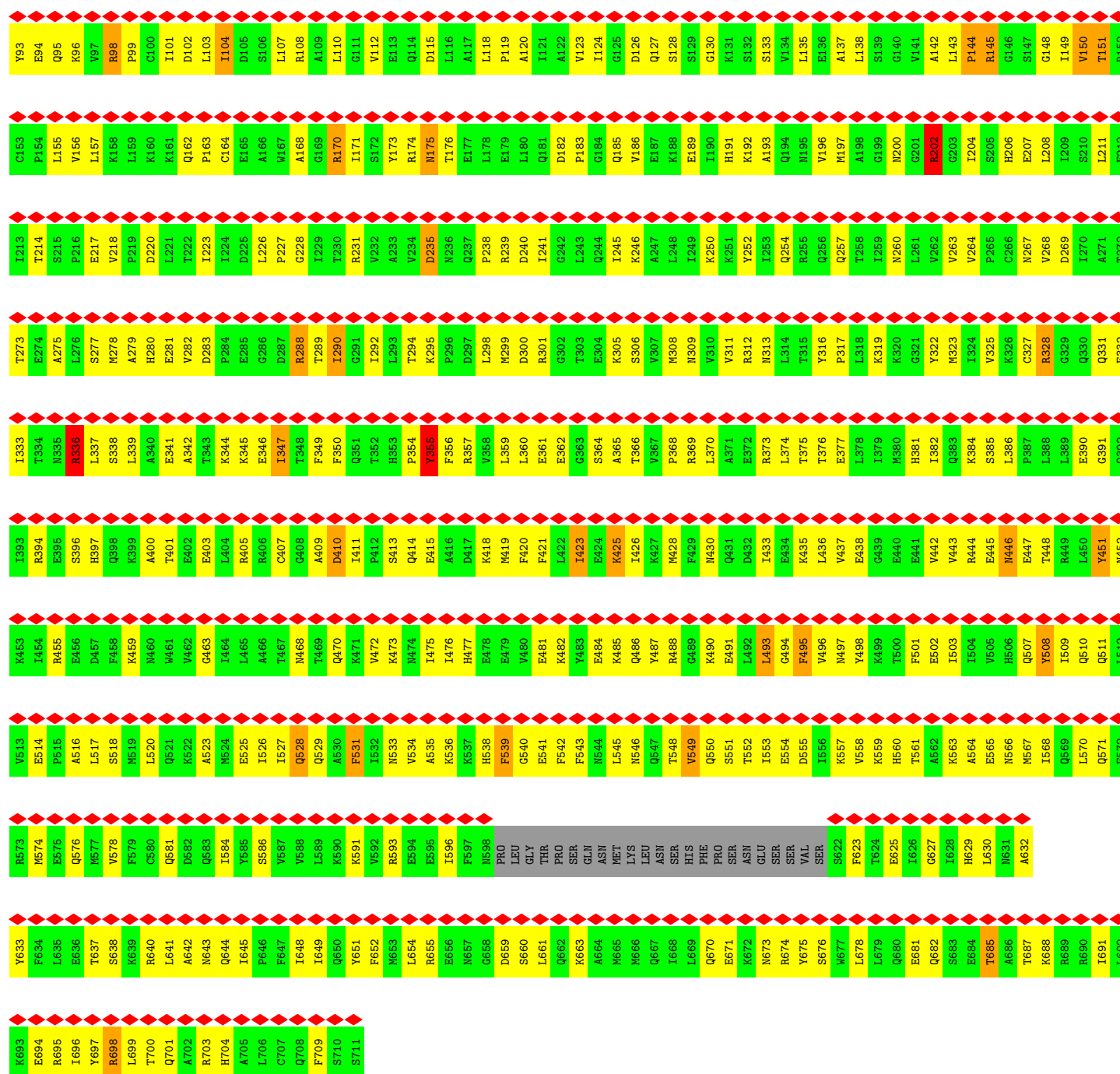
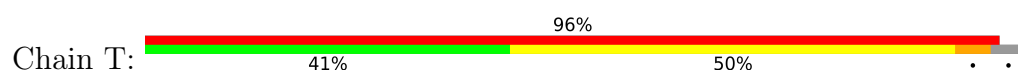




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• Molecule 1: Interferon-induced GTP-binding protein Mx2

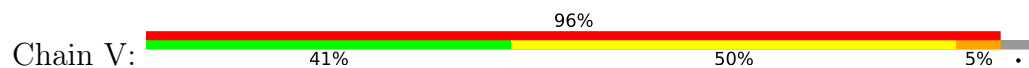


• Molecule 1: Interferon-induced GTP-binding protein Mx2

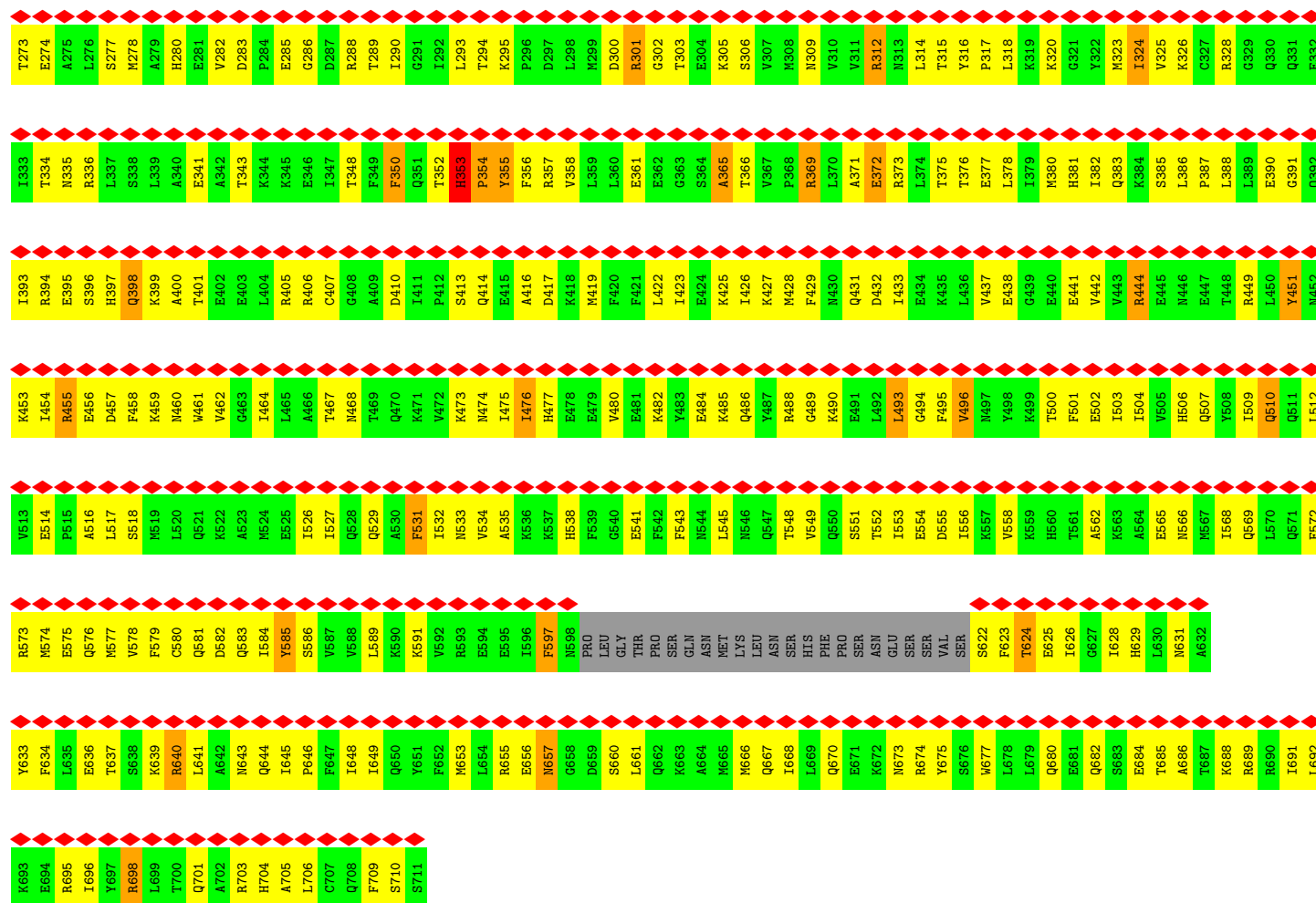


K693	R695	I696	R698	L699	T700	Q701	A702	R703	H704	A705	L706	C707	Q708	F709	S710	S711																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														</
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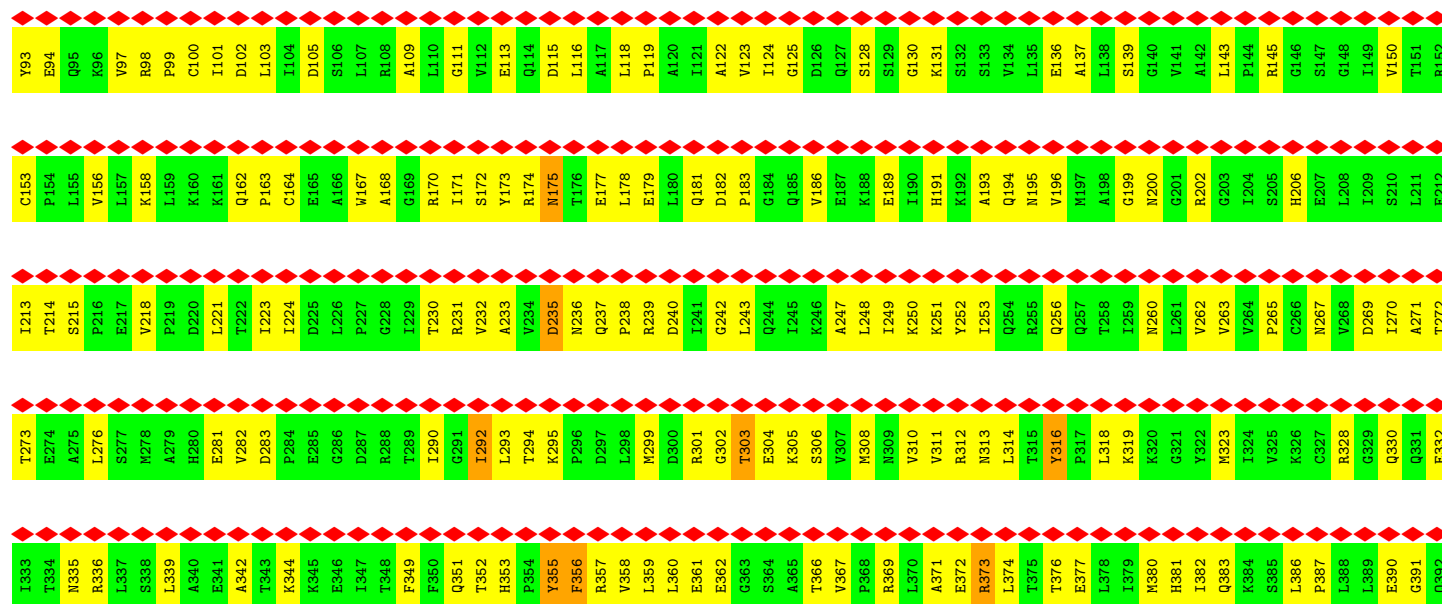
• Molecule 1: Interferon-induced GTP-binding protein Mx2

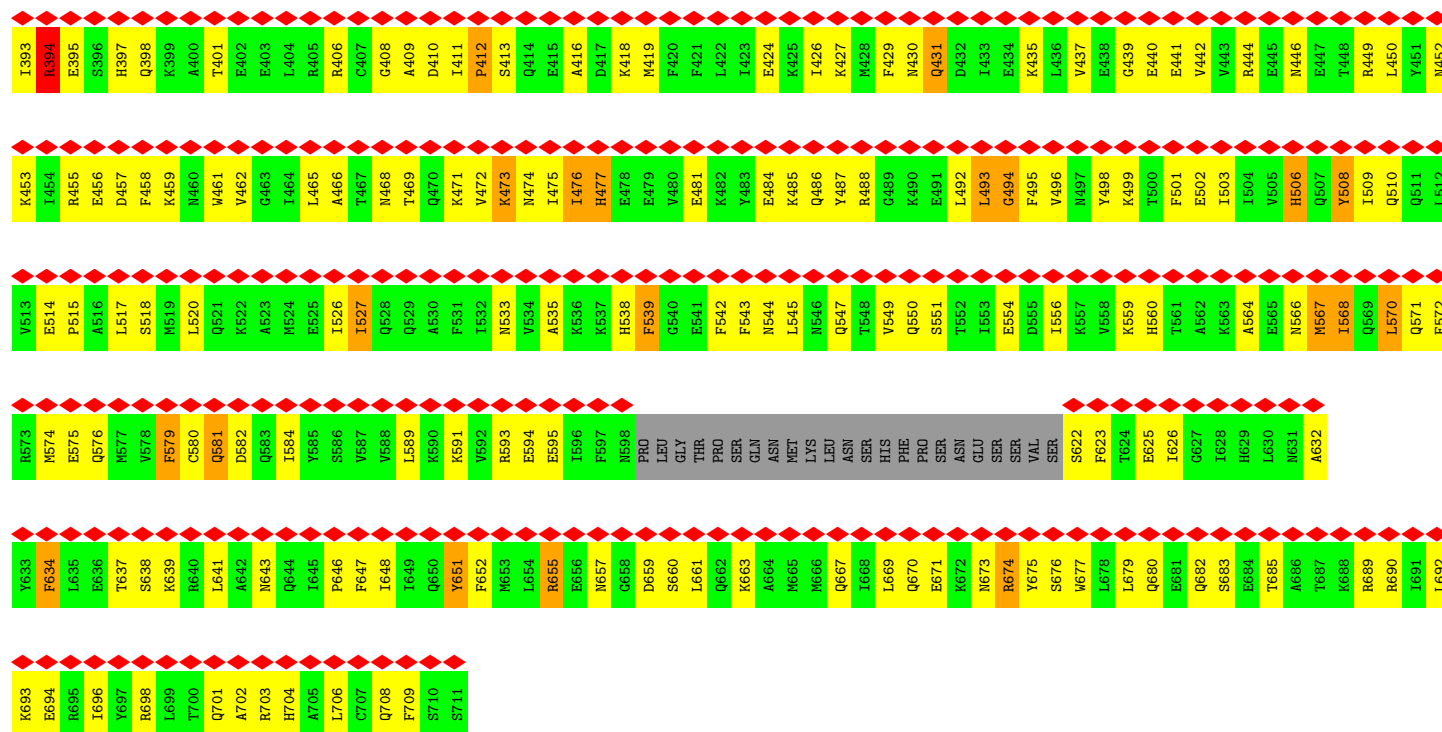


Y93	E94	Q95	K96	V97	R98	P99	C100	I101	D102	L103	I104	I105	S106	L107	R108	A109	L110	G111	V112	E113	Q114	D115	L116	A117	L118	P119	A120	I121	A122	V123	I124	G125	D126	Q127	S128	E129	Q130	K131	S132	S133	V134	L135	E136	A137	L138	S139	G140	V141	A142	L143	P144	R145	A146	S147	G148	T149	I150	T151	R152
C153	P154	L155	V156	L157	K158	L159	K160	K161	Q162	P163	C164	E165	A166	V167	A168	G169	R170	I171	S172	Y173	R174	N175	T176	E177	L178	E179	L180	Q181	D182	P183	G184	Q185	V186	E187	K188	E189	I190	H191	K192	A193	Q194	N195	V196	H197	A198	G199	N200	G201	R202	G203	I204	S205	H206	E207	L208	I209	S210	L211	E212
I213	T214	S215	P216	E217	V218	P219	D220	K221	Q222	I223	I224	D225	A226	P227	G228	I229	T230	R231	V232	A233	V234	D235	N236	Q237	E238	R239	D240	I241	G242	L243	Q244	I245	K246	A247	L248	I249	K250	K251	V252	I253	Q254	R255	Q256	P257	T258	I259	N260	L261	V262	V263	V264	P265	C266	N267	V268	D269	S270	A271	T272

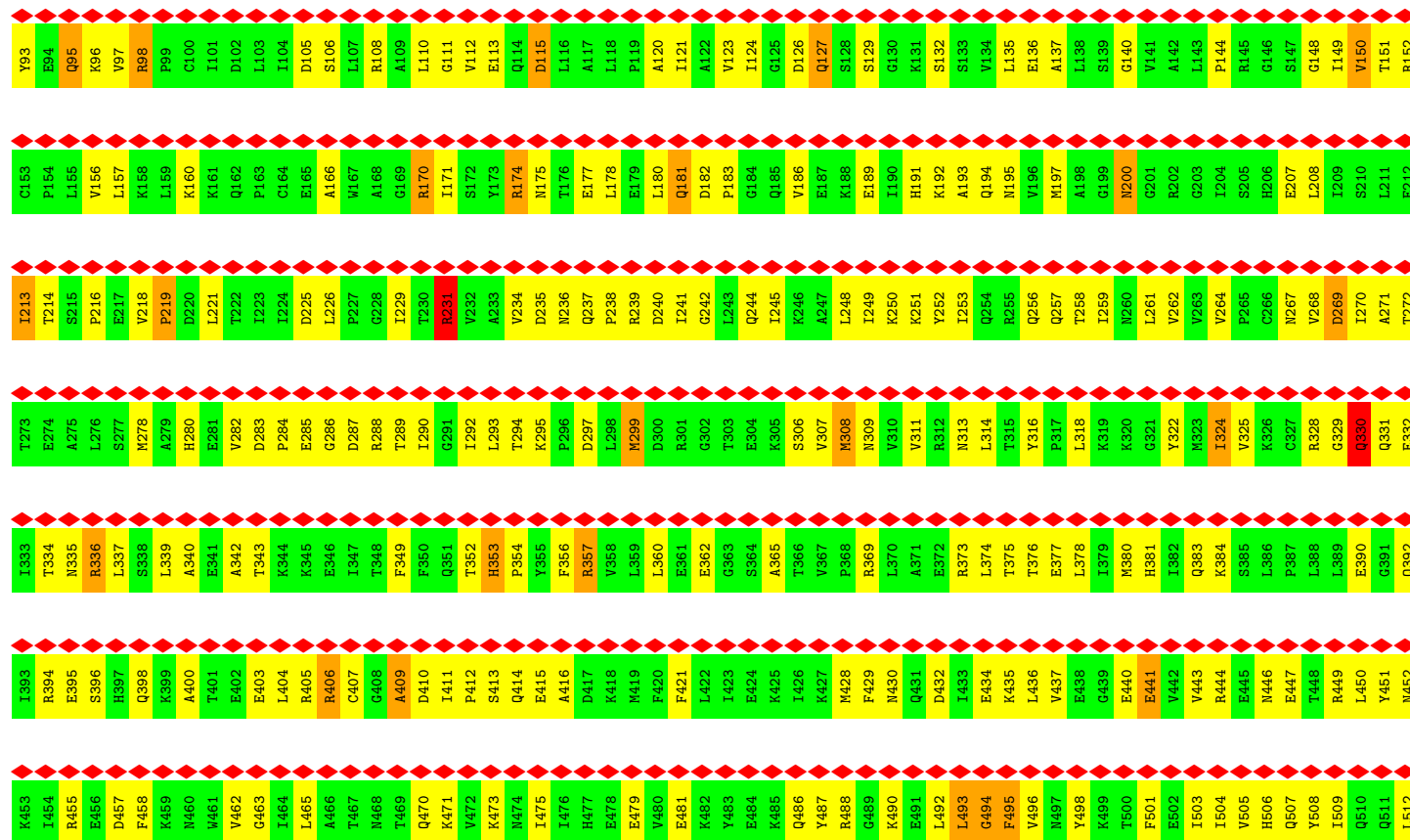
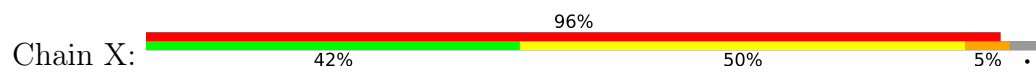


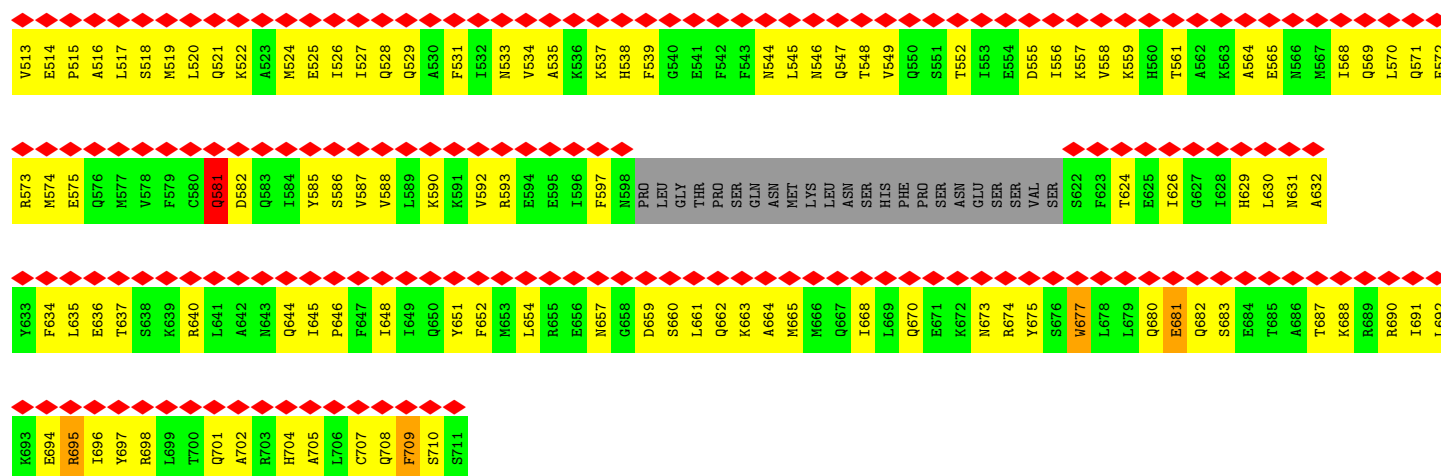
● Molecule 1: Interferon-induced GTP-binding protein Mx2



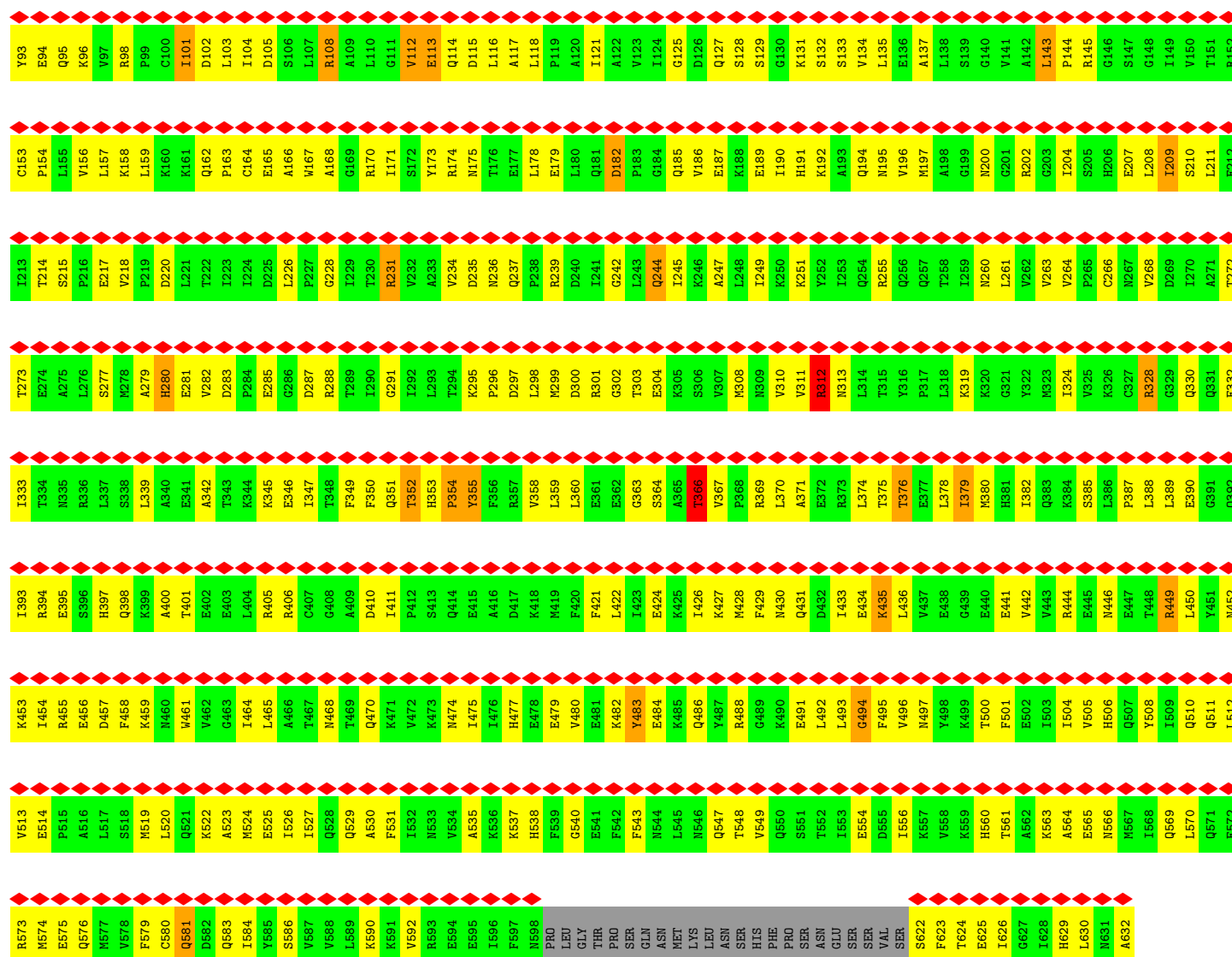


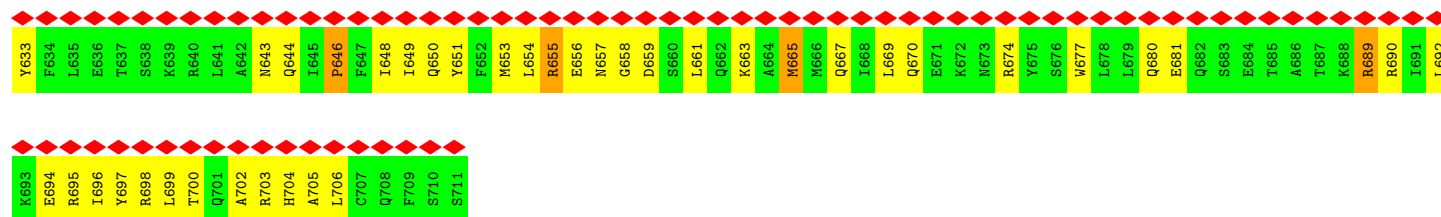
• Molecule 1: Interferon-induced GTP-binding protein Mx2



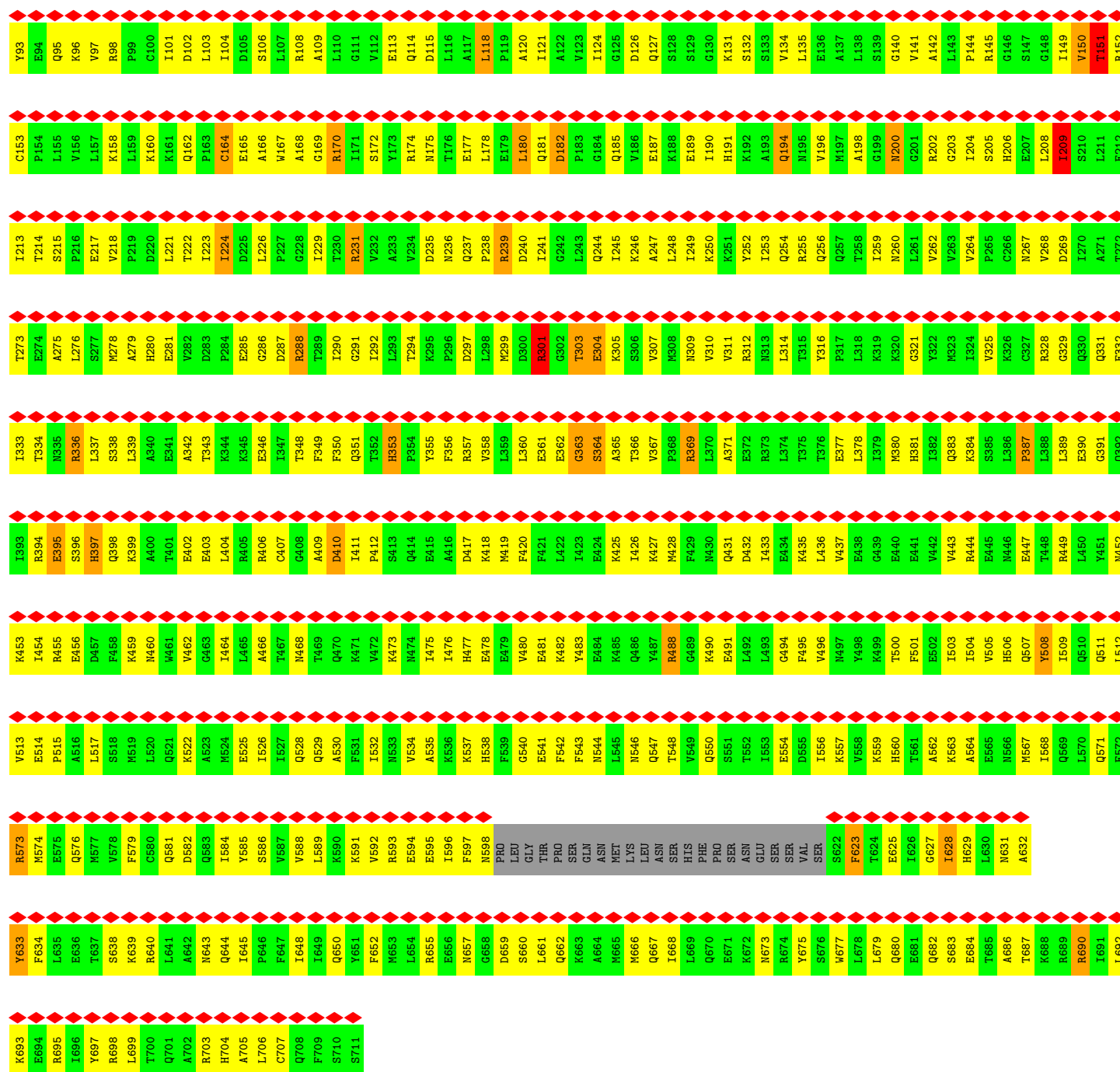


• Molecule 1: Interferon-induced GTP-binding protein Mx2





• Molecule 1: Interferon-induced GTP-binding protein Mx2



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=58.4°, rise=8.25 Å, axial sym=C1	Depositor
Number of segments used	44955	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	93000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.199	Depositor
Minimum map value	-0.091	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	4.5	Depositor
Map size (Å)	516.14996, 516.14996, 516.14996	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.147, 1.147, 1.147	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	2.18	148/4880 (3.0%)	2.54	370/6573 (5.6%)
1	1	2.18	136/4880 (2.8%)	2.58	423/6573 (6.4%)
1	2	2.24	155/4880 (3.2%)	2.53	350/6573 (5.3%)
1	3	2.17	142/4880 (2.9%)	2.59	377/6573 (5.7%)
1	4	2.18	133/4880 (2.7%)	2.61	413/6573 (6.3%)
1	5	2.19	157/4880 (3.2%)	2.57	402/6573 (6.1%)
1	6	2.20	145/4880 (3.0%)	2.52	354/6573 (5.4%)
1	7	2.20	155/4880 (3.2%)	2.54	371/6573 (5.6%)
1	8	2.19	133/4880 (2.7%)	2.56	385/6573 (5.9%)
1	9	2.21	153/4880 (3.1%)	2.51	358/6573 (5.4%)
1	A	2.14	120/4880 (2.5%)	2.58	372/6573 (5.7%)
1	B	2.16	133/4880 (2.7%)	2.59	409/6573 (6.2%)
1	C	2.19	157/4880 (3.2%)	2.57	367/6573 (5.6%)
1	D	2.21	150/4880 (3.1%)	2.52	365/6573 (5.6%)
1	E	2.21	172/4880 (3.5%)	2.56	399/6573 (6.1%)
1	F	2.13	135/4880 (2.8%)	2.62	391/6573 (5.9%)
1	G	2.20	158/4880 (3.2%)	2.60	392/6573 (6.0%)
1	H	2.17	147/4880 (3.0%)	2.58	411/6573 (6.3%)
1	I	2.18	153/4880 (3.1%)	2.56	382/6573 (5.8%)
1	J	2.23	163/4880 (3.3%)	2.58	403/6573 (6.1%)
1	K	2.23	161/4880 (3.3%)	2.57	416/6573 (6.3%)
1	L	2.22	170/4880 (3.5%)	2.55	372/6573 (5.7%)
1	M	2.22	158/4880 (3.2%)	2.55	389/6573 (5.9%)
1	N	2.18	152/4880 (3.1%)	2.60	395/6573 (6.0%)
1	O	2.24	169/4880 (3.5%)	2.55	371/6573 (5.6%)
1	P	2.23	162/4880 (3.3%)	2.57	388/6573 (5.9%)
1	Q	2.21	149/4880 (3.1%)	2.54	388/6573 (5.9%)
1	R	2.18	150/4880 (3.1%)	2.61	403/6573 (6.1%)
1	S	2.19	143/4880 (2.9%)	2.57	391/6573 (5.9%)
1	T	2.21	155/4880 (3.2%)	2.61	399/6573 (6.1%)
1	U	2.23	171/4880 (3.5%)	2.59	410/6573 (6.2%)
1	V	2.19	166/4880 (3.4%)	2.60	410/6573 (6.2%)
1	W	2.20	139/4880 (2.8%)	2.57	371/6573 (5.6%)
1	X	2.17	136/4880 (2.8%)	2.57	385/6573 (5.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Y	2.20	135/4880 (2.8%)	2.53	367/6573 (5.6%)
1	Z	2.18	140/4880 (2.9%)	2.61	403/6573 (6.1%)
1	a	2.21	149/4880 (3.1%)	2.60	422/6573 (6.4%)
1	b	2.14	134/4880 (2.7%)	2.58	379/6573 (5.8%)
1	c	2.14	129/4880 (2.6%)	2.55	379/6573 (5.8%)
1	d	2.20	149/4880 (3.1%)	2.59	404/6573 (6.1%)
1	e	2.22	183/4880 (3.8%)	2.55	390/6573 (5.9%)
1	f	2.17	149/4880 (3.1%)	2.55	378/6573 (5.8%)
1	g	2.19	152/4880 (3.1%)	2.62	425/6573 (6.5%)
1	h	2.16	135/4880 (2.8%)	2.61	411/6573 (6.3%)
1	i	2.18	156/4880 (3.2%)	2.56	339/6573 (5.2%)
1	j	2.20	147/4880 (3.0%)	2.52	378/6573 (5.8%)
1	k	2.16	138/4880 (2.8%)	2.58	390/6573 (5.9%)
1	l	2.18	143/4880 (2.9%)	2.59	406/6573 (6.2%)
1	m	2.20	158/4880 (3.2%)	2.54	377/6573 (5.7%)
1	n	2.20	157/4880 (3.2%)	2.56	377/6573 (5.7%)
1	o	2.18	140/4880 (2.9%)	2.59	411/6573 (6.3%)
1	p	2.22	166/4880 (3.4%)	2.61	398/6573 (6.1%)
1	q	2.16	136/4880 (2.8%)	2.59	383/6573 (5.8%)
1	r	2.17	134/4880 (2.7%)	2.56	385/6573 (5.9%)
1	s	2.19	134/4880 (2.7%)	2.51	345/6573 (5.2%)
1	t	2.20	149/4880 (3.1%)	2.60	409/6573 (6.2%)
1	u	2.18	153/4880 (3.1%)	2.60	392/6573 (6.0%)
1	v	2.22	147/4880 (3.0%)	2.58	385/6573 (5.9%)
1	w	2.18	144/4880 (3.0%)	2.58	398/6573 (6.1%)
1	x	2.20	148/4880 (3.0%)	2.59	393/6573 (6.0%)
1	y	2.15	145/4880 (3.0%)	2.57	382/6573 (5.8%)
1	z	2.17	149/4880 (3.1%)	2.58	374/6573 (5.7%)
All	All	2.19	9225/302560 (3.0%)	2.57	24062/407526 (5.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	9
1	1	0	10
1	2	0	22
1	3	0	22
1	4	0	14
1	5	0	17

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	6	0	11
1	7	0	15
1	8	0	17
1	9	0	19
1	A	0	23
1	B	0	17
1	C	0	17
1	D	0	17
1	E	0	18
1	F	0	27
1	G	0	19
1	H	0	20
1	I	0	18
1	J	0	15
1	K	0	18
1	L	0	23
1	M	0	13
1	N	0	21
1	O	0	16
1	P	0	19
1	Q	0	19
1	R	0	13
1	S	0	16
1	T	0	16
1	U	0	17
1	V	0	20
1	W	0	17
1	X	0	20
1	Y	0	12
1	Z	0	19
1	a	0	14
1	b	0	19
1	c	0	16
1	d	0	21
1	e	0	18
1	f	0	18
1	g	0	14
1	h	0	17
1	i	0	15
1	j	0	27
1	k	0	16
1	l	0	18

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	m	0	17
1	n	0	16
1	o	0	14
1	p	0	17
1	q	0	20
1	r	0	17
1	s	0	20
1	t	0	17
1	u	0	16
1	v	0	21
1	w	0	12
1	x	0	25
1	y	0	18
1	z	0	22
All	All	0	1091

The worst 5 of 9225 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	v	295	LYS	CA-C	16.20	1.64	1.53
1	n	363	GLY	CA-C	15.48	1.61	1.51
1	A	645	ILE	CA-CB	-14.06	1.46	1.54
1	Y	295	LYS	CA-C	13.69	1.62	1.53
1	X	290	ILE	C-N	13.10	1.40	1.33

The worst 5 of 24062 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4	645	ILE	N-CA-CB	18.00	121.84	110.50
1	L	111	GLY	O-C-N	-16.90	109.53	122.71
1	m	560	HIS	CA-CB-CG	-16.45	97.35	113.80
1	Q	597	PHE	N-CA-C	15.81	130.08	111.11
1	S	493	LEU	CA-C-N	15.44	133.60	122.33

There are no chirality outliers.

5 of 1091 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	170	ARG	Sidechain
1	0	239	ARG	Sidechain
1	0	255	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	0	369	ARG	Sidechain
1	0	98	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	4807	0	4935	9	0
1	1	4807	0	4935	11	0
1	2	4807	0	4935	5	0
1	3	4807	0	4935	10	0
1	4	4807	0	4935	7	0
1	5	4807	0	4935	7	0
1	6	4807	0	4935	7	0
1	7	4807	0	4935	8	0
1	8	4807	0	4935	8	0
1	9	4807	0	4935	6	0
1	A	4807	0	4935	7	0
1	B	4807	0	4935	8	0
1	C	4807	0	4935	13	0
1	D	4807	0	4935	6	0
1	E	4807	0	4935	10	0
1	F	4807	0	4935	12	0
1	G	4807	0	4935	8	0
1	H	4807	0	4935	5	0
1	I	4807	0	4935	5	0
1	J	4807	0	4935	8	0
1	K	4807	0	4935	7	0
1	L	4807	0	4935	8	0
1	M	4807	0	4935	12	0
1	N	4807	0	4935	11	0
1	O	4807	0	4935	6	0
1	P	4807	0	4935	9	0
1	Q	4807	0	4935	7	0
1	R	4807	0	4935	6	0
1	S	4807	0	4935	9	0
1	T	4807	0	4935	7	0
1	U	4807	0	4935	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	V	4807	0	4935	9	0
1	W	4807	0	4935	9	0
1	X	4807	0	4935	7	0
1	Y	4807	0	4935	12	0
1	Z	4807	0	4935	6	0
1	a	4807	0	4935	10	0
1	b	4807	0	4935	7	0
1	c	4807	0	4935	6	0
1	d	4807	0	4935	7	0
1	e	4807	0	4935	4	0
1	f	4807	0	4935	9	0
1	g	4807	0	4935	10	0
1	h	4807	0	4935	7	0
1	i	4807	0	4935	7	0
1	j	4807	0	4935	8	0
1	k	4807	0	4935	9	0
1	l	4807	0	4935	9	0
1	m	4807	0	4935	5	0
1	n	4807	0	4935	11	0
1	o	4807	0	4935	11	0
1	p	4807	0	4935	13	0
1	q	4807	0	4935	10	0
1	r	4807	0	4935	12	0
1	s	4807	0	4935	9	0
1	t	4807	0	4935	7	0
1	u	4807	0	4935	9	0
1	v	4807	0	4935	6	0
1	w	4807	0	4935	6	0
1	x	4807	0	4935	13	0
1	y	4807	0	4935	12	0
1	z	4807	0	4935	13	0
All	All	298034	0	305970	497	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

The worst 5 of 497 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:150:VAL:HG13	1:H:228:GLY:H	1.40	0.85
1:2:241:ILE:H	1:2:241:ILE:HD13	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:123:VAL:HG22	1:l:261:LEU:HD23	1.73	0.69
1:y:180:LEU:HD13	1:y:186:VAL:HG22	1.76	0.66
1:b:98:ARG:HH22	1:b:220:ASP:CG	2.07	0.62

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	592/619 (96%)	556 (94%)	30 (5%)	6 (1%)	12	47
1	1	592/619 (96%)	556 (94%)	27 (5%)	9 (2%)	8	38
1	2	592/619 (96%)	555 (94%)	33 (6%)	4 (1%)	18	55
1	3	592/619 (96%)	561 (95%)	27 (5%)	4 (1%)	18	55
1	4	592/619 (96%)	554 (94%)	27 (5%)	11 (2%)	6	32
1	5	592/619 (96%)	541 (91%)	38 (6%)	13 (2%)	5	29
1	6	592/619 (96%)	550 (93%)	34 (6%)	8 (1%)	9	39
1	7	592/619 (96%)	550 (93%)	34 (6%)	8 (1%)	9	39
1	8	592/619 (96%)	554 (94%)	31 (5%)	7 (1%)	10	42
1	9	592/619 (96%)	550 (93%)	36 (6%)	6 (1%)	12	47
1	A	592/619 (96%)	547 (92%)	33 (6%)	12 (2%)	6	31
1	B	592/619 (96%)	553 (93%)	31 (5%)	8 (1%)	9	39
1	C	592/619 (96%)	546 (92%)	36 (6%)	10 (2%)	7	35
1	D	592/619 (96%)	542 (92%)	40 (7%)	10 (2%)	7	35
1	E	592/619 (96%)	555 (94%)	29 (5%)	8 (1%)	9	39
1	F	592/619 (96%)	551 (93%)	29 (5%)	12 (2%)	6	31
1	G	592/619 (96%)	551 (93%)	31 (5%)	10 (2%)	7	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	592/619 (96%)	551 (93%)	32 (5%)	9 (2%)	8	38
1	I	592/619 (96%)	546 (92%)	37 (6%)	9 (2%)	8	38
1	J	592/619 (96%)	549 (93%)	33 (6%)	10 (2%)	7	35
1	K	592/619 (96%)	549 (93%)	30 (5%)	13 (2%)	5	29
1	L	592/619 (96%)	547 (92%)	33 (6%)	12 (2%)	6	31
1	M	592/619 (96%)	553 (93%)	34 (6%)	5 (1%)	16	53
1	N	592/619 (96%)	552 (93%)	33 (6%)	7 (1%)	10	42
1	O	592/619 (96%)	551 (93%)	35 (6%)	6 (1%)	12	47
1	P	592/619 (96%)	552 (93%)	31 (5%)	9 (2%)	8	38
1	Q	592/619 (96%)	547 (92%)	38 (6%)	7 (1%)	10	42
1	R	592/619 (96%)	552 (93%)	35 (6%)	5 (1%)	16	53
1	S	592/619 (96%)	545 (92%)	36 (6%)	11 (2%)	6	32
1	T	592/619 (96%)	549 (93%)	36 (6%)	7 (1%)	10	42
1	U	592/619 (96%)	547 (92%)	35 (6%)	10 (2%)	7	35
1	V	592/619 (96%)	550 (93%)	36 (6%)	6 (1%)	12	47
1	W	592/619 (96%)	556 (94%)	30 (5%)	6 (1%)	12	47
1	X	592/619 (96%)	550 (93%)	30 (5%)	12 (2%)	6	31
1	Y	592/619 (96%)	550 (93%)	37 (6%)	5 (1%)	16	53
1	Z	592/619 (96%)	550 (93%)	28 (5%)	14 (2%)	4	27
1	a	592/619 (96%)	551 (93%)	35 (6%)	6 (1%)	12	47
1	b	592/619 (96%)	555 (94%)	31 (5%)	6 (1%)	12	47
1	c	592/619 (96%)	554 (94%)	29 (5%)	9 (2%)	8	38
1	d	592/619 (96%)	552 (93%)	31 (5%)	9 (2%)	8	38
1	e	592/619 (96%)	555 (94%)	31 (5%)	6 (1%)	12	47
1	f	592/619 (96%)	548 (93%)	35 (6%)	9 (2%)	8	38
1	g	592/619 (96%)	554 (94%)	29 (5%)	9 (2%)	8	38
1	h	592/619 (96%)	559 (94%)	25 (4%)	8 (1%)	9	39
1	i	592/619 (96%)	558 (94%)	27 (5%)	7 (1%)	10	42
1	j	592/619 (96%)	552 (93%)	29 (5%)	11 (2%)	6	32
1	k	592/619 (96%)	560 (95%)	23 (4%)	9 (2%)	8	38
1	l	592/619 (96%)	557 (94%)	27 (5%)	8 (1%)	9	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	m	592/619 (96%)	550 (93%)	35 (6%)	7 (1%)	10	42
1	n	592/619 (96%)	543 (92%)	38 (6%)	11 (2%)	6	32
1	o	592/619 (96%)	550 (93%)	35 (6%)	7 (1%)	10	42
1	p	592/619 (96%)	539 (91%)	39 (7%)	14 (2%)	4	27
1	q	592/619 (96%)	549 (93%)	31 (5%)	12 (2%)	6	31
1	r	592/619 (96%)	555 (94%)	29 (5%)	8 (1%)	9	39
1	s	592/619 (96%)	553 (93%)	36 (6%)	3 (0%)	24	63
1	t	592/619 (96%)	554 (94%)	27 (5%)	11 (2%)	6	32
1	u	592/619 (96%)	561 (95%)	22 (4%)	9 (2%)	8	38
1	v	592/619 (96%)	551 (93%)	33 (6%)	8 (1%)	9	39
1	w	592/619 (96%)	552 (93%)	30 (5%)	10 (2%)	7	35
1	x	592/619 (96%)	558 (94%)	27 (5%)	7 (1%)	10	42
1	y	592/619 (96%)	553 (93%)	32 (5%)	7 (1%)	10	42
1	z	592/619 (96%)	553 (93%)	33 (6%)	6 (1%)	12	47
All	All	36704/38378 (96%)	34194 (93%)	1984 (5%)	526 (1%)	11	39

5 of 526 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	495	PHE
1	4	175	ASN
1	4	414	GLN
1	6	200	ASN
1	8	413	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	533/555 (96%)	513 (96%)	20 (4%)	29	51
1	1	533/555 (96%)	515 (97%)	18 (3%)	32	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2	533/555 (96%)	516 (97%)	17 (3%)	34	55
1	3	533/555 (96%)	519 (97%)	14 (3%)	40	60
1	4	533/555 (96%)	510 (96%)	23 (4%)	26	47
1	5	533/555 (96%)	516 (97%)	17 (3%)	34	55
1	6	533/555 (96%)	518 (97%)	15 (3%)	38	59
1	7	533/555 (96%)	513 (96%)	20 (4%)	29	51
1	8	533/555 (96%)	515 (97%)	18 (3%)	32	54
1	9	533/555 (96%)	512 (96%)	21 (4%)	28	49
1	A	533/555 (96%)	517 (97%)	16 (3%)	36	57
1	B	533/555 (96%)	510 (96%)	23 (4%)	26	47
1	C	533/555 (96%)	519 (97%)	14 (3%)	40	60
1	D	533/555 (96%)	516 (97%)	17 (3%)	34	55
1	E	533/555 (96%)	513 (96%)	20 (4%)	29	51
1	F	533/555 (96%)	510 (96%)	23 (4%)	26	47
1	G	533/555 (96%)	520 (98%)	13 (2%)	43	63
1	H	533/555 (96%)	521 (98%)	12 (2%)	44	63
1	I	533/555 (96%)	523 (98%)	10 (2%)	50	66
1	J	533/555 (96%)	520 (98%)	13 (2%)	43	63
1	K	533/555 (96%)	517 (97%)	16 (3%)	36	57
1	L	533/555 (96%)	520 (98%)	13 (2%)	43	63
1	M	533/555 (96%)	516 (97%)	17 (3%)	34	55
1	N	533/555 (96%)	522 (98%)	11 (2%)	47	65
1	O	533/555 (96%)	519 (97%)	14 (3%)	40	60
1	P	533/555 (96%)	518 (97%)	15 (3%)	38	59
1	Q	533/555 (96%)	517 (97%)	16 (3%)	36	57
1	R	533/555 (96%)	518 (97%)	15 (3%)	38	59
1	S	533/555 (96%)	518 (97%)	15 (3%)	38	59
1	T	533/555 (96%)	515 (97%)	18 (3%)	32	54
1	U	533/555 (96%)	516 (97%)	17 (3%)	34	55
1	V	533/555 (96%)	515 (97%)	18 (3%)	32	54
1	W	533/555 (96%)	516 (97%)	17 (3%)	34	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	X	533/555 (96%)	518 (97%)	15 (3%)	38	59
1	Y	533/555 (96%)	516 (97%)	17 (3%)	34	55
1	Z	533/555 (96%)	516 (97%)	17 (3%)	34	55
1	a	533/555 (96%)	520 (98%)	13 (2%)	43	63
1	b	533/555 (96%)	513 (96%)	20 (4%)	29	51
1	c	533/555 (96%)	522 (98%)	11 (2%)	47	65
1	d	533/555 (96%)	510 (96%)	23 (4%)	26	47
1	e	533/555 (96%)	513 (96%)	20 (4%)	29	51
1	f	533/555 (96%)	516 (97%)	17 (3%)	34	55
1	g	533/555 (96%)	513 (96%)	20 (4%)	29	51
1	h	533/555 (96%)	513 (96%)	20 (4%)	29	51
1	i	533/555 (96%)	514 (96%)	19 (4%)	31	52
1	j	533/555 (96%)	519 (97%)	14 (3%)	40	60
1	k	533/555 (96%)	512 (96%)	21 (4%)	28	49
1	l	533/555 (96%)	513 (96%)	20 (4%)	29	51
1	m	533/555 (96%)	523 (98%)	10 (2%)	50	66
1	n	533/555 (96%)	507 (95%)	26 (5%)	22	44
1	o	533/555 (96%)	521 (98%)	12 (2%)	44	63
1	p	533/555 (96%)	521 (98%)	12 (2%)	44	63
1	q	533/555 (96%)	515 (97%)	18 (3%)	32	54
1	r	533/555 (96%)	515 (97%)	18 (3%)	32	54
1	s	533/555 (96%)	521 (98%)	12 (2%)	44	63
1	t	533/555 (96%)	514 (96%)	19 (4%)	31	52
1	u	533/555 (96%)	510 (96%)	23 (4%)	26	47
1	v	533/555 (96%)	514 (96%)	19 (4%)	31	52
1	w	533/555 (96%)	521 (98%)	12 (2%)	44	63
1	x	533/555 (96%)	510 (96%)	23 (4%)	26	47
1	y	533/555 (96%)	521 (98%)	12 (2%)	44	63
1	z	533/555 (96%)	513 (96%)	20 (4%)	29	51
All	All	33046/34410 (96%)	31997 (97%)	1049 (3%)	35	55

5 of 1049 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	581	GLN
1	U	249	ILE
1	S	577	MET
1	Z	301	ARG
1	l	270	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 651 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	331	GLN
1	S	644	GLN
1	J	430	ASN
1	I	330	GLN
1	N	538	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

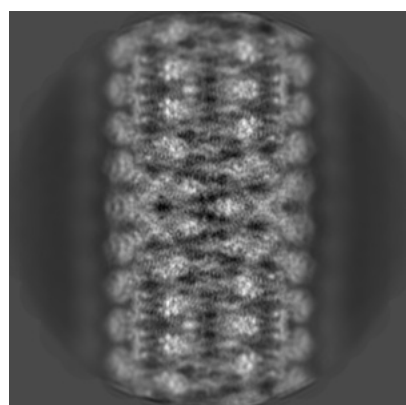
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8577. These allow visual inspection of the internal detail of the map and identification of artifacts.

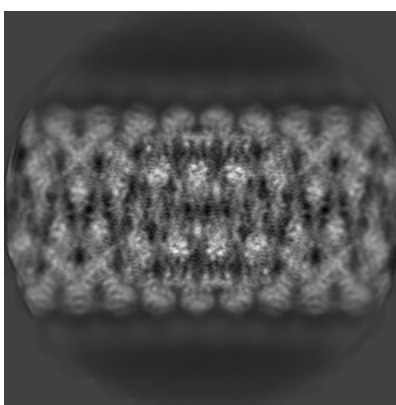
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

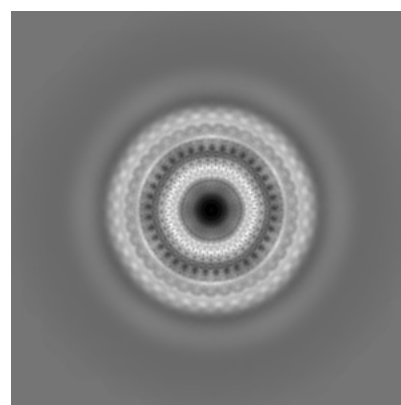
6.1.1 Primary map



X



Y

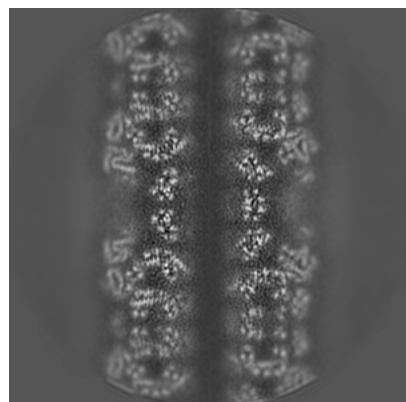


Z

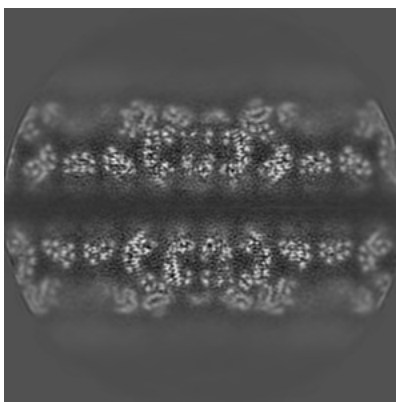
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

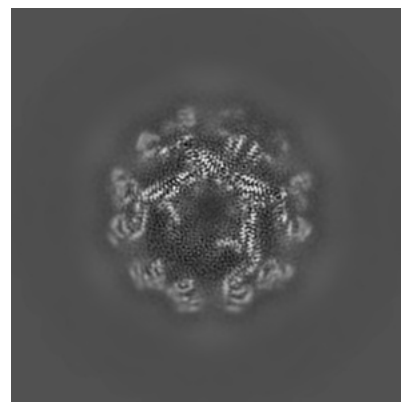
6.2.1 Primary map



X Index: 225



Y Index: 225

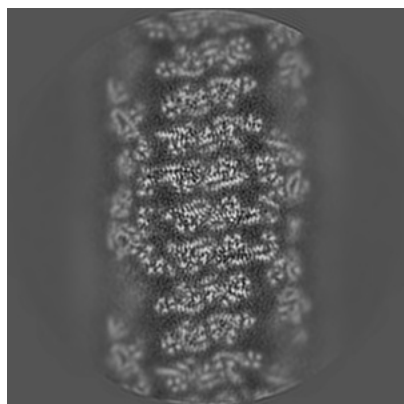


Z Index: 225

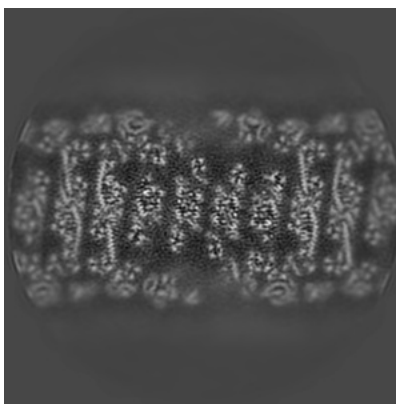
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

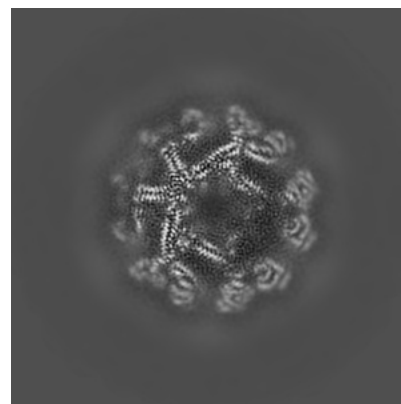
6.3.1 Primary map



X Index: 264



Y Index: 178

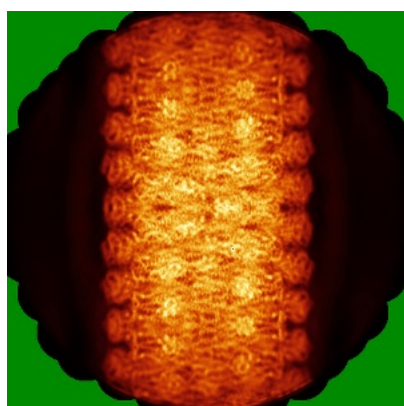


Z Index: 236

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

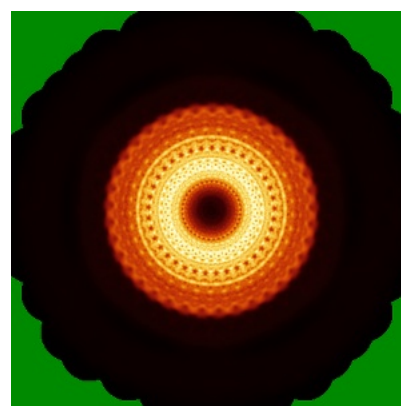
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views

6.5.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 4.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

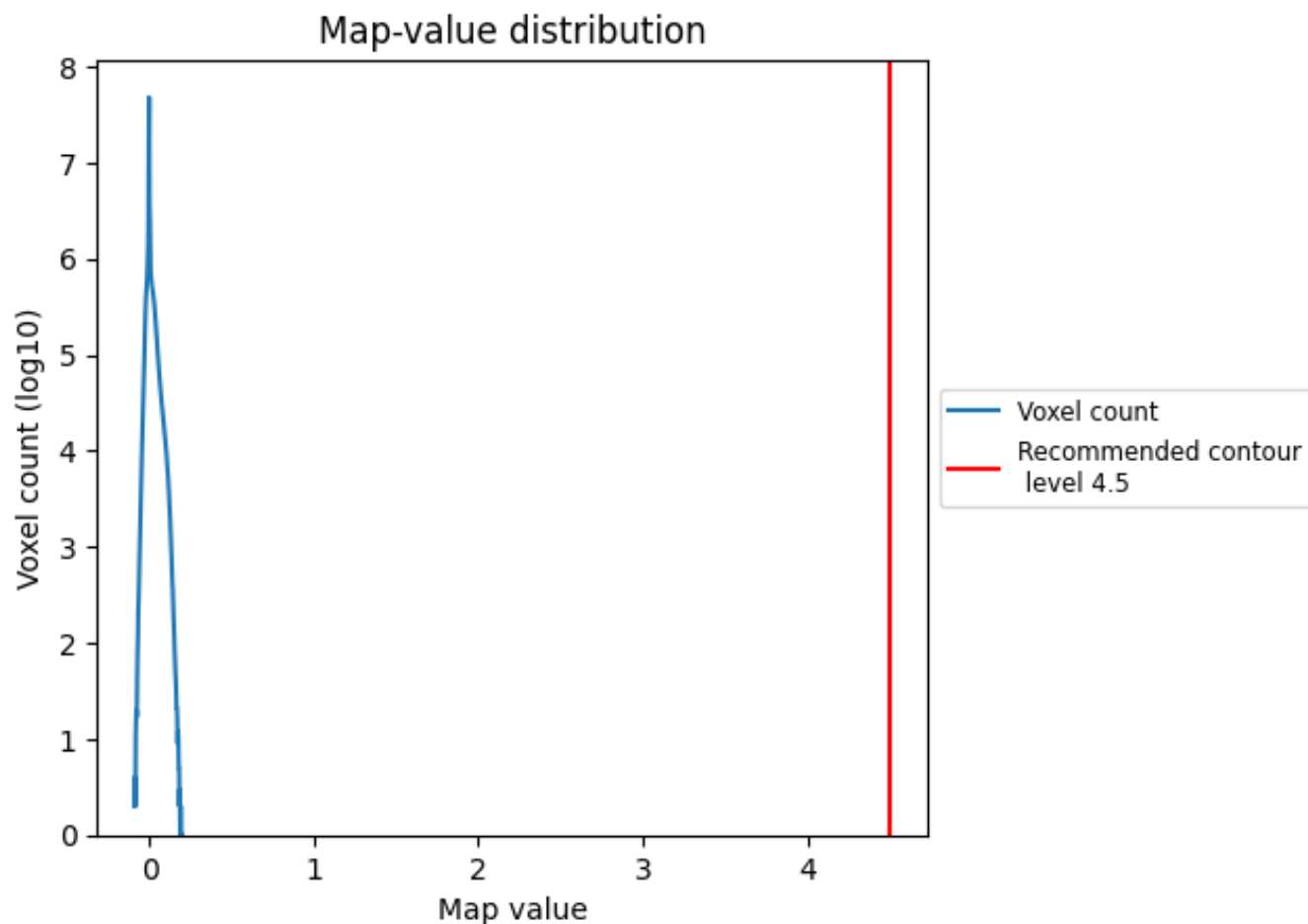
6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

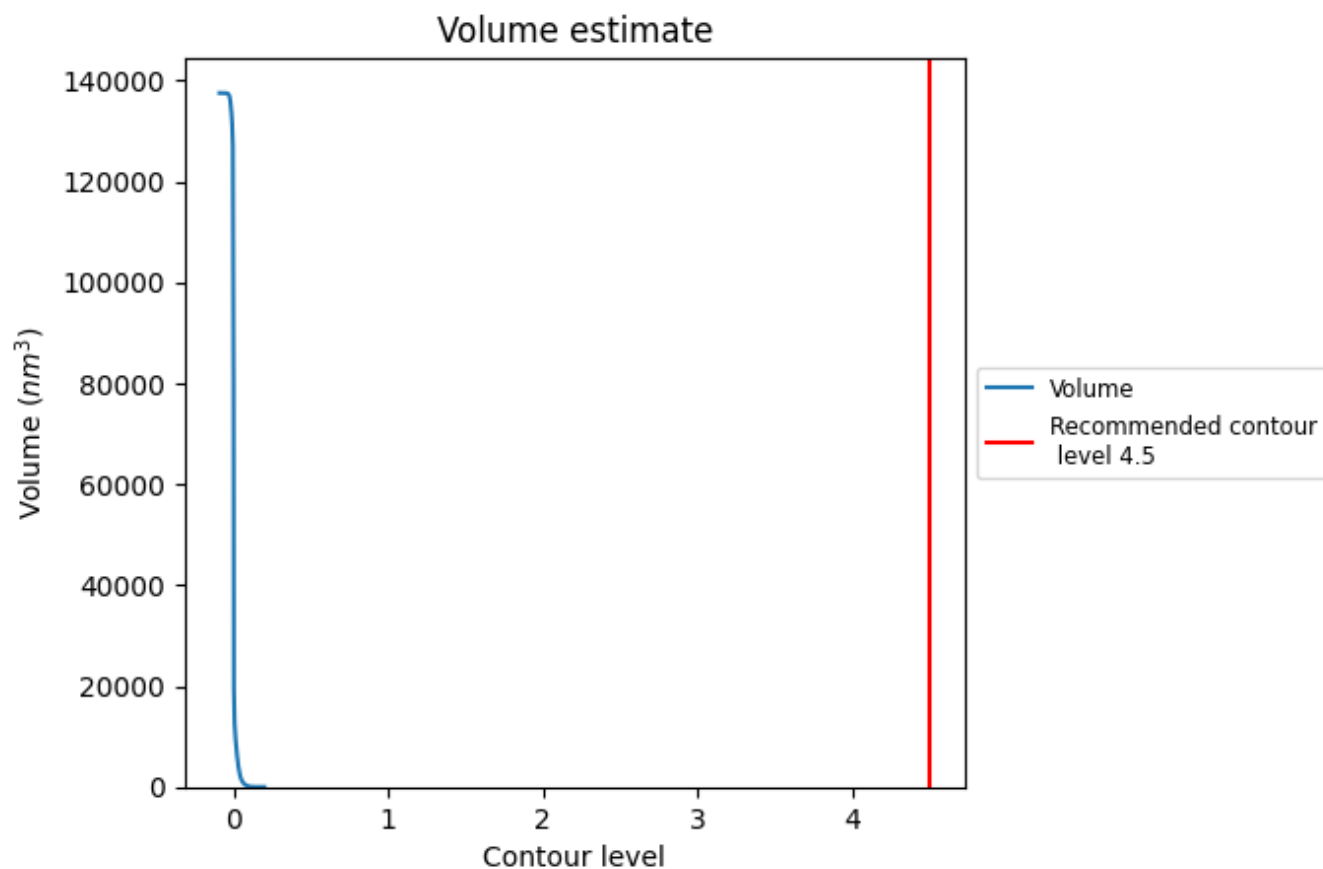
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



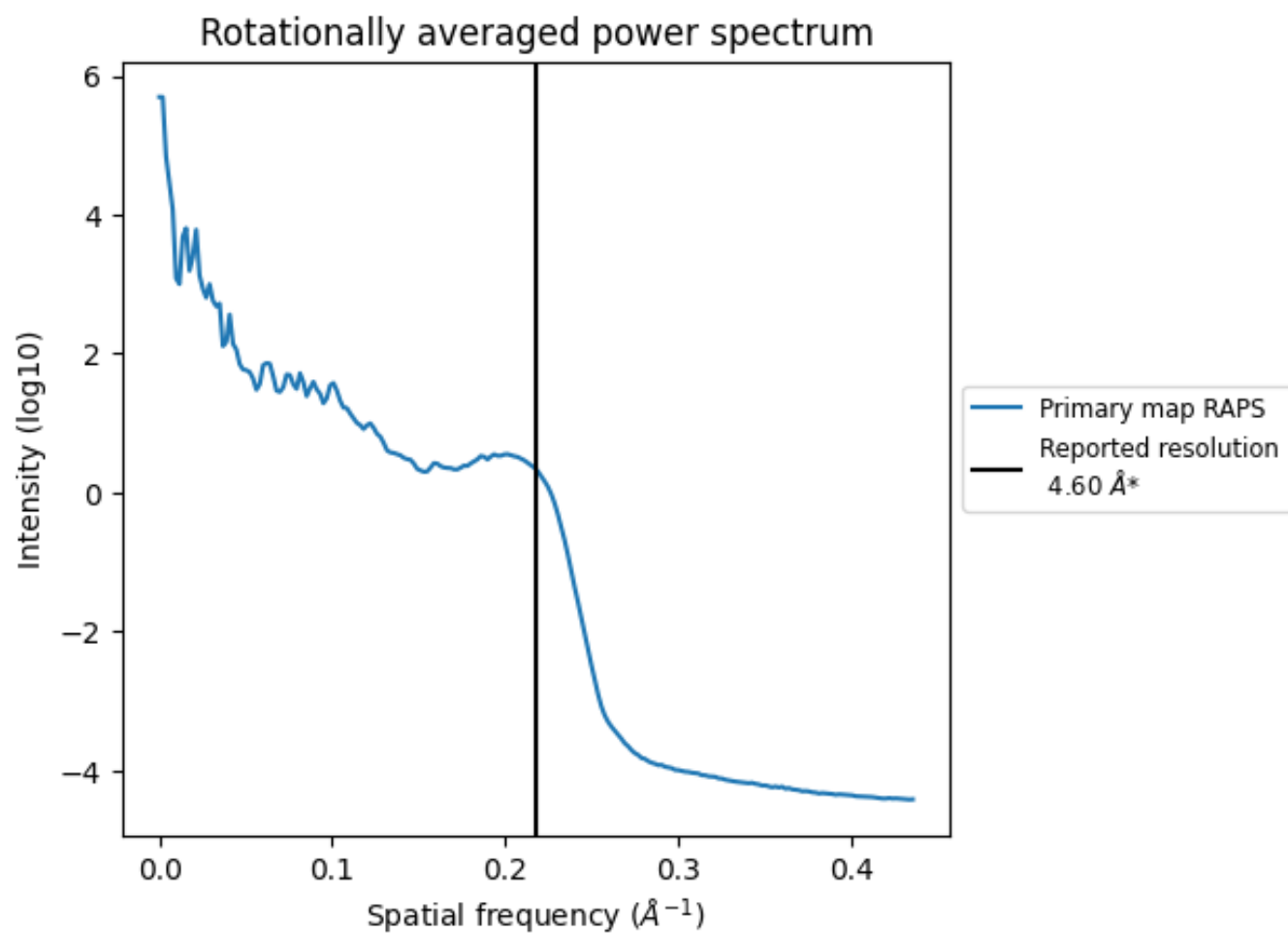
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate [i](#)



The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

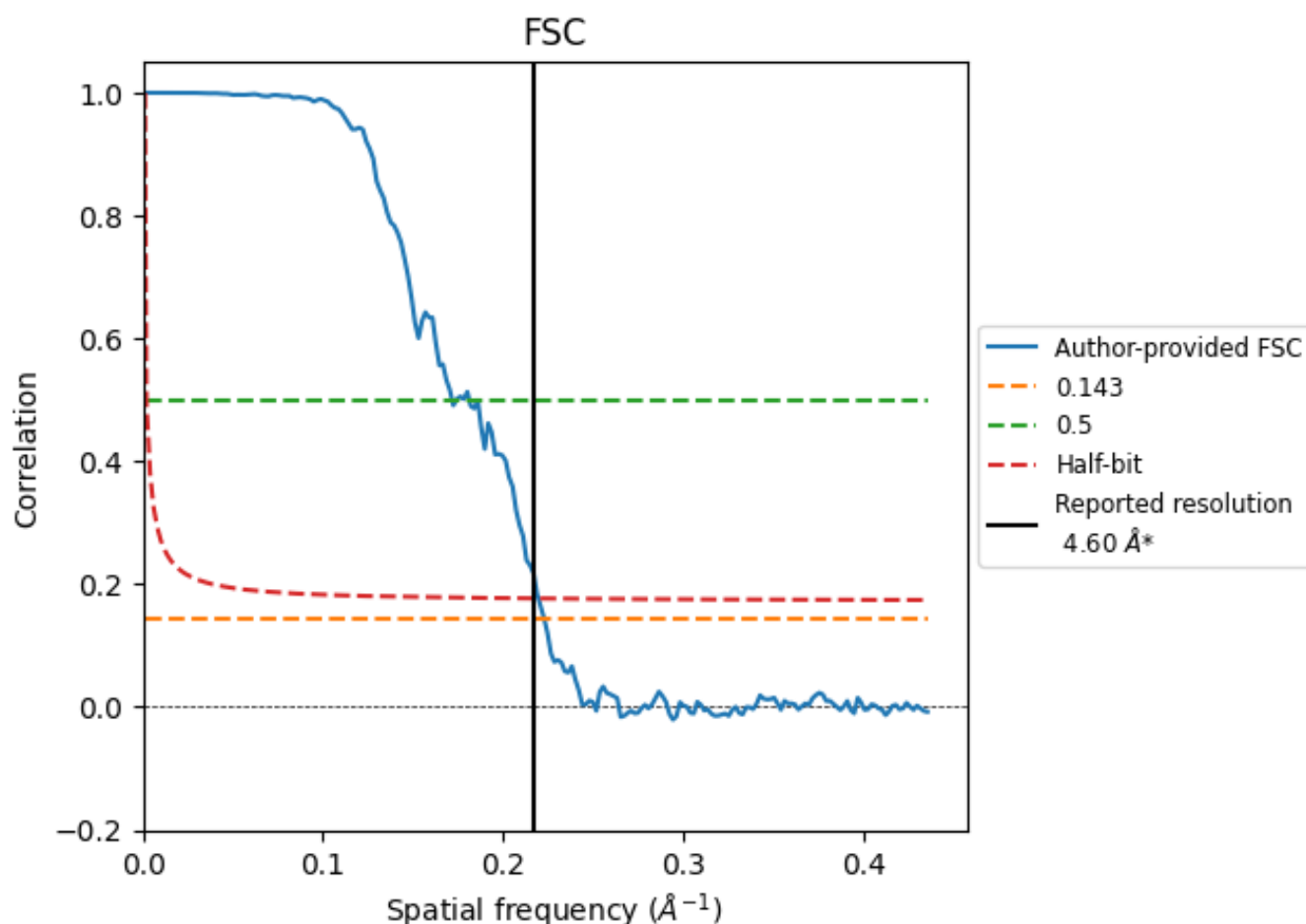


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

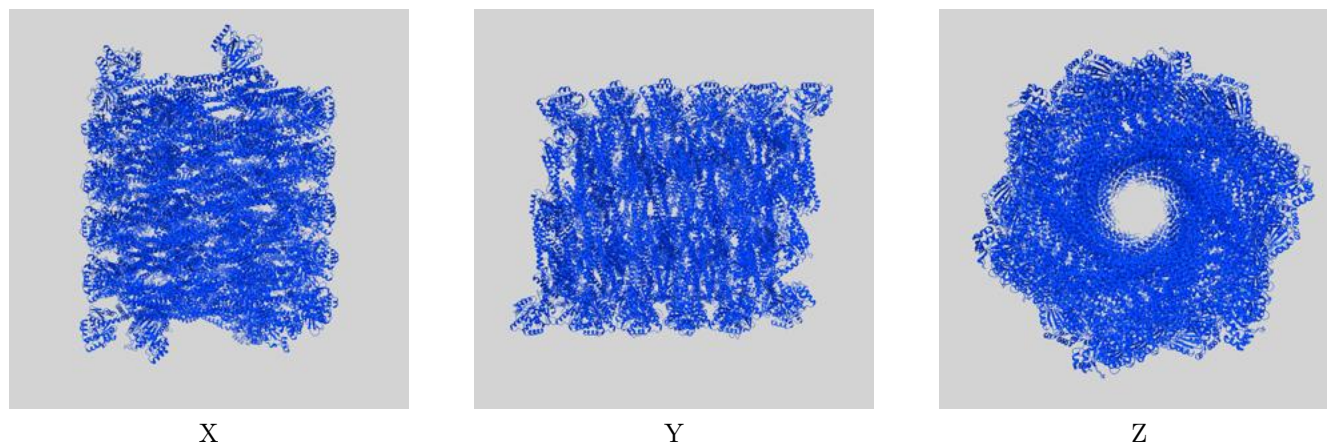
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.49	5.82	4.55
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

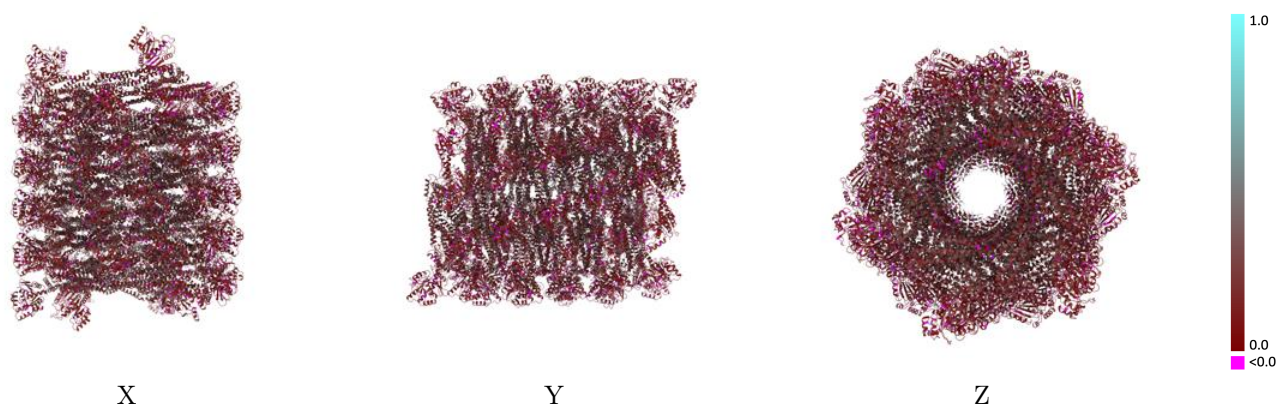
This section contains information regarding the fit between EMDB map EMD-8577 and PDB model 5UOT. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



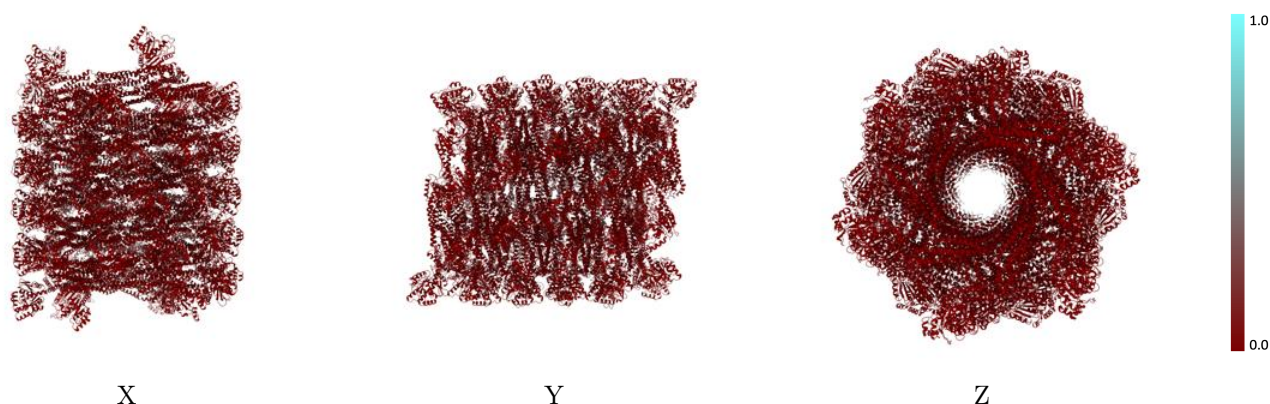
The images above show the 3D surface view of the map at the recommended contour level 4.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



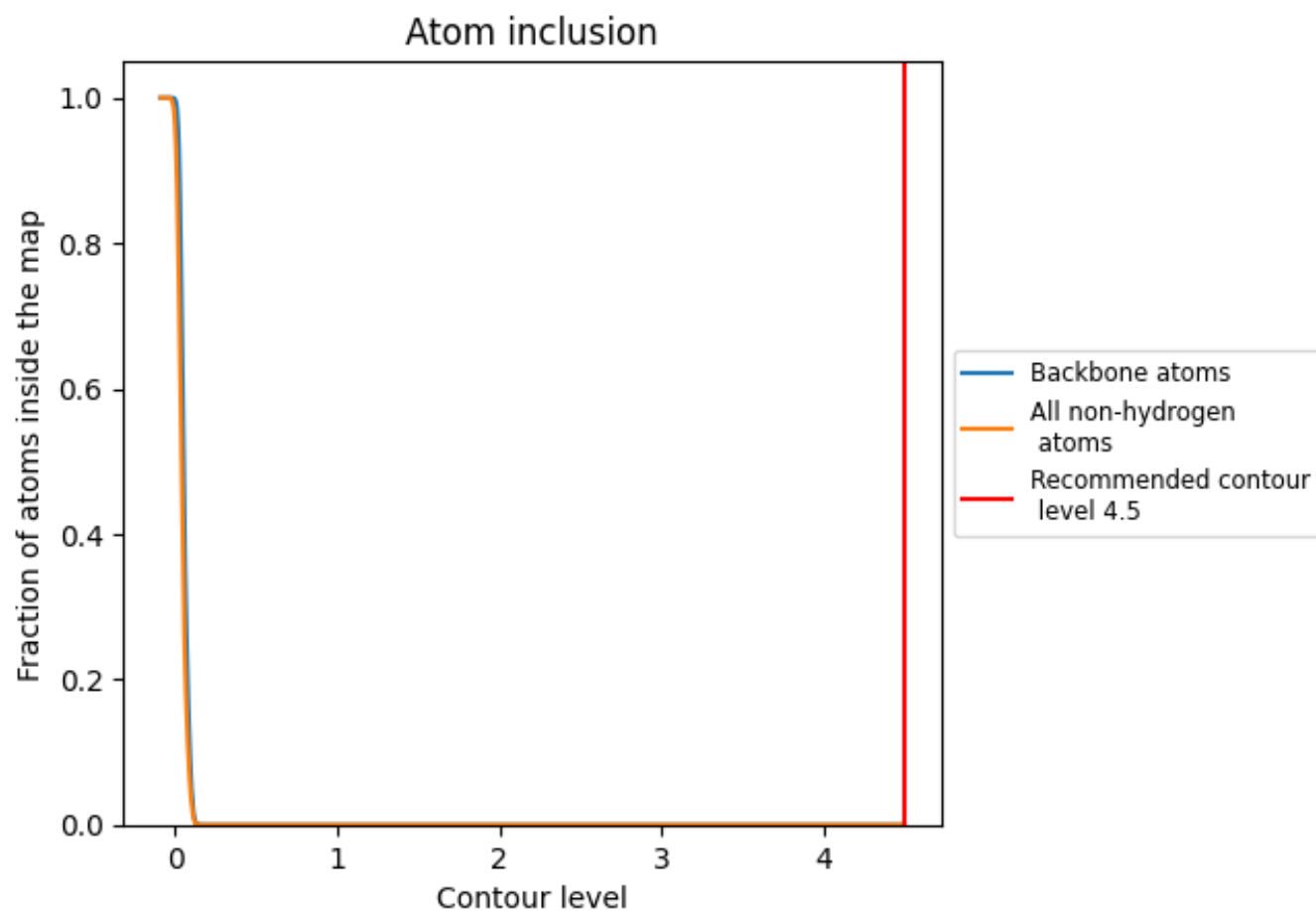
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (4.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 0% of all backbone atoms, 0% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0000	0.1970
0	0.0000	0.1820
1	0.0000	0.1840
2	0.0000	0.1960
3	0.0000	0.1880
4	0.0000	0.2080
5	0.0000	0.1910
6	0.0000	0.2090
7	0.0000	0.2050
8	0.0000	0.1880
9	0.0000	0.2100
A	0.0000	0.2020
B	0.0000	0.2020
C	0.0000	0.2030
D	0.0000	0.1980
E	0.0000	0.2040
F	0.0000	0.2010
G	0.0000	0.2040
H	0.0000	0.2050
I	0.0000	0.1940
J	0.0000	0.2030
K	0.0000	0.1910
L	0.0000	0.2020
M	0.0000	0.1930
N	0.0000	0.1900
O	0.0000	0.1900
P	0.0000	0.1880
Q	0.0000	0.1900
R	0.0000	0.1910
S	0.0000	0.1940
T	0.0000	0.1810
U	0.0000	0.1800
V	0.0000	0.1870
W	0.0000	0.1740
X	0.0000	0.1820



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Chain	Atom inclusion	Q-score
Y	 0.0000	 0.1800
Z	 0.0000	 0.1680
a	 0.0000	 0.1910
b	 0.0000	 0.2130
c	 0.0000	 0.1960
d	 0.0000	 0.1880
e	 0.0000	 0.1930
f	 0.0000	 0.1960
g	 0.0000	 0.2170
h	 0.0000	 0.2080
i	 0.0000	 0.2120
j	 0.0000	 0.2010
k	 0.0000	 0.1890
l	 0.0000	 0.2100
m	 0.0000	 0.1940
n	 0.0000	 0.2120
o	 0.0000	 0.1970
p	 0.0000	 0.1910
q	 0.0000	 0.2110
r	 0.0000	 0.1920
s	 0.0000	 0.2120
t	 0.0000	 0.2090
u	 0.0000	 0.2170
v	 0.0000	 0.2030
w	 0.0000	 0.1910
x	 0.0000	 0.2170
y	 0.0000	 0.1890
z	 0.0000	 0.2150