



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 10:21 AM UTC

PDB ID : 7T81 / pdb_00007t81
EMDB ID : EMD-25741
Title : Model of Munc13-1 C1-C2B-MUN-C2C 2D crystal between lipid bilayers.
Authors : Grushin, K.; Sindelar, C.V.
Deposited on : 2021-12-15
Resolution : 10.00 Å(reported)

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:

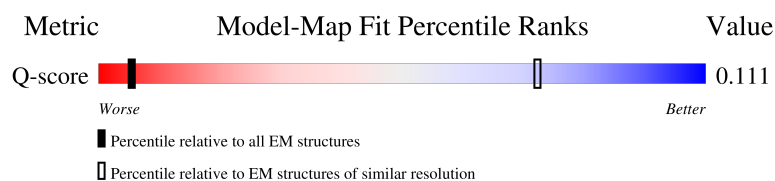
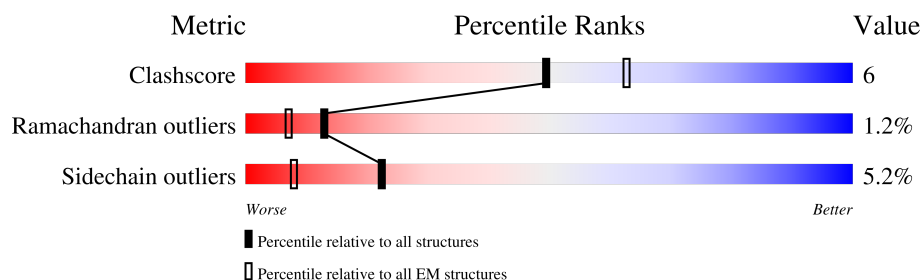
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 10.00 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	147 (9.50 - 10.50)

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	A	1154	 6% 85% 12% ..
1	C	1154	 6% 85% 12% ..
1	D	1154	 6% 85% 12% ..
1	E	1154	 6% 85% 12% ..

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Mol	Chain	Length	Quality of chain
1	F	1154	6% 84% 12% ..
1	G	1154	6% 85% 12% ..
1	H	1154	17% 81% 15% ..
1	I	1154	21% 82% 14% ..
1	J	1154	20% 81% 14% ..
1	K	1154	16% 82% 14% ..
1	L	1154	21% 82% 14% ..
1	M	1154	20% 81% 15% ..
1	N	1154	17% 82% 14% ..
1	O	1154	21% 83% 13% ..
1	P	1154	20% 81% 15% ..
1	Q	1154	16% 82% 14% ..
1	R	1154	21% 83% 13% ..
1	S	1154	19% 82% 14% ..
1	T	1154	16% 82% 14% ..
1	U	1154	21% 82% 14% ..
1	V	1154	20% 82% 14% ..
1	W	1154	16% 81% 14% ..
1	X	1154	21% 82% 14% ..
1	Y	1154	20% 82% 14% ..

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 432240 atoms, of which 215424 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 Protein unc-13 homolog A.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	C	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	D	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	E	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	F	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	G	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	H	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	I	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	J	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	K	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	L	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	M	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	N	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	O	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	P	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	Q	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		
1	R	1132	Total	C	H	N	O	S	0	0
			18010	5715	8976	1545	1719	55		

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	S	1132	Total 18010	C 5715	H 8976	N 1545	O 1719	S 55	0	0
1	T	1132	Total 18010	C 5715	H 8976	N 1545	O 1719	S 55	0	0
1	U	1132	Total 18010	C 5715	H 8976	N 1545	O 1719	S 55	0	0
1	V	1132	Total 18010	C 5715	H 8976	N 1545	O 1719	S 55	0	0
1	W	1132	Total 18010	C 5715	H 8976	N 1545	O 1719	S 55	0	0
1	X	1132	Total 18010	C 5715	H 8976	N 1545	O 1719	S 55	0	0
1	Y	1132	Total 18010	C 5715	H 8976	N 1545	O 1719	S 55	0	0

There are 264 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	expression tag	UNP Q62768
A	-6	PRO	-	expression tag	UNP Q62768
A	-5	LEU	-	expression tag	UNP Q62768
A	-4	GLY	-	expression tag	UNP Q62768
A	-3	SER	-	expression tag	UNP Q62768
A	-2	GLU	-	expression tag	UNP Q62768
A	-1	PHE	-	expression tag	UNP Q62768
A	0	MET	-	expression tag	UNP Q62768
A	228	TRP	LEU	conflict	UNP Q62768
A	880	GLU	-	linker	UNP Q62768
A	881	PHE	-	linker	UNP Q62768
C	-7	GLY	-	expression tag	UNP Q62768
C	-6	PRO	-	expression tag	UNP Q62768
C	-5	LEU	-	expression tag	UNP Q62768
C	-4	GLY	-	expression tag	UNP Q62768
C	-3	SER	-	expression tag	UNP Q62768
C	-2	GLU	-	expression tag	UNP Q62768
C	-1	PHE	-	expression tag	UNP Q62768
C	0	MET	-	expression tag	UNP Q62768
C	228	TRP	LEU	conflict	UNP Q62768
C	880	GLU	-	linker	UNP Q62768
C	881	PHE	-	linker	UNP Q62768
D	-7	GLY	-	expression tag	UNP Q62768
D	-6	PRO	-	expression tag	UNP Q62768
D	-5	LEU	-	expression tag	UNP Q62768

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-4	GLY	-	expression tag	UNP Q62768
D	-3	SER	-	expression tag	UNP Q62768
D	-2	GLU	-	expression tag	UNP Q62768
D	-1	PHE	-	expression tag	UNP Q62768
D	0	MET	-	expression tag	UNP Q62768
D	228	TRP	LEU	conflict	UNP Q62768
D	880	GLU	-	linker	UNP Q62768
D	881	PHE	-	linker	UNP Q62768
E	-7	GLY	-	expression tag	UNP Q62768
E	-6	PRO	-	expression tag	UNP Q62768
E	-5	LEU	-	expression tag	UNP Q62768
E	-4	GLY	-	expression tag	UNP Q62768
E	-3	SER	-	expression tag	UNP Q62768
E	-2	GLU	-	expression tag	UNP Q62768
E	-1	PHE	-	expression tag	UNP Q62768
E	0	MET	-	expression tag	UNP Q62768
E	228	TRP	LEU	conflict	UNP Q62768
E	880	GLU	-	linker	UNP Q62768
E	881	PHE	-	linker	UNP Q62768
F	-7	GLY	-	expression tag	UNP Q62768
F	-6	PRO	-	expression tag	UNP Q62768
F	-5	LEU	-	expression tag	UNP Q62768
F	-4	GLY	-	expression tag	UNP Q62768
F	-3	SER	-	expression tag	UNP Q62768
F	-2	GLU	-	expression tag	UNP Q62768
F	-1	PHE	-	expression tag	UNP Q62768
F	0	MET	-	expression tag	UNP Q62768
F	228	TRP	LEU	conflict	UNP Q62768
F	880	GLU	-	linker	UNP Q62768
F	881	PHE	-	linker	UNP Q62768
G	-7	GLY	-	expression tag	UNP Q62768
G	-6	PRO	-	expression tag	UNP Q62768
G	-5	LEU	-	expression tag	UNP Q62768
G	-4	GLY	-	expression tag	UNP Q62768
G	-3	SER	-	expression tag	UNP Q62768
G	-2	GLU	-	expression tag	UNP Q62768
G	-1	PHE	-	expression tag	UNP Q62768
G	0	MET	-	expression tag	UNP Q62768
G	228	TRP	LEU	conflict	UNP Q62768
G	880	GLU	-	linker	UNP Q62768
G	881	PHE	-	linker	UNP Q62768
H	-7	GLY	-	expression tag	UNP Q62768

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-6	PRO	-	expression tag	UNP Q62768
H	-5	LEU	-	expression tag	UNP Q62768
H	-4	GLY	-	expression tag	UNP Q62768
H	-3	SER	-	expression tag	UNP Q62768
H	-2	GLU	-	expression tag	UNP Q62768
H	-1	PHE	-	expression tag	UNP Q62768
H	0	MET	-	expression tag	UNP Q62768
H	228	TRP	LEU	conflict	UNP Q62768
H	880	GLU	-	linker	UNP Q62768
H	881	PHE	-	linker	UNP Q62768
I	-7	GLY	-	expression tag	UNP Q62768
I	-6	PRO	-	expression tag	UNP Q62768
I	-5	LEU	-	expression tag	UNP Q62768
I	-4	GLY	-	expression tag	UNP Q62768
I	-3	SER	-	expression tag	UNP Q62768
I	-2	GLU	-	expression tag	UNP Q62768
I	-1	PHE	-	expression tag	UNP Q62768
I	0	MET	-	expression tag	UNP Q62768
I	228	TRP	LEU	conflict	UNP Q62768
I	880	GLU	-	linker	UNP Q62768
I	881	PHE	-	linker	UNP Q62768
J	-7	GLY	-	expression tag	UNP Q62768
J	-6	PRO	-	expression tag	UNP Q62768
J	-5	LEU	-	expression tag	UNP Q62768
J	-4	GLY	-	expression tag	UNP Q62768
J	-3	SER	-	expression tag	UNP Q62768
J	-2	GLU	-	expression tag	UNP Q62768
J	-1	PHE	-	expression tag	UNP Q62768
J	0	MET	-	expression tag	UNP Q62768
J	228	TRP	LEU	conflict	UNP Q62768
J	880	GLU	-	linker	UNP Q62768
J	881	PHE	-	linker	UNP Q62768
K	-7	GLY	-	expression tag	UNP Q62768
K	-6	PRO	-	expression tag	UNP Q62768
K	-5	LEU	-	expression tag	UNP Q62768
K	-4	GLY	-	expression tag	UNP Q62768
K	-3	SER	-	expression tag	UNP Q62768
K	-2	GLU	-	expression tag	UNP Q62768
K	-1	PHE	-	expression tag	UNP Q62768
K	0	MET	-	expression tag	UNP Q62768
K	228	TRP	LEU	conflict	UNP Q62768
K	880	GLU	-	linker	UNP Q62768

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Chain	Residue	Modelled	Actual	Comment	Reference
K	881	PHE	-	linker	UNP Q62768
L	-7	GLY	-	expression tag	UNP Q62768
L	-6	PRO	-	expression tag	UNP Q62768
L	-5	LEU	-	expression tag	UNP Q62768
L	-4	GLY	-	expression tag	UNP Q62768
L	-3	SER	-	expression tag	UNP Q62768
L	-2	GLU	-	expression tag	UNP Q62768
L	-1	PHE	-	expression tag	UNP Q62768
L	0	MET	-	expression tag	UNP Q62768
L	228	TRP	LEU	conflict	UNP Q62768
L	880	GLU	-	linker	UNP Q62768
L	881	PHE	-	linker	UNP Q62768
M	-7	GLY	-	expression tag	UNP Q62768
M	-6	PRO	-	expression tag	UNP Q62768
M	-5	LEU	-	expression tag	UNP Q62768
M	-4	GLY	-	expression tag	UNP Q62768
M	-3	SER	-	expression tag	UNP Q62768
M	-2	GLU	-	expression tag	UNP Q62768
M	-1	PHE	-	expression tag	UNP Q62768
M	0	MET	-	expression tag	UNP Q62768
M	228	TRP	LEU	conflict	UNP Q62768
M	880	GLU	-	linker	UNP Q62768
M	881	PHE	-	linker	UNP Q62768
N	-7	GLY	-	expression tag	UNP Q62768
N	-6	PRO	-	expression tag	UNP Q62768
N	-5	LEU	-	expression tag	UNP Q62768
N	-4	GLY	-	expression tag	UNP Q62768
N	-3	SER	-	expression tag	UNP Q62768
N	-2	GLU	-	expression tag	UNP Q62768
N	-1	PHE	-	expression tag	UNP Q62768
N	0	MET	-	expression tag	UNP Q62768
N	228	TRP	LEU	conflict	UNP Q62768
N	880	GLU	-	linker	UNP Q62768
N	881	PHE	-	linker	UNP Q62768
O	-7	GLY	-	expression tag	UNP Q62768
O	-6	PRO	-	expression tag	UNP Q62768
O	-5	LEU	-	expression tag	UNP Q62768
O	-4	GLY	-	expression tag	UNP Q62768
O	-3	SER	-	expression tag	UNP Q62768
O	-2	GLU	-	expression tag	UNP Q62768
O	-1	PHE	-	expression tag	UNP Q62768
O	0	MET	-	expression tag	UNP Q62768

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Chain	Residue	Modelled	Actual	Comment	Reference
O	228	TRP	LEU	conflict	UNP Q62768
O	880	GLU	-	linker	UNP Q62768
O	881	PHE	-	linker	UNP Q62768
P	-7	GLY	-	expression tag	UNP Q62768
P	-6	PRO	-	expression tag	UNP Q62768
P	-5	LEU	-	expression tag	UNP Q62768
P	-4	GLY	-	expression tag	UNP Q62768
P	-3	SER	-	expression tag	UNP Q62768
P	-2	GLU	-	expression tag	UNP Q62768
P	-1	PHE	-	expression tag	UNP Q62768
P	0	MET	-	expression tag	UNP Q62768
P	228	TRP	LEU	conflict	UNP Q62768
P	880	GLU	-	linker	UNP Q62768
P	881	PHE	-	linker	UNP Q62768
Q	-7	GLY	-	expression tag	UNP Q62768
Q	-6	PRO	-	expression tag	UNP Q62768
Q	-5	LEU	-	expression tag	UNP Q62768
Q	-4	GLY	-	expression tag	UNP Q62768
Q	-3	SER	-	expression tag	UNP Q62768
Q	-2	GLU	-	expression tag	UNP Q62768
Q	-1	PHE	-	expression tag	UNP Q62768
Q	0	MET	-	expression tag	UNP Q62768
Q	228	TRP	LEU	conflict	UNP Q62768
Q	880	GLU	-	linker	UNP Q62768
Q	881	PHE	-	linker	UNP Q62768
R	-7	GLY	-	expression tag	UNP Q62768
R	-6	PRO	-	expression tag	UNP Q62768
R	-5	LEU	-	expression tag	UNP Q62768
R	-4	GLY	-	expression tag	UNP Q62768
R	-3	SER	-	expression tag	UNP Q62768
R	-2	GLU	-	expression tag	UNP Q62768
R	-1	PHE	-	expression tag	UNP Q62768
R	0	MET	-	expression tag	UNP Q62768
R	228	TRP	LEU	conflict	UNP Q62768
R	880	GLU	-	linker	UNP Q62768
R	881	PHE	-	linker	UNP Q62768
S	-7	GLY	-	expression tag	UNP Q62768
S	-6	PRO	-	expression tag	UNP Q62768
S	-5	LEU	-	expression tag	UNP Q62768
S	-4	GLY	-	expression tag	UNP Q62768
S	-3	SER	-	expression tag	UNP Q62768
S	-2	GLU	-	expression tag	UNP Q62768

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Chain	Residue	Modelled	Actual	Comment	Reference
S	-1	PHE	-	expression tag	UNP Q62768
S	0	MET	-	expression tag	UNP Q62768
S	228	TRP	LEU	conflict	UNP Q62768
S	880	GLU	-	linker	UNP Q62768
S	881	PHE	-	linker	UNP Q62768
T	-7	GLY	-	expression tag	UNP Q62768
T	-6	PRO	-	expression tag	UNP Q62768
T	-5	LEU	-	expression tag	UNP Q62768
T	-4	GLY	-	expression tag	UNP Q62768
T	-3	SER	-	expression tag	UNP Q62768
T	-2	GLU	-	expression tag	UNP Q62768
T	-1	PHE	-	expression tag	UNP Q62768
T	0	MET	-	expression tag	UNP Q62768
T	228	TRP	LEU	conflict	UNP Q62768
T	880	GLU	-	linker	UNP Q62768
T	881	PHE	-	linker	UNP Q62768
U	-7	GLY	-	expression tag	UNP Q62768
U	-6	PRO	-	expression tag	UNP Q62768
U	-5	LEU	-	expression tag	UNP Q62768
U	-4	GLY	-	expression tag	UNP Q62768
U	-3	SER	-	expression tag	UNP Q62768
U	-2	GLU	-	expression tag	UNP Q62768
U	-1	PHE	-	expression tag	UNP Q62768
U	0	MET	-	expression tag	UNP Q62768
U	228	TRP	LEU	conflict	UNP Q62768
U	880	GLU	-	linker	UNP Q62768
U	881	PHE	-	linker	UNP Q62768
V	-7	GLY	-	expression tag	UNP Q62768
V	-6	PRO	-	expression tag	UNP Q62768
V	-5	LEU	-	expression tag	UNP Q62768
V	-4	GLY	-	expression tag	UNP Q62768
V	-3	SER	-	expression tag	UNP Q62768
V	-2	GLU	-	expression tag	UNP Q62768
V	-1	PHE	-	expression tag	UNP Q62768
V	0	MET	-	expression tag	UNP Q62768
V	228	TRP	LEU	conflict	UNP Q62768
V	880	GLU	-	linker	UNP Q62768
V	881	PHE	-	linker	UNP Q62768
W	-7	GLY	-	expression tag	UNP Q62768
W	-6	PRO	-	expression tag	UNP Q62768
W	-5	LEU	-	expression tag	UNP Q62768
W	-4	GLY	-	expression tag	UNP Q62768

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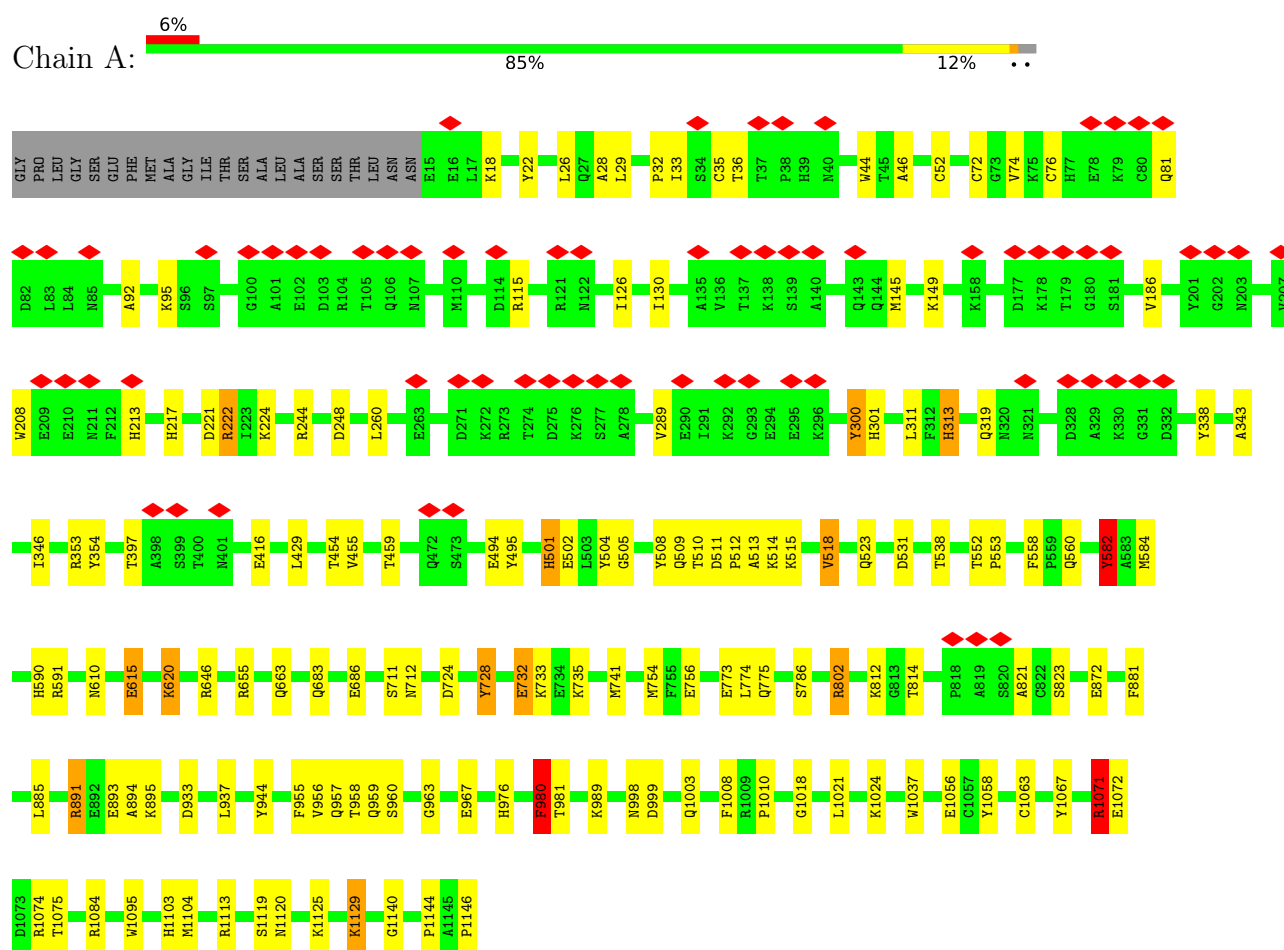
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Chain	Residue	Modelled	Actual	Comment	Reference
W	-3	SER	-	expression tag	UNP Q62768
W	-2	GLU	-	expression tag	UNP Q62768
W	-1	PHE	-	expression tag	UNP Q62768
W	0	MET	-	expression tag	UNP Q62768
W	228	TRP	LEU	conflict	UNP Q62768
W	880	GLU	-	linker	UNP Q62768
W	881	PHE	-	linker	UNP Q62768
X	-7	GLY	-	expression tag	UNP Q62768
X	-6	PRO	-	expression tag	UNP Q62768
X	-5	LEU	-	expression tag	UNP Q62768
X	-4	GLY	-	expression tag	UNP Q62768
X	-3	SER	-	expression tag	UNP Q62768
X	-2	GLU	-	expression tag	UNP Q62768
X	-1	PHE	-	expression tag	UNP Q62768
X	0	MET	-	expression tag	UNP Q62768
X	228	TRP	LEU	conflict	UNP Q62768
X	880	GLU	-	linker	UNP Q62768
X	881	PHE	-	linker	UNP Q62768
Y	-7	GLY	-	expression tag	UNP Q62768
Y	-6	PRO	-	expression tag	UNP Q62768
Y	-5	LEU	-	expression tag	UNP Q62768
Y	-4	GLY	-	expression tag	UNP Q62768
Y	-3	SER	-	expression tag	UNP Q62768
Y	-2	GLU	-	expression tag	UNP Q62768
Y	-1	PHE	-	expression tag	UNP Q62768
Y	0	MET	-	expression tag	UNP Q62768
Y	228	TRP	LEU	conflict	UNP Q62768
Y	880	GLU	-	linker	UNP Q62768
Y	881	PHE	-	linker	UNP Q62768

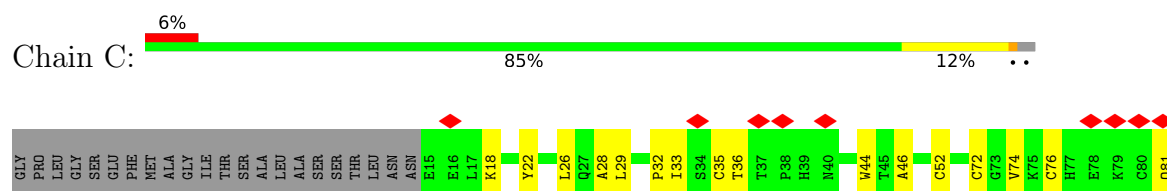
3 Residue-property plots

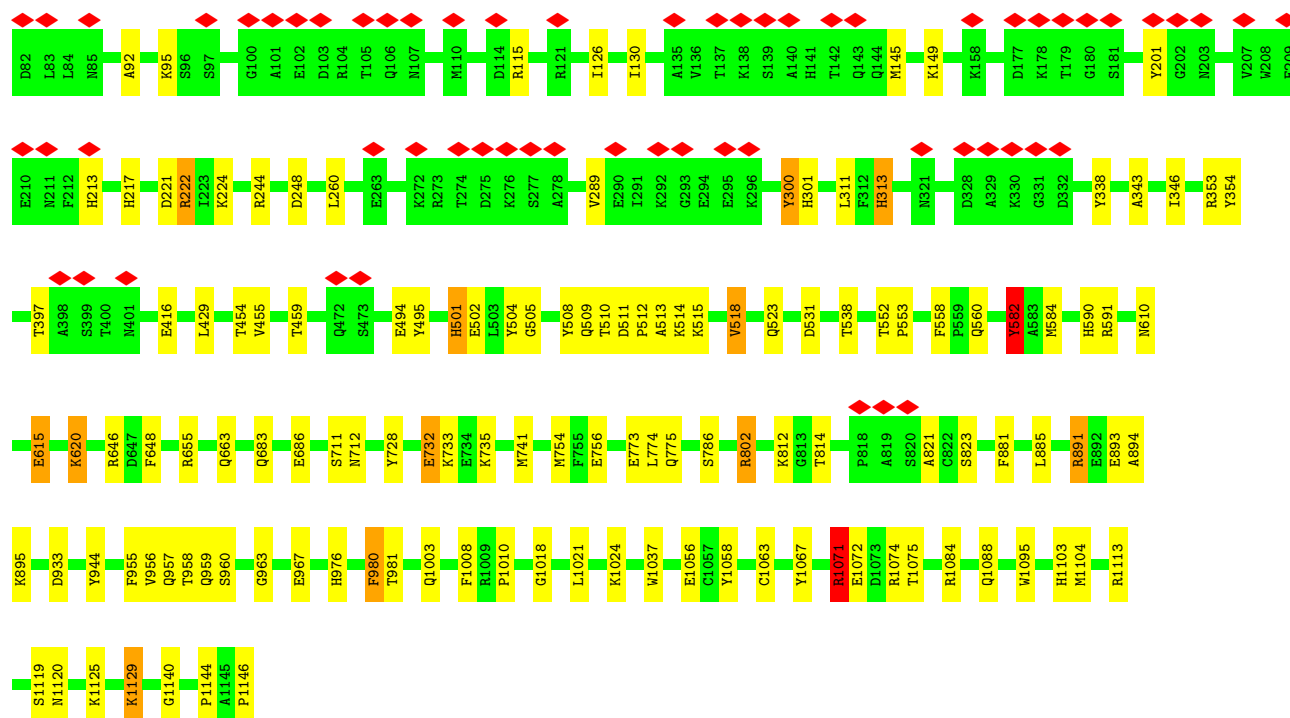
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Protein unc-13 homolog A

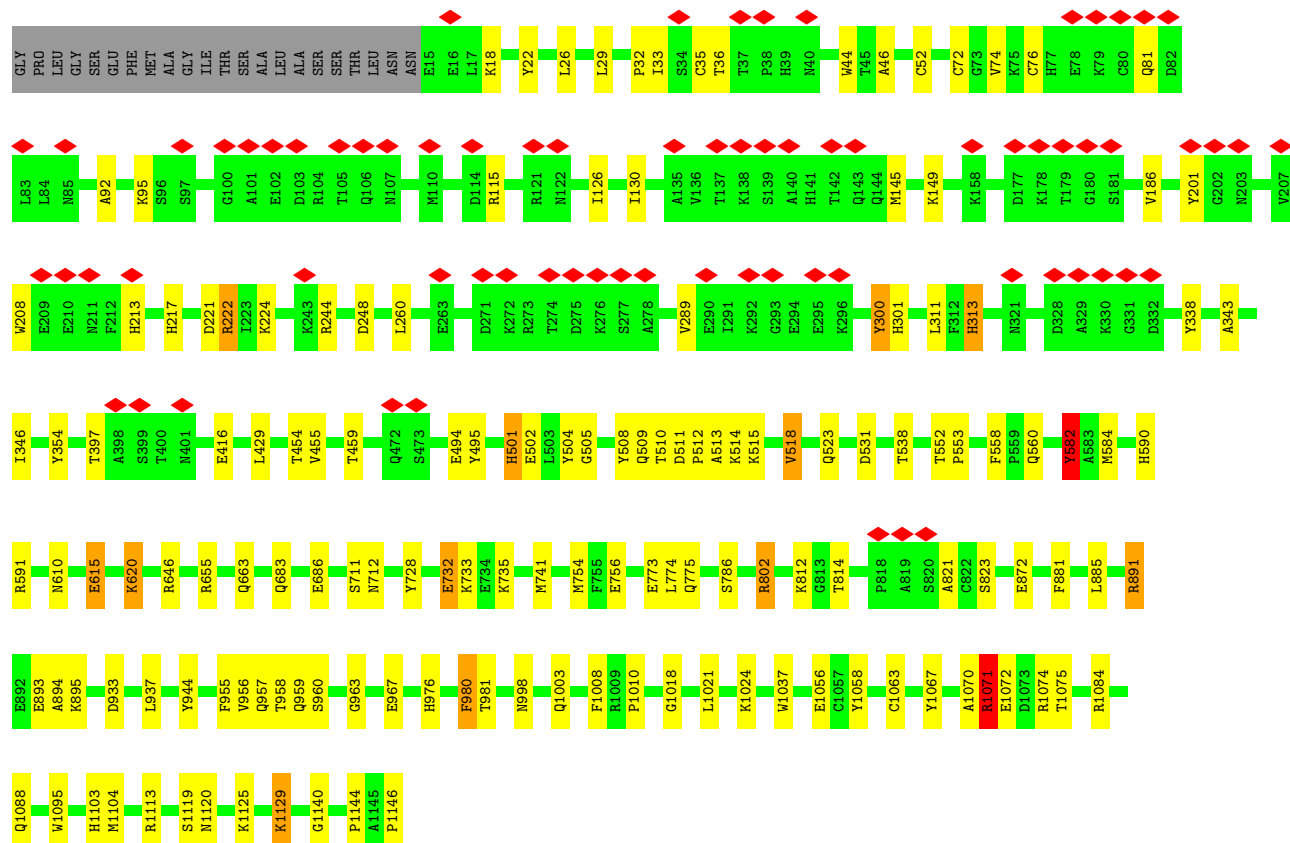
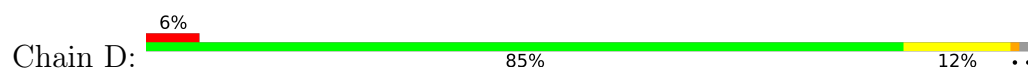


• Molecule 1: Protein unc-13 homolog A

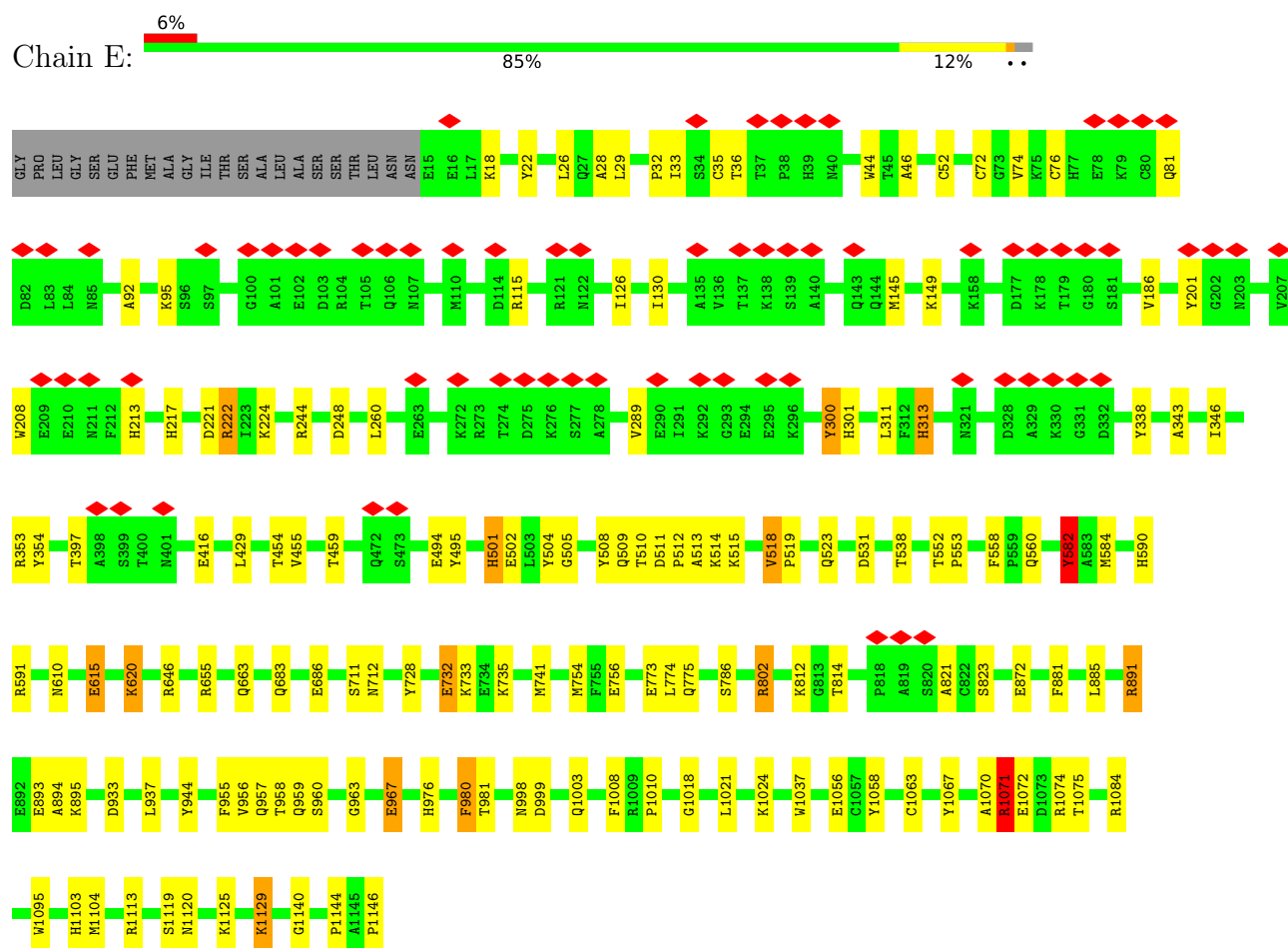




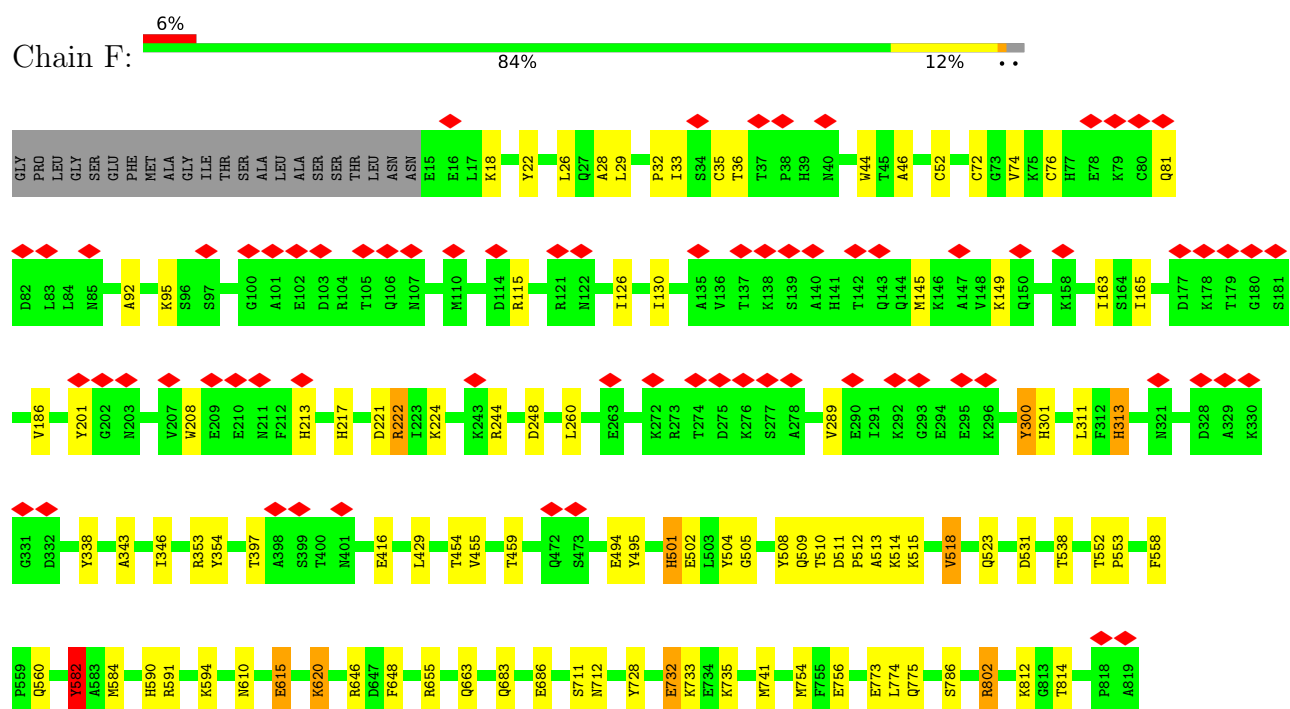
• Molecule 1: Protein unc-13 homolog A

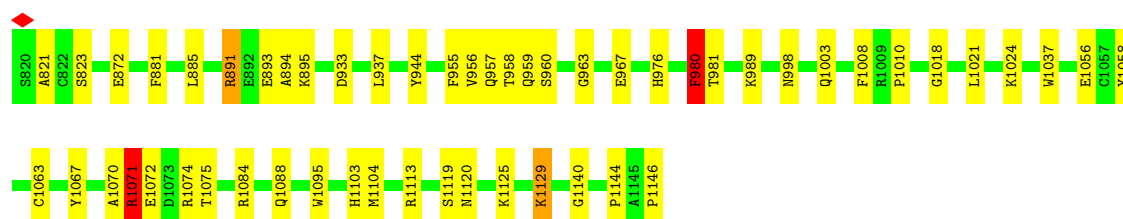


- Molecule 1: Protein unc-13 homolog A

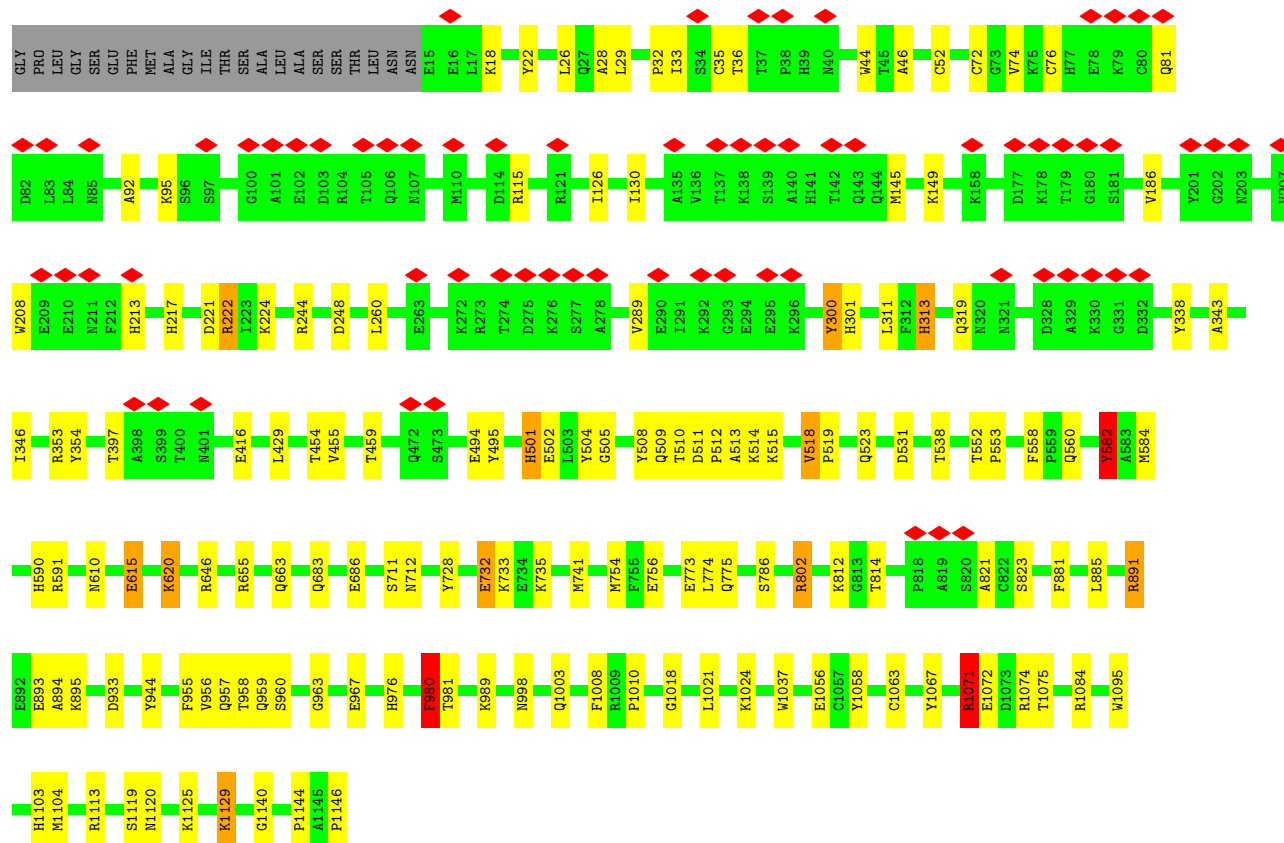
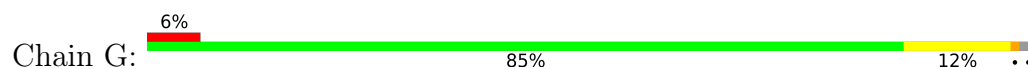


- Molecule 1: Protein unc-13 homolog A

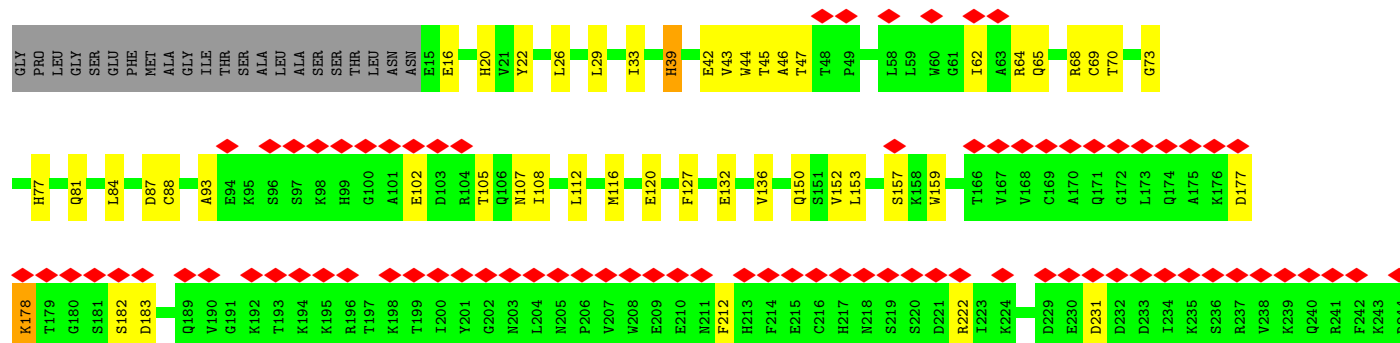
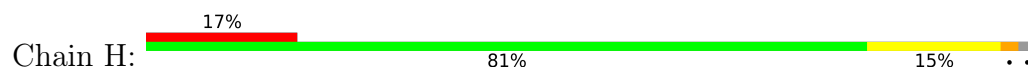


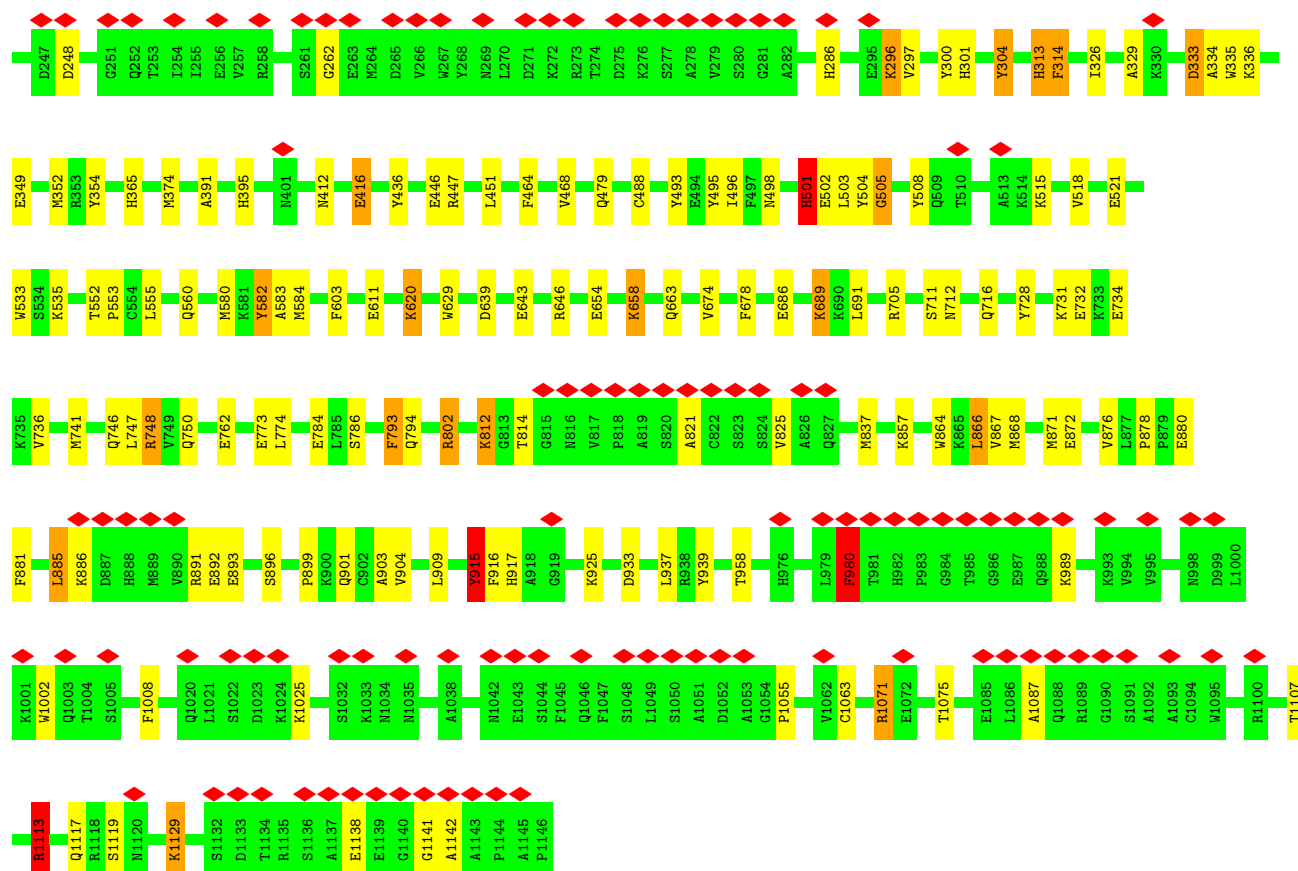


• Molecule 1: Protein unc-13 homolog A

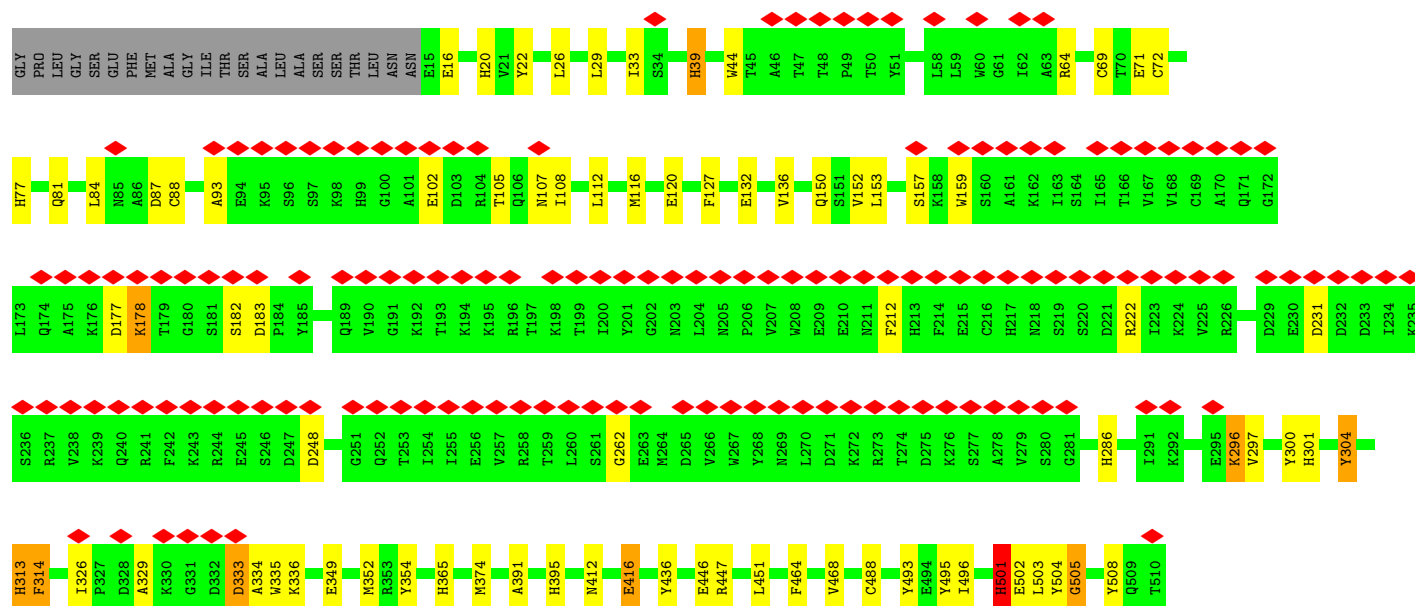
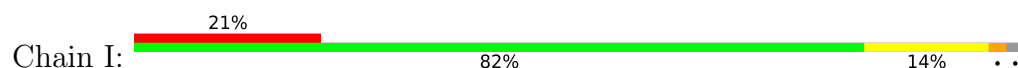


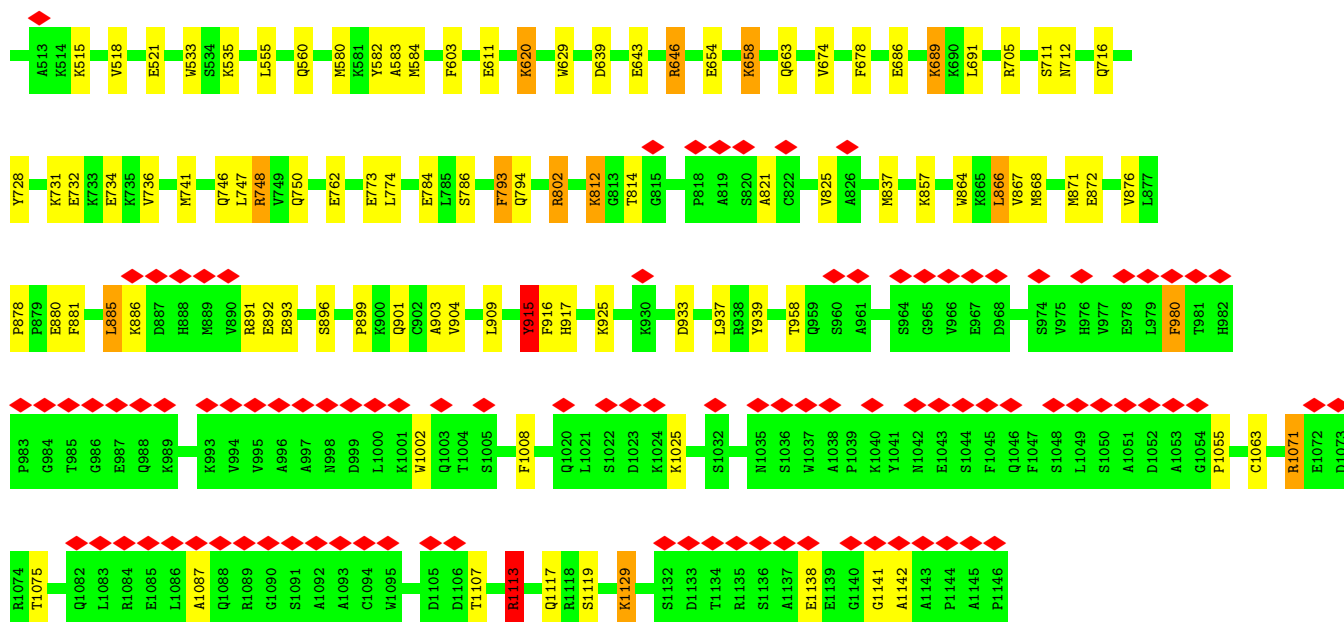
• Molecule 1: Protein unc-13 homolog A



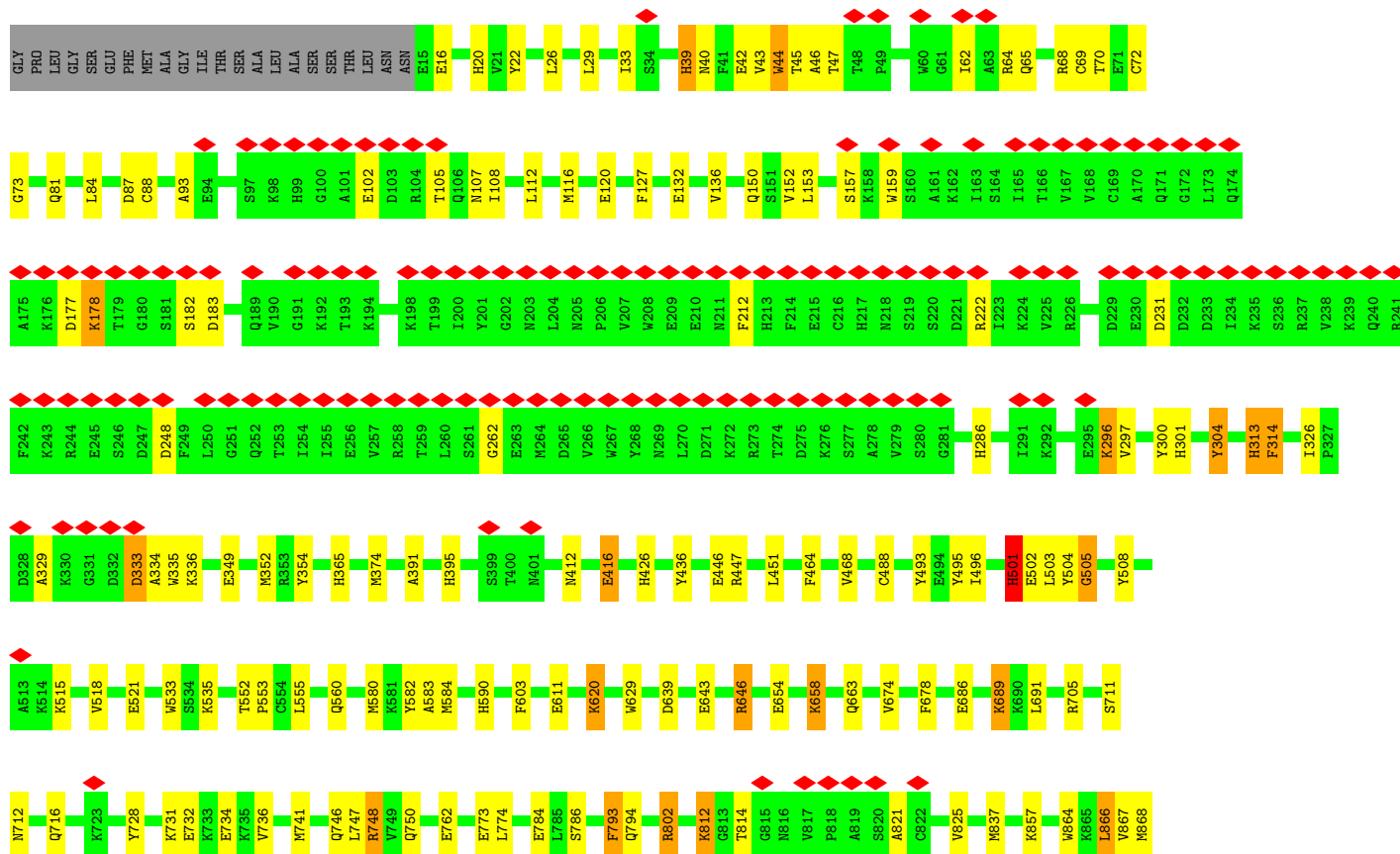
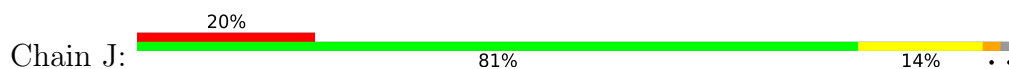


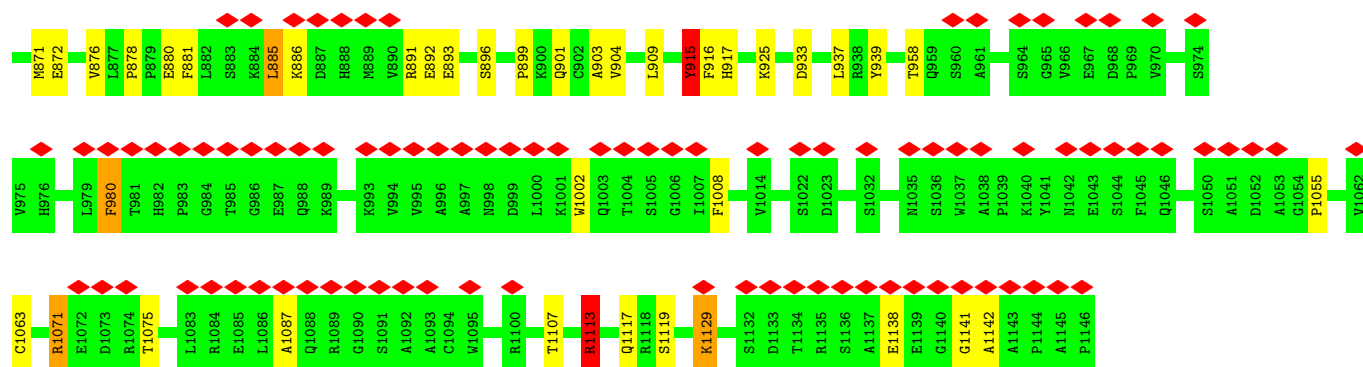
• Molecule 1: Protein unc-13 homolog A



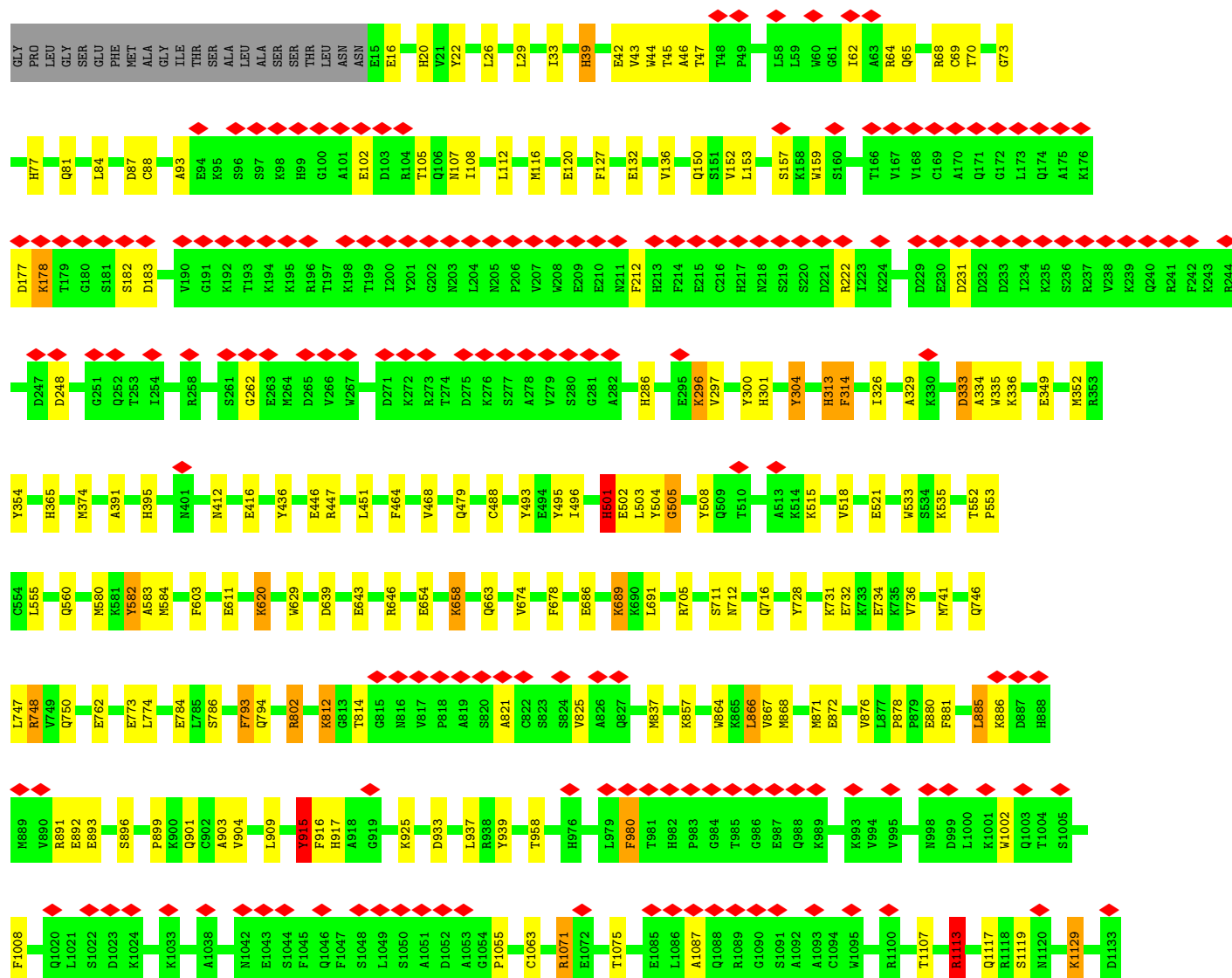
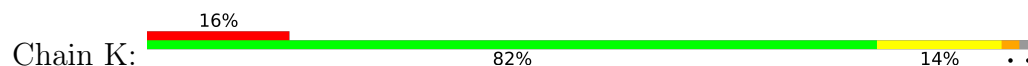


• Molecule 1: Protein unc-13 homolog A



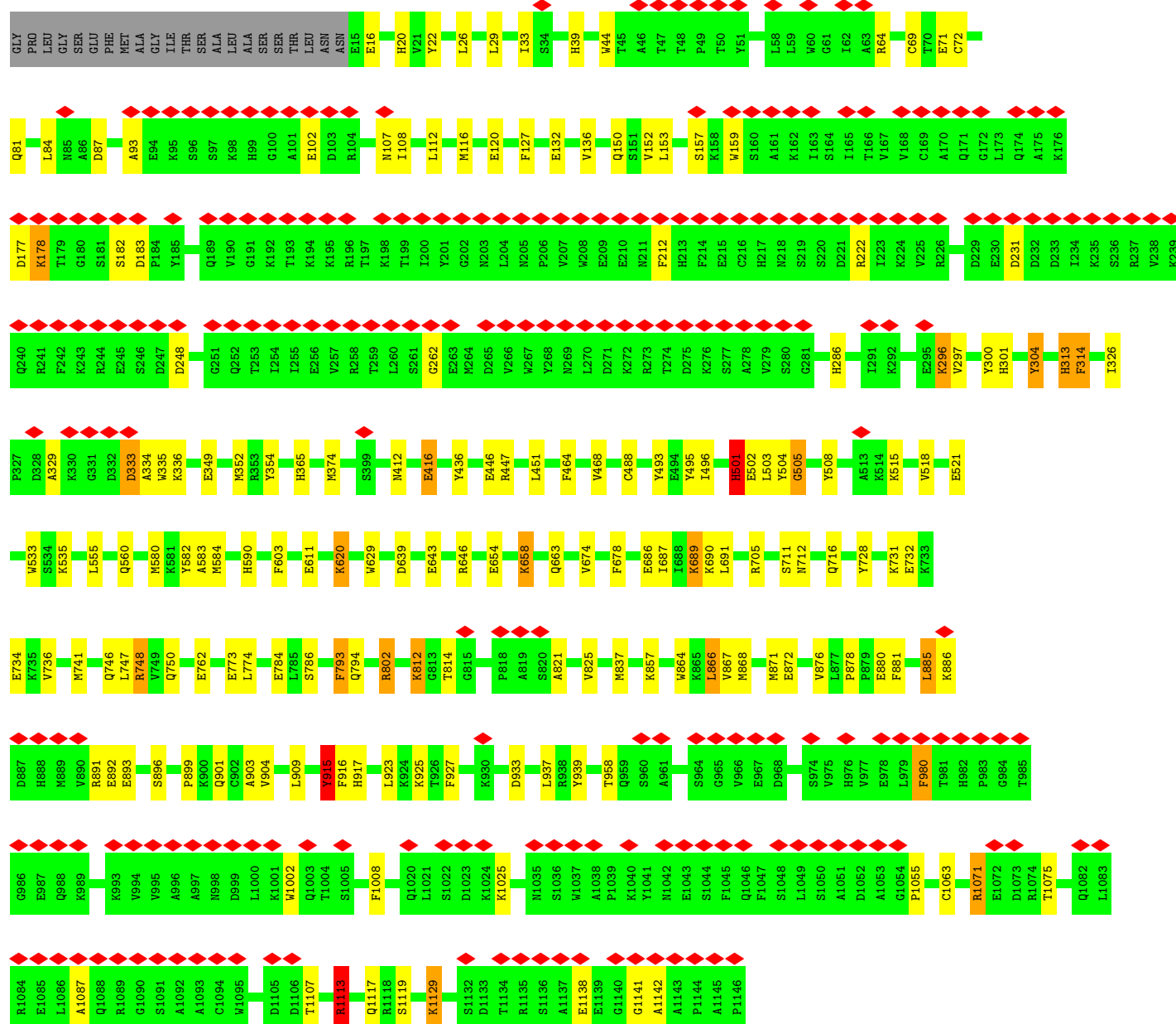
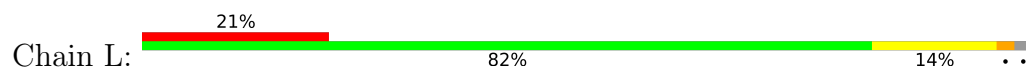


• Molecule 1: Protein unc-13 homolog A

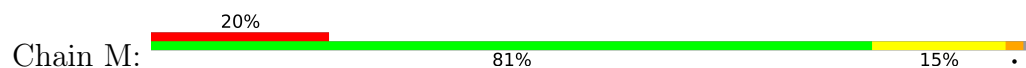


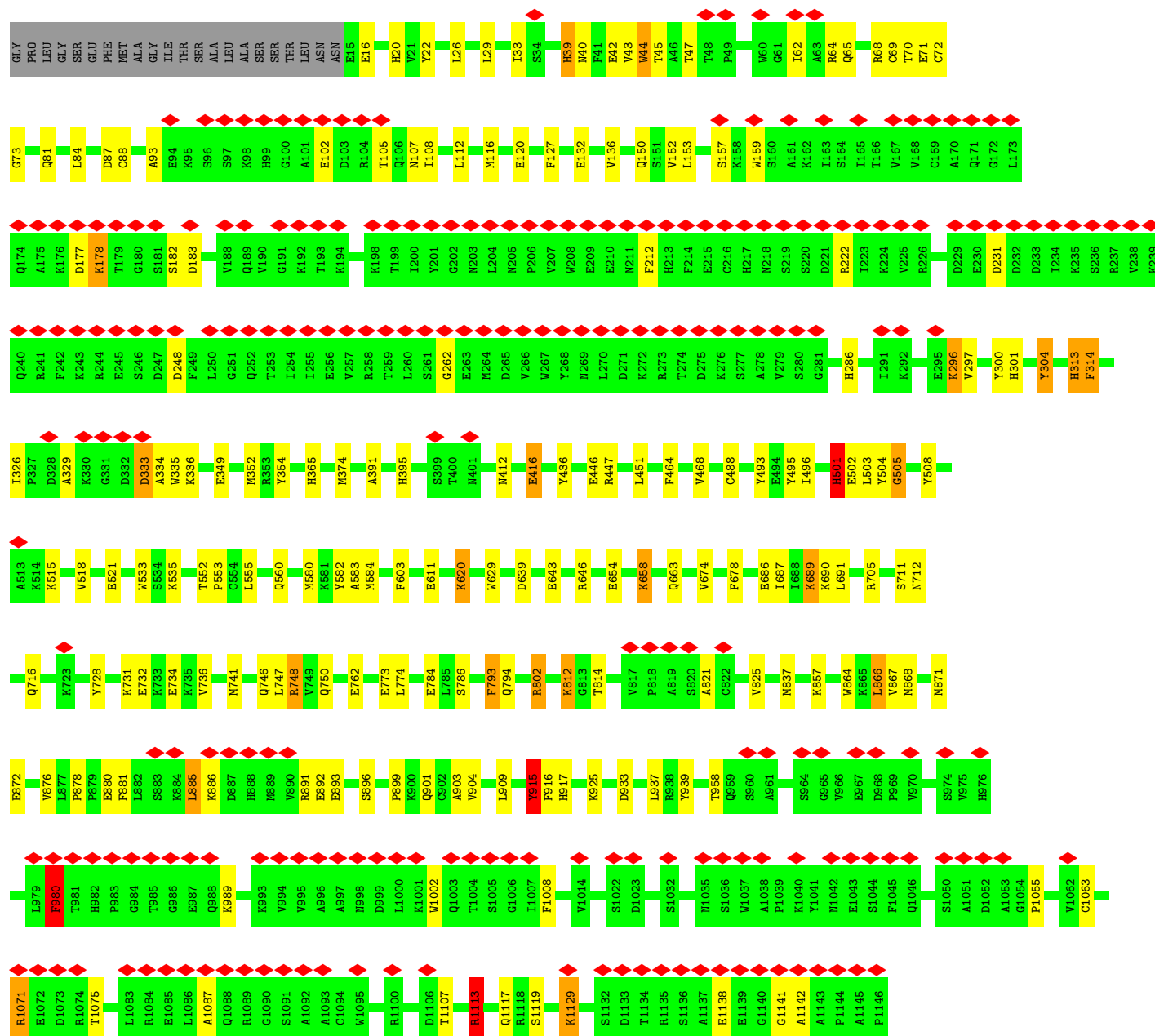


• Molecule 1: Protein unc-13 homolog A

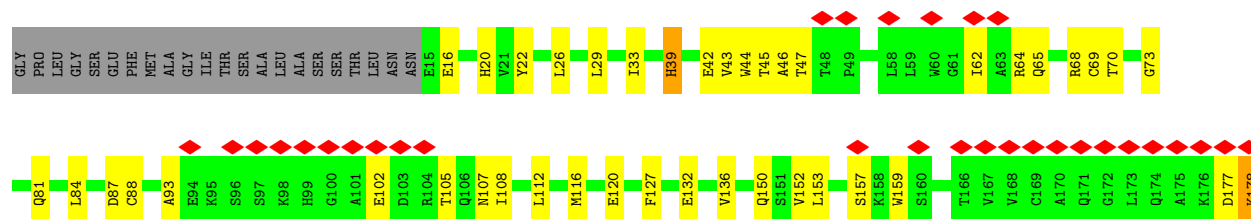
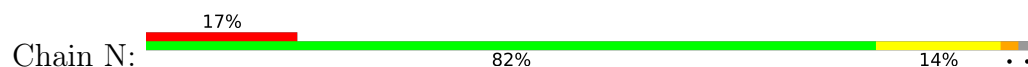


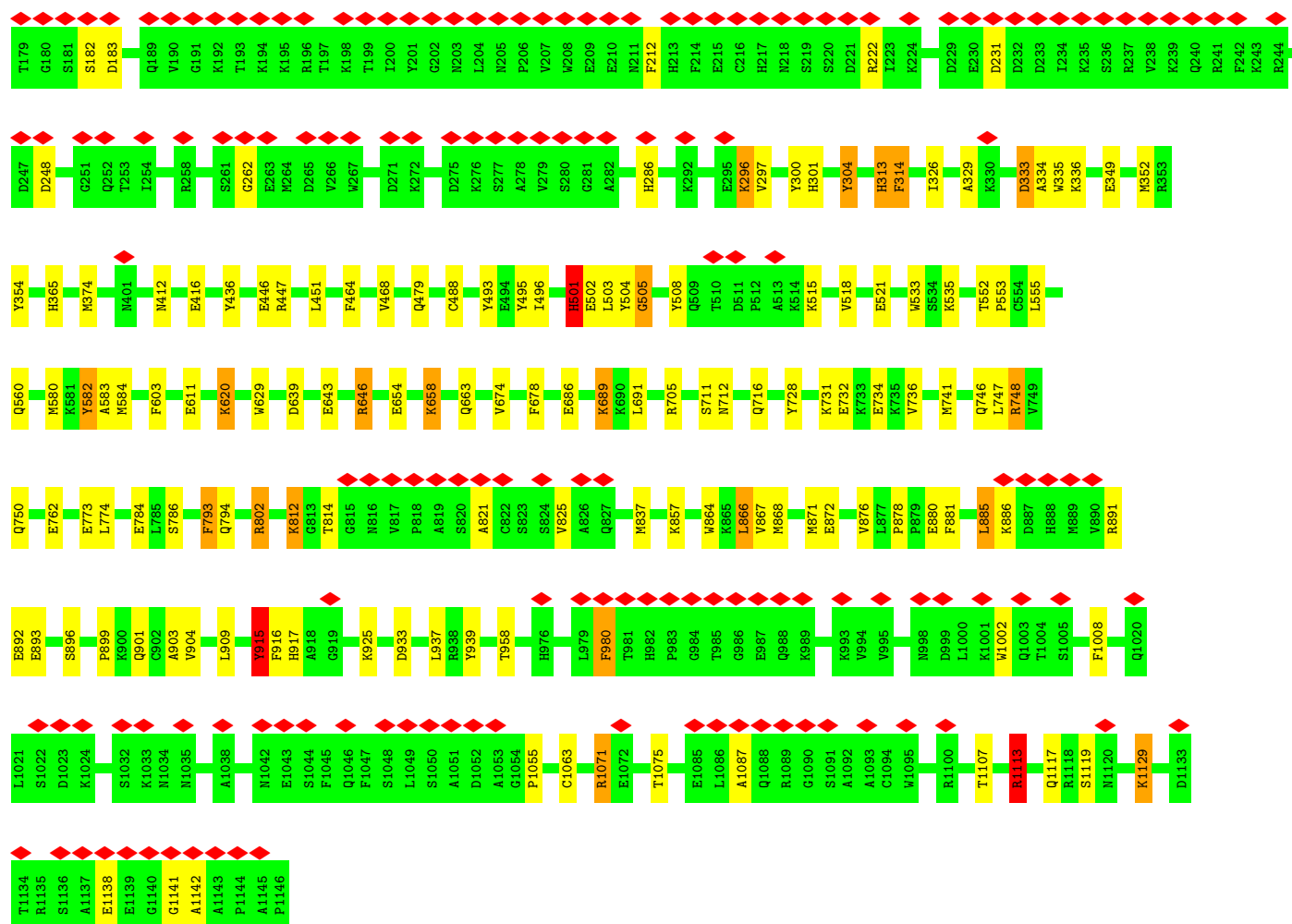
• Molecule 1: Protein unc-13 homolog A



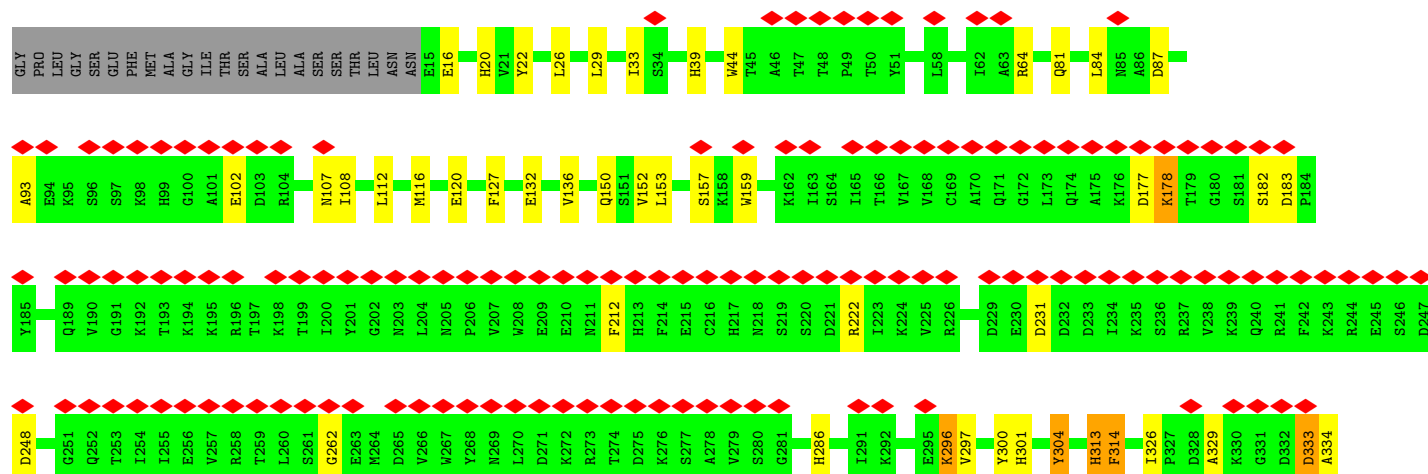
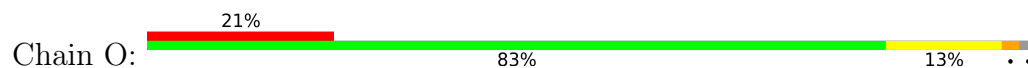


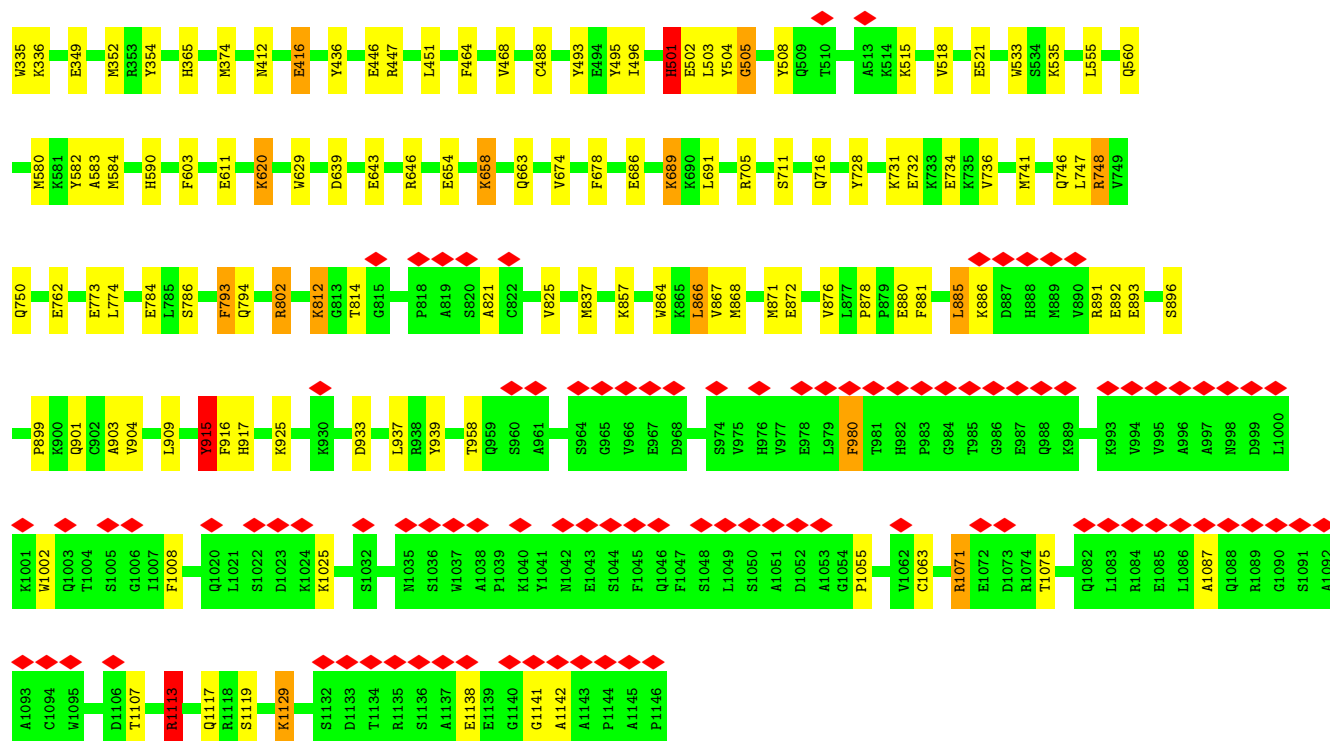
• Molecule 1: Protein unc-13 homolog A



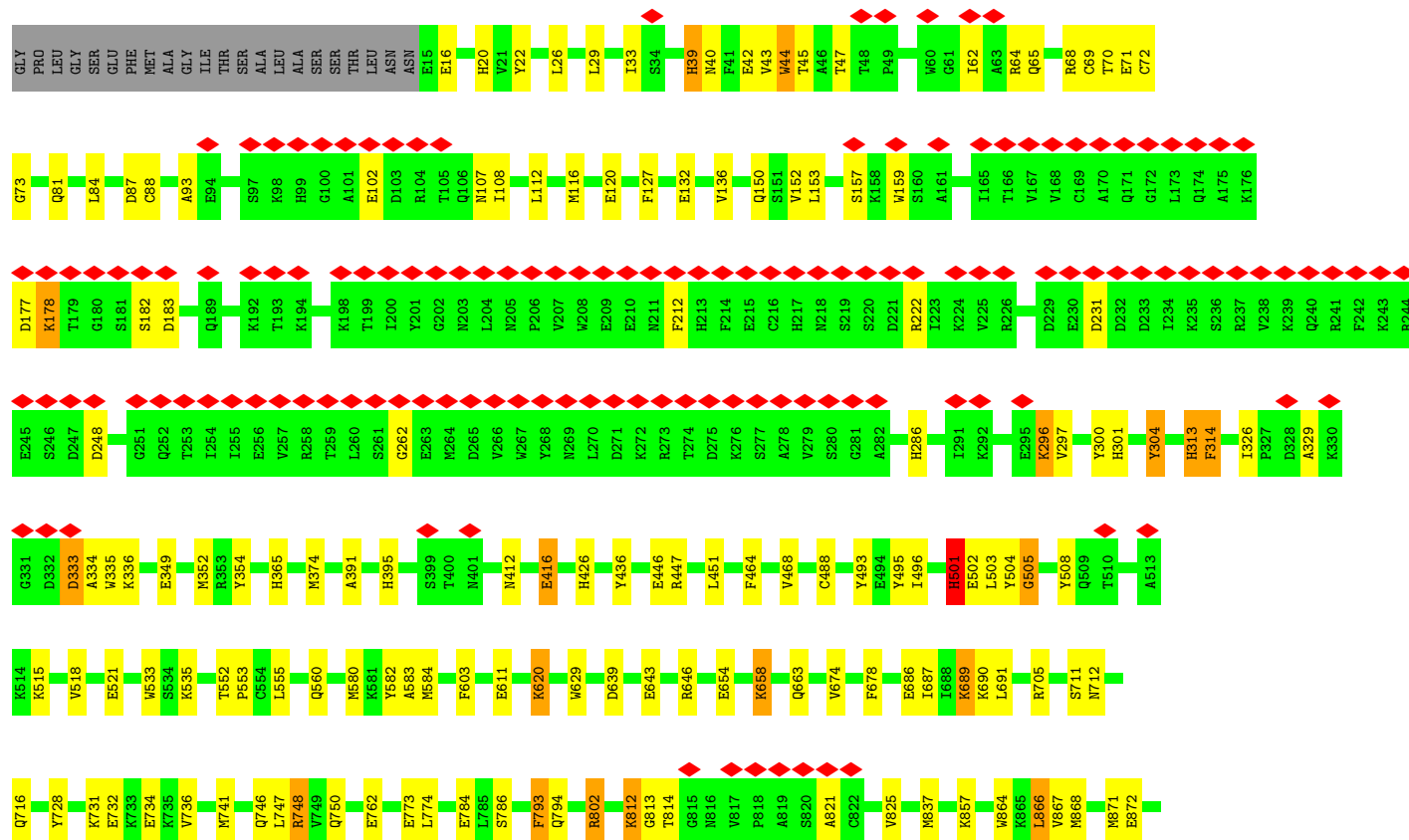
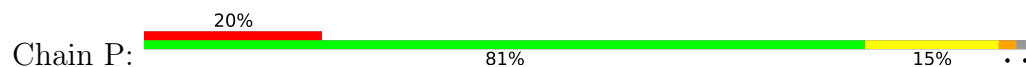


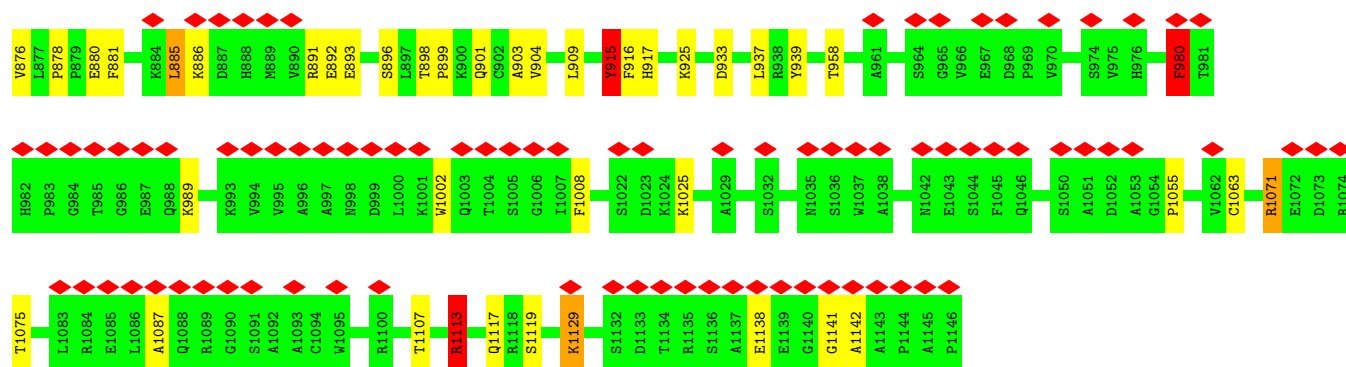
• Molecule 1: Protein unc-13 homolog A



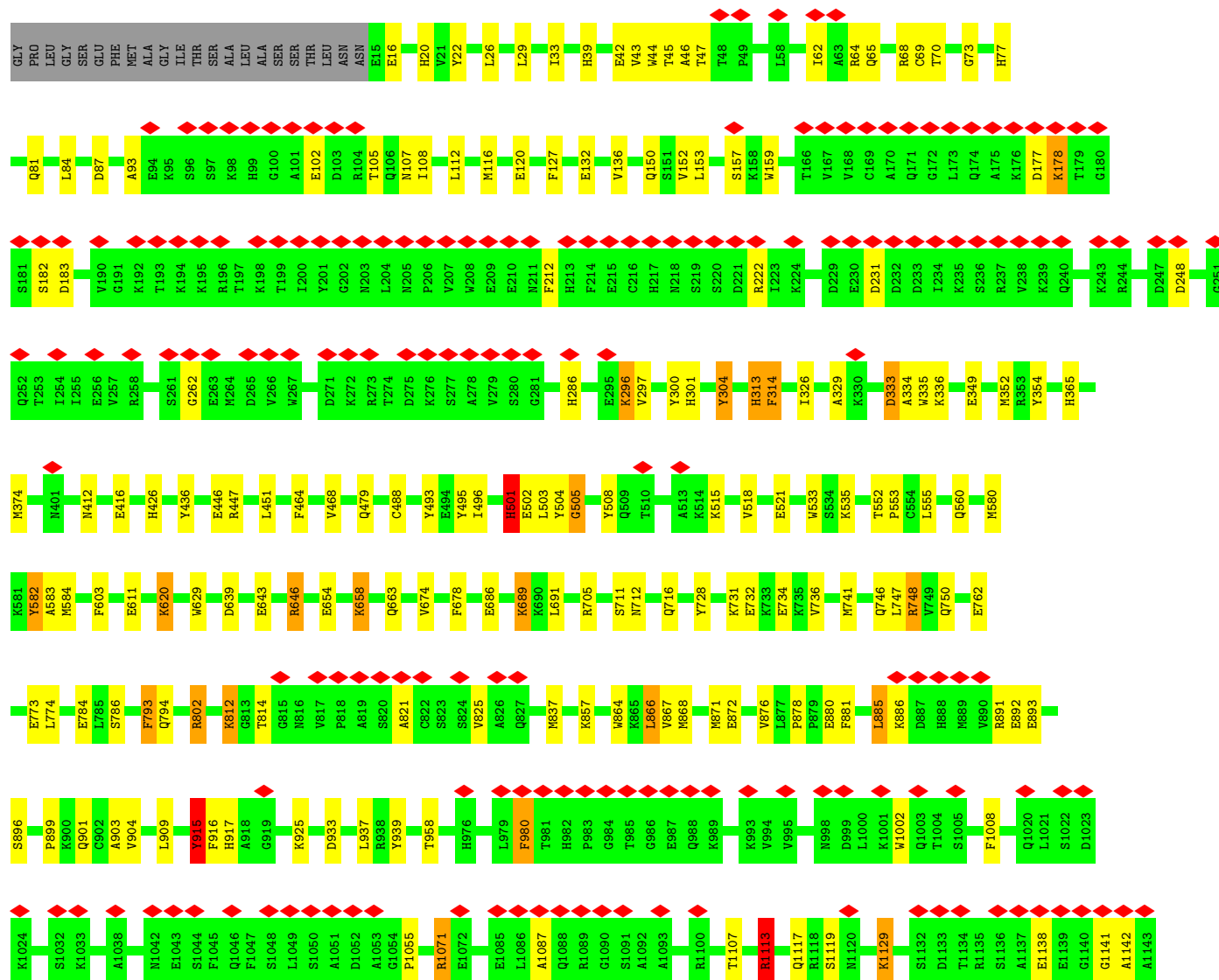
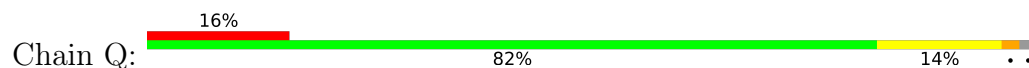


• Molecule 1: Protein unc-13 homolog A



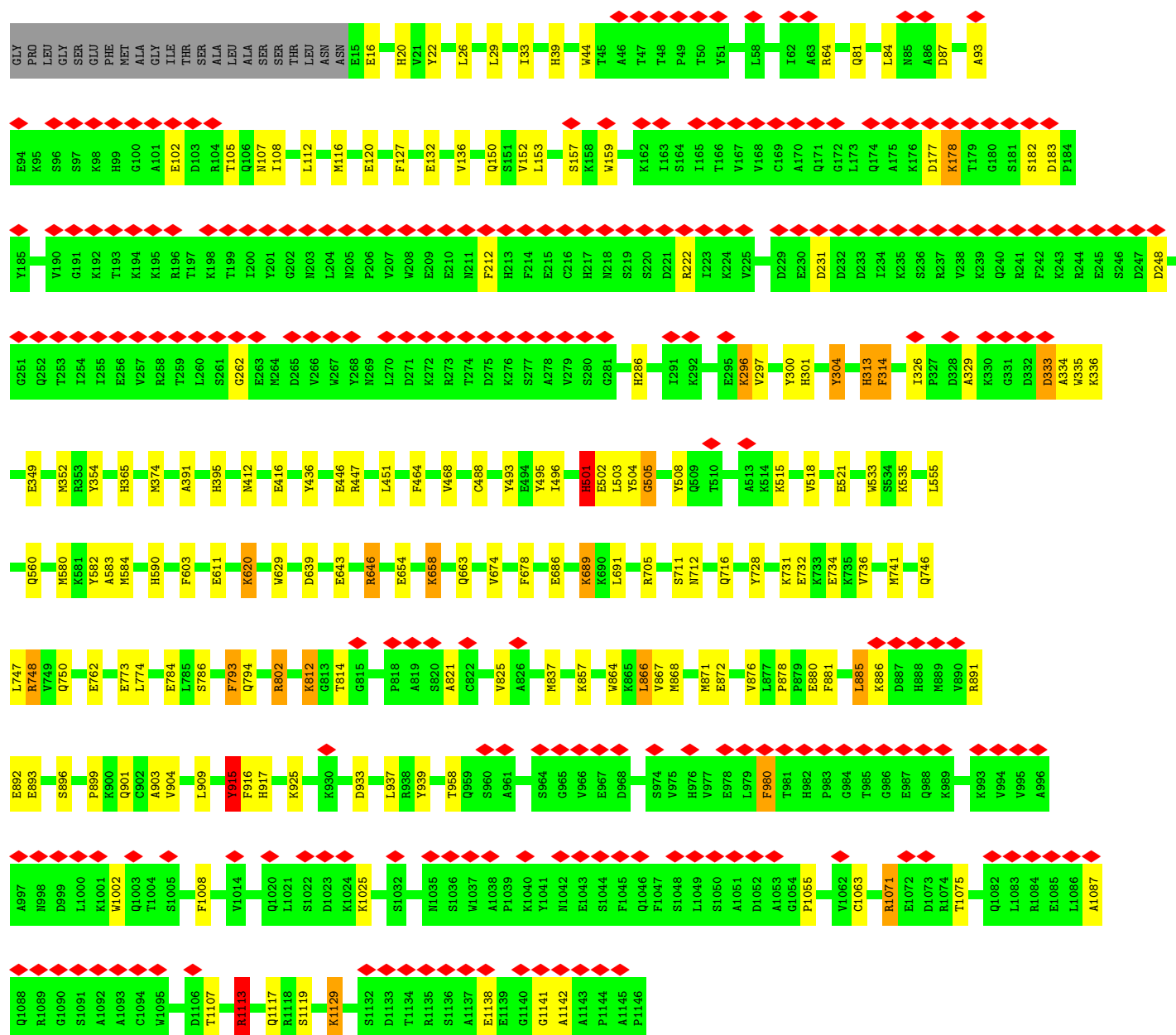
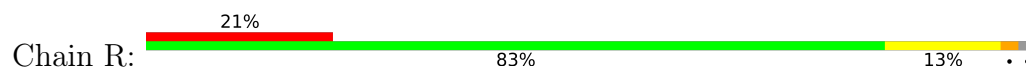


• Molecule 1: Protein unc-13 homolog A

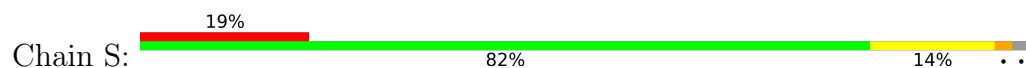


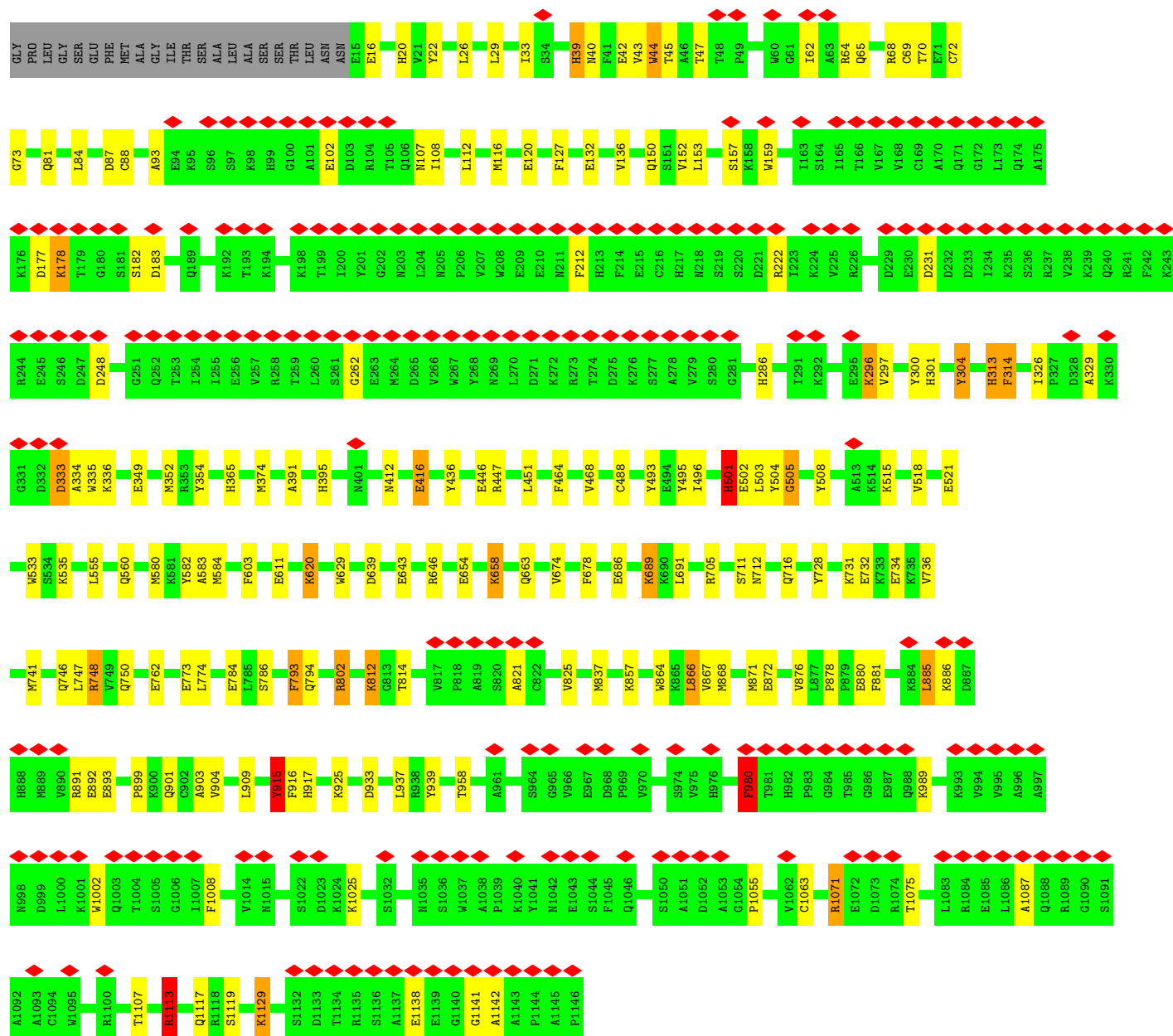


• Molecule 1: Protein unc-13 homolog A

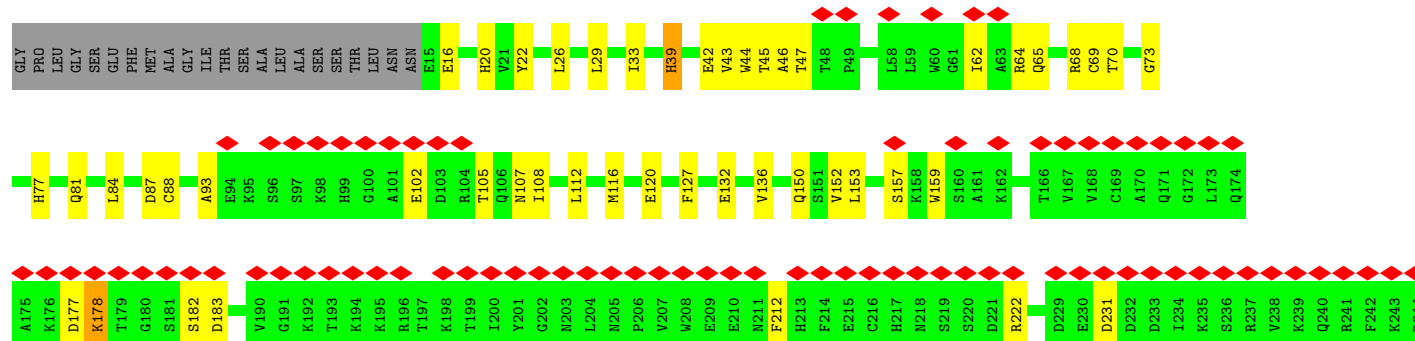
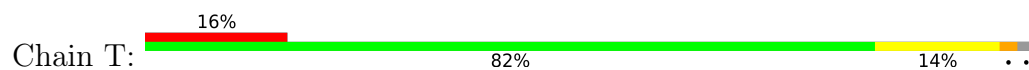


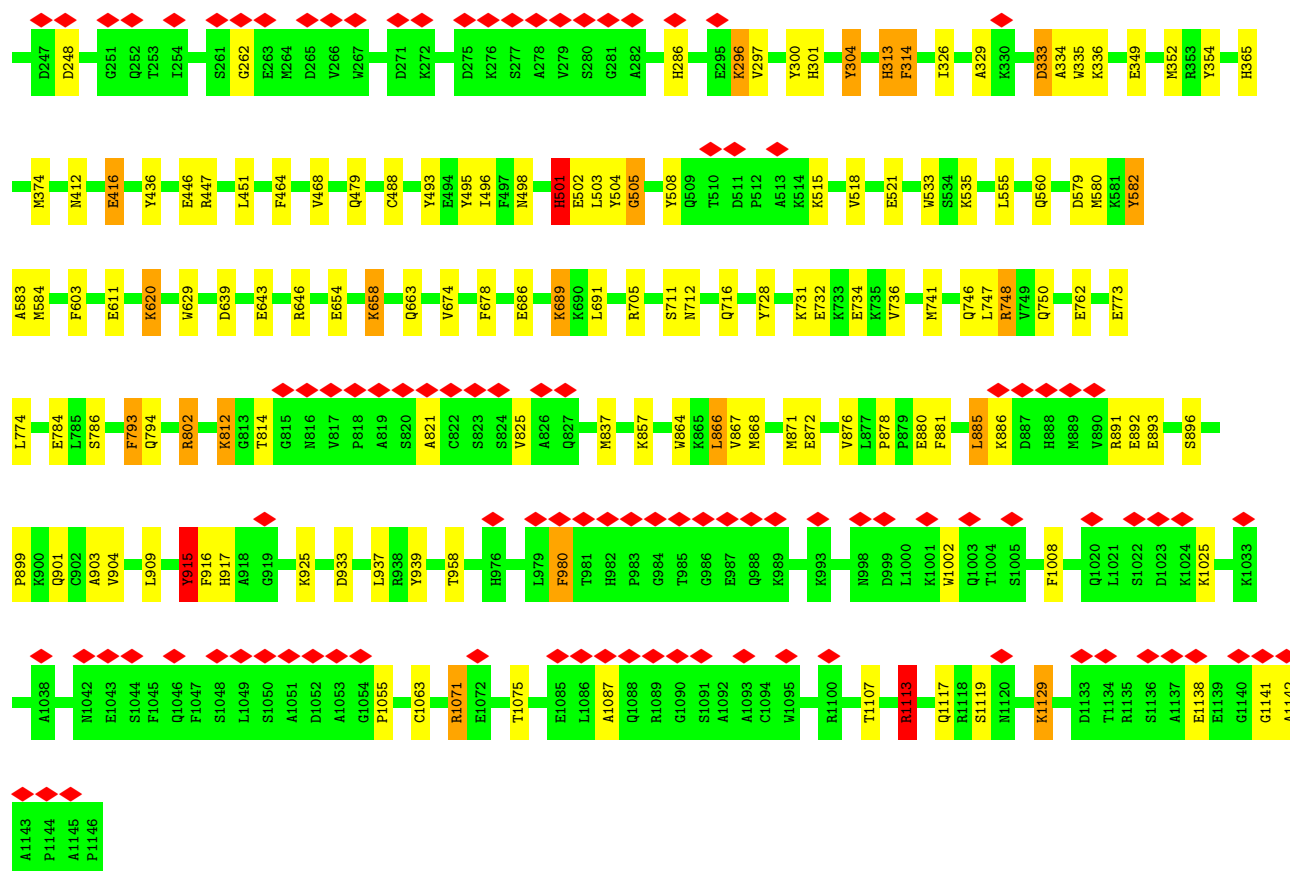
• Molecule 1: Protein unc-13 homolog A



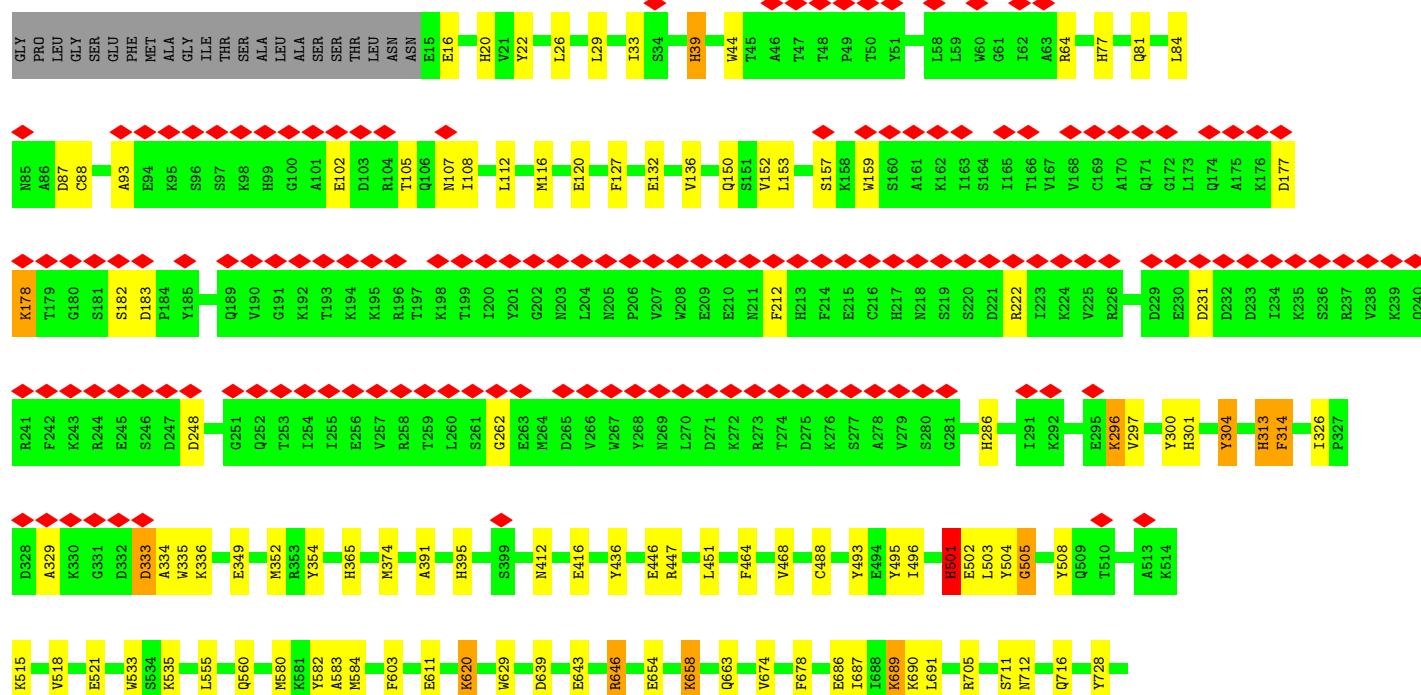
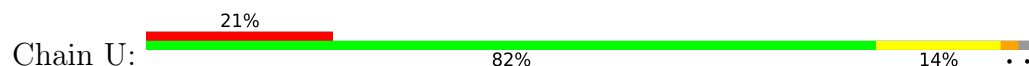


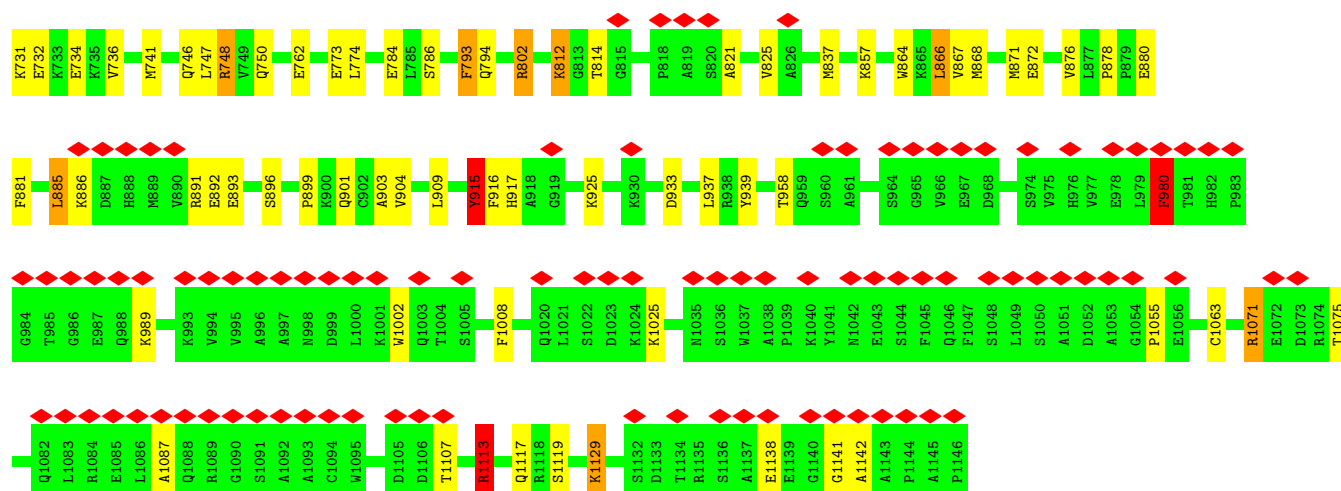
• Molecule 1: Protein unc-13 homolog A



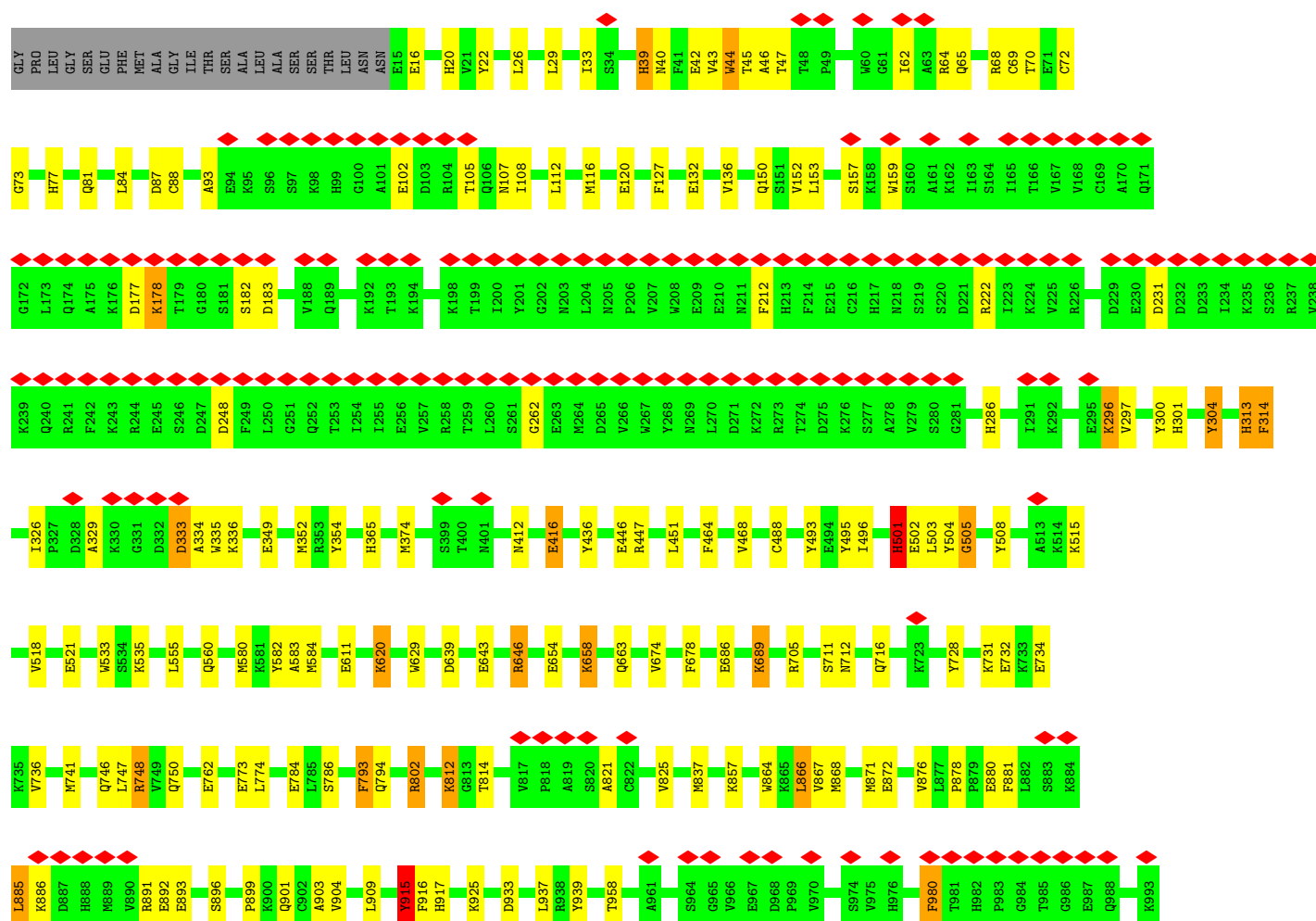
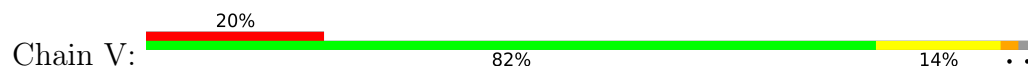


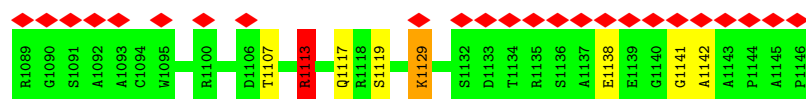
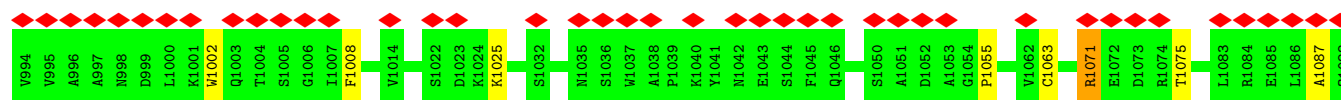
• Molecule 1: Protein unc-13 homolog A



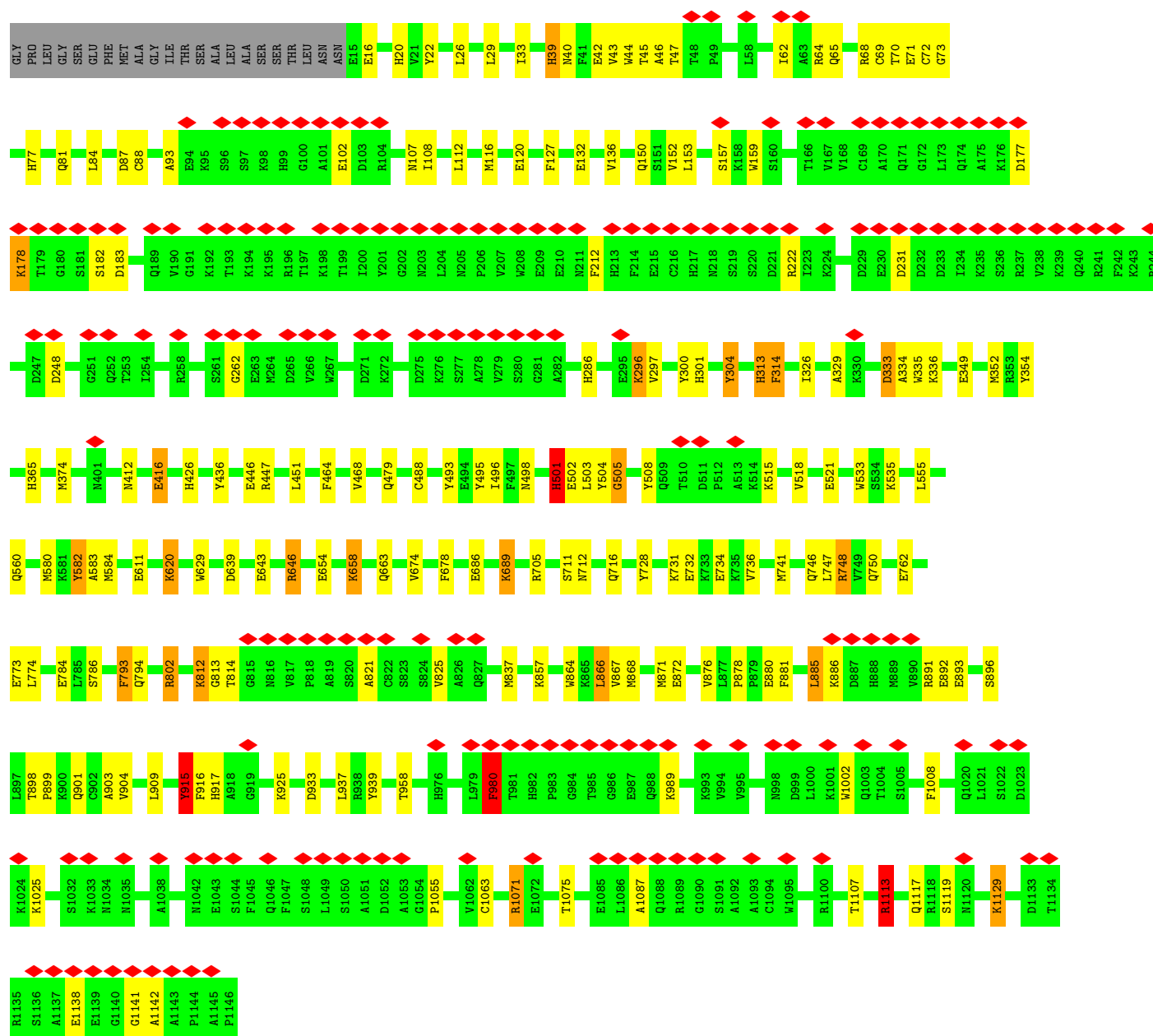
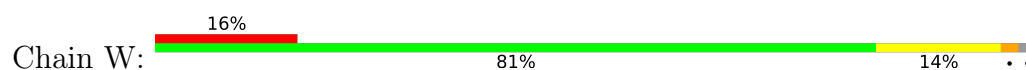


• Molecule 1: Protein unc-13 homolog A

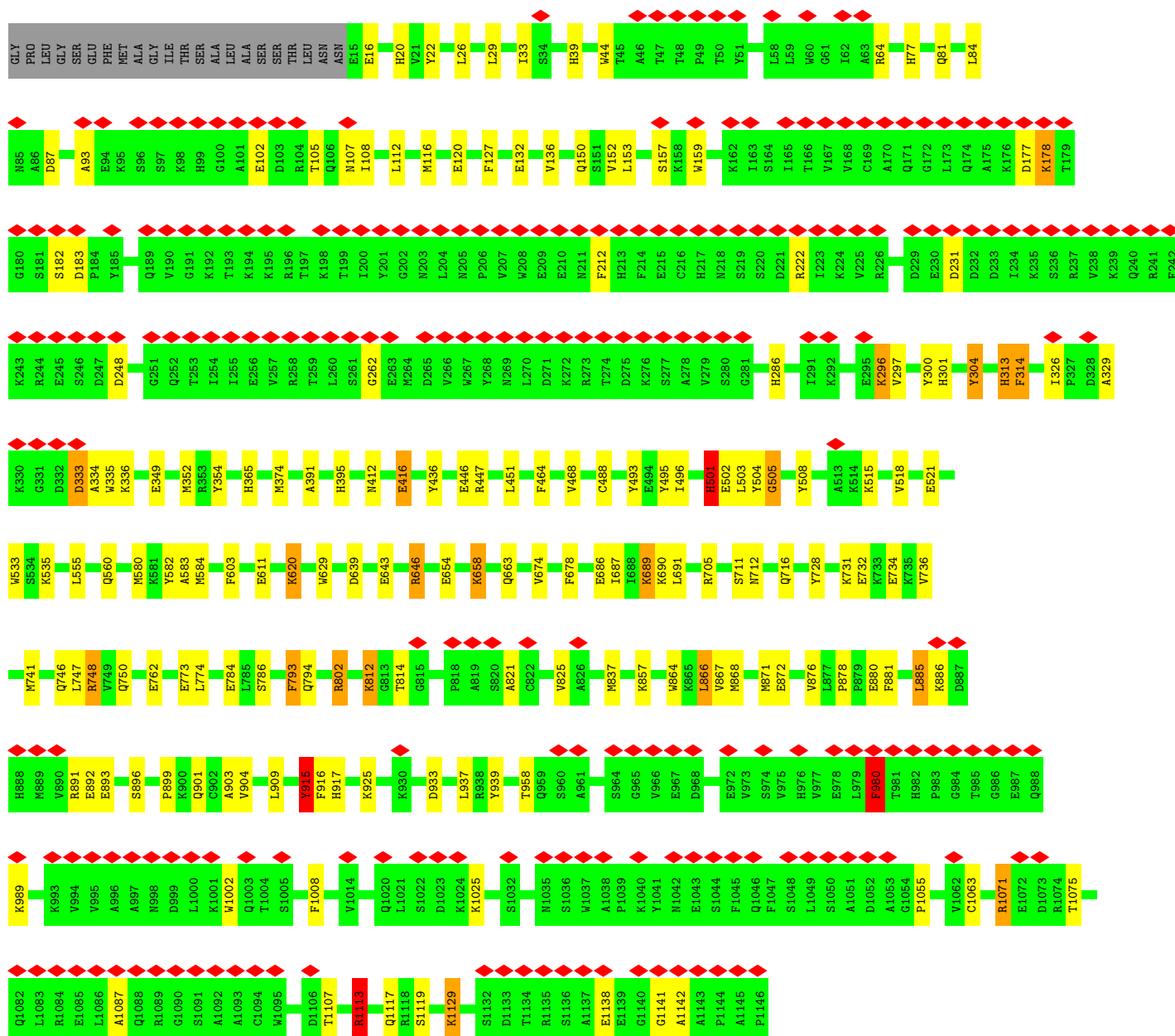
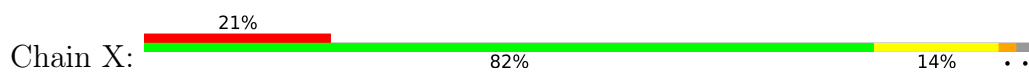




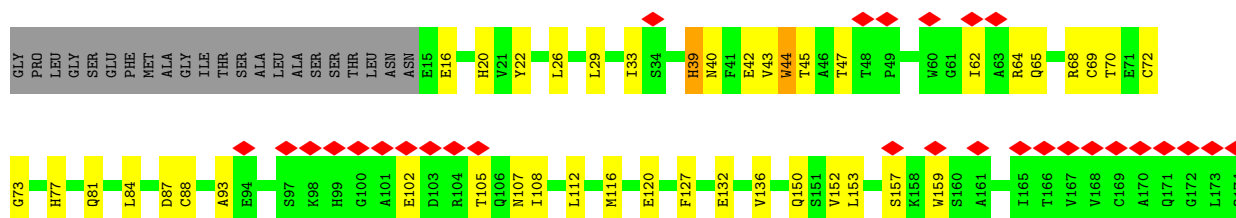
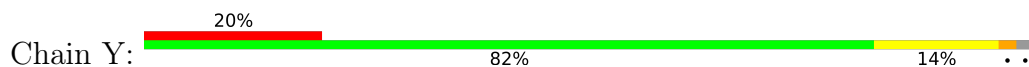
• Molecule 1: Protein unc-13 homolog A

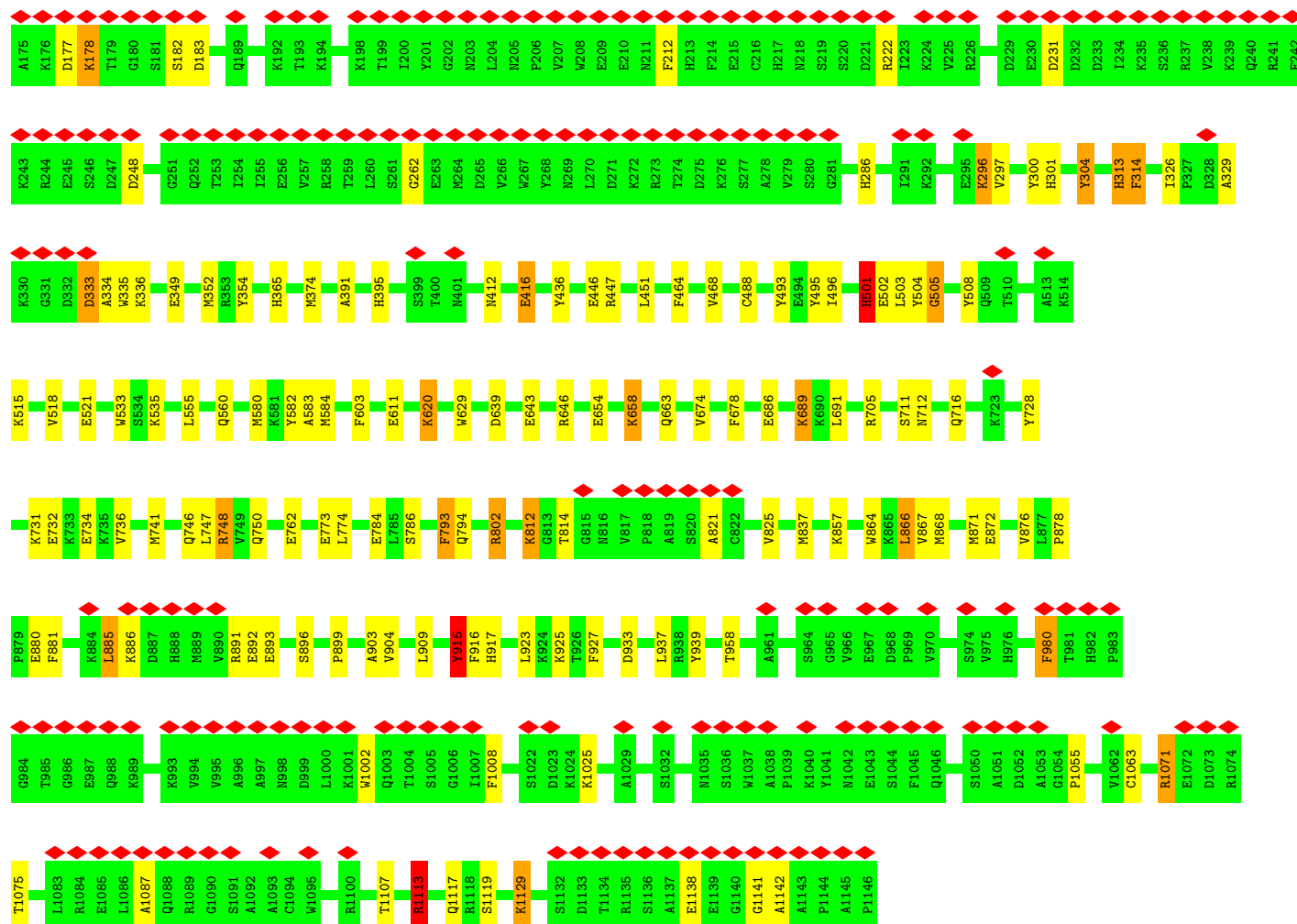


• Molecule 1: Protein unc-13 homolog A



• Molecule 1: Protein unc-13 homolog A





4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of subtomograms used	7	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	110	Depositor
Minimum defocus (nm)	3500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.862	Depositor
Minimum map value	-0.175	Depositor
Average map value	0.030	Depositor
Map value standard deviation	0.076	Depositor
Recommended contour level	0.23	Depositor
Map size ($\text{\AA}$)	680.39996, 680.39996, 680.39996	wwPDB
Map dimensions	324, 324, 324	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.1, 2.1, 2.1	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	A	0.78	0/9220	1.33	18/12466 (0.1%)
1	C	0.78	0/9220	1.33	17/12466 (0.1%)
1	D	0.78	0/9220	1.33	17/12466 (0.1%)
1	E	0.78	0/9220	1.33	17/12466 (0.1%)
1	F	0.78	0/9220	1.33	17/12466 (0.1%)
1	G	0.78	0/9220	1.33	18/12466 (0.1%)
1	H	0.79	0/9220	1.41	16/12466 (0.1%)
1	I	0.79	0/9220	1.41	17/12466 (0.1%)
1	J	0.79	0/9220	1.41	18/12466 (0.1%)
1	K	0.79	0/9220	1.41	16/12466 (0.1%)
1	L	0.79	0/9220	1.41	16/12466 (0.1%)
1	M	0.79	0/9220	1.41	15/12466 (0.1%)
1	N	0.79	0/9220	1.41	16/12466 (0.1%)
1	O	0.79	0/9220	1.41	17/12466 (0.1%)
1	P	0.79	0/9220	1.41	16/12466 (0.1%)
1	Q	0.79	0/9220	1.41	18/12466 (0.1%)
1	R	0.79	0/9220	1.41	17/12466 (0.1%)
1	S	0.79	0/9220	1.41	15/12466 (0.1%)
1	T	0.79	0/9220	1.41	16/12466 (0.1%)
1	U	0.79	0/9220	1.41	17/12466 (0.1%)
1	V	0.79	0/9220	1.41	17/12466 (0.1%)
1	W	0.79	0/9220	1.41	18/12466 (0.1%)
1	X	0.79	0/9220	1.41	17/12466 (0.1%)
1	Y	0.79	0/9220	1.41	16/12466 (0.1%)
All	All	0.79	0/221280	1.39	402/299184 (0.1%)

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	A	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	10
1	D	0	10
1	E	0	10
1	F	0	10
1	G	0	9
1	H	0	14
1	I	0	14
1	J	0	14
1	K	0	14
1	L	0	14
1	M	0	14
1	N	0	14
1	O	0	14
1	P	0	14
1	Q	0	14
1	R	0	14
1	S	0	14
1	T	0	14
1	U	0	14
1	V	0	14
1	W	0	14
1	X	0	14
1	Y	0	14
All	All	0	310

There are no bond length outliers.

The worst 5 of 402 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	W	980	PHE	CA-CB-CG	10.33	124.13	113.80
1	L	980	PHE	CA-CB-CG	10.32	124.12	113.80
1	N	980	PHE	CA-CB-CG	10.29	124.09	113.80
1	R	980	PHE	CA-CB-CG	10.27	124.07	113.80
1	O	980	PHE	CA-CB-CG	10.27	124.07	113.80

There are no chirality outliers.

5 of 310 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	244	ARG	Sidechain
1	A	300	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	A	495	TYR	Sidechain
1	A	582	TYR	Sidechain
1	A	591	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	A	9034	8976	8957	199	0
1	C	9034	8976	8957	191	0
1	D	9034	8976	8960	196	0
1	E	9034	8976	8959	202	0
1	F	9034	8976	8958	201	0
1	G	9034	8976	8958	199	0
1	H	9034	8976	8966	164	0
1	I	9034	8976	8973	66	0
1	J	9034	8976	8967	150	0
1	K	9034	8976	8966	153	0
1	L	9034	8976	8973	66	0
1	M	9034	8976	8967	160	0
1	N	9034	8976	8965	163	0
1	O	9034	8976	8973	64	0
1	P	9034	8976	8967	150	0
1	Q	9034	8976	8966	149	0
1	R	9034	8976	8973	64	0
1	S	9034	8976	8968	147	0
1	T	9034	8976	8966	155	0
1	U	9034	8976	8973	67	0
1	V	9034	8976	8966	163	0
1	W	9034	8976	8966	173	0
1	X	9034	8976	8973	68	0
1	Y	9034	8976	8968	156	0
All	All	216816	215424	215185	2475	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 6.

The worst 5 of 2475 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:E:1003:GLN:HE22	1:F:655:ARG:CD	1.08	1.64
1:A:655:ARG:CD	1:G:1003:GLN:HE22	1.10	1.62
1:A:1003:GLN:HE22	1:C:655:ARG:CD	1.08	1.60
1:C:1003:GLN:HE22	1:D:655:ARG:CD	1.10	1.58
1:C:1003:GLN:CD	1:D:655:ARG:HD3	1.26	1.57

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	A	1130/1154 (98%)	1060 (94%)	60 (5%)	10 (1%)	14	51
1	C	1130/1154 (98%)	1059 (94%)	61 (5%)	10 (1%)	14	51
1	D	1130/1154 (98%)	1060 (94%)	60 (5%)	10 (1%)	14	51
1	E	1130/1154 (98%)	1060 (94%)	60 (5%)	10 (1%)	14	51
1	F	1130/1154 (98%)	1060 (94%)	60 (5%)	10 (1%)	14	51
1	G	1130/1154 (98%)	1060 (94%)	60 (5%)	10 (1%)	14	51
1	H	1130/1154 (98%)	1030 (91%)	85 (8%)	15 (1%)	9	42
1	I	1130/1154 (98%)	1030 (91%)	85 (8%)	15 (1%)	9	42
1	J	1130/1154 (98%)	1030 (91%)	86 (8%)	14 (1%)	10	44
1	K	1130/1154 (98%)	1029 (91%)	87 (8%)	14 (1%)	10	44
1	L	1130/1154 (98%)	1030 (91%)	85 (8%)	15 (1%)	9	42
1	M	1130/1154 (98%)	1030 (91%)	86 (8%)	14 (1%)	10	44
1	N	1130/1154 (98%)	1031 (91%)	85 (8%)	14 (1%)	10	44
1	O	1130/1154 (98%)	1030 (91%)	85 (8%)	15 (1%)	9	42
1	P	1130/1154 (98%)	1030 (91%)	85 (8%)	15 (1%)	9	42
1	Q	1130/1154 (98%)	1029 (91%)	87 (8%)	14 (1%)	10	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	1130/1154 (98%)	1030 (91%)	85 (8%)	15 (1%)	9	42
1	S	1130/1154 (98%)	1030 (91%)	86 (8%)	14 (1%)	10	44
1	T	1130/1154 (98%)	1030 (91%)	85 (8%)	15 (1%)	9	42
1	U	1130/1154 (98%)	1031 (91%)	84 (7%)	15 (1%)	9	42
1	V	1130/1154 (98%)	1030 (91%)	85 (8%)	15 (1%)	9	42
1	W	1130/1154 (98%)	1031 (91%)	84 (7%)	15 (1%)	9	42
1	X	1130/1154 (98%)	1029 (91%)	86 (8%)	15 (1%)	9	42
1	Y	1130/1154 (98%)	1030 (91%)	85 (8%)	15 (1%)	9	42
All	All	27120/27696 (98%)	24899 (92%)	1897 (7%)	324 (1%)	13	44

5 of 324 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	894	ALA
1	C	894	ALA
1	D	894	ALA
1	E	894	ALA
1	F	894	ALA

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	A	1006/1022 (98%)	971 (96%)	35 (4%)	32	53
1	C	1006/1022 (98%)	971 (96%)	35 (4%)	32	53
1	D	1006/1022 (98%)	971 (96%)	35 (4%)	32	53
1	E	1006/1022 (98%)	971 (96%)	35 (4%)	32	53
1	F	1006/1022 (98%)	971 (96%)	35 (4%)	32	53
1	G	1006/1022 (98%)	971 (96%)	35 (4%)	32	53
1	H	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	I	1006/1022 (98%)	947 (94%)	59 (6%)	18	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	K	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	L	1006/1022 (98%)	947 (94%)	59 (6%)	18	39
1	M	1006/1022 (98%)	947 (94%)	59 (6%)	18	39
1	N	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	O	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	P	1006/1022 (98%)	947 (94%)	59 (6%)	18	39
1	Q	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	R	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	S	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	T	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	U	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	V	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	W	1006/1022 (98%)	947 (94%)	59 (6%)	18	39
1	X	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
1	Y	1006/1022 (98%)	948 (94%)	58 (6%)	18	40
All	All	24144/24528 (98%)	22885 (95%)	1259 (5%)	22	42

5 of 1259 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	T	248	ASP
1	X	44	TRP
1	T	773	GLU
1	T	222	ARG
1	V	178	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 487 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	680	GLN
1	X	65	GLN
1	Q	77	HIS
1	W	810	GLN
1	Y	269	ASN

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.

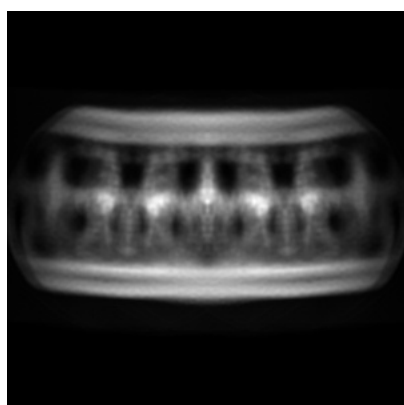
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25741. These allow visual inspection of the internal detail of the map and identification of artifacts.

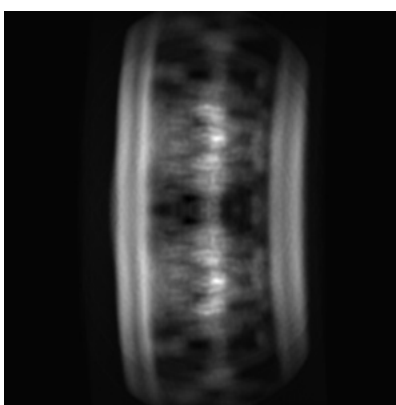
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

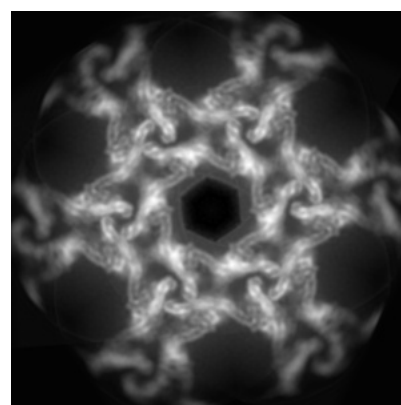
6.1.1 Primary map



X



Y

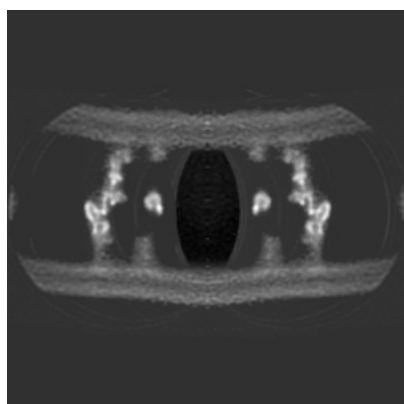


Z

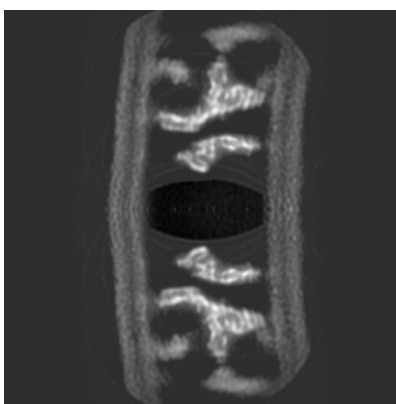
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

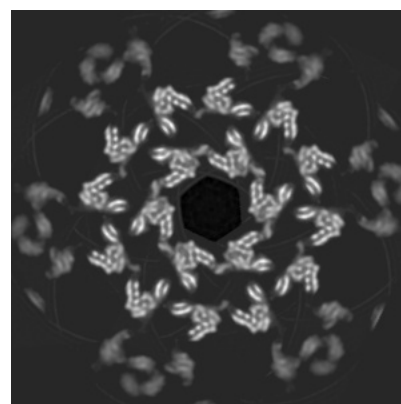
6.2.1 Primary map



X Index: 162



Y Index: 162

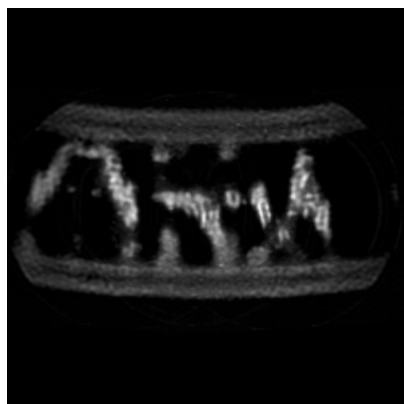


Z Index: 162

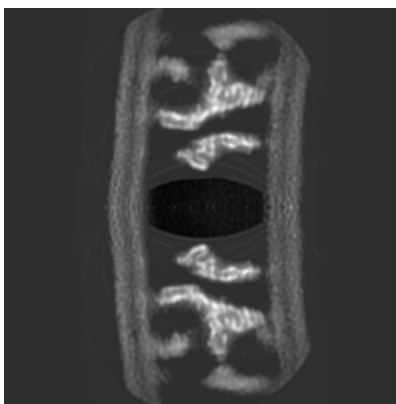
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

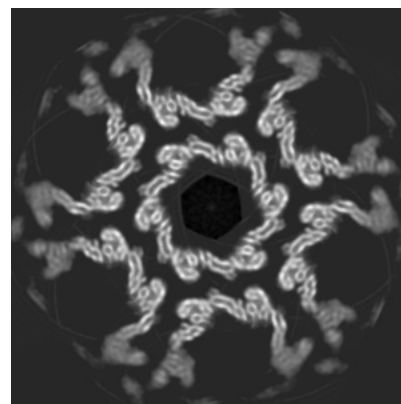
6.3.1 Primary map



X Index: 121



Y Index: 162

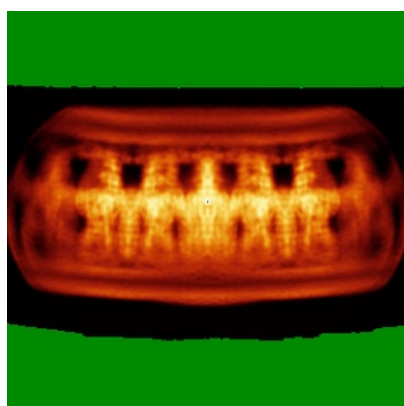


Z Index: 170

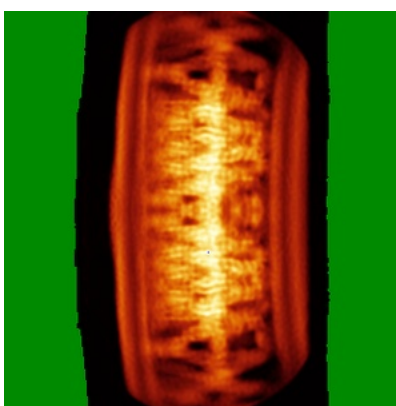
The images above show the largest variance slices of the map in three orthogonal directions.

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

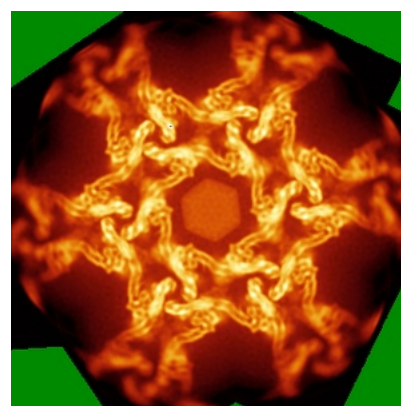
6.4.1 Primary map



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 [i](#)

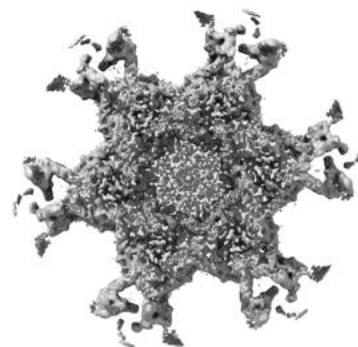
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.23. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

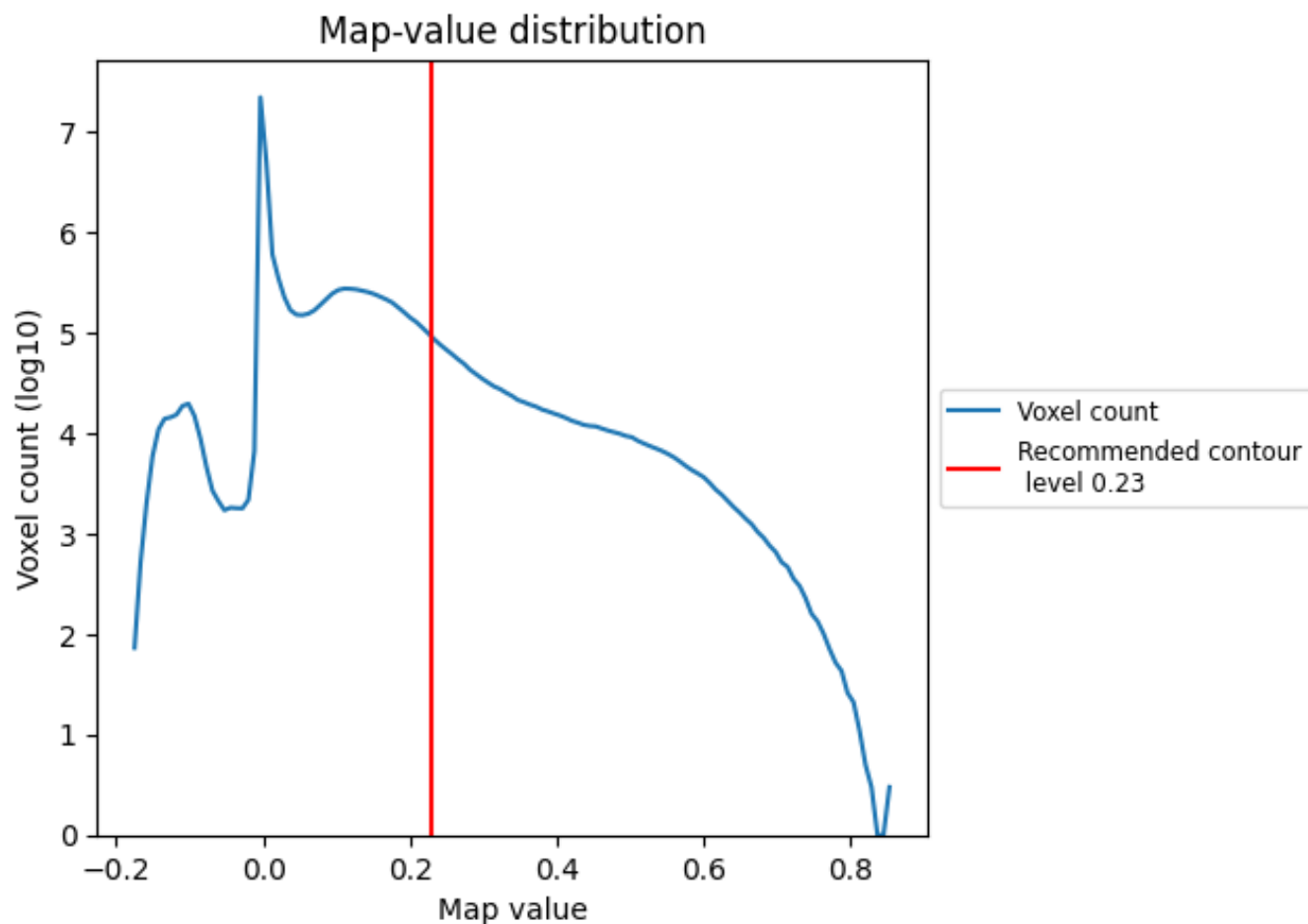
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

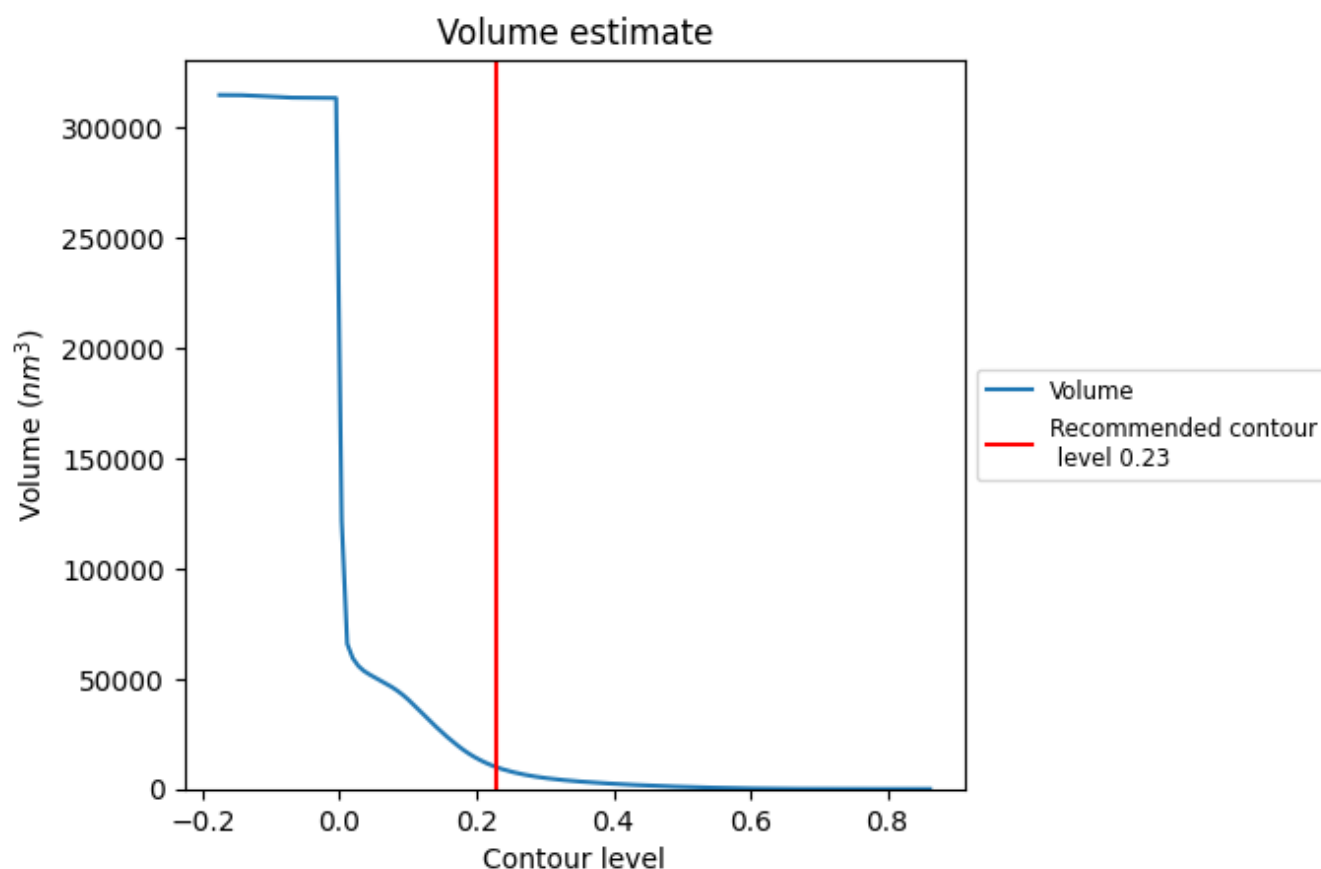
This section contains the results of statistical analysis of the map.

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.

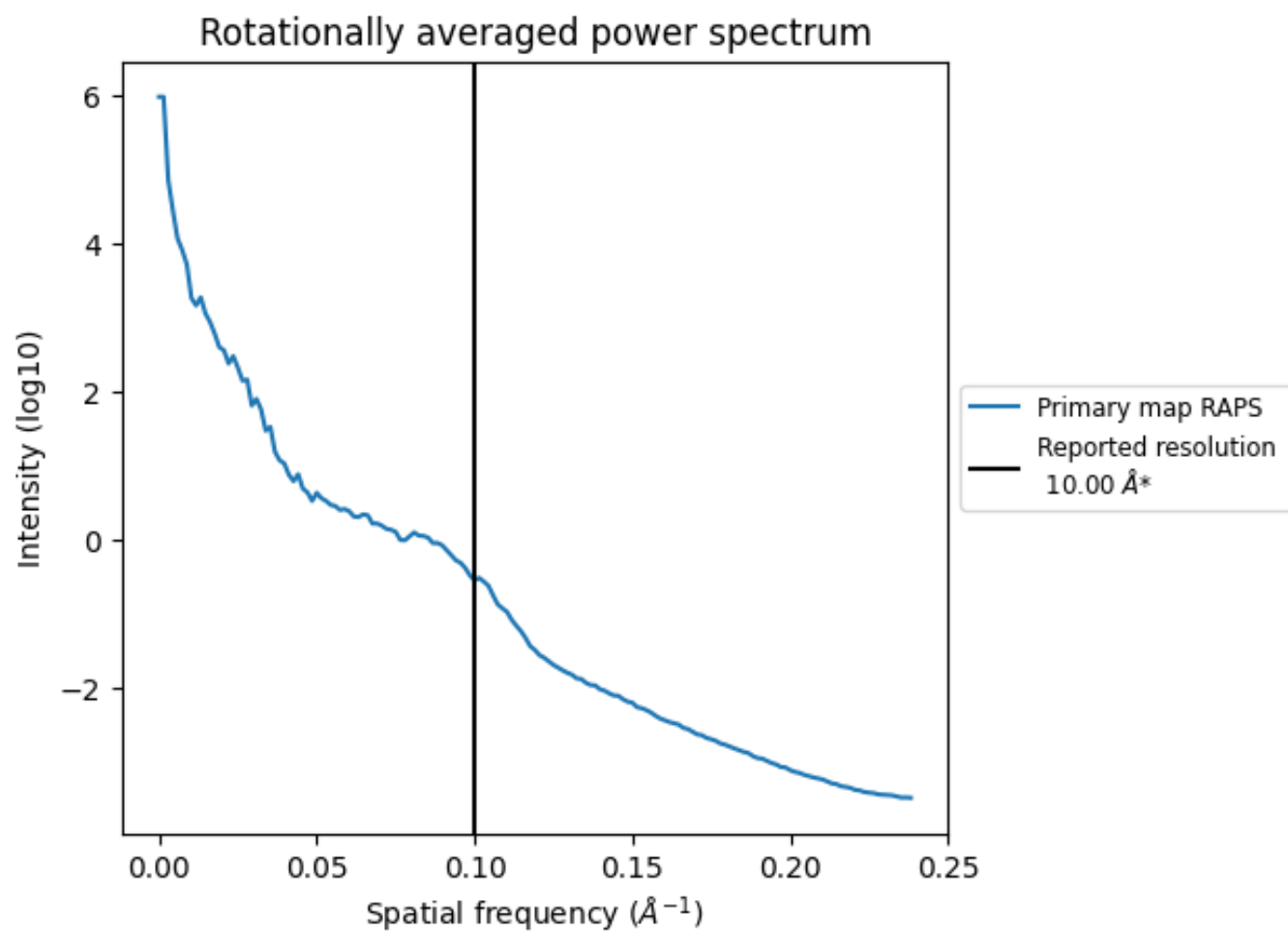
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 9801 nm^3 ; this corresponds to an approximate mass of 8853 kDa.

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 0.100 Å⁻¹

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

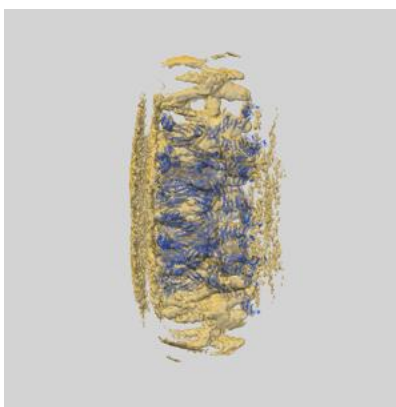
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25741 and PDB model 7T81. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

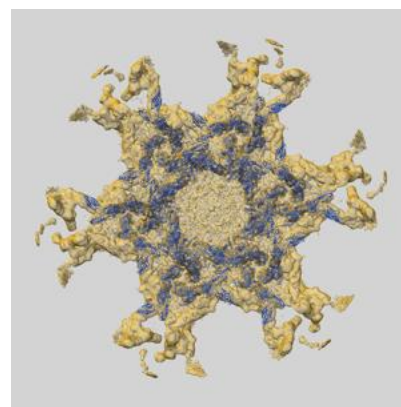
9.1 Map-model overlay [i](#)



X



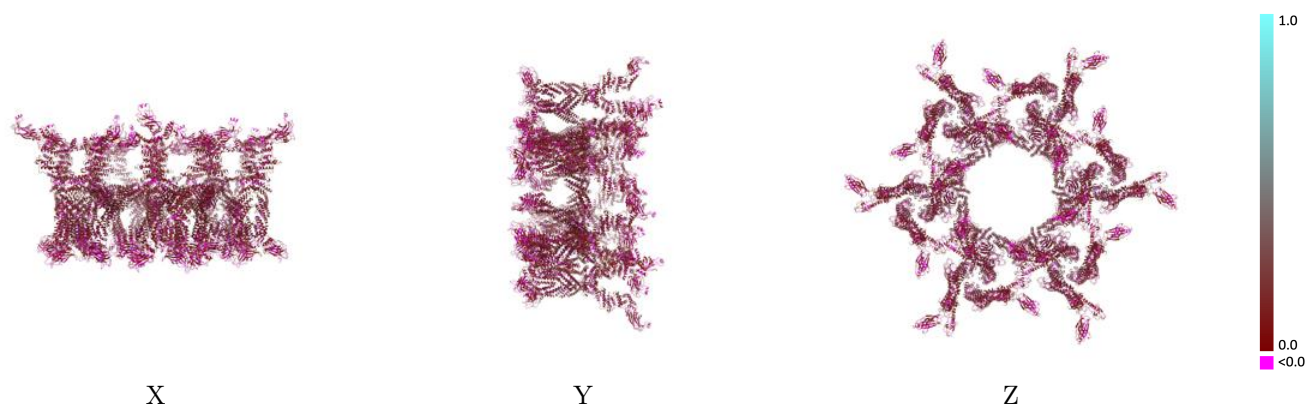
Y



Z

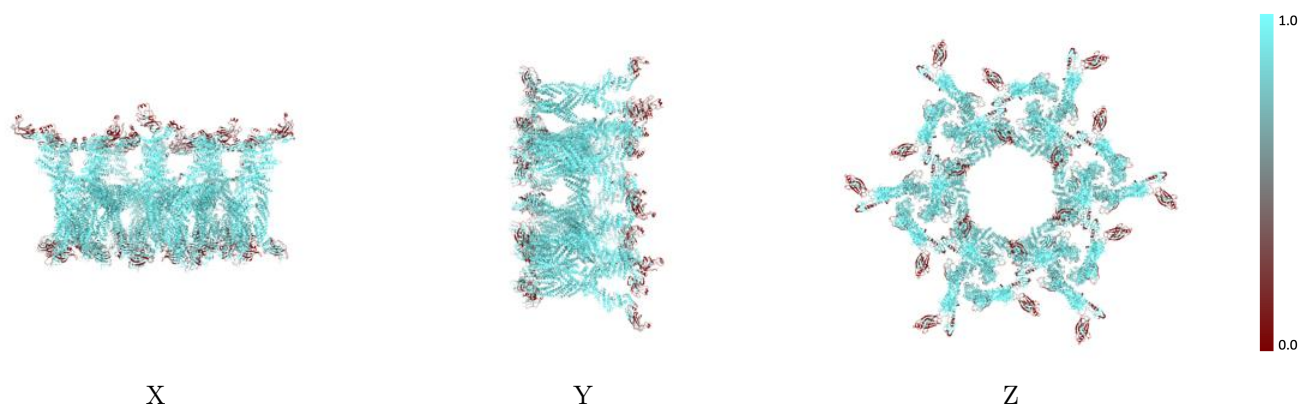
The images above show the 3D surface view of the map at the recommended contour level 0.23 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



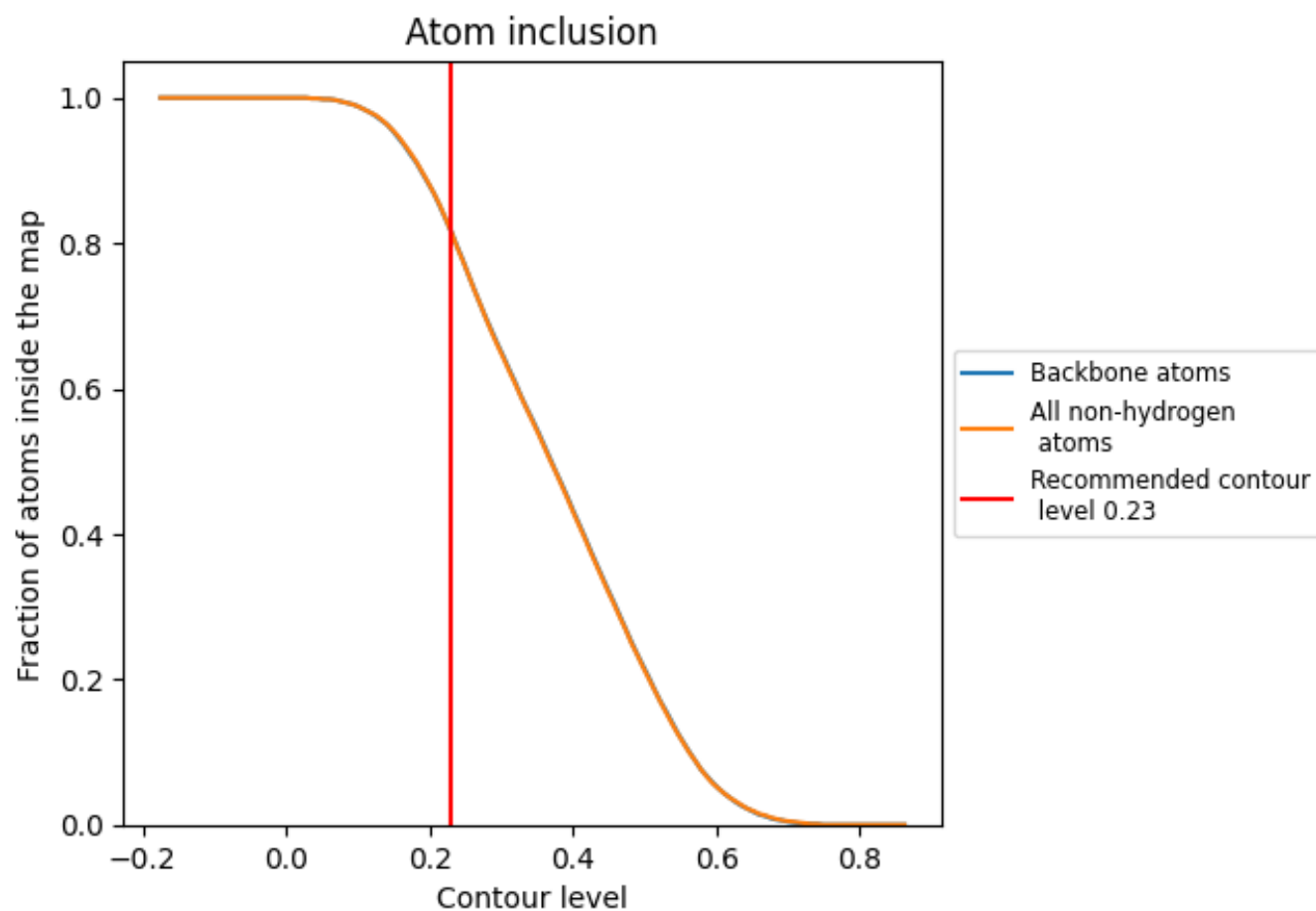
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.23).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 82% 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 (0.23) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8160	 0.1110
A	 0.9120	 0.1120
C	 0.9110	 0.1120
D	 0.9110	 0.1120
E	 0.9100	 0.1120
F	 0.9100	 0.1120
G	 0.9110	 0.1120
H	 0.8110	 0.1100
I	 0.7630	 0.1120
J	 0.7710	 0.1090
K	 0.8130	 0.1100
L	 0.7610	 0.1100
M	 0.7690	 0.1100
N	 0.8110	 0.1110
O	 0.7640	 0.1110
P	 0.7750	 0.1100
Q	 0.8180	 0.1090
R	 0.7700	 0.1110
S	 0.7790	 0.1100
T	 0.8140	 0.1090
U	 0.7590	 0.1090
V	 0.7690	 0.1100
W	 0.8110	 0.1100
X	 0.7650	 0.1100
Y	 0.7720	 0.1100

