



wwPDB EM Validation Summary Report ⓘ

Apr 18, 2026 – 09:03 am BST

PDB ID : 9SWA / pdb_00009swa
EMDB ID : EMD-55303
Title : Adenovirus dodecahedron
Authors : Kabasakal, B.V.; Buzas, D.; Bufton, J.; Berger-Schaffitzel, C.; Berger, I.
Deposited on : 2025-10-04
Resolution : 2.20 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:

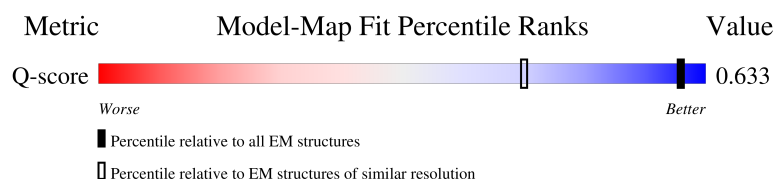
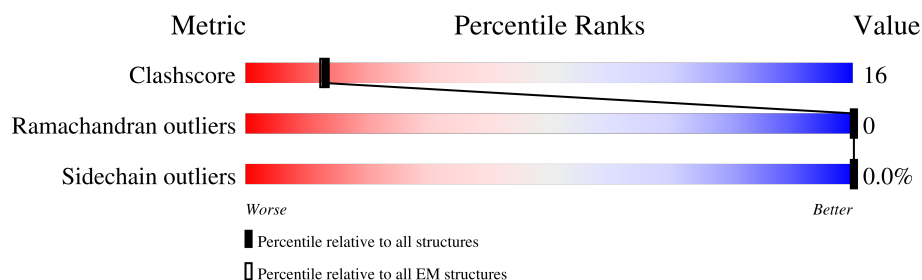
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.20 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	3184 (1.71 - 2.70)

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	1	543	80% 64% 15% • 20%
1	2	543	80% 63% 16% • 20%
1	3	543	80% 64% 15% • 20%
1	4	543	80% 63% 16% • 20%

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Mol	Chain	Length	Quality of chain
1	5	543	
1	6	543	
1	7	543	
1	8	543	
1	9	543	
1	A	543	
1	B	543	
1	C	543	
1	D	543	
1	E	543	
1	F	543	
1	G	543	
1	H	543	
1	I	543	
1	J	543	
1	K	543	
1	L	543	
1	M	543	
1	N	543	
1	O	543	
1	P	543	
1	Q	543	
1	R	543	
1	S	543	
1	T	543	

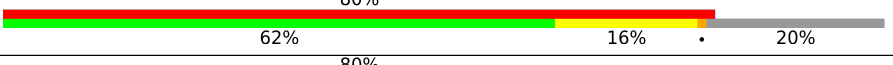
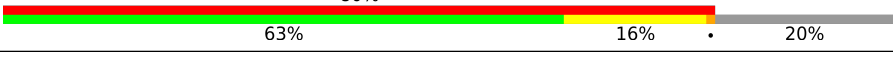
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Mol	Chain	Length	Quality of chain
1	V	543	
1	W	543	
1	X	543	
1	Y	543	
1	Z	543	
1	a	543	
1	b	543	
1	c	543	
1	d	543	
1	e	543	
1	f	543	
1	g	543	
1	h	543	
1	i	543	
1	j	543	
1	k	543	
1	l	543	
1	m	543	
1	n	543	
1	o	543	
1	p	543	
1	q	543	
1	r	543	
1	s	543	
1	t	543	

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Mol	Chain	Length	Quality of chain
1	u	543	 80% 63% 16% • 20%
1	v	543	 80% 63% 16% • 20%
1	w	543	 80% 63% 16% • 20%
1	x	543	 80% 64% 15% • 20%
1	y	543	 80% 62% 16% • 20%
1	z	543	 80% 63% 16% • 20%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 210432 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 Penton protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	2	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	3	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	4	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	5	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	6	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	7	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	8	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	9	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	A	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	B	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	C	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	D	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	E	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	F	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	G	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	H	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	I	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	J	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	K	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	L	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	M	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	N	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	O	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	P	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	Q	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	R	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	S	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	T	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	V	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	W	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	X	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	Y	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	Z	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	a	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	b	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	c	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	d	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	e	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	f	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	g	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	h	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	i	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	j	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	k	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	l	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	m	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	n	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	o	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	p	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	q	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	r	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	s	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	t	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	u	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	v	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	w	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	x	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		
1	y	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	z	435	Total	C	N	O	S	1	0
			3507	2217	604	673	13		

There are 720 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	57	SER	ALA	conflict	UNP G9G849
1	153	GLU	-	insertion	UNP G9G849
1	154	PHE	-	insertion	UNP G9G849
1	161	PRO	-	insertion	UNP G9G849
1	162	GLY	-	insertion	UNP G9G849
1	310	ARG	-	insertion	UNP G9G849
1	322	ASP	-	insertion	UNP G9G849
1	323	VAL	-	insertion	UNP G9G849
1	334	GLU	-	insertion	UNP G9G849
1	335	LEU	-	insertion	UNP G9G849
1	347	SER	-	insertion	UNP G9G849
1	348	ARG	-	insertion	UNP G9G849
2	57	SER	ALA	conflict	UNP G9G849
2	153	GLU	-	insertion	UNP G9G849
2	154	PHE	-	insertion	UNP G9G849
2	161	PRO	-	insertion	UNP G9G849
2	162	GLY	-	insertion	UNP G9G849
2	310	ARG	-	insertion	UNP G9G849
2	322	ASP	-	insertion	UNP G9G849
2	323	VAL	-	insertion	UNP G9G849
2	334	GLU	-	insertion	UNP G9G849
2	335	LEU	-	insertion	UNP G9G849
2	347	SER	-	insertion	UNP G9G849
2	348	ARG	-	insertion	UNP G9G849
3	57	SER	ALA	conflict	UNP G9G849
3	153	GLU	-	insertion	UNP G9G849
3	154	PHE	-	insertion	UNP G9G849
3	161	PRO	-	insertion	UNP G9G849
3	162	GLY	-	insertion	UNP G9G849
3	310	ARG	-	insertion	UNP G9G849
3	322	ASP	-	insertion	UNP G9G849
3	323	VAL	-	insertion	UNP G9G849
3	334	GLU	-	insertion	UNP G9G849
3	335	LEU	-	insertion	UNP G9G849
3	347	SER	-	insertion	UNP G9G849
3	348	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
4	57	SER	ALA	conflict	UNP G9G849
4	153	GLU	-	insertion	UNP G9G849
4	154	PHE	-	insertion	UNP G9G849
4	161	PRO	-	insertion	UNP G9G849
4	162	GLY	-	insertion	UNP G9G849
4	310	ARG	-	insertion	UNP G9G849
4	322	ASP	-	insertion	UNP G9G849
4	323	VAL	-	insertion	UNP G9G849
4	334	GLU	-	insertion	UNP G9G849
4	335	LEU	-	insertion	UNP G9G849
4	347	SER	-	insertion	UNP G9G849
4	348	ARG	-	insertion	UNP G9G849
5	57	SER	ALA	conflict	UNP G9G849
5	153	GLU	-	insertion	UNP G9G849
5	154	PHE	-	insertion	UNP G9G849
5	161	PRO	-	insertion	UNP G9G849
5	162	GLY	-	insertion	UNP G9G849
5	310	ARG	-	insertion	UNP G9G849
5	322	ASP	-	insertion	UNP G9G849
5	323	VAL	-	insertion	UNP G9G849
5	334	GLU	-	insertion	UNP G9G849
5	335	LEU	-	insertion	UNP G9G849
5	347	SER	-	insertion	UNP G9G849
5	348	ARG	-	insertion	UNP G9G849
6	57	SER	ALA	conflict	UNP G9G849
6	153	GLU	-	insertion	UNP G9G849
6	154	PHE	-	insertion	UNP G9G849
6	161	PRO	-	insertion	UNP G9G849
6	162	GLY	-	insertion	UNP G9G849
6	310	ARG	-	insertion	UNP G9G849
6	322	ASP	-	insertion	UNP G9G849
6	323	VAL	-	insertion	UNP G9G849
6	334	GLU	-	insertion	UNP G9G849
6	335	LEU	-	insertion	UNP G9G849
6	347	SER	-	insertion	UNP G9G849
6	348	ARG	-	insertion	UNP G9G849
7	57	SER	ALA	conflict	UNP G9G849
7	153	GLU	-	insertion	UNP G9G849
7	154	PHE	-	insertion	UNP G9G849
7	161	PRO	-	insertion	UNP G9G849
7	162	GLY	-	insertion	UNP G9G849
7	310	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
7	322	ASP	-	insertion	UNP G9G849
7	323	VAL	-	insertion	UNP G9G849
7	334	GLU	-	insertion	UNP G9G849
7	335	LEU	-	insertion	UNP G9G849
7	347	SER	-	insertion	UNP G9G849
7	348	ARG	-	insertion	UNP G9G849
8	57	SER	ALA	conflict	UNP G9G849
8	153	GLU	-	insertion	UNP G9G849
8	154	PHE	-	insertion	UNP G9G849
8	161	PRO	-	insertion	UNP G9G849
8	162	GLY	-	insertion	UNP G9G849
8	310	ARG	-	insertion	UNP G9G849
8	322	ASP	-	insertion	UNP G9G849
8	323	VAL	-	insertion	UNP G9G849
8	334	GLU	-	insertion	UNP G9G849
8	335	LEU	-	insertion	UNP G9G849
8	347	SER	-	insertion	UNP G9G849
8	348	ARG	-	insertion	UNP G9G849
9	57	SER	ALA	conflict	UNP G9G849
9	153	GLU	-	insertion	UNP G9G849
9	154	PHE	-	insertion	UNP G9G849
9	161	PRO	-	insertion	UNP G9G849
9	162	GLY	-	insertion	UNP G9G849
9	310	ARG	-	insertion	UNP G9G849
9	322	ASP	-	insertion	UNP G9G849
9	323	VAL	-	insertion	UNP G9G849
9	334	GLU	-	insertion	UNP G9G849
9	335	LEU	-	insertion	UNP G9G849
9	347	SER	-	insertion	UNP G9G849
9	348	ARG	-	insertion	UNP G9G849
A	57	SER	ALA	conflict	UNP G9G849
A	153	GLU	-	insertion	UNP G9G849
A	154	PHE	-	insertion	UNP G9G849
A	161	PRO	-	insertion	UNP G9G849
A	162	GLY	-	insertion	UNP G9G849
A	310	ARG	-	insertion	UNP G9G849
A	322	ASP	-	insertion	UNP G9G849
A	323	VAL	-	insertion	UNP G9G849
A	334	GLU	-	insertion	UNP G9G849
A	335	LEU	-	insertion	UNP G9G849
A	347	SER	-	insertion	UNP G9G849
A	348	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
B	57	SER	ALA	conflict	UNP G9G849
B	153	GLU	-	insertion	UNP G9G849
B	154	PHE	-	insertion	UNP G9G849
B	161	PRO	-	insertion	UNP G9G849
B	162	GLY	-	insertion	UNP G9G849
B	310	ARG	-	insertion	UNP G9G849
B	322	ASP	-	insertion	UNP G9G849
B	323	VAL	-	insertion	UNP G9G849
B	334	GLU	-	insertion	UNP G9G849
B	335	LEU	-	insertion	UNP G9G849
B	347	SER	-	insertion	UNP G9G849
B	348	ARG	-	insertion	UNP G9G849
C	57	SER	ALA	conflict	UNP G9G849
C	153	GLU	-	insertion	UNP G9G849
C	154	PHE	-	insertion	UNP G9G849
C	161	PRO	-	insertion	UNP G9G849
C	162	GLY	-	insertion	UNP G9G849
C	310	ARG	-	insertion	UNP G9G849
C	322	ASP	-	insertion	UNP G9G849
C	323	VAL	-	insertion	UNP G9G849
C	334	GLU	-	insertion	UNP G9G849
C	335	LEU	-	insertion	UNP G9G849
C	347	SER	-	insertion	UNP G9G849
C	348	ARG	-	insertion	UNP G9G849
D	57	SER	ALA	conflict	UNP G9G849
D	153	GLU	-	insertion	UNP G9G849
D	154	PHE	-	insertion	UNP G9G849
D	161	PRO	-	insertion	UNP G9G849
D	162	GLY	-	insertion	UNP G9G849
D	310	ARG	-	insertion	UNP G9G849
D	322	ASP	-	insertion	UNP G9G849
D	323	VAL	-	insertion	UNP G9G849
D	334	GLU	-	insertion	UNP G9G849
D	335	LEU	-	insertion	UNP G9G849
D	347	SER	-	insertion	UNP G9G849
D	348	ARG	-	insertion	UNP G9G849
E	57	SER	ALA	conflict	UNP G9G849
E	153	GLU	-	insertion	UNP G9G849
E	154	PHE	-	insertion	UNP G9G849
E	161	PRO	-	insertion	UNP G9G849
E	162	GLY	-	insertion	UNP G9G849
E	310	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
E	322	ASP	-	insertion	UNP G9G849
E	323	VAL	-	insertion	UNP G9G849
E	334	GLU	-	insertion	UNP G9G849
E	335	LEU	-	insertion	UNP G9G849
E	347	SER	-	insertion	UNP G9G849
E	348	ARG	-	insertion	UNP G9G849
F	57	SER	ALA	conflict	UNP G9G849
F	153	GLU	-	insertion	UNP G9G849
F	154	PHE	-	insertion	UNP G9G849
F	161	PRO	-	insertion	UNP G9G849
F	162	GLY	-	insertion	UNP G9G849
F	310	ARG	-	insertion	UNP G9G849
F	322	ASP	-	insertion	UNP G9G849
F	323	VAL	-	insertion	UNP G9G849
F	334	GLU	-	insertion	UNP G9G849
F	335	LEU	-	insertion	UNP G9G849
F	347	SER	-	insertion	UNP G9G849
F	348	ARG	-	insertion	UNP G9G849
G	57	SER	ALA	conflict	UNP G9G849
G	153	GLU	-	insertion	UNP G9G849
G	154	PHE	-	insertion	UNP G9G849
G	161	PRO	-	insertion	UNP G9G849
G	162	GLY	-	insertion	UNP G9G849
G	310	ARG	-	insertion	UNP G9G849
G	322	ASP	-	insertion	UNP G9G849
G	323	VAL	-	insertion	UNP G9G849
G	334	GLU	-	insertion	UNP G9G849
G	335	LEU	-	insertion	UNP G9G849
G	347	SER	-	insertion	UNP G9G849
G	348	ARG	-	insertion	UNP G9G849
H	57	SER	ALA	conflict	UNP G9G849
H	153	GLU	-	insertion	UNP G9G849
H	154	PHE	-	insertion	UNP G9G849
H	161	PRO	-	insertion	UNP G9G849
H	162	GLY	-	insertion	UNP G9G849
H	310	ARG	-	insertion	UNP G9G849
H	322	ASP	-	insertion	UNP G9G849
H	323	VAL	-	insertion	UNP G9G849
H	334	GLU	-	insertion	UNP G9G849
H	335	LEU	-	insertion	UNP G9G849
H	347	SER	-	insertion	UNP G9G849
H	348	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
I	57	SER	ALA	conflict	UNP G9G849
I	153	GLU	-	insertion	UNP G9G849
I	154	PHE	-	insertion	UNP G9G849
I	161	PRO	-	insertion	UNP G9G849
I	162	GLY	-	insertion	UNP G9G849
I	310	ARG	-	insertion	UNP G9G849
I	322	ASP	-	insertion	UNP G9G849
I	323	VAL	-	insertion	UNP G9G849
I	334	GLU	-	insertion	UNP G9G849
I	335	LEU	-	insertion	UNP G9G849
I	347	SER	-	insertion	UNP G9G849
I	348	ARG	-	insertion	UNP G9G849
J	57	SER	ALA	conflict	UNP G9G849
J	153	GLU	-	insertion	UNP G9G849
J	154	PHE	-	insertion	UNP G9G849
J	161	PRO	-	insertion	UNP G9G849
J	162	GLY	-	insertion	UNP G9G849
J	310	ARG	-	insertion	UNP G9G849
J	322	ASP	-	insertion	UNP G9G849
J	323	VAL	-	insertion	UNP G9G849
J	334	GLU	-	insertion	UNP G9G849
J	335	LEU	-	insertion	UNP G9G849
J	347	SER	-	insertion	UNP G9G849
J	348	ARG	-	insertion	UNP G9G849
K	57	SER	ALA	conflict	UNP G9G849
K	153	GLU	-	insertion	UNP G9G849
K	154	PHE	-	insertion	UNP G9G849
K	161	PRO	-	insertion	UNP G9G849
K	162	GLY	-	insertion	UNP G9G849
K	310	ARG	-	insertion	UNP G9G849
K	322	ASP	-	insertion	UNP G9G849
K	323	VAL	-	insertion	UNP G9G849
K	334	GLU	-	insertion	UNP G9G849
K	335	LEU	-	insertion	UNP G9G849
K	347	SER	-	insertion	UNP G9G849
K	348	ARG	-	insertion	UNP G9G849
L	57	SER	ALA	conflict	UNP G9G849
L	153	GLU	-	insertion	UNP G9G849
L	154	PHE	-	insertion	UNP G9G849
L	161	PRO	-	insertion	UNP G9G849
L	162	GLY	-	insertion	UNP G9G849
L	310	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
L	322	ASP	-	insertion	UNP G9G849
L	323	VAL	-	insertion	UNP G9G849
L	334	GLU	-	insertion	UNP G9G849
L	335	LEU	-	insertion	UNP G9G849
L	347	SER	-	insertion	UNP G9G849
L	348	ARG	-	insertion	UNP G9G849
M	57	SER	ALA	conflict	UNP G9G849
M	153	GLU	-	insertion	UNP G9G849
M	154	PHE	-	insertion	UNP G9G849
M	161	PRO	-	insertion	UNP G9G849
M	162	GLY	-	insertion	UNP G9G849
M	310	ARG	-	insertion	UNP G9G849
M	322	ASP	-	insertion	UNP G9G849
M	323	VAL	-	insertion	UNP G9G849
M	334	GLU	-	insertion	UNP G9G849
M	335	LEU	-	insertion	UNP G9G849
M	347	SER	-	insertion	UNP G9G849
M	348	ARG	-	insertion	UNP G9G849
N	57	SER	ALA	conflict	UNP G9G849
N	153	GLU	-	insertion	UNP G9G849
N	154	PHE	-	insertion	UNP G9G849
N	161	PRO	-	insertion	UNP G9G849
N	162	GLY	-	insertion	UNP G9G849
N	310	ARG	-	insertion	UNP G9G849
N	322	ASP	-	insertion	UNP G9G849
N	323	VAL	-	insertion	UNP G9G849
N	334	GLU	-	insertion	UNP G9G849
N	335	LEU	-	insertion	UNP G9G849
N	347	SER	-	insertion	UNP G9G849
N	348	ARG	-	insertion	UNP G9G849
O	57	SER	ALA	conflict	UNP G9G849
O	153	GLU	-	insertion	UNP G9G849
O	154	PHE	-	insertion	UNP G9G849
O	161	PRO	-	insertion	UNP G9G849
O	162	GLY	-	insertion	UNP G9G849
O	310	ARG	-	insertion	UNP G9G849
O	322	ASP	-	insertion	UNP G9G849
O	323	VAL	-	insertion	UNP G9G849
O	334	GLU	-	insertion	UNP G9G849
O	335	LEU	-	insertion	UNP G9G849
O	347	SER	-	insertion	UNP G9G849
O	348	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
P	57	SER	ALA	conflict	UNP G9G849
P	153	GLU	-	insertion	UNP G9G849
P	154	PHE	-	insertion	UNP G9G849
P	161	PRO	-	insertion	UNP G9G849
P	162	GLY	-	insertion	UNP G9G849
P	310	ARG	-	insertion	UNP G9G849
P	322	ASP	-	insertion	UNP G9G849
P	323	VAL	-	insertion	UNP G9G849
P	334	GLU	-	insertion	UNP G9G849
P	335	LEU	-	insertion	UNP G9G849
P	347	SER	-	insertion	UNP G9G849
P	348	ARG	-	insertion	UNP G9G849
Q	57	SER	ALA	conflict	UNP G9G849
Q	153	GLU	-	insertion	UNP G9G849
Q	154	PHE	-	insertion	UNP G9G849
Q	161	PRO	-	insertion	UNP G9G849
Q	162	GLY	-	insertion	UNP G9G849
Q	310	ARG	-	insertion	UNP G9G849
Q	322	ASP	-	insertion	UNP G9G849
Q	323	VAL	-	insertion	UNP G9G849
Q	334	GLU	-	insertion	UNP G9G849
Q	335	LEU	-	insertion	UNP G9G849
Q	347	SER	-	insertion	UNP G9G849
Q	348	ARG	-	insertion	UNP G9G849
R	57	SER	ALA	conflict	UNP G9G849
R	153	GLU	-	insertion	UNP G9G849
R	154	PHE	-	insertion	UNP G9G849
R	161	PRO	-	insertion	UNP G9G849
R	162	GLY	-	insertion	UNP G9G849
R	310	ARG	-	insertion	UNP G9G849
R	322	ASP	-	insertion	UNP G9G849
R	323	VAL	-	insertion	UNP G9G849
R	334	GLU	-	insertion	UNP G9G849
R	335	LEU	-	insertion	UNP G9G849
R	347	SER	-	insertion	UNP G9G849
R	348	ARG	-	insertion	UNP G9G849
S	57	SER	ALA	conflict	UNP G9G849
S	153	GLU	-	insertion	UNP G9G849
S	154	PHE	-	insertion	UNP G9G849
S	161	PRO	-	insertion	UNP G9G849
S	162	GLY	-	insertion	UNP G9G849
S	310	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
S	322	ASP	-	insertion	UNP G9G849
S	323	VAL	-	insertion	UNP G9G849
S	334	GLU	-	insertion	UNP G9G849
S	335	LEU	-	insertion	UNP G9G849
S	347	SER	-	insertion	UNP G9G849
S	348	ARG	-	insertion	UNP G9G849
T	57	SER	ALA	conflict	UNP G9G849
T	153	GLU	-	insertion	UNP G9G849
T	154	PHE	-	insertion	UNP G9G849
T	161	PRO	-	insertion	UNP G9G849
T	162	GLY	-	insertion	UNP G9G849
T	310	ARG	-	insertion	UNP G9G849
T	322	ASP	-	insertion	UNP G9G849
T	323	VAL	-	insertion	UNP G9G849
T	334	GLU	-	insertion	UNP G9G849
T	335	LEU	-	insertion	UNP G9G849
T	347	SER	-	insertion	UNP G9G849
T	348	ARG	-	insertion	UNP G9G849
V	57	SER	ALA	conflict	UNP G9G849
V	153	GLU	-	insertion	UNP G9G849
V	154	PHE	-	insertion	UNP G9G849
V	161	PRO	-	insertion	UNP G9G849
V	162	GLY	-	insertion	UNP G9G849
V	310	ARG	-	insertion	UNP G9G849
V	322	ASP	-	insertion	UNP G9G849
V	323	VAL	-	insertion	UNP G9G849
V	334	GLU	-	insertion	UNP G9G849
V	335	LEU	-	insertion	UNP G9G849
V	347	SER	-	insertion	UNP G9G849
V	348	ARG	-	insertion	UNP G9G849
W	57	SER	ALA	conflict	UNP G9G849
W	153	GLU	-	insertion	UNP G9G849
W	154	PHE	-	insertion	UNP G9G849
W	161	PRO	-	insertion	UNP G9G849
W	162	GLY	-	insertion	UNP G9G849
W	310	ARG	-	insertion	UNP G9G849
W	322	ASP	-	insertion	UNP G9G849
W	323	VAL	-	insertion	UNP G9G849
W	334	GLU	-	insertion	UNP G9G849
W	335	LEU	-	insertion	UNP G9G849
W	347	SER	-	insertion	UNP G9G849
W	348	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
X	57	SER	ALA	conflict	UNP G9G849
X	153	GLU	-	insertion	UNP G9G849
X	154	PHE	-	insertion	UNP G9G849
X	161	PRO	-	insertion	UNP G9G849
X	162	GLY	-	insertion	UNP G9G849
X	310	ARG	-	insertion	UNP G9G849
X	322	ASP	-	insertion	UNP G9G849
X	323	VAL	-	insertion	UNP G9G849
X	334	GLU	-	insertion	UNP G9G849
X	335	LEU	-	insertion	UNP G9G849
X	347	SER	-	insertion	UNP G9G849
X	348	ARG	-	insertion	UNP G9G849
Y	57	SER	ALA	conflict	UNP G9G849
Y	153	GLU	-	insertion	UNP G9G849
Y	154	PHE	-	insertion	UNP G9G849
Y	161	PRO	-	insertion	UNP G9G849
Y	162	GLY	-	insertion	UNP G9G849
Y	310	ARG	-	insertion	UNP G9G849
Y	322	ASP	-	insertion	UNP G9G849
Y	323	VAL	-	insertion	UNP G9G849
Y	334	GLU	-	insertion	UNP G9G849
Y	335	LEU	-	insertion	UNP G9G849
Y	347	SER	-	insertion	UNP G9G849
Y	348	ARG	-	insertion	UNP G9G849
Z	57	SER	ALA	conflict	UNP G9G849
Z	153	GLU	-	insertion	UNP G9G849
Z	154	PHE	-	insertion	UNP G9G849
Z	161	PRO	-	insertion	UNP G9G849
Z	162	GLY	-	insertion	UNP G9G849
Z	310	ARG	-	insertion	UNP G9G849
Z	322	ASP	-	insertion	UNP G9G849
Z	323	VAL	-	insertion	UNP G9G849
Z	334	GLU	-	insertion	UNP G9G849
Z	335	LEU	-	insertion	UNP G9G849
Z	347	SER	-	insertion	UNP G9G849
Z	348	ARG	-	insertion	UNP G9G849
a	57	SER	ALA	conflict	UNP G9G849
a	153	GLU	-	insertion	UNP G9G849
a	154	PHE	-	insertion	UNP G9G849
a	161	PRO	-	insertion	UNP G9G849
a	162	GLY	-	insertion	UNP G9G849
a	310	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
a	322	ASP	-	insertion	UNP G9G849
a	323	VAL	-	insertion	UNP G9G849
a	334	GLU	-	insertion	UNP G9G849
a	335	LEU	-	insertion	UNP G9G849
a	347	SER	-	insertion	UNP G9G849
a	348	ARG	-	insertion	UNP G9G849
b	57	SER	ALA	conflict	UNP G9G849
b	153	GLU	-	insertion	UNP G9G849
b	154	PHE	-	insertion	UNP G9G849
b	161	PRO	-	insertion	UNP G9G849
b	162	GLY	-	insertion	UNP G9G849
b	310	ARG	-	insertion	UNP G9G849
b	322	ASP	-	insertion	UNP G9G849
b	323	VAL	-	insertion	UNP G9G849
b	334	GLU	-	insertion	UNP G9G849
b	335	LEU	-	insertion	UNP G9G849
b	347	SER	-	insertion	UNP G9G849
b	348	ARG	-	insertion	UNP G9G849
c	57	SER	ALA	conflict	UNP G9G849
c	153	GLU	-	insertion	UNP G9G849
c	154	PHE	-	insertion	UNP G9G849
c	161	PRO	-	insertion	UNP G9G849
c	162	GLY	-	insertion	UNP G9G849
c	310	ARG	-	insertion	UNP G9G849
c	322	ASP	-	insertion	UNP G9G849
c	323	VAL	-	insertion	UNP G9G849
c	334	GLU	-	insertion	UNP G9G849
c	335	LEU	-	insertion	UNP G9G849
c	347	SER	-	insertion	UNP G9G849
c	348	ARG	-	insertion	UNP G9G849
d	57	SER	ALA	conflict	UNP G9G849
d	153	GLU	-	insertion	UNP G9G849
d	154	PHE	-	insertion	UNP G9G849
d	161	PRO	-	insertion	UNP G9G849
d	162	GLY	-	insertion	UNP G9G849
d	310	ARG	-	insertion	UNP G9G849
d	322	ASP	-	insertion	UNP G9G849
d	323	VAL	-	insertion	UNP G9G849
d	334	GLU	-	insertion	UNP G9G849
d	335	LEU	-	insertion	UNP G9G849
d	347	SER	-	insertion	UNP G9G849
d	348	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
e	57	SER	ALA	conflict	UNP G9G849
e	153	GLU	-	insertion	UNP G9G849
e	154	PHE	-	insertion	UNP G9G849
e	161	PRO	-	insertion	UNP G9G849
e	162	GLY	-	insertion	UNP G9G849
e	310	ARG	-	insertion	UNP G9G849
e	322	ASP	-	insertion	UNP G9G849
e	323	VAL	-	insertion	UNP G9G849
e	334	GLU	-	insertion	UNP G9G849
e	335	LEU	-	insertion	UNP G9G849
e	347	SER	-	insertion	UNP G9G849
e	348	ARG	-	insertion	UNP G9G849
f	57	SER	ALA	conflict	UNP G9G849
f	153	GLU	-	insertion	UNP G9G849
f	154	PHE	-	insertion	UNP G9G849
f	161	PRO	-	insertion	UNP G9G849
f	162	GLY	-	insertion	UNP G9G849
f	310	ARG	-	insertion	UNP G9G849
f	322	ASP	-	insertion	UNP G9G849
f	323	VAL	-	insertion	UNP G9G849
f	334	GLU	-	insertion	UNP G9G849
f	335	LEU	-	insertion	UNP G9G849
f	347	SER	-	insertion	UNP G9G849
f	348	ARG	-	insertion	UNP G9G849
g	57	SER	ALA	conflict	UNP G9G849
g	153	GLU	-	insertion	UNP G9G849
g	154	PHE	-	insertion	UNP G9G849
g	161	PRO	-	insertion	UNP G9G849
g	162	GLY	-	insertion	UNP G9G849
g	310	ARG	-	insertion	UNP G9G849
g	322	ASP	-	insertion	UNP G9G849
g	323	VAL	-	insertion	UNP G9G849
g	334	GLU	-	insertion	UNP G9G849
g	335	LEU	-	insertion	UNP G9G849
g	347	SER	-	insertion	UNP G9G849
g	348	ARG	-	insertion	UNP G9G849
h	57	SER	ALA	conflict	UNP G9G849
h	153	GLU	-	insertion	UNP G9G849
h	154	PHE	-	insertion	UNP G9G849
h	161	PRO	-	insertion	UNP G9G849
h	162	GLY	-	insertion	UNP G9G849
h	310	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
h	322	ASP	-	insertion	UNP G9G849
h	323	VAL	-	insertion	UNP G9G849
h	334	GLU	-	insertion	UNP G9G849
h	335	LEU	-	insertion	UNP G9G849
h	347	SER	-	insertion	UNP G9G849
h	348	ARG	-	insertion	UNP G9G849
i	57	SER	ALA	conflict	UNP G9G849
i	153	GLU	-	insertion	UNP G9G849
i	154	PHE	-	insertion	UNP G9G849
i	161	PRO	-	insertion	UNP G9G849
i	162	GLY	-	insertion	UNP G9G849
i	310	ARG	-	insertion	UNP G9G849
i	322	ASP	-	insertion	UNP G9G849
i	323	VAL	-	insertion	UNP G9G849
i	334	GLU	-	insertion	UNP G9G849
i	335	LEU	-	insertion	UNP G9G849
i	347	SER	-	insertion	UNP G9G849
i	348	ARG	-	insertion	UNP G9G849
j	57	SER	ALA	conflict	UNP G9G849
j	153	GLU	-	insertion	UNP G9G849
j	154	PHE	-	insertion	UNP G9G849
j	161	PRO	-	insertion	UNP G9G849
j	162	GLY	-	insertion	UNP G9G849
j	310	ARG	-	insertion	UNP G9G849
j	322	ASP	-	insertion	UNP G9G849
j	323	VAL	-	insertion	UNP G9G849
j	334	GLU	-	insertion	UNP G9G849
j	335	LEU	-	insertion	UNP G9G849
j	347	SER	-	insertion	UNP G9G849
j	348	ARG	-	insertion	UNP G9G849
k	57	SER	ALA	conflict	UNP G9G849
k	153	GLU	-	insertion	UNP G9G849
k	154	PHE	-	insertion	UNP G9G849
k	161	PRO	-	insertion	UNP G9G849
k	162	GLY	-	insertion	UNP G9G849
k	310	ARG	-	insertion	UNP G9G849
k	322	ASP	-	insertion	UNP G9G849
k	323	VAL	-	insertion	UNP G9G849
k	334	GLU	-	insertion	UNP G9G849
k	335	LEU	-	insertion	UNP G9G849
k	347	SER	-	insertion	UNP G9G849
k	348	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
l	57	SER	ALA	conflict	UNP G9G849
l	153	GLU	-	insertion	UNP G9G849
l	154	PHE	-	insertion	UNP G9G849
l	161	PRO	-	insertion	UNP G9G849
l	162	GLY	-	insertion	UNP G9G849
l	310	ARG	-	insertion	UNP G9G849
l	322	ASP	-	insertion	UNP G9G849
l	323	VAL	-	insertion	UNP G9G849
l	334	GLU	-	insertion	UNP G9G849
l	335	LEU	-	insertion	UNP G9G849
l	347	SER	-	insertion	UNP G9G849
l	348	ARG	-	insertion	UNP G9G849
m	57	SER	ALA	conflict	UNP G9G849
m	153	GLU	-	insertion	UNP G9G849
m	154	PHE	-	insertion	UNP G9G849
m	161	PRO	-	insertion	UNP G9G849
m	162	GLY	-	insertion	UNP G9G849
m	310	ARG	-	insertion	UNP G9G849
m	322	ASP	-	insertion	UNP G9G849
m	323	VAL	-	insertion	UNP G9G849
m	334	GLU	-	insertion	UNP G9G849
m	335	LEU	-	insertion	UNP G9G849
m	347	SER	-	insertion	UNP G9G849
m	348	ARG	-	insertion	UNP G9G849
n	57	SER	ALA	conflict	UNP G9G849
n	153	GLU	-	insertion	UNP G9G849
n	154	PHE	-	insertion	UNP G9G849
n	161	PRO	-	insertion	UNP G9G849
n	162	GLY	-	insertion	UNP G9G849
n	310	ARG	-	insertion	UNP G9G849
n	322	ASP	-	insertion	UNP G9G849
n	323	VAL	-	insertion	UNP G9G849
n	334	GLU	-	insertion	UNP G9G849
n	335	LEU	-	insertion	UNP G9G849
n	347	SER	-	insertion	UNP G9G849
n	348	ARG	-	insertion	UNP G9G849
o	57	SER	ALA	conflict	UNP G9G849
o	153	GLU	-	insertion	UNP G9G849
o	154	PHE	-	insertion	UNP G9G849
o	161	PRO	-	insertion	UNP G9G849
o	162	GLY	-	insertion	UNP G9G849
o	310	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
o	322	ASP	-	insertion	UNP G9G849
o	323	VAL	-	insertion	UNP G9G849
o	334	GLU	-	insertion	UNP G9G849
o	335	LEU	-	insertion	UNP G9G849
o	347	SER	-	insertion	UNP G9G849
o	348	ARG	-	insertion	UNP G9G849
p	57	SER	ALA	conflict	UNP G9G849
p	153	GLU	-	insertion	UNP G9G849
p	154	PHE	-	insertion	UNP G9G849
p	161	PRO	-	insertion	UNP G9G849
p	162	GLY	-	insertion	UNP G9G849
p	310	ARG	-	insertion	UNP G9G849
p	322	ASP	-	insertion	UNP G9G849
p	323	VAL	-	insertion	UNP G9G849
p	334	GLU	-	insertion	UNP G9G849
p	335	LEU	-	insertion	UNP G9G849
p	347	SER	-	insertion	UNP G9G849
p	348	ARG	-	insertion	UNP G9G849
q	57	SER	ALA	conflict	UNP G9G849
q	153	GLU	-	insertion	UNP G9G849
q	154	PHE	-	insertion	UNP G9G849
q	161	PRO	-	insertion	UNP G9G849
q	162	GLY	-	insertion	UNP G9G849
q	310	ARG	-	insertion	UNP G9G849
q	322	ASP	-	insertion	UNP G9G849
q	323	VAL	-	insertion	UNP G9G849
q	334	GLU	-	insertion	UNP G9G849
q	335	LEU	-	insertion	UNP G9G849
q	347	SER	-	insertion	UNP G9G849
q	348	ARG	-	insertion	UNP G9G849
r	57	SER	ALA	conflict	UNP G9G849
r	153	GLU	-	insertion	UNP G9G849
r	154	PHE	-	insertion	UNP G9G849
r	161	PRO	-	insertion	UNP G9G849
r	162	GLY	-	insertion	UNP G9G849
r	310	ARG	-	insertion	UNP G9G849
r	322	ASP	-	insertion	UNP G9G849
r	323	VAL	-	insertion	UNP G9G849
r	334	GLU	-	insertion	UNP G9G849
r	335	LEU	-	insertion	UNP G9G849
r	347	SER	-	insertion	UNP G9G849
r	348	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
s	57	SER	ALA	conflict	UNP G9G849
s	153	GLU	-	insertion	UNP G9G849
s	154	PHE	-	insertion	UNP G9G849
s	161	PRO	-	insertion	UNP G9G849
s	162	GLY	-	insertion	UNP G9G849
s	310	ARG	-	insertion	UNP G9G849
s	322	ASP	-	insertion	UNP G9G849
s	323	VAL	-	insertion	UNP G9G849
s	334	GLU	-	insertion	UNP G9G849
s	335	LEU	-	insertion	UNP G9G849
s	347	SER	-	insertion	UNP G9G849
s	348	ARG	-	insertion	UNP G9G849
t	57	SER	ALA	conflict	UNP G9G849
t	153	GLU	-	insertion	UNP G9G849
t	154	PHE	-	insertion	UNP G9G849
t	161	PRO	-	insertion	UNP G9G849
t	162	GLY	-	insertion	UNP G9G849
t	310	ARG	-	insertion	UNP G9G849
t	322	ASP	-	insertion	UNP G9G849
t	323	VAL	-	insertion	UNP G9G849
t	334	GLU	-	insertion	UNP G9G849
t	335	LEU	-	insertion	UNP G9G849
t	347	SER	-	insertion	UNP G9G849
t	348	ARG	-	insertion	UNP G9G849
u	57	SER	ALA	conflict	UNP G9G849
u	153	GLU	-	insertion	UNP G9G849
u	154	PHE	-	insertion	UNP G9G849
u	161	PRO	-	insertion	UNP G9G849
u	162	GLY	-	insertion	UNP G9G849
u	310	ARG	-	insertion	UNP G9G849
u	322	ASP	-	insertion	UNP G9G849
u	323	VAL	-	insertion	UNP G9G849
u	334	GLU	-	insertion	UNP G9G849
u	335	LEU	-	insertion	UNP G9G849
u	347	SER	-	insertion	UNP G9G849
u	348	ARG	-	insertion	UNP G9G849
v	57	SER	ALA	conflict	UNP G9G849
v	153	GLU	-	insertion	UNP G9G849
v	154	PHE	-	insertion	UNP G9G849
v	161	PRO	-	insertion	UNP G9G849
v	162	GLY	-	insertion	UNP G9G849
v	310	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
v	322	ASP	-	insertion	UNP G9G849
v	323	VAL	-	insertion	UNP G9G849
v	334	GLU	-	insertion	UNP G9G849
v	335	LEU	-	insertion	UNP G9G849
v	347	SER	-	insertion	UNP G9G849
v	348	ARG	-	insertion	UNP G9G849
w	57	SER	ALA	conflict	UNP G9G849
w	153	GLU	-	insertion	UNP G9G849
w	154	PHE	-	insertion	UNP G9G849
w	161	PRO	-	insertion	UNP G9G849
w	162	GLY	-	insertion	UNP G9G849
w	310	ARG	-	insertion	UNP G9G849
w	322	ASP	-	insertion	UNP G9G849
w	323	VAL	-	insertion	UNP G9G849
w	334	GLU	-	insertion	UNP G9G849
w	335	LEU	-	insertion	UNP G9G849
w	347	SER	-	insertion	UNP G9G849
w	348	ARG	-	insertion	UNP G9G849
x	57	SER	ALA	conflict	UNP G9G849
x	153	GLU	-	insertion	UNP G9G849
x	154	PHE	-	insertion	UNP G9G849
x	161	PRO	-	insertion	UNP G9G849
x	162	GLY	-	insertion	UNP G9G849
x	310	ARG	-	insertion	UNP G9G849
x	322	ASP	-	insertion	UNP G9G849
x	323	VAL	-	insertion	UNP G9G849
x	334	GLU	-	insertion	UNP G9G849
x	335	LEU	-	insertion	UNP G9G849
x	347	SER	-	insertion	UNP G9G849
x	348	ARG	-	insertion	UNP G9G849
y	57	SER	ALA	conflict	UNP G9G849
y	153	GLU	-	insertion	UNP G9G849
y	154	PHE	-	insertion	UNP G9G849
y	161	PRO	-	insertion	UNP G9G849
y	162	GLY	-	insertion	UNP G9G849
y	310	ARG	-	insertion	UNP G9G849
y	322	ASP	-	insertion	UNP G9G849
y	323	VAL	-	insertion	UNP G9G849
y	334	GLU	-	insertion	UNP G9G849
y	335	LEU	-	insertion	UNP G9G849
y	347	SER	-	insertion	UNP G9G849
y	348	ARG	-	insertion	UNP G9G849

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Chain	Residue	Modelled	Actual	Comment	Reference
z	57	SER	ALA	conflict	UNP G9G849
z	153	GLU	-	insertion	UNP G9G849
z	154	PHE	-	insertion	UNP G9G849
z	161	PRO	-	insertion	UNP G9G849
z	162	GLY	-	insertion	UNP G9G849
z	310	ARG	-	insertion	UNP G9G849
z	322	ASP	-	insertion	UNP G9G849
z	323	VAL	-	insertion	UNP G9G849
z	334	GLU	-	insertion	UNP G9G849
z	335	LEU	-	insertion	UNP G9G849
z	347	SER	-	insertion	UNP G9G849
z	348	ARG	-	insertion	UNP G9G849

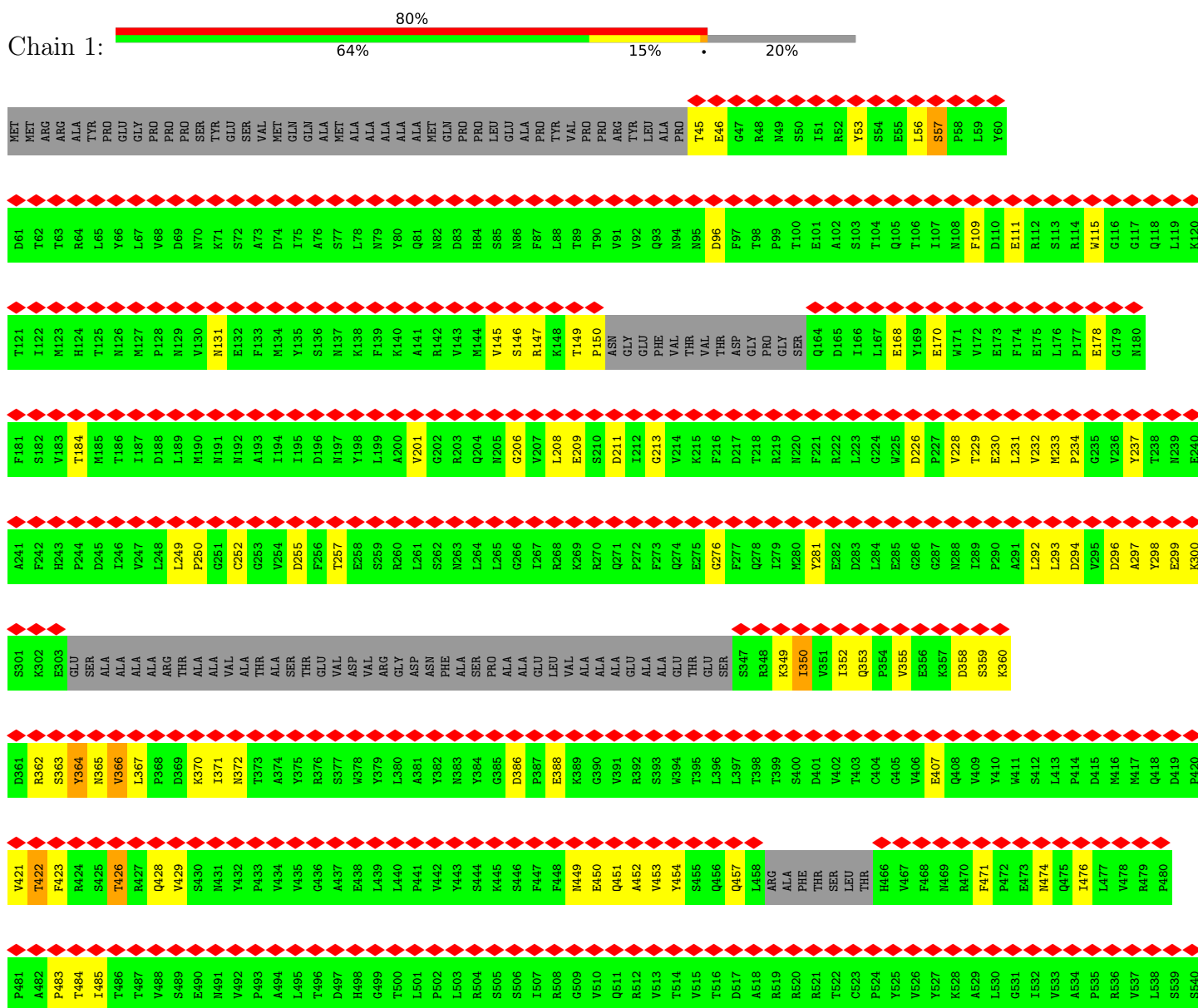
- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
2	1	1	Total K 1 1	0
2	2	1	Total K 1 1	0
2	3	1	Total K 1 1	0
2	4	1	Total K 1 1	0
2	5	1	Total K 1 1	0
2	6	1	Total K 1 1	0
2	7	1	Total K 1 1	0
2	8	1	Total K 1 1	0
2	9	1	Total K 1 1	0
2	B	1	Total K 1 1	0
2	I	1	Total K 1 1	0
2	R	1	Total K 1 1	0

3 Residue-property plots

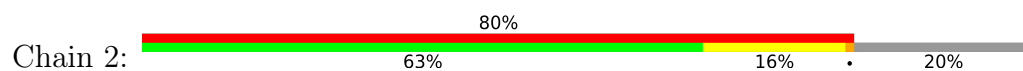
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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





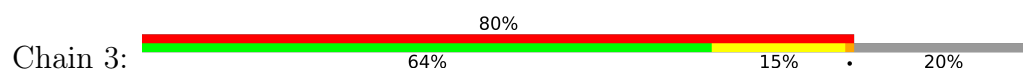
• Molecule 1: Penton protein



MET	MET	ARG	ARG	ALA	TYR	PRO	GLU	GLY	PRO	PRO	PRO	SER	TYR	GLU	SER	VAL	MET	GLN	GLN	ALA	ALA	ALA	ALA	MET	GLN	PRO	PRO	PRO	LEU	ALA	ALA	PRO	PRO	TYR	VAL	PRO	PRO	ARG	TYR	LEU	ALA	ALA	PRO	T45	E46	G47	R48	N49	S50	I51	R52	Y53	S54	E55	L56	S57	P58	L59	Y60		
D61	T62	T63	T63	R64	L65	Y66	L67	L67	P68	D69	N70	K71	S72	A73	D74	I75	A76	S77	L78	N79	Y80	Q81	N82	D83	H84	S85	N86	F87	L88	T89	T90	V91	V92	Q93	N94	N95	D96	F97	T98	P99	T100	E101	A102	S103	T104	Q105	T106	I107	N108	F109	D110	E111	R112	S113	R114	W115	G116	Q117	Q118	L119	K120
T121	T122	M123	H124	T125	N126	M127	P128	N129	V130	N131	E132	F133	M134	Y135	S136	N137	K138	F139	K140	A141	R142	V143	M144	V145	S146	R147	K148	T149	P150	ASN	GLY	GLU	PHE	VAL	THR	THR	ASP	GLY	PRO	GLY	SER	Q164	D165	I166	L167	E168	Y169	E170	W171	V172	E173	F174	E175	L176	P177	E178	G179	N180			
F181	S182	V183	T184	M185	T186	I187	D188	L189	M190	N191	N192	A193	I194	I195	D196	N197	Y198	L199	A200	V201	G202	R203	Q204	R205	G206	V207	L208	E209	S210	D211	I212	G213	V214	K215	F216	D217	T218	R219	N220	F221	R222	L223	G224	W225	D226	P227	V228	T229	E230	L231	V232	N233	P234	G235	V236	Y237	N239	E240			
A241	F242	H243	P244	D245	T246	V247	L248	L249	P250	G251	C252	G253	V254	D255	F256	T257	E258	S259	R260	L261	S262	N263	L264	L265	G266	L267	R268	K269	R270	Q271	P272	F273	Q274	E275	G276	F277	Q278	I279	N280	Y281	E282	D283	L284	E285	G286	G287	N288	I289	P290	L291	L292	L293	D294	V295	D296	A297	E299	K300			
S301	K302	E303	GLU	SER	ALA	ALA	ALA	ALA	ARG	THR	ALA	VAL	THR	ALA	THR	SER	THR	GLU	VAL	ASP	VAL	ARG	GLY	ASP	ASN	PHE	ALA	SER	PRO	ALA	ALA	GLU	THR	GLU	SER	S347	R348	K349	I350	V351	I352	Q353	P354	V355	E356	K357	D358	S359	K360												
D361	R362	S363	Y364	N365	Y366	L367	P368	D369	K370	I371	N372	T373	A374	Y375	R376	S377	W378	Y379	L380	A381	Y382	N383	Y384	G385	D386	F387	E388	K389	G390	Y391	R392	S393	W394	T395	L396	L397	T398	T399	S400	D401	V402	T403	C404	G405	V406	E407	Q408	Y409	Y410	W411	S412	L413	P414	D415	M416	M417	Q418	D419	P420		
V421	T422	F423	R424	S425	T426	R427	Q428	V429	S430	N431	Y432	P433	V434	V435	G436	A437	E438	L439	L440	P441	V442	Y443	S444	K445	S446	F447	F448	N449	E450	Q451	A452	V453	Y454	S455	Q456	Q457	L458	ARG	ALA	PHE	THR	SER	LEU	THR	H466	V467	F468	N469	F471	P472	N473	N474	Q475	L476	L477	V478	R479	P480			
P481	A482	P483	T484	L485	T486	T487	V488	S489	E490	N491	V492	P493	A494	L495	T496	D497	H498	G499	T500	L501	P502	L503	R504	S505	S506	I507	R508	G509	V510	Q511	R512	V513	T514	V515	T516	D517	A518	R519	R520	R521	T522	C523	P524	Y525	V526	Y527	K528	A529	L530	G531	T532	V533	A534	P535	R536	V537	L538	S539	S540		



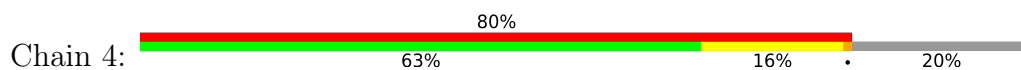
• Molecule 1: Penton protein



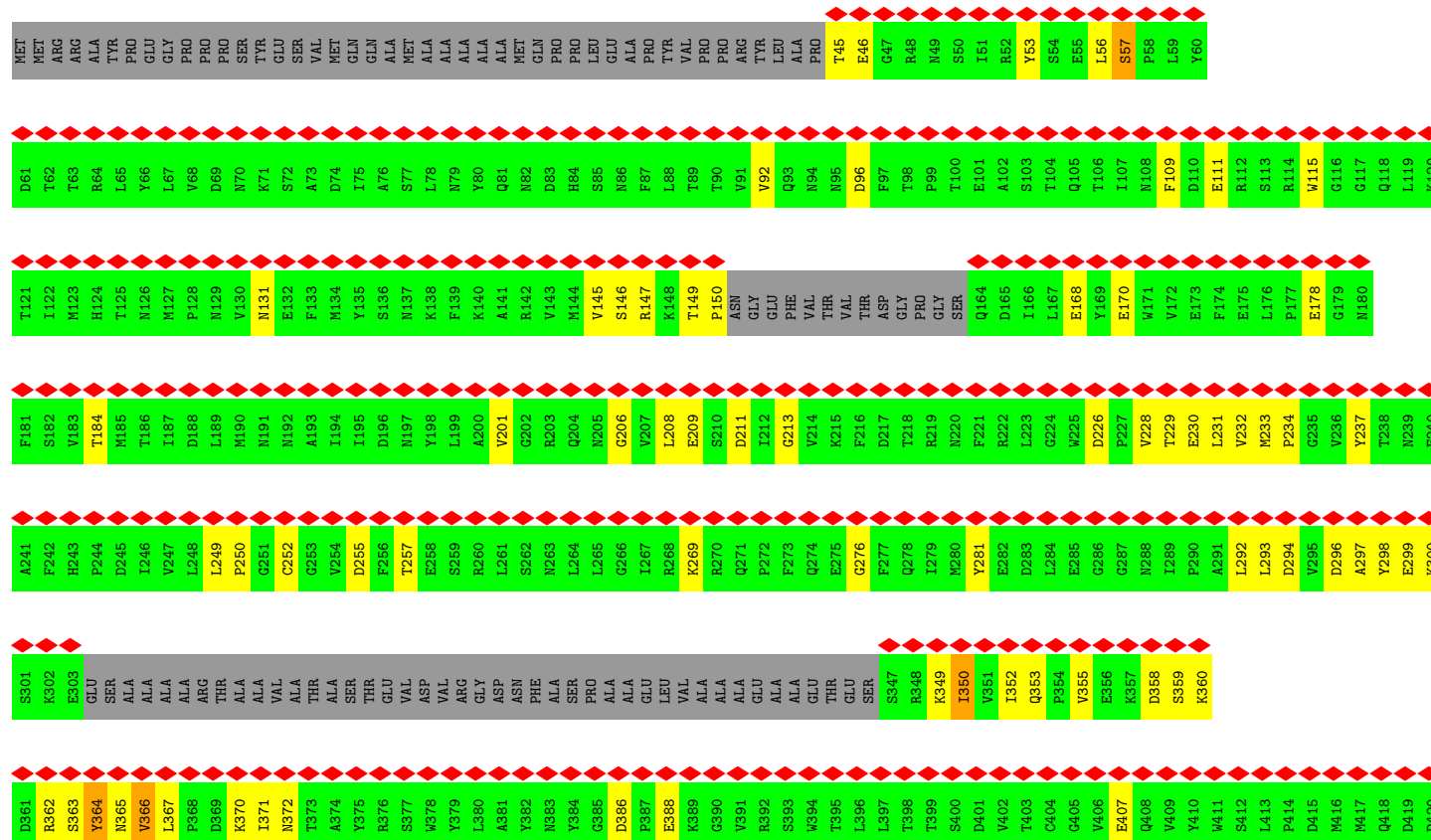
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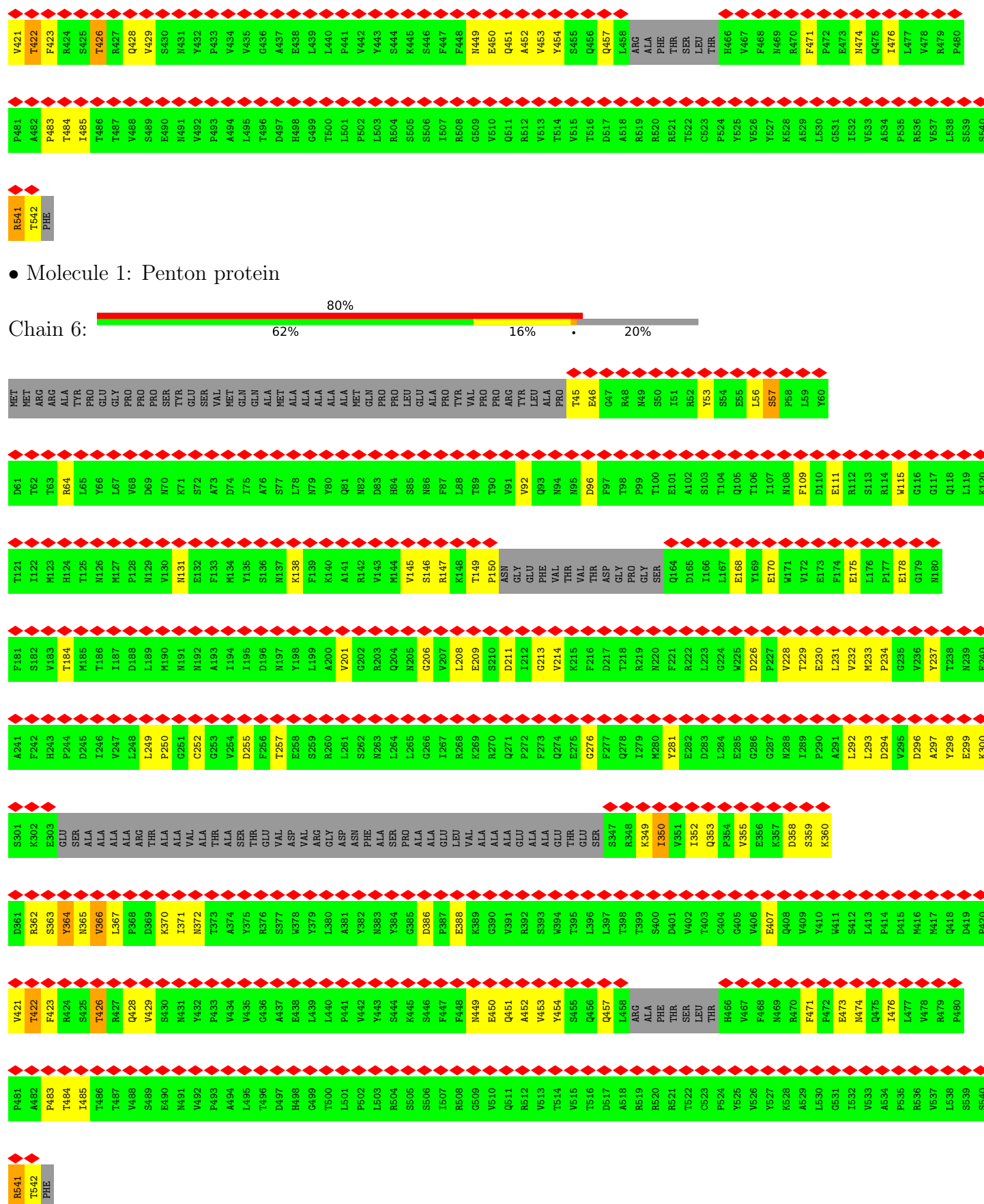
D61	T121	F181	A241	S301	D361	V421	P481	R541
T62	I122	S182	F242	K302	R362	T422	A482	T542
T63	M123	V183	H243	E303	S363	F423	P483	PHE
R64	H124	T184	P244	GLU	Y364	R424	T484	
L65	T125	M185	D245	SER	N365	S425	I485	
L67	M127	T186	I246	ALA	V366	T426	T486	
V68	M128	T187	V247	ALA	L367	R427	T487	
D69	P128	D188	L248	ALA	P368	Q428	V488	
N70	N129	D189	L249	ARG	S369	V429	S489	
K71	V130	M190	P250	THR	K370	S430	E490	
S72	N131	N191	G251	ALA	I371	M431	N491	
A73	E132	N192	C252	VAL	N372	V432	V492	
D74	F133	A193	G253	ALA	T373	P433	P493	
I75	M134	I194	V254	THR	A374	V434	A494	
A76	Y135	I195	D255	SER	Y375	V435	L495	
S77	S136	D196	F256	THR	R376	G436	T496	
L78	K137	Y197	T257	GLU	S377	A437	D497	
N79	N138	Y198	E258	VAL	W378	E438	G498	
Y80	F139	L199	S259	VAL	Y379	L439	G499	
Q81	K140	A200	R260	ARG	L380	L440	T500	
N82	A141	V201	L261	GLY	A381	P441	L501	
D83	R142	G202	S262	ASN	Y382	V442	P502	
H84	V143	R203	N263	ASP	N383	Y443	L503	
S85	M144	Q204	L264	ALA	Y384	S444	R504	
N86	V145	N205	L265	SER	G385	K445	S505	
F87	S146	G206	G266	PRO	D386	S446	S506	
L88	R147	V207	I267	ALA	P387	F447	L507	
T89	K148	L208	R268	GLU	E388	F448	R508	
T90	T149	E209	K269	LEU	K389	M449	G509	
V91	P150	S210	R270	ALA	G390	E450	V510	
V92	ASN	D211	Q271	ALA	V391	Q451	Q511	
Q93	GLY	I212	P272	GLU	R392	A452	R512	
N94	PHE	G213	F273	ALA	S393	V453	V513	
N95	VAL	V214	Q274	ALA	W394	Y454	T514	
D96	THR	K215	E275	GLU	T395	S455	V515	
F97	VAL	F216	G276	THR	L396	Q456	T516	
P99	THR	R217	F277	GLU	L397	Q457	D517	
T100	ASP	D218	Q278	SER	T398	L458	A518	
E101	PRO	R219	I279	R347	T399	ARG	R519	
A102	GLY	R220	Y281	K349	S400	PHE	R520	
S103	SER	F221	E282	I350	D401	THR	R521	
T104	Q164	D165	E283	V351	V402	SER	T522	
Q105	D166	L223	L284	I352	T403	LEU	C523	
T106	L167	G224	E285	Q353	C404	THR	P524	
I107	E168	W225	G286	P354	G405		V525	
N108	Y169	D226	G287	V355	V406	H466	V526	
F109	E170	P227	N288	E356	E407	V467	Y527	
D110	W171	V228	I289	K357	Q408	M469	K528	
E111	V172	T229	P290	D358	V409	R470	A529	
R112	E173	E230	A291	S359	Y410	F471	L530	
S113	F174	L231	L292	K360	W411	P472	G531	
R114	E175	V232	L293		S412	E473	T532	
W115	L176	M233	D294		L413	M474	V533	
G116	P177	P234	V295		P414	Q475	A534	
G117	E178	G235	D296		D415	L476	P535	
Q118	G179	V236	D297		M416	L477	R536	
L119	N180	Y237	Y298		Q417	V478	V537	
K120		N239	E299		D419	P480	S539	
		E240	K300		P420		S540	

• Molecule 1: Penton protein



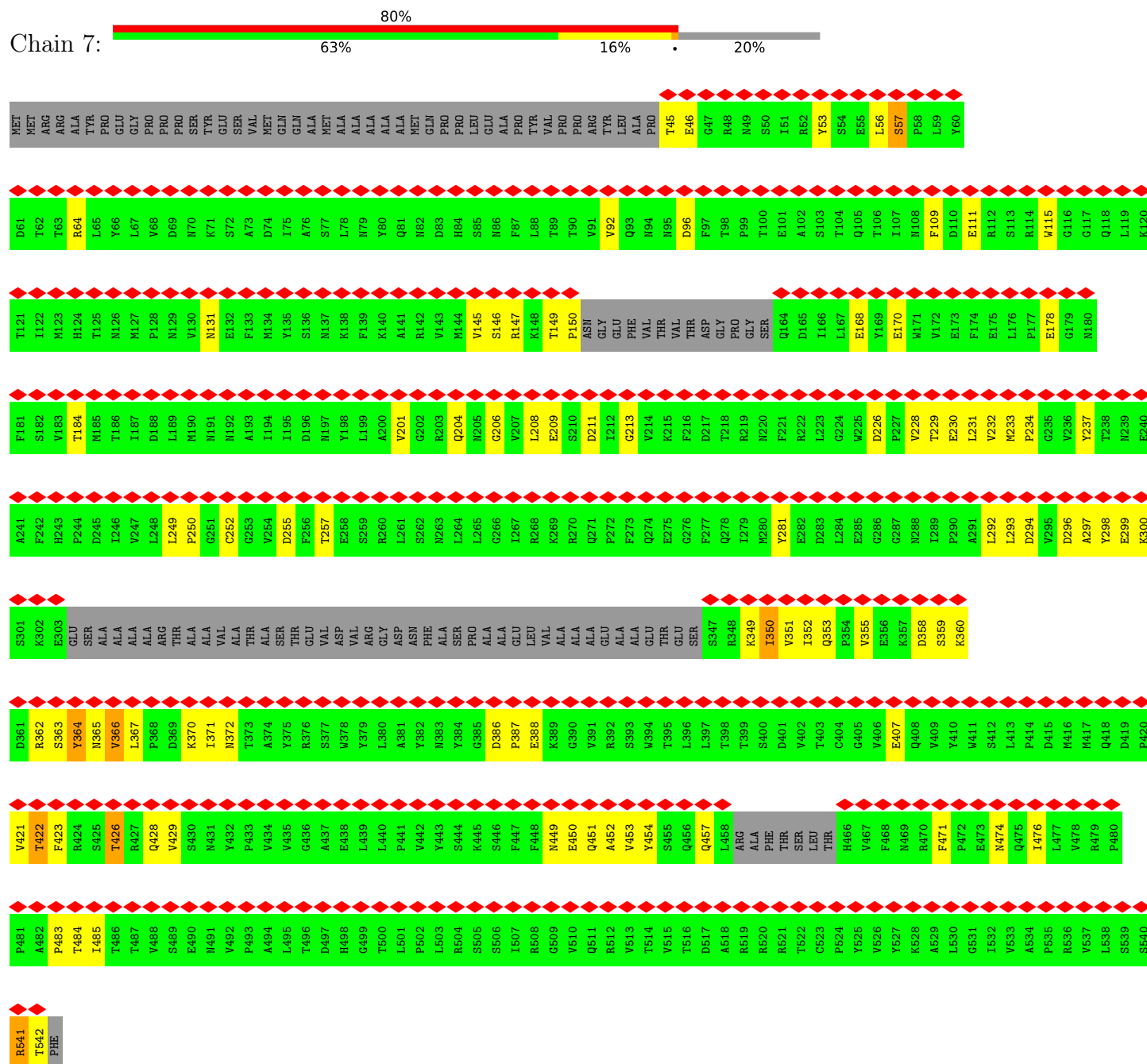
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ARG	T62	I122	S182	ARG	T62	I122	S182
ALA	T63	M123	V183	ALA	T63	M123	V183
TYR	R64	H124	T184	TYR	R64	H124	T184
PRO	L65	T125	M185	PRO	L65	T125	M185
GLY	V66	M127	T186	GLY	V66	M127	T186
PRO	L67	M128	T187	PRO	L67	M128	T187
PRO	V68	P128	D188	PRO	V68	P128	D188
PRO	D69	N129	D189	PRO	D69	N129	D189
SER	N70	M130	M190	SER	N70	M130	M190
TYR	K71	N131	N191	TYR	K71	N131	N191
GLU	S72	E132	N192	GLU	S72	E132	N192
SER	A73	F133	A193	SER	A73	F133	A193
VAL	D74	M134	I194	VAL	D74	M134	I194
MET	I75	Y135	I195	MET	I75	Y135	I195
GLN	A76	S136	D196	GLN	A76	S136	D196
GLN	S77	N137	Y197	GLN	S77	N137	Y197
ALA	L78	K138	Y198	ALA	L78	K138	Y198
ALA	N79	F139	L199	ALA	N79	F139	L199
ALA	Y80	K140	A200	ALA	Y80	K140	A200
ALA	Q81	A141	V201	ALA	Q81	A141	V201
MET	N82	R142	G202	MET	N82	R142	G202
GLN	D83	V143	R203	GLN	D83	V143	R203
PRO	H84	M144	Q204	PRO	H84	M144	Q204
LEU	S85	V145	N205	LEU	S85	V145	N205
GLU	N86	S146	G206	GLU	N86	S146	G206
ALA	F87	R147	V207	ALA	F87	R147	V207
PRO	L88	K148	L208	PRO	L88	K148	L208
TYR	T89	T149	E209	TYR	T89	T149	E209
VAL	T90	S210	S210	VAL	T90	S210	S210
PRO	V91	D211	D211	PRO	V91	D211	D211
ARG	V92	I212	I212	ARG	V92	I212	I212
TYR	Q93	G213	G213	TYR	Q93	G213	G213
LEU	N94	V214	V214	LEU	N94	V214	V214
ALA	N95	K215	K215	ALA	N95	K215	K215
PRO	D96	F216	F216	PRO	D96	F216	F216
ALA	F97	D217	D217	ALA	F97	D217	D217
THR	T98	T218	T218	THR	T98	T218	T218
THR	P99	R219	R219	THR	P99	R219	R219
THR	T100	N220	N220	THR	T100	N220	N220
PRO	E101	F221	F221	PRO	E101	F221	F221
ALA	A102	D165	D165	ALA	A102	D165	D165
ALA	S103	I166	I166	ALA	S103	I166	I166
ALA	T104	L167	L167	ALA	T104	L167	L167
THR	Q105	E168	E168	THR	Q105	E168	E168
THR	T106	Y169	Y169	THR	T106	Y169	Y169
THR	I107	E170	E170	THR	I107	E170	E170
THR	N108	W171	W171	THR	N108	W171	W171
THR	F109	V172	V172	THR	F109	V172	V172
THR	D110	E173	E173	THR	D110	E173	E173
THR	E111	F174	F174	THR	E111	F174	F174
THR	R112	E175	E175	THR	R112	E175	E175
THR	S113	L176	L176	THR	S113	L176	L176
THR	R114	P177	P177	THR	R114	P177	P177
THR	W115	E178	E178	THR	W115	E178	E178
THR	G116	G179	G179	THR	G116	G179	G179
THR	Q118	N180	N180	THR	Q118	N180	N180
THR	L119			THR	L119		
THR	K120			THR	K120		





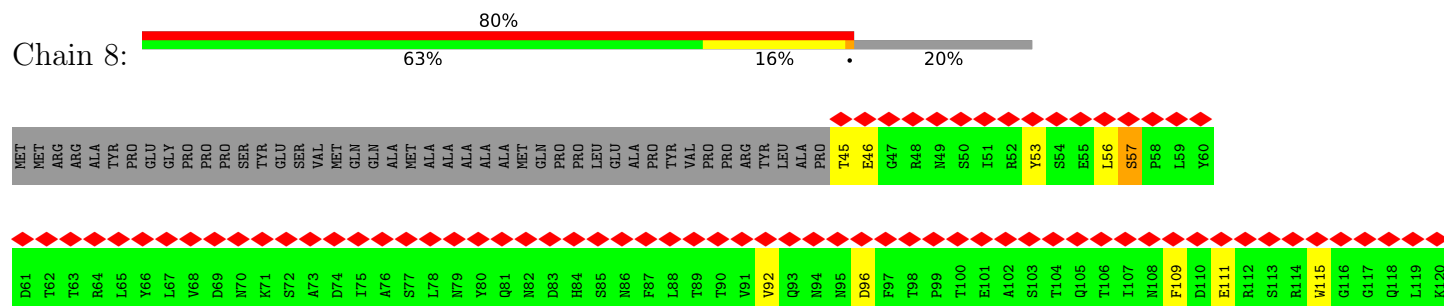
● Molecule 1: Penton protein

Chain 7:



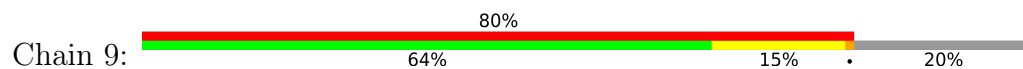
● Molecule 1: Penton protein

Chain 8:

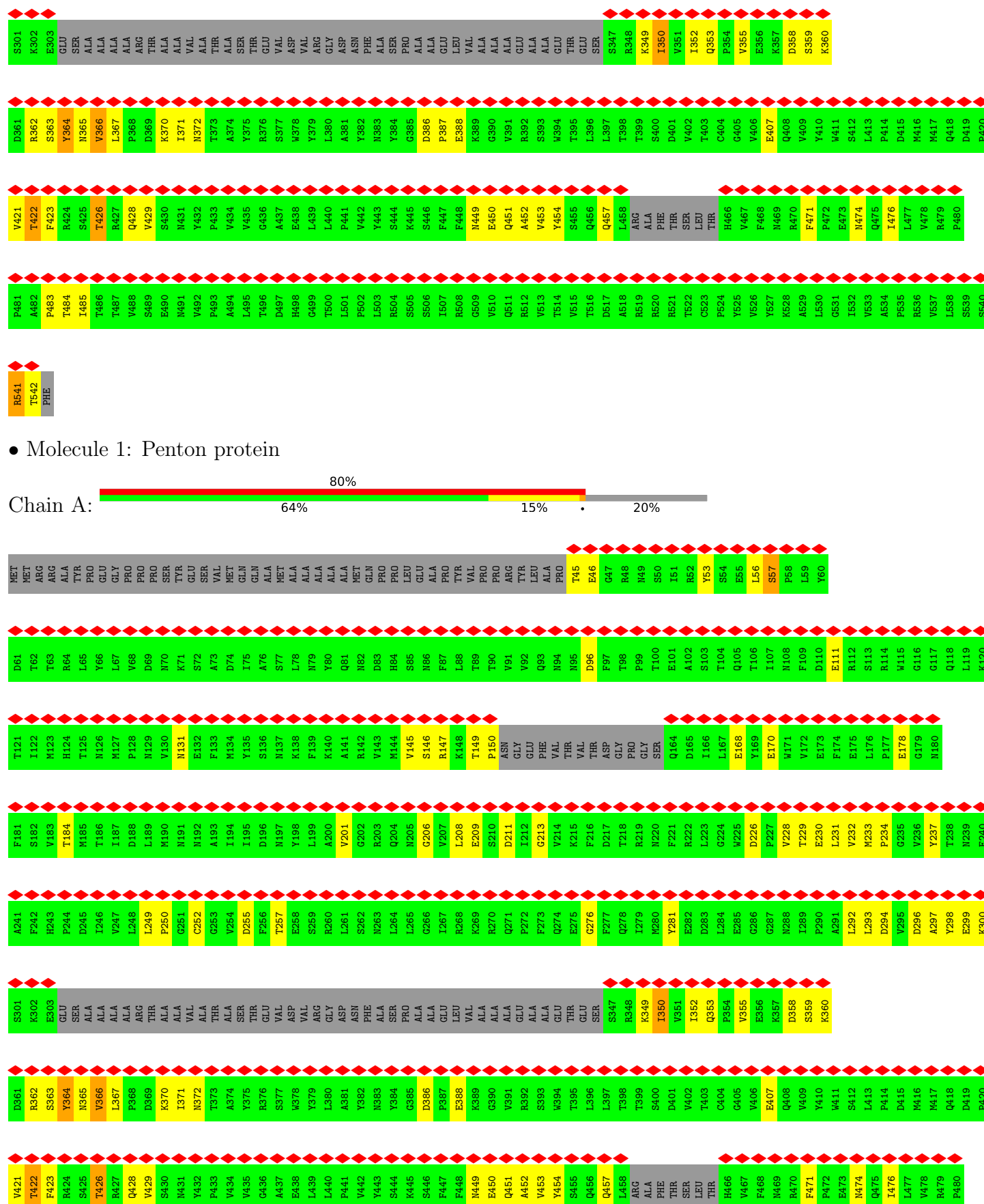


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M123	V183	H243	E303	S363	F423	P483	PHE
H124	T184	P244	GLU	Y364	R424	T484	
T125	M185	D245	SER	N365	S425	T485	
M126	T186	I246	ALA	V366	T426	T486	
M127	I187	V247	ALA	L367	R427	T487	
P128	D188	L248	ALA	P368	Q428	V488	
M129	L189	L249	ARG	D369	V429	S489	
V130	M190	P250	THR	K370	S430	E490	
M131	N191	G251	ALA	I371	M431	M491	
E132	N192	C252	VAL	N372	Y432	V492	
F133	A193	G253	ALA	T373	P433	P493	
M134	I194	V254	THR	A374	V434	A494	
Y135	I195	D255	ALA	Y375	V435	L495	
S136	D196	F256	THR	R376	G436	T496	
N137	Y197	T257	GLU	S377	A437	D497	
K138	Y198	E258	VAL	W378	E438	H498	
F139	L199	S259	ARG	Y379	L439	G499	
K140	A200	R260	GLY	L380	L440	T500	
A141	V201	L261	ASP	A381	P441	L501	
R142	G202	S262	ASN	Y382	V442	P502	
V143	R203	N263	PHE	N383	Y443	L503	
M144	Q204	L264	ALA	Y384	S444	R504	
V145	N205	L265	PRO	G385	K445	S505	
S146	G206	G266	ALA	D386	S446	S506	
R147	V207	I267	GLU	F387	F447	I507	
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T149	E209	K269	VAL	K389	M449	G509	
ASN	S210	R270	ALA	G390	E450	V510	
GLY	D211	Q271	ALA	V391	Q451	Q511	
PHE	I212	P272	GLU	R392	A452	R512	
VAL	G213	F273	ALA	S393	V453	V513	
THR	V214	Q274	GLU	W394	Y454	T514	
VAL	K215	E275	THR	T395	S455	V515	
THR	F216	G276	GLU	L396	Q456	T516	
ASP	D217	F277	SER	L397	Q457	D517	
PRO	T218	Q278	R347	T398	L458	A518	
GLY	R219	I279	R348	T399	ARG	R519	
PRO	N220	M280	K349	S400	ALA	R520	
SER	F221	Y281	I350	D401	PHE	R521	
Q164	R222	E282	V351	A402	THR	T522	
D165	L223	D283	I352	T403	SER	C523	
I166	G224	L284	Q353	C404	LEU	P524	
L167	W225	E285	P354	G405	THR	Y525	
E168	W226	G286	V355	V406	H466	V526	
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V172	E230	P290	S359	M410	F471	A529	
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F174	V232	L292		S412	E473	G531	
L176	M233	L293		L413	M474	V532	
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P177	G235	V295		D415	I476	A534	
E178	D236	D296		M416	L477	P535	
G179	Y237	A297		M417	V478	R536	
N180	T238	Y298		Q418	R479	V537	
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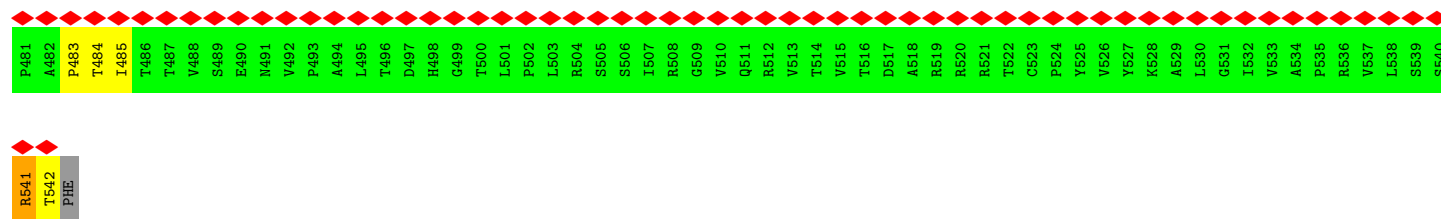
• Molecule 1: Penton protein



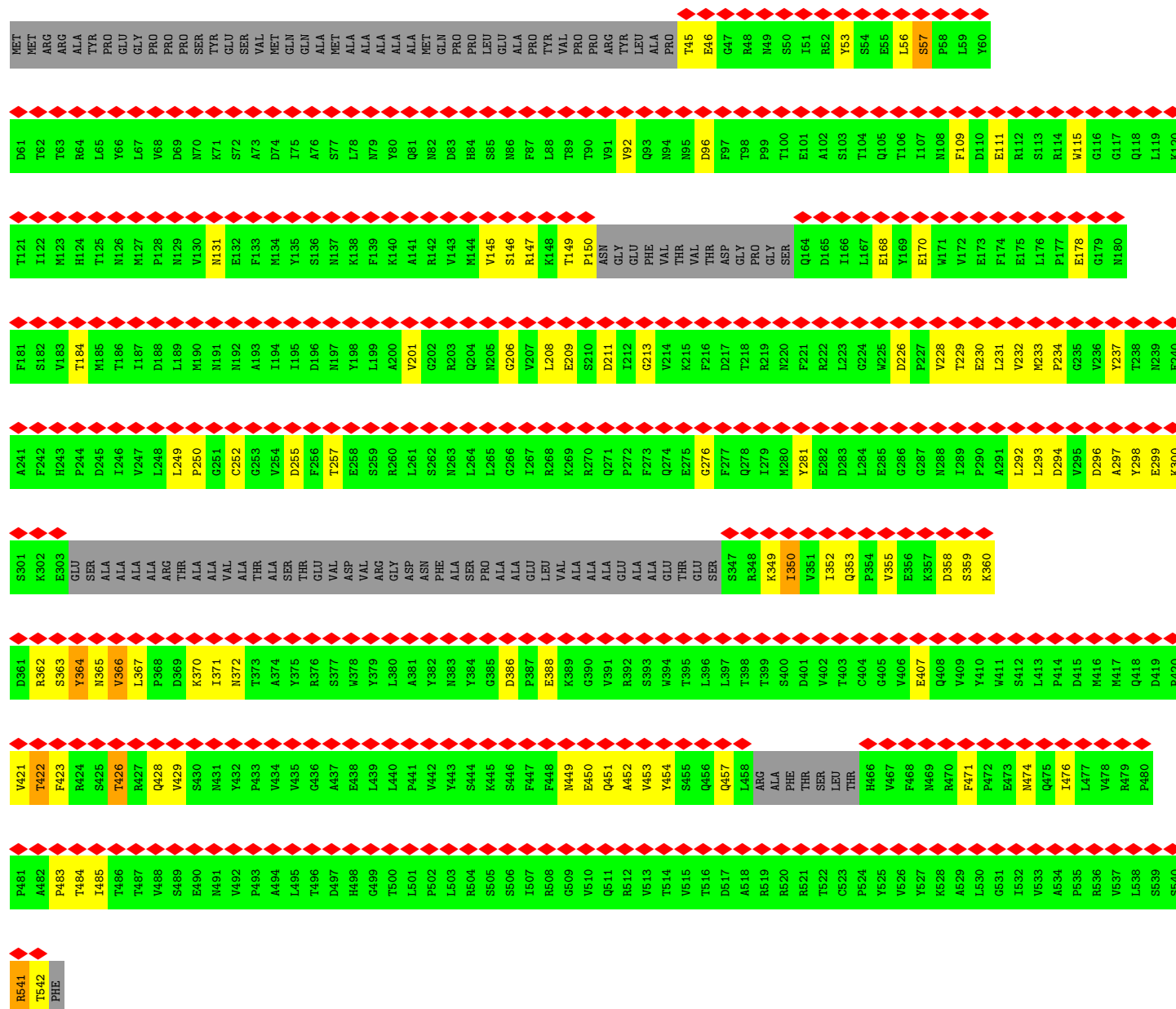
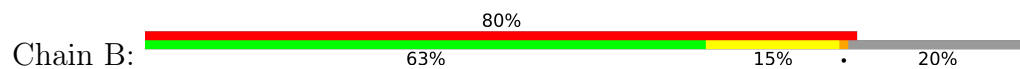
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ALA	R64	H124	T184	P244
TYR	L65	T125	M185	D245
PRO	Y66	M126	T186	I246
GLY	L67	M127	I187	V247
PRO	V68	P128	D188	L248
PRO	D69	M129	L189	L249
PRO	N70	V130	M190	P250
SER	K71	M131	N191	G251
TYR	S72	E132	N192	C252
GLU	A73	F133	A193	G253
SER	D74	M134	I194	V254
VAL	I75	Y135	I195	D255
MET	A76	S136	D196	F256
GLN	S77	M137	Y197	T257
GLN	L78	K138	Y198	E258
ALA	S79	F139	L199	S259
ALA	Y80	K140	A200	R260
ALA	Q81	A141	V201	L261
ALA	N82	R142	G202	S262
GLN	D83	V143	R203	N263
PRO	H84	M144	Q204	L264
PRO	S85	V145	N205	L265
LEU	N86	S146	G206	G266
ALA	F87	R147	V207	I267
ALA	L88	K148	L208	R268
TYR	T89	T149	E209	K269
VAL	T90	P150	S210	R270
PRO	Y91	ASN	D211	Q271
ARG	V92	GLY	I212	P272
TYR	Q93	PHE	G213	F273
ALA	N94	VAL	V214	Q274
PRO	N95	THR	K215	E275
T45	D96	VAL	F216	G276
E46	F97	THR	D217	F277
G47	T98	ASP	T218	Q278
R48	P99	PRO	R219	I279
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R51	A102		R222	E282
R52	S103		L223	D283
Y53	T104		G224	L284
S54	Q105		W225	E285
E55	T106		E168	L167
L56	T107		E169	I166
S57	N108		D226	E168
P58	F109		P227	Y169
L59	D110		V228	E170
Y60	E111		W171	E171
	R112		V172	V172
	S113		E230	E230
	R114		L231	L231
	W115		V232	V232
	G116		M233	M233
	G117		P234	P234
	L119		G235	G235
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			Y237	Y237
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			N239	N239
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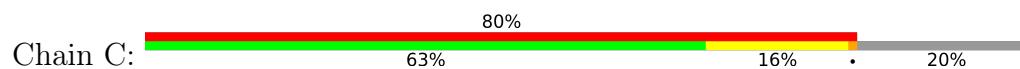
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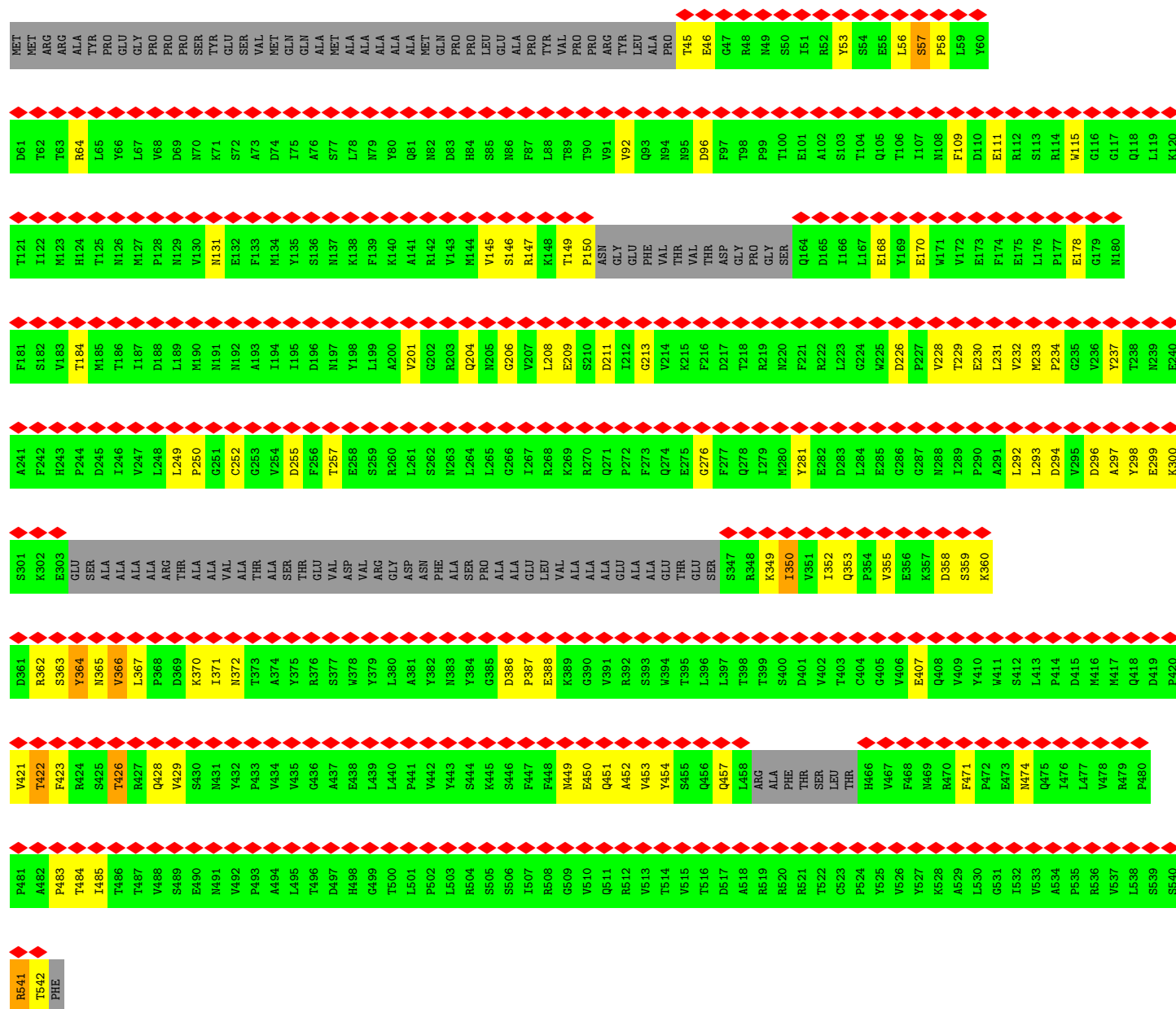


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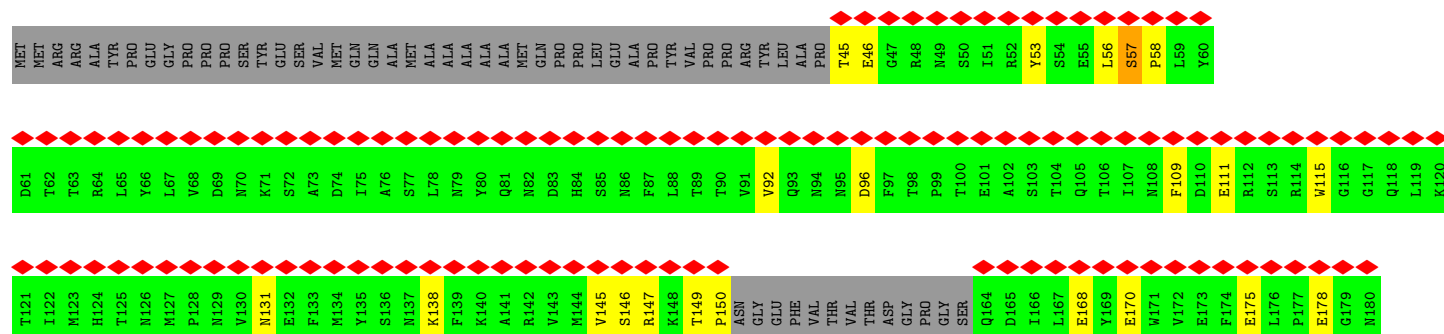


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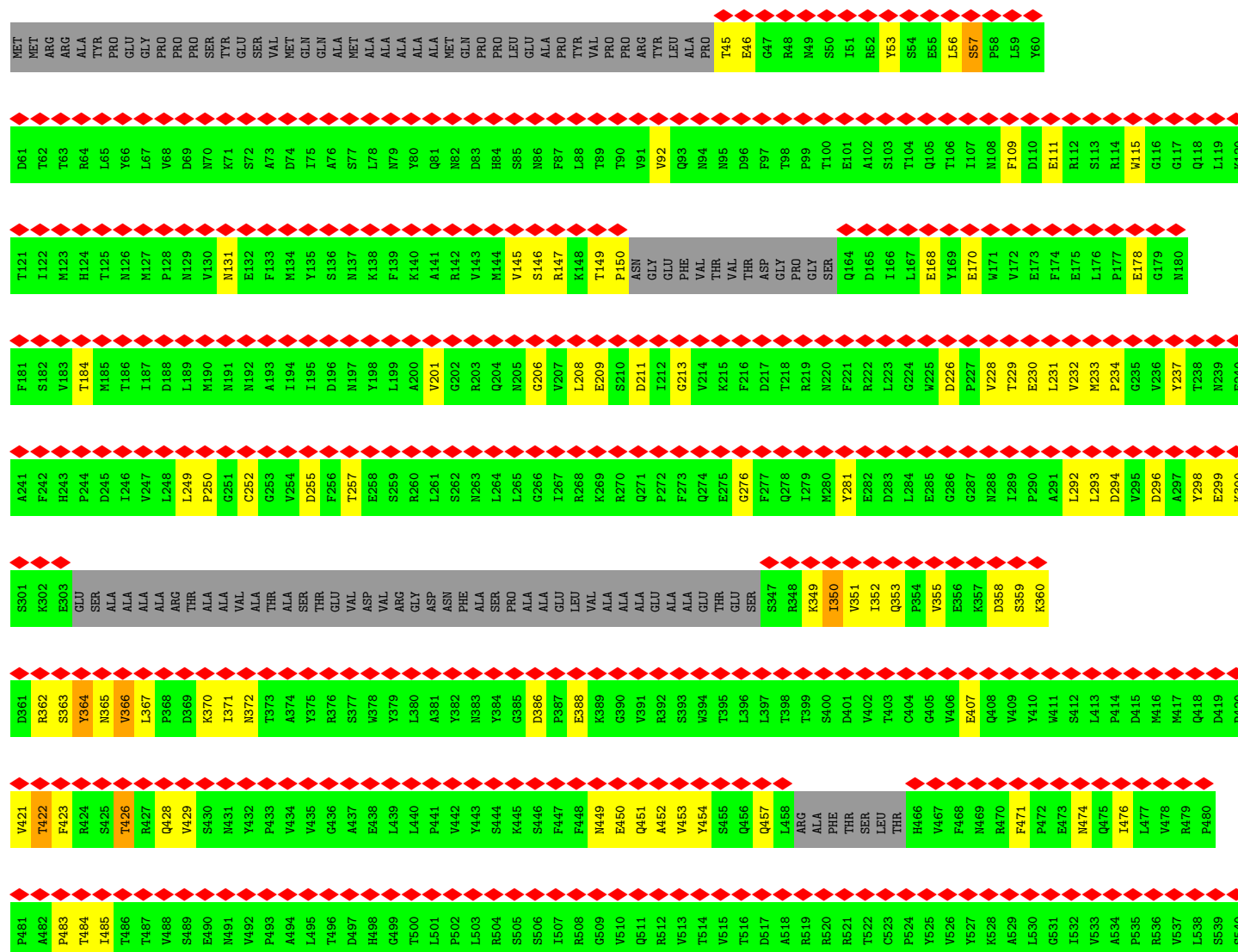
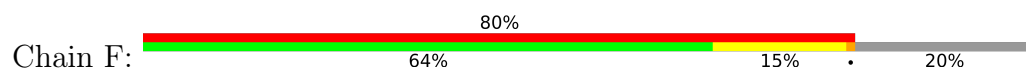


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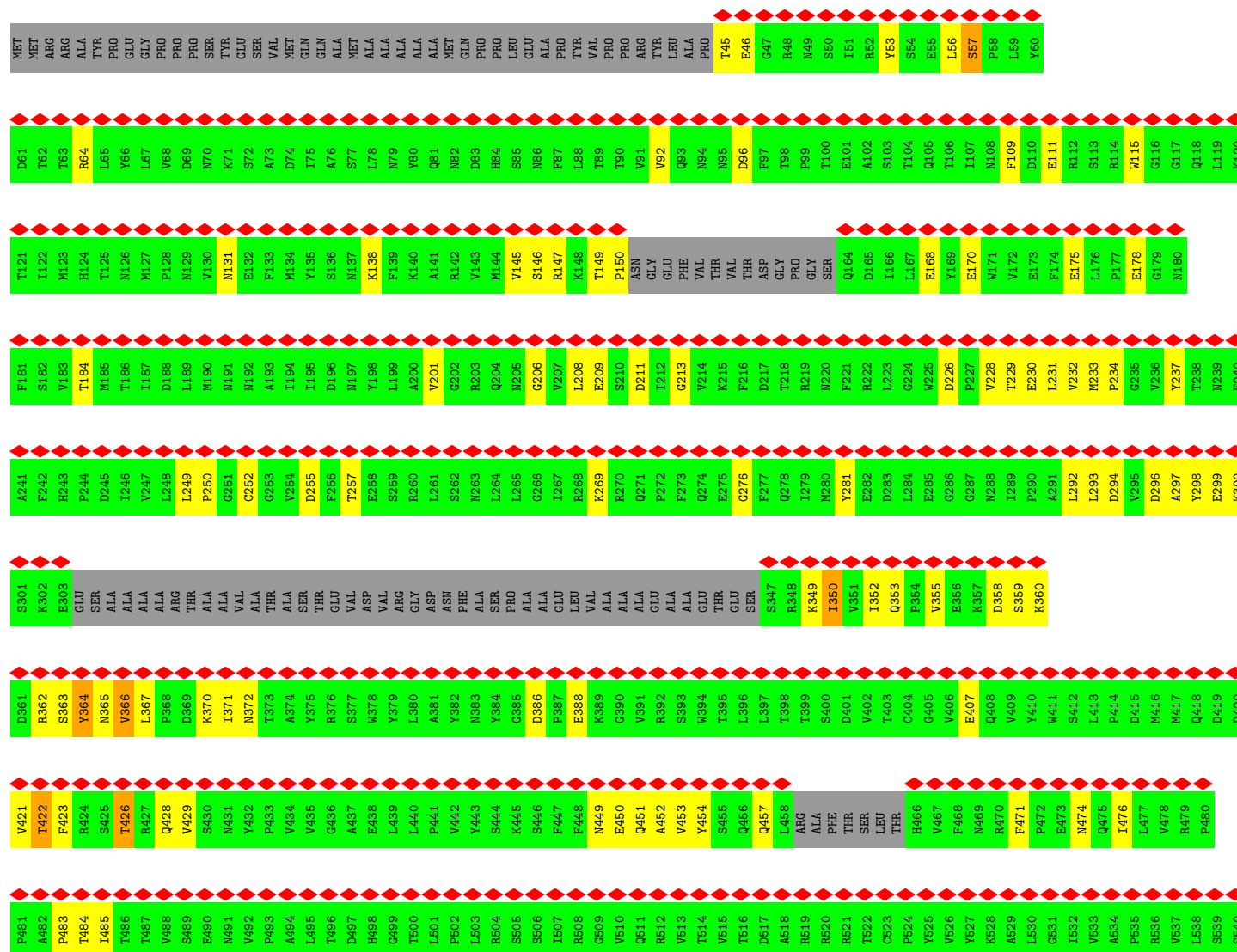
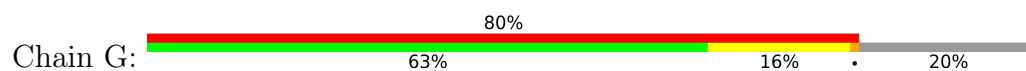


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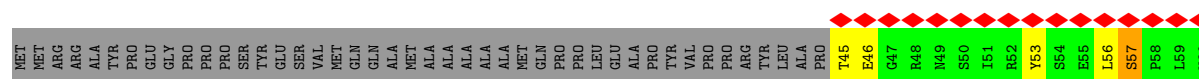




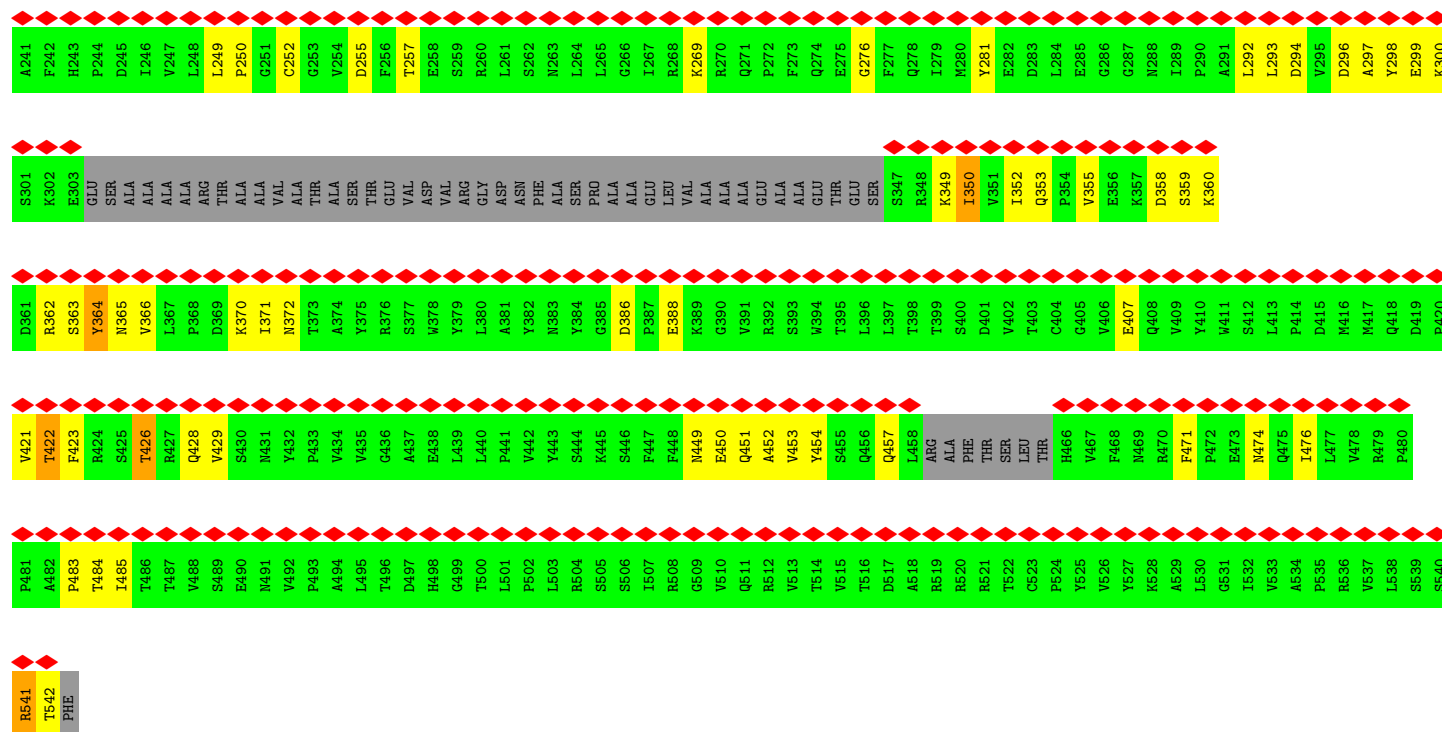
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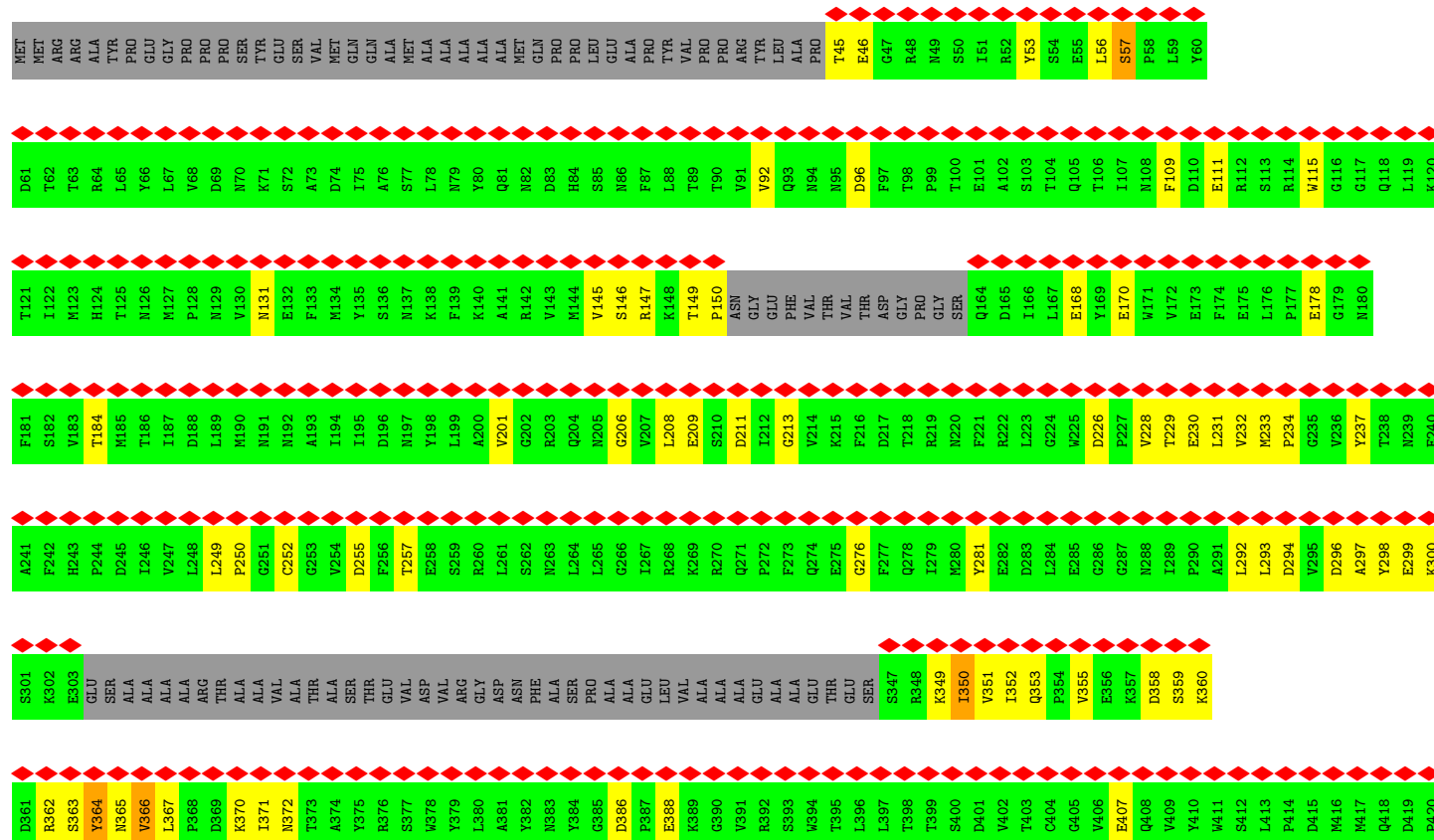
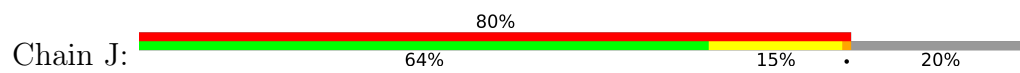
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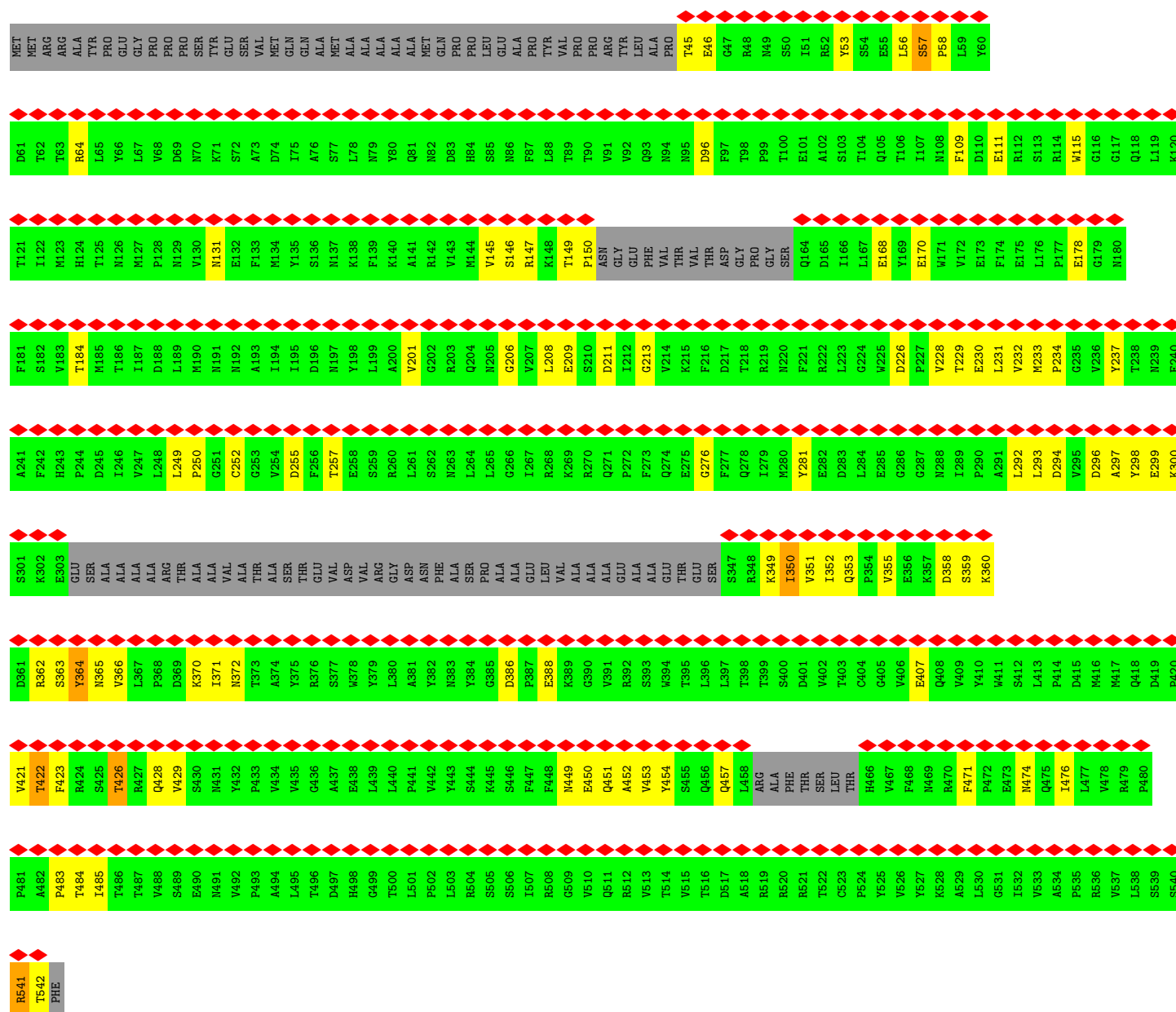






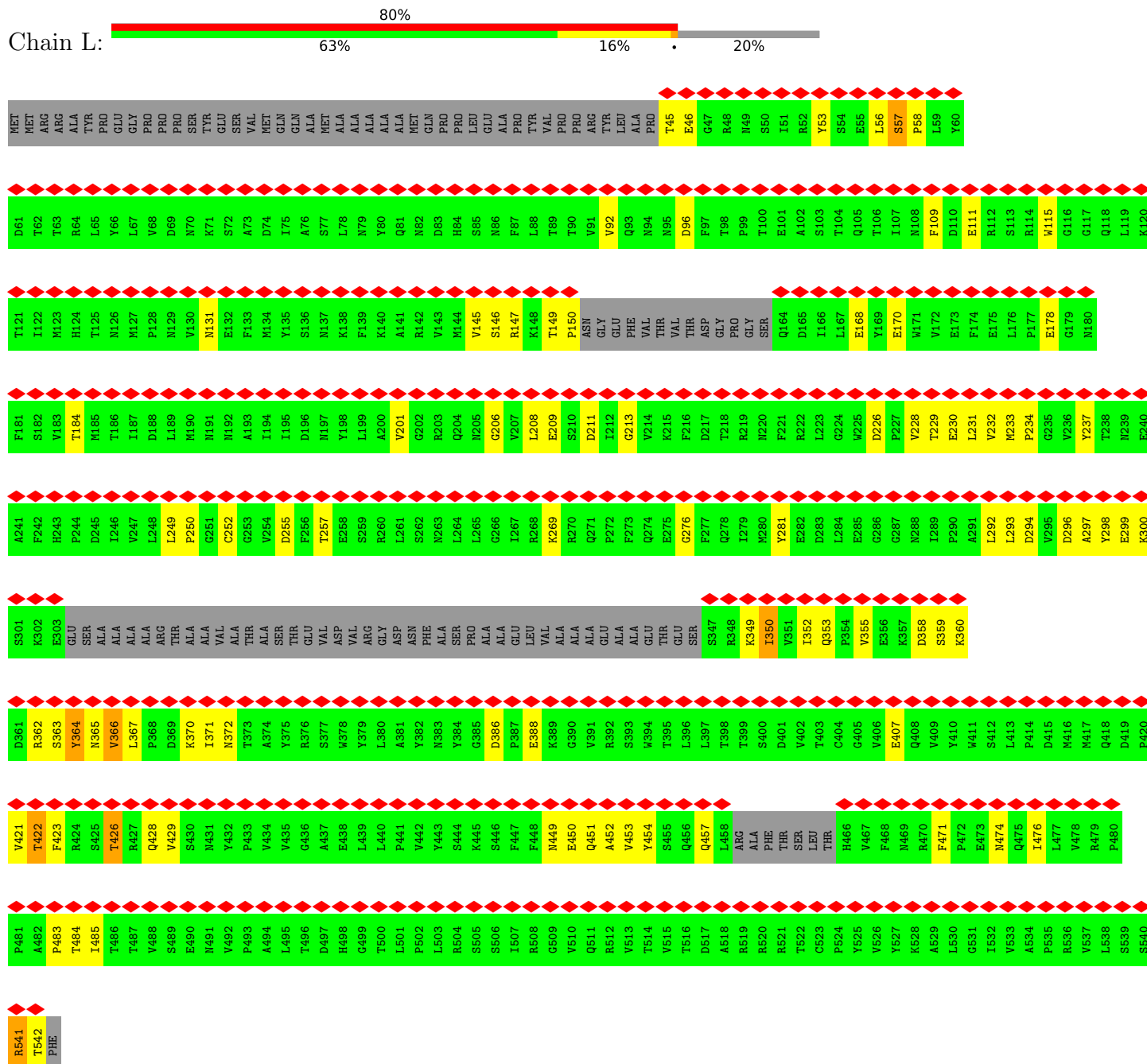
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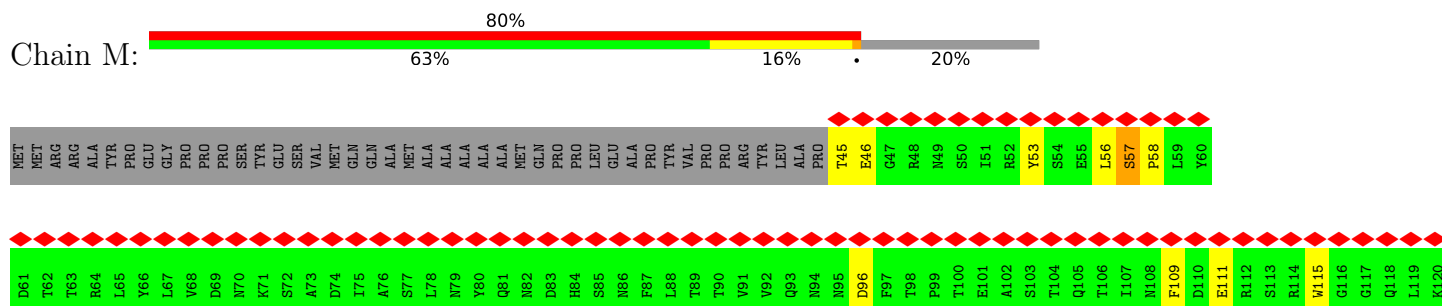
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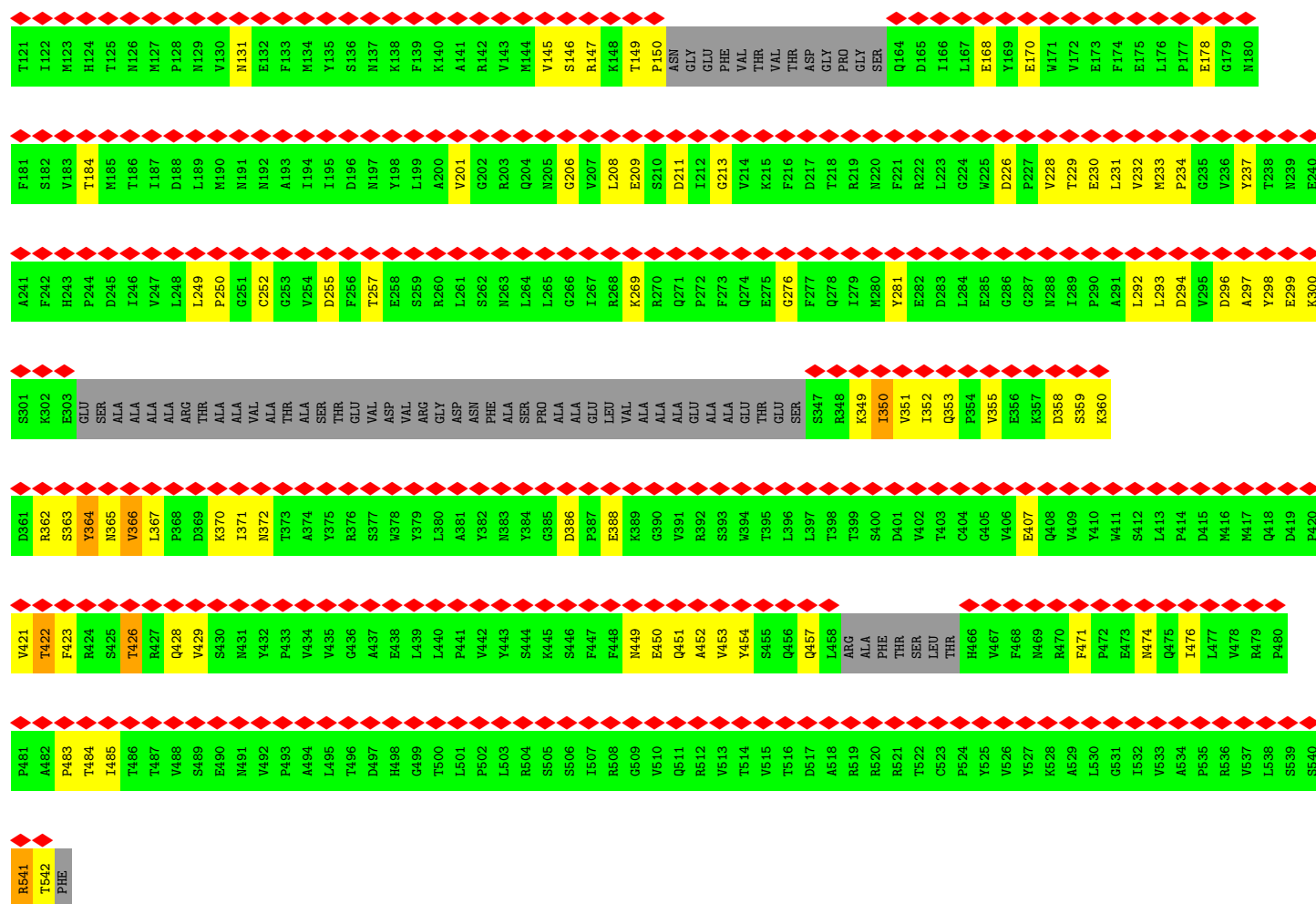
Chain L:



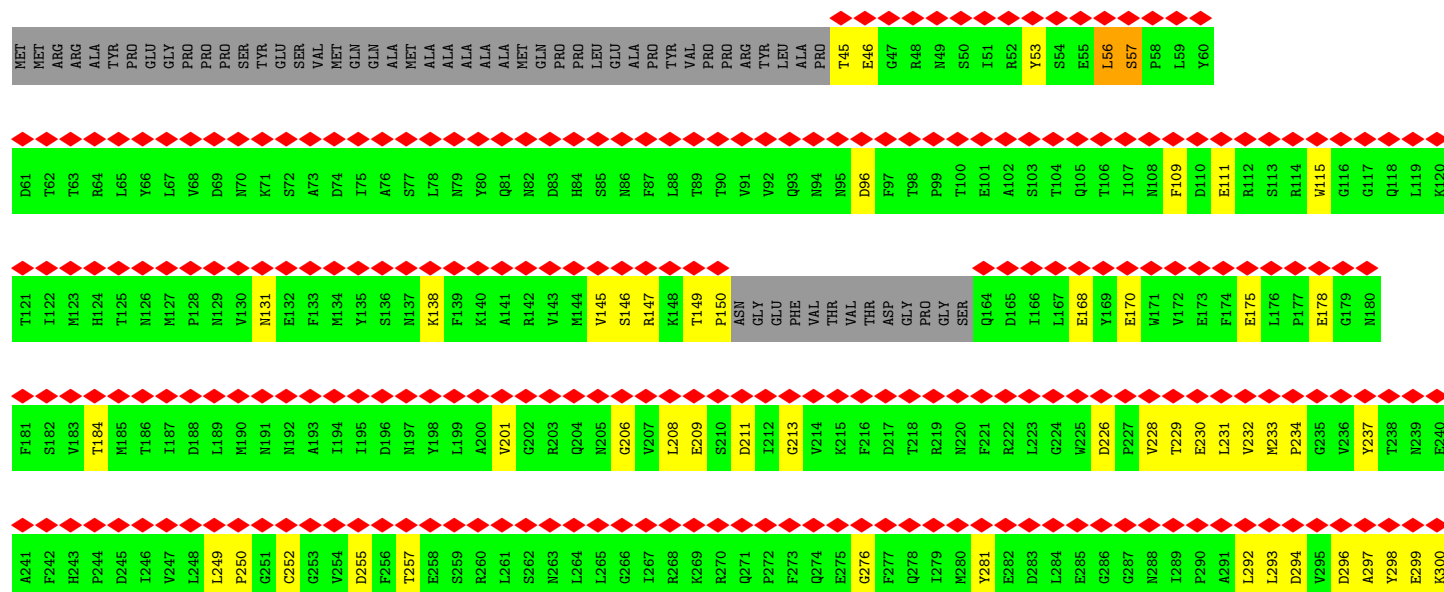
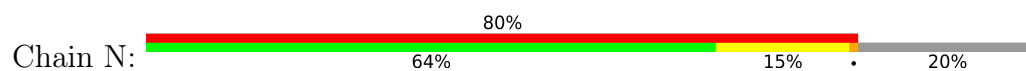
- Molecule 1: Penton protein

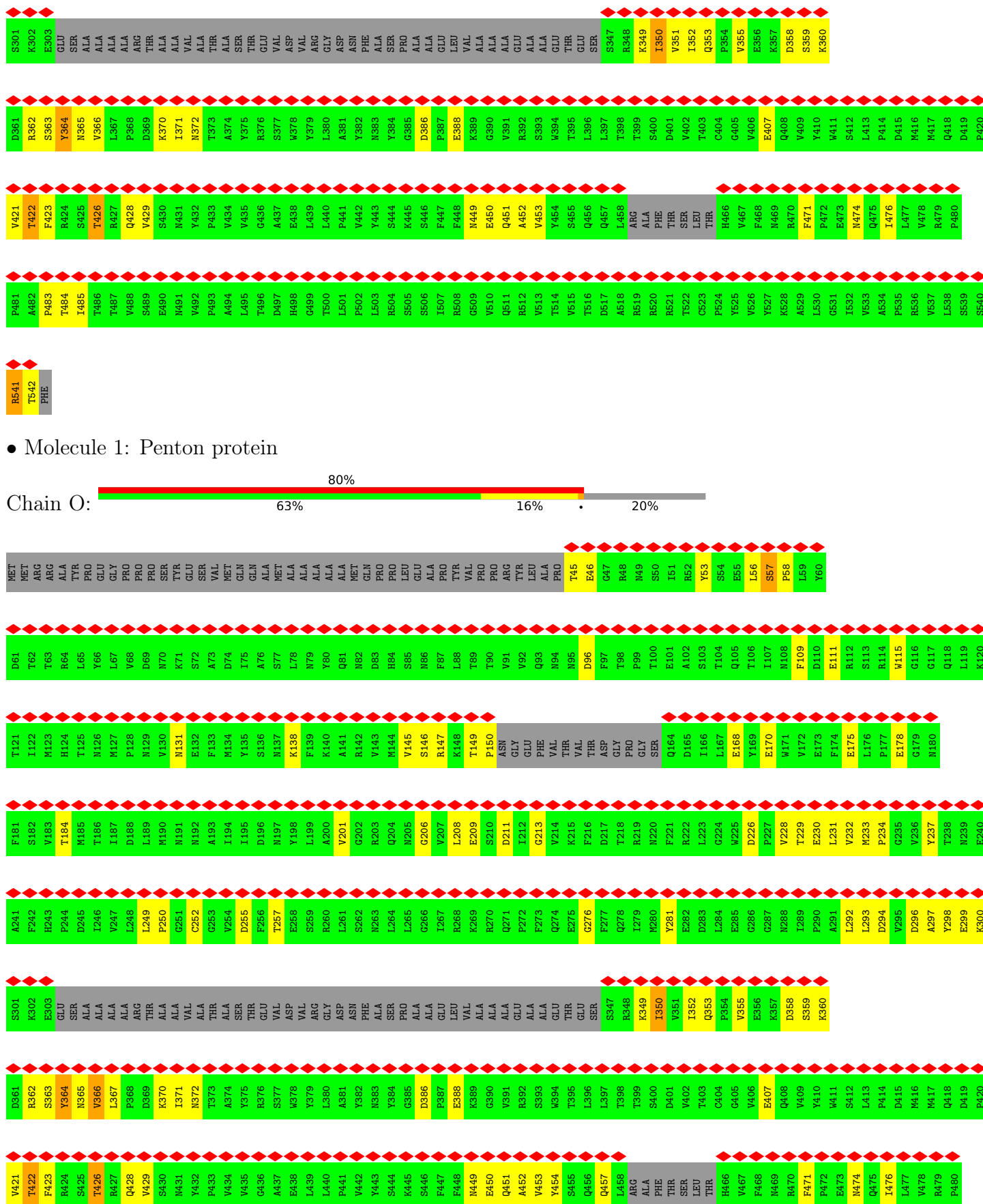
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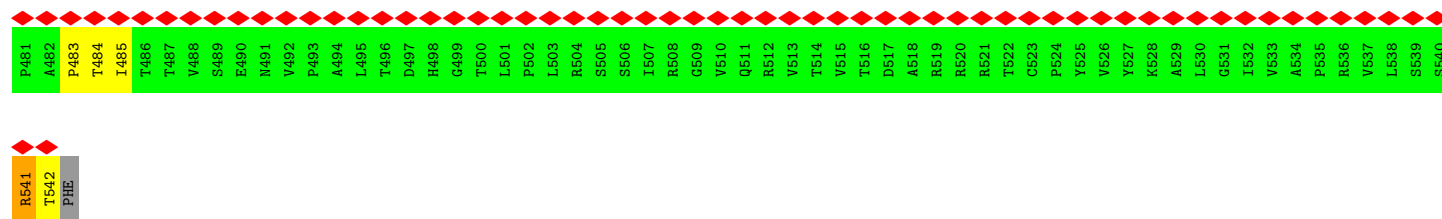




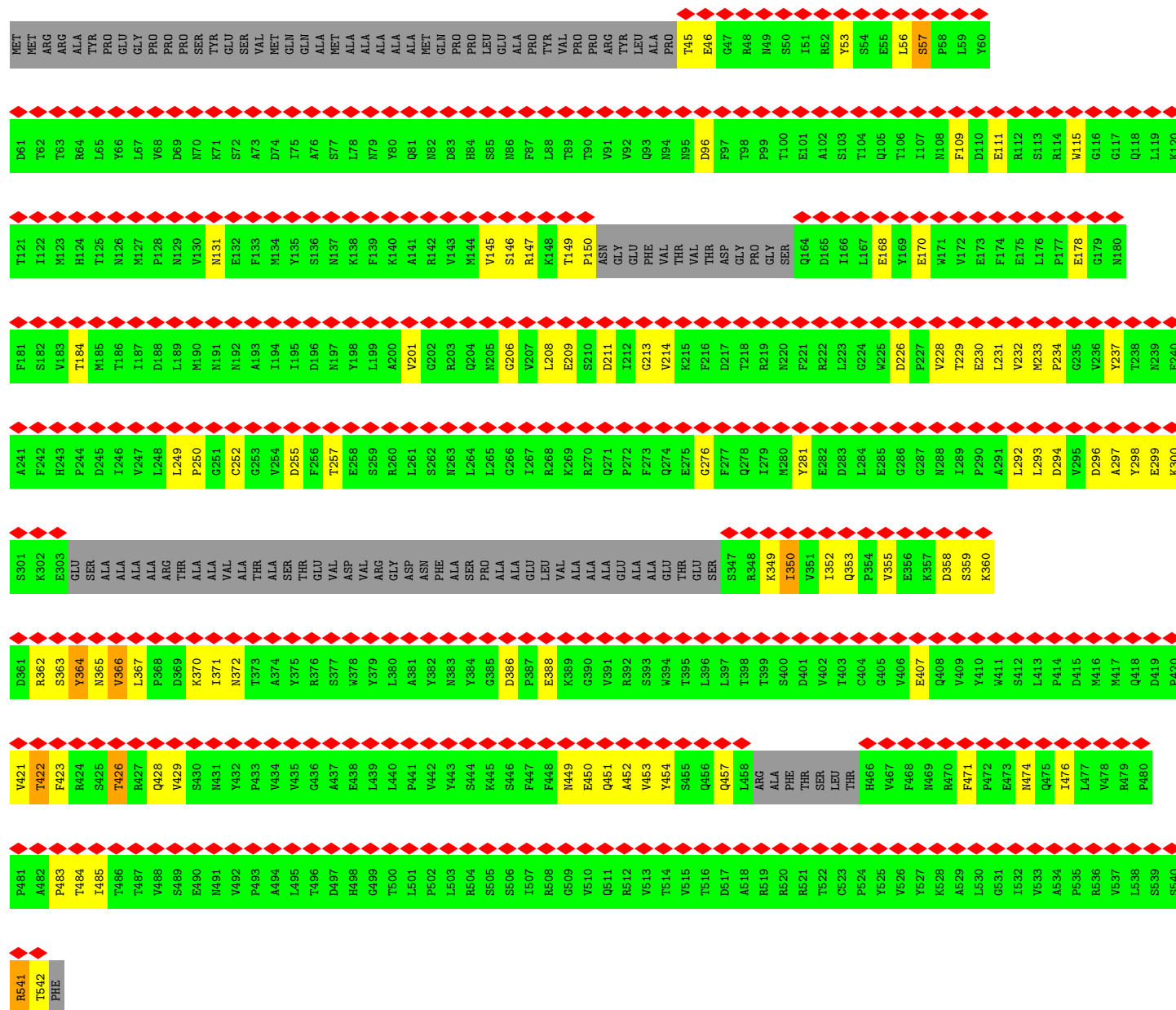
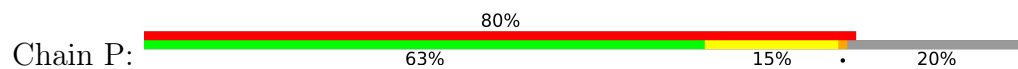
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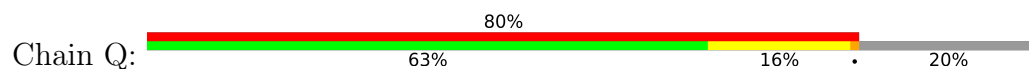


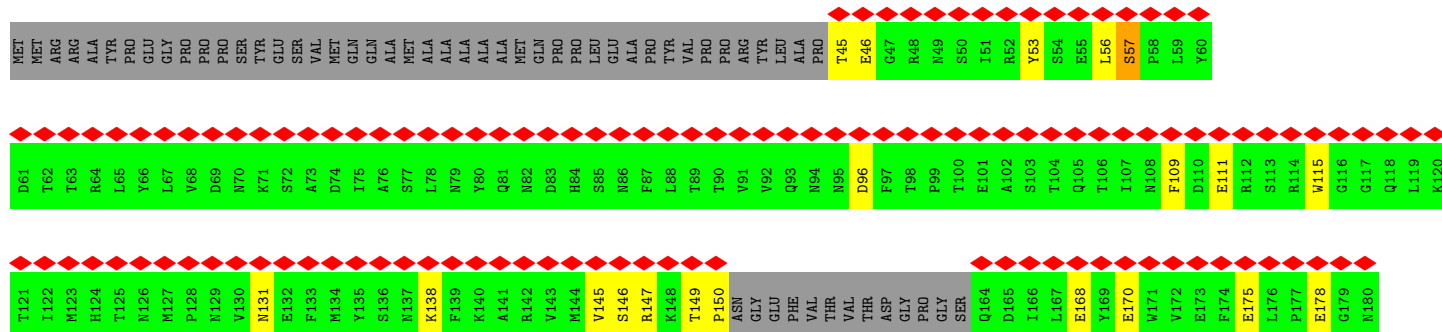
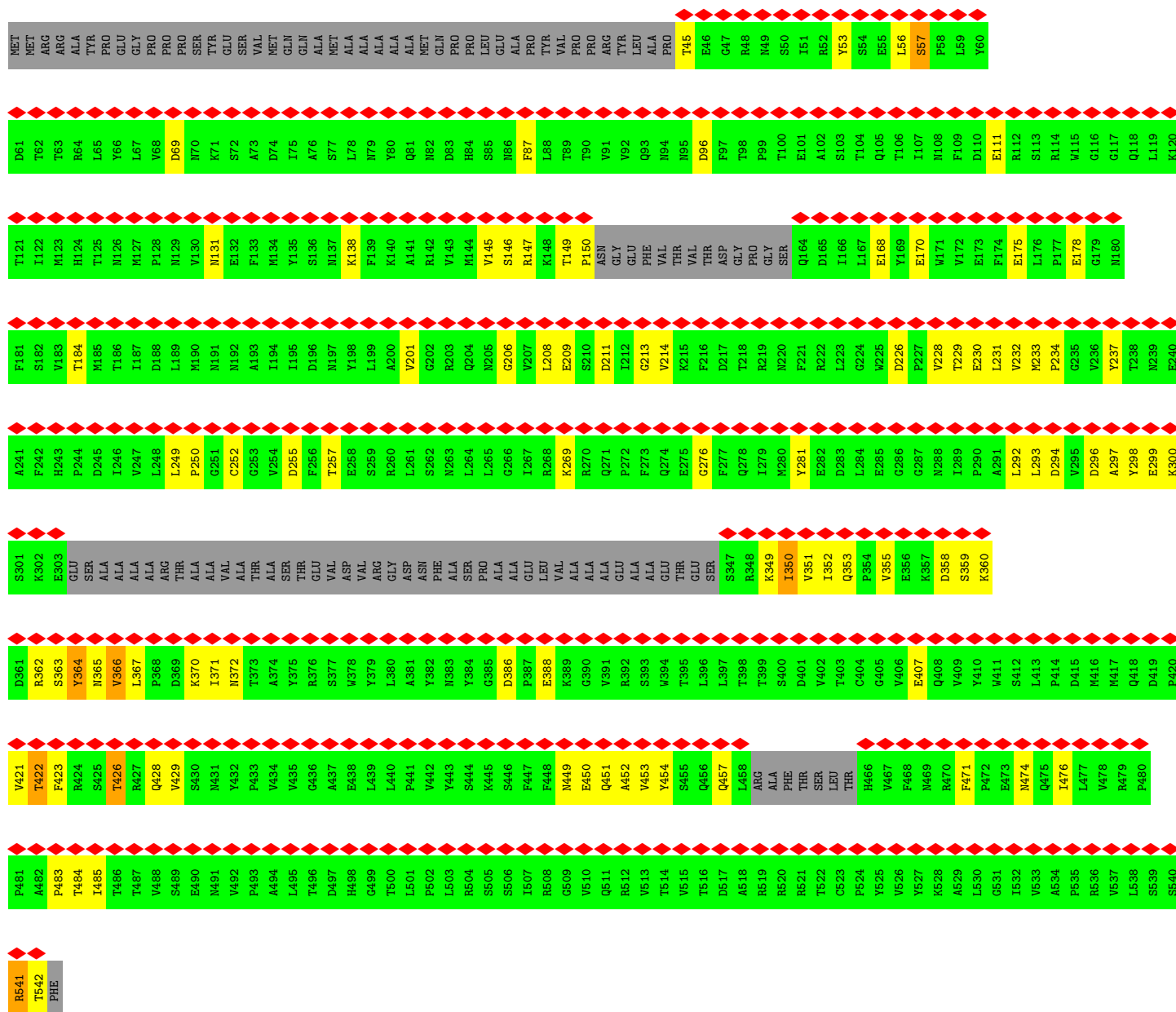


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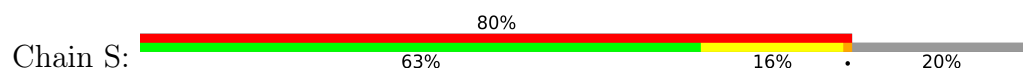
• Molecule 1: Penton protein





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V183	H243	E303	S363	F423	P483	PHE
T184	P244	GLU	Y364	R424	T484	
M185	I245	SER	N365	S425	T485	
T186	I246	ALA	V366	T426	T486	
I187	V247	ALA	L367	R427	T487	
D188	L248	ALA	P368	Q428	V488	
L189	L249	ARG	D369	V429	S489	
M190	P250	THR	K370	S430	E490	
N191	G251	ALA	I371	N431	M491	
N192	C252	VAL	N372	Y432	V492	
A193	G253	ALA	T373	P433	P493	
I194	V254	THR	A374	V434	A494	
I195	D255	SER	Y375	V435	L495	
D196	F256	THR	R376	G436	T496	
N197	T257	GLU	S377	A437	D497	
Y198	E258	VAL	W378	E438	H498	
L199	S259	VAL	Y379	L439	G499	
A200	R260	ARG	L380	L440	T500	
V201	L261	GLY	A381	P441	L501	
G202	S262	ASP	Y382	V442	P502	
R203	N263	ASN	N383	Y443	L503	
Q204	L264	ALA	Y384	S444	R504	
N205	L265	SER	R385	K445	S505	
G206	G266	PRO	D386	S446	S506	
V207	I267	ALA	P387	F447	I507	
L208	R268	GLU	E388	F448	R508	
E209	K269	LEU	K389	N449	G509	
S210	R270	VAL	G390	E450	V510	
D211	Q271	ALA	V391	Q451	Q511	
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G213	F273	GLU	S393	V453	V513	
V214	Q274	ALA	W394	V454	T514	
K215	E275	GLU	T395	S455	V515	
F216	G276	THR	L396	Q456	T516	
D217	F277	GLU	L397	Q457	D517	
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N220	M280	R348	S400	ALA	R520	
F221	Y281	PHE	D401	THR	R521	
R222	E282	I350	V402	SER	T522	
L223	D283	V351	T403	LEU	C523	
G224	L284	Q353	C404	THR	P524	
W225	E285	P354	G405	H466	Y525	
D226	G286	V355	V406	V467	V526	
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T229	I289	D358	V409	R470	A529	
E230	P290	S359	Y410	F471	L530	
L231	A291	K360	W411	P472	G531	
V232	L292		S412	E473	I532	
M233	L293		L413	N474	V533	
P234	D294		P414	Q475	A534	
G235	V295		D415	I476	P535	
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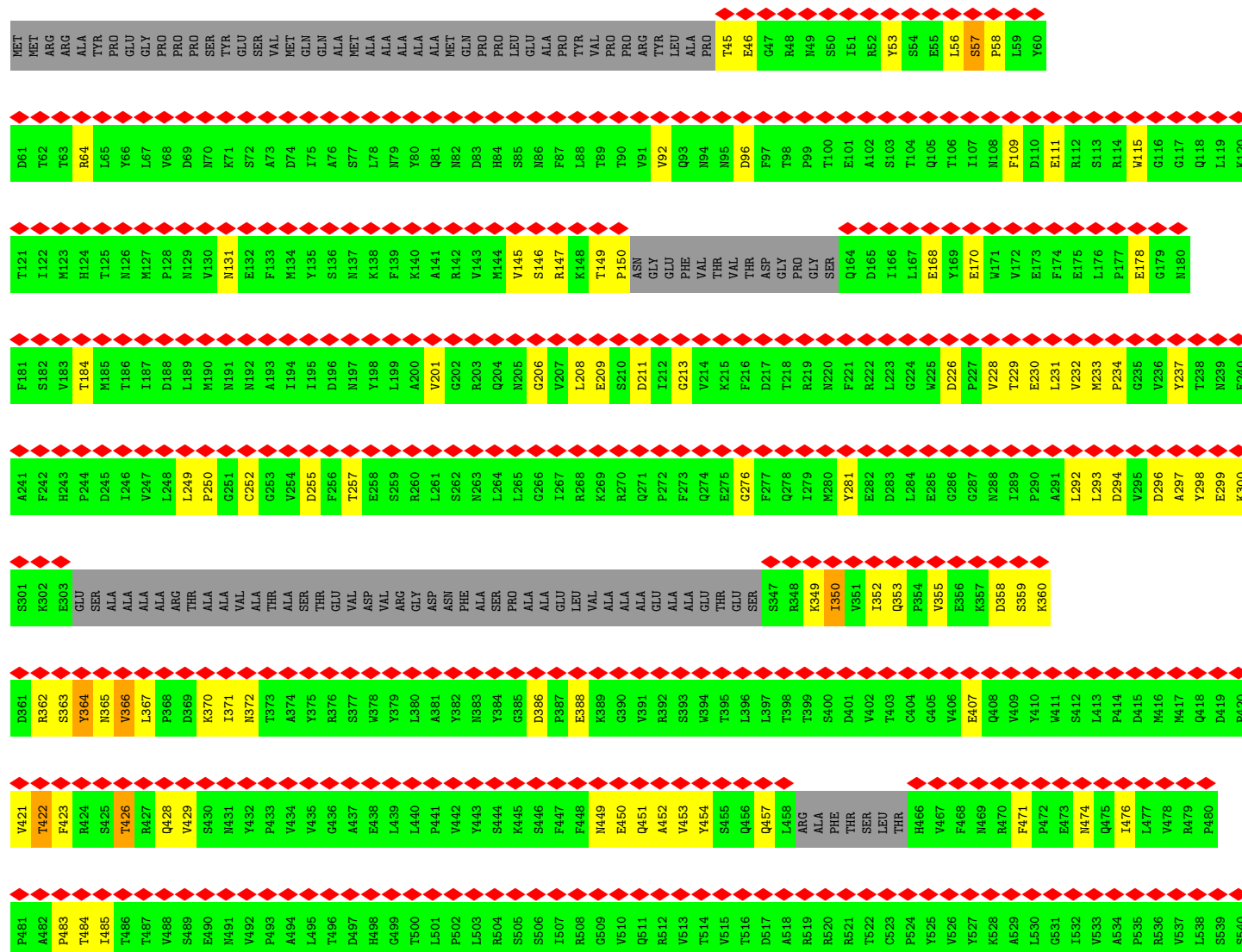
• Molecule 1: Penton protein



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ARG	T63	M123	V183	H243	E303
ALA	R64	H124	T184	P244	GLU
TYR	L65	T125	M185	I245	SER
PRO	V66	M126	T186	I246	ALA
GLY	L67	M127	I187	V247	ALA
PRO	V68	P128	D188	L248	ALA
PRO	D69	M129	L189	L249	ARG
SER	N70	V130	M190	P250	THR
TYR	K71	M131	N191	G251	ALA
GLU	S72	E132	N192	C252	ALA
SER	A73	F133	A193	G253	THR
VAL	D74	M134	I194	V254	ALA
MET	I75	Y135	I195	D255	ALA
GLN	A76	S136	D196	F256	SER
ALA	S77	M137	N197	T257	THR
ALA	L78	K138	Y198	E258	GLU
ALA	N79	F139	L199	S259	VAL
ALA	Q81	K140	A200	R260	VAL
ALA	N82	A141	V201	L261	GLY
MET	D83	R142	G202	S262	ASP
GLN	H84	V143	R203	N263	ASN
PRO	S85	M144	Q204	L264	ALA
LEU	N86	V145	N205	L265	SER
ALA	F87	S146	G206	G266	PRO
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TYR	T89	K148	L208	R268	ALA
PRO	T90	T149	E209	K269	LEU
PRO	V91	P150	S210	R270	VAL
ARG	V92	ASN	D211	Q271	ALA
LEU	Q93	GLY	I212	P272	ALA
ALA	N94	PHE	G213	F273	ALA
PRO	N95	VAL	V214	Q274	GLU
T45	D96	THR	K215	E275	THR
E46	F97	VAL	F216	G276	GLU
G47	T98	THR	D217	F277	SER
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S50	T100	GLY	R219	I279	R348
I51	E101	GLY	N220	M280	K349
R52	A102	SER	F221	Y281	I350
Y53	S103	LEU	R222	E282	V351
S54	T104	D165	L223	D283	I352
E55	Q105	I166	G224	L284	Q353
L56	T106	L167	W225	E285	P354
S57	I107	E168	D226	G286	V355
P58	N108	Y169	P227	G287	E356
L59	F109	E170	V228	N288	K357
Y60	D110	W171	T229	I289	D358
	E111	E172	E230	P290	S359
	R112	F174	L231	A291	K360
	S113	E175	V232	L292	
	R114	L176	M233	L293	
	W115	P177	P234	D294	
	G116	E178	G235	V295	
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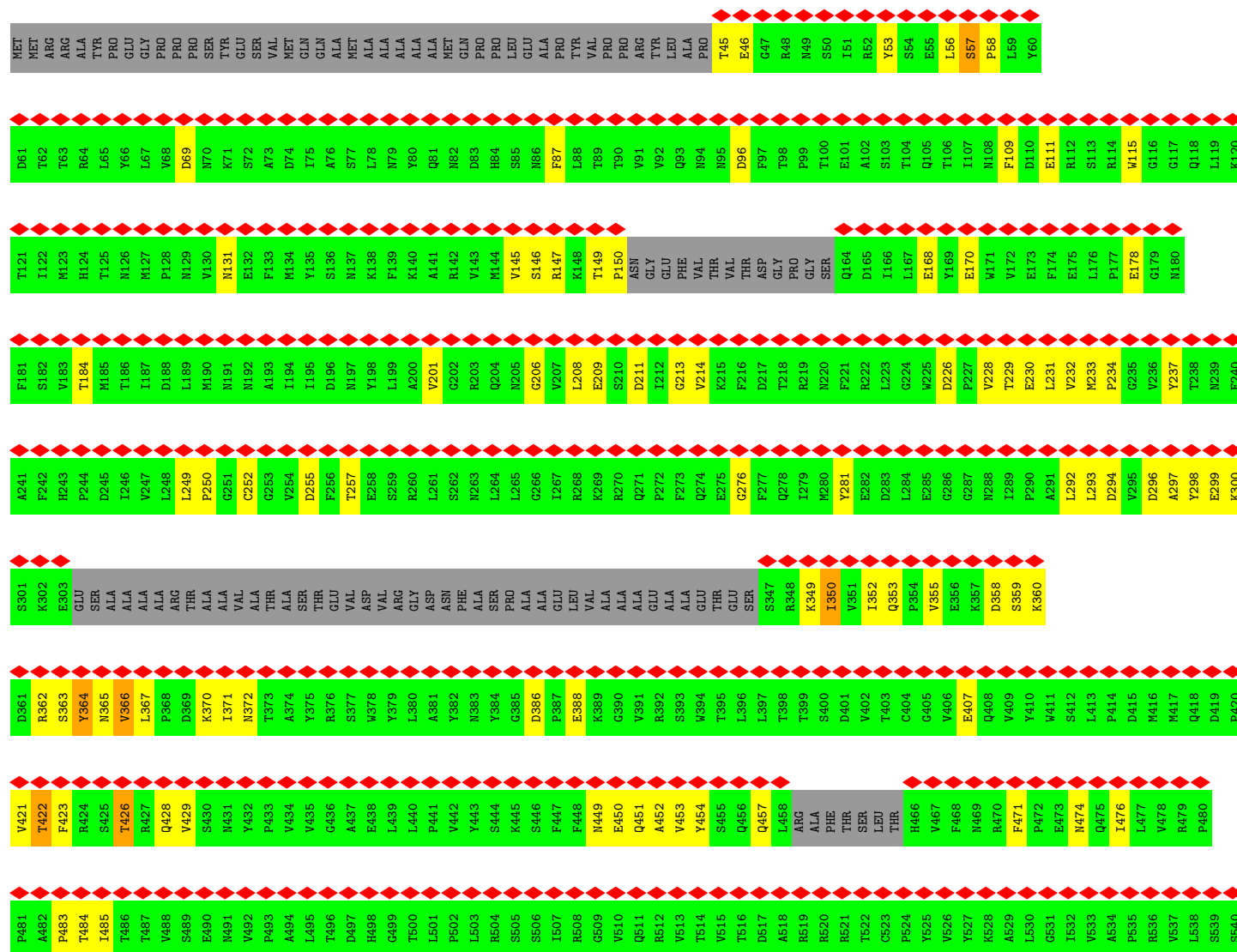
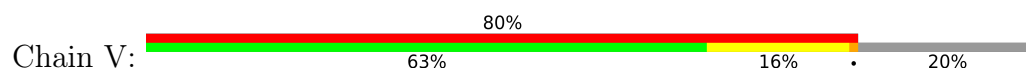


• Molecule 1: Penton protein

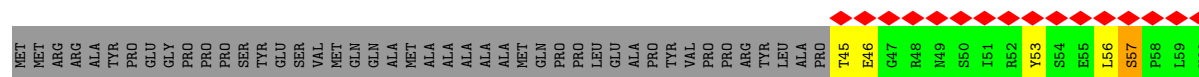
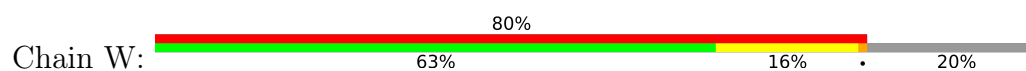




• Molecule 1: Penton protein

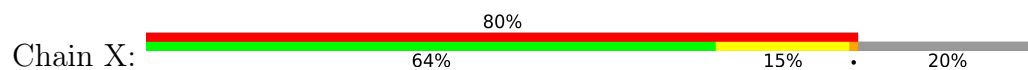


• Molecule 1: Penton protein

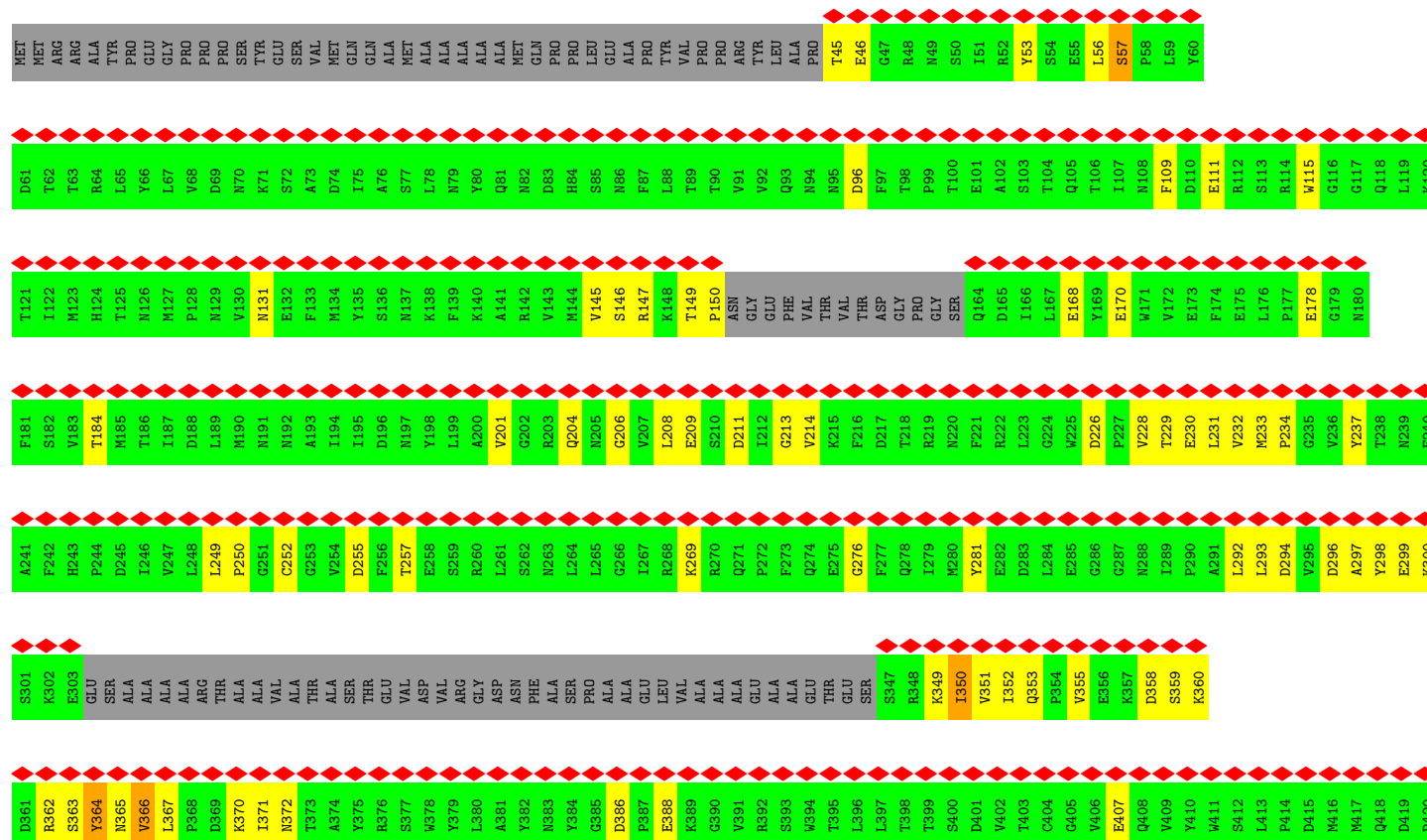


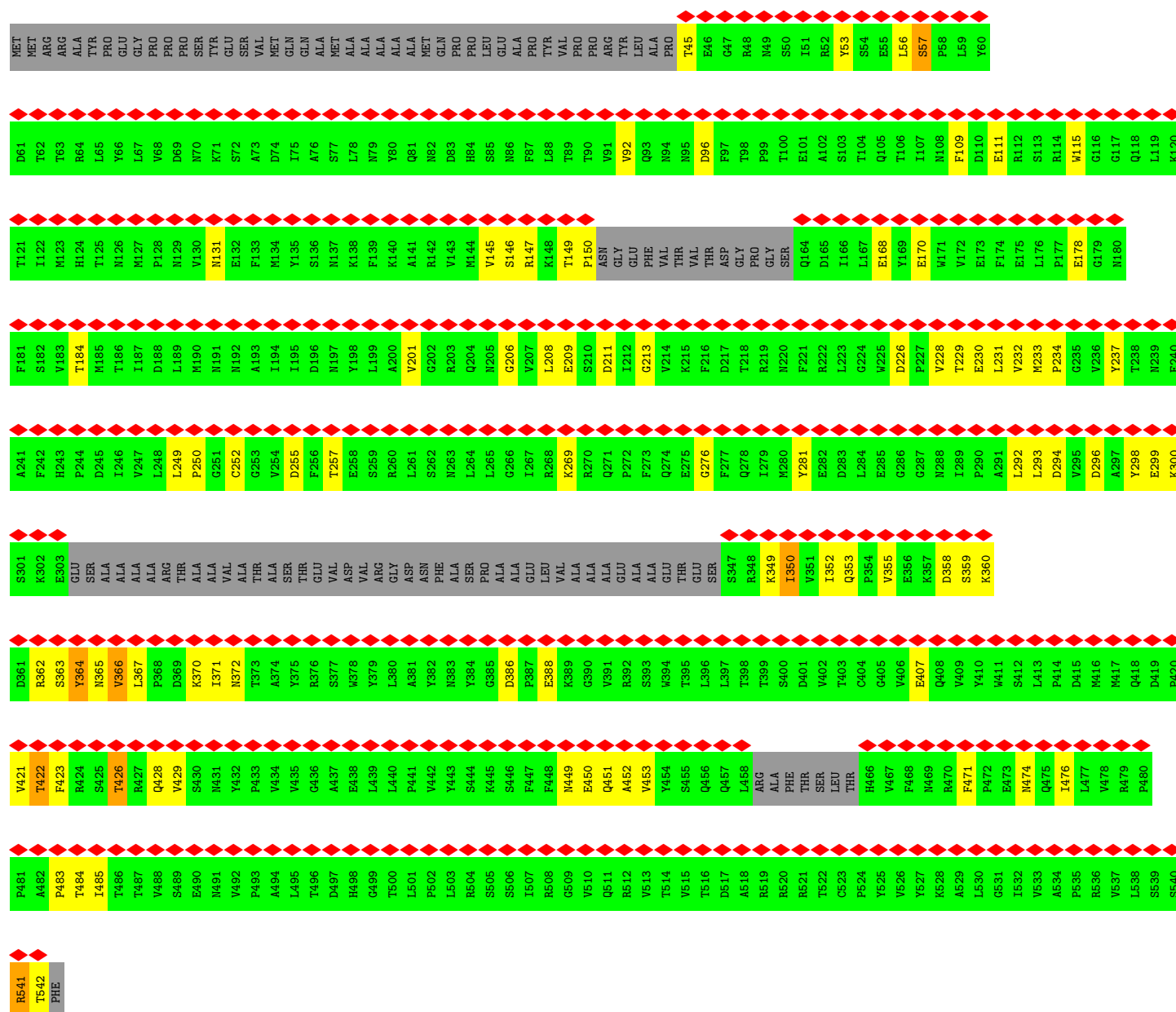
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R64	H124	T184	P244	GLU	Y364	R424	T484	
L65	T125	M185	I245	SER	N365	S425	I485	
Y66	M126	T186	I246	ALA	N366	T426	T486	
L67	M127	I187	V247	ALA	L367	R427	T487	
V68	P128	D188	L248	ALA	P368	Q428	V488	
D69	M129	L189	L249	ARG	D369	V429	S489	
N70	V130	M190	P250	THR	K370	V429	E490	
K71	N131	N191	G251	ALA	I371	S430	N491	
S72	E132	N192	C252	VAL	N372	M431	V492	
A73	F133	A193	G253	ALA	T373	P432	P493	
D74	M134	I194	V254	THR	A374	V434	A494	
I75	Y135	I195	D255	SER	Y375	V435	L495	
A76	S136	D196	F256	THR	R376	G436	T496	
S77	M137	Y197	T257	GLU	S377	A437	D497	
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Y80	K140	A200	R260	ARG	L380	L440	T500	
Q81	A141	V201	L261	GLY	A381	P441	L501	
N82	R142	G202	S262	ASP	Y382	V442	P502	
D83	V143	R203	N263	ASN	N383	Y443	L503	
H84	M144	Q204	L264	ALA	Y384	S444	R504	
S85	V145	N205	L265	SER	G385	K445	S505	
N86	S146	G206	G266	PRO	D386	S446	S506	
F87	R147	V207	I267	ALA	P387	F447	L507	
L88	K148	L208	R268	GLU	E388	F448	R508	
T89	T149	E209	K269	LEU	K389	M449	G509	
T90	S210	G211	R270	VAL	G390	E450	V510	
V91	D211	I212	Q271	ALA	V391	Q451	Q511	
V92	G213	G214	P272	GLU	R392	A452	R512	
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S103	D165	R222	E283	V351	V402	SER	T522	
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Q105	L167	G224	L284	P354	C404	THR	P524	
T106	E168	W225	E285	V355	G405	H466	Y525	
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N108	E170	P227	G287	K357	E407	M469	Y527	
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R112	F174	L231	A291		W411	E473	G531	
S113	E175	V232	L292		S412	M474	T532	
R114	P177	M233	L293		L413	Q475	V533	
W115	E178	G235	D294		D415	L476	P535	
G116	G179	V236	V295		M416	L477	R536	
G117	T237	Y237	D296		Q417	V478	V537	
Q118	N239	E240	A297		M418	R479	L538	
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• Molecule 1: Penton protein

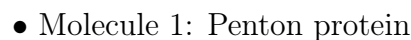


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ALA	T63	M123	V183	ALA	T63	M123	V183
TYR	R64	H124	T184	TYR	R64	H124	T184
PRO	L65	T125	M185	PRO	L65	T125	M185
GLY	Y66	M126	T186	GLY	Y66	M126	T186
PRO	L67	M127	I187	PRO	L67	M127	I187
PRO	V68	P128	D188	PRO	V68	P128	D188
PRO	D69	M129	L189	PRO	D69	M129	L189
SER	N70	V130	M190	SER	N70	V130	M190
TYR	K71	N131	N191	TYR	K71	N131	N191
GLU	S72	E132	N192	GLU	S72	E132	N192
SER	A73	F133	A193	SER	A73	F133	A193
VAL	D74	M134	I194	VAL	D74	M134	I194
MET	I75	Y135	I195	MET	I75	Y135	I195
GLN	A76	S136	D196	GLN	A76	S136	D196
ALA	S77	M137	Y197	ALA	S77	M137	Y197
ALA	L78	K138	Y198	ALA	L78	K138	Y198
ALA	N79	F139	L199	ALA	N79	F139	L199
ALA	Y80	K140	A200	ALA	Y80	K140	A200
ALA	Q81	A141	V201	ALA	Q81	A141	V201
MET	N82	R142	G202	MET	N82	R142	G202
GLN	D83	V143	R203	GLN	D83	V143	R203
PRO	H84	M144	Q204	PRO	H84	M144	Q204
LEU	S85	V145	N205	LEU	S85	V145	N205
GLU	N86	S146	G206	GLU	N86	S146	G206
ALA	F87	R147	V207	ALA	F87	R147	V207
PRO	L88	K148	L208	PRO	L88	K148	L208
TYR	T89	T149	E209	TYR	T89	T149	E209
VAL	T90	S210	G211	VAL	T90	S210	G211
PRO	V91	D211	I212	PRO	V91	D211	I212
ARG	V92	G213	G214	ARG	V92	G213	G214
LEU	Q93	N94	V214	LEU	Q93	N94	V214
ALA	N95	K215	F216	ALA	N95	K215	F216
PRO	D96	THR	F217	PRO	D96	THR	F217
ALA	F97	ASP	D217	ALA	F97	ASP	D217
PRO	T98	GLY	T218	PRO	T98	GLY	T218
GLY	P99	PRO	R219	GLY	P99	PRO	R219
SER	T100	SER	N220	SER	T100	SER	N220
Q164	E101	Q164	R221	Q164	E101	Q164	R221
D165	A102	D165	R222	D165	A102	D165	R222
I166	S103	I166	L223	I166	S103	I166	L223
L167	T104	L167	G224	L167	T104	L167	G224
E168	Q105	E168	W225	E168	Q105	E168	W225
Y169	T106	Y169	D226	Y169	T106	Y169	D226
E170	I107	E170	P227	E170	I107	E170	P227
W171	N108	W171	V228	W171	N108	W171	V228
V172	F109	V172	T229	V172	F109	V172	T229
E173	D110	E173	E230	E173	D110	E173	E230
F174	D110	F174	L231	F174	D110	F174	L231
E175	R112	E175	V232	E175	R112	E175	V232
P177	S113	P177	M233	P177	S113	P177	M233
E178	R114	E178	P234	E178	R114	E178	P234
G179	W115	G179	G235	G179	W115	G179	G235
N180	G116	N180	V236	N180	G116	N180	V236
	G117		Y237		G117		Y237
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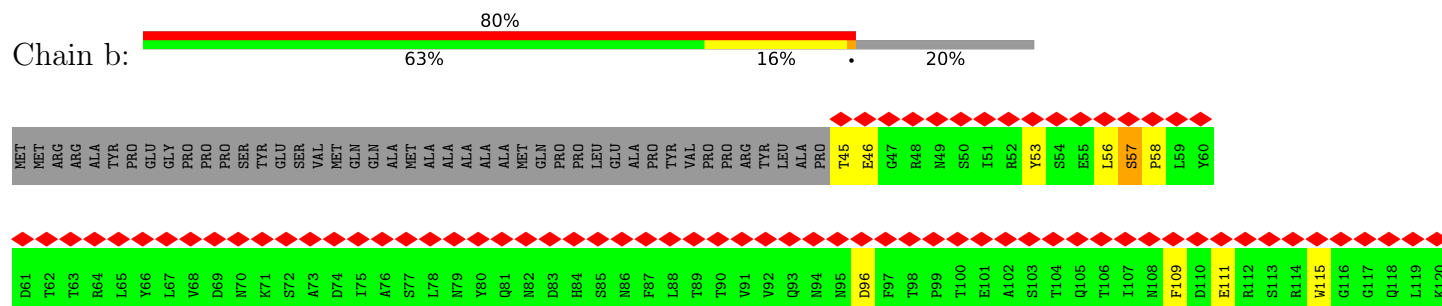


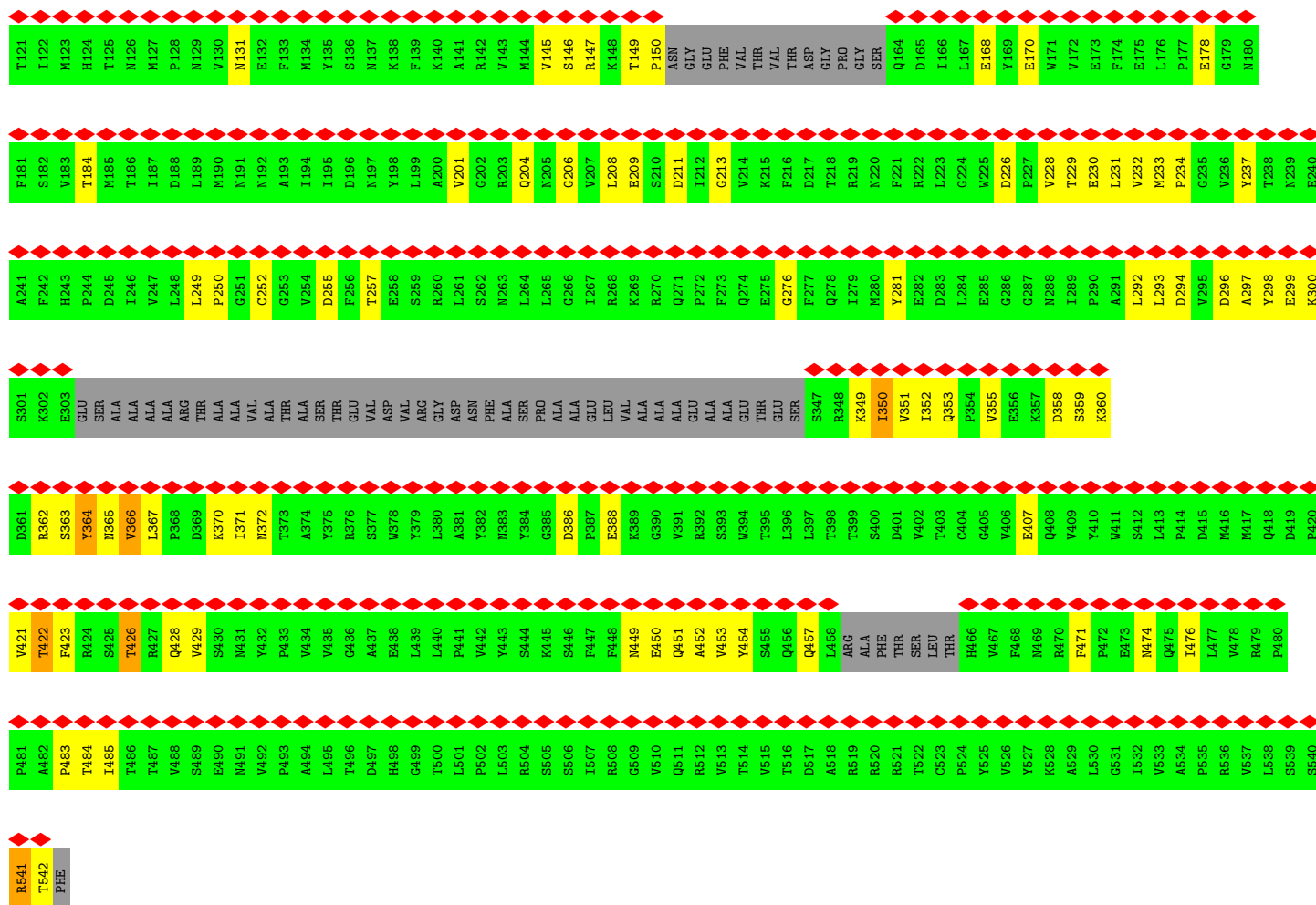


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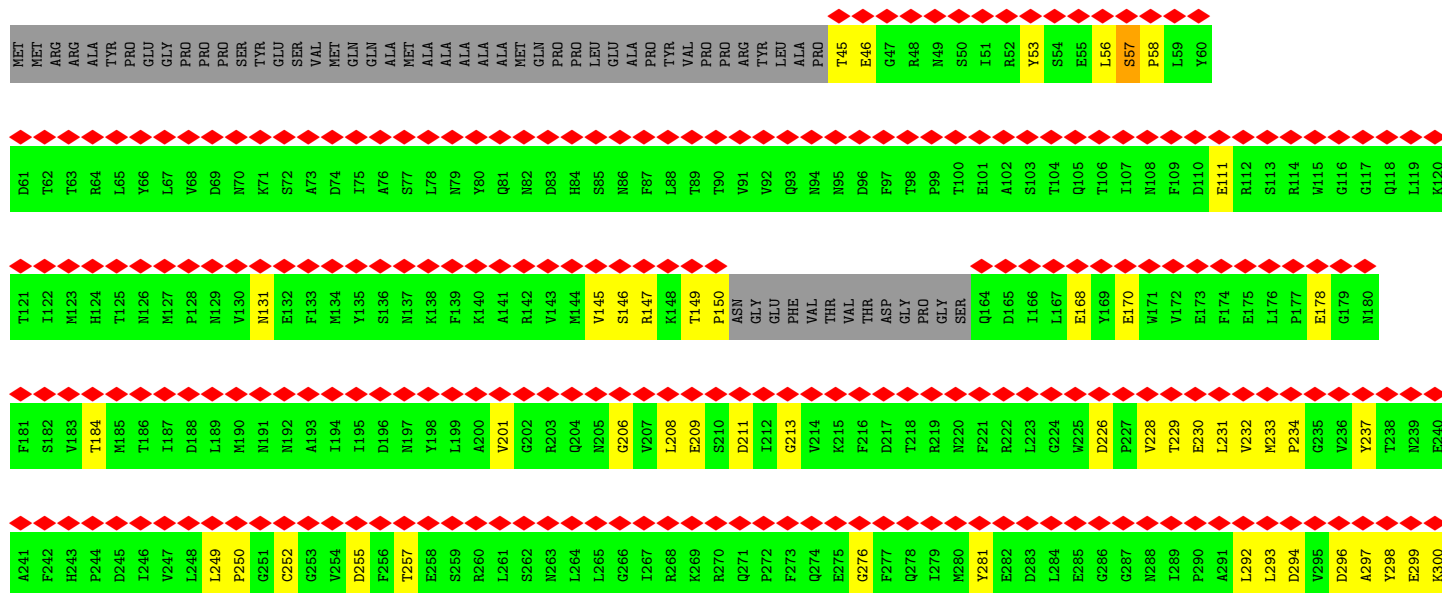
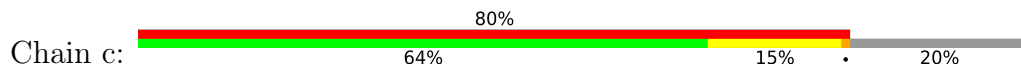


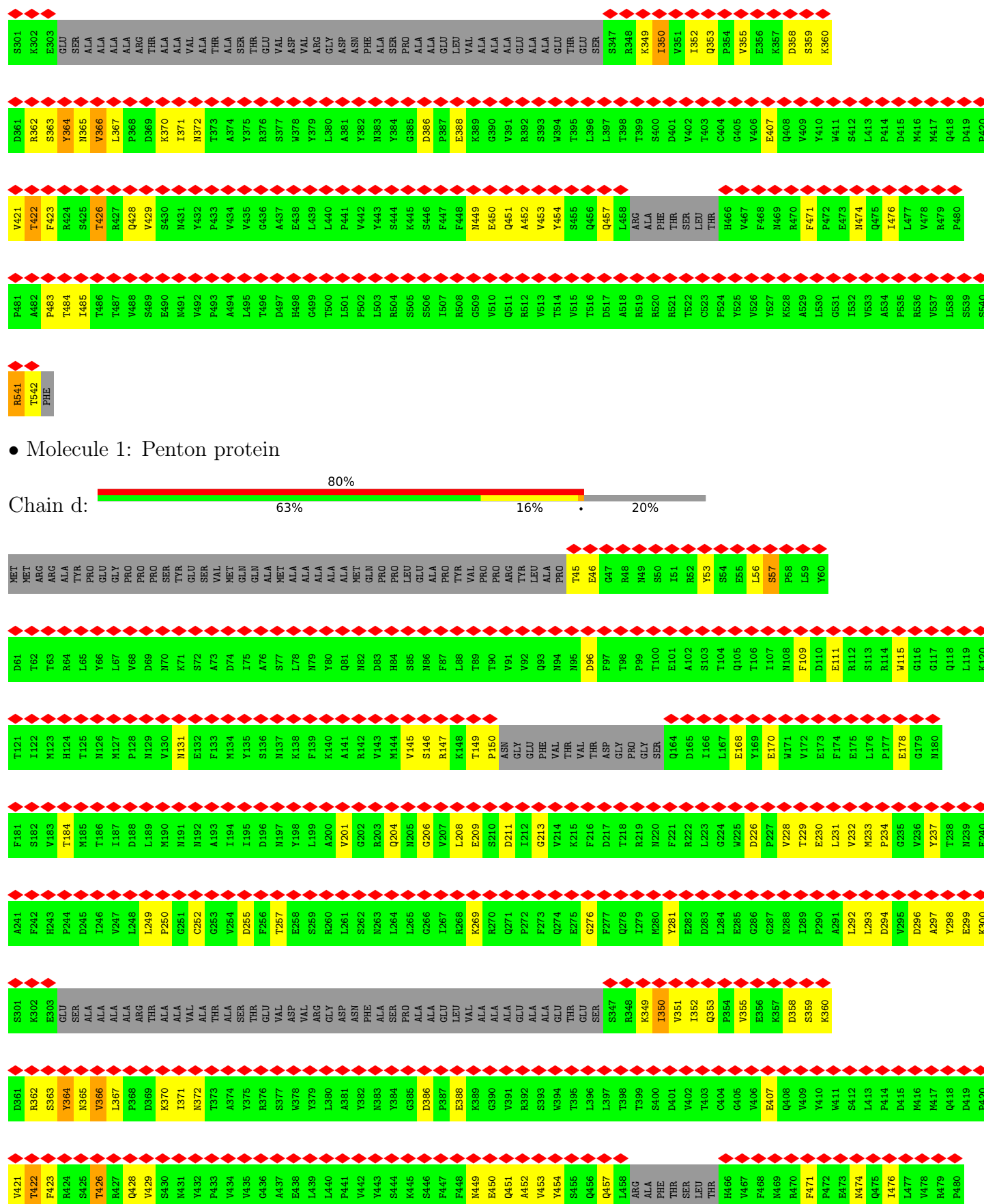
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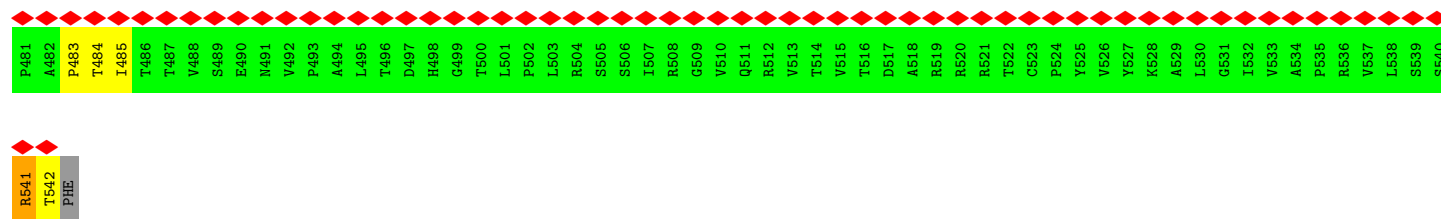




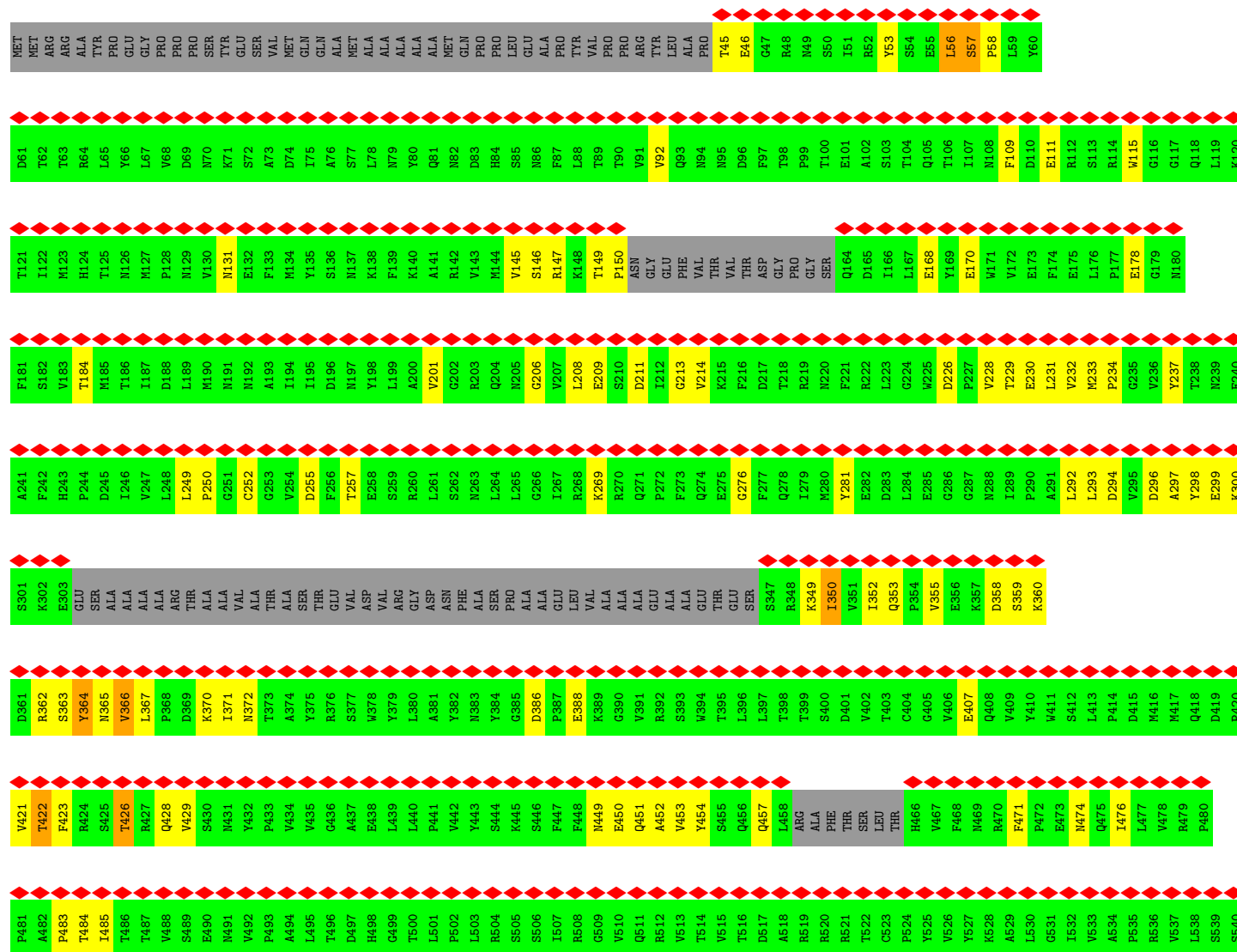
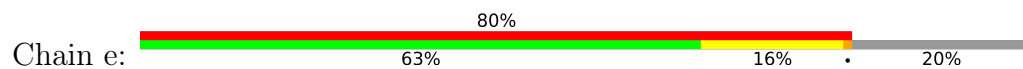
• Molecule 1: Penton protein



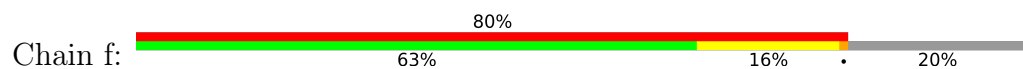




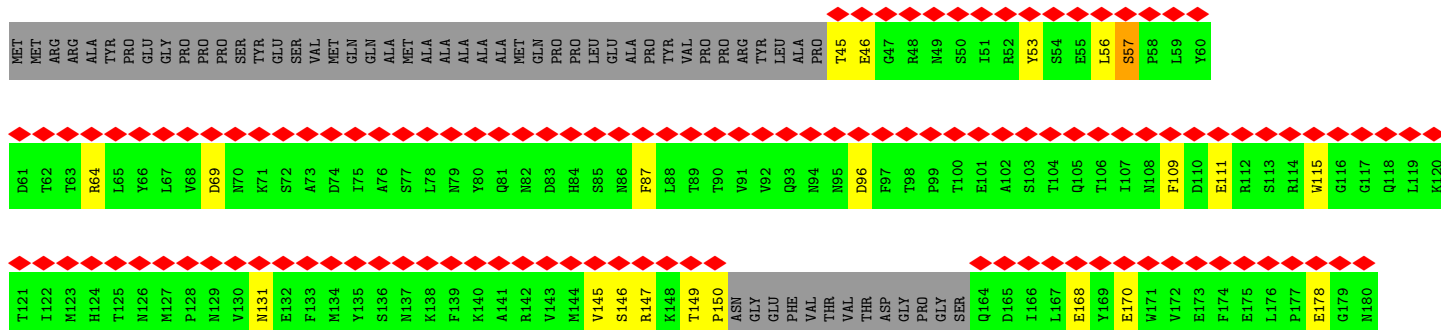
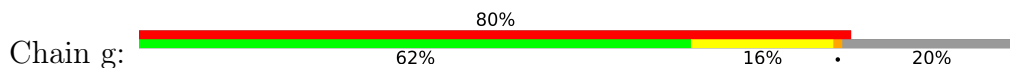
• Molecule 1: Penton protein



• Molecule 1: Penton protein

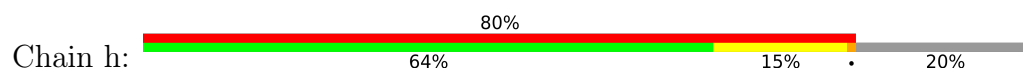


- Molecule 1: Penton protein



F181	A241	S301	D361	V421	P481	R541
S182	F242	K302	R362	T422	A482	T542
V183	H243	E303	S363	F423	P483	PHE
T184	P244	GLU	Y364	R424	T484	
M185	I245	SER	N365	S425	T485	
T186	I246	ALA	V366	T426	T486	
I187	V247	ALA	L367	R427	T487	
D188	L248	ALA	P368	Q428	V488	
L189	L249	ARG	D369	V429	S489	
M190	P250	THR	K370	S430	E490	
N191	G251	ALA	I371	N431	M491	
N192	C252	VAL	N372	Y432	V492	
A193	G253	ALA	T373	P433	P493	
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D196	F256	THR	R376	G436	T496	
N197	T257	GLU	S377	A437	D497	
Y198	E258	ASP	W378	E438	H498	
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D226	G286	V355	V406	V467	V526	
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T229	I289	D358	V409	R470	A529	
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L231	A291	K360	W411	P472	G531	
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V236	D296		M416	L477	R536	
Y237	A297		M417	V478	V537	
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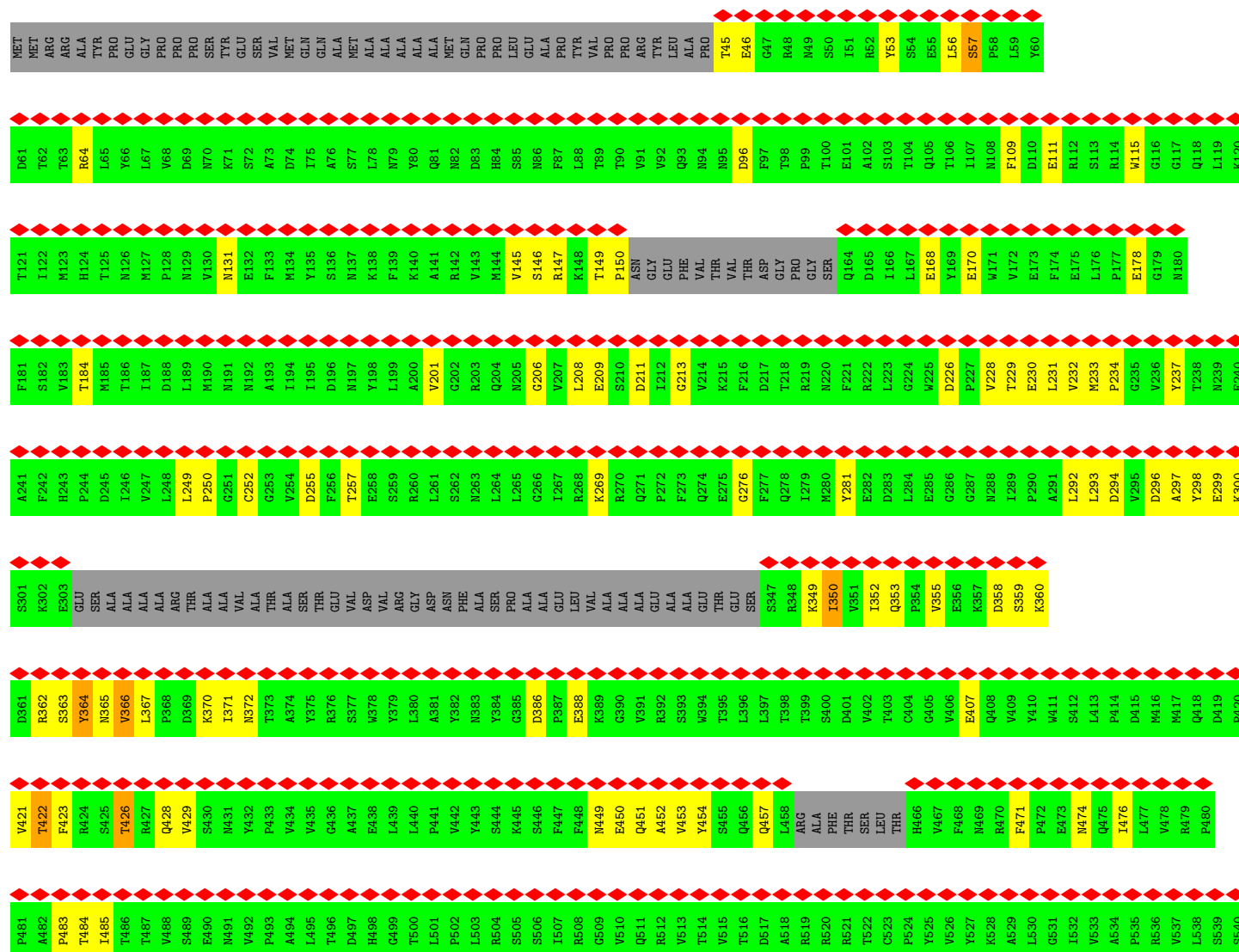
• Molecule 1: Penton protein



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ALA	R64	H124	T184	P244	GLU
TYR	L65	T125	M185	I245	SER
PRO	V66	M126	T186	I246	ALA
GLY	L67	M127	I187	V247	ALA
PRO	V68	P128	D188	L248	ALA
PRO	D69	M129	L189	L249	ARG
PRO	N70	V130	M190	P250	THR
SER	K71	M131	N191	G251	ALA
TYR	S72	E132	N192	C252	ALA
GLU	D73	F133	A193	G253	THR
VAL	A74	M134	I194	V254	ALA
MET	D75	M135	I195	D255	ALA
GLN	I76	Y136	D196	F256	SER
GLN	A76	S136	N197	T257	THR
ALA	S77	M137	Y198	E258	GLU
ALA	L78	K138	L199	S259	VAL
ALA	N79	F139	A200	R260	ARG
ALA	Y80	K140	V201	L261	GLY
ALA	Q81	A141	G202	S262	ASP
ALA	N82	R142	R203	N263	ASN
GLN	D83	V143	Q204	L264	ALA
PRO	H84	M144	N205	L265	SER
LEU	S85	V145	G206	G266	PRO
LEU	N86	R146	V207	I267	ALA
ALA	F87	L147	L208	R268	GLU
TYR	L88	K148	E209	K269	LEU
VAL	T89	T149	S210	R270	VAL
PRO	T90	P150	D211	Q271	ALA
PRO	V91	GLY	I212	P272	ALA
ARG	V92	GLU	G213	F273	ALA
TYR	Q93	PHE	V214	Q274	ALA
LEU	N94	VAL	K215	E275	GLU
ALA	N95	THR	F216	G276	THR
PRO	D96	VAL	D217	F277	SER
T45	F97	THR	T218	Q278	R347
E46	T98	ASP	R219	I279	R348
G47	P99	GLY	N220	M280	K349
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S50	A102	THR	L223	D283	I352
I51	S103	D165	G224	L284	Q353
R52	T104	I166	W225	E285	P354
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E55	Q105	Y169	V228	N288	K357
L56	I107	E170	T229	I289	D358
S57	N108	W171	E230	P290	S359
P58	F109	V172	L231	A291	K360
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	R114	W115	V236	D296	
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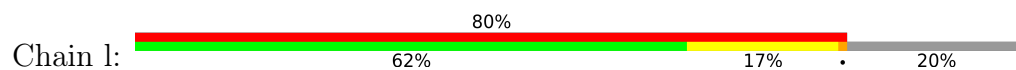


• Molecule 1: Penton protein

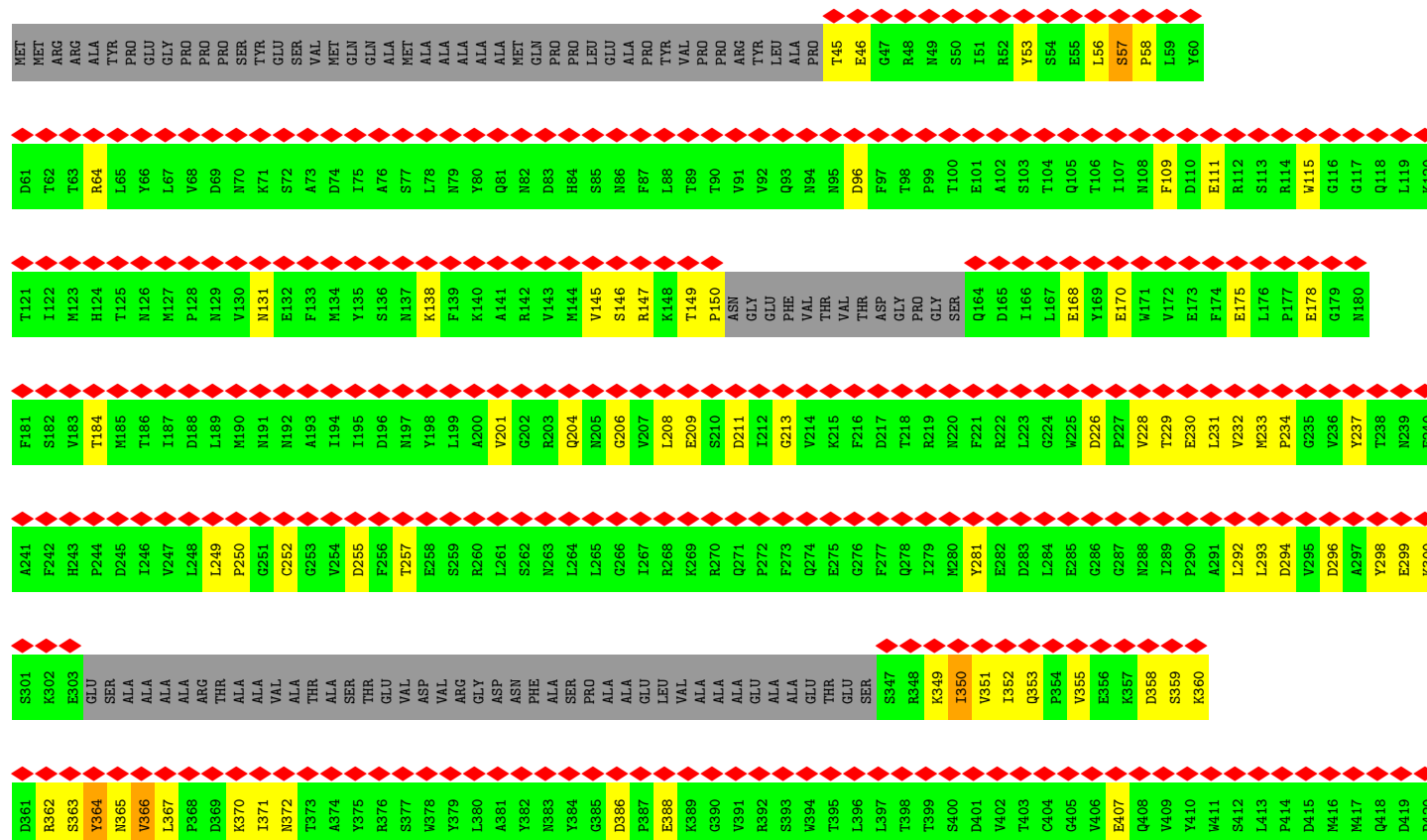


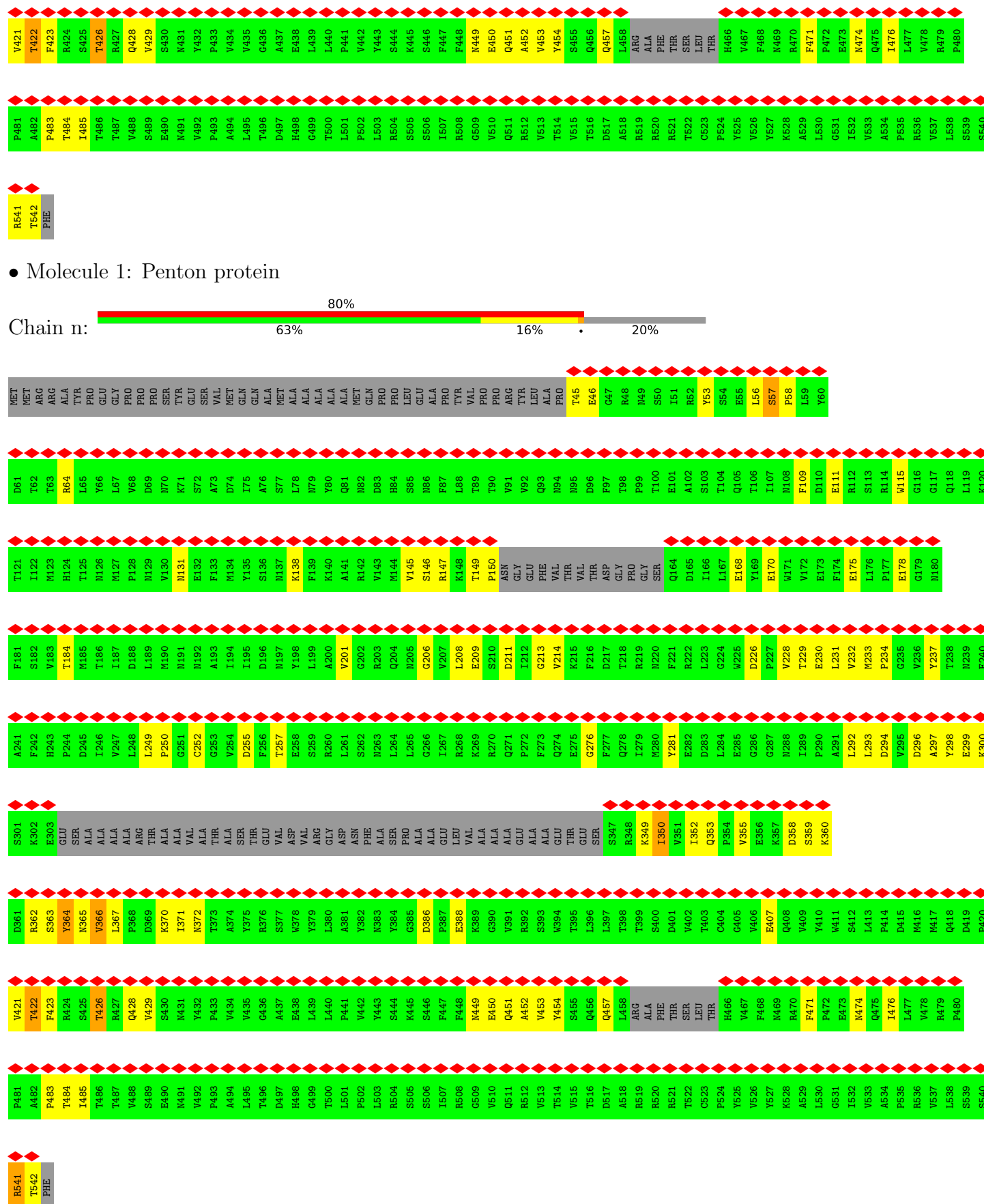
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R64	H124	T184	P244	GLU	Y364	R424	T484	
L65	T125	M185	D245	SER	N365	S425	I485	
Y66	M126	T186	I246	ALA	V366	T426	T486	
L67	M127	I187	V247	ALA	L367	R427	T487	
V68	P128	D188	L248	ALA	P368	Q428	V488	
D69	M129	L189	L249	ARG	P369	V429	S489	
N70	V130	M190	P250	THR	K370	S430	E490	
K71	N131	N191	G251	ALA	I371	M431	N491	
S72	E132	N192	C252	VAL	N372	V432	V492	
A73	F133	A193	G253	ALA	T373	P433	P493	
D74	M134	I194	V254	THR	A374	V434	A494	
I75	Y135	I195	D255	SER	Y375	V435	L495	
A76	S136	D196	F256	THR	R376	G436	T496	
S77	K137	Y197	T257	GLU	S377	A437	D497	
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Y80	K140	A200	R260	ARG	L380	L440	T500	
Q81	A141	V201	L261	GLY	A381	P441	L501	
N82	R142	G202	S262	ASN	Y382	V442	P502	
D83	V143	R203	N263	ASP	N383	Y443	L503	
H84	M144	Q204	L264	ALA	Y384	S444	R504	
S85	V145	N205	L265	SER	G385	K445	S505	
N86	S146	G206	G266	PRO	D386	S446	S506	
F87	R147	V207	I267	ALA	P387	F447	L507	
L88	K148	L208	R268	GLU	E388	F448	R508	
T89	T149	E209	K269	LEU	K389	M449	G509	
T90	P150	S210	R270	VAL	G390	E450	V510	
V91	ASN	D211	Q271	ALA	V391	Q451	Q511	
V92	GLY	I212	P272	ALA	R392	A452	R512	
Q93	PHE	G213	F273	ALA	S393	V453	V513	
N94	VAL	V214	Q274	ALA	W394	Y454	T514	
N95	THR	K215	E275	THR	T395	S455	V515	
D96	VAL	F216	G276	GLU	L396	Q456	T516	
F97	THR	D217	F277	SER	L397	Q457	D517	
T98	GLY	T218	Q278	R347	T398	L458	A518	
P99	PRO	R219	I279	R348	T399	ARG	R519	
T100	GLY	R219	I279	K349	S400	PHE	R520	
E101	SER	N220	Y281	I350	D401	THR	R521	
A102	Q164	R222	E282	V351	V402	SER	T522	
S103	D165	L223	D283	I352	T403	LEU	C523	
T104	I166	G224	L284	Q353	C404	THR	P524	
Q105	L167	W225	E285	P354	G405	H466	Y525	
T106	E168	D226	G286	V355	V406	V467	V526	
I107	Y169	D227	G287	E356	E407	M469	Y527	
N108	E170	V228	N288	K357	Q408	R470	K528	
F109	W171	T229	I289	D358	V409	F471	A529	
D110	V172	E230	P290	S359	Y410	P472	L530	
E111	F173	L231	A291	K360	W411	E473	G531	
R112	E175	V232	L292		S412	M474	I532	
S113	P176	M233	L293		L413	Q475	V533	
R114	P177	P234	D294		P414	L476	A534	
W115	E178	G235	V295		D415	L477	P535	
G116	G179	V236	D296		M416	V478	R536	
G117	T237	Y237	A297		Q417	R479	V537	
Q118	N239	E240	Y298		M418	P480	L538	
L119			E299		D419		S539	
K120			K300		P420		S540	

• Molecule 1: Penton protein

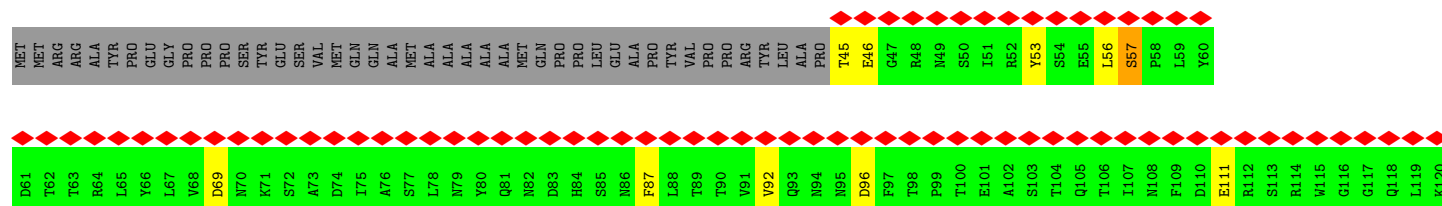
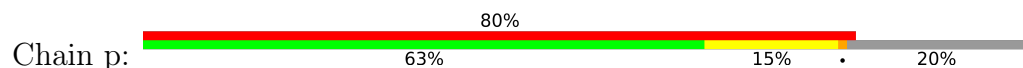
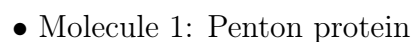


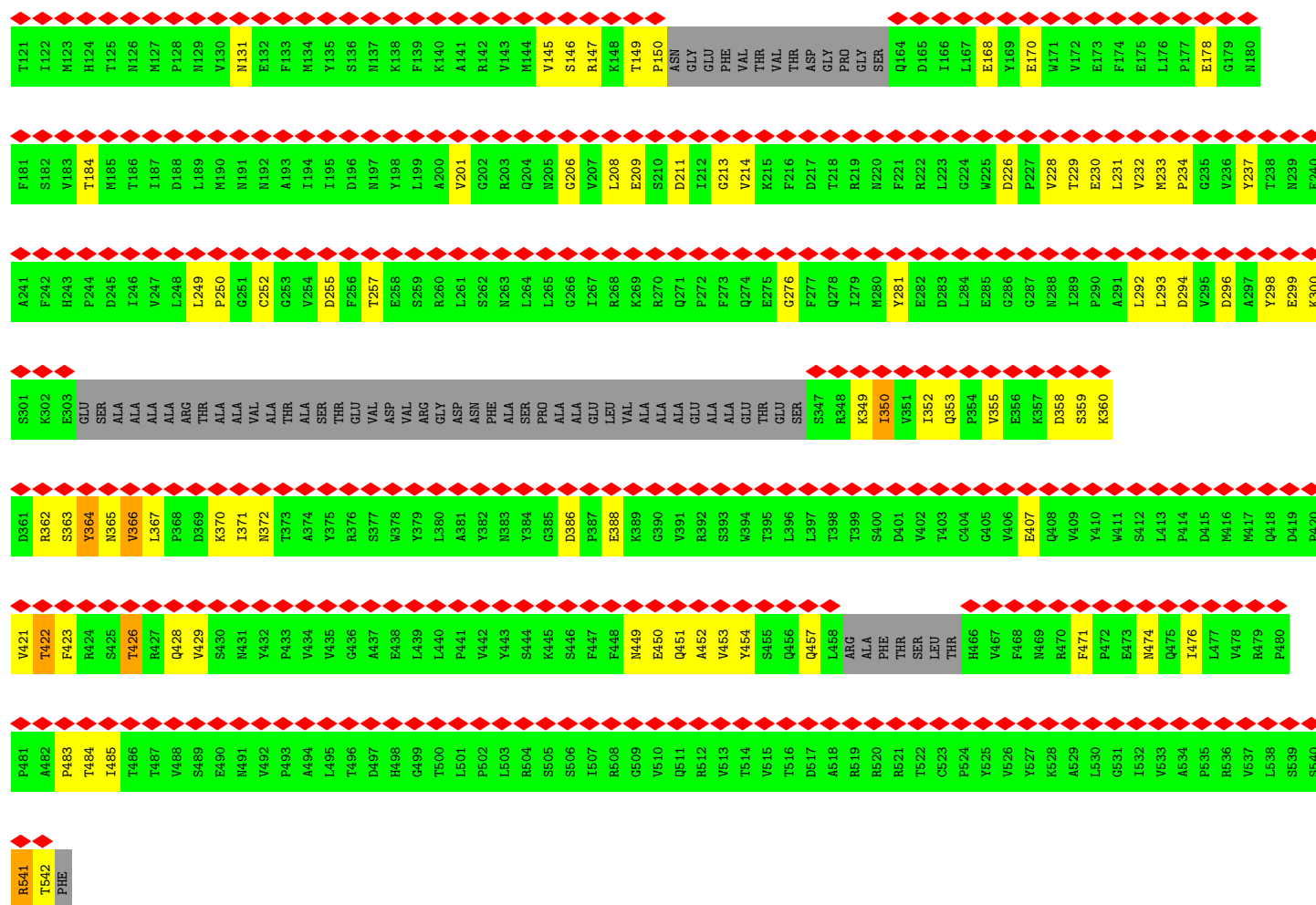
MET	D61	T121	F181	MET	D61	T121	F181
ARG	T62	I122	S182	ARG	T62	I122	S182
ALA	T63	M123	V183	ALA	T63	M123	V183
TYR	R64	H124	T184	TYR	R64	H124	T184
PRO	L65	T125	M185	PRO	L65	T125	M185
GLY	Y66	M126	T186	GLY	Y66	M126	T186
PRO	L67	M127	I187	PRO	L67	M127	I187
PRO	V68	P128	D188	PRO	V68	P128	D188
PRO	D69	M129	L189	PRO	D69	M129	L189
SER	N70	V130	M190	SER	N70	V130	M190
TYR	K71	N131	N191	TYR	K71	N131	N191
GLU	S72	E132	N192	GLU	S72	E132	N192
SER	A73	F133	A193	SER	A73	F133	A193
VAL	D74	M134	I194	VAL	D74	M134	I194
MET	I75	Y135	I195	MET	I75	Y135	I195
GLN	A76	S136	D196	GLN	A76	S136	D196
ALA	S77	K137	Y197	ALA	S77	K137	Y197
MET	L78	N138	Y198	MET	L78	N138	Y198
ALA	N79	F139	L199	ALA	N79	F139	L199
ALA	Y80	K140	A200	ALA	Y80	K140	A200
ALA	Q81	A141	V201	ALA	Q81	A141	V201
MET	N82	R142	G202	MET	N82	R142	G202
GLN	D83	V143	R203	GLN	D83	V143	R203
PRO	H84	M144	Q204	PRO	H84	M144	Q204
LEU	S85	N205	N205	LEU	S85	N205	N205
GLU	N86	G206	G206	GLU	N86	G206	G206
ALA	F87	V207	V207	ALA	F87	V207	V207
PRO	L88	K148	L208	PRO	L88	K148	L208
TYR	T89	T149	E209	TYR	T89	T149	E209
VAL	T90	S210	S210	VAL	T90	S210	S210
PRO	V91	D211	D211	PRO	V91	D211	D211
ARG	V92	I212	I212	ARG	V92	I212	I212
LEU	Q93	G213	G213	LEU	Q93	G213	G213
ALA	N94	V214	V214	ALA	N94	V214	V214
PRO	N95	K215	K215	PRO	N95	K215	K215
T45	D96	F216	F216	T45	D96	F216	F216
E46	F97	D217	D217	E46	F97	D217	D217
G47	T98	T218	T218	G47	T98	T218	T218
R48	P99	R219	R219	R48	P99	R219	R219
S50	T100	N220	N220	S50	T100	N220	N220
T51	E101	R221	R221	T51	E101	R221	R221
R52	A102	R222	R222	R52	A102	R222	R222
Y53	S103	L223	L223	Y53	S103	L223	L223
S54	T104	G224	G224	S54	T104	G224	G224
E55	Q105	W225	W225	E55	Q105	W225	W225
L56	T106	D226	D226	L56	T106	D226	D226
S57	I107	P227	P227	S57	I107	P227	P227
P58	N108	V228	V228	P58	N108	V228	V228
L59	F109	T229	T229	L59	F109	T229	T229
Y60	D110	E230	E230	Y60	D110	E230	E230
	E111	L231	L231		E111	L231	L231
	R112	V232	V232		R112	V232	V232
	S113	M233	M233		S113	M233	M233
	R114	P234	P234		R114	P234	P234
	W115	G235	G235		W115	G235	G235
	G116	V236	V236		G116	V236	V236
	G117	Y237	Y237		G117	Y237	Y237
	Q118	N239	N239		Q118	N239	N239
	L119				L119		
	K120				K120		



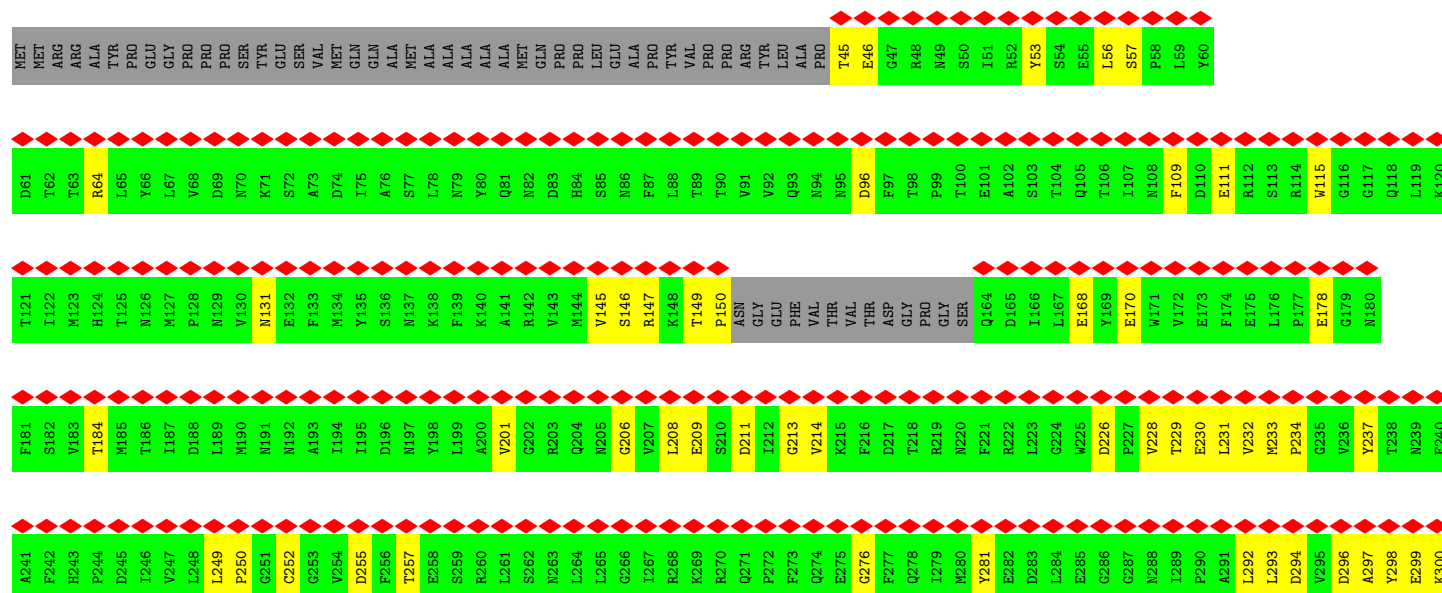
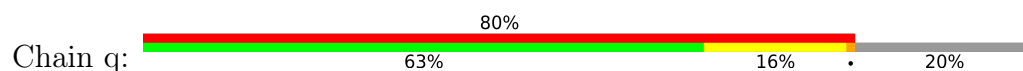


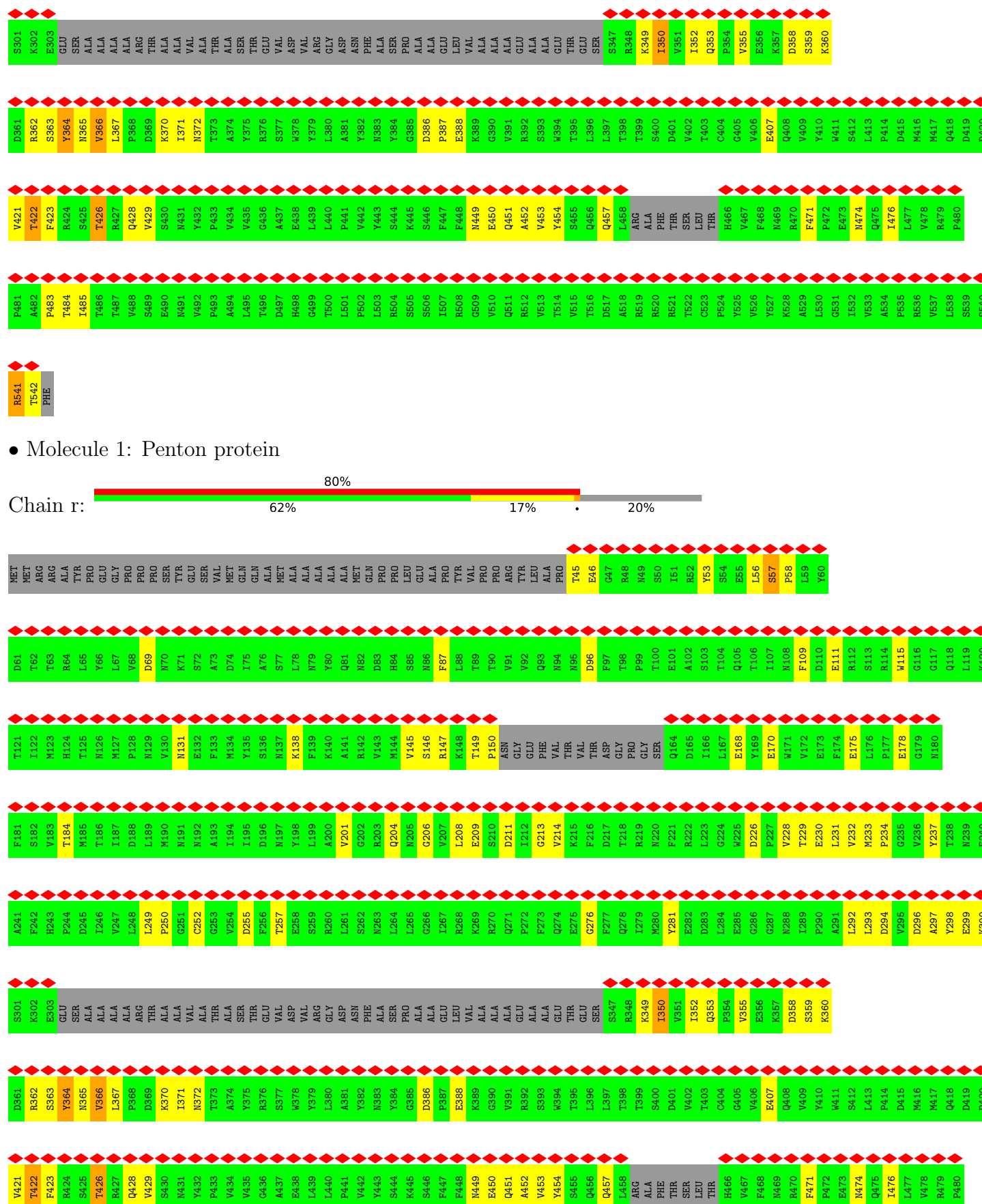
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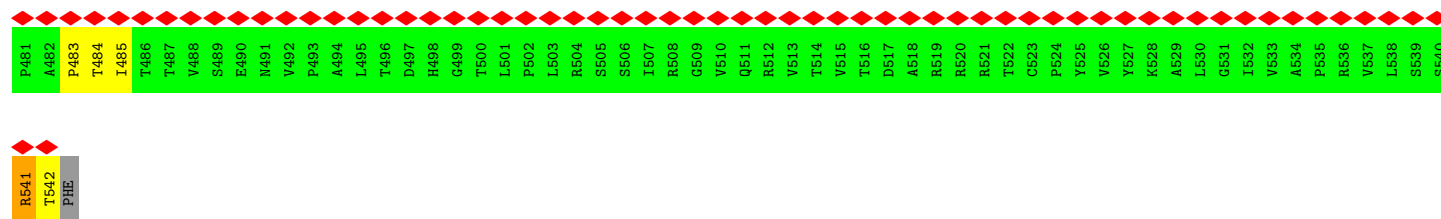




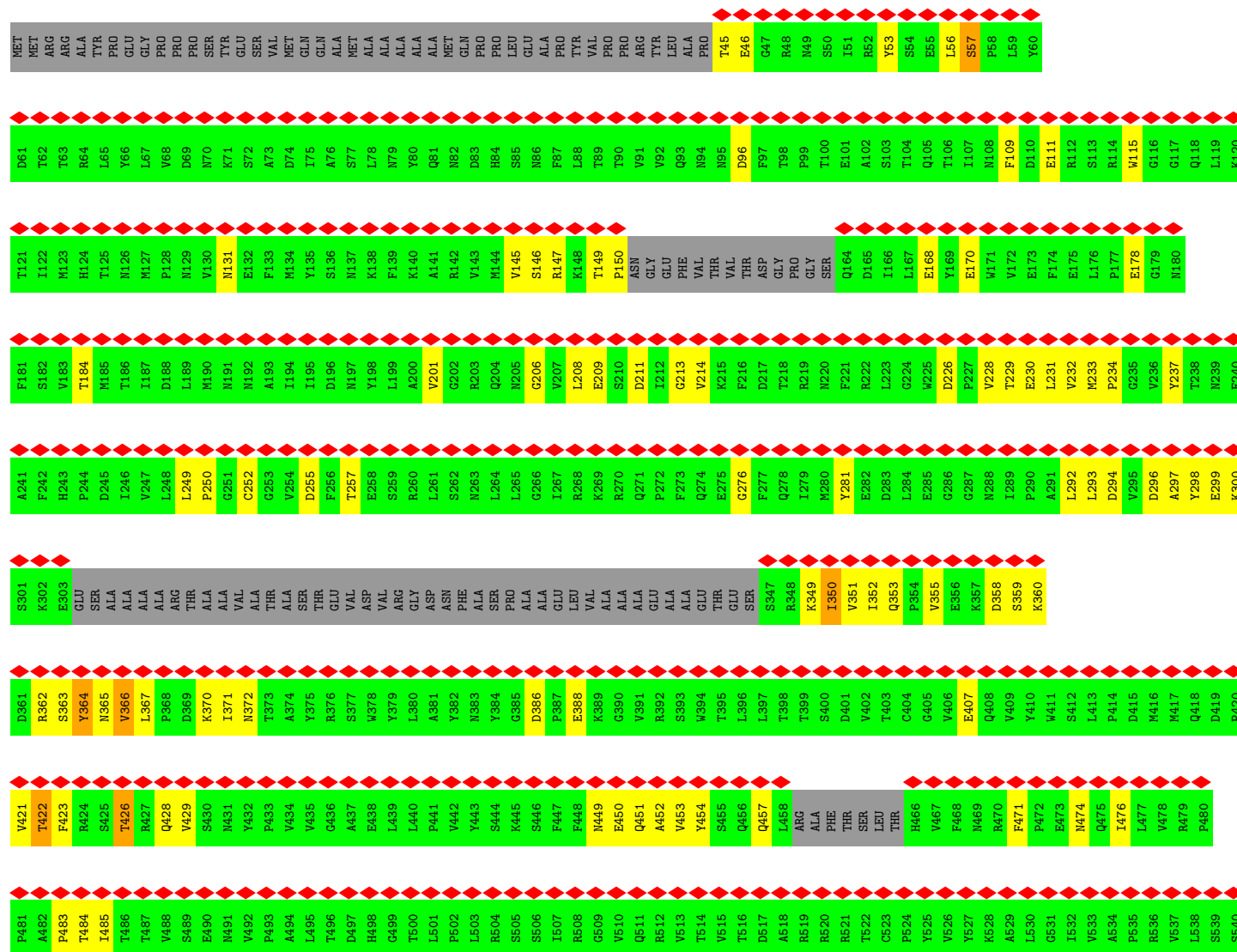
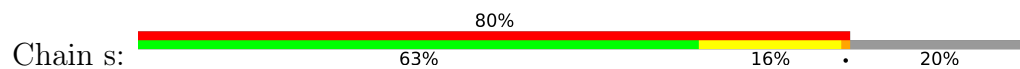
• Molecule 1: Penton protein







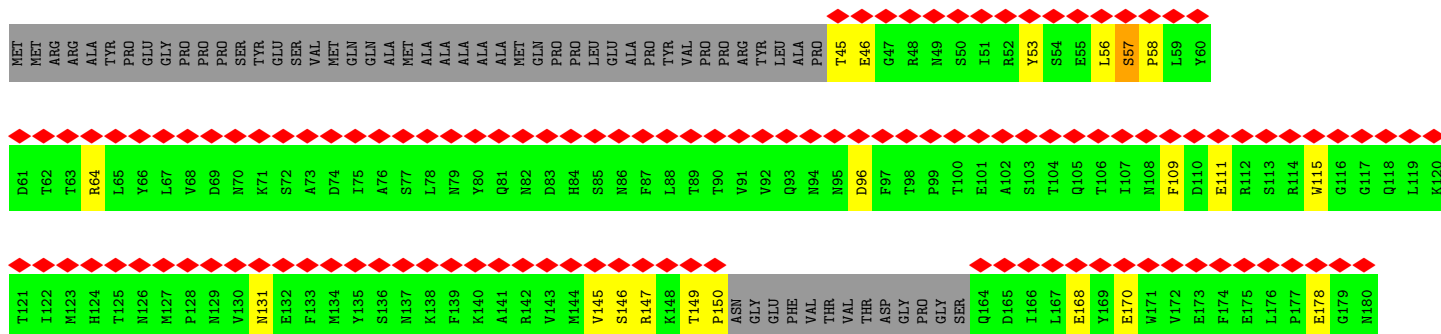
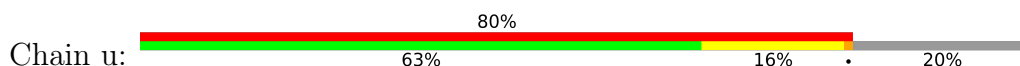
• Molecule 1: Penton protein



• Molecule 1: Penton protein

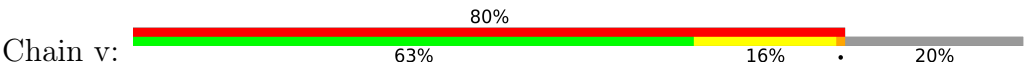


- Molecule 1: Penton protein



F181	A241	S301	D361	V421	P481	R541
S182	F242	K302	R362	T422	A482	T542
V183	H243	E303	S363	F423	P483	PHE
T184	P244	GLU	Y364	R424	T484	
M185	I245	SER	N365	S425	T485	
T186	I246	ALA	V366	T426	T486	
I187	V247	ALA	L367	R427	T487	
D188	L248	ALA	P368	Q428	V488	
L189	L249	ARG	D369	V429	S489	
M190	P250	THR	K370	S430	E490	
N191	G251	ALA	I371	N431	N491	
N192	C252	VAL	N372	Y432	V492	
A193	G253	ALA	T373	P433	P493	
I194	V254	THR	A374	V434	A494	
I195	D255	SER	Y375	V435	L495	
D196	F256	THR	R376	G436	T496	
N197	T257	GLU	S377	A437	D497	
Y198	E258	ASP	W378	E438	H498	
L199	S259	VAL	Y379	L439	G499	
A200	R260	ARG	L380	L440	T500	
V201	L261	GLY	A381	P441	L501	
G202	S262	ASP	Y382	V442	P502	
R203	N263	ASN	N383	Y443	L503	
Q204	L264	ALA	Y384	S444	R504	
N205	L265	SER	G385	K445	S505	
G206	G266	PRO	D386	S446	S506	
V207	I267	ALA	P387	F447	I507	
L208	R268	GLU	E388	F448	R508	
E209	K269	LEU	K389	N449	G509	
S210	R270	VAL	G390	E450	V510	
D211	Q271	ALA	V391	Q451	Q511	
I212	P272	ALA	R392	A452	R512	
G213	F273	GLU	S393	V453	V513	
V214	Q274	ALA	W394	V454	T514	
K215	E275	GLU	T395	S455	V515	
F216	G276	THR	L396	Q456	T516	
D217	F277	GLU	L397	Q457	D517	
T218	Q278	SER	T398	L458	A518	
R219	I279	R347	T399	ARG	R519	
N220	M280	R348	S400	ALA	N49	
F221	Y281	PHE	D401	THR	R520	
R222	E282	V351	V402	SER	R521	
L223	D283	R352	T403	LEU	T522	
G224	L284	Q353	C404	THR	C523	
W225	E285	P354	G405	H466	P524	
D226	G286	V355	V406	V467	Y525	
P227	G287	E356	E407	F468	V526	
V228	N288	K357	Q408	N469	Y527	
T229	I289	D358	V409	R470	K528	
E230	P290	S359	Y410	F471	A529	
L231	A291	K360	W411	F472	L530	
V232	L292		S412	E473	G531	
M233	L293		L413	N474	I532	
P234	D294		P414	Q475	V533	
G235	V295		D415	I476	A534	
V236	D296		M416	L477	P535	
Y237	A297		M417	V478	R536	
T238	Y298		Q418	R479	V537	
N239	E299		D419	P480	L538	
E240	K300		P420		S539	
					S540	

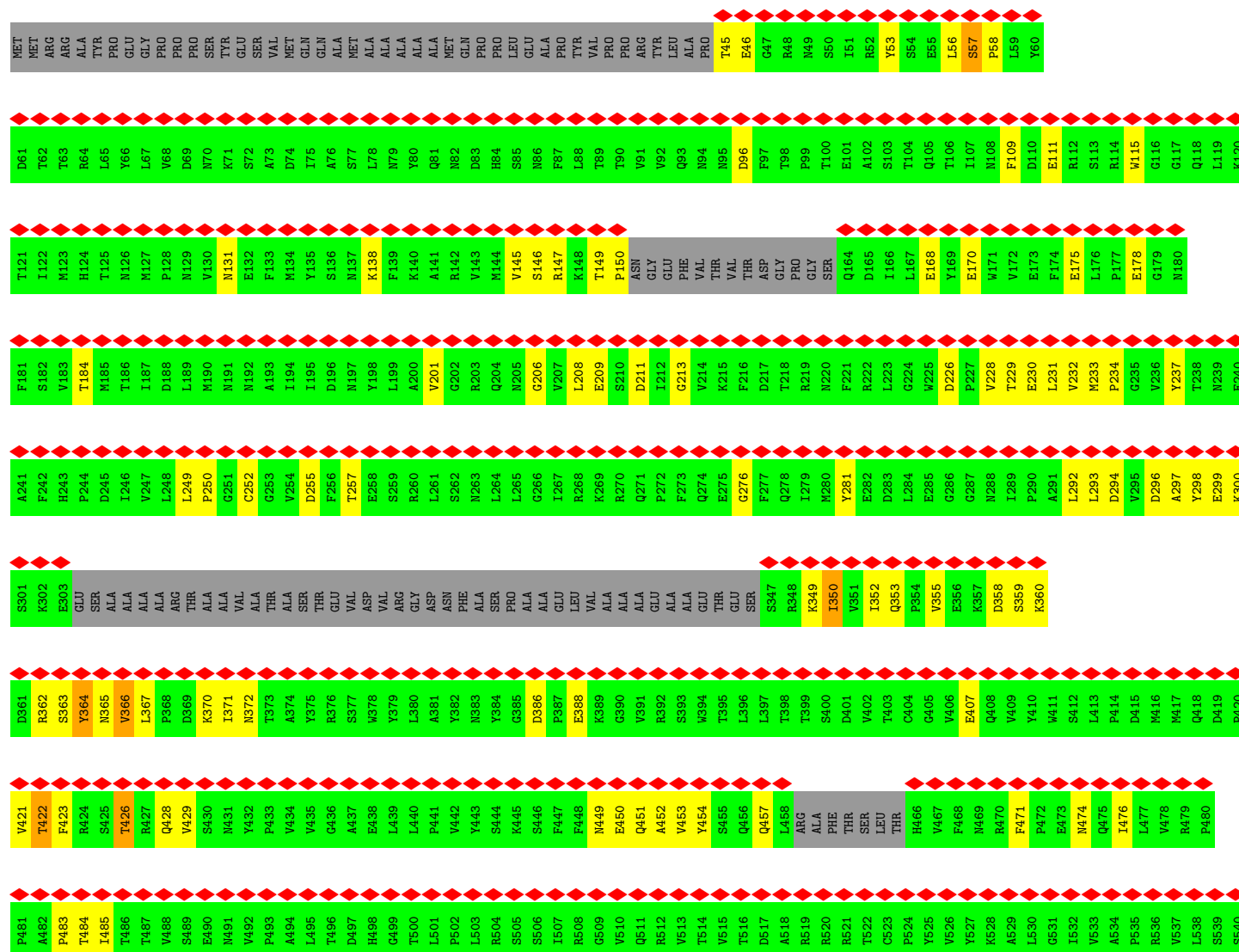
● Molecule 1: Penton protein



MET	D61	T121	F181	A241	S301
MET	T62	I122	S182	F242	K302
ARG	T63	M123	V183	H243	E303
ALA	R64	H124	T184	P244	GLU
TYR	L65	T125	M185	I245	SER
PRO	V66	M126	T186	I246	ALA
GLY	L67	M127	I187	V247	ALA
PRO	V68	P128	D188	L248	ALA
PRO	D69	L129	L189	L249	ARG
PRO	N70	V130	M190	P250	THR
SER	K71	M131	N191	G251	ALA
TYR	S72	E132	N192	C252	ALA
GLU	D73	F133	A193	G253	THR
SER	A74	M134	I194	V254	ALA
VAL	D75	Y135	I195	D255	ALA
GLN	I76	S136	D196	F256	SER
GLN	A76	M137	N197	T257	THR
ALA	S77	K138	Y198	E258	GLU
ALA	L78	F139	L199	S259	VAL
ALA	N79	K140	A200	R260	ARG
ALA	Q81	A141	V201	L261	GLY
ALA	N82	R142	G202	S262	ASP
GLN	D83	V143	R203	N263	ASN
PRO	H84	M144	Q204	L264	ALA
LEU	S85	V145	N205	L265	SER
LEU	N86	S146	G206	G266	PRO
ALA	F87	R147	V207	I267	ALA
TYR	L88	K148	L208	R268	GLU
VAL	T89	T149	E209	K269	LEU
PRO	T90	P150	S210	R270	VAL
PRO	V91	ASN	D211	Q271	ALA
ARG	V92	GLY	I212	P272	ALA
TYR	Q93	PHE	G213	F273	GLU
LEU	N94	VAL	V214	Q274	ALA
ALA	N95	THR	K215	E275	GLU
PRO	D96	VAL	F216	G276	THR
T45	F97	THR	D217	F277	SER
E46	T98	ASP	T218	Q278	R347
G47	P99	GLY	R219	I279	R348
R48	T100	PRO	N220	M280	K349
N49	E101	GLY	F221	Y281	I350
S50	A102	SER	R222	E282	V351
I51	S103	THR	L223	D283	R352
R52	T104	D165	G224	L284	I353
Y53	Q105	I166	W225	E285	P354
S54	T106	L167	D226	G286	V355
E55	Q107	E168	P227	G287	E356
L56	N108	Y169	V228	N288	K357
S57	F109	E170	T229	I289	D358
P58	D110	W171	E230	P290	S359
L59	E111	V172	L231	A291	K360
Y60	R112	F173	V232	L292	
	S113	E175	M233	L293	
	R114	L176	P234	D294	
	W115	P177	G235	V295	
	G116	E178	V236	D296	
	G117	G179	Y237	A297	
	L118	M180	T238	Y298	
	L119		N239	E299	
	K120		E240	K300	

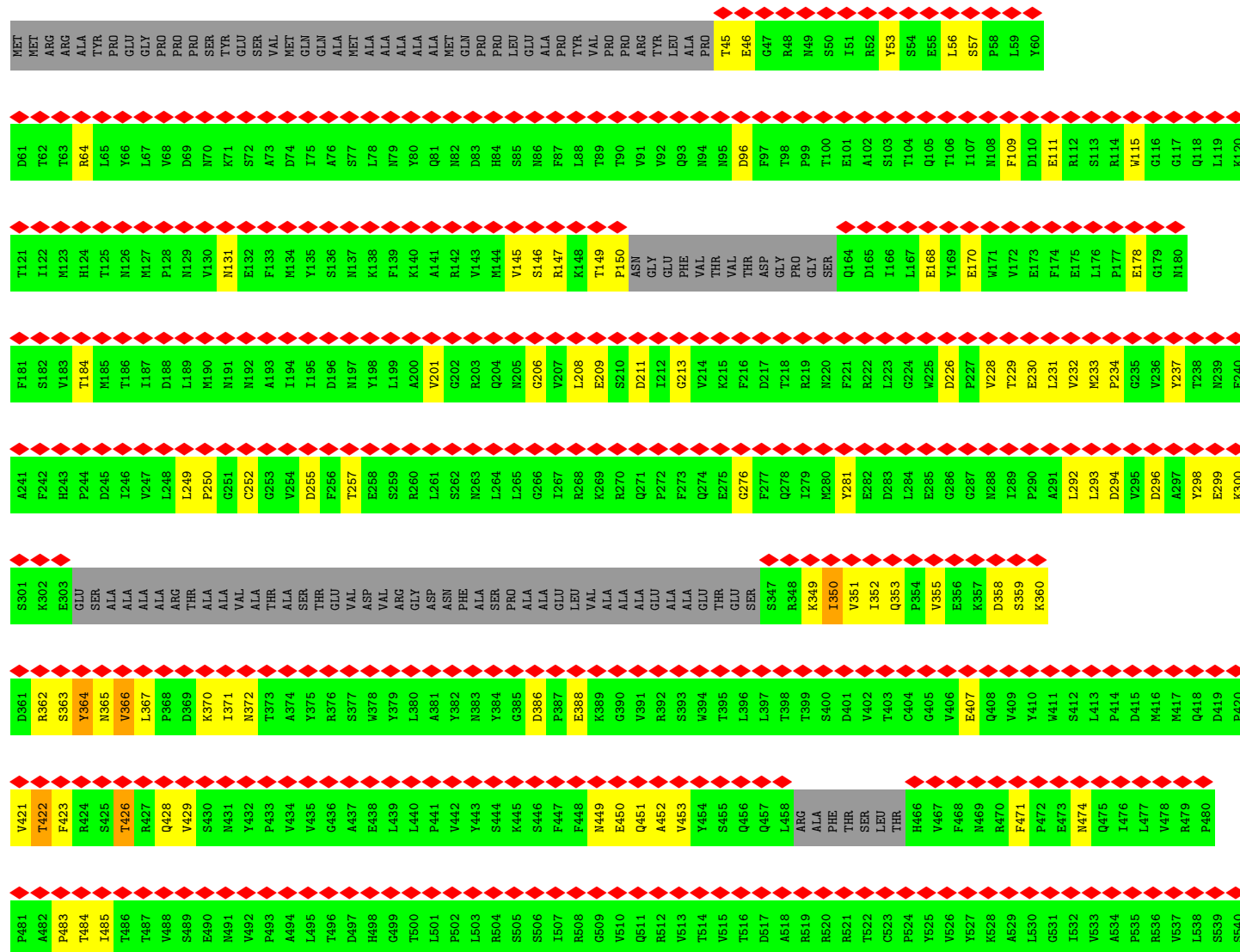
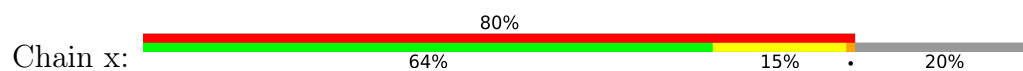


• Molecule 1: Penton protein

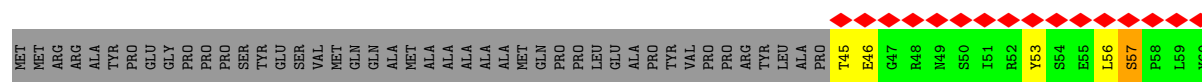
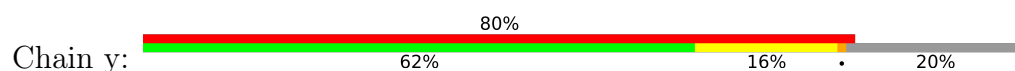




• Molecule 1: Penton protein



• Molecule 1: Penton protein





R541	T542	PHE	P481	A482	P483	T484	L485	T486	T487	V488	S489	E490	M491	V492	P493	A494	L495	T496	D497	H498	G499	T500	L501	P502	L503	R504	S505	S506	L507	R508	G509	V510	O511	R512	V513	T514	V515	T516	D517	A518	R519	R520	R521	T522	C523	P524	V525	V526	V527	K528	L529	L530	G531	T532	V533	A534	P535	R536	V537	L538	S539	S540																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
			D361	R362	S363	Y364	N365	V366	L367	P368	D369	K370	L371	N372	T373	A374	Y375	R376	S377	W378	Y379	L380	A381	Y382	N383	Y384	G385	D386	P387	E388	K389	G390	V391	R392	S393	W394	T395	L396	L397	T398	T399	S400	D401	V402	T403	C404	G405	V406	E407	Q408	V409	Y410	W411	S412	L413	P414	D415	W416	W417	Q418	D419	P420																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
V421	T422	F423	R424	S425	T426	R427	Q428	V429	S430	M431	V432	P433	A434	V435	A436	A437	E438	L439	L440	P441	V442	Y443	S444	K445	S446	F447	P448	M449	E450	Q451	A452	V453	Y454	S455	Q456	Q457	L458	ARG	ALA	PHE	THR	SER	LEU	THR	H466	V467	F468	M469	R470	F471	P472	E473	M474	Q475	I476	L477	V478	R479	P480																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	147098	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44.01	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.270	Depositor
Minimum map value	-0.143	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	419.99997, 419.99997, 419.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section:
K

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	1	0.30	0/3588	0.69	14/4880 (0.3%)
1	2	0.30	0/3588	0.68	14/4880 (0.3%)
1	3	0.30	0/3588	0.68	14/4880 (0.3%)
1	4	0.30	1/3588 (0.0%)	0.69	14/4880 (0.3%)
1	5	0.30	0/3588	0.68	14/4880 (0.3%)
1	6	0.30	0/3588	0.69	15/4880 (0.3%)
1	7	0.30	0/3588	0.69	14/4880 (0.3%)
1	8	0.30	0/3588	0.69	15/4880 (0.3%)
1	9	0.30	0/3588	0.69	14/4880 (0.3%)
1	A	0.30	0/3588	0.69	14/4880 (0.3%)
1	B	0.30	0/3588	0.69	14/4880 (0.3%)
1	C	0.30	0/3588	0.69	14/4880 (0.3%)
1	D	0.30	0/3588	0.68	14/4880 (0.3%)
1	E	0.30	0/3588	0.69	14/4880 (0.3%)
1	F	0.30	0/3588	0.68	14/4880 (0.3%)
1	G	0.30	0/3588	0.68	14/4880 (0.3%)
1	H	0.30	0/3588	0.69	14/4880 (0.3%)
1	I	0.30	0/3588	0.68	14/4880 (0.3%)
1	J	0.30	0/3588	0.69	14/4880 (0.3%)
1	K	0.30	0/3588	0.68	14/4880 (0.3%)
1	L	0.30	0/3588	0.69	14/4880 (0.3%)
1	M	0.30	0/3588	0.69	14/4880 (0.3%)
1	N	0.30	0/3588	0.69	14/4880 (0.3%)
1	O	0.30	0/3588	0.69	14/4880 (0.3%)
1	P	0.30	0/3588	0.69	15/4880 (0.3%)
1	Q	0.30	0/3588	0.68	15/4880 (0.3%)
1	R	0.30	0/3588	0.69	14/4880 (0.3%)
1	S	0.30	0/3588	0.69	15/4880 (0.3%)
1	T	0.30	0/3588	0.69	14/4880 (0.3%)
1	V	0.30	0/3588	0.69	15/4880 (0.3%)
1	W	0.30	0/3588	0.69	14/4880 (0.3%)
1	X	0.30	0/3588	0.69	14/4880 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Y	0.30	0/3588	0.69	15/4880 (0.3%)
1	Z	0.30	0/3588	0.69	14/4880 (0.3%)
1	a	0.30	0/3588	0.68	14/4880 (0.3%)
1	b	0.30	0/3588	0.68	14/4880 (0.3%)
1	c	0.30	0/3588	0.68	14/4880 (0.3%)
1	d	0.30	0/3588	0.69	14/4880 (0.3%)
1	e	0.30	0/3588	0.69	15/4880 (0.3%)
1	f	0.30	0/3588	0.68	15/4880 (0.3%)
1	g	0.30	0/3588	0.69	15/4880 (0.3%)
1	h	0.30	0/3588	0.69	14/4880 (0.3%)
1	i	0.30	0/3588	0.69	14/4880 (0.3%)
1	j	0.30	0/3588	0.69	14/4880 (0.3%)
1	k	0.30	0/3588	0.69	14/4880 (0.3%)
1	l	0.30	0/3588	0.69	14/4880 (0.3%)
1	m	0.30	0/3588	0.69	14/4880 (0.3%)
1	n	0.30	0/3588	0.69	15/4880 (0.3%)
1	o	0.30	0/3588	0.69	15/4880 (0.3%)
1	p	0.30	0/3588	0.68	15/4880 (0.3%)
1	q	0.30	0/3588	0.69	15/4880 (0.3%)
1	r	0.30	0/3588	0.69	15/4880 (0.3%)
1	s	0.30	0/3588	0.69	15/4880 (0.3%)
1	t	0.30	0/3588	0.69	14/4880 (0.3%)
1	u	0.30	0/3588	0.69	14/4880 (0.3%)
1	v	0.30	0/3588	0.69	15/4880 (0.3%)
1	w	0.30	0/3588	0.69	14/4880 (0.3%)
1	x	0.30	0/3588	0.69	14/4880 (0.3%)
1	y	0.30	0/3588	0.69	14/4880 (0.3%)
1	z	0.30	0/3588	0.69	14/4880 (0.3%)
All	All	0.30	1/215280 (0.0%)	0.69	857/292800 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	4	366	VAL	CA-CB	-5.00	1.47	1.53

The worst 5 of 857 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	u	426	THR	N-CA-C	8.32	124.25	113.18
1	E	426	THR	N-CA-C	8.32	124.24	113.18
1	o	426	THR	N-CA-C	8.32	124.24	113.18
1	z	426	THR	N-CA-C	8.32	124.24	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	w	426	THR	N-CA-C	8.31	124.24	113.18

There are no chirality outliers.

There are no planarity outliers.

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	1	3507	0	3435	115	0
1	2	3507	0	3435	121	0
1	3	3507	0	3435	114	0
1	4	3507	0	3435	126	0
1	5	3507	0	3435	119	0
1	6	3507	0	3435	127	0
1	7	3507	0	3435	126	0
1	8	3507	0	3435	125	0
1	9	3507	0	3435	119	0
1	A	3507	0	3435	120	0
1	B	3507	0	3435	125	0
1	C	3507	0	3435	130	0
1	D	3507	0	3435	119	0
1	E	3507	0	3435	127	0
1	F	3507	0	3435	121	0
1	G	3507	0	3435	126	0
1	H	3507	0	3435	120	0
1	I	3507	0	3435	118	0
1	J	3507	0	3435	124	0
1	K	3507	0	3435	121	0
1	L	3507	0	3435	126	0
1	M	3507	0	3435	122	0
1	N	3507	0	3435	121	0
1	O	3507	0	3435	119	0
1	P	3507	0	3435	124	0
1	Q	3507	0	3435	121	0
1	R	3507	0	3435	124	0
1	S	3507	0	3435	119	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	T	3507	0	3435	126	0
1	V	3507	0	3435	124	0
1	W	3507	0	3435	121	0
1	X	3507	0	3435	122	0
1	Y	3507	0	3435	124	0
1	Z	3507	0	3435	120	0
1	a	3507	0	3435	120	0
1	b	3507	0	3435	124	0
1	c	3507	0	3435	119	0
1	d	3507	0	3435	120	0
1	e	3507	0	3435	124	0
1	f	3507	0	3435	122	0
1	g	3507	0	3435	122	0
1	h	3507	0	3435	124	0
1	i	3507	0	3435	125	0
1	j	3507	0	3435	123	0
1	k	3507	0	3435	120	0
1	l	3507	0	3435	122	0
1	m	3507	0	3435	123	0
1	n	3507	0	3435	117	0
1	o	3507	0	3435	122	0
1	p	3507	0	3435	117	0
1	q	3507	0	3435	124	0
1	r	3507	0	3435	127	0
1	s	3507	0	3435	118	0
1	t	3507	0	3435	120	0
1	u	3507	0	3435	124	0
1	v	3507	0	3435	124	0
1	w	3507	0	3435	122	0
1	x	3507	0	3435	119	0
1	y	3507	0	3435	124	0
1	z	3507	0	3435	122	0
2	1	1	0	0	0	0
2	2	1	0	0	0	0
2	3	1	0	0	0	0
2	4	1	0	0	0	0
2	5	1	0	0	0	0
2	6	1	0	0	0	0
2	7	1	0	0	0	0
2	8	1	0	0	0	0
2	9	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	1	0	0	0	0
2	R	1	0	0	0	0
All	All	210432	0	206100	6784	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 16.

The worst 5 of 6784 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:j:426:THR:CG2	1:j:428:GLN:HG2	1.56	1.36
1:E:426:THR:CG2	1:E:428:GLN:HG2	1.56	1.36
1:t:426:THR:CG2	1:t:428:GLN:HG2	1.56	1.36
1:x:426:THR:CG2	1:x:428:GLN:HG2	1.56	1.36
1:f:426:THR:CG2	1:f:428:GLN:HG2	1.56	1.36

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	1	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	2	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	3	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	4	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	5	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	6	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	7	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	8	428/543 (79%)	388 (91%)	40 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	9	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	A	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	B	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	C	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	D	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	E	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	F	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	G	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	H	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	I	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	J	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	K	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	L	428/543 (79%)	387 (90%)	41 (10%)	0	100	100
1	M	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	N	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	O	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	P	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	Q	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	R	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	S	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	T	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	V	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	W	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	X	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	Y	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	Z	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	a	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	b	428/543 (79%)	387 (90%)	41 (10%)	0	100	100
1	c	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	d	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	e	428/543 (79%)	388 (91%)	40 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	f	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	g	428/543 (79%)	387 (90%)	41 (10%)	0	100	100
1	h	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	i	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	j	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	k	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	l	428/543 (79%)	387 (90%)	41 (10%)	0	100	100
1	m	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	n	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	o	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	p	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	q	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	r	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	s	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	t	428/543 (79%)	387 (90%)	41 (10%)	0	100	100
1	u	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	v	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	w	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	x	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	y	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
1	z	428/543 (79%)	388 (91%)	40 (9%)	0	100	100
All	All	25680/32580 (79%)	23275 (91%)	2405 (9%)	0	100	100

There are no Ramachandran outliers to report.

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	1	396/472 (84%)	396 (100%)	0	100	100
1	2	396/472 (84%)	396 (100%)	0	100	100
1	3	396/472 (84%)	396 (100%)	0	100	100
1	4	396/472 (84%)	396 (100%)	0	100	100
1	5	396/472 (84%)	396 (100%)	0	100	100
1	6	396/472 (84%)	395 (100%)	1 (0%)	86	93
1	7	396/472 (84%)	396 (100%)	0	100	100
1	8	396/472 (84%)	396 (100%)	0	100	100
1	9	396/472 (84%)	396 (100%)	0	100	100
1	A	396/472 (84%)	396 (100%)	0	100	100
1	B	396/472 (84%)	396 (100%)	0	100	100
1	C	396/472 (84%)	396 (100%)	0	100	100
1	D	396/472 (84%)	396 (100%)	0	100	100
1	E	396/472 (84%)	395 (100%)	1 (0%)	86	93
1	F	396/472 (84%)	396 (100%)	0	100	100
1	G	396/472 (84%)	396 (100%)	0	100	100
1	H	396/472 (84%)	396 (100%)	0	100	100
1	I	396/472 (84%)	396 (100%)	0	100	100
1	J	396/472 (84%)	396 (100%)	0	100	100
1	K	396/472 (84%)	396 (100%)	0	100	100
1	L	396/472 (84%)	396 (100%)	0	100	100
1	M	396/472 (84%)	396 (100%)	0	100	100
1	N	396/472 (84%)	396 (100%)	0	100	100
1	O	396/472 (84%)	396 (100%)	0	100	100
1	P	396/472 (84%)	396 (100%)	0	100	100
1	Q	396/472 (84%)	396 (100%)	0	100	100
1	R	396/472 (84%)	396 (100%)	0	100	100
1	S	396/472 (84%)	396 (100%)	0	100	100
1	T	396/472 (84%)	396 (100%)	0	100	100
1	V	396/472 (84%)	396 (100%)	0	100	100
1	W	396/472 (84%)	396 (100%)	0	100	100
1	X	396/472 (84%)	395 (100%)	1 (0%)	86	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Y	396/472 (84%)	396 (100%)	0	100	100
1	Z	396/472 (84%)	396 (100%)	0	100	100
1	a	396/472 (84%)	396 (100%)	0	100	100
1	b	396/472 (84%)	396 (100%)	0	100	100
1	c	396/472 (84%)	396 (100%)	0	100	100
1	d	396/472 (84%)	396 (100%)	0	100	100
1	e	396/472 (84%)	396 (100%)	0	100	100
1	f	396/472 (84%)	396 (100%)	0	100	100
1	g	396/472 (84%)	396 (100%)	0	100	100
1	h	396/472 (84%)	396 (100%)	0	100	100
1	i	396/472 (84%)	396 (100%)	0	100	100
1	j	396/472 (84%)	396 (100%)	0	100	100
1	k	396/472 (84%)	396 (100%)	0	100	100
1	l	396/472 (84%)	396 (100%)	0	100	100
1	m	396/472 (84%)	396 (100%)	0	100	100
1	n	396/472 (84%)	396 (100%)	0	100	100
1	o	396/472 (84%)	396 (100%)	0	100	100
1	p	396/472 (84%)	396 (100%)	0	100	100
1	q	396/472 (84%)	396 (100%)	0	100	100
1	r	396/472 (84%)	396 (100%)	0	100	100
1	s	396/472 (84%)	396 (100%)	0	100	100
1	t	396/472 (84%)	396 (100%)	0	100	100
1	u	396/472 (84%)	396 (100%)	0	100	100
1	v	396/472 (84%)	396 (100%)	0	100	100
1	w	396/472 (84%)	396 (100%)	0	100	100
1	x	396/472 (84%)	396 (100%)	0	100	100
1	y	396/472 (84%)	396 (100%)	0	100	100
1	z	396/472 (84%)	396 (100%)	0	100	100
All	All	23760/28320 (84%)	23757 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	6	473	GLU
1	E	473	GLU
1	X	473	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 173 such sidechains are listed below:

Mol	Chain	Res	Type
1	h	239	ASN
1	r	118	GLN
1	i	372	ASN
1	m	372	ASN
1	s	475	GLN

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](#)

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

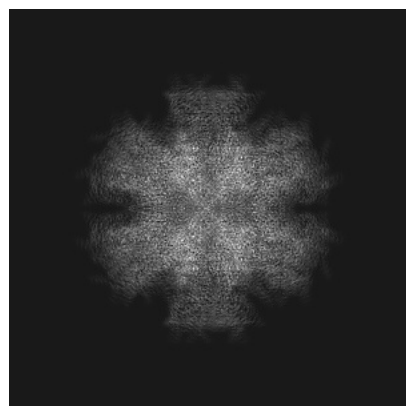
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55303. These allow visual inspection of the internal detail of the map and identification of artifacts.

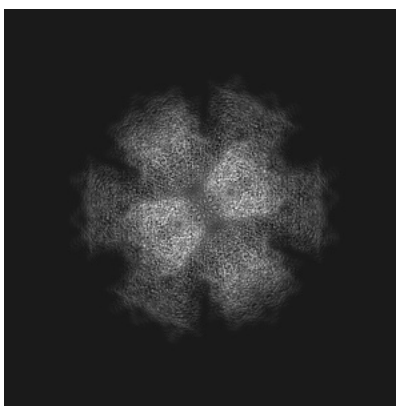
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

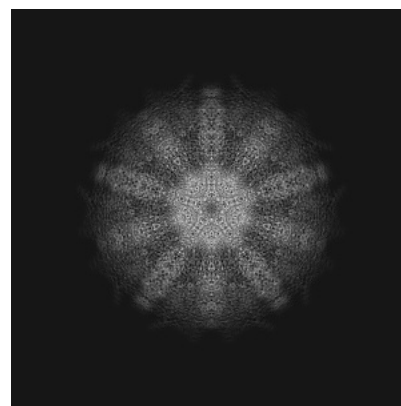
6.1.1 Primary map



X

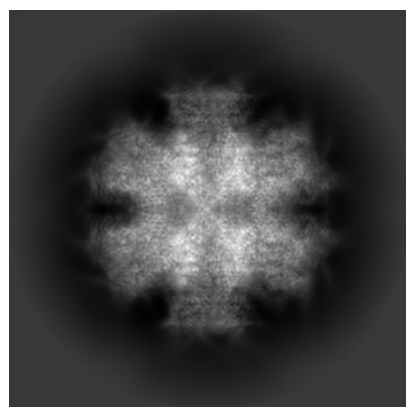


Y

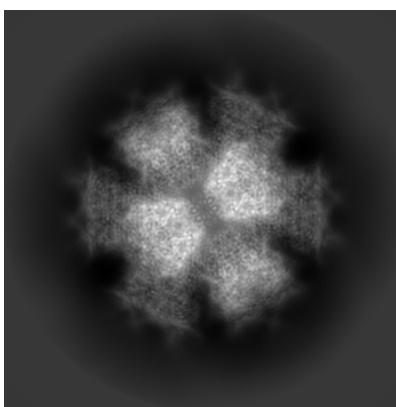


Z

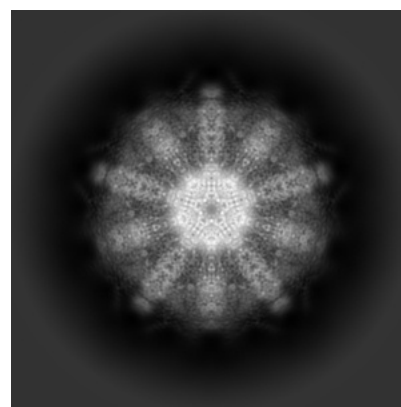
6.1.2 Raw map



X



Y

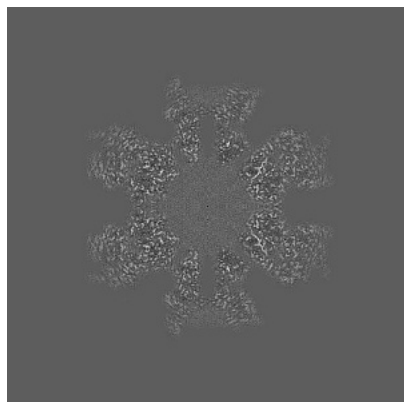


Z

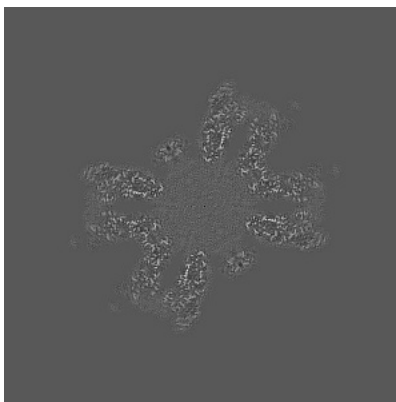
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

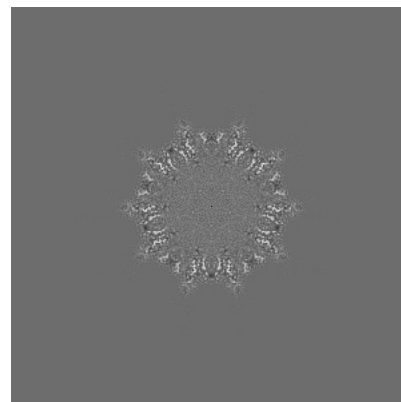
6.2.1 Primary map



X Index: 200

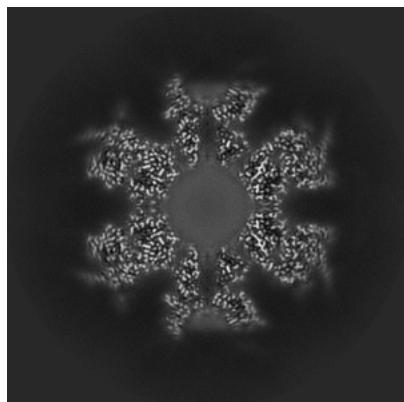


Y Index: 200

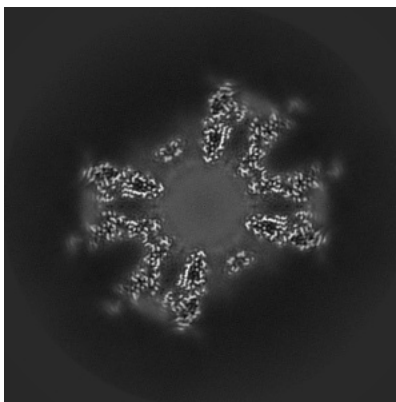


Z Index: 200

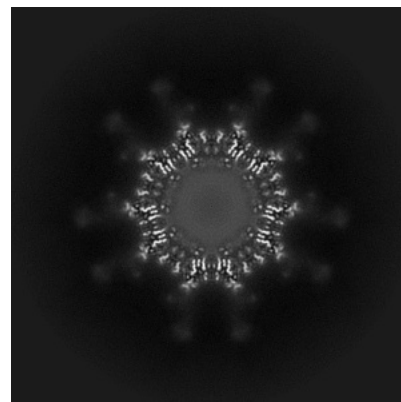
6.2.2 Raw map



X Index: 200



Y Index: 200

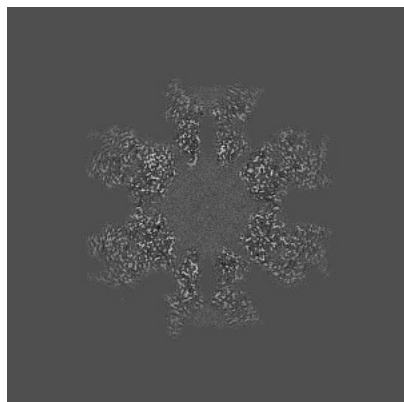


Z Index: 200

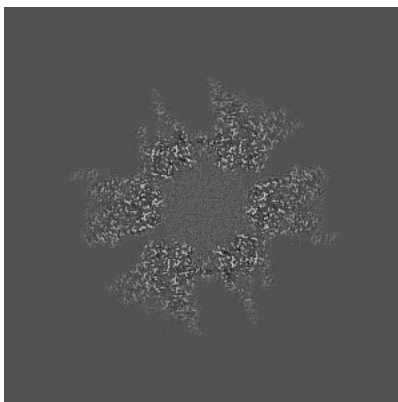
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

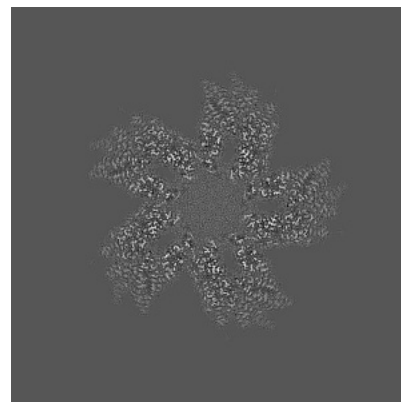
6.3.1 Primary map



X Index: 199

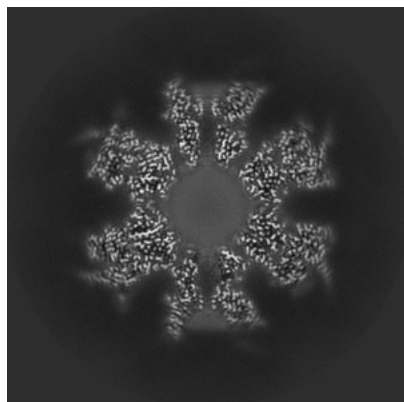


Y Index: 184

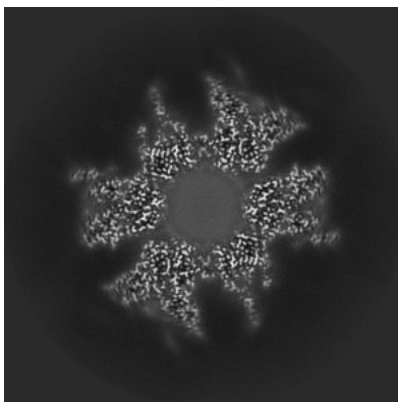


Z Index: 227

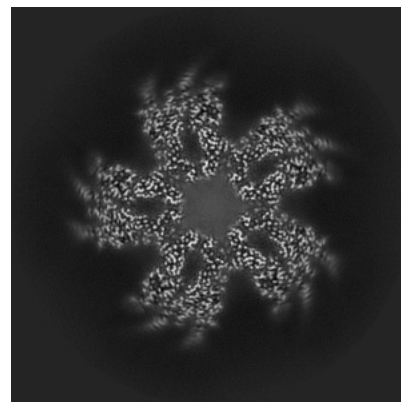
6.3.2 Raw map



X Index: 198



Y Index: 184

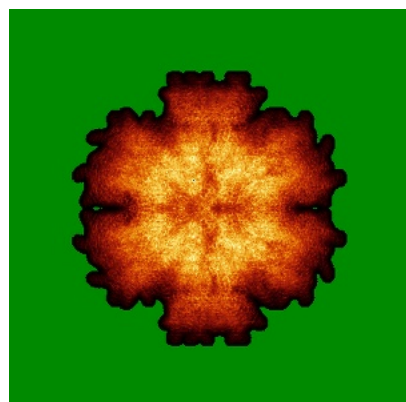


Z Index: 169

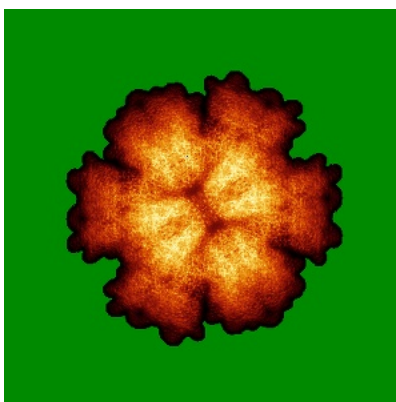
The images above show the largest variance slices of the map in three orthogonal directions.

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

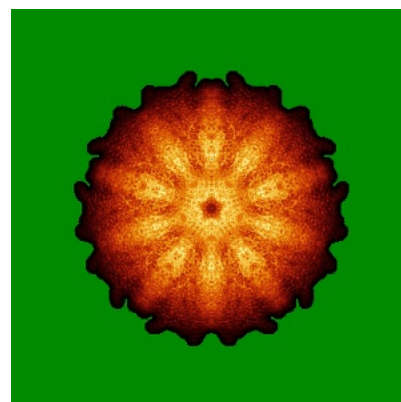
6.4.1 Primary map



X

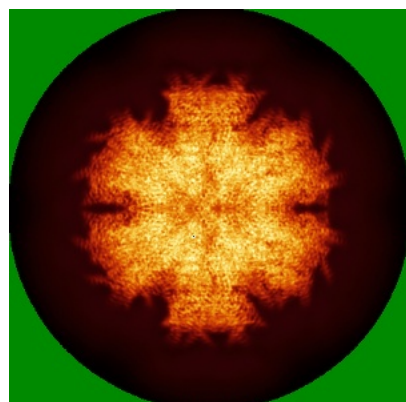


Y

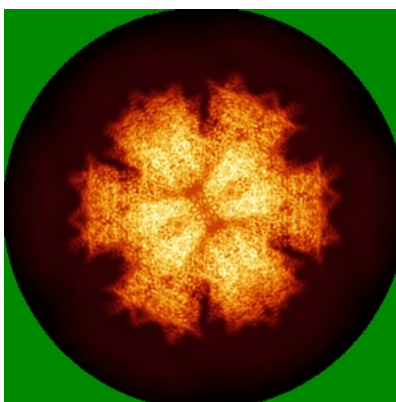


Z

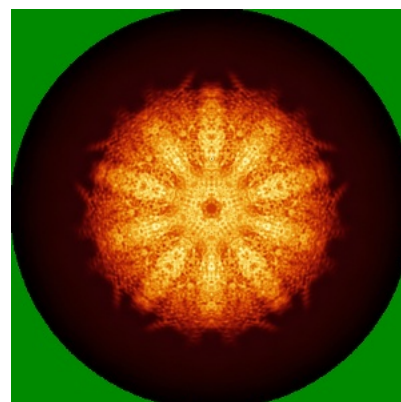
6.4.2 Raw map



X



Y

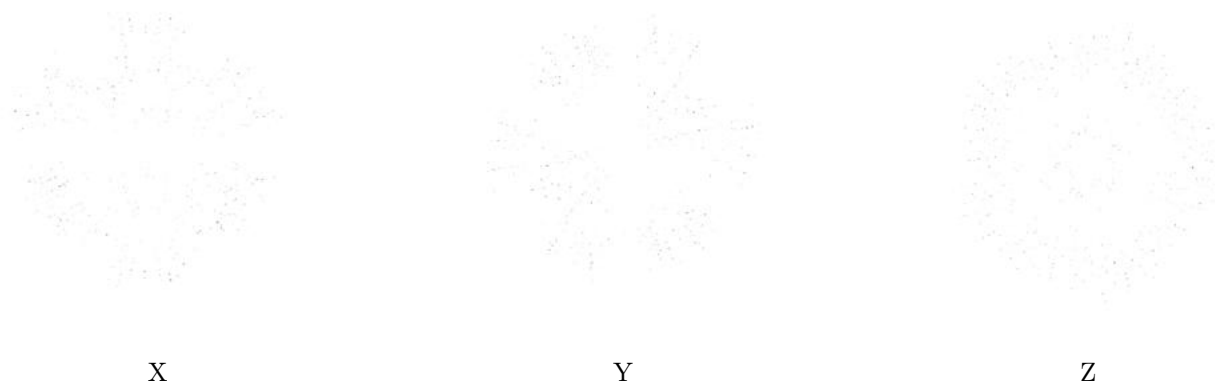


Z

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.

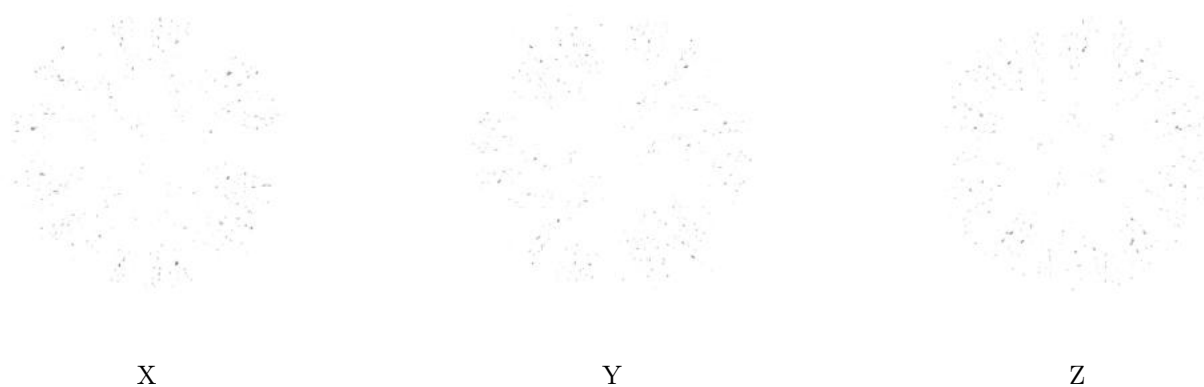
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

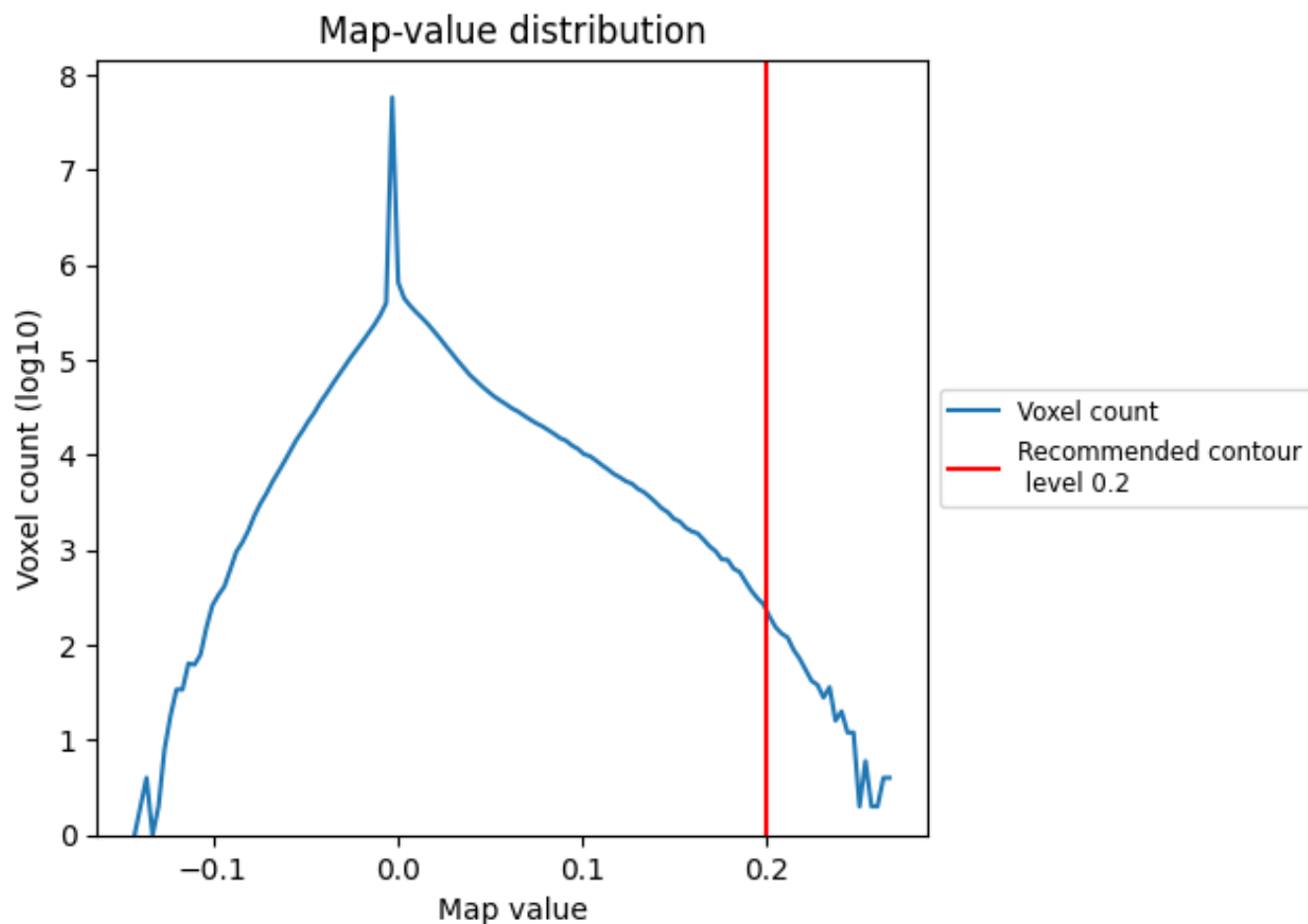
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

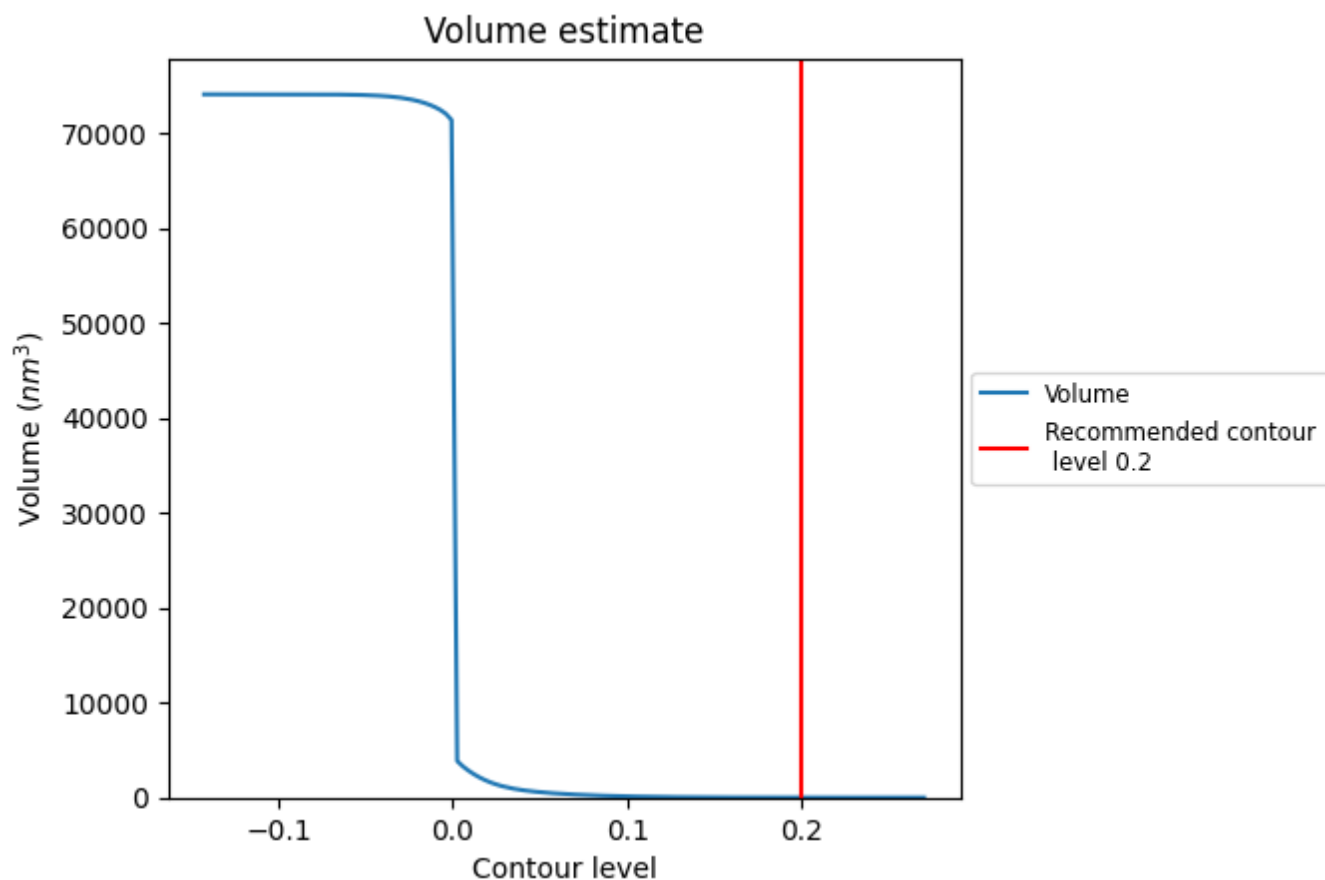
This section contains the results of statistical analysis of the map.

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.

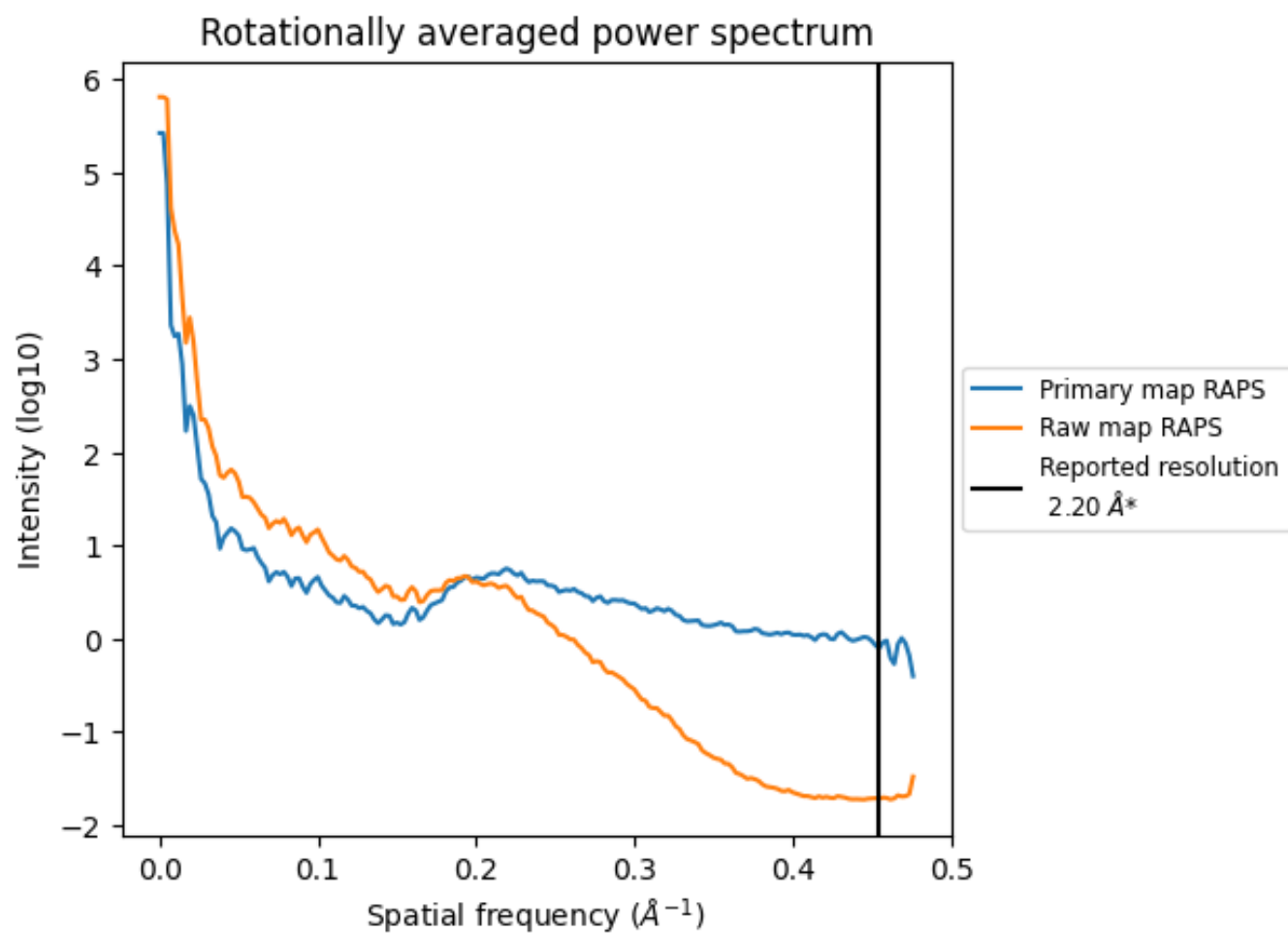
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1 nm³; this corresponds to an approximate mass of 1 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 ⓘ

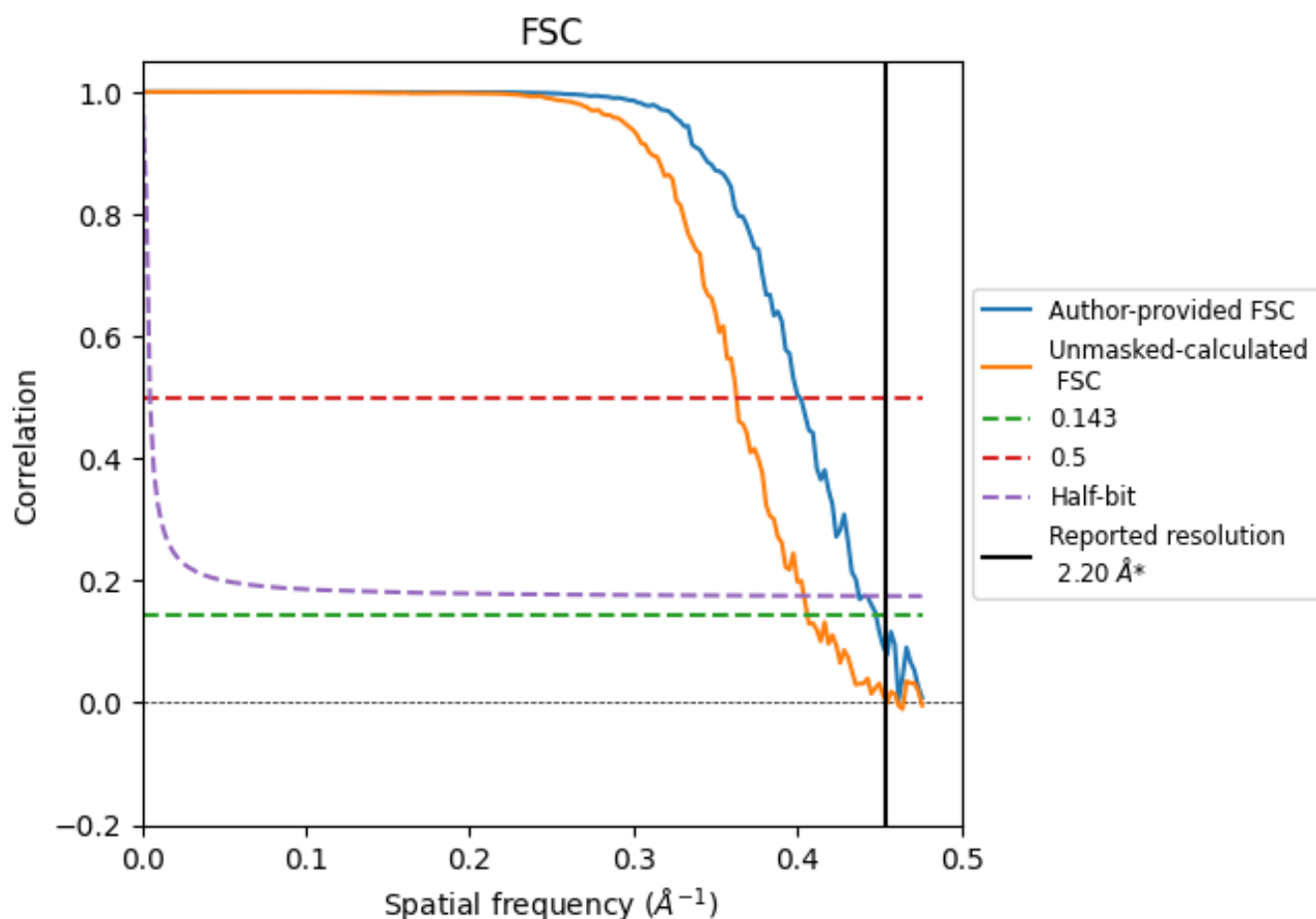


*Reported resolution corresponds to spatial frequency of 0.455 Å⁻¹

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 $0.455 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

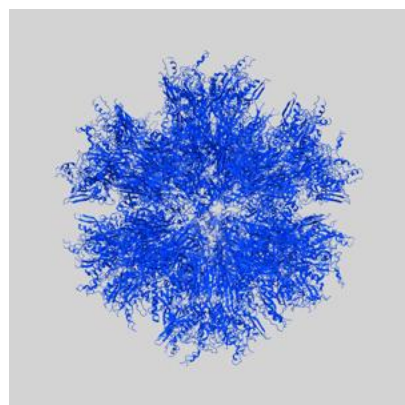
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	2.23	2.49	2.28
Unmasked-calculated*	2.46	2.76	2.48

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.46 differs from the reported value 2.2 by more than 10 %

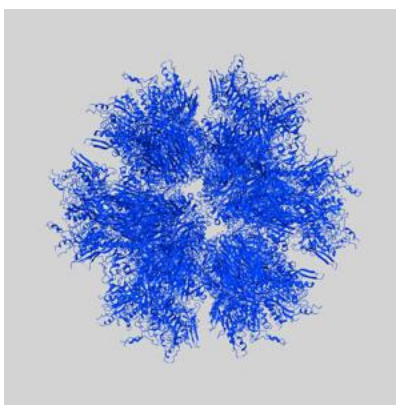
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55303 and PDB model 9SWA. Per-residue inclusion information can be found in section [3](#) on page [27](#).

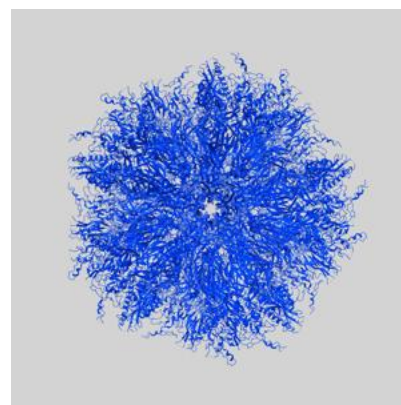
9.1 Map-model overlay [i](#)



X



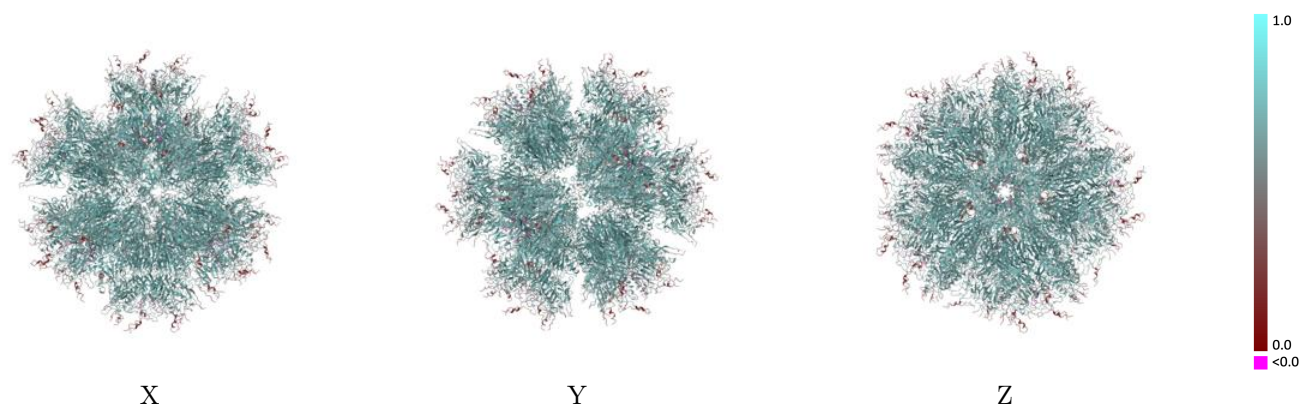
Y



Z

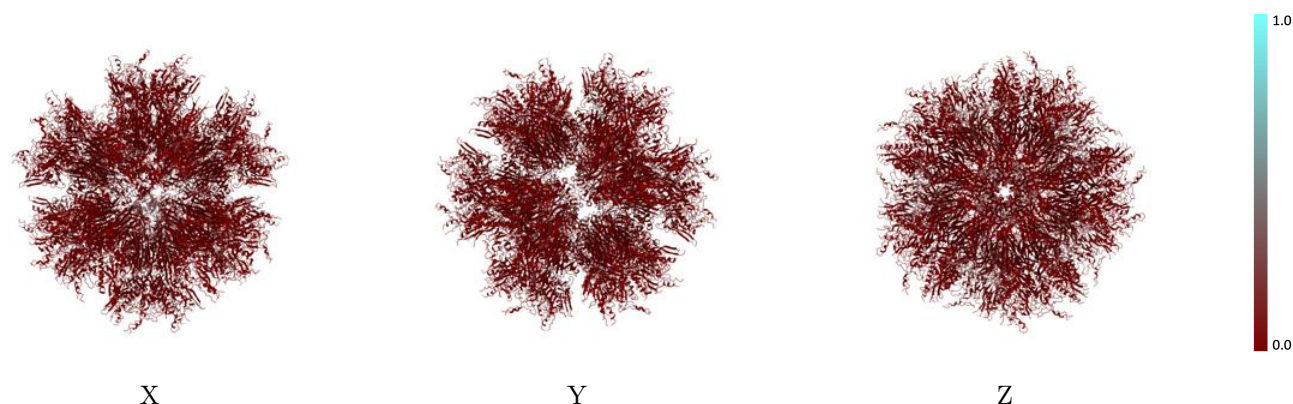
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



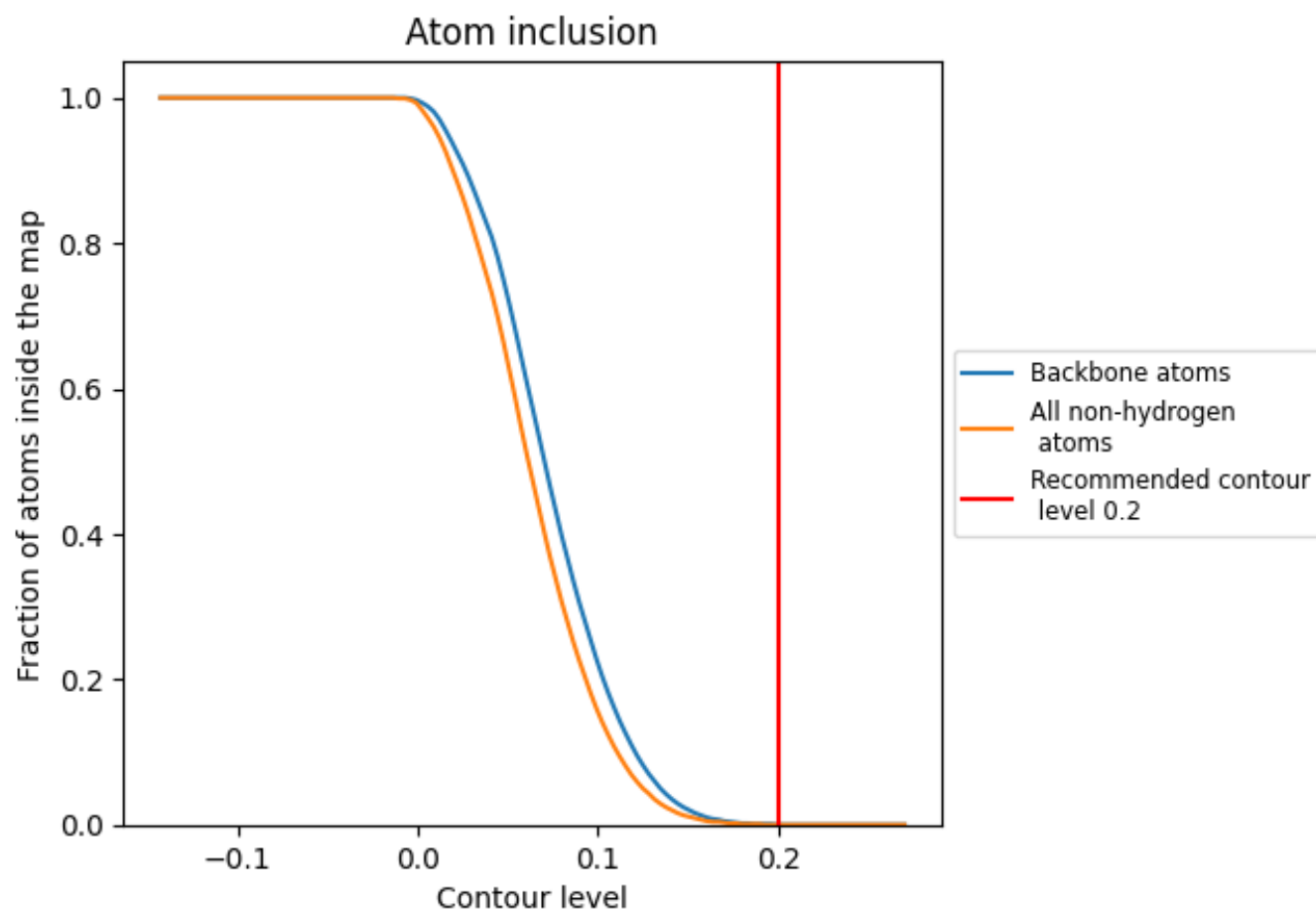
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.0000	 0.6330
1	 0.0000	 0.6350
2	 0.0010	 0.6330
3	 0.0000	 0.6310
4	 0.0000	 0.6310
5	 0.0000	 0.6340
6	 0.0010	 0.6340
7	 0.0000	 0.6330
8	 0.0000	 0.6320
9	 0.0000	 0.6360
A	 0.0000	 0.6300
B	 0.0000	 0.6330
C	 0.0000	 0.6320
D	 0.0000	 0.6330
E	 0.0000	 0.6320
F	 0.0000	 0.6380
G	 0.0000	 0.6340
H	 0.0000	 0.6350
I	 0.0000	 0.6350
J	 0.0010	 0.6320
K	 0.0000	 0.6350
L	 0.0000	 0.6380
M	 0.0000	 0.6290
N	 0.0000	 0.6320
O	 0.0000	 0.6310
P	 0.0000	 0.6360
Q	 0.0000	 0.6310
R	 0.0000	 0.6330
S	 0.0000	 0.6360
T	 0.0000	 0.6330
V	 0.0000	 0.6330
W	 0.0000	 0.6340
X	 0.0000	 0.6310
Y	 0.0000	 0.6330
Z	 0.0000	 0.6330



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Chain	Atom inclusion	Q-score
a	 0.0000	 0.6350
b	 0.0000	 0.6300
c	 0.0000	 0.6360
d	 0.0000	 0.6310
e	 0.0000	 0.6340
f	 0.0000	 0.6310
g	 0.0000	 0.6320
h	 0.0010	 0.6310
i	 0.0000	 0.6330
j	 0.0000	 0.6320
k	 0.0000	 0.6340
l	 0.0000	 0.6320
m	 0.0000	 0.6310
n	 0.0000	 0.6340
o	 0.0000	 0.6310
p	 0.0000	 0.6330
q	 0.0000	 0.6330
r	 0.0000	 0.6370
s	 0.0000	 0.6350
t	 0.0000	 0.6350
u	 0.0000	 0.6310
v	 0.0000	 0.6370
w	 0.0000	 0.6320
x	 0.0000	 0.6340
y	 0.0000	 0.6320
z	 0.0000	 0.6320