



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 10:16 PM UTC

PDB ID : 8RVE / pdb_00008rve
EMDB ID : EMD-16844
Title : Vimentin intermediate filament
Authors : Eibauer, M.; Medalia, O.
Deposited on : 2024-02-01
Resolution : 7.20 Å(reported)
Based on initial model : .

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:

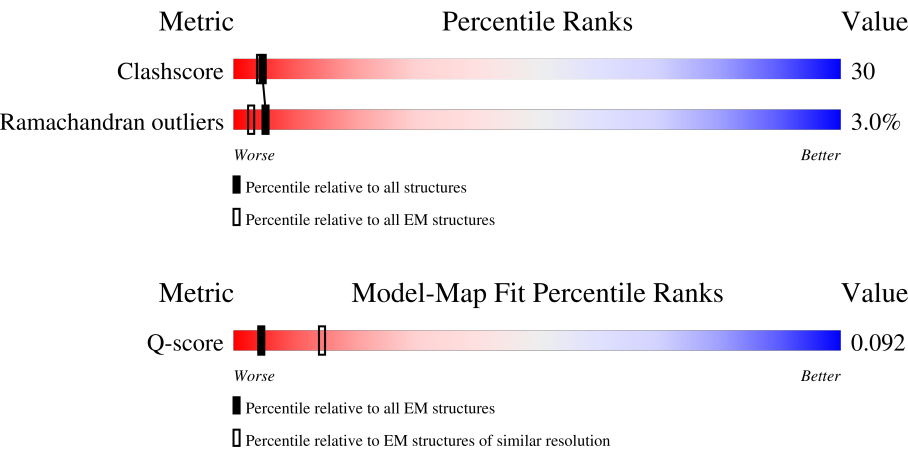
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 7.20 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	-
Q-score	-	25397	444 (6.70 - 7.70)

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	0	466	6% 47% 5% .. 46%
1	1	466	24% 51% 6% . 41%
1	2	466	22% 52% . .. 43%
1	3	466	24% 30% 11% 59%
1	4	466	28% 27% 14% . 58%

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Mol	Chain	Length	Quality of chain
1	5	466	
1	6	466	
1	7	466	
1	8	466	
1	9	466	
1	A	466	
1	AA	466	
1	AB	466	
1	AC	466	
1	AD	466	
1	AE	466	
1	AF	466	
1	AG	466	
1	AH	466	
1	AI	466	
1	AJ	466	
1	AK	466	
1	AL	466	
1	AM	466	
1	AN	466	
1	AO	466	
1	AP	466	
1	B	466	
1	C	466	
1	D	466	

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Mol	Chain	Length	Quality of chain
1	E	466	
1	F	466	
1	G	466	
1	H	466	
1	I	466	
1	J	466	
1	K	466	
1	L	466	
1	M	466	
1	N	466	
1	O	466	
1	P	466	
1	Q	466	
1	R	466	
1	S	466	
1	T	466	
1	U	466	
1	V	466	
1	W	466	
1	X	466	
1	Y	466	
1	Z	466	
1	a	466	
1	b	466	
1	c	466	

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Mol	Chain	Length	Quality of chain
1	d	466	
1	e	466	
1	f	466	
1	g	466	
1	h	466	
1	i	466	
1	j	466	
1	k	466	
1	l	466	
1	m	466	
1	n	466	
1	o	466	
1	p	466	
1	q	466	
1	r	466	
1	s	466	
1	t	466	
1	u	466	
1	v	466	
1	w	466	
1	x	466	
1	y	466	
1	z	466	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 54788 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 Vimentin.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	253	Total	C	N	O	0	0
			1012	506	253	253		
1	1	273	Total	C	N	O	0	0
			1092	546	273	273		
1	2	266	Total	C	N	O	0	0
			1064	532	266	266		
1	3	191	Total	C	N	O	0	0
			764	382	191	191		
1	4	195	Total	C	N	O	0	0
			780	390	195	195		
1	5	267	Total	C	N	O	0	0
			1068	534	267	267		
1	6	263	Total	C	N	O	0	0
			1052	526	263	263		
1	7	142	Total	C	N	O	0	0
			568	284	142	142		
1	8	147	Total	C	N	O	0	0
			588	294	147	147		
1	9	252	Total	C	N	O	0	0
			1008	504	252	252		
1	A	281	Total	C	N	O	0	0
			1124	562	281	281		
1	AA	95	Total	C	N	O	0	0
			380	190	95	95		
1	AB	100	Total	C	N	O	0	0
			400	200	100	100		
1	AC	223	Total	C	N	O	0	0
			892	446	223	223		
1	AD	222	Total	C	N	O	0	0
			888	444	222	222		
1	AE	49	Total	C	N	O	0	0
			196	98	49	49		
1	AF	54	Total	C	N	O	0	0
			216	108	54	54		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	AG	199	Total	C	N	O	0	0
			796	398	199	199		
1	AH	199	Total	C	N	O	0	0
			796	398	199	199		
1	AI	167	Total	C	N	O	0	0
			668	334	167	167		
1	AJ	170	Total	C	N	O	0	0
			680	340	170	170		
1	AK	136	Total	C	N	O	0	0
			544	272	136	136		
1	AL	141	Total	C	N	O	0	0
			564	282	141	141		
1	AM	81	Total	C	N	O	0	0
			324	162	81	81		
1	AN	85	Total	C	N	O	0	0
			340	170	85	85		
1	AO	34	Total	C	N	O	0	0
			136	68	34	34		
1	AP	39	Total	C	N	O	0	0
			156	78	39	39		
1	B	269	Total	C	N	O	0	0
			1076	538	269	269		
1	C	281	Total	C	N	O	0	0
			1124	562	281	281		
1	D	278	Total	C	N	O	0	0
			1112	556	278	278		
1	E	33	Total	C	N	O	0	0
			132	66	33	33		
1	F	35	Total	C	N	O	0	0
			140	70	35	35		
1	G	52	Total	C	N	O	0	0
			208	104	52	52		
1	H	54	Total	C	N	O	0	0
			216	108	54	54		
1	I	79	Total	C	N	O	0	0
			316	158	79	79		
1	J	83	Total	C	N	O	0	0
			332	166	83	83		
1	K	107	Total	C	N	O	0	0
			428	214	107	107		
1	L	113	Total	C	N	O	0	0
			452	226	113	113		

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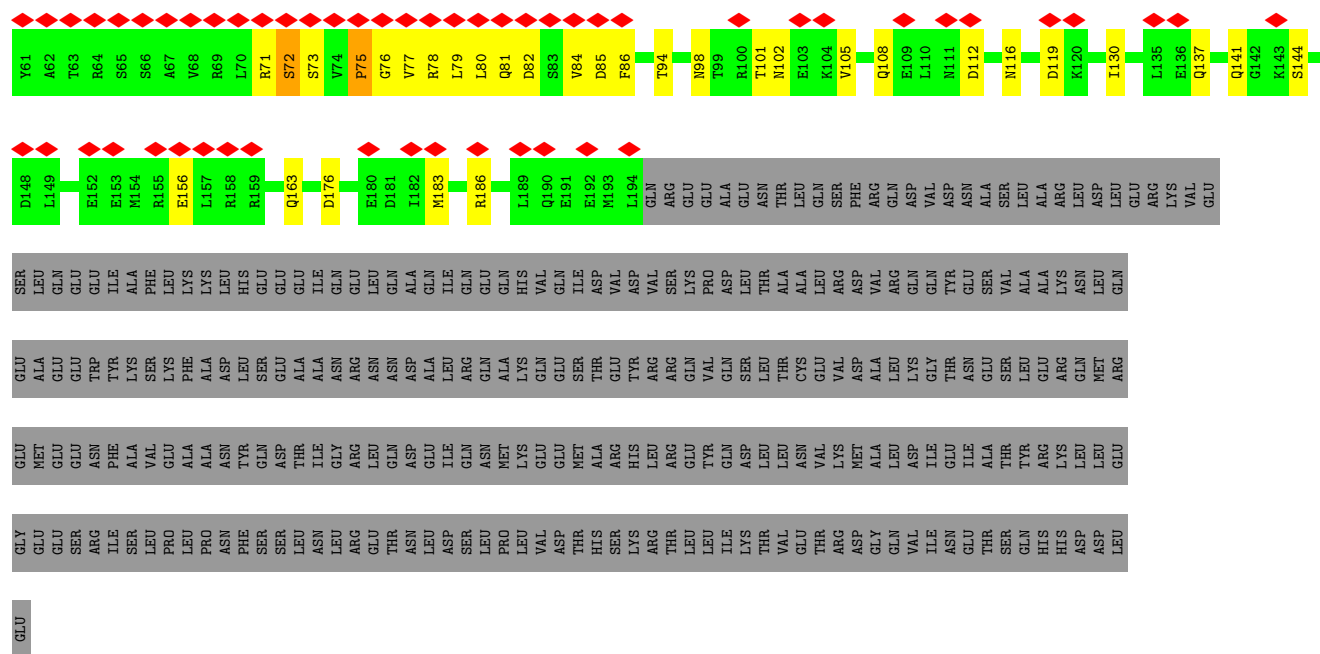
Mol	Chain	Residues	Atoms				AltConf	Trace
1	M	136	Total 544	C 272	N 136	O 136	0	0
1	N	142	Total 568	C 284	N 142	O 142	0	0
1	O	165	Total 660	C 330	N 165	O 165	0	0
1	P	170	Total 680	C 340	N 170	O 170	0	0
1	Q	14	Total 56	C 28	N 14	O 14	0	0
1	R	14	Total 56	C 28	N 14	O 14	0	0
1	S	194	Total 776	C 388	N 194	O 194	0	0
1	T	199	Total 796	C 398	N 199	O 199	0	0
1	U	53	Total 212	C 106	N 53	O 53	0	0
1	V	57	Total 228	C 114	N 57	O 57	0	0
1	W	194	Total 776	C 388	N 194	O 194	0	0
1	X	194	Total 776	C 388	N 194	O 194	0	0
1	Y	99	Total 396	C 198	N 99	O 99	0	0
1	Z	102	Total 408	C 204	N 102	O 102	0	0
1	a	209	Total 836	C 418	N 209	O 209	0	0
1	b	205	Total 820	C 410	N 205	O 205	0	0
1	c	148	Total 592	C 296	N 148	O 148	0	0
1	d	150	Total 600	C 300	N 150	O 150	0	0
1	e	214	Total 856	C 428	N 214	O 214	0	0
1	f	209	Total 836	C 418	N 209	O 209	0	0
1	g	194	Total 776	C 388	N 194	O 194	0	0

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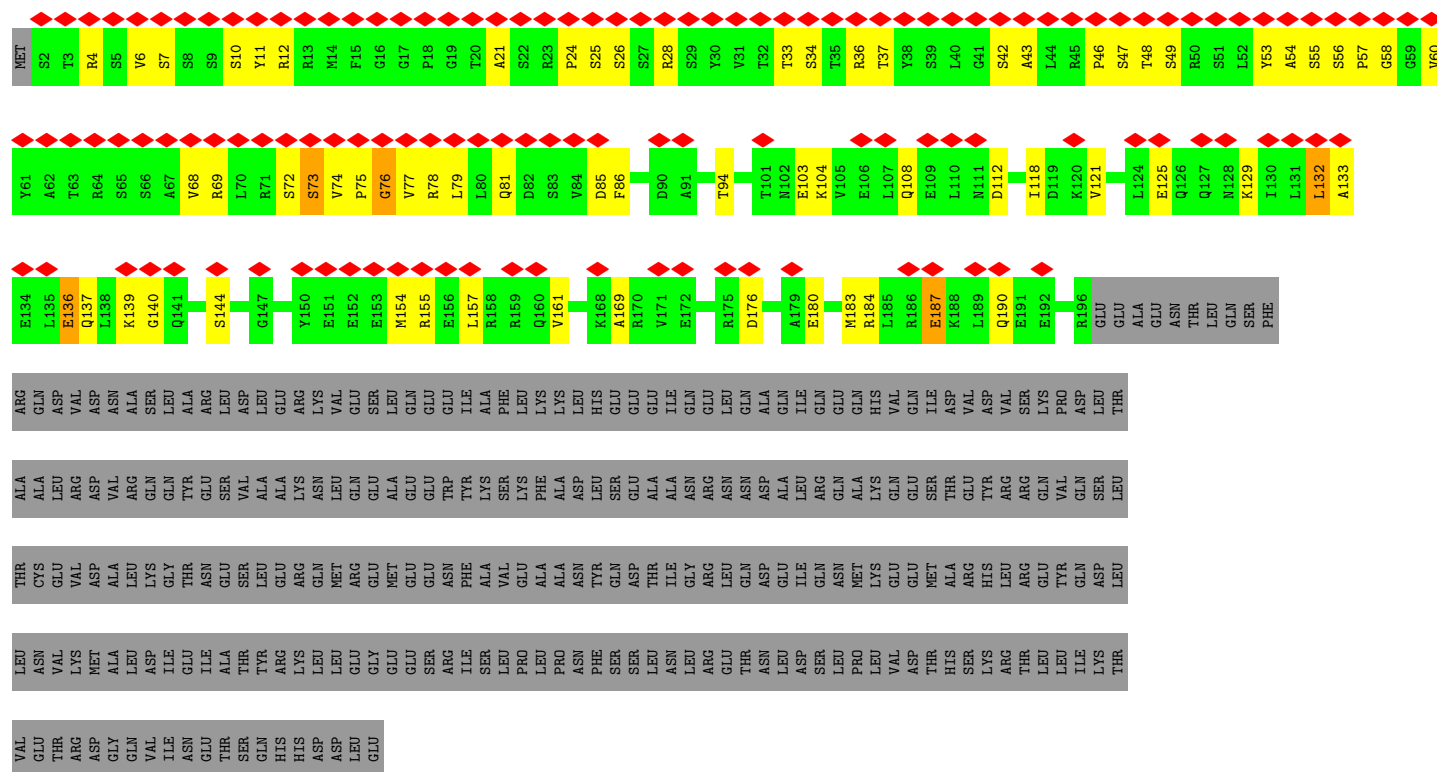
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Mol	Chain	Residues	Atoms				AltConf	Trace
1	h	193	Total	C	N	O	0	0
			772	386	193	193		
1	i	246	Total	C	N	O	0	0
			984	492	246	246		
1	j	237	Total	C	N	O	0	0
			948	474	237	237		
1	k	224	Total	C	N	O	0	0
			896	448	224	224		
1	l	225	Total	C	N	O	0	0
			900	450	225	225		
1	m	265	Total	C	N	O	0	0
			1060	530	265	265		
1	n	253	Total	C	N	O	0	0
			1012	506	253	253		
1	o	254	Total	C	N	O	0	0
			1016	508	254	254		
1	p	253	Total	C	N	O	0	0
			1012	506	253	253		
1	q	283	Total	C	N	O	0	0
			1132	566	283	283		
1	r	278	Total	C	N	O	0	0
			1112	556	278	278		
1	s	277	Total	C	N	O	0	0
			1108	554	277	277		
1	t	266	Total	C	N	O	0	0
			1064	532	266	266		
1	u	258	Total	C	N	O	0	0
			1032	516	258	258		
1	v	254	Total	C	N	O	0	0
			1016	508	254	254		
1	w	259	Total	C	N	O	0	0
			1036	518	259	259		
1	x	250	Total	C	N	O	0	0
			1000	500	250	250		
1	y	224	Total	C	N	O	0	0
			896	448	224	224		
1	z	228	Total	C	N	O	0	0
			912	456	228	228		



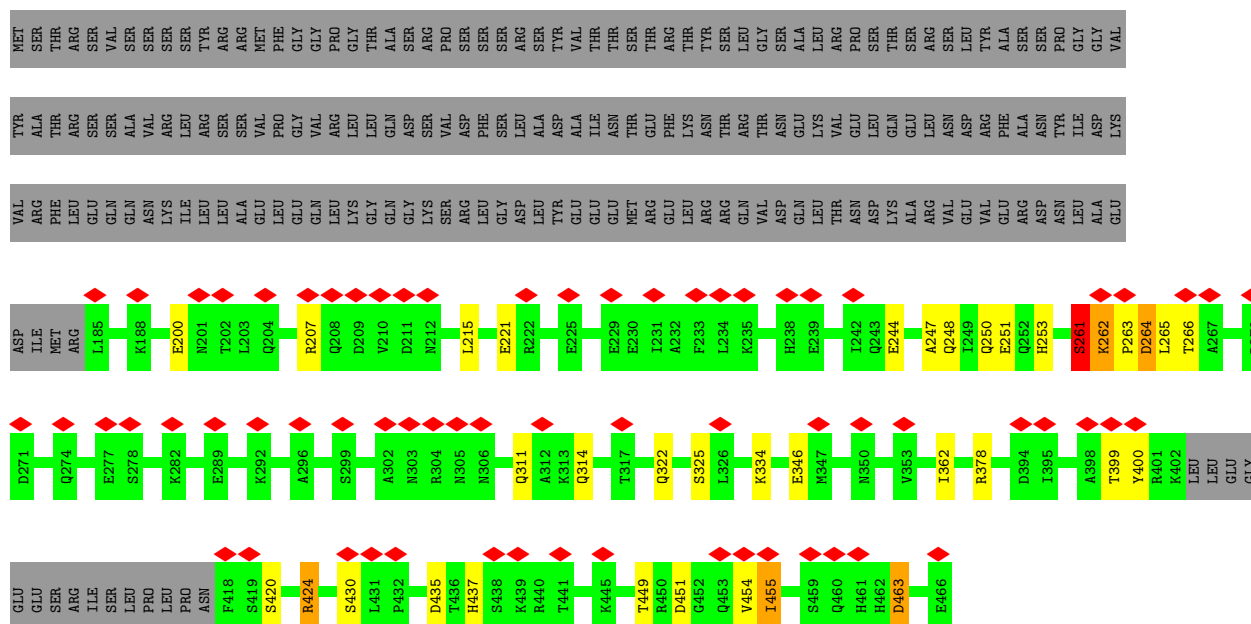


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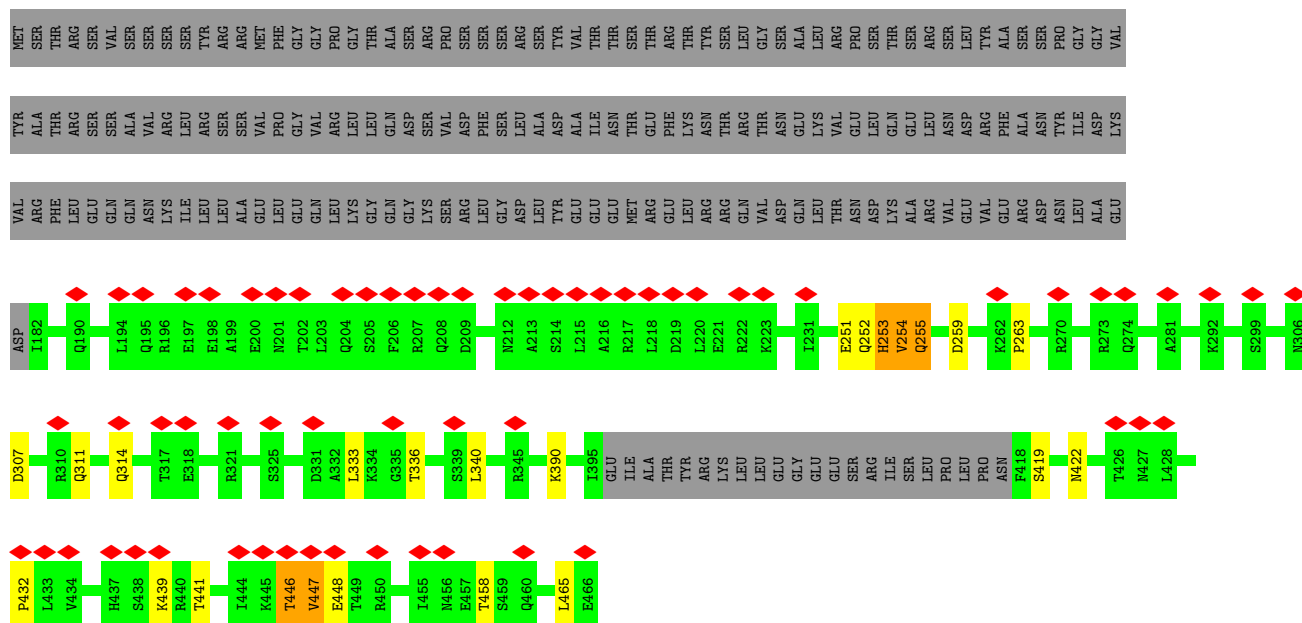


- Molecule 1: Vimentin

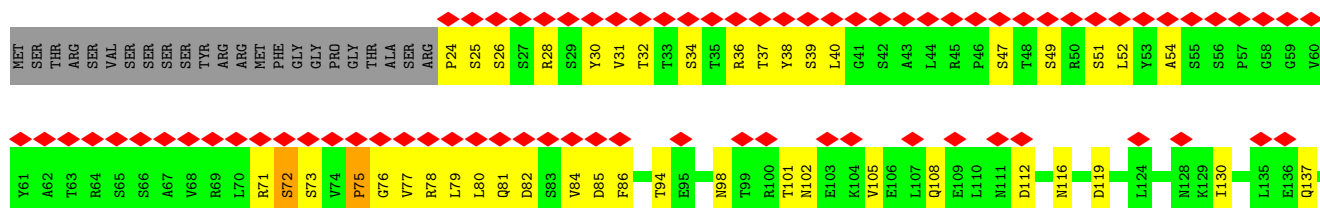


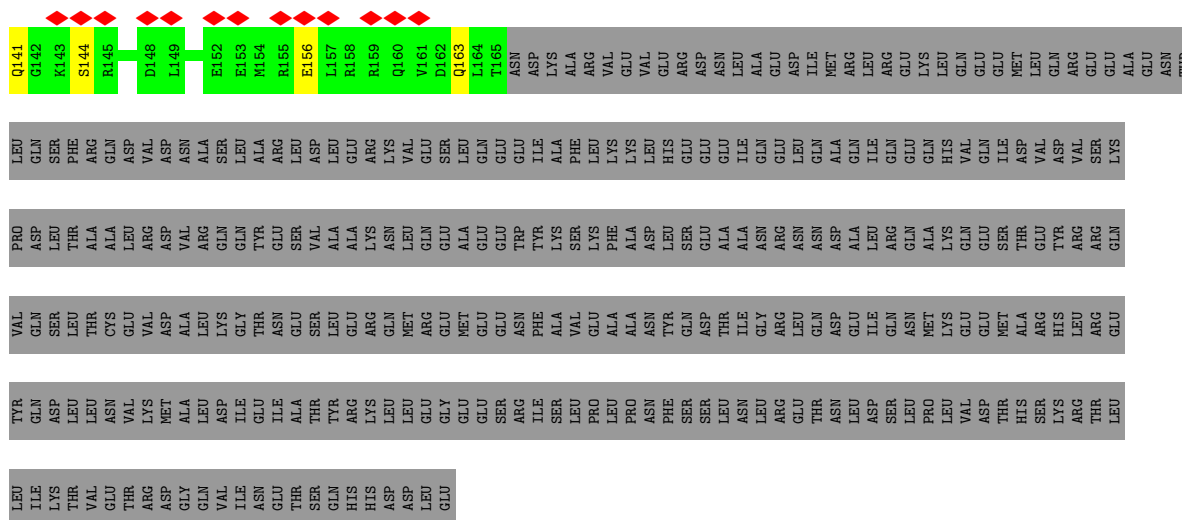


• Molecule 1: Vimentin

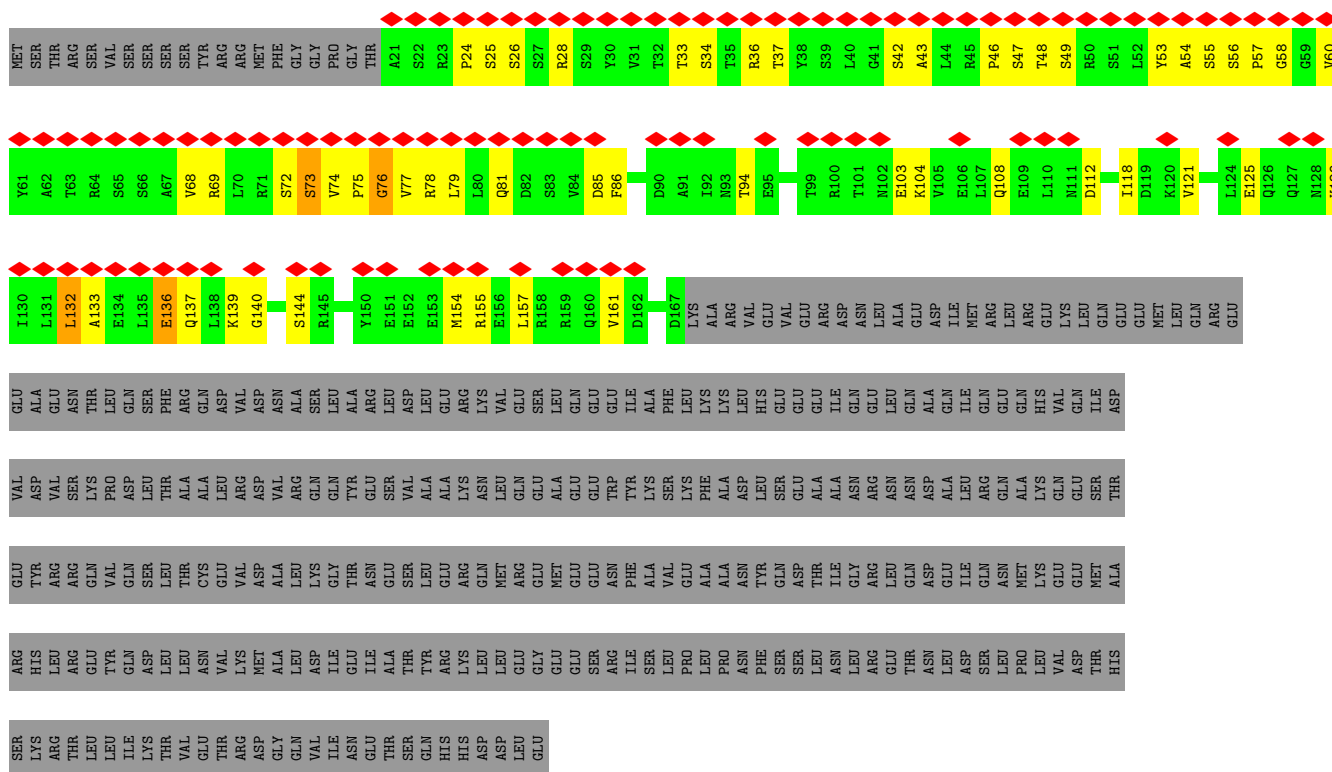


• Molecule 1: Vimentin

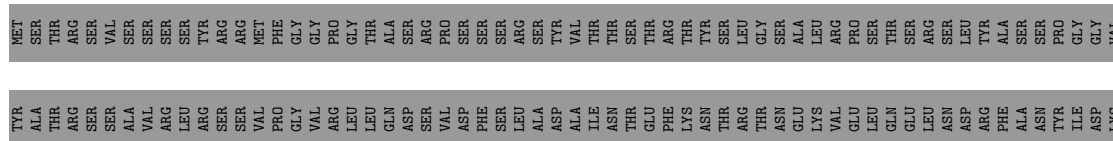


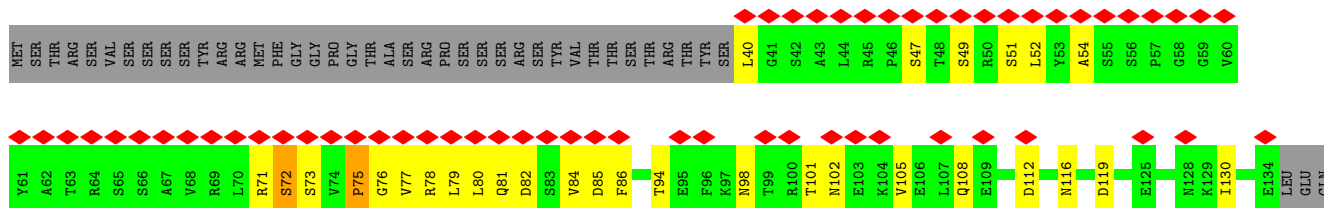


- Molecule 1: Vimentin



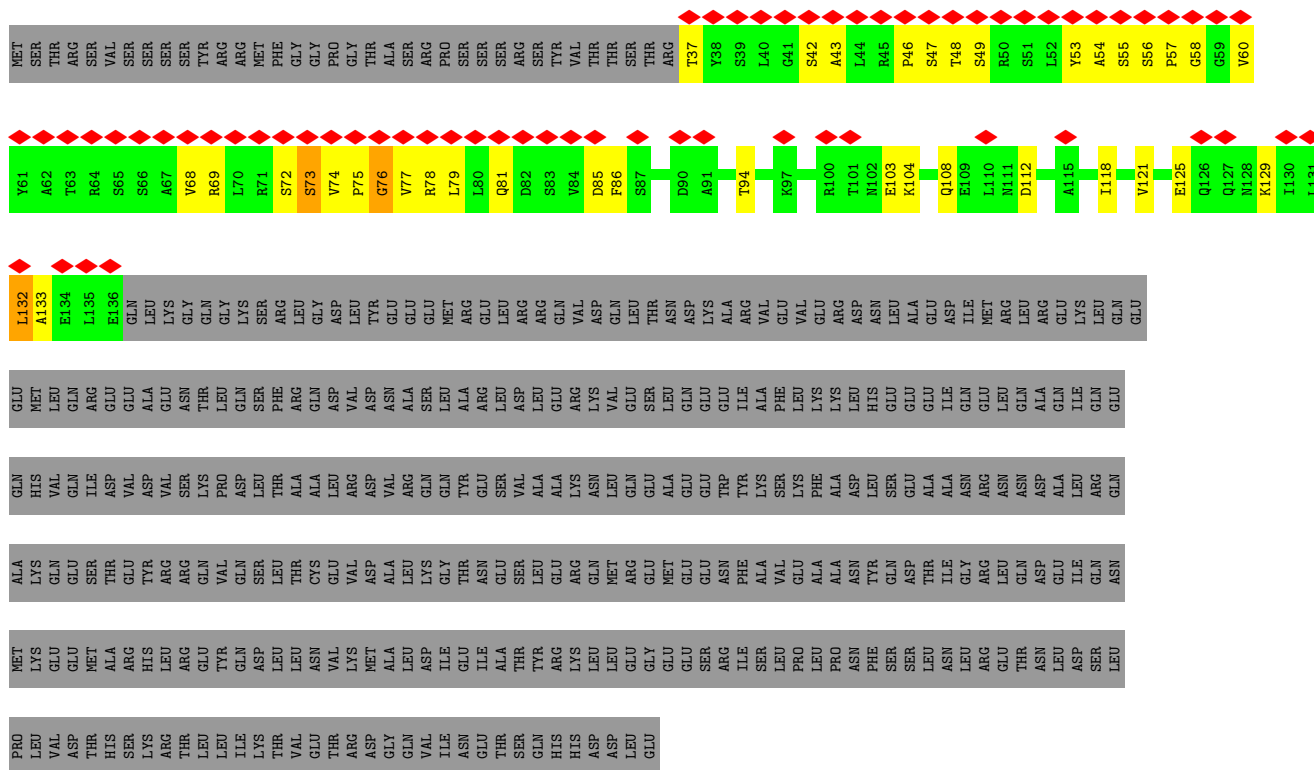
- Molecule 1: Vimentin



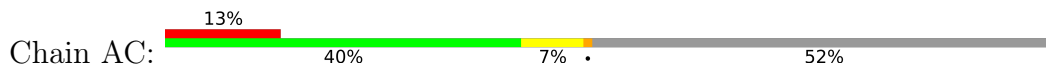


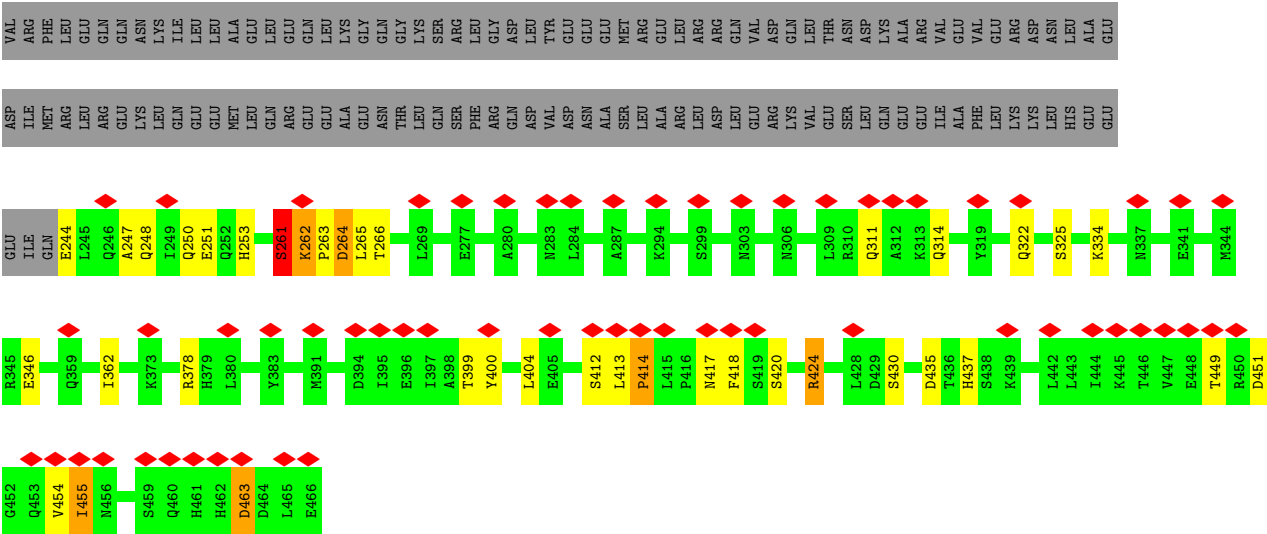
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ARG	LEU	ARG	VAL
THR	ARG	SER	LYS
LEU	GLN	GLY	THR
LEU	TYR	VAL	PRO
ILE	GLN	GLN	ASP
THR	ASP	LEU	LEU
THR	LEU	THR	ALA
VAL	LEU	THR	ALA
GLU	ASN	CYS	ALA
THR	VAL	GLU	LEU
ARG	LYS	VAL	ARG
ASP	MET	ASP	ASP
GLY	ALA	ALA	VAL
GLN	LEU	GLN	ARG
VAL	ASP	LYS	GLN
ILE	ILE	GLY	GLN
ASN	GLU	THR	TYR
GLU	ILE	ASN	GLU
THR	ALA	GLU	SER
THR	SER	SER	VAL
GLN	TYR	LEU	ALA
HIS	ARG	GLU	ALA
HIS	LYS	ARG	LYS
ASP	LEU	GLN	ASN
ASP	LEU	MET	LEU
LEU	GLU	ARG	GLN
GLU	GLY	GLU	GLU
	GLU	MET	ALA
	GLU	GLU	GLU
	SER	ASN	TRP
	ILE	PHE	TYR
	SER	ALA	LYS
	LEU	VAL	SER
	PRO	GLU	LYS
	LEU	ALA	PHE
	PRO	ALA	ALA
	ASN	ASN	ASP
	PHE	TYR	LEU
	SER	GLN	SER
	SER	THR	GLU
	ASN	ILE	ALA
	LEU	GLY	ASN
	ARG	GLY	ARG
	GLU	LEU	ASN
	THR	GLN	ASN
	PRO	ASN	GLN
	LEU	GLU	ALA
	ASP	ILE	ILE
	SER	GLN	ARG
	LEU	ASN	GLN
	PRO	MET	ALA
	LEU	LYS	HIS
	VAL	GLU	GLN
	ASP	GLU	VAL
	THR	MET	GLN
	HIS	ALA	SER

- Molecule 1: Vimentin

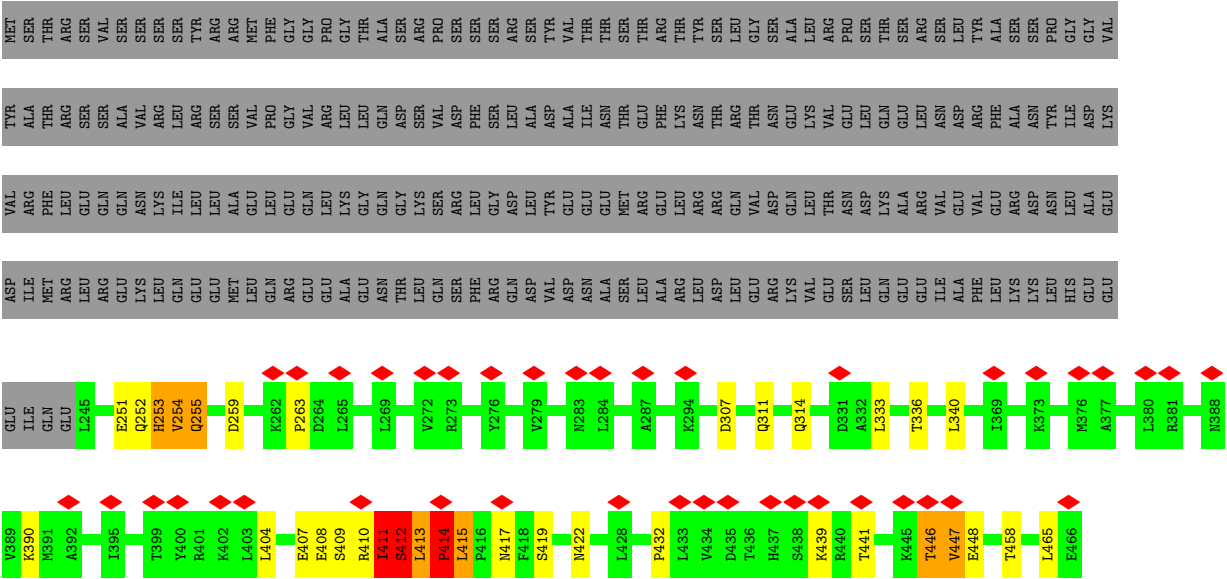
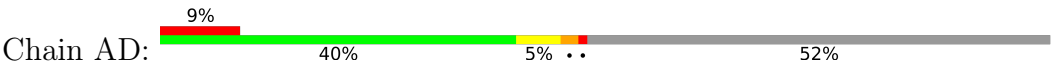


- Molecule 1: Vimentin

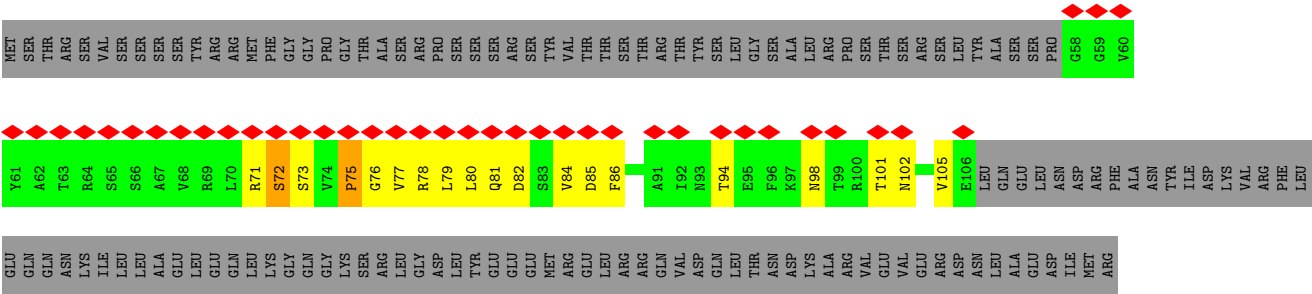
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• Molecule 1: Vimentin



• Molecule 1: Vimentin

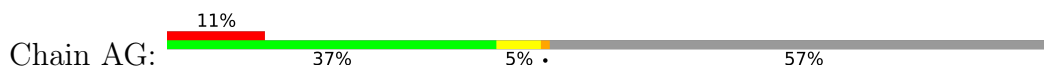


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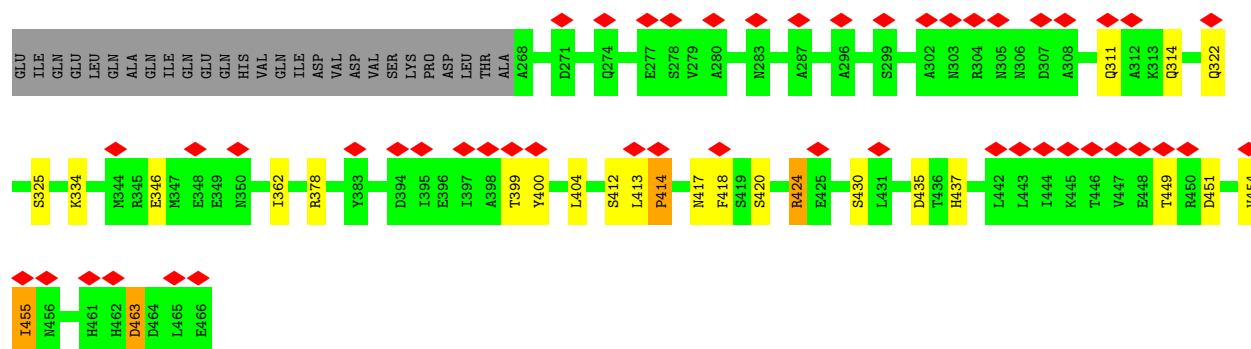
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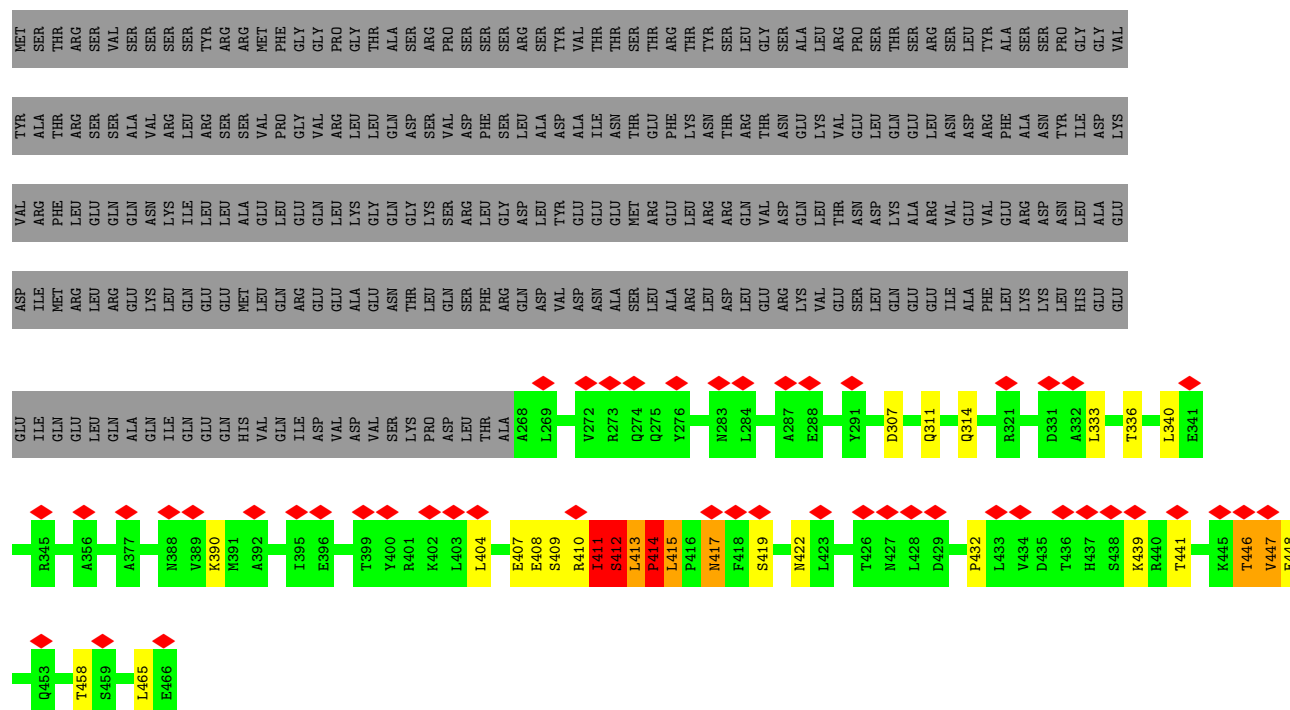
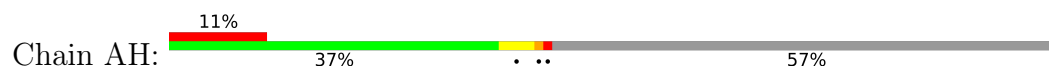
- Molecule 1: Vimentin



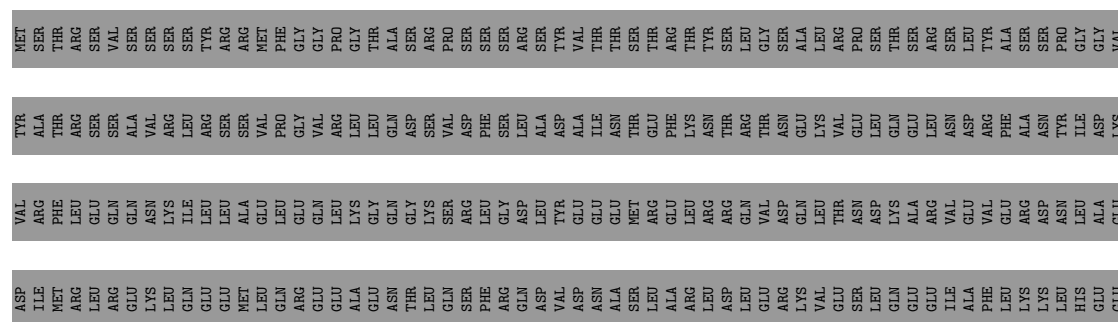
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ILE	THR	ARG	ALA	SER
MET	ARG	LEU	ARG	ARG
LEU	LEU	GLU	SER	VAL
GLU	ARG	GLN	ALA	SER
LYS	GLU	ASN	VAL	SER
LEU	LEU	LYS	ARG	SER
GLN	GLN	ILE	LEU	SER
GLU	GLU	LEU	ARG	TYR
GLU	GLU	LEU	SER	ARG
MET	MET	ALA	SER	ARG
LEU	LEU	GLU	VAL	MET
GLN	GLN	LEU	PRO	PHE
ARG	ARG	GLU	GLY	GLY
GLU	GLU	GLN	VAL	GLY
GLU	GLU	LEU	ARG	PRO
ALA	ALA	LYS	LEU	GLY
GLU	GLU	GLY	LEU	THR
ASN	ASN	GLN	GLN	ALA
THR	THR	GLY	ASP	SER
LEU	LEU	LYS	SER	ARG
GLN	GLN	SER	VAL	PRO
SER	SER	ARG	ASP	SER
PHE	PHE	LEU	PHE	SER
ARG	ARG	GLY	SER	SER
GLN	GLN	ASP	LEU	ARG
ASP	ASP	LEU	ALA	SER
VAL	VAL	TYR	ASP	TYR
ASP	ASP	GLU	ALA	VAL
ASN	ASN	GLU	ILE	THR
ALA	ALA	GLU	ASN	THR
SER	SER	MET	THR	SER
LEU	LEU	ARG	GLU	THR
ALA	ALA	GLU	PHE	ARG
ARG	ARG	LEU	LYS	THR
LEU	LEU	ARG	ASN	TYR
ASP	ASP	ARG	THR	SER
LEU	LEU	GLN	ARG	LEU
GLU	GLU	VAL	THR	GLY
ARG	ARG	ASP	ASN	SER
LYS	LYS	GLN	GLU	LEU
VAL	VAL	THR	LYS	ALA
GLU	GLU	THR	VAL	ARG
SER	SER	ASN	GLU	PRO
LEU	LEU	ASP	LEU	SER
GLN	GLN	LYS	GLN	THR
GLU	GLU	ALA	GLU	SER
ILE	ILE	VAL	ASN	ARG
GLU	GLU	GLU	LEU	SER
PHE	PHE	VAL	ARG	TYR
LEU	LEU	GLU	PHE	ALA
LYS	LYS	ARG	ALA	SER
THR	THR	ASP	ASN	SER
LEU	LEU	ASN	TYR	PRO
HIS	HIS	LEU	ILE	GLY
GLU	GLU	ALA	ASP	GLY
GLU	GLU	GLN	THR	VAL

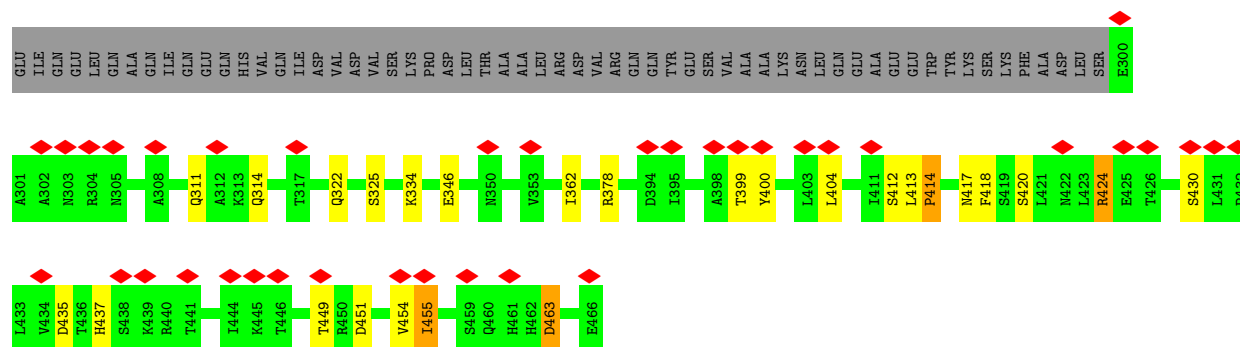


• Molecule 1: Vimentin

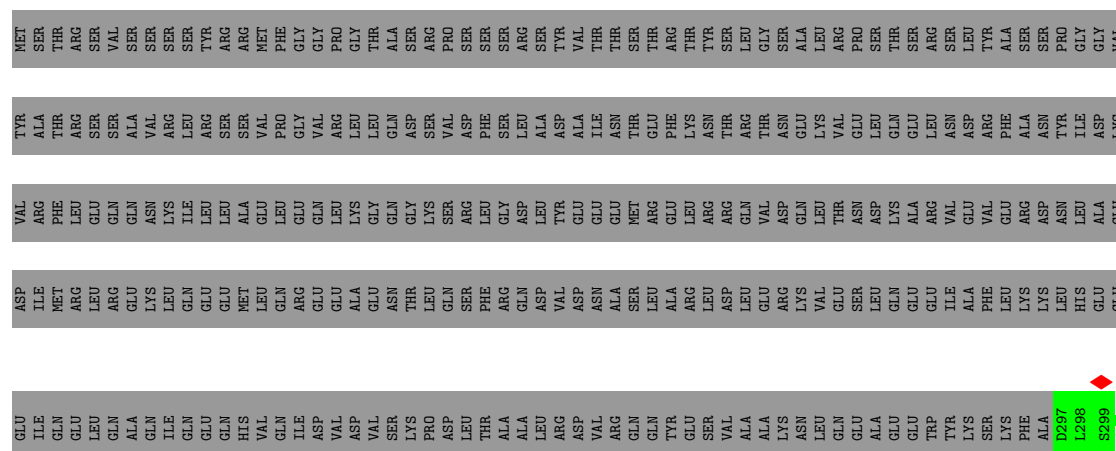


• Molecule 1: Vimentin

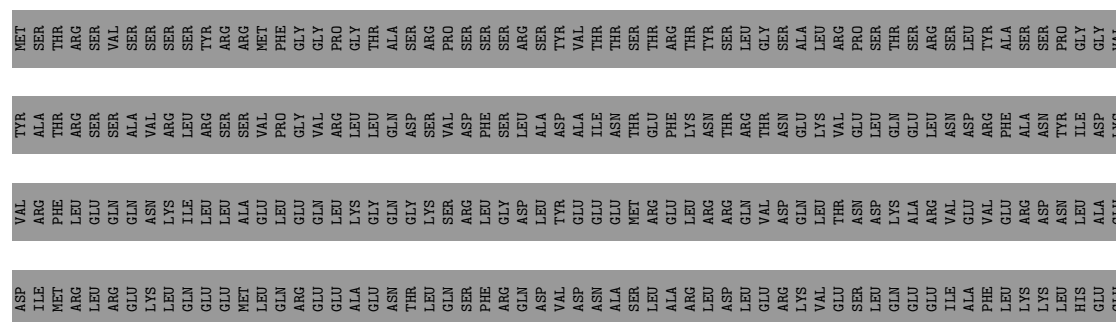


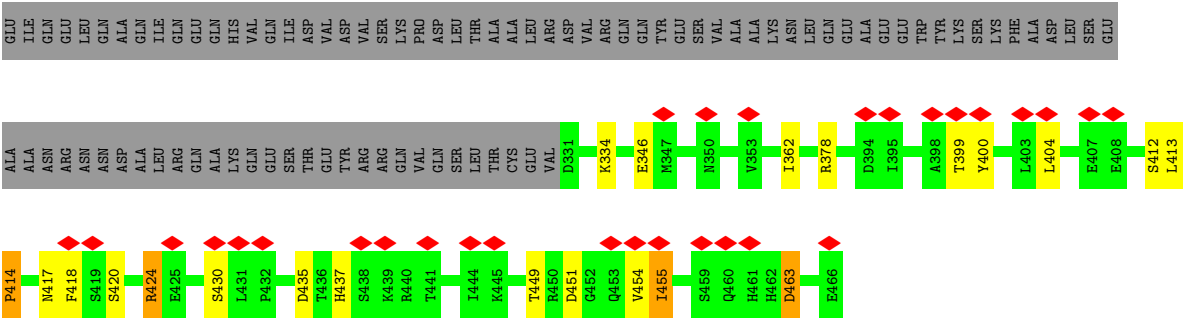


• Molecule 1: Vimentin

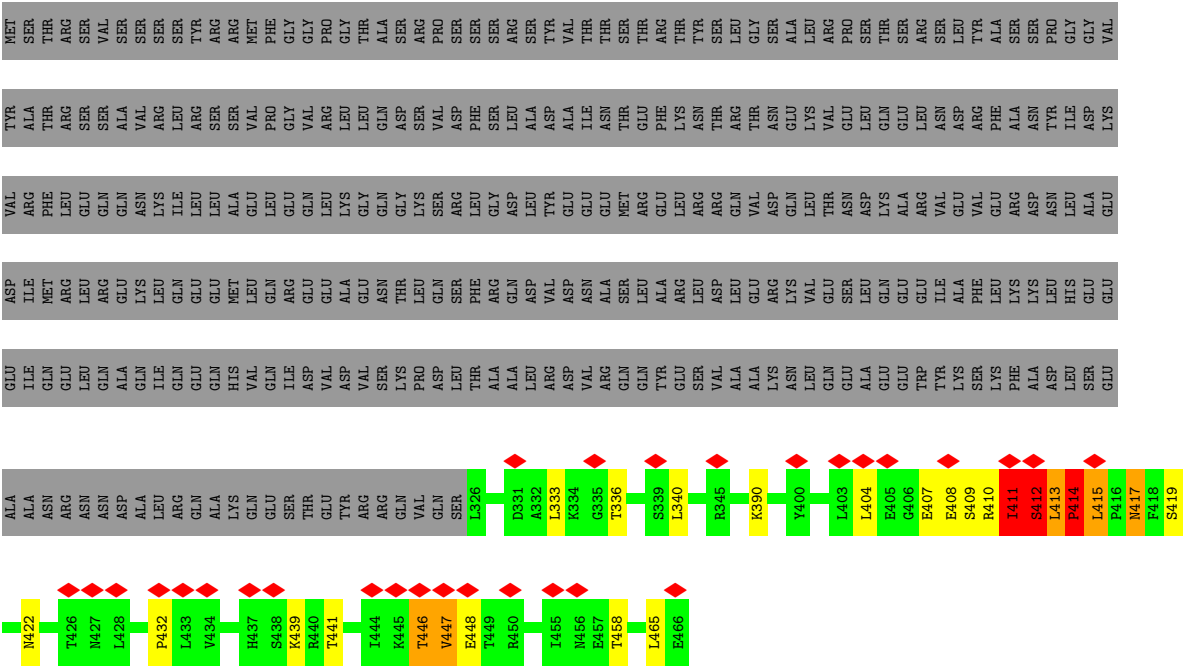


• Molecule 1: Vimentin

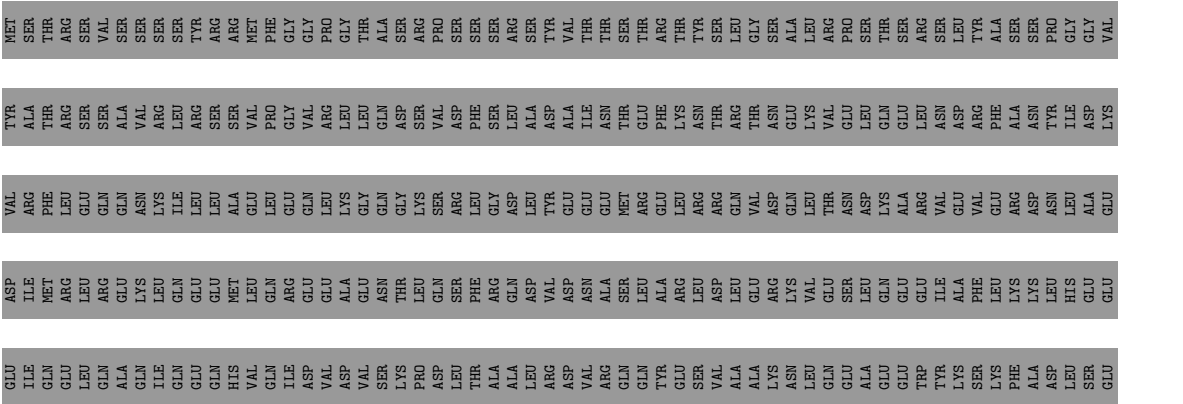


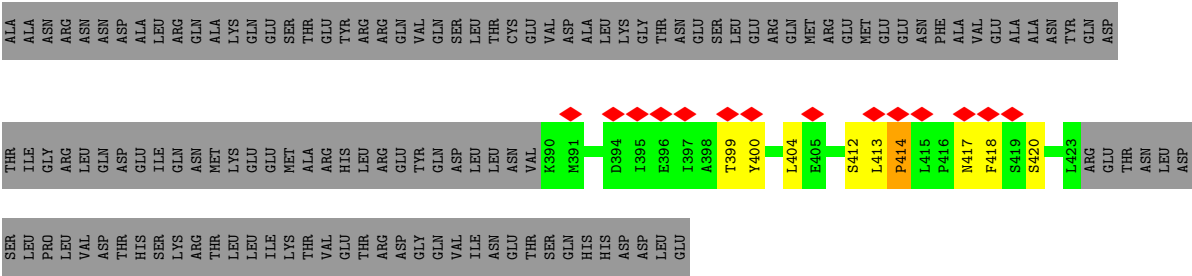


● Molecule 1: Vimentin



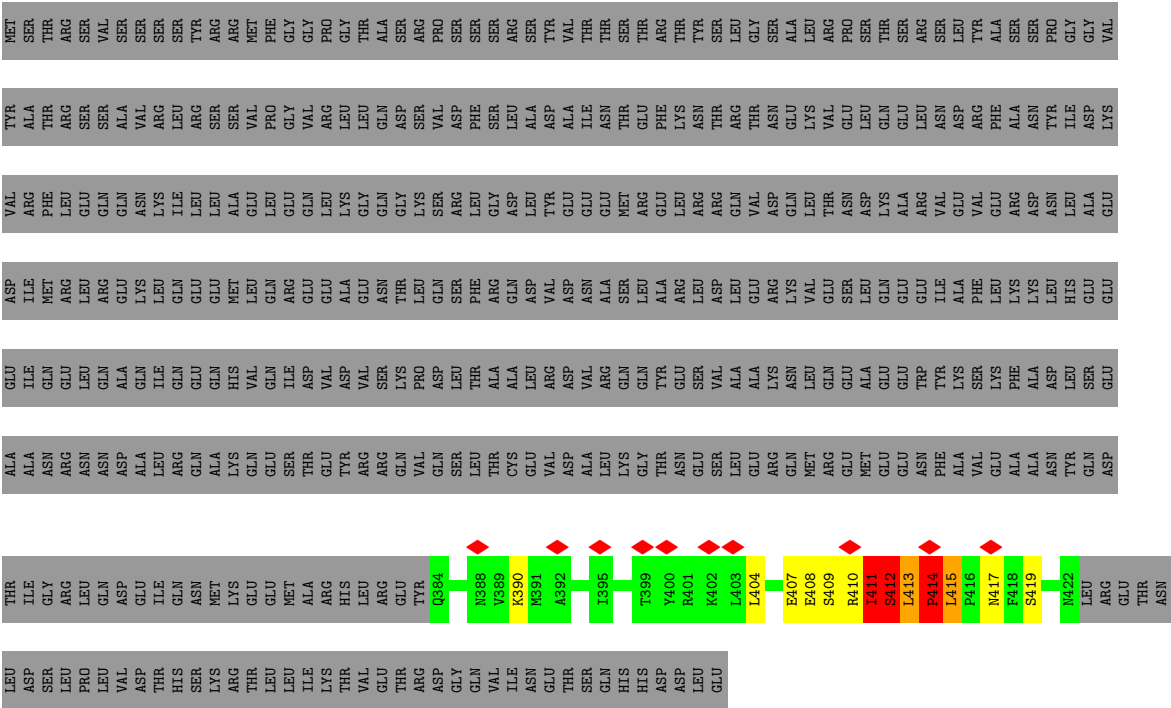
● Molecule 1: Vimentin





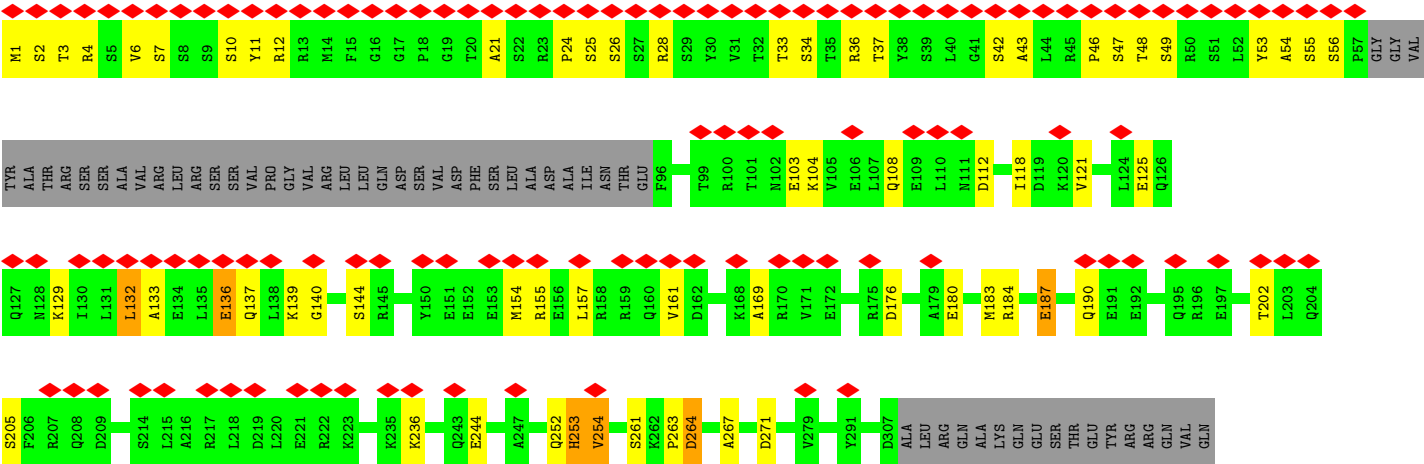
● Molecule 1: Vimentin

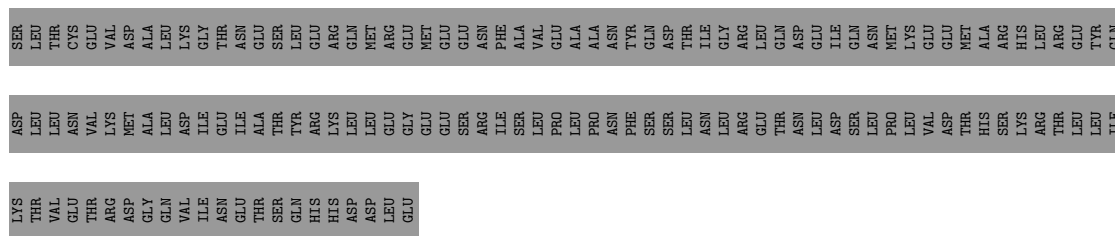
Chain AP: 6% 92%



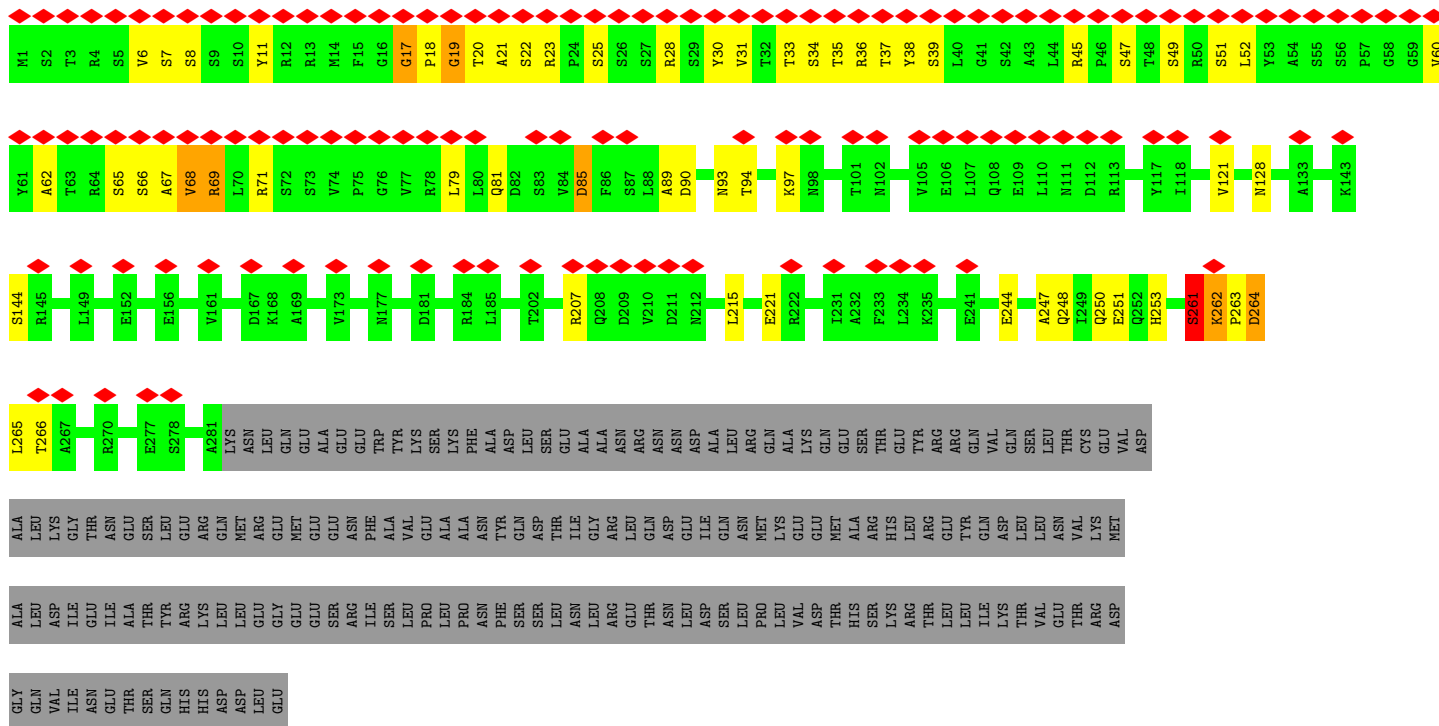
● Molecule 1: Vimentin

Chain B: 26% 44% 13% 42%

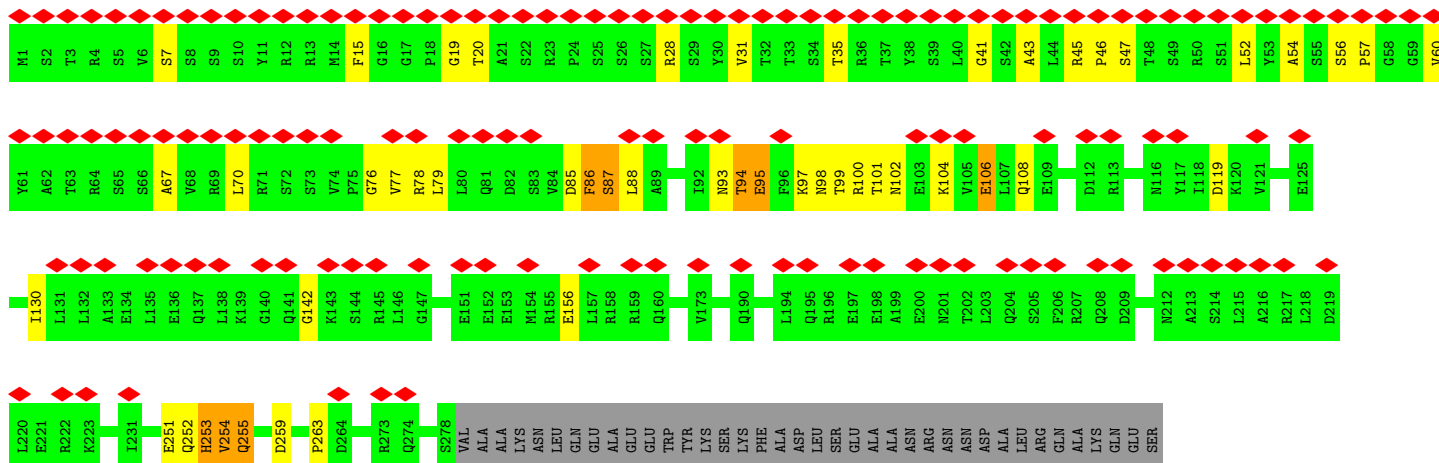




- Molecule 1: Vimentin



- Molecule 1: Vimentin



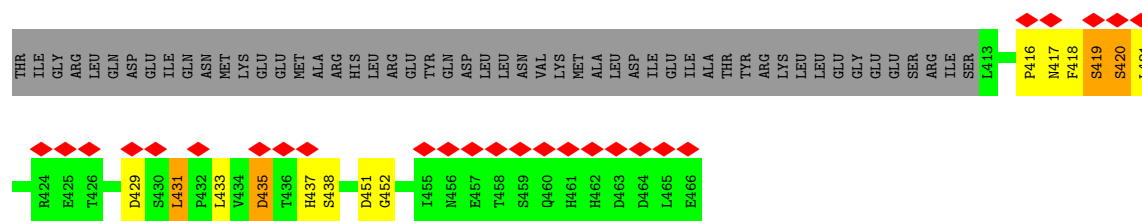
- Molecule 1: Vimentin



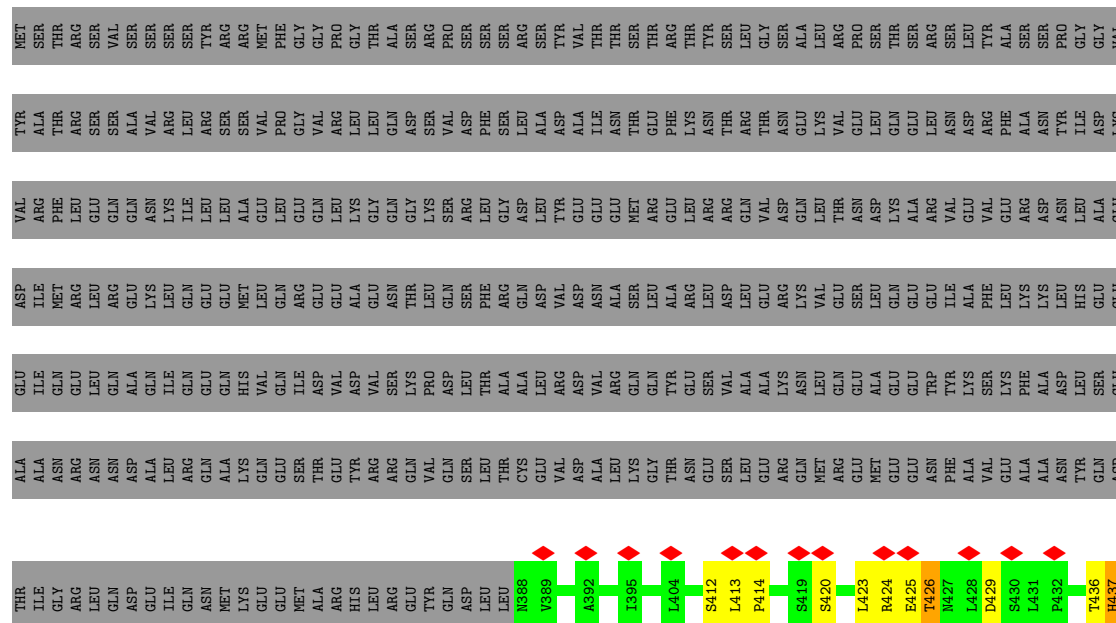
LEU	ASN	ASN	GLY	THR	ALA	GLU	ASP	VAL	TYR	MET
ASN	LEU	ASN	ARG	GLN	ASN	ILE	ILE	PHE	ALA	SER
ARG	LEU	ASN	ARG	GLN	ASN	GLU	ARG	PHE	THR	SER
THR	THR	ASN	LEU	GLN	ASN	GLN	ARG	GLN	SER	ARG
ASN	ASN	ASP	GLN	ASP	ASP	ALA	ARG	GLN	ALA	SER
LEU	ASN	ALA	GLU	GLU	ALA	ILE	LYS	ASN	VAL	SER
LEU	ASN	GLN	ARG	GLN	ILE	ILE	GLN	ARG	ARG	SER
PRO	ASN	GLN	ASN	ASN	GLN	GLU	GLU	LEU	ARG	TYR
LEU	LYS	LYS	MET	LYS	GLN	HIS	MET	ALA	SER	ARG
V434	GLU	GLN	GLU	GLU	VAL	VAL	LEU	GLU	PRO	MET
D435	GLU	GLN	GLU	GLU	GLN	GLN	GLN	LEU	VAL	ARG
T436	MET	SER	MET	ALA	THR	ASP	ARG	GLY	GLY	VAL
H437	ALA	THR	ALA	ALA	THR	VAL	GLU	GLN	ARG	PRO
S438	HIS	TYR	TYR	TYR	TYR	ASP	ALA	LYS	LEU	GLY
K439	LEU	GLN	LEU	GLN	GLN	VAL	GLN	GLN	THR	ALA
R440	ARG	ARG	ARG	ARG	GLN	SER	ASN	GLN	ASP	ALA
K445	TYR	TYR	GLN	GLN	VAL	PRO	LEU	LYS	SER	ARG
T446	ASP	ASP	GLN	ASP	GLN	LEU	SER	SER	ASP	PRO
V447	LEU	LEU	LEU	LEU	THR	THR	PHE	GLY	PHE	SER
E448	LEU	THR	THR	THR	ALA	ALA	ARG	GLY	SER	SER
T449	ASN	ASN	ASN	ASN	CYS	ALA	GLN	ASP	LEU	ALA
R450	VAL	VAL	VAL	VAL	GLU	LEU	ASP	TYR	ALA	SER
D451	LYS	LYS	LYS	LYS	VAL	ARG	VAL	TYR	ASP	TYR
G452	MET	ALA	ALA	ALA	ASP	ASP	ASP	GLU	ALA	THR
Q453	LEU	LEU	LEU	LEU	ALA	VAL	ASN	GLU	ILE	THR
V454	ASP	ASP	ASP	ASP	LYS	GLN	SER	GLU	ASN	THR
I455	ILE	ILE	GLY	GLY	THR	GLN	LEU	ARG	GLU	THR
N456	ILE	ILE	THR	THR	ASN	TYR	ARG	LEU	LYS	ARG
E457	ALA	GLU	GLU	GLU	GLU	GLU	ARG	LEU	LYS	TYR
T458	THR	SER	SER	THR	VAL	VAL	ASP	ARG	ASN	SER
S459	TYR	LEU	LEU	TYR	ALA	ALA	LEU	VAL	ARG	LEU
Q460	ARG	GLU	ARG	GLY	GLU	LYS	GLU	ASP	THR	GLY
H461	LYS	ARG	GLU	GLU	ARG	ASN	ARG	ASP	ASN	SER
H462	LEU	GLN	GLU	LEU	GLN	ASN	VAL	GLN	GLU	ALA
D463	LEU	MET	LEU	LEU	LEU	LYS	LYS	LEU	LYS	THR
D464	GLU	ARG	GLU	GLU	GLU	GLN	ARG	THR	VAL	ARG
L465	GLY	GLY	GLY	GLY	GLY	ALA	LEU	ASP	GLU	SER
E466	GLU	SER	GLU	GLU	GLU	GLU	GLN	LYS	GLU	THR
	ARG	ASN	THR	ILE	PHE	TRP	GLU	VAL	ASN	ARG
	SER	SER	SER	ILE	VAL	TYR	ILE	VAL	ASP	THR
	PRO	VAL	VAL	LEU	VAL	LYS	PHE	VAL	ARG	TYR
	GLU	GLU	GLU	PRO	GLU	LYS	LEU	GLU	PHE	ALA
	LEU	ALA	ALA	LEU	ALA	PHE	LEU	ARG	SER	ALA
	ASN	ASN	ASN	PRO	ALA	LYS	LYS	ASP	ASN	SER
	PHE	ASN	ASN	ASN	ASN	ASP	LEU	ASN	TYR	GLY
	THR	THR	THR	THR	GLN	SER	HIS	ASN	ILE	GLY
	SER	SER	SER	SER	GLN	THR	GLU	GLU	ASP	VAL

- Molecule 1: Vimentin

[illegible]



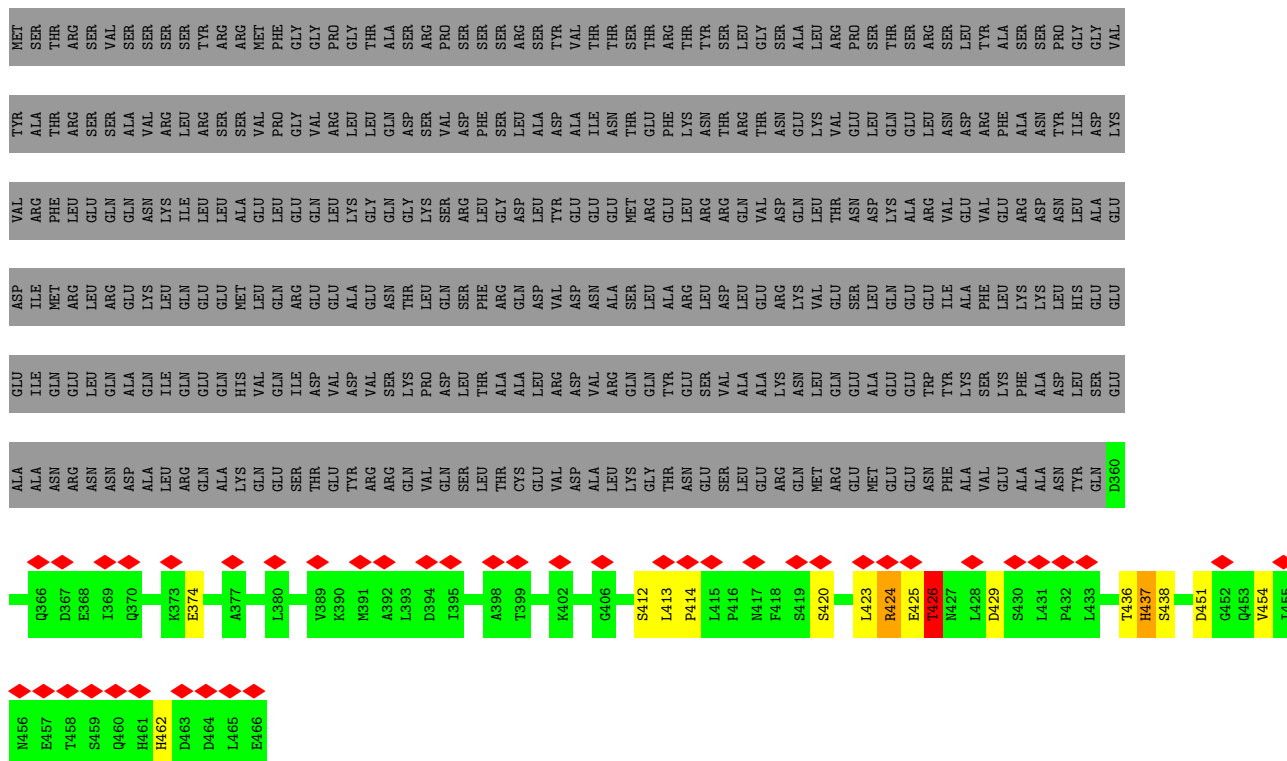
• Molecule 1: Vimentin



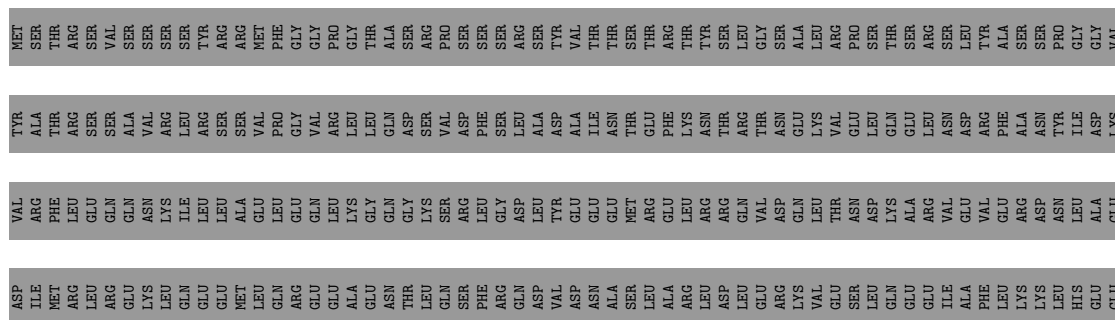
• Molecule 1: Vimentin

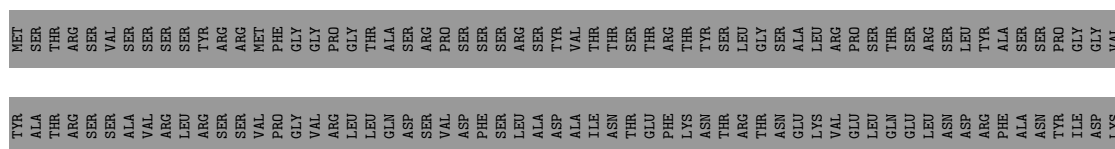


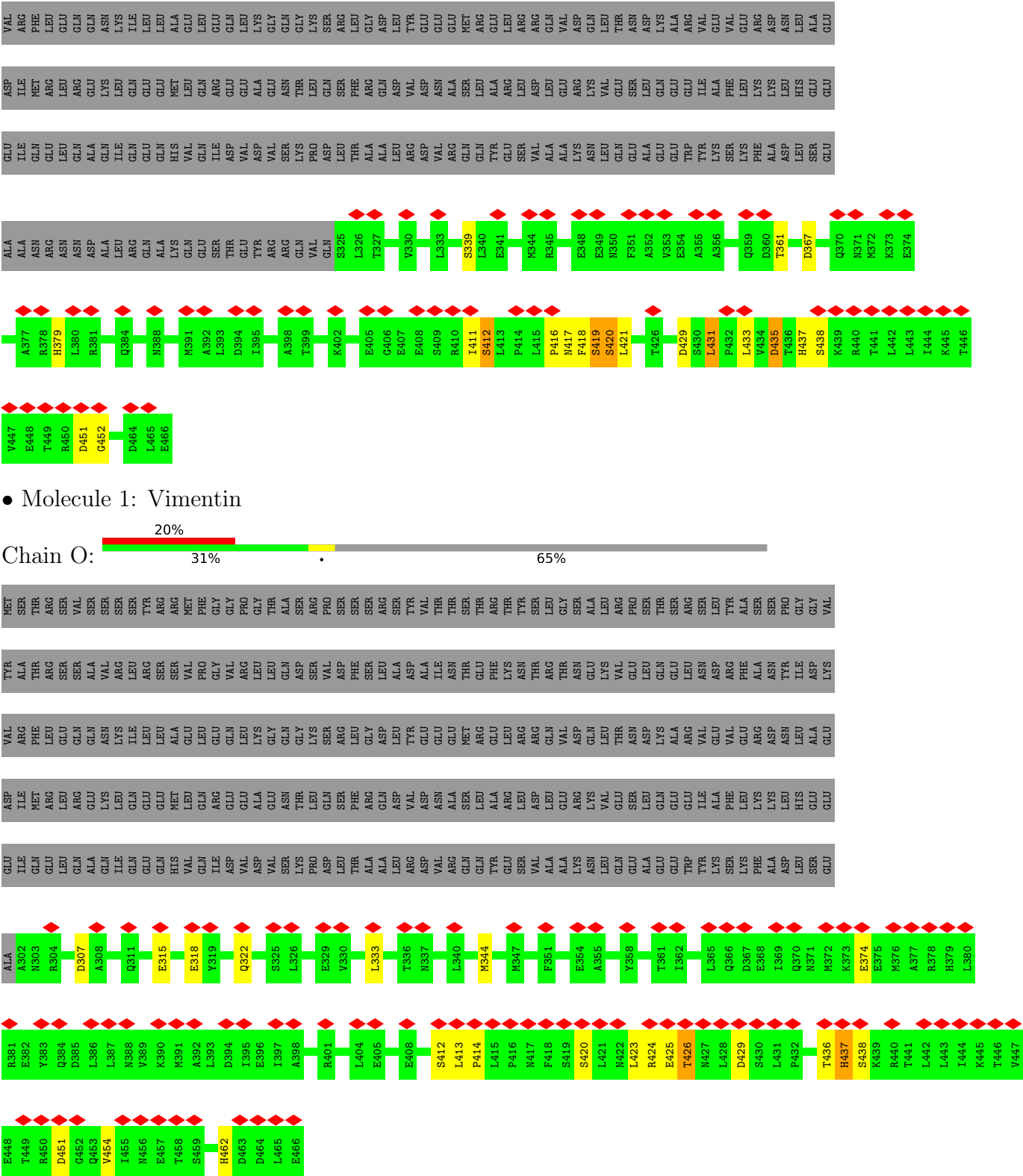
- Molecule 1: Vimentin



- Molecule 1: Vimentin

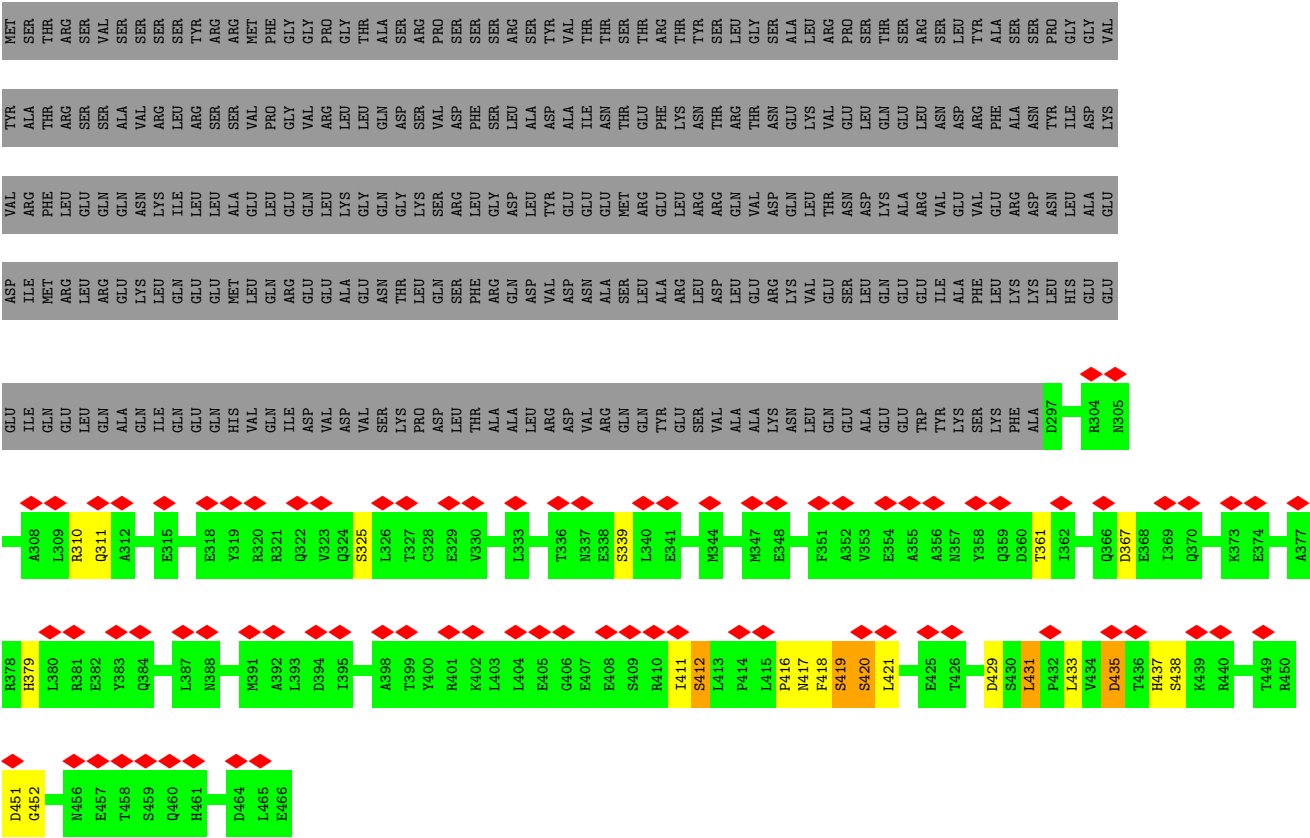




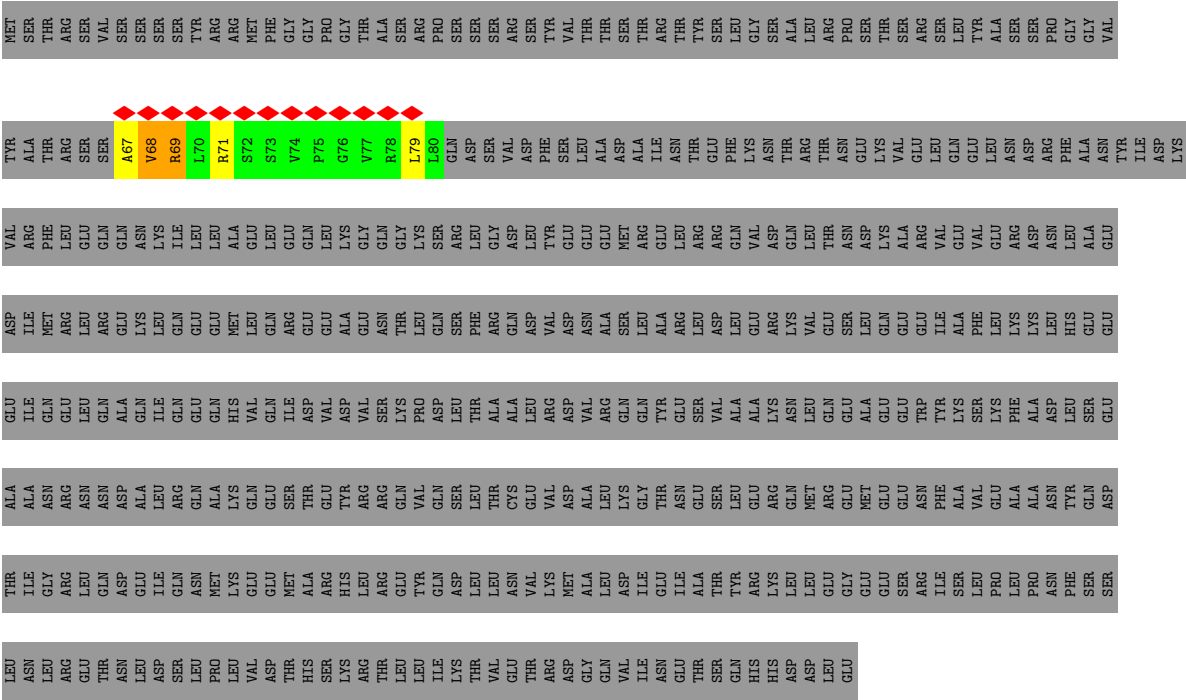


• Molecule 1: Vimentin





● Molecule 1: Vimentin



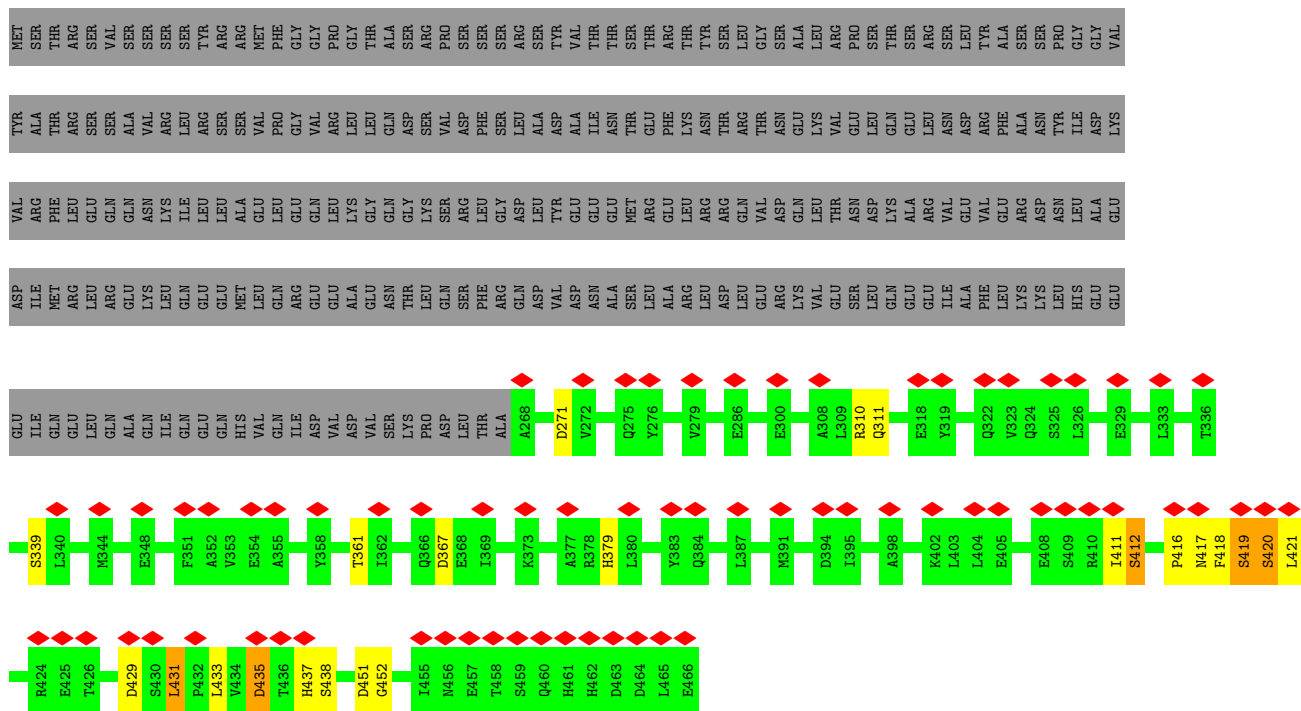
● Molecule 1: Vimentin

[illegible]

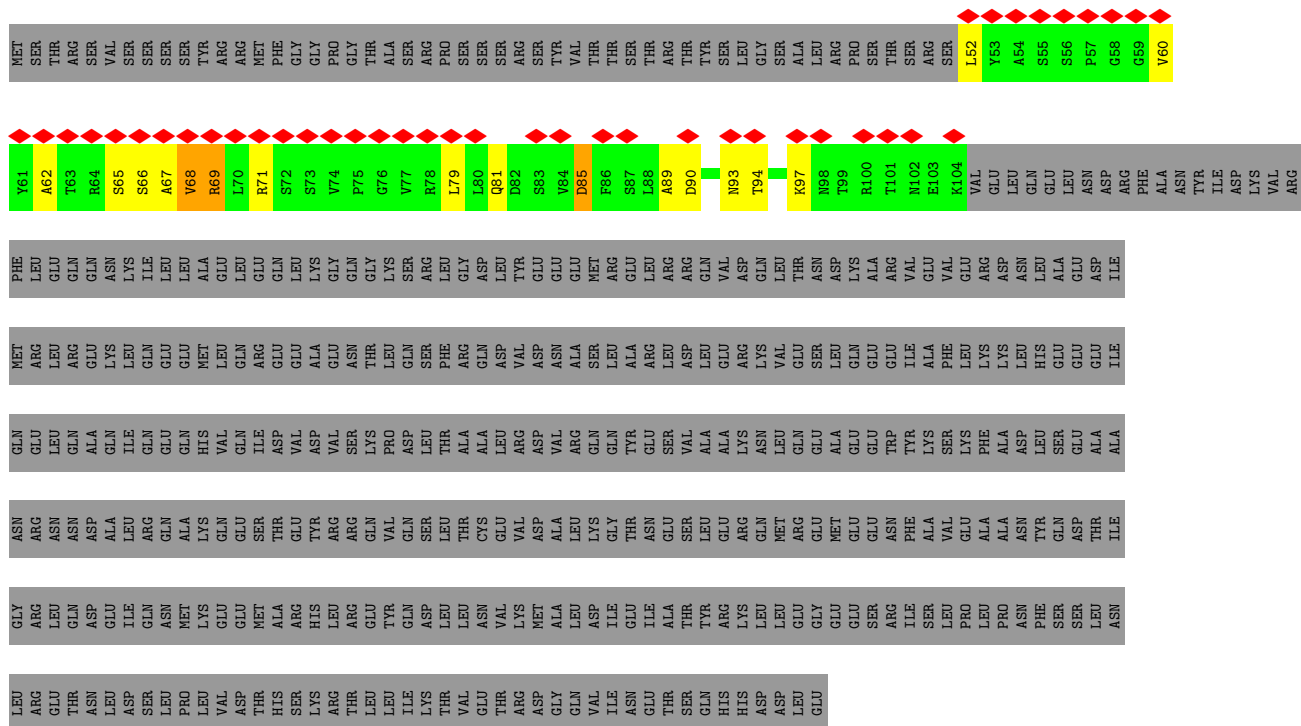
Chain S:

[illegible]

Chain T: 15% 38% 57%



- Molecule 1: Vimentin

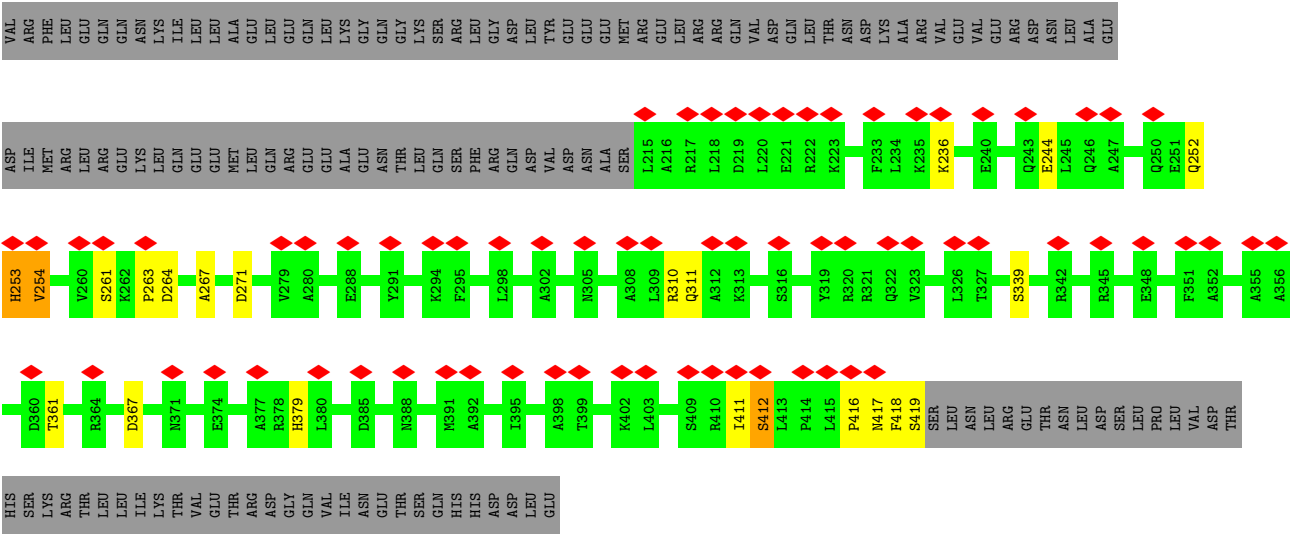


- Molecule 1: Vimentin

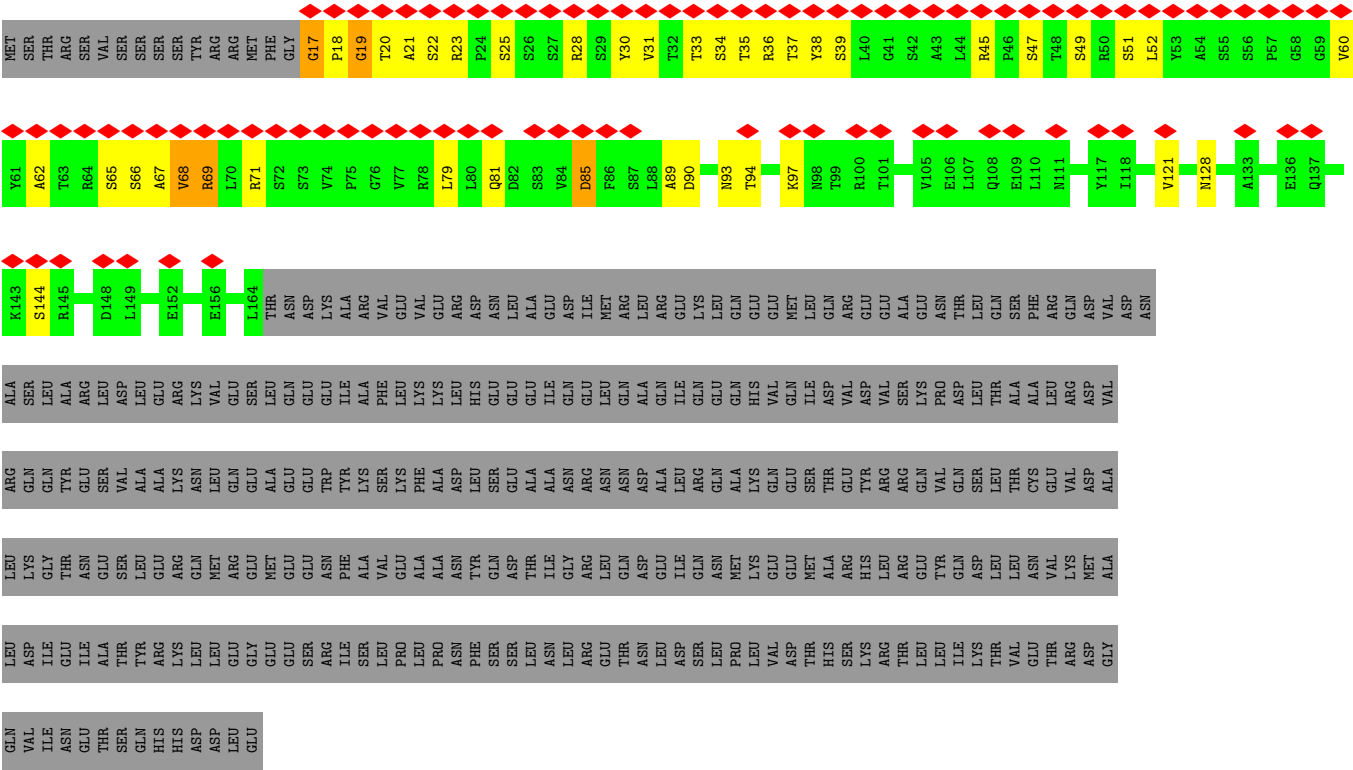




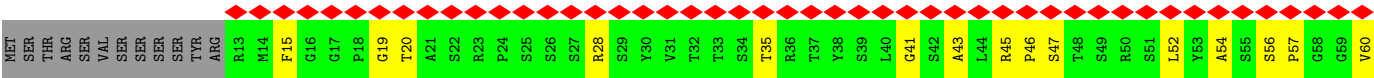


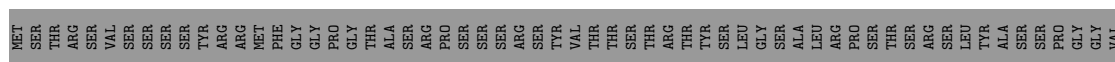


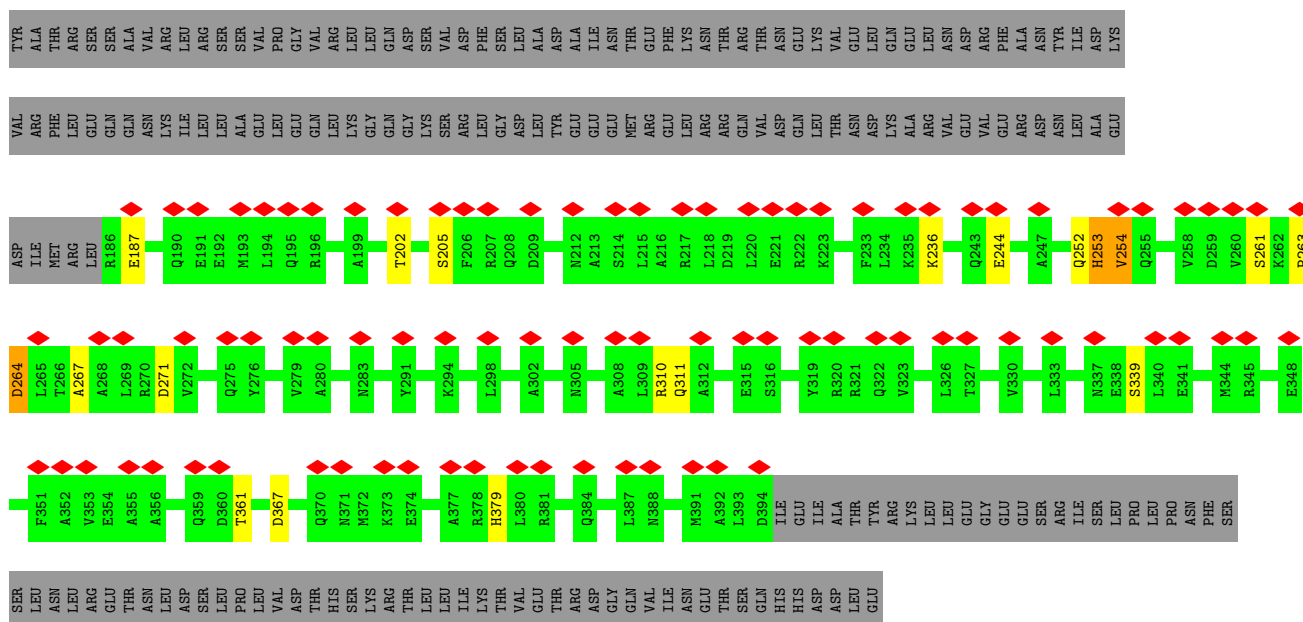
• Molecule 1: Vimentin



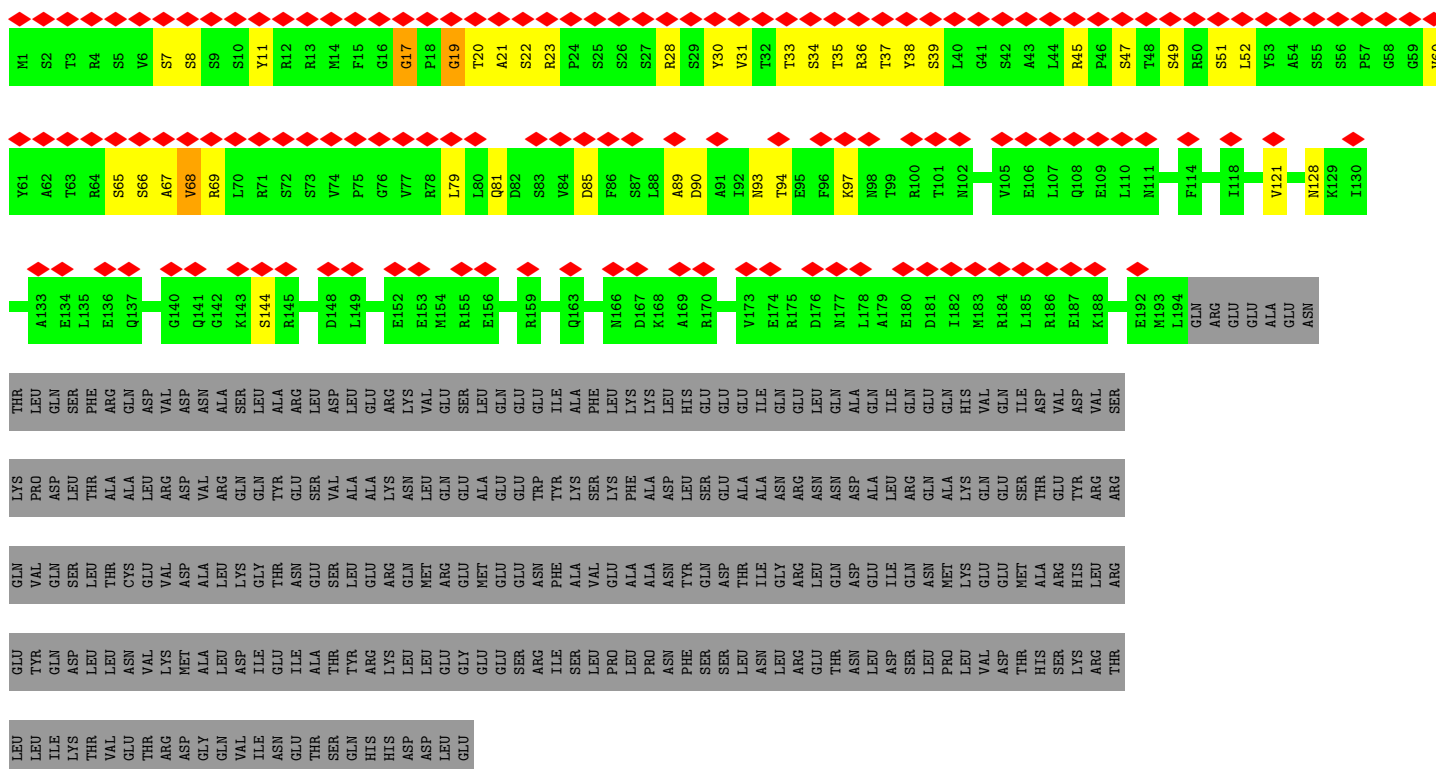
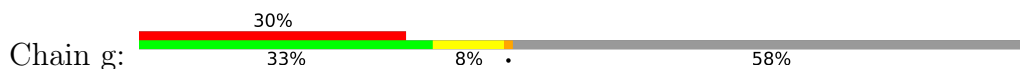
• Molecule 1: Vimentin





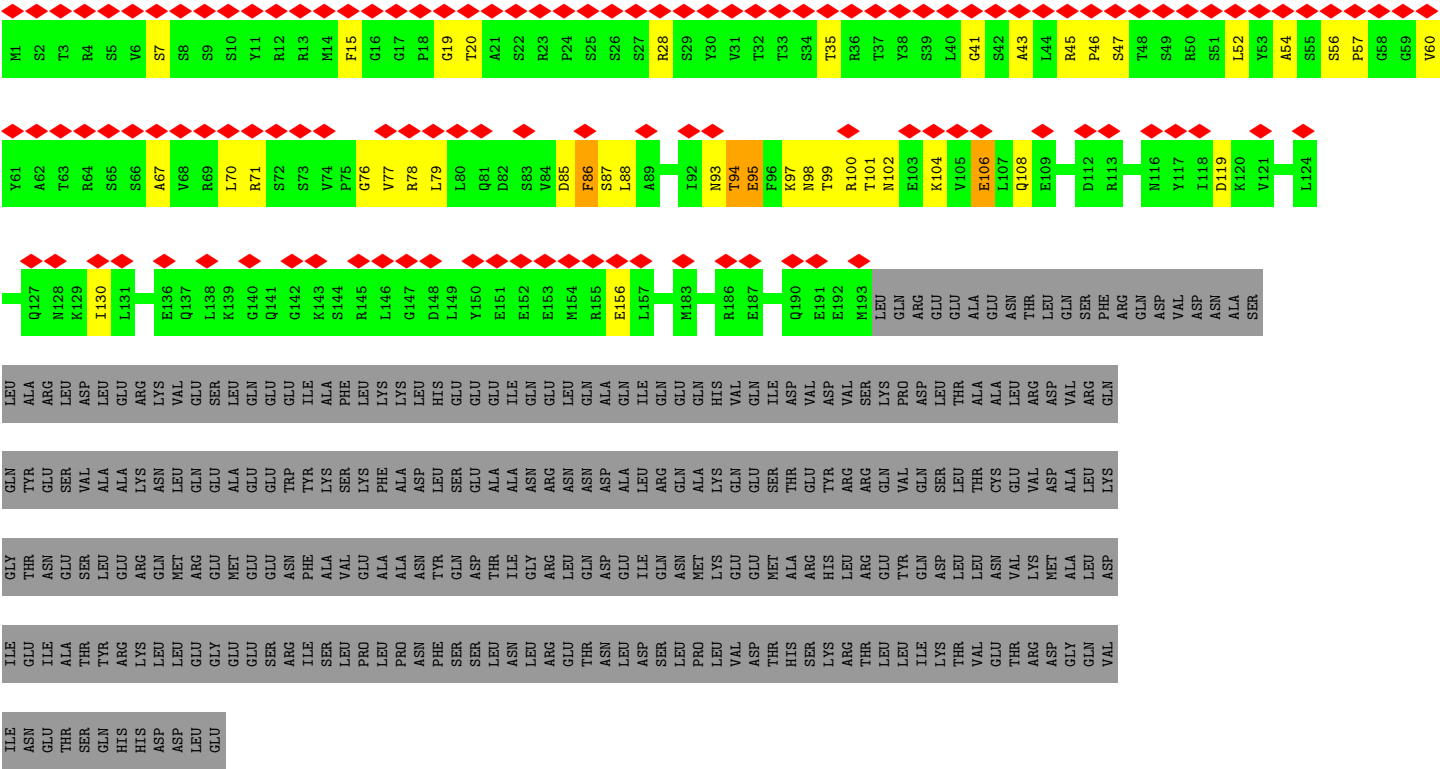


• Molecule 1: Vimentin

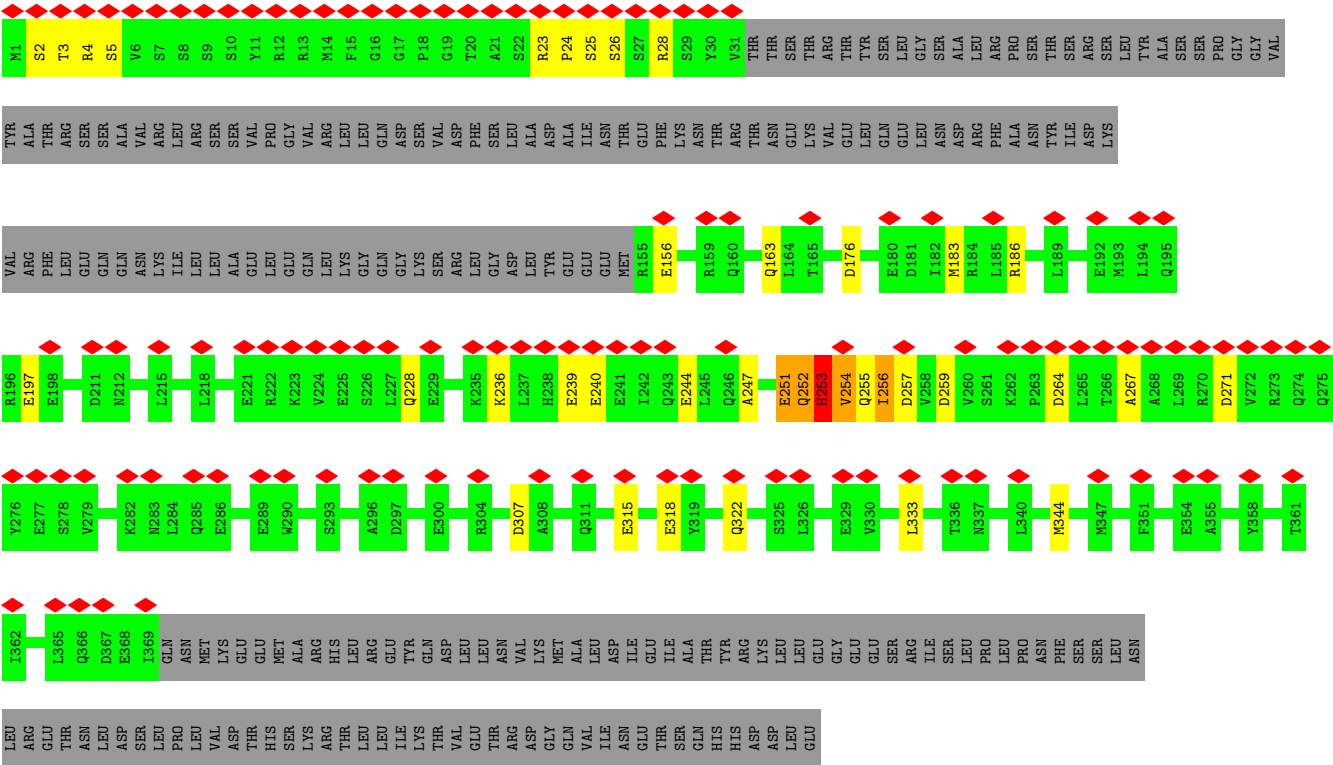


• Molecule 1: Vimentin



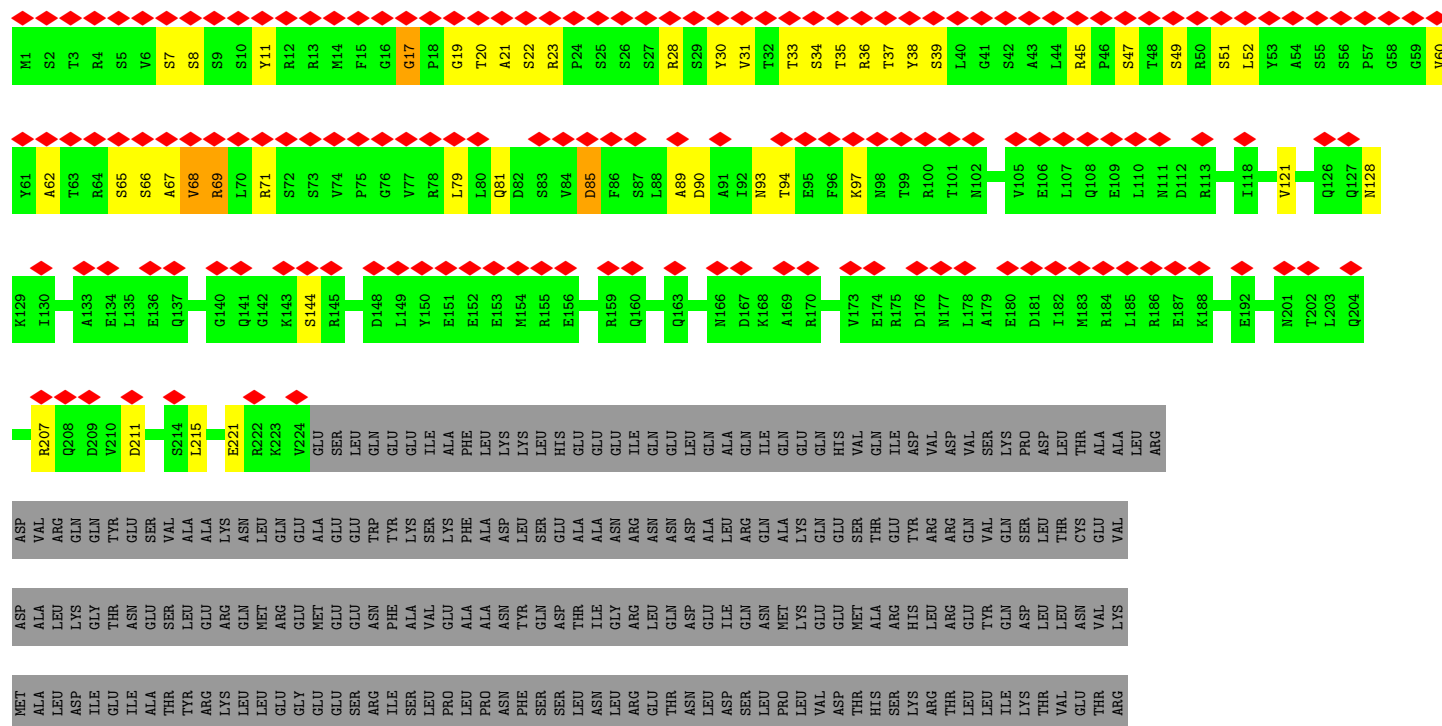


● Molecule 1: Vimentin



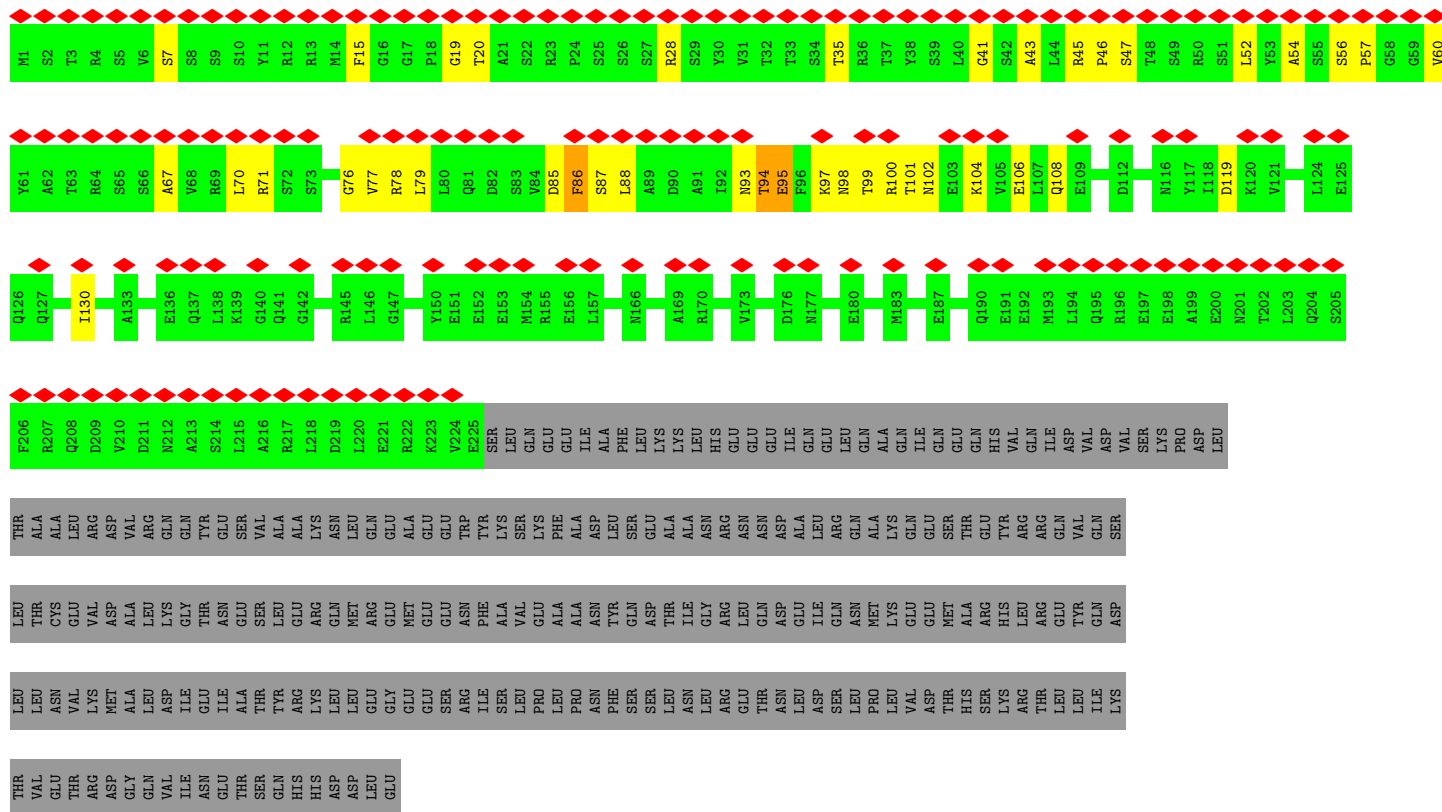
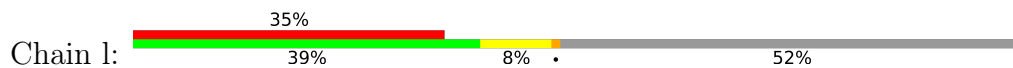
● Molecule 1: Vimentin

- Molecule 1: Vimentin

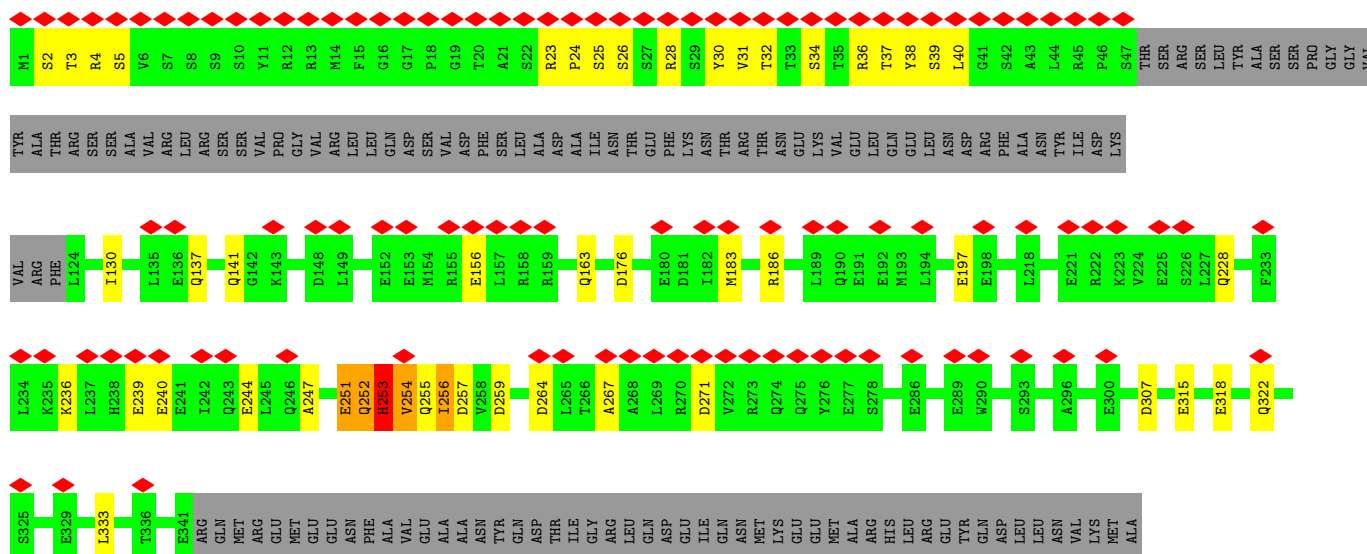


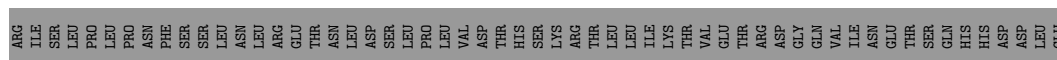
ASP
GLY
GLN
VAL
ILE
ASN
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THR
SER
GLN
HIS
HIS
ASP
ASP
LEU
GLU

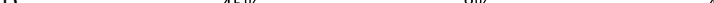
• Molecule 1: Vimentin

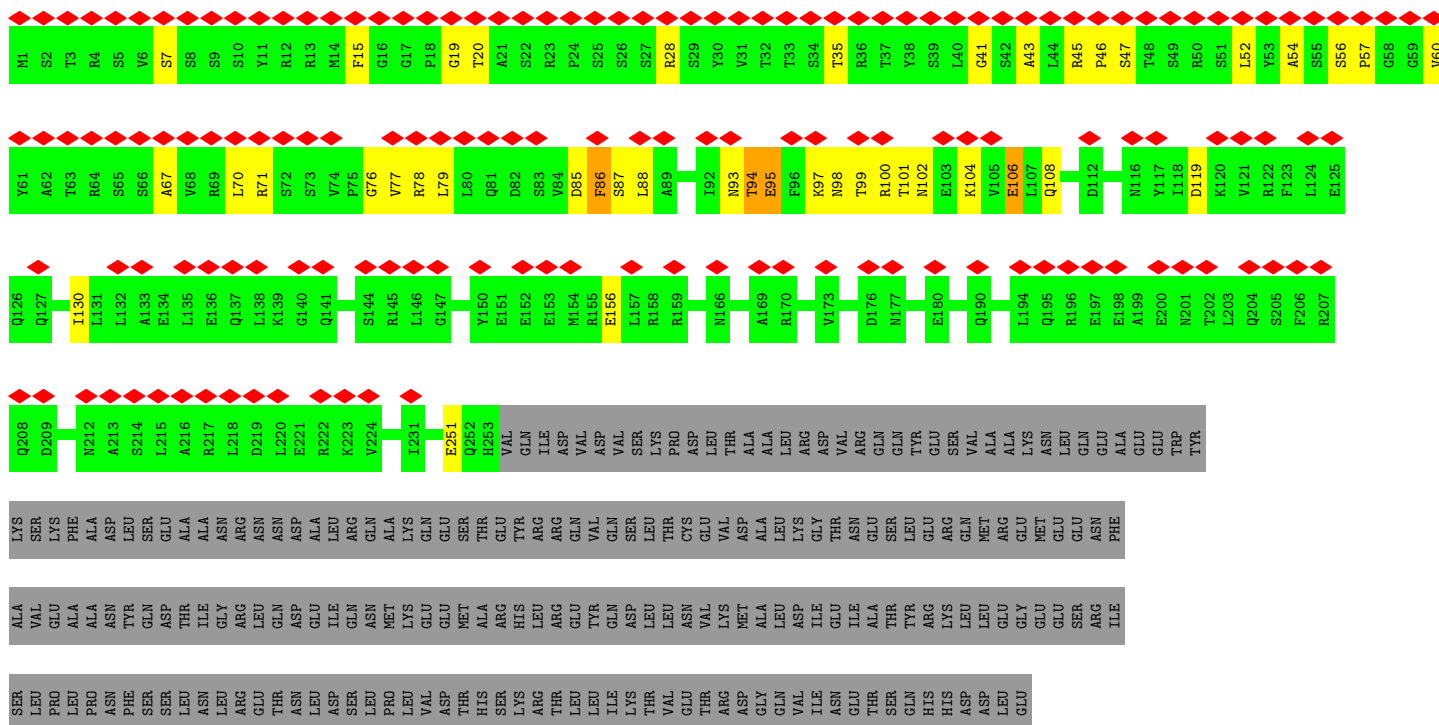


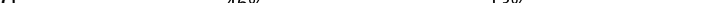
• Molecule 1: Vimentin

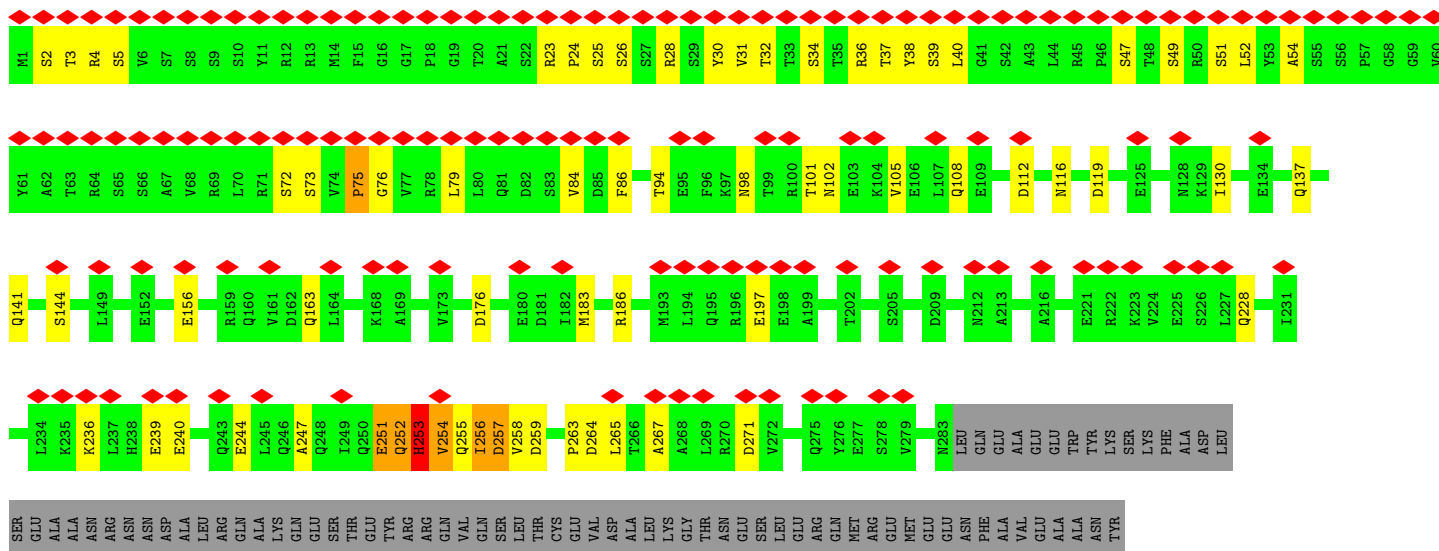


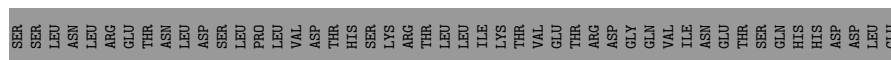


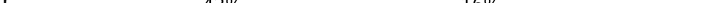
Chain p: 

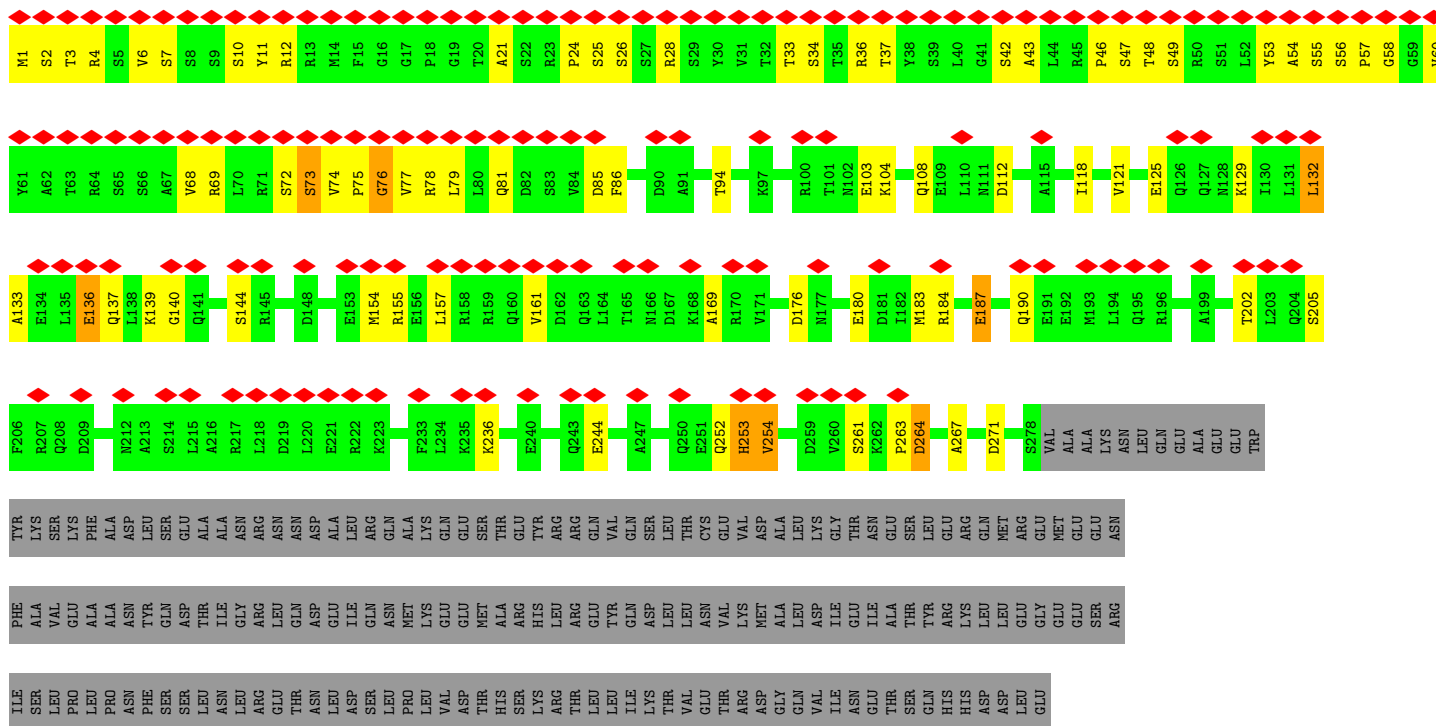


Chain q: 

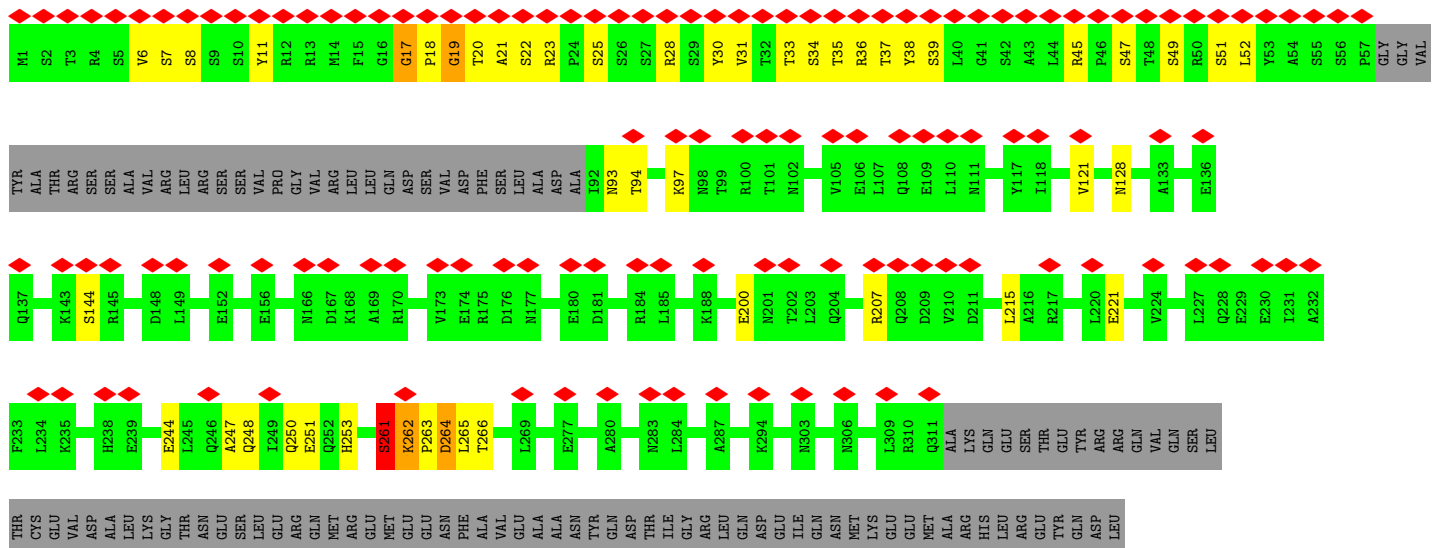




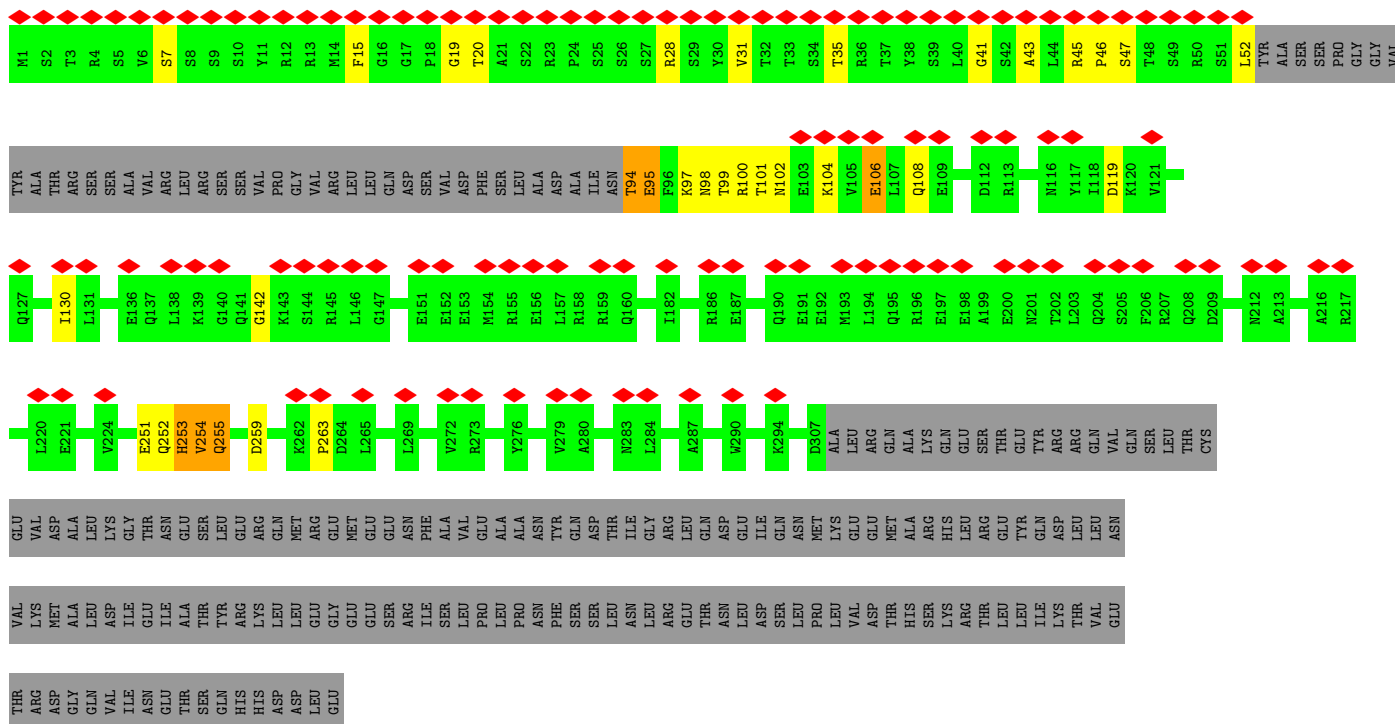
Chain r: 



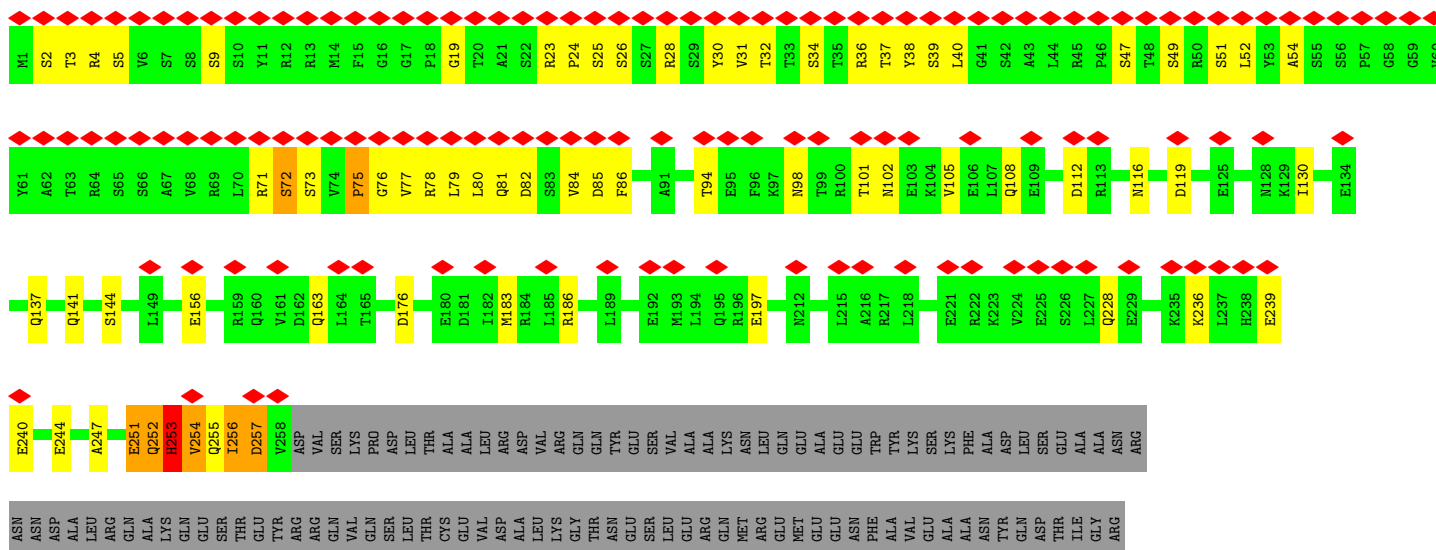
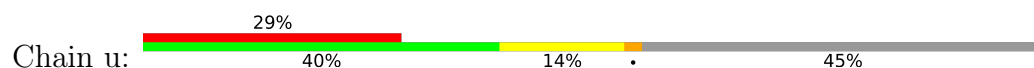
Chain s: 28% 49% 9% 14%



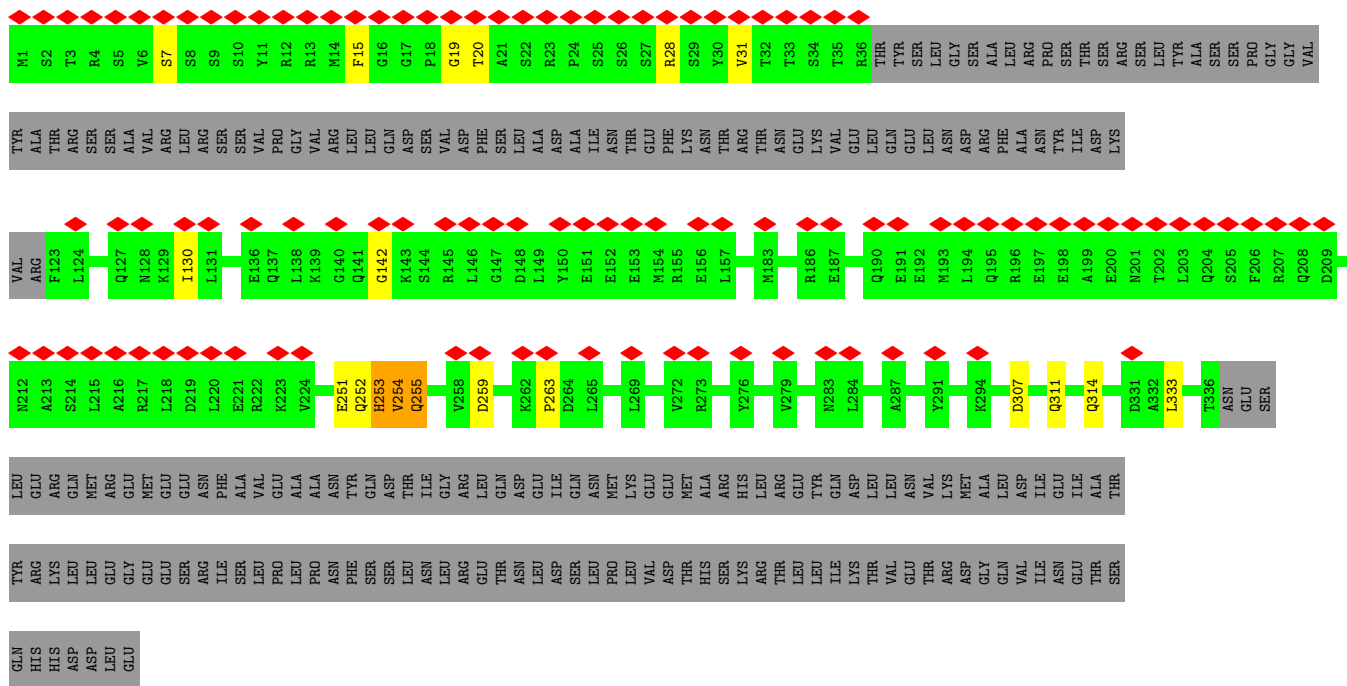
- Molecule 1: Vimentin



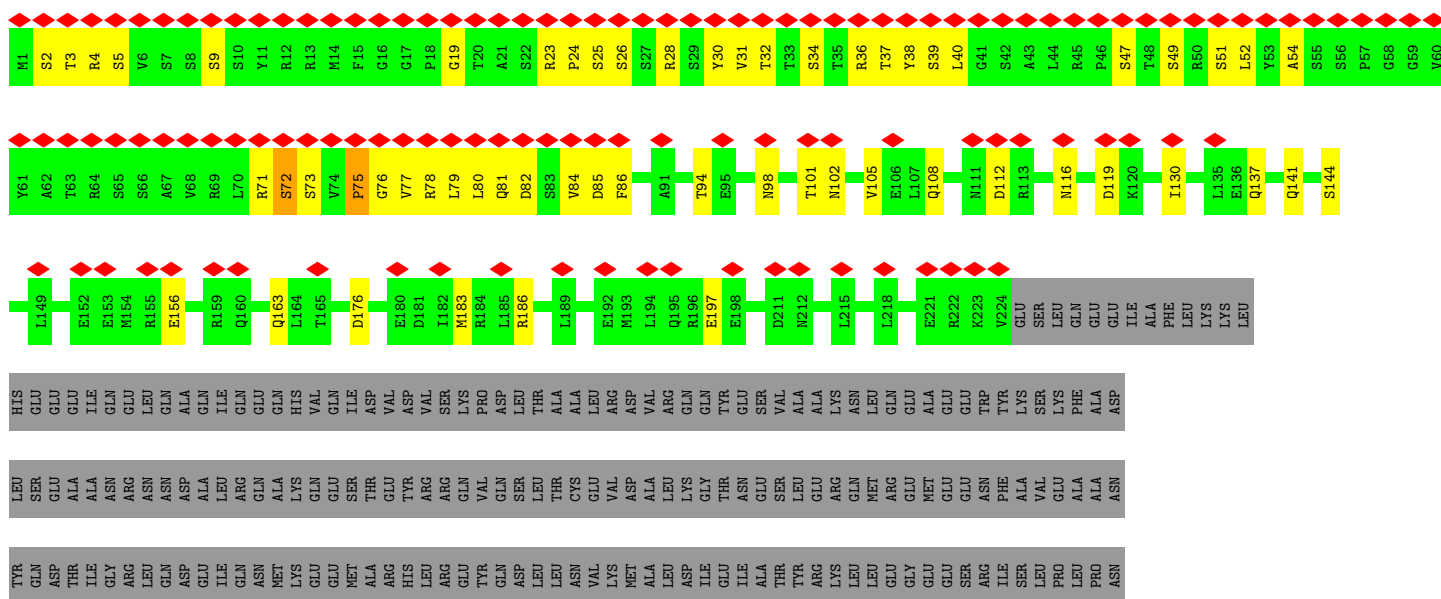
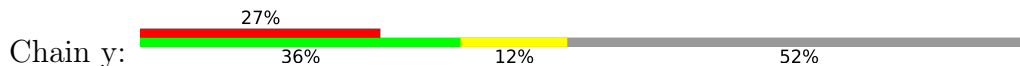
- Molecule 1: Vimentin

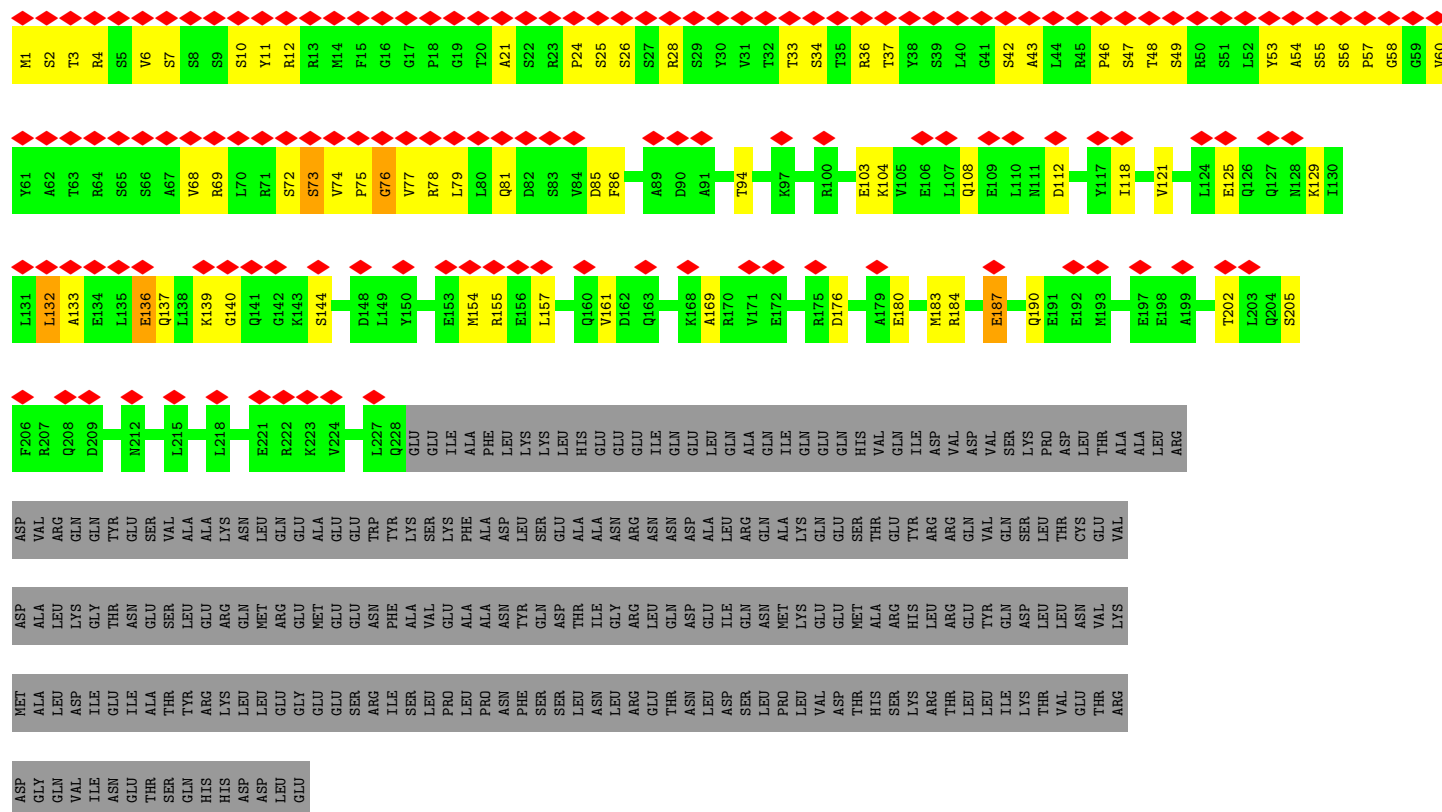


- Molecule 1: Vimentin



- Molecule 1: Vimentin





4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=73.7308°, rise=42.461 Å, axial sym=C1	Depositor
Number of segments used	236920	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	62	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.016	Depositor
Minimum map value	-0.003	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	380.798, 380.798, 380.798	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0021, 1.0021, 1.0021	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	1.08	6/1011 (0.6%)	1.88	21/1262 (1.7%)
1	1	1.13	1/1088 (0.1%)	2.65	14/1353 (1.0%)
1	2	0.89	0/1061	1.75	10/1321 (0.8%)
1	3	0.93	0/763	1.68	5/952 (0.5%)
1	4	0.89	0/779	1.66	3/972 (0.3%)
1	5	1.14	1/1065 (0.1%)	2.72	17/1326 (1.3%)
1	6	0.87	0/1050	1.75	10/1309 (0.8%)
1	7	0.92	0/567	1.68	5/707 (0.7%)
1	8	0.88	0/587	1.64	3/732 (0.4%)
1	9	1.18	1/1006 (0.1%)	2.79	19/1254 (1.5%)
1	A	1.00	3/1122 (0.3%)	1.84	14/1399 (1.0%)
1	AA	0.94	0/379	1.71	3/472 (0.6%)
1	AB	0.90	0/399	1.66	3/497 (0.6%)
1	AC	1.22	1/890 (0.1%)	2.90	19/1109 (1.7%)
1	AD	1.11	6/887 (0.7%)	1.93	21/1107 (1.9%)
1	AE	0.94	0/195	1.70	3/242 (1.2%)
1	AF	0.91	0/215	1.70	3/267 (1.1%)
1	AG	0.89	0/795	1.84	14/992 (1.4%)
1	AH	1.12	6/795 (0.8%)	1.85	16/992 (1.6%)
1	AI	0.89	0/667	1.84	14/832 (1.7%)
1	AJ	1.16	6/679 (0.9%)	1.86	16/847 (1.9%)
1	AK	0.90	0/543	1.84	12/677 (1.8%)
1	AL	1.22	6/563 (1.1%)	1.91	16/702 (2.3%)
1	AM	0.96	0/323	2.01	9/402 (2.2%)
1	AN	1.35	6/339 (1.8%)	2.03	11/422 (2.6%)
1	AO	1.12	0/135	2.00	2/167 (1.2%)
1	AP	1.83	6/155 (3.9%)	2.50	11/192 (5.7%)
1	B	0.95	1/1074 (0.1%)	1.71	7/1339 (0.5%)
1	C	1.14	1/1122 (0.1%)	2.60	9/1399 (0.6%)
1	D	0.87	0/1111	1.70	7/1387 (0.5%)
1	E	0.82	0/131	1.68	5/162 (3.1%)
1	F	0.86	0/139	1.67	2/172 (1.2%)
1	G	0.86	0/207	1.75	6/257 (2.3%)
1	H	0.94	0/215	1.62	2/267 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	I	0.89	0/315	1.72	6/392 (1.5%)
1	J	0.96	0/331	1.65	3/412 (0.7%)
1	K	0.87	0/427	1.69	6/532 (1.1%)
1	L	0.92	0/451	1.63	3/562 (0.5%)
1	M	0.86	0/543	1.70	6/677 (0.9%)
1	N	0.90	0/567	1.63	3/707 (0.4%)
1	O	0.85	0/659	1.70	6/822 (0.7%)
1	P	0.88	0/679	1.65	5/847 (0.6%)
1	Q	0.87	0/55	1.43	0/67
1	R	0.70	0/55	1.09	0/67
1	S	0.85	0/775	1.69	6/967 (0.6%)
1	T	0.87	0/795	1.63	5/992 (0.5%)
1	U	0.89	0/211	1.65	2/262 (0.8%)
1	V	0.88	0/227	1.60	2/282 (0.7%)
1	W	1.02	3/775 (0.4%)	1.92	12/967 (1.2%)
1	X	1.01	1/775 (0.1%)	1.78	12/967 (1.2%)
1	Y	0.86	0/395	1.63	2/492 (0.4%)
1	Z	0.86	0/407	1.55	2/507 (0.4%)
1	a	1.00	3/835 (0.4%)	1.90	10/1042 (1.0%)
1	b	0.97	1/819 (0.1%)	1.74	10/1022 (1.0%)
1	c	0.85	0/591	1.63	4/737 (0.5%)
1	d	0.86	0/599	1.56	2/747 (0.3%)
1	e	0.99	3/855 (0.4%)	1.86	10/1067 (0.9%)
1	f	0.94	1/835 (0.1%)	1.75	9/1042 (0.9%)
1	g	0.86	0/775	1.60	4/967 (0.4%)
1	h	0.87	0/771	1.62	2/962 (0.2%)
1	i	1.00	3/982 (0.3%)	1.86	10/1224 (0.8%)
1	j	0.94	1/946 (0.1%)	1.78	9/1179 (0.8%)
1	k	0.85	0/895	1.60	4/1117 (0.4%)
1	l	0.85	0/899	1.60	2/1122 (0.2%)
1	m	0.99	3/1058 (0.3%)	1.83	12/1319 (0.9%)
1	n	0.95	1/1010 (0.1%)	1.74	9/1259 (0.7%)
1	o	0.85	0/1015	1.62	4/1267 (0.3%)
1	p	0.86	0/1011	1.60	2/1262 (0.2%)
1	q	1.02	3/1131 (0.3%)	1.84	15/1412 (1.1%)
1	r	0.96	1/1111 (0.1%)	1.74	10/1387 (0.7%)
1	s	1.13	1/1105 (0.1%)	2.60	7/1376 (0.5%)
1	t	0.85	0/1062	1.71	5/1324 (0.4%)
1	u	1.01	3/1031 (0.3%)	1.81	14/1287 (1.1%)
1	v	0.94	1/1015 (0.1%)	1.71	5/1267 (0.4%)
1	w	1.15	1/1033 (0.1%)	2.68	9/1286 (0.7%)
1	x	0.85	0/998	1.72	5/1244 (0.4%)
1	y	0.93	0/895	1.68	5/1117 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	z	0.87	0/911	1.67	3/1137 (0.3%)
All	All	0.98	81/54687 (0.1%)	1.90	594/68182 (0.9%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	0	0	23
1	1	0	20
1	2	0	16
1	3	0	19
1	4	0	21
1	5	0	22
1	6	0	17
1	7	0	17
1	8	0	16
1	9	0	24
1	A	0	33
1	AA	0	16
1	AB	0	11
1	AC	0	23
1	AD	0	23
1	AE	0	9
1	AF	0	7
1	AG	0	18
1	AH	0	21
1	AI	0	18
1	AJ	0	21
1	AK	0	15
1	AL	0	18
1	AM	0	10
1	AN	0	11
1	AO	0	6
1	AP	0	8
1	B	0	24
1	C	0	15
1	D	0	16
1	E	0	3
1	G	0	11
1	H	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	I	0	12
1	J	0	7
1	K	0	13
1	L	0	10
1	M	0	15
1	N	0	11
1	O	0	19
1	P	0	13
1	Q	0	1
1	S	0	19
1	T	0	13
1	U	0	1
1	V	0	6
1	W	0	30
1	X	0	18
1	Y	0	3
1	Z	0	9
1	a	0	25
1	b	0	16
1	c	0	5
1	d	0	10
1	e	0	25
1	f	0	16
1	g	0	7
1	h	0	13
1	i	0	26
1	j	0	18
1	k	0	11
1	l	0	11
1	m	0	26
1	n	0	23
1	o	0	11
1	p	0	13
1	q	0	36
1	r	0	31
1	s	0	14
1	t	0	12
1	u	0	33
1	v	0	27
1	w	0	17
1	x	0	11
1	y	0	20

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	z	0	23
All	All	0	1217

The worst 5 of 81 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	261	SER	C-N	-24.30	0.83	1.33
1	5	261	SER	C-N	-24.30	0.83	1.33
1	s	261	SER	C-N	-24.30	0.83	1.33
1	9	261	SER	C-N	-24.29	0.83	1.33
1	AC	261	SER	C-N	-24.29	0.83	1.33

The worst 5 of 594 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	261	SER	O-C-N	-73.73	37.32	122.84
1	5	261	SER	O-C-N	-73.72	37.33	122.84
1	w	261	SER	O-C-N	-73.71	37.34	122.84
1	9	261	SER	O-C-N	-73.71	37.34	122.84
1	s	261	SER	O-C-N	-73.70	37.35	122.84

There are no chirality outliers.

5 of 1217 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	253	HIS	Peptide
1	0	255	GLN	Mainchain
1	0	263	PRO	Peptide
1	0	307	ASP	Mainchain
1	0	311	GLN	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	1012	0	256	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1092	0	279	37	0
1	2	1064	0	276	1	0
1	3	764	0	202	90	0
1	4	780	0	201	143	0
1	5	1068	0	267	27	0
1	6	1052	0	265	2	0
1	7	568	0	149	88	0
1	8	588	0	149	126	0
1	9	1008	0	253	26	0
1	A	1124	0	291	79	0
1	AA	380	0	99	54	0
1	AB	400	0	102	94	0
1	AC	892	0	224	26	0
1	AD	888	0	225	6	0
1	AE	196	0	53	35	0
1	AF	216	0	56	50	0
1	AG	796	0	203	4	0
1	AH	796	0	203	5	0
1	AI	668	0	171	4	0
1	AJ	680	0	174	5	0
1	AK	544	0	140	4	0
1	AL	564	0	145	5	0
1	AM	324	0	81	0	0
1	AN	340	0	85	5	0
1	AO	136	0	33	0	0
1	AP	156	0	38	5	0
1	B	1076	0	271	134	0
1	C	1124	0	282	145	0
1	D	1112	0	289	97	0
1	E	132	0	34	3	0
1	F	140	0	36	6	0
1	G	208	0	51	3	0
1	H	216	0	51	26	0
1	I	316	0	79	3	0
1	J	332	0	82	29	0
1	K	428	0	109	4	0
1	L	452	0	114	29	0
1	M	544	0	140	3	0
1	N	568	0	145	29	0
1	O	660	0	169	3	0
1	P	680	0	173	28	0
1	Q	56	0	13	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	56	0	11	9	0
1	S	776	0	198	3	0
1	T	796	0	202	29	0
1	U	212	0	49	55	0
1	V	228	0	55	68	0
1	W	776	0	195	11	0
1	X	776	0	194	24	0
1	Y	396	0	92	81	0
1	Z	408	0	101	92	0
1	a	836	0	211	11	0
1	b	820	0	206	21	0
1	c	592	0	148	112	0
1	d	600	0	159	100	0
1	e	856	0	216	12	0
1	f	836	0	211	1	0
1	g	776	0	198	124	0
1	h	772	0	205	100	0
1	i	984	0	251	39	0
1	j	948	0	242	45	0
1	k	896	0	228	120	0
1	l	900	0	237	100	0
1	m	1060	0	274	63	0
1	n	1012	0	260	87	0
1	o	1016	0	258	134	0
1	p	1012	0	265	101	0
1	q	1132	0	295	89	0
1	r	1112	0	285	159	0
1	s	1108	0	279	112	0
1	t	1064	0	276	63	0
1	u	1032	0	271	118	0
1	v	1016	0	262	160	0
1	w	1036	0	266	77	0
1	x	1000	0	262	9	0
1	y	896	0	237	101	0
1	z	912	0	236	158	0
All	All	54788	0	13993	2073	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 30.

The worst 5 of 2073 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)
1:4:125:GLU:CA	1:p:104:LYS:C	1.76	1.59
1:8:125:GLU:CA	1:D:104:LYS:C	1.76	1.59
1:B:125:GLU:CA	1:Z:104:LYS:C	1.76	1.58
1:AB:125:GLU:CA	1:t:104:LYS:C	1.76	1.56
1:d:104:LYS:C	1:r:125:GLU:CA	1.76	1.56

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	251/466 (54%)	220 (88%)	19 (8%)	12 (5%)	2	16
1	1	265/466 (57%)	234 (88%)	25 (9%)	6 (2%)	5	28
1	2	260/466 (56%)	238 (92%)	14 (5%)	8 (3%)	3	22
1	3	189/466 (41%)	156 (82%)	29 (15%)	4 (2%)	5	30
1	4	193/466 (41%)	162 (84%)	26 (14%)	5 (3%)	4	25
1	5	261/466 (56%)	228 (87%)	28 (11%)	5 (2%)	6	32
1	6	259/466 (56%)	237 (92%)	14 (5%)	8 (3%)	3	22
1	7	140/466 (30%)	117 (84%)	21 (15%)	2 (1%)	9	40
1	8	106/466 (23%)	91 (86%)	12 (11%)	3 (3%)	4	24
1	9	195/466 (42%)	164 (84%)	28 (14%)	3 (2%)	8	40
1	A	250/466 (54%)	215 (86%)	28 (11%)	7 (3%)	4	24
1	AA	93/466 (20%)	77 (83%)	15 (16%)	1 (1%)	11	46
1	AB	98/466 (21%)	85 (87%)	11 (11%)	2 (2%)	6	31
1	AC	219/466 (47%)	181 (83%)	31 (14%)	7 (3%)	3	21
1	AD	220/466 (47%)	189 (86%)	19 (9%)	12 (6%)	1	14
1	AE	47/466 (10%)	36 (77%)	10 (21%)	1 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AF	52/466 (11%)	40 (77%)	10 (19%)	2 (4%)	2	19
1	AG	197/466 (42%)	168 (85%)	23 (12%)	6 (3%)	3	22
1	AH	197/466 (42%)	172 (87%)	17 (9%)	8 (4%)	2	18
1	AI	165/466 (35%)	136 (82%)	23 (14%)	6 (4%)	2	20
1	AJ	168/466 (36%)	143 (85%)	17 (10%)	8 (5%)	2	16
1	AK	134/466 (29%)	105 (78%)	23 (17%)	6 (4%)	2	17
1	AL	139/466 (30%)	115 (83%)	16 (12%)	8 (6%)	1	14
1	AM	79/466 (17%)	63 (80%)	12 (15%)	4 (5%)	1	15
1	AN	83/466 (18%)	68 (82%)	11 (13%)	4 (5%)	2	16
1	AO	32/466 (7%)	25 (78%)	3 (9%)	4 (12%)	0	4
1	AP	37/466 (8%)	26 (70%)	7 (19%)	4 (11%)	0	6
1	B	265/466 (57%)	240 (91%)	21 (8%)	4 (2%)	8	40
1	C	225/466 (48%)	185 (82%)	32 (14%)	8 (4%)	2	20
1	D	249/466 (53%)	224 (90%)	18 (7%)	7 (3%)	4	24
1	E	31/466 (7%)	19 (61%)	11 (36%)	1 (3%)	3	21
1	F	33/466 (7%)	26 (79%)	4 (12%)	3 (9%)	0	8
1	G	50/466 (11%)	31 (62%)	18 (36%)	1 (2%)	6	31
1	H	52/466 (11%)	36 (69%)	11 (21%)	5 (10%)	0	7
1	I	77/466 (16%)	55 (71%)	19 (25%)	3 (4%)	2	19
1	J	81/466 (17%)	65 (80%)	11 (14%)	5 (6%)	1	13
1	K	105/466 (22%)	83 (79%)	19 (18%)	3 (3%)	3	23
1	L	111/466 (24%)	95 (86%)	11 (10%)	5 (4%)	2	17
1	M	134/466 (29%)	112 (84%)	19 (14%)	3 (2%)	5	29
1	N	140/466 (30%)	124 (89%)	11 (8%)	5 (4%)	2	20
1	O	163/466 (35%)	141 (86%)	19 (12%)	3 (2%)	6	34
1	P	168/466 (36%)	152 (90%)	11 (6%)	5 (3%)	3	22
1	Q	12/466 (3%)	6 (50%)	4 (33%)	2 (17%)	0	2
1	R	12/466 (3%)	9 (75%)	2 (17%)	1 (8%)	0	9
1	S	192/466 (41%)	170 (88%)	19 (10%)	3 (2%)	7	38
1	T	197/466 (42%)	181 (92%)	11 (6%)	5 (2%)	4	26
1	U	51/466 (11%)	37 (72%)	10 (20%)	4 (8%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	V	55/466 (12%)	43 (78%)	9 (16%)	3 (6%)	1	14
1	W	192/466 (41%)	172 (90%)	13 (7%)	7 (4%)	2	20
1	X	192/466 (41%)	175 (91%)	11 (6%)	6 (3%)	3	22
1	Y	97/466 (21%)	78 (80%)	15 (16%)	4 (4%)	2	18
1	Z	100/466 (22%)	84 (84%)	13 (13%)	3 (3%)	3	22
1	a	139/466 (30%)	130 (94%)	5 (4%)	4 (3%)	3	23
1	b	19/466 (4%)	17 (90%)	2 (10%)	0	100	100
1	c	146/466 (31%)	119 (82%)	21 (14%)	6 (4%)	2	18
1	d	69/466 (15%)	61 (88%)	5 (7%)	3 (4%)	2	17
1	e	185/466 (40%)	175 (95%)	7 (4%)	3 (2%)	7	38
1	f	95/466 (20%)	89 (94%)	5 (5%)	1 (1%)	11	46
1	j	140/466 (30%)	129 (92%)	9 (6%)	2 (1%)	9	40
1	k	127/466 (27%)	105 (83%)	18 (14%)	4 (3%)	3	22
1	q	159/466 (34%)	148 (93%)	6 (4%)	5 (3%)	3	22
1	r	276/466 (59%)	240 (87%)	30 (11%)	6 (2%)	5	29
1	s	271/466 (58%)	243 (90%)	23 (8%)	5 (2%)	6	34
1	t	262/466 (56%)	240 (92%)	16 (6%)	6 (2%)	5	28
1	u	256/466 (55%)	216 (84%)	35 (14%)	5 (2%)	6	31
1	v	252/466 (54%)	219 (87%)	28 (11%)	5 (2%)	6	31
1	w	253/466 (54%)	230 (91%)	18 (7%)	5 (2%)	6	31
1	x	246/466 (53%)	228 (93%)	12 (5%)	6 (2%)	4	27
1	y	222/466 (48%)	186 (84%)	32 (14%)	4 (2%)	6	34
1	z	226/466 (48%)	195 (86%)	26 (12%)	5 (2%)	5	29
All	All	10656/32620 (33%)	9204 (86%)	1132 (11%)	320 (3%)	5	22

5 of 320 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	413	LEU
1	0	414	PRO
1	1	18	PRO
1	1	265	LEU
1	5	265	LEU

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1	2
1	5	2
1	9	2
1	AC	2
1	C	2
1	s	2
1	w	2

The worst 5 of 14 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	263:PRO	C	264:ASP	N	2.24
1	5	263:PRO	C	264:ASP	N	2.24
1	9	263:PRO	C	264:ASP	N	2.24
1	AC	263:PRO	C	264:ASP	N	2.24
1	C	263:PRO	C	264:ASP	N	2.24

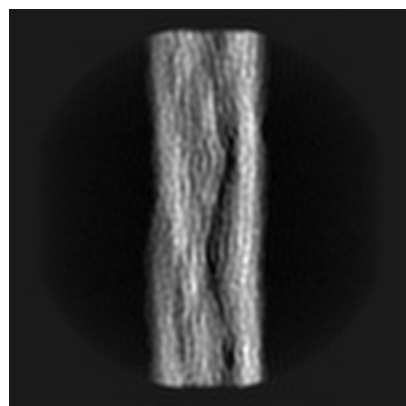
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16844. These allow visual inspection of the internal detail of the map and identification of artifacts.

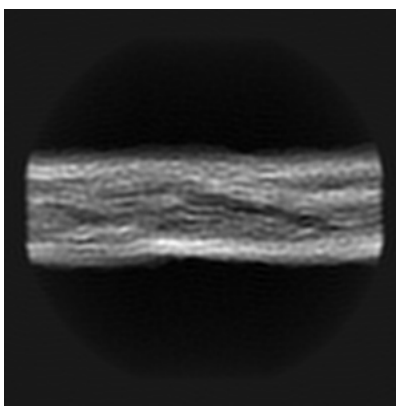
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

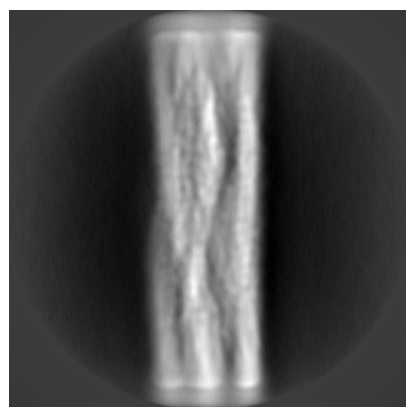


Y

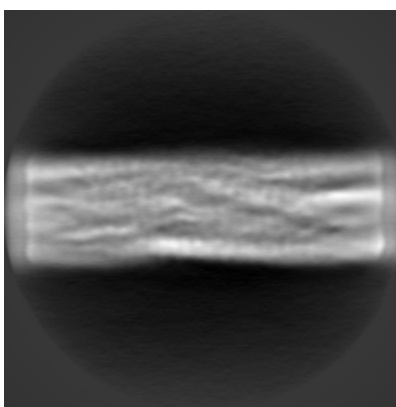


Z

6.1.2 Raw map



X



Y

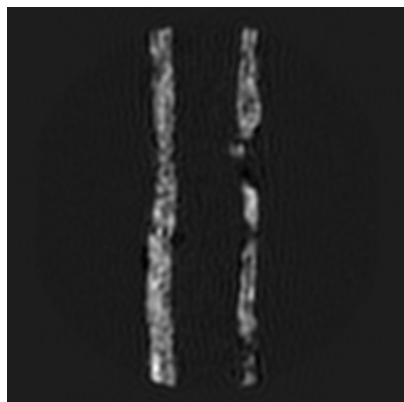


Z

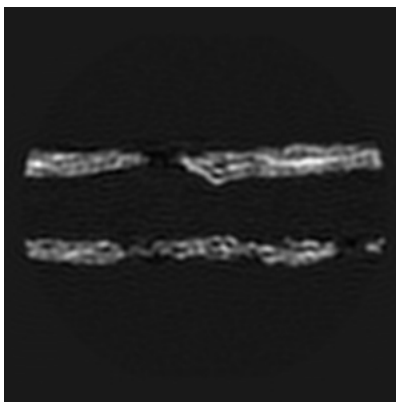
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 190

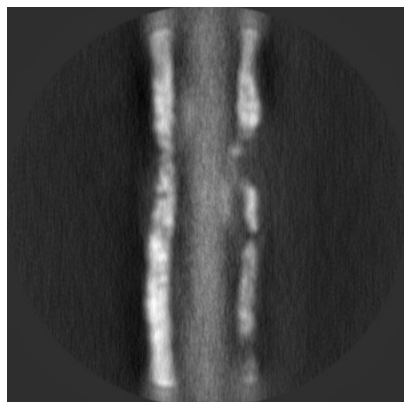


Y Index: 190

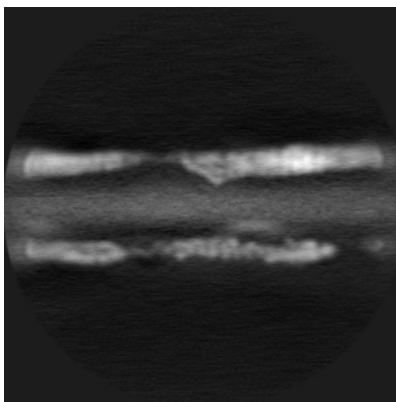


Z Index: 190

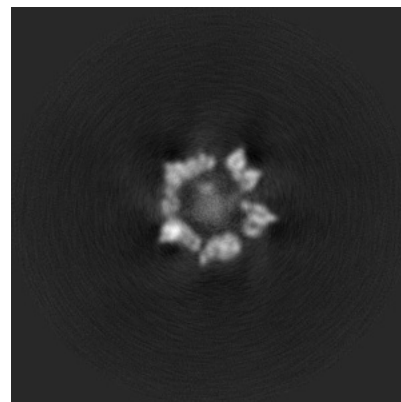
6.2.2 Raw map



X Index: 190



Y Index: 190

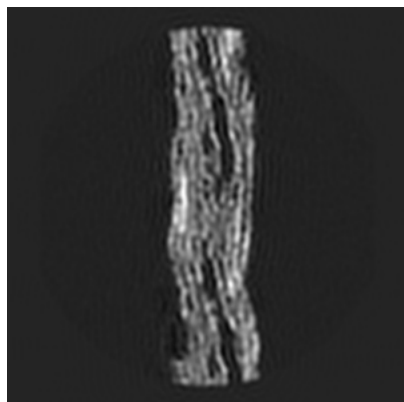


Z Index: 190

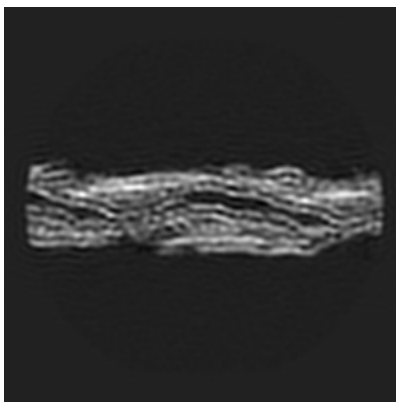
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 155

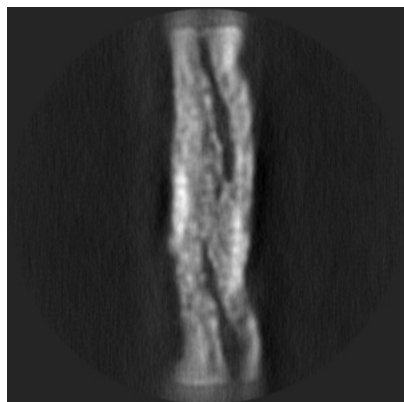


Y Index: 229

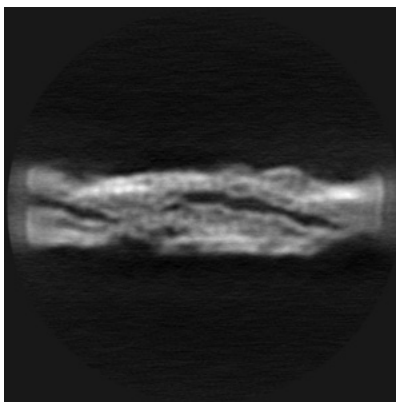


Z Index: 160

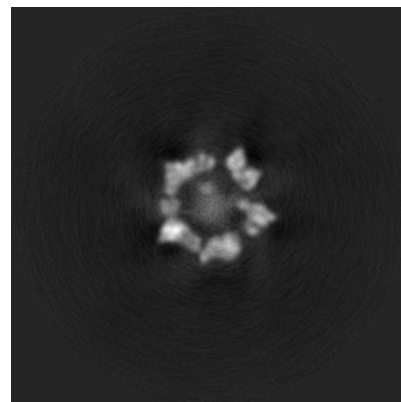
6.3.2 Raw map



X Index: 153



Y Index: 229

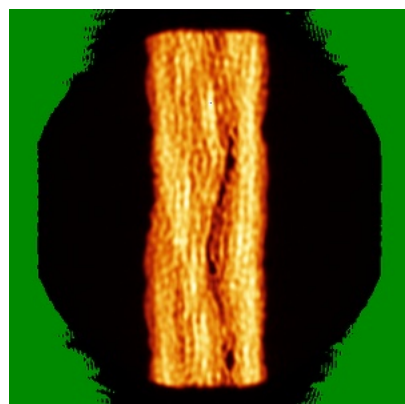


Z Index: 194

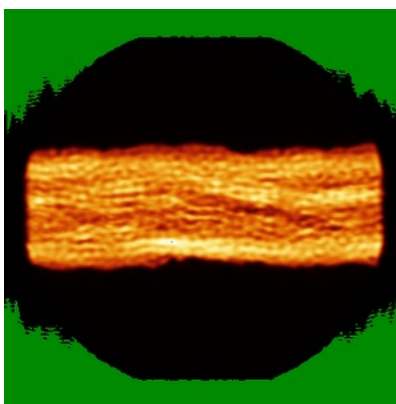
The images above show the largest variance slices of the map in three orthogonal directions.

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

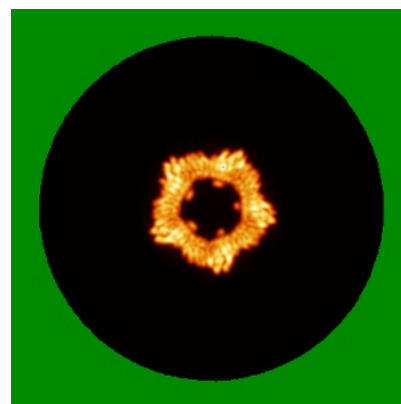
6.4.1 Primary map



X

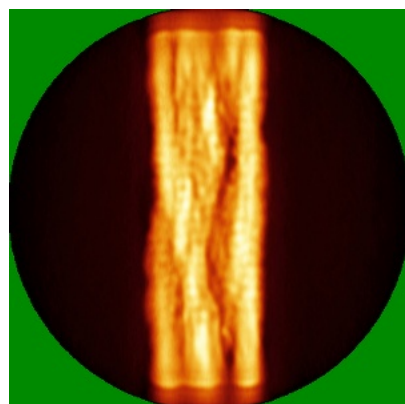


Y

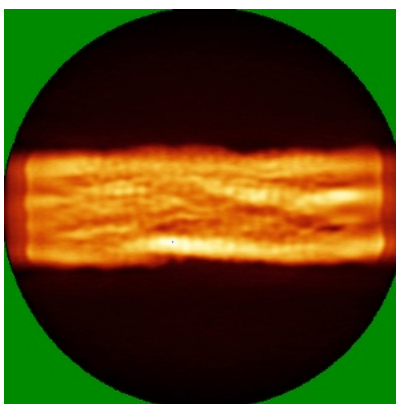


Z

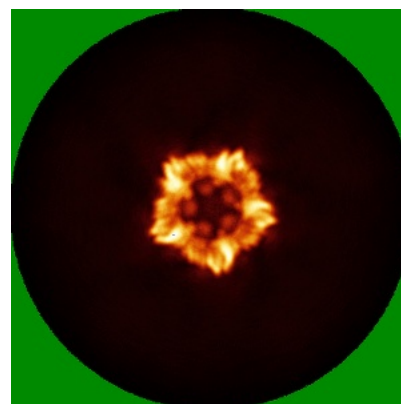
6.4.2 Raw map



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 0.005. 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 shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

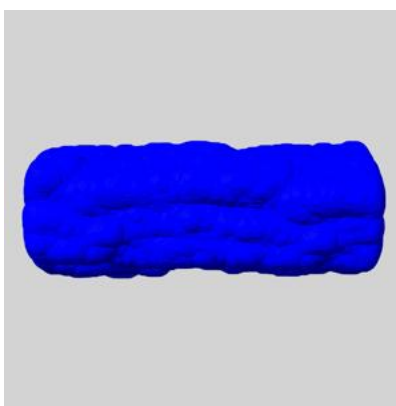
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

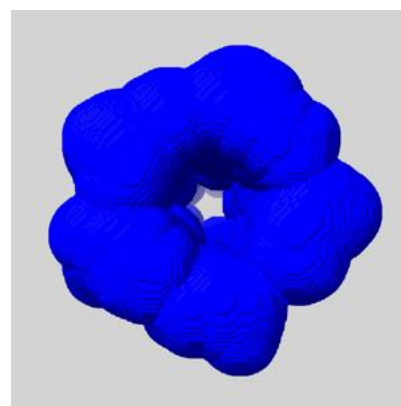
6.6.1 emd_16844_msk_1.map [i](#)



X



Y

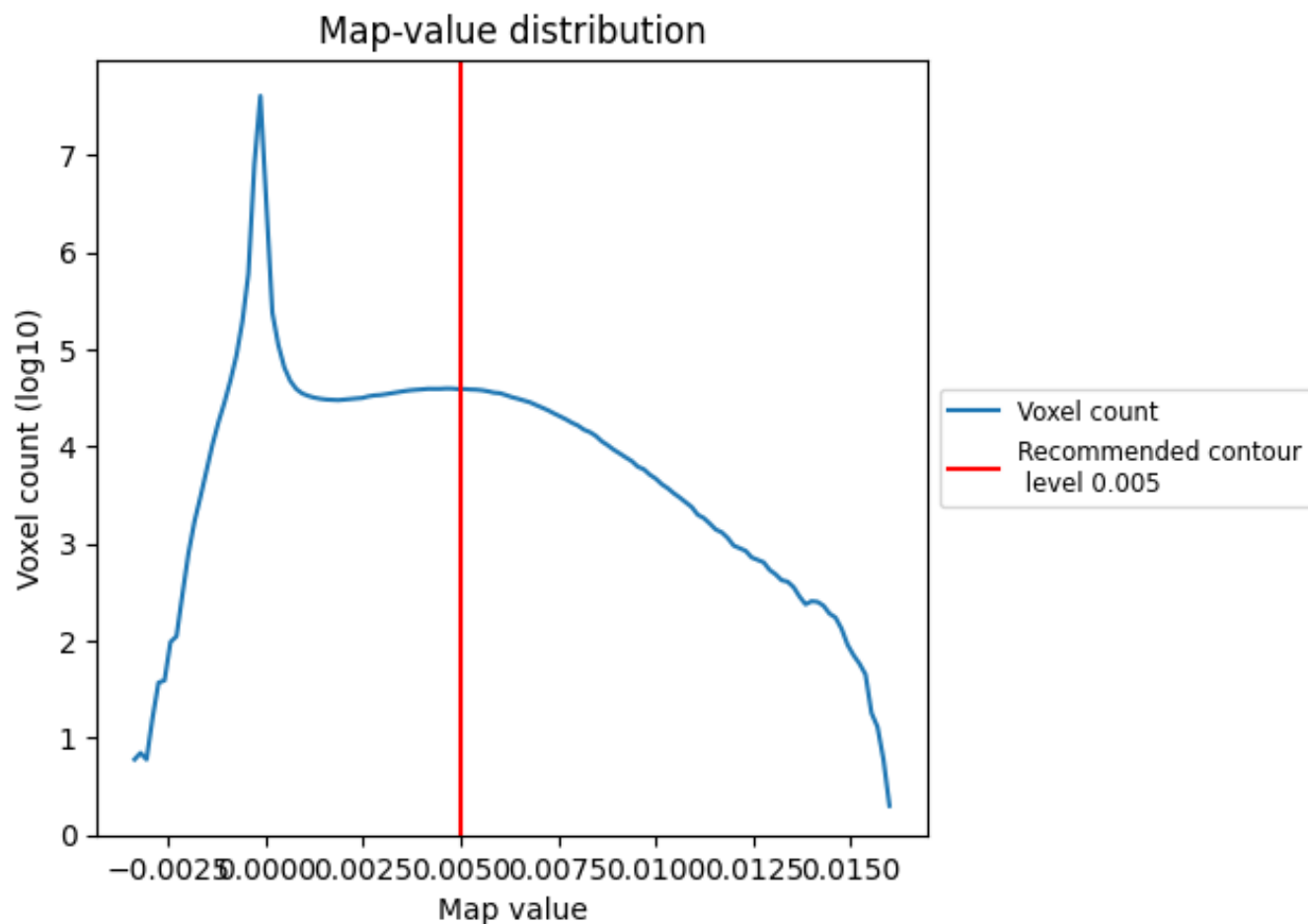


Z

7 Map analysis [i](#)

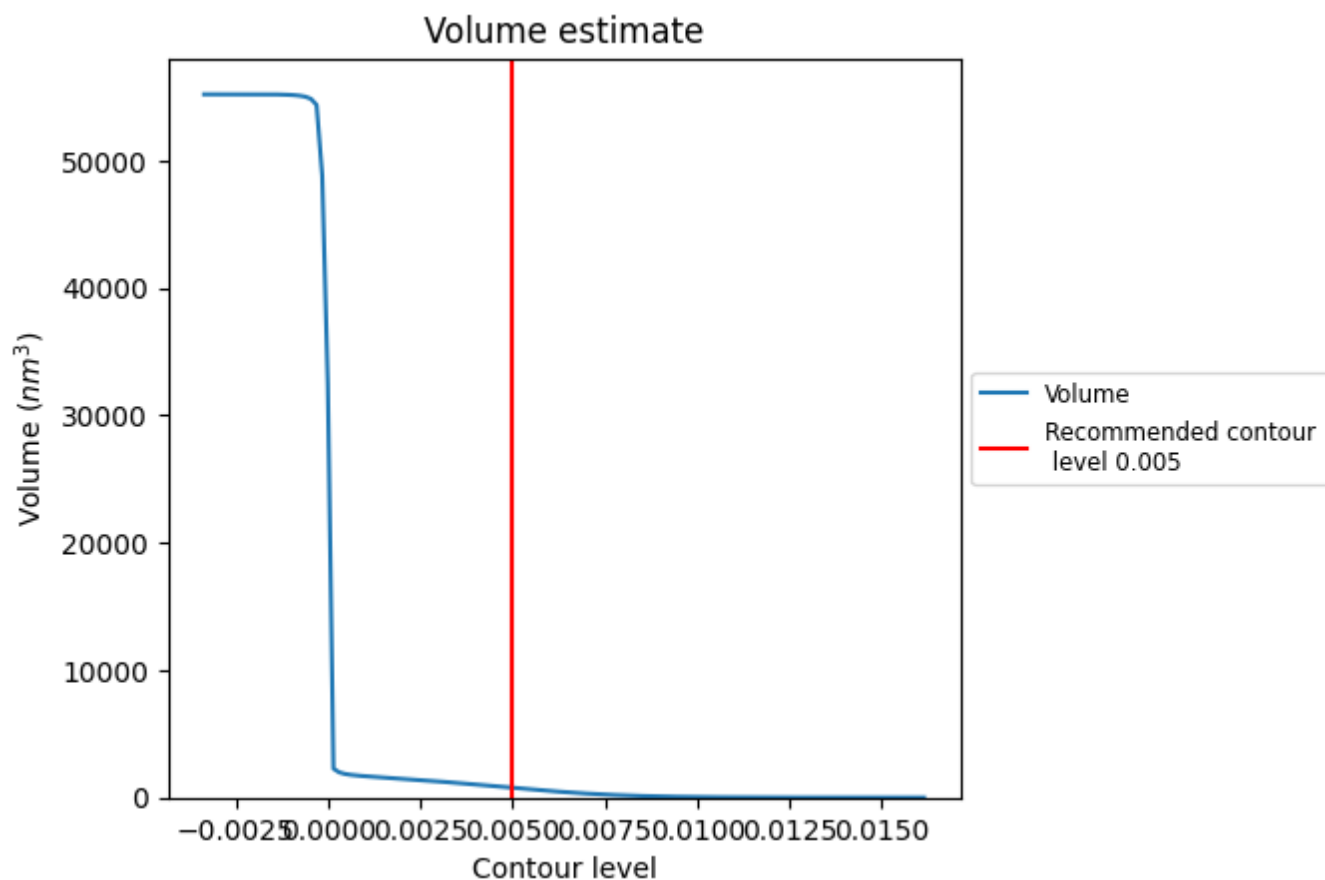
This section contains the results of statistical analysis of the map.

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.

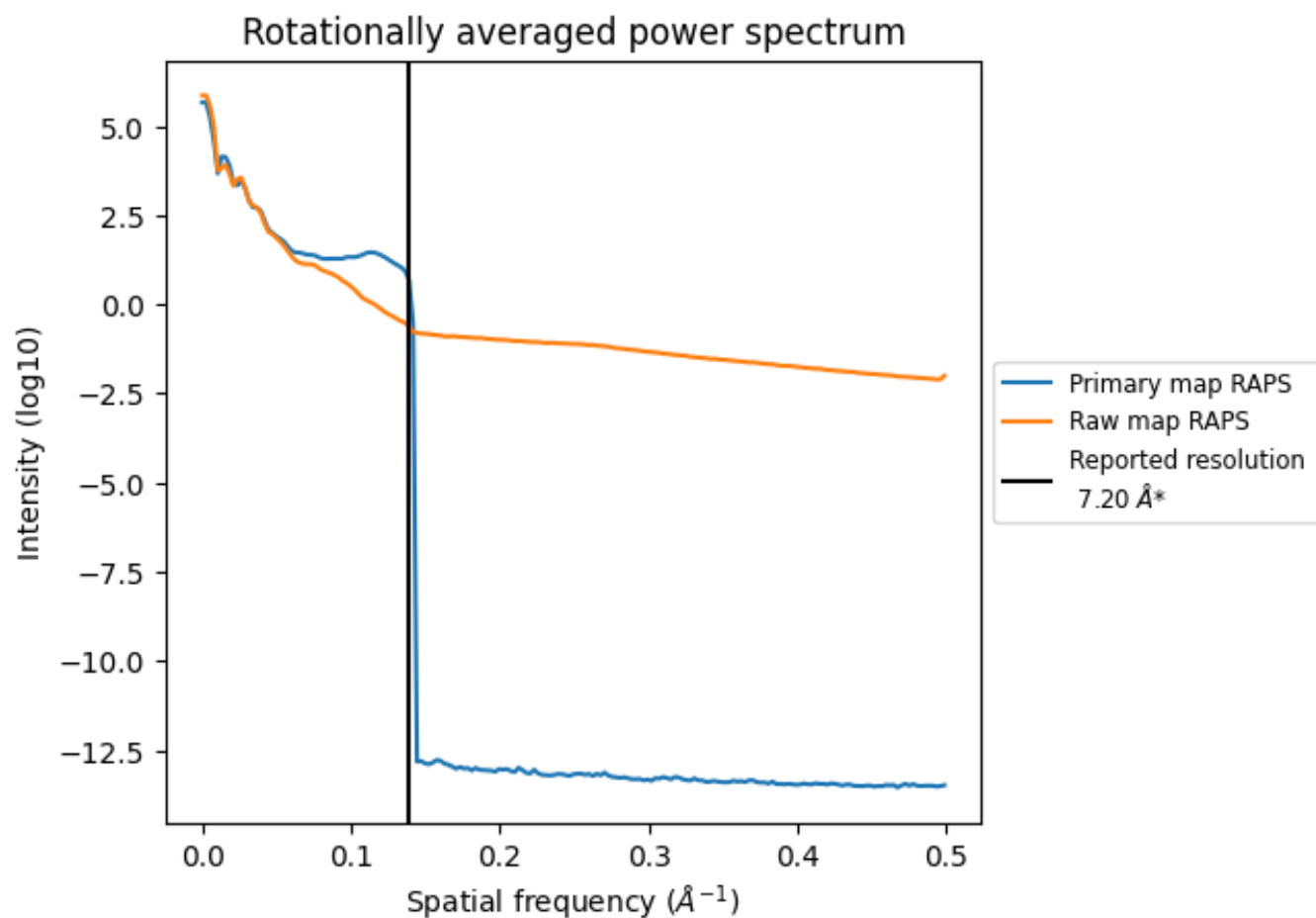
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 768 nm³; this corresponds to an approximate mass of 694 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 ⓘ

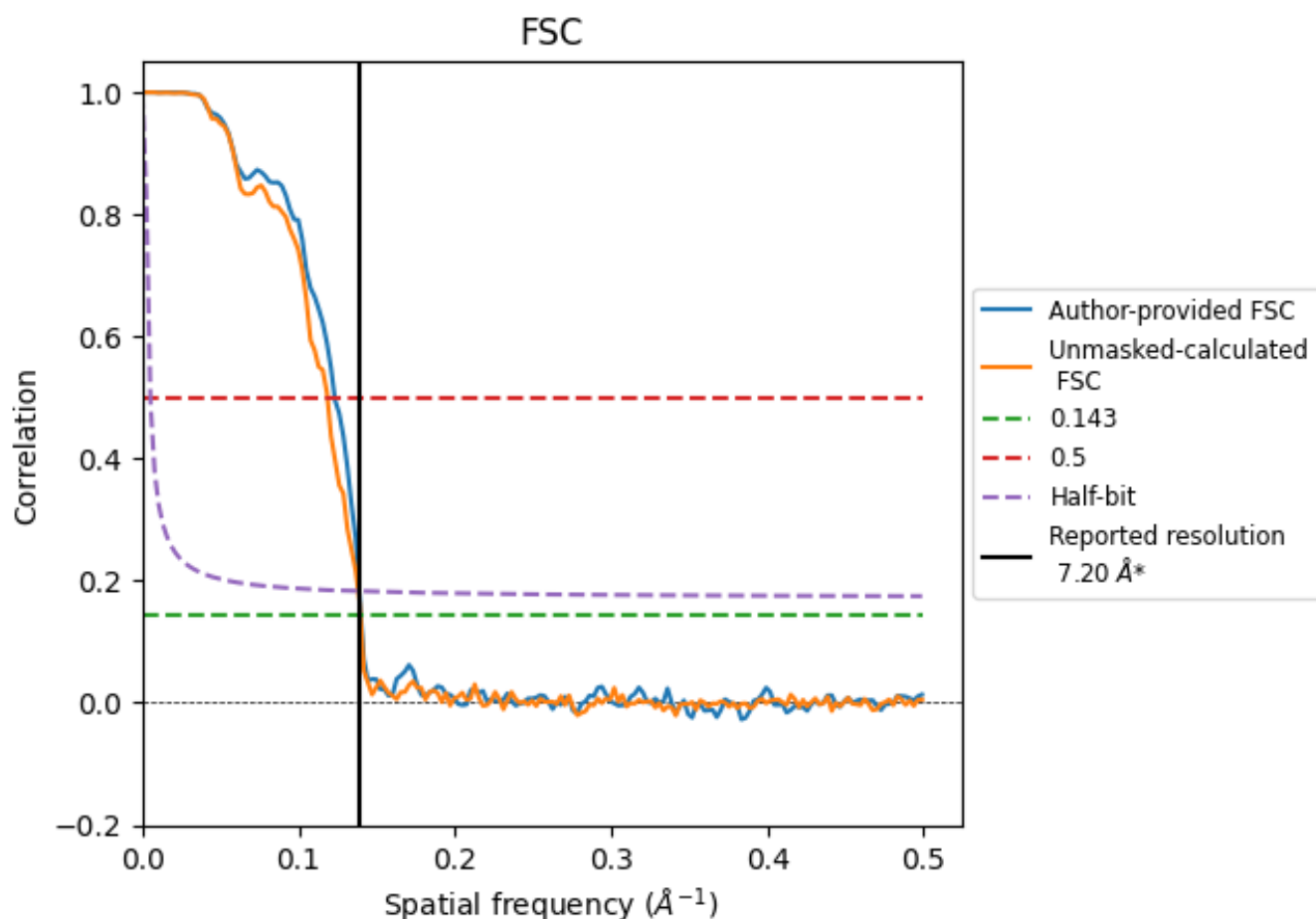


*Reported resolution corresponds to spatial frequency of 0.139 Å⁻¹

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 $0.139 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

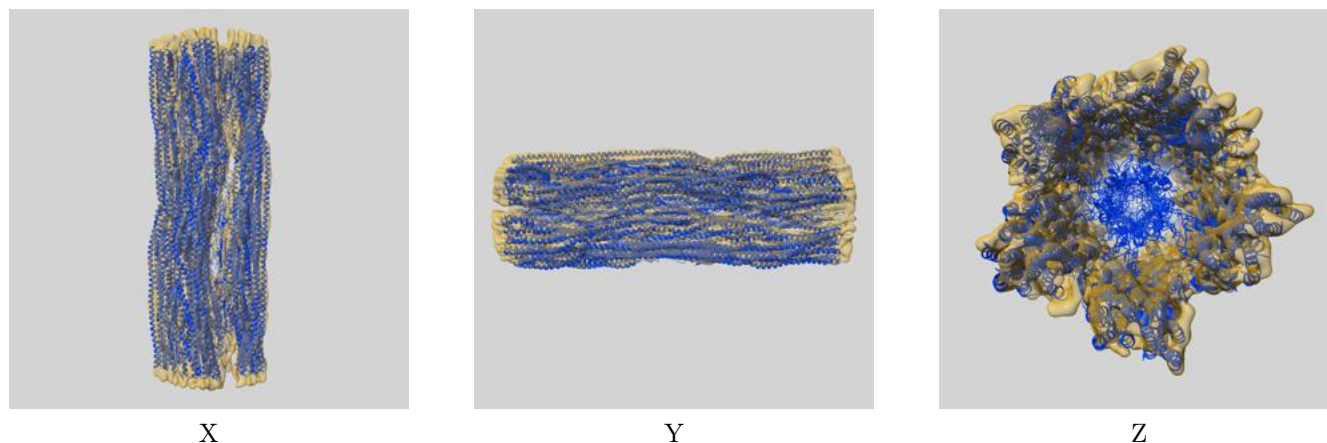
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.20	-	-
Author-provided FSC curve	7.15	8.12	7.20
Unmasked-calculated*	7.16	8.44	7.24

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

9 Map-model fit [i](#)

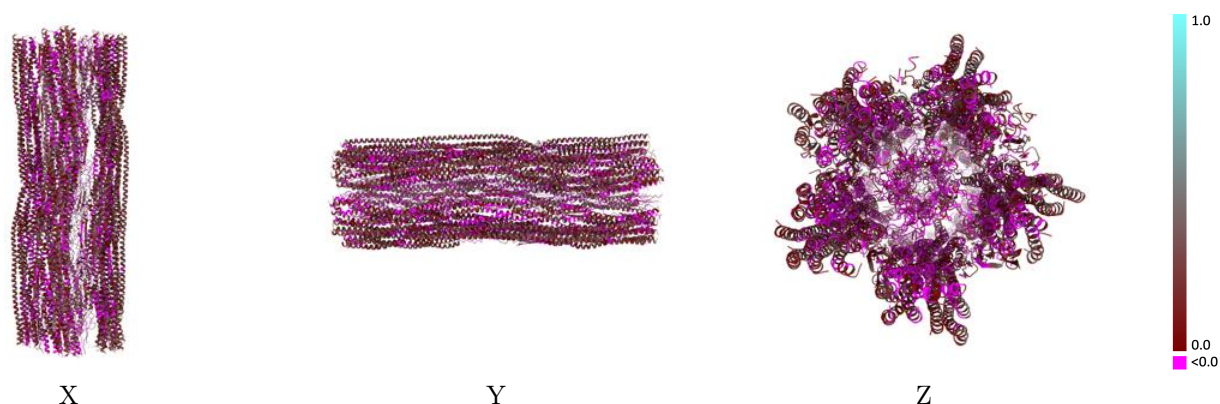
This section contains information regarding the fit between EMDB map EMD-16844 and PDB model 8RVE. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



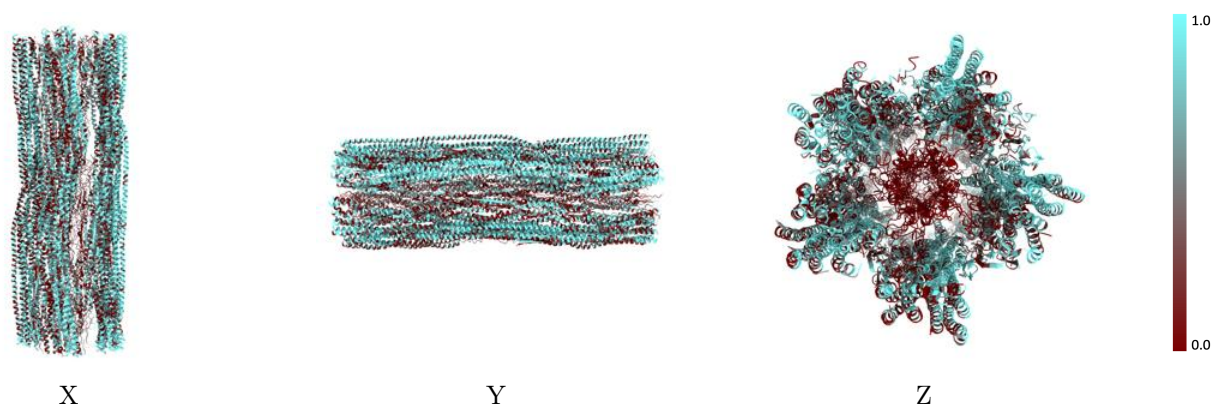
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



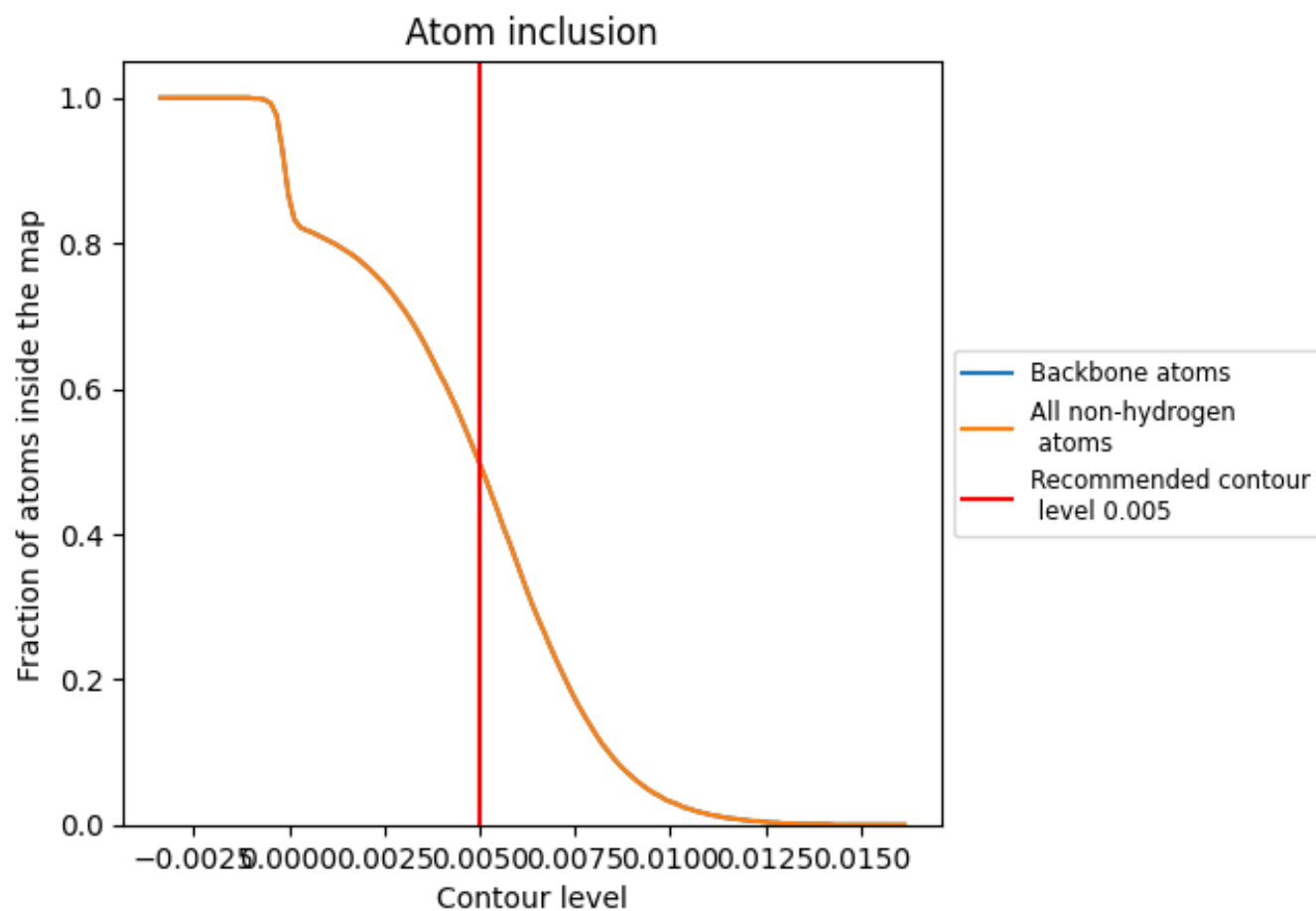
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 50% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4970	 0.0920
0	 0.8250	 0.1680
1	 0.5410	 0.0730
2	 0.5630	 0.0820
3	 0.3770	 0.0510
4	 0.2820	 0.0750
5	 0.6830	 0.0840
6	 0.7030	 0.1090
7	 0.3500	 0.0680
8	 0.2760	 0.0540
9	 0.6940	 0.1300
A	 0.5140	 0.0930
AA	 0.3160	 0.0240
AB	 0.3000	 0.0570
AC	 0.6500	 0.0890
AD	 0.7540	 0.1890
AE	 0.2040	 -0.0010
AF	 0.2590	 0.0200
AG	 0.6810	 0.0890
AH	 0.6870	 0.1600
AI	 0.7200	 0.0860
AJ	 0.6650	 0.0950
AK	 0.7100	 0.0940
AL	 0.7310	 0.1290
AM	 0.6940	 0.1020
AN	 0.7940	 0.1600
AO	 0.5510	 0.0780
AP	 0.6150	 0.1930
B	 0.4970	 0.1110
C	 0.4750	 0.1070
D	 0.4510	 0.0870
E	 0.3560	 0.0870
F	 0.4640	 0.0610
G	 0.4180	 0.1060
H	 0.4310	 0.0640



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Chain	Atom inclusion	Q-score
I	 0.6490	 0.1830
J	 0.5060	 0.0960
K	 0.5510	 0.1580
L	 0.5350	 0.1280
M	 0.4780	 0.1290
N	 0.4910	 0.1420
O	 0.4090	 0.1240
P	 0.4590	 0.1490
Q	 0.0540	 0.0500
R	 0.1250	 0.0700
S	 0.5750	 0.1620
T	 0.5680	 0.1650
U	 0.1740	 0.0250
V	 0.1670	 -0.0820
W	 0.7650	 0.2040
X	 0.7730	 0.1980
Y	 0.2830	 0.0730
Z	 0.2870	 0.0490
a	 0.6840	 0.1720
b	 0.6110	 0.1650
c	 0.3140	 0.0730
d	 0.2930	 0.0250
e	 0.5310	 0.1250
f	 0.5020	 0.1390
g	 0.2440	 0.0460
h	 0.3120	 -0.0040
i	 0.4550	 0.0750
j	 0.4950	 0.1140
k	 0.2530	 0.0370
l	 0.2490	 0.0010
m	 0.5130	 0.0800
n	 0.4900	 0.1180
o	 0.3540	 0.0750
p	 0.3580	 0.0410
q	 0.4180	 0.0470
r	 0.3760	 0.0690
s	 0.4700	 0.0930
t	 0.4990	 0.0710
u	 0.4290	 0.0280
v	 0.3550	 0.0400
w	 0.4820	 0.0720
x	 0.5250	 0.0540

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Chain	Atom inclusion	Q-score
y	 0.4100	 0.0390
z	 0.3190	 0.0280