



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 03:47 AM UTC

PDB ID : 2Y9J / pdb_00002y9j
EMDB ID : EMD-1874
Title : THREE-DIMENSIONAL MODEL OF SALMONELLA'S NEEDLE COMPLEX AT SUBNANOMETER RESOLUTION
Authors : Schraidt, O.; Marlovits, T.C.
Deposited on : 2011-02-15
Resolution : 6.40 Å(reported)
Based on initial model : 2Y9J

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

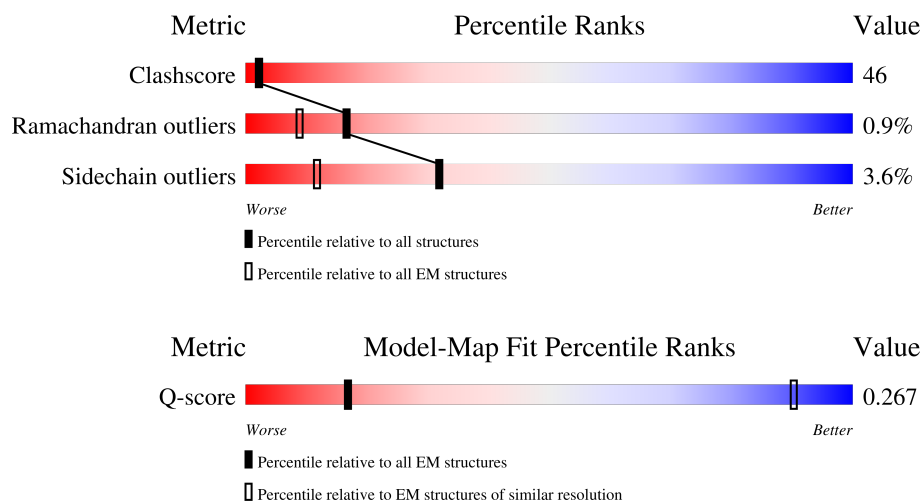
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.40 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	544 (5.90 - 6.90)

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

Mol	Chain	Length	Quality of chain
1	A	186	18% 78% 21%
1	B	186	18% 78% 21%
1	C	186	18% 78% 20%
1	D	186	18% 78% 21%

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Mol	Chain	Length	Quality of chain
1	E	186	
1	F	186	
1	G	186	
1	H	186	
1	I	186	
1	J	186	
1	K	186	
1	L	186	
1	M	186	
1	N	186	
1	O	186	
1	P	186	
1	Q	186	
1	R	186	
1	S	186	
1	T	186	
1	U	186	
1	V	186	
1	W	186	
1	X	186	
2	Y	170	
2	Z	170	
2	a	170	
2	b	170	
2	c	170	

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Mol	Chain	Length	Quality of chain
2	d	170	
2	e	170	
2	f	170	
2	g	170	
2	h	170	
2	i	170	
2	j	170	
2	k	170	
2	l	170	
2	m	170	
2	n	170	
2	o	170	
2	p	170	
2	q	170	
2	r	170	
2	s	170	
2	t	170	
2	u	170	
2	v	170	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 70704 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 PROTEIN PRGH.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	B	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	C	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	D	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	E	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	F	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	G	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	H	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	I	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	J	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	K	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	L	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	M	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	N	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	O	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	P	186	Total 1541	C 976	N 280	O 281	S 4	0	0
1	Q	186	Total 1541	C 976	N 280	O 281	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	186	Total	C	N	O	S	0	0
			1541	976	280	281	4		
1	S	186	Total	C	N	O	S	0	0
			1541	976	280	281	4		
1	T	186	Total	C	N	O	S	0	0
			1541	976	280	281	4		
1	U	186	Total	C	N	O	S	0	0
			1541	976	280	281	4		
1	V	186	Total	C	N	O	S	0	0
			1541	976	280	281	4		
1	W	186	Total	C	N	O	S	0	0
			1541	976	280	281	4		
1	X	186	Total	C	N	O	S	0	0
			1541	976	280	281	4		

- Molecule 2 is a protein called LIPOPROTEIN PRGK.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Y	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	Z	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	a	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	b	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	c	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	d	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	e	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	f	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	g	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	h	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	i	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	j	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	k	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	l	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	m	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	n	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	o	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	p	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	q	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	r	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	s	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	t	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	u	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		
2	v	170	Total	C	N	O	S	0	0
			1339	845	233	258	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	A	66	Total	O	0
			66	66	
3	B	66	Total	O	0
			66	66	
3	C	66	Total	O	0
			66	66	
3	D	66	Total	O	0
			66	66	
3	E	66	Total	O	0
			66	66	
3	F	66	Total	O	0
			66	66	
3	G	66	Total	O	0
			66	66	

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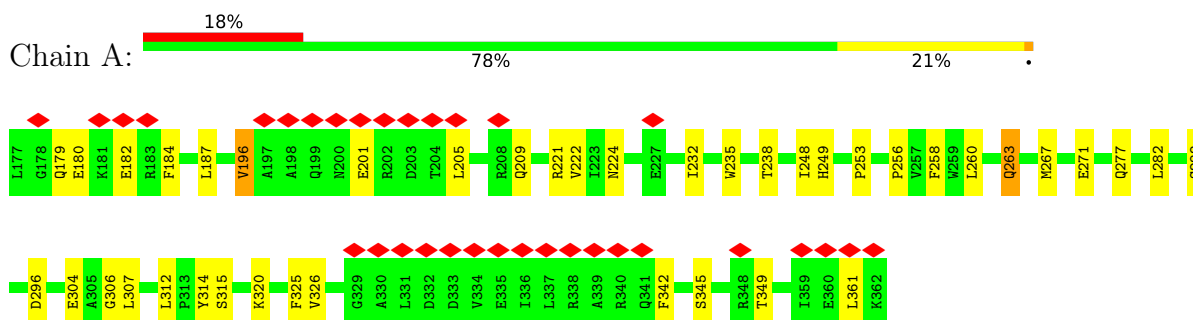
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Mol	Chain	Residues	Atoms		AltConf
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3	I	66	Total 66	O 66	0
3	J	66	Total 66	O 66	0
3	K	66	Total 66	O 66	0
3	L	66	Total 66	O 66	0
3	M	66	Total 66	O 66	0
3	N	66	Total 66	O 66	0
3	O	66	Total 66	O 66	0
3	P	66	Total 66	O 66	0
3	Q	66	Total 66	O 66	0
3	R	66	Total 66	O 66	0
3	S	66	Total 66	O 66	0
3	T	66	Total 66	O 66	0
3	U	66	Total 66	O 66	0
3	V	66	Total 66	O 66	0
3	W	66	Total 66	O 66	0
3	X	66	Total 66	O 66	0

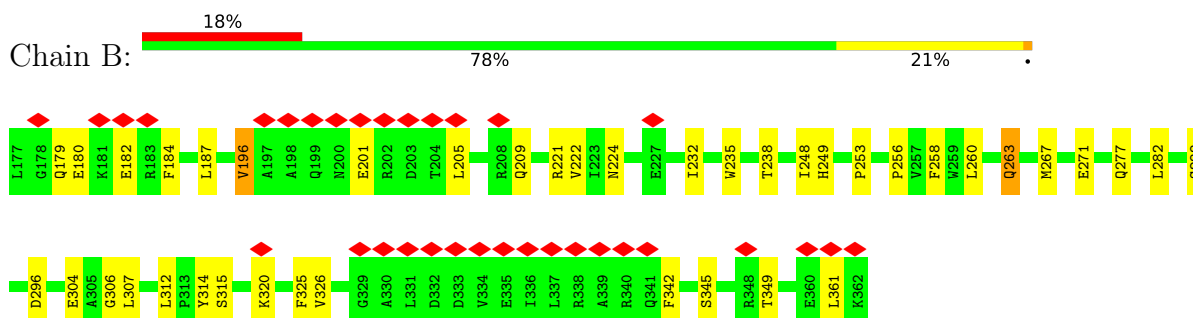
3 Residue-property plots

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.

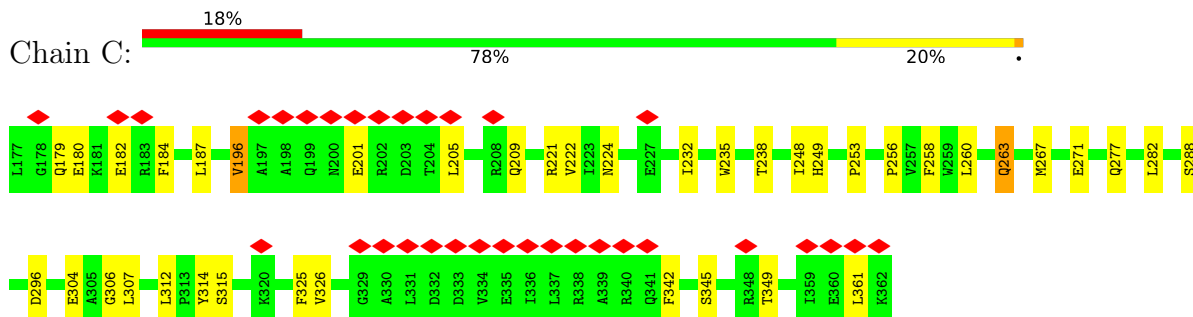
- Molecule 1: PROTEIN PRGH



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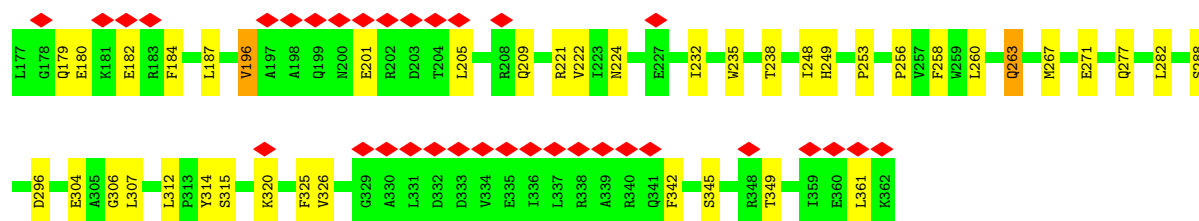


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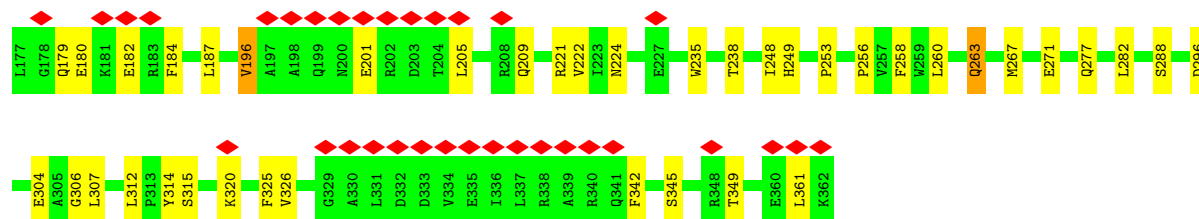
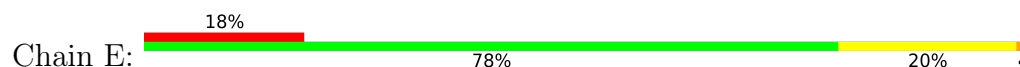


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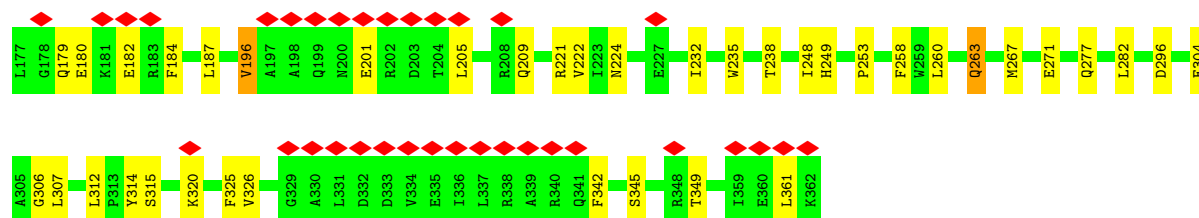
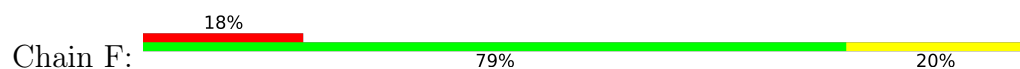




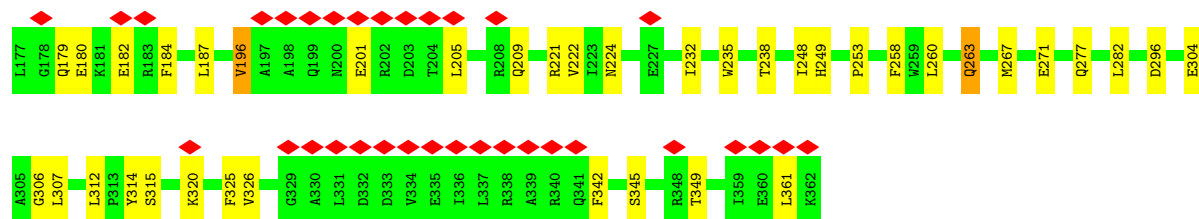
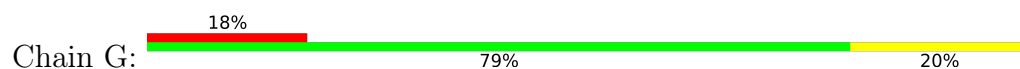
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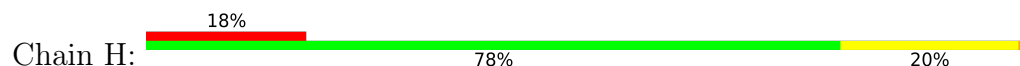
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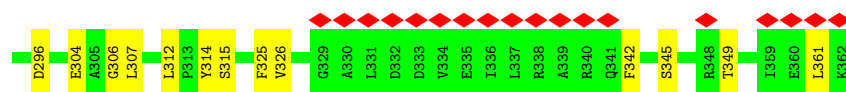


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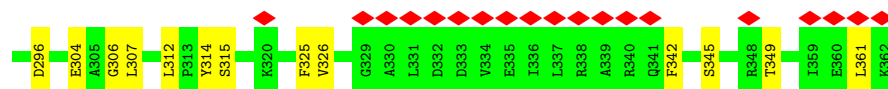
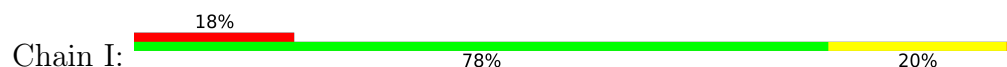


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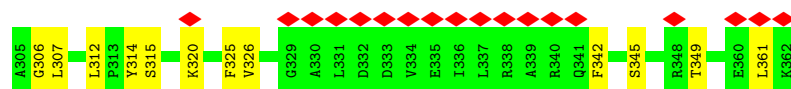
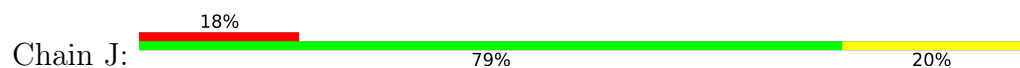




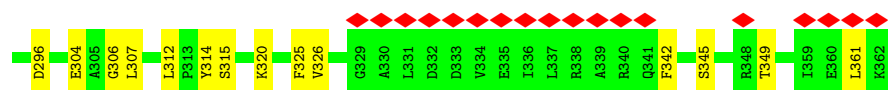
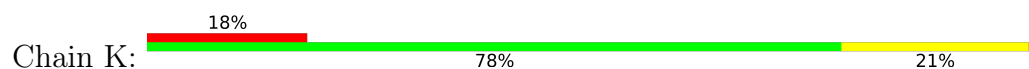
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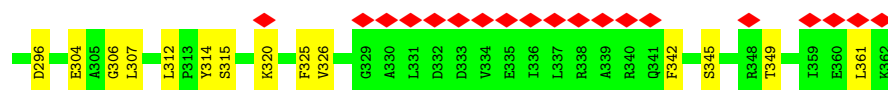
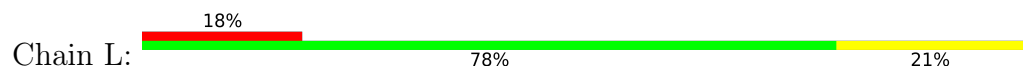
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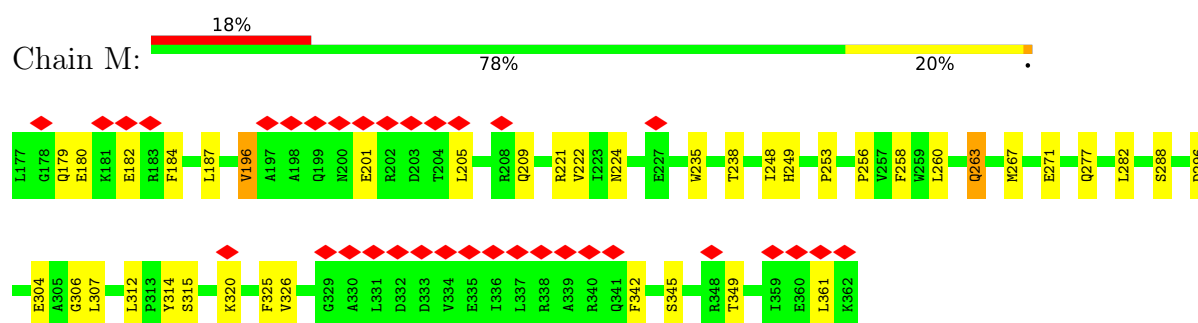
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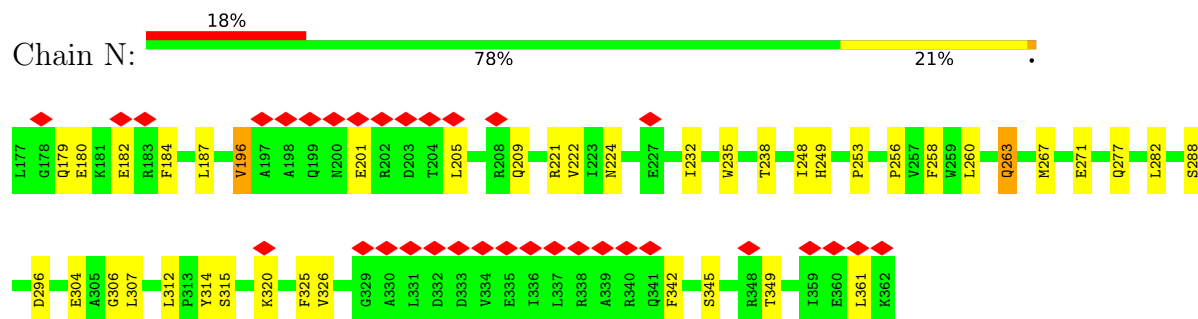
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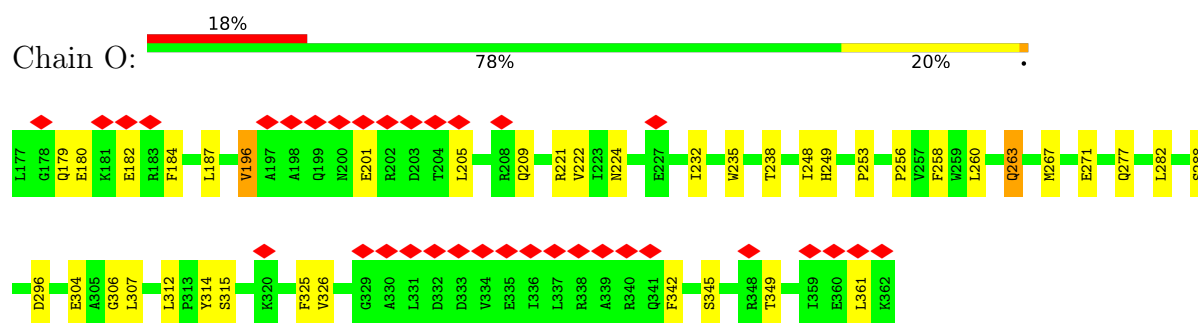
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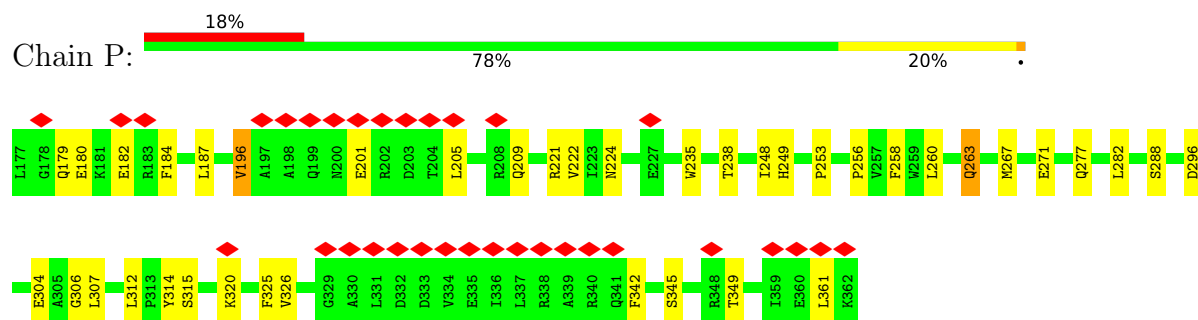
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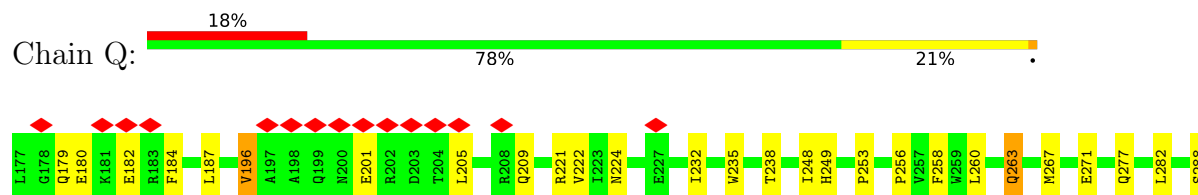
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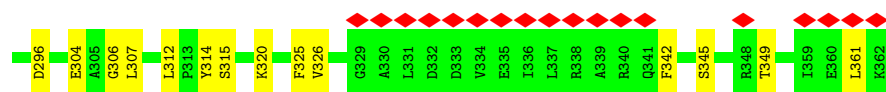


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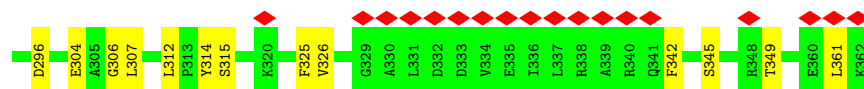
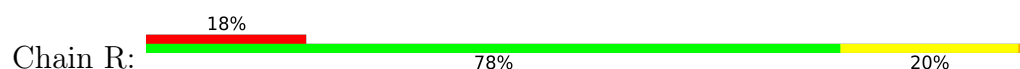


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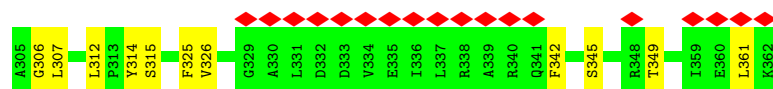
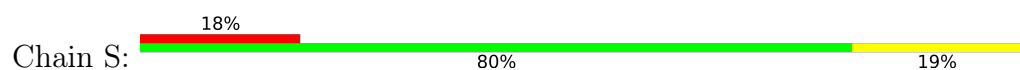




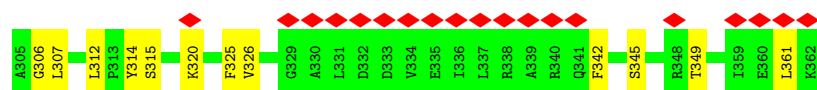
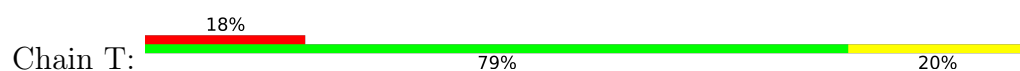
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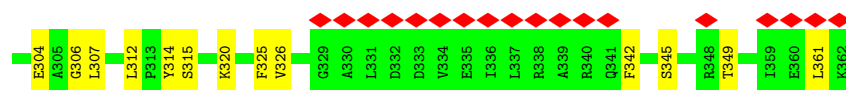
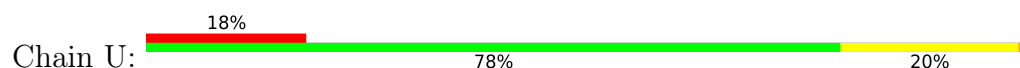
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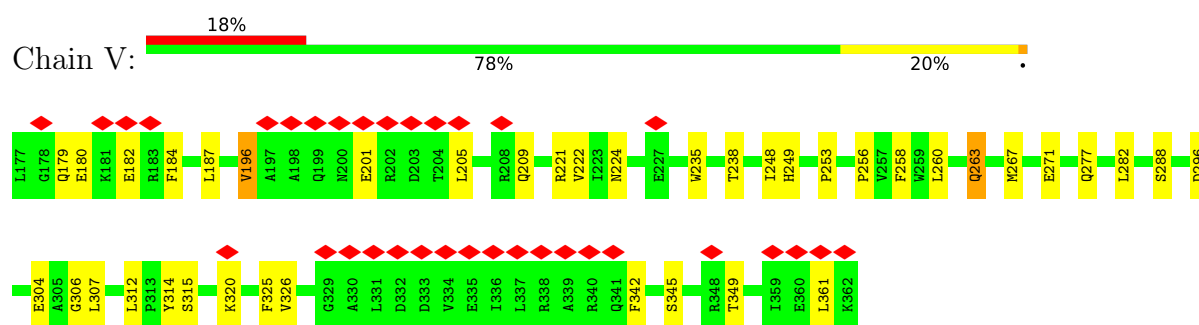
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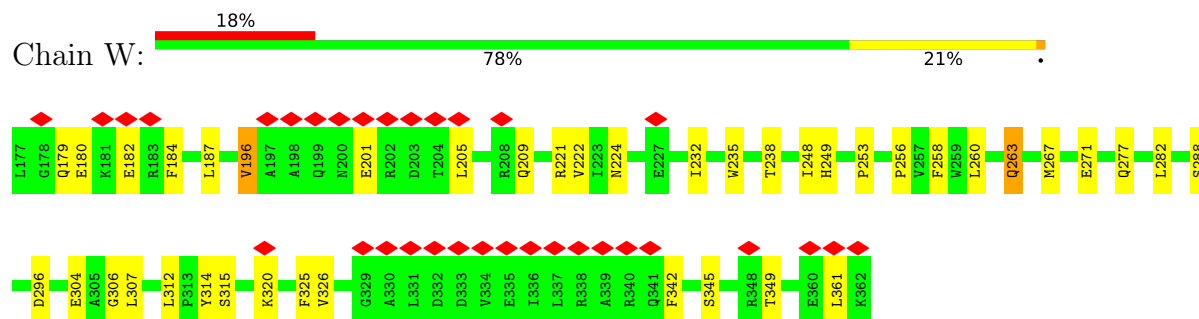
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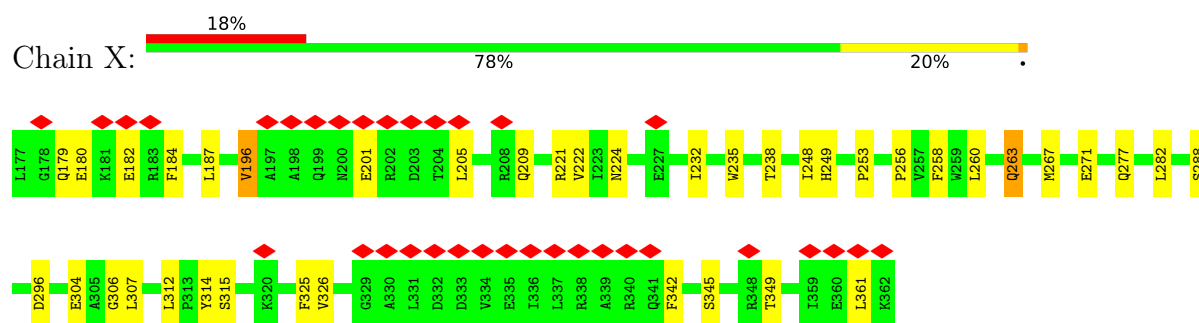
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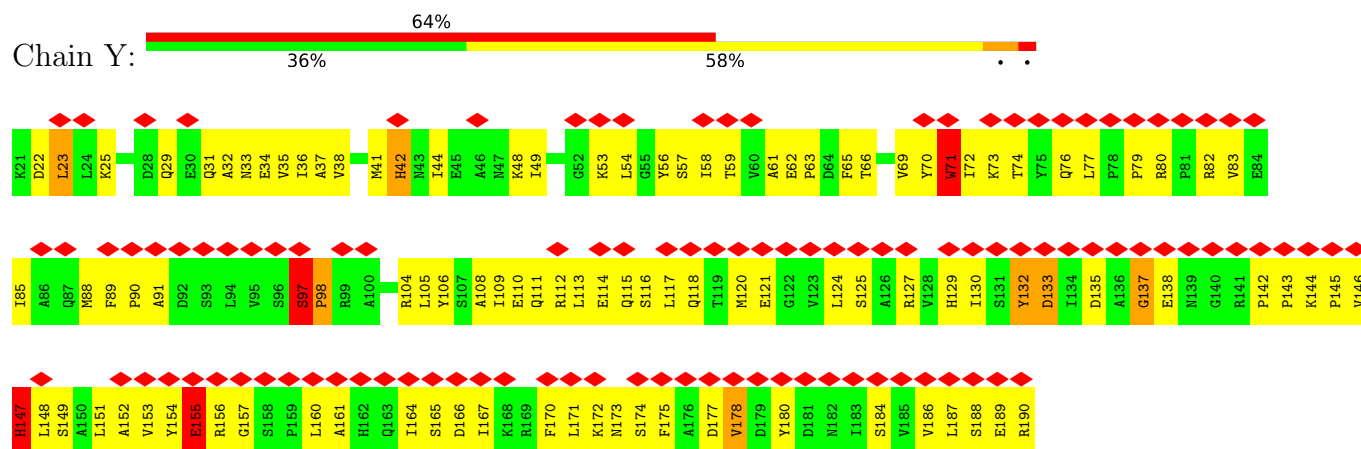
• Molecule 1: PROTEIN PRGH



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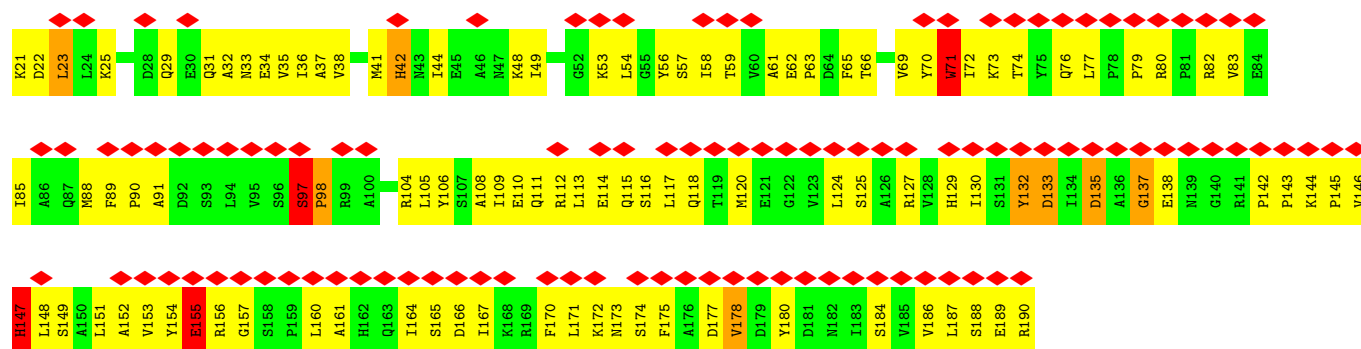


• Molecule 2: LIPOPROTEIN PRGK



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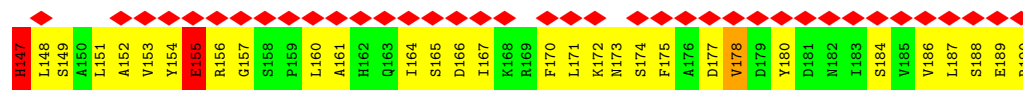


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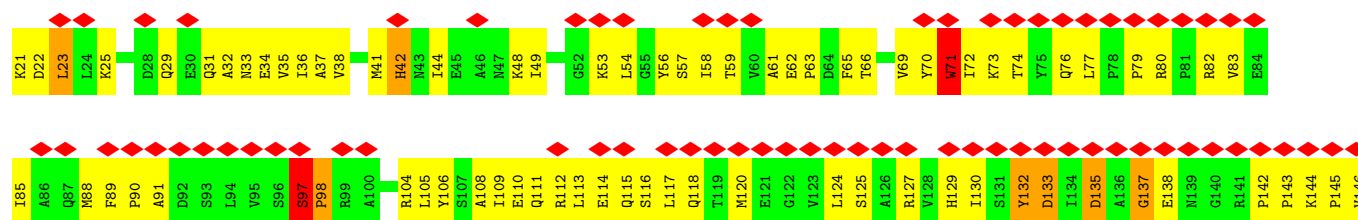


• Molecule 2: LIPOPROTEIN PRGK

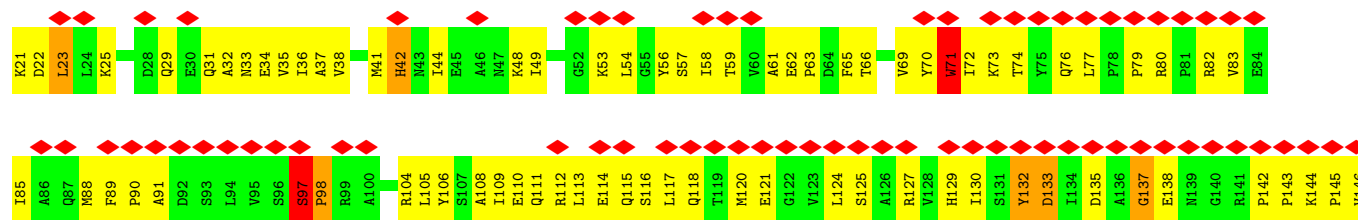




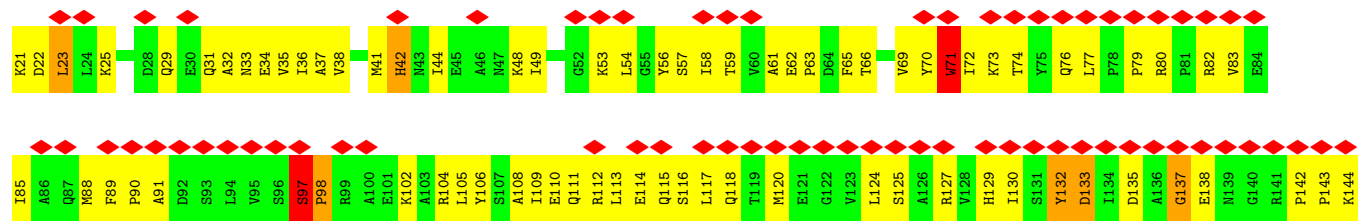
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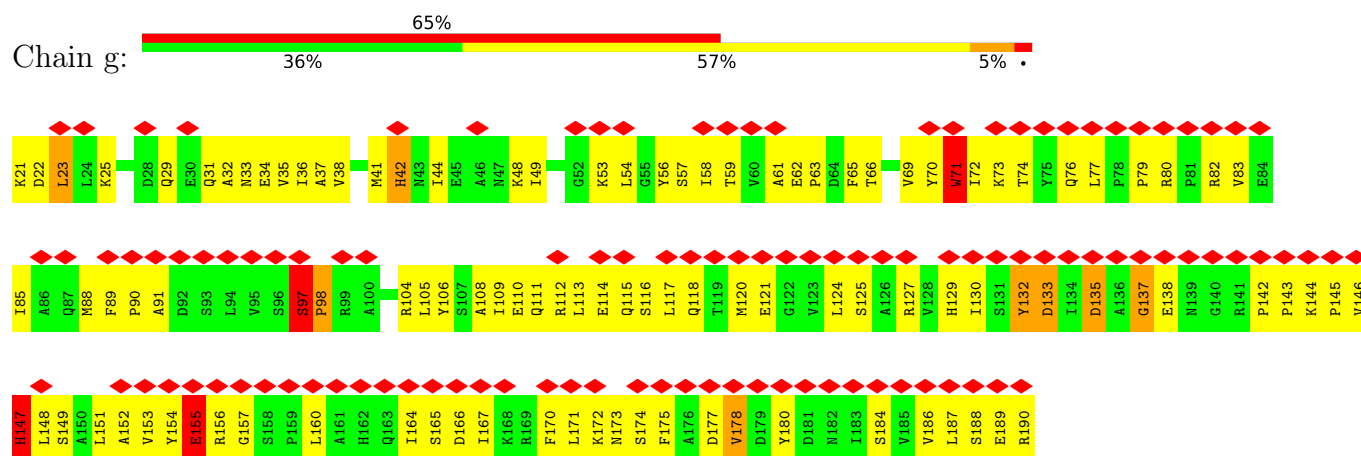


• Molecule 2: LIPOPROTEIN PRGK

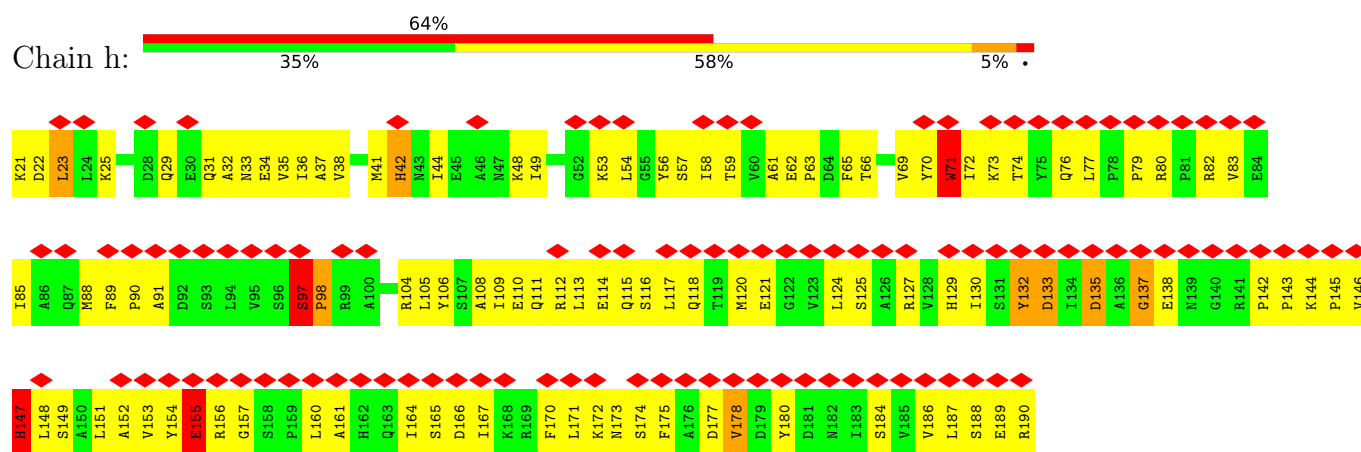


• Molecule 2: LIPOPROTEIN PRGK

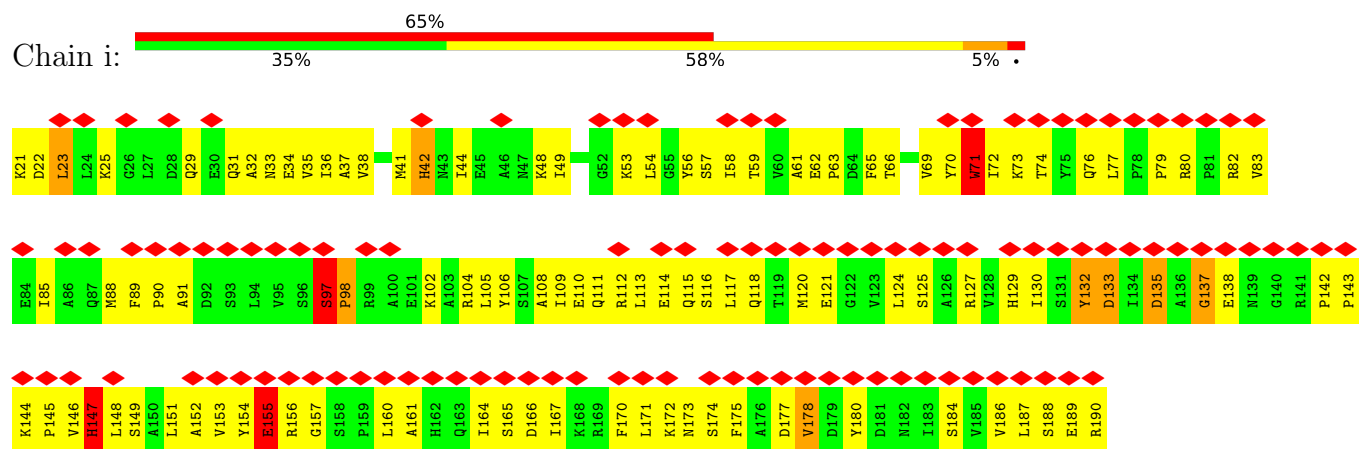




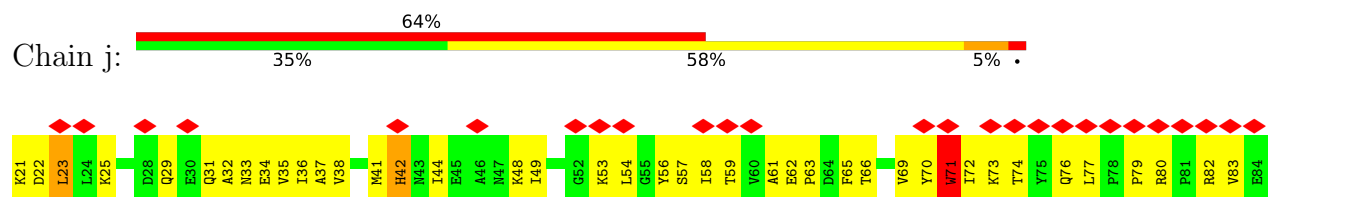
• Molecule 2: LIPOPROTEIN PRGK



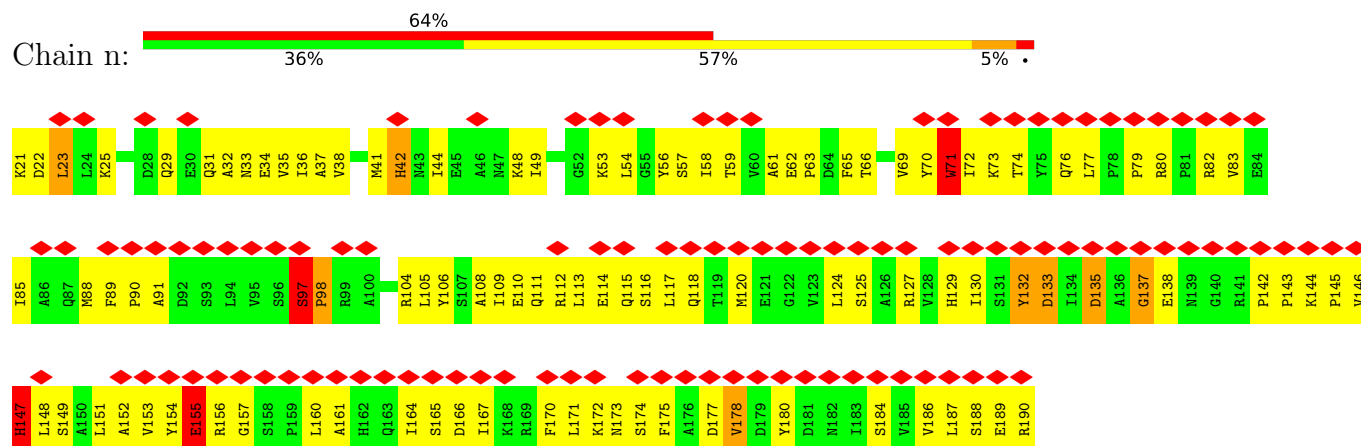
• Molecule 2: LIPOPROTEIN PRGK



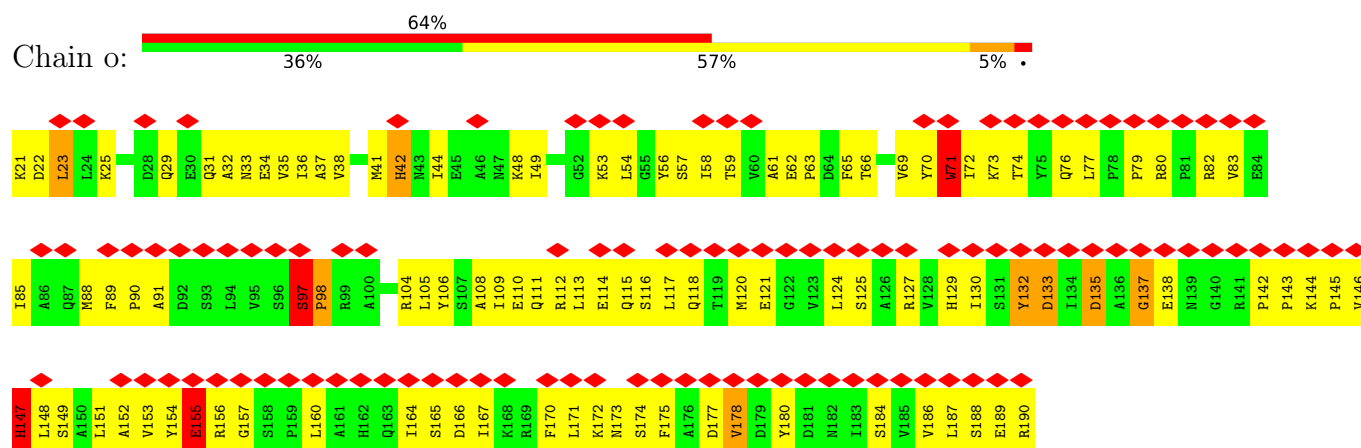
• Molecule 2: LIPOPROTEIN PRGK



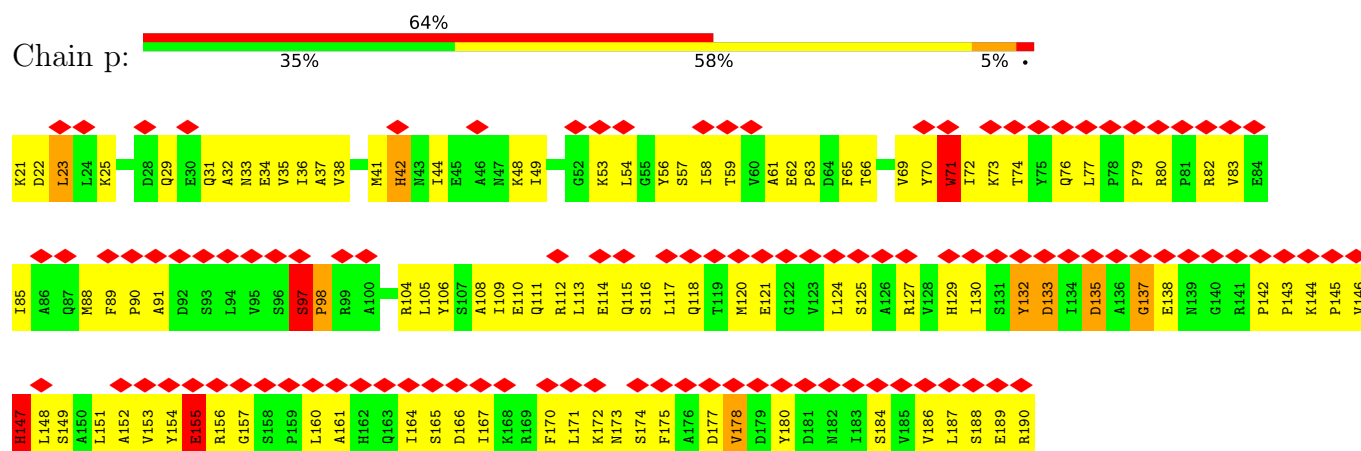
- Molecule 2: LIPOPROTEIN PRGK



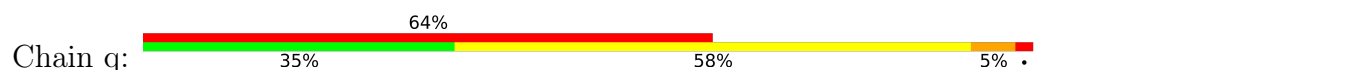
- Molecule 2: LIPOPROTEIN PRGK

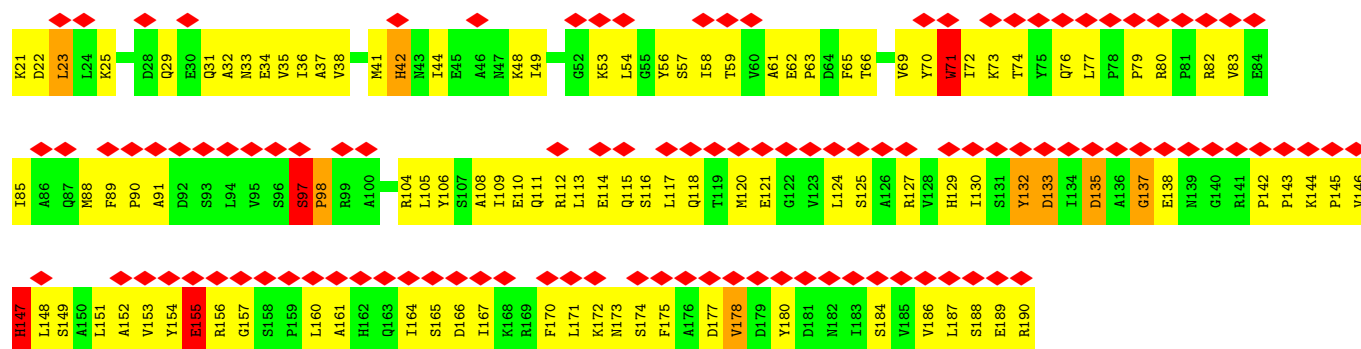


- Molecule 2: LIPOPROTEIN PRGK

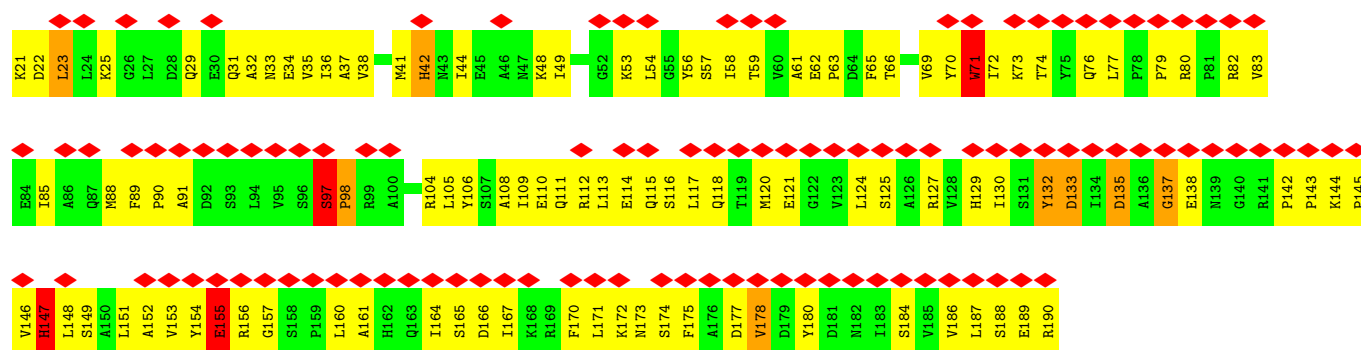


- Molecule 2: LIPOPROTEIN PRGK

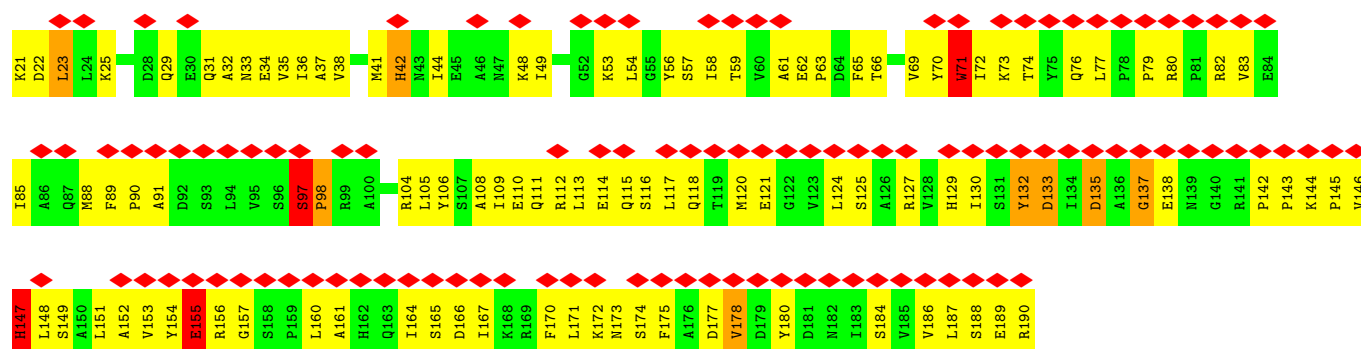




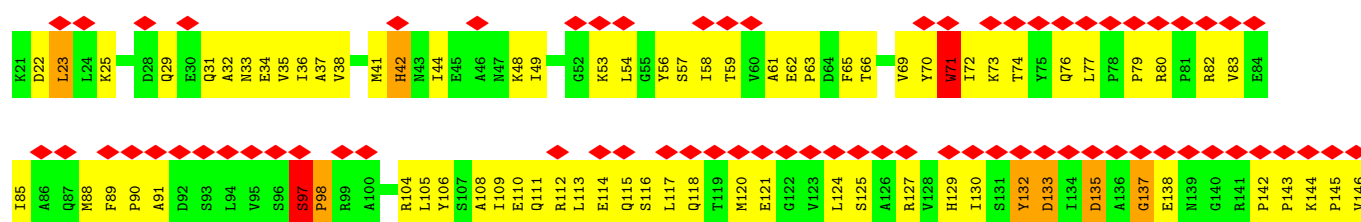
• Molecule 2: LIPOPROTEIN PRGK

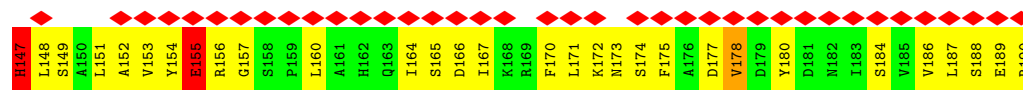


• Molecule 2: LIPOPROTEIN PRGK

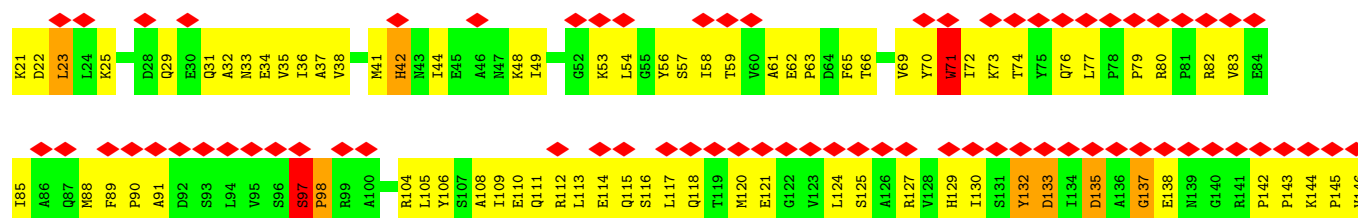


• Molecule 2: LIPOPROTEIN PRGK

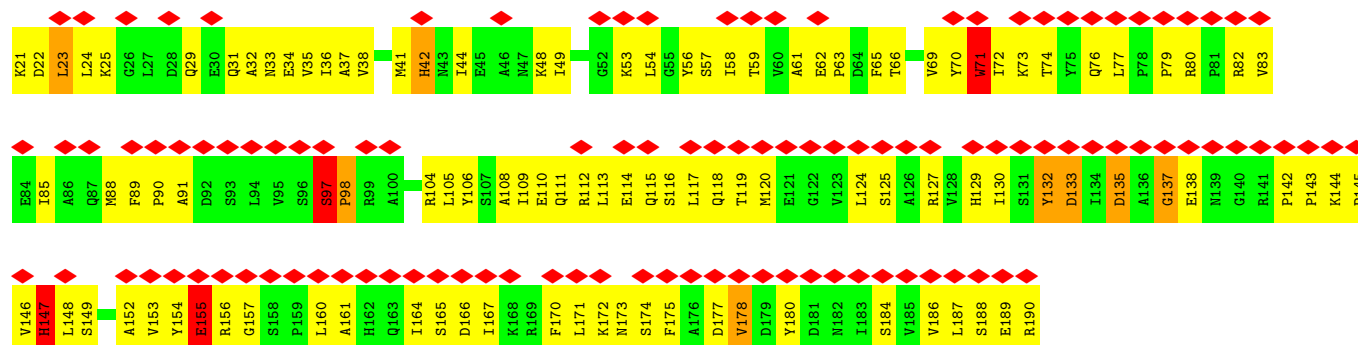




• Molecule 2: LIPOPROTEIN PRGK



• Molecule 2: LIPOPROTEIN PRGK



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C24	Depositor
Number of particles used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	EACH MICROGRAPH	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	93000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	0.213	Depositor
Minimum map value	-0.187	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.076	Depositor
Map size ($\text{\AA}$)	399.0, 399.0, 399.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.33, 1.33, 1.33	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	B	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	C	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	D	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	E	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	F	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	G	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	H	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	I	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	J	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	K	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	L	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	M	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	N	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	O	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	P	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	Q	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	R	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	S	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	T	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	U	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	V	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	W	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
1	X	0.78	1/1573 (0.1%)	0.92	2/2122 (0.1%)
2	Y	1.08	6/1365 (0.4%)	1.26	4/1850 (0.2%)
2	Z	1.07	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	a	1.08	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	b	1.07	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	c	1.07	7/1365 (0.5%)	1.26	4/1850 (0.2%)
2	d	1.07	7/1365 (0.5%)	1.26	4/1850 (0.2%)
2	e	1.07	6/1365 (0.4%)	1.26	4/1850 (0.2%)
2	f	1.07	6/1365 (0.4%)	1.27	4/1850 (0.2%)
2	g	1.08	7/1365 (0.5%)	1.26	4/1850 (0.2%)
2	h	1.07	8/1365 (0.6%)	1.27	4/1850 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	i	1.07	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	j	1.07	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	k	1.08	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	l	1.07	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	m	1.07	7/1365 (0.5%)	1.26	4/1850 (0.2%)
2	n	1.08	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	o	1.07	7/1365 (0.5%)	1.26	4/1850 (0.2%)
2	p	1.07	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	q	1.07	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	r	1.07	7/1365 (0.5%)	1.27	4/1850 (0.2%)
2	s	1.08	7/1365 (0.5%)	1.27	6/1850 (0.3%)
2	t	1.08	7/1365 (0.5%)	1.27	6/1850 (0.3%)
2	u	1.07	7/1365 (0.5%)	1.26	4/1850 (0.2%)
2	v	1.07	7/1365 (0.5%)	1.26	4/1850 (0.2%)
All	All	0.93	190/70512 (0.3%)	1.09	148/95328 (0.2%)

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
2	Y	0	3
2	Z	0	3
2	a	0	3
2	b	0	3
2	c	0	3
2	d	0	3
2	e	0	3
2	f	0	3
2	g	0	3
2	h	0	3
2	i	0	3
2	j	0	3
2	k	0	3
2	l	0	3
2	m	0	3
2	n	0	3
2	o	0	3
2	p	0	3
2	q	0	3
2	r	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	s	0	3
2	t	0	3
2	u	0	3
2	v	0	3
All	All	0	72

The worst 5 of 190 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	v	97	SER	C-O	-7.62	1.14	1.24
2	p	97	SER	C-O	-7.59	1.14	1.24
2	g	97	SER	C-O	-7.55	1.14	1.24
2	a	97	SER	C-O	-7.55	1.14	1.24
2	c	97	SER	C-O	-7.54	1.14	1.24

The worst 5 of 148 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	o	178	VAL	CG1-CB-CG2	-6.19	97.17	110.80
2	p	178	VAL	CG1-CB-CG2	-6.18	97.20	110.80
2	q	178	VAL	CG1-CB-CG2	-6.18	97.21	110.80
2	f	178	VAL	CG1-CB-CG2	-6.18	97.21	110.80
2	k	178	VAL	CG1-CB-CG2	-6.18	97.21	110.80

There are no chirality outliers.

5 of 72 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Y	155	GLU	Mainchain
2	Y	71	TRP	Mainchain
2	Y	97	SER	Peptide
2	Z	71	TRP	Mainchain
2	Z	97	SER	Peptide

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	A	1541	0	1530	25	0
1	B	1541	0	1530	26	0
1	C	1541	0	1530	24	0
1	D	1541	0	1530	26	0
1	E	1541	0	1530	25	0
1	F	1541	0	1530	25	0
1	G	1541	0	1530	24	0
1	H	1541	0	1530	25	0
1	I	1541	0	1530	25	0
1	J	1541	0	1530	24	0
1	K	1541	0	1530	26	0
1	L	1541	0	1530	26	0
1	M	1541	0	1530	25	0
1	N	1541	0	1530	26	0
1	O	1541	0	1530	24	0
1	P	1541	0	1530	24	0
1	Q	1541	0	1530	26	0
1	R	1541	0	1530	25	0
1	S	1541	0	1530	24	0
1	T	1541	0	1530	25	0
1	U	1541	0	1530	24	0
1	V	1541	0	1530	24	0
1	W	1541	0	1530	26	0
1	X	1541	0	1530	24	0
2	Y	1339	0	1331	381	0
2	Z	1339	0	1332	377	0
2	a	1339	0	1331	388	0
2	b	1339	0	1331	383	0
2	c	1339	0	1331	390	0
2	d	1339	0	1331	382	0
2	e	1339	0	1331	390	0
2	f	1339	0	1331	388	0
2	g	1339	0	1331	394	0
2	h	1339	0	1331	382	0
2	i	1339	0	1331	386	0
2	j	1339	0	1331	383	0
2	k	1339	0	1331	386	0
2	l	1339	0	1331	388	0
2	m	1339	0	1331	370	0
2	n	1339	0	1331	386	0
2	o	1339	0	1331	389	0
2	p	1339	0	1331	384	0
2	q	1339	0	1331	382	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	r	1339	0	1331	382	0
2	s	1339	0	1332	385	0
2	t	1339	0	1331	386	0
2	u	1339	0	1331	388	0
2	v	1339	0	1332	385	0
3	A	66	0	0	0	0
3	B	66	0	0	0	0
3	C	66	0	0	0	0
3	D	66	0	0	0	0
3	E	66	0	0	0	0
3	F	66	0	0	0	0
3	G	66	0	0	0	0
3	H	66	0	0	0	0
3	I	66	0	0	0	0
3	J	66	0	0	0	0
3	K	66	0	0	0	0
3	L	66	0	0	0	0
3	M	66	0	0	0	0
3	N	66	0	0	0	0
3	O	66	0	0	0	0
3	P	66	0	0	0	0
3	Q	66	0	0	0	0
3	R	66	0	0	0	0
3	S	66	0	0	0	0
3	T	66	0	0	0	0
3	U	66	0	0	0	0
3	V	66	0	0	0	0
3	W	66	0	0	0	0
3	X	66	0	0	0	0
All	All	70704	0	68667	6391	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 46.

The worst 5 of 6391 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)
2:m:170:PHE:CZ	2:v:186:VAL:HG21	1.25	1.70
2:j:170:PHE:CE1	2:s:186:VAL:HG21	1.13	1.64
2:b:186:VAL:HG21	2:d:170:PHE:CE1	1.14	1.64
2:i:186:VAL:HG21	2:q:170:PHE:CE1	1.12	1.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:170:PHE:CE1	2:m:186:VAL:HG21	1.16	1.62

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	B	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	C	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	D	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	E	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	F	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	G	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	H	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	I	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	J	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	K	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	L	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	M	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	N	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	O	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	P	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	Q	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	R	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	S	184/186 (99%)	180 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	U	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	V	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	W	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
1	X	184/186 (99%)	180 (98%)	4 (2%)	0	100	100
2	Y	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	Z	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	a	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	b	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	c	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	d	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	e	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	f	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	g	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	h	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	i	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	j	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	k	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	l	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	m	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	n	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	o	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	p	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	q	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	r	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	s	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	t	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	u	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
2	v	168/170 (99%)	157 (94%)	8 (5%)	3 (2%)	6	34
All	All	8448/8544 (99%)	8088 (96%)	288 (3%)	72 (1%)	16	50

5 of 72 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Y	97	SER
2	Z	97	SER
2	a	97	SER
2	b	97	SER
2	c	97	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	B	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	C	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	D	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	E	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	F	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	G	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	H	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	I	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	J	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	K	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	L	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	M	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	N	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	O	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	P	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	Q	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	R	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	S	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	T	160/160 (100%)	150 (94%)	10 (6%)	16	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	U	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	V	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	W	160/160 (100%)	150 (94%)	10 (6%)	16	37
1	X	160/160 (100%)	150 (94%)	10 (6%)	16	37
2	Y	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	Z	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	a	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	b	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	c	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	d	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	e	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	f	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	g	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	h	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	i	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	j	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	k	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	l	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	m	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	n	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	o	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	p	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	q	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	r	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	s	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	t	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	u	146/146 (100%)	145 (99%)	1 (1%)	76	81
2	v	146/146 (100%)	145 (99%)	1 (1%)	76	81
All	All	7344/7344 (100%)	7080 (96%)	264 (4%)	32	52

5 of 264 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	209	GLN
1	X	345	SER
2	s	23	LEU
1	J	315	SER
1	J	263	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 320 such sidechains are listed below:

Mol	Chain	Res	Type
2	j	118	GLN
2	r	76	GLN
2	k	111	GLN
2	n	118	GLN
2	t	40	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

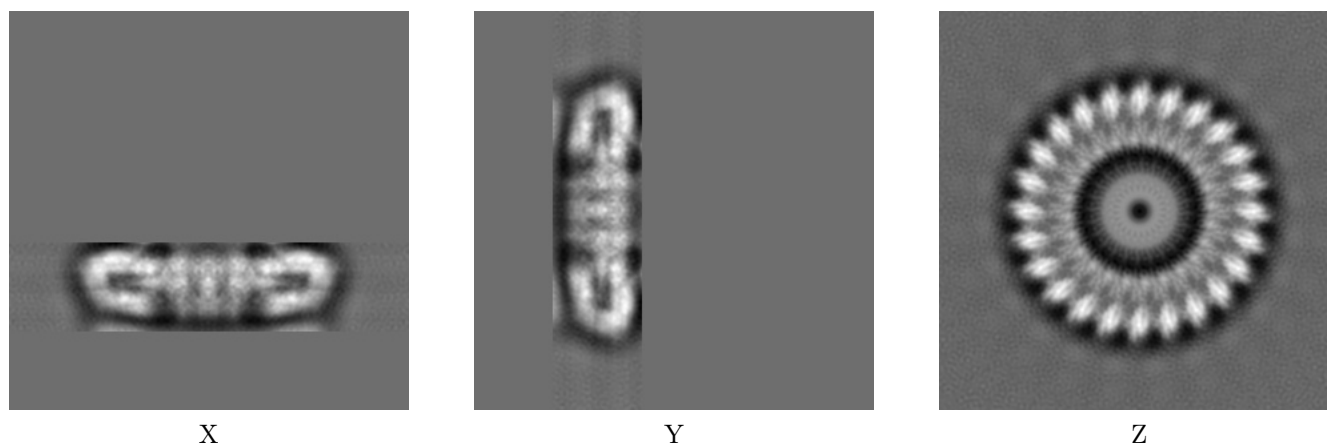
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1874. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

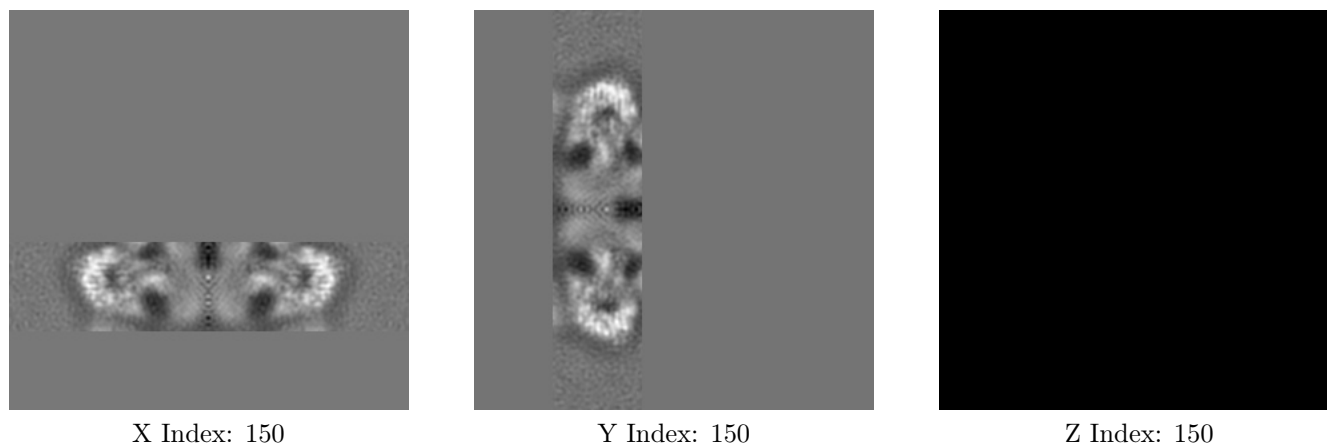
6.1.1 Primary map



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

6.2 Central slices [i](#)

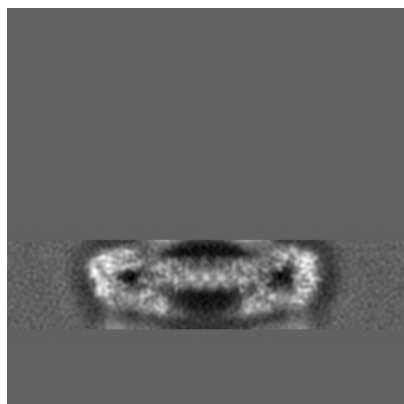
6.2.1 Primary map



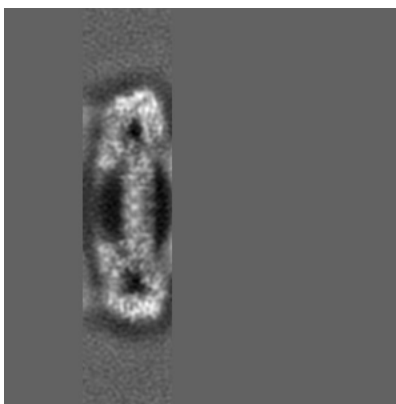
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

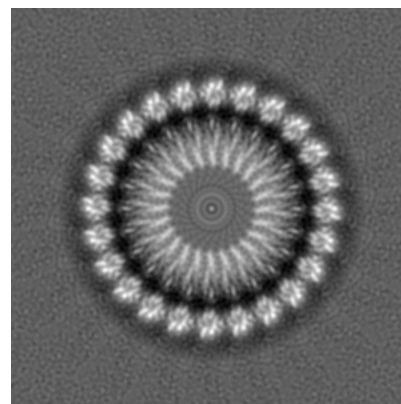
6.3.1 Primary map



X Index: 192



Y Index: 191

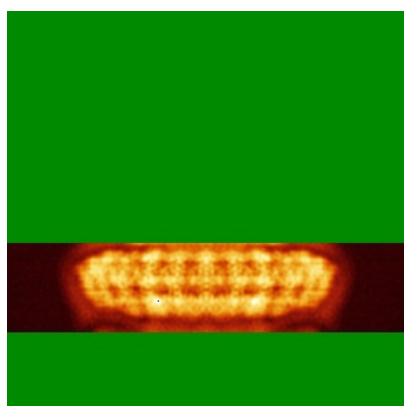


Z Index: 98

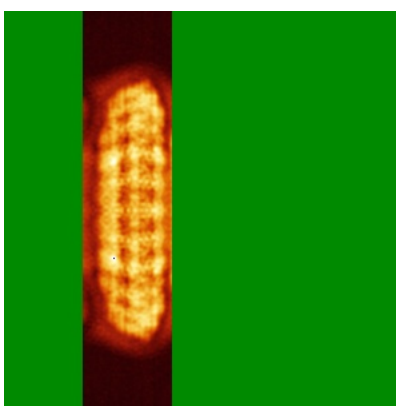
The images above show the largest variance slices of the map in three orthogonal directions.

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

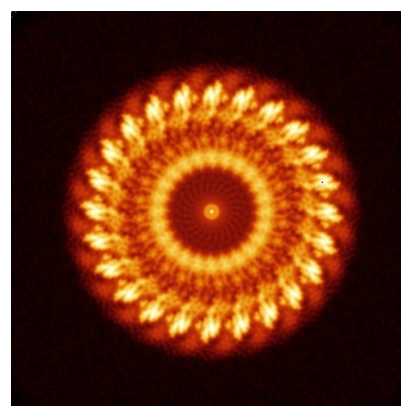
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.076. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

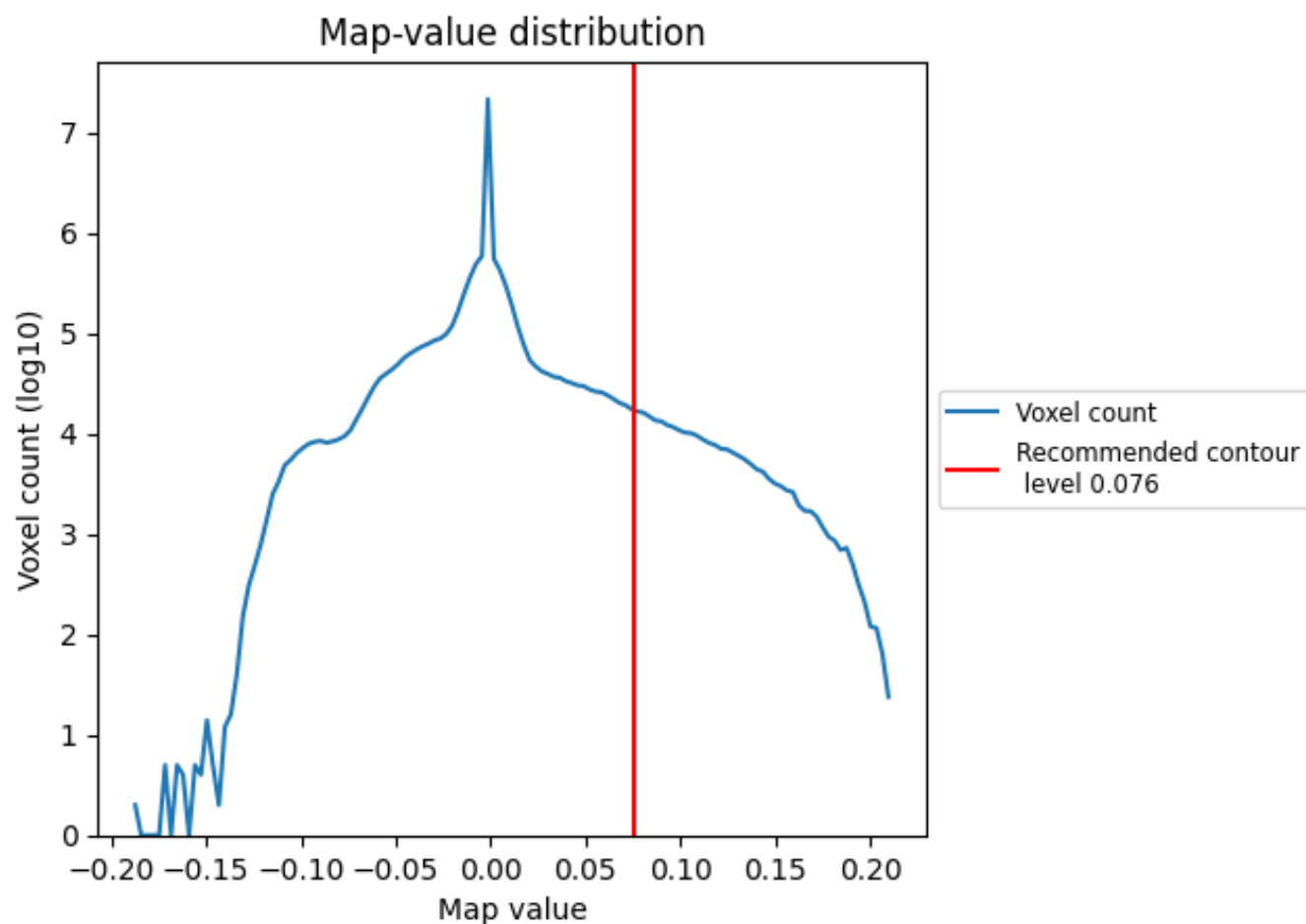
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

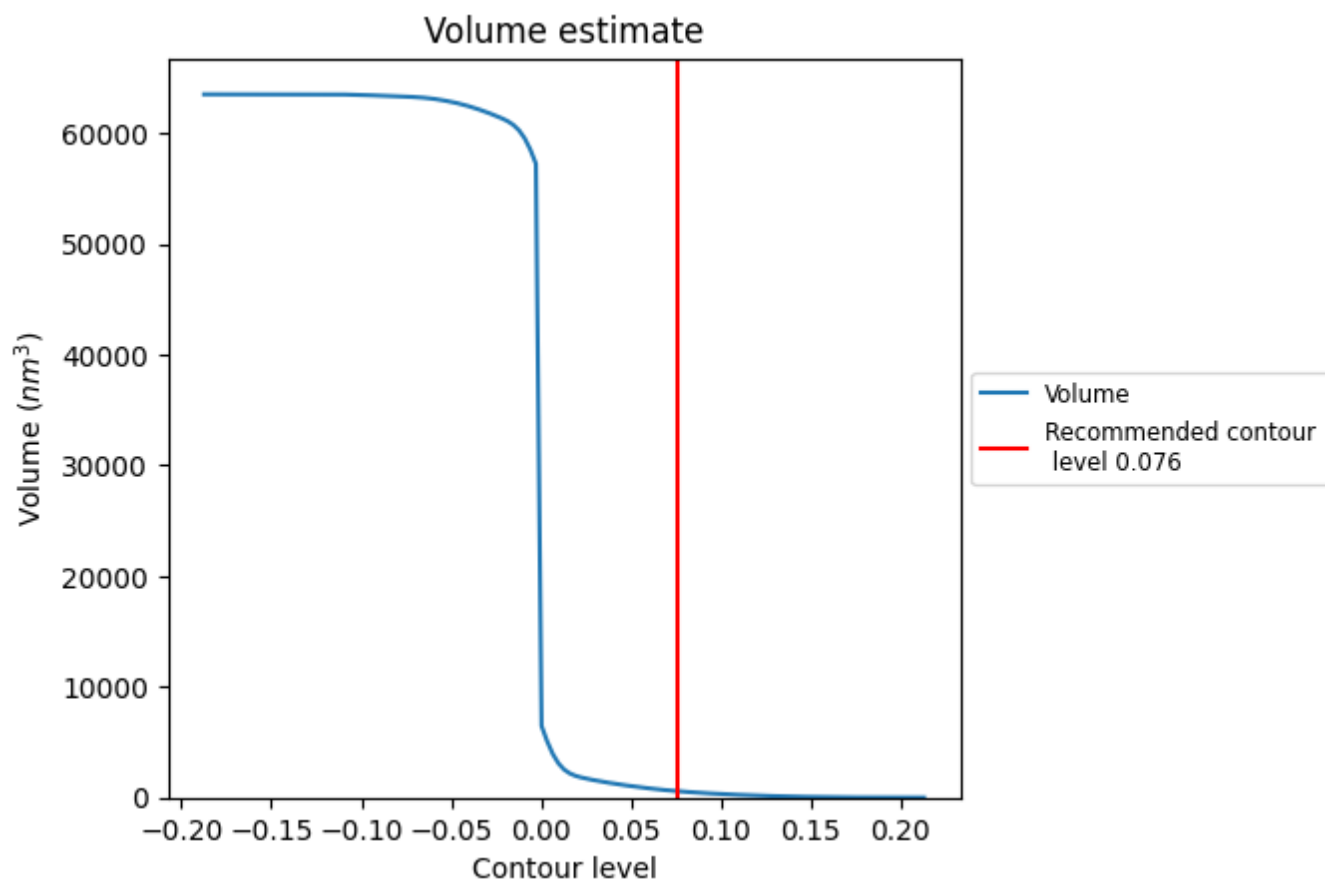
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

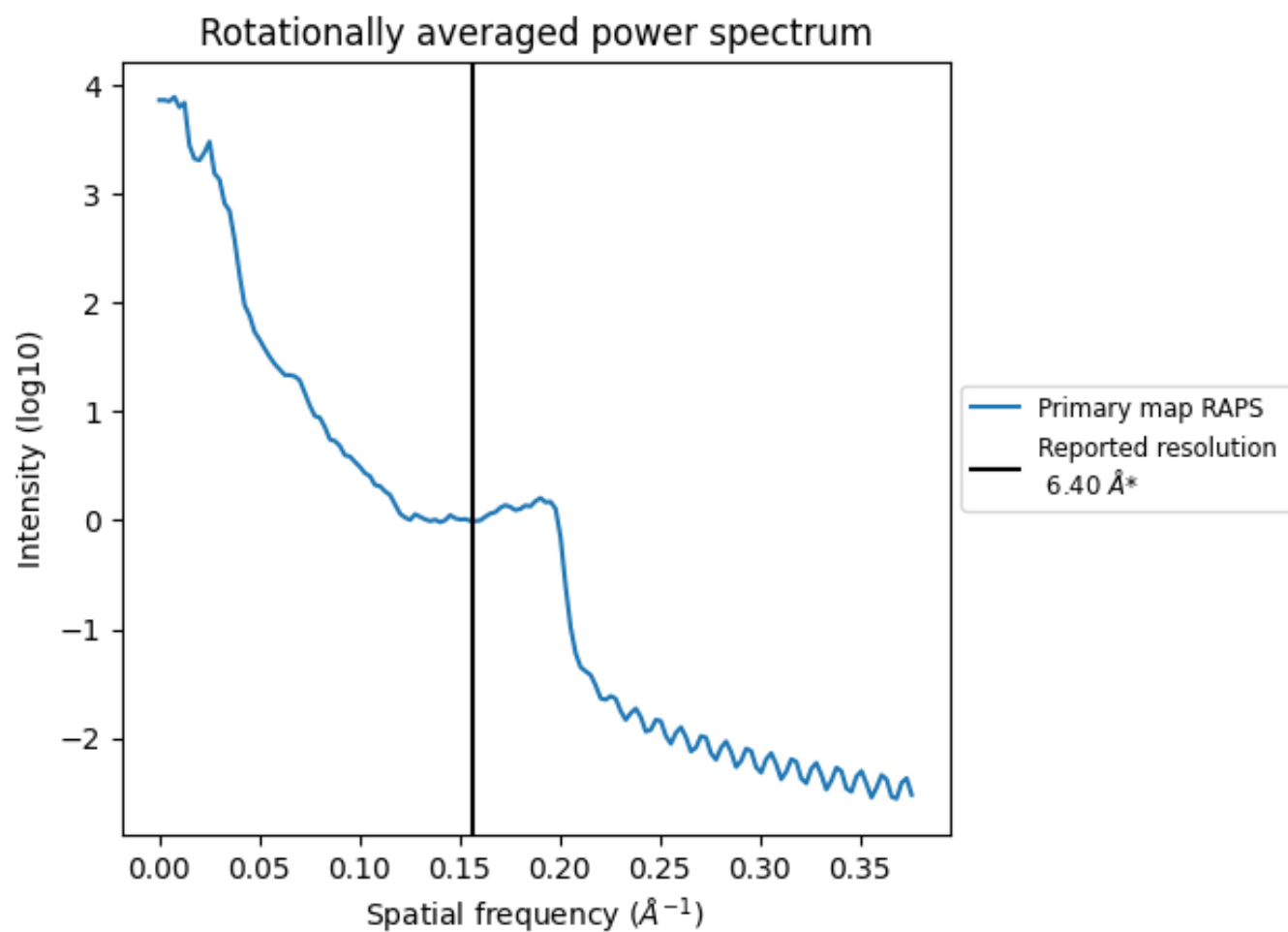
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 576 nm³; this corresponds to an approximate mass of 520 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 0.156 Å⁻¹

8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

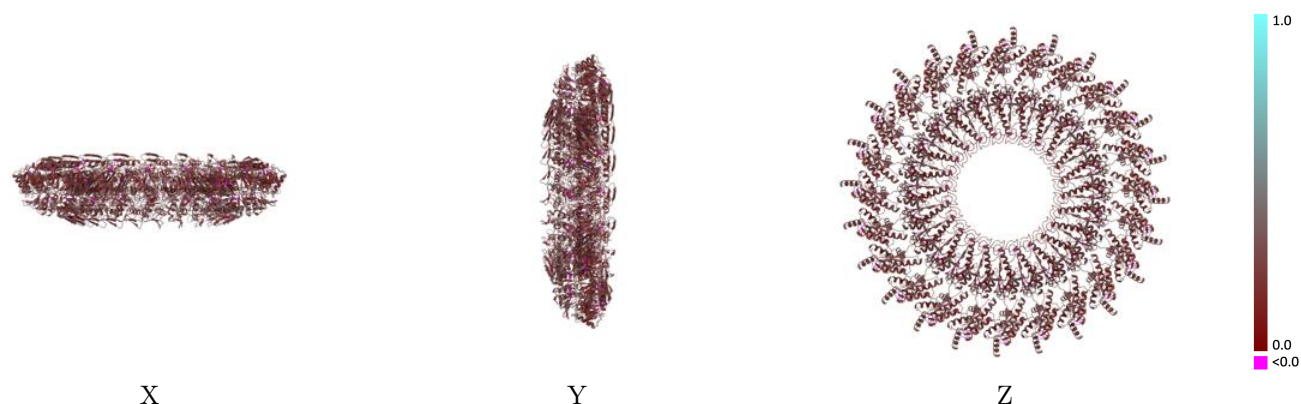
This section contains information regarding the fit between EMDB map EMD-1874 and PDB model 2Y9J. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



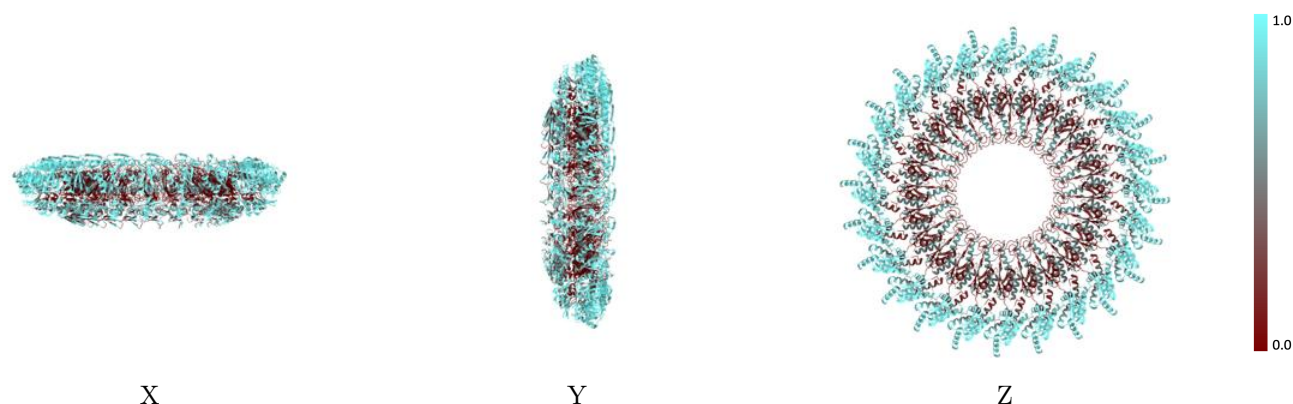
The images above show the 3D surface view of the map at the recommended contour level 0.076 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



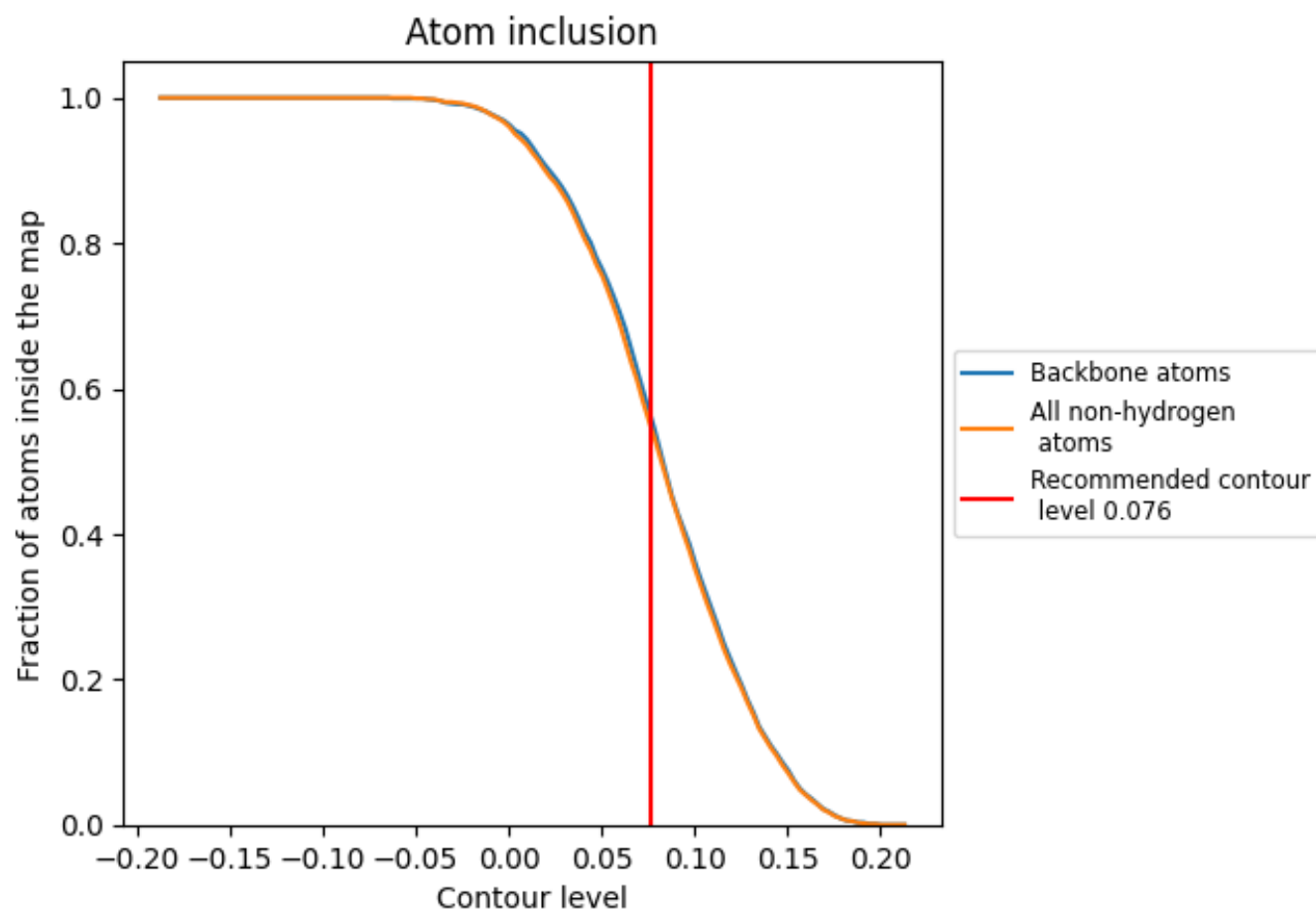
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.076).

9.4 Atom inclusion [i](#)



At the recommended contour level, 56% of all backbone atoms, 55% 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 (0.076) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5500	0.2670
A	0.7620	0.2780
B	0.7620	0.2790
C	0.7620	0.2800
D	0.7600	0.2810
E	0.7600	0.2790
F	0.7610	0.2830
G	0.7620	0.2820
H	0.7600	0.2800
I	0.7610	0.2820
J	0.7630	0.2800
K	0.7620	0.2810
L	0.7600	0.2830
M	0.7610	0.2790
N	0.7620	0.2810
O	0.7610	0.2790
P	0.7620	0.2790
Q	0.7620	0.2820
R	0.7620	0.2800
S	0.7610	0.2800
T	0.7600	0.2810
U	0.7600	0.2820
V	0.7600	0.2800
W	0.7620	0.2770
X	0.7600	0.2820
Y	0.3220	0.2510
Z	0.3220	0.2520
a	0.3220	0.2510
b	0.3200	0.2510
c	0.3250	0.2540
d	0.3220	0.2520
e	0.3260	0.2520
f	0.3230	0.2510
g	0.3200	0.2510
h	0.3220	0.2530

1.0

0.0

<0.0

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Chain	Atom inclusion	Q-score
i	 0.3230	 0.2530
j	 0.3220	 0.2530
k	 0.3230	 0.2510
l	 0.3200	 0.2500
m	 0.3230	 0.2520
n	 0.3250	 0.2530
o	 0.3220	 0.2520
p	 0.3200	 0.2510
q	 0.3230	 0.2540
r	 0.3230	 0.2520
s	 0.3180	 0.2510
t	 0.3250	 0.2530
u	 0.3200	 0.2520
v	 0.3160	 0.2490