



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:15 AM UTC

PDB ID : 3ZBI / pdb_00003zbi
EMDB ID : EMD-2233
Title : Fitting result in the O-layer of the subnanometer structure of the bacterial pKM101 type IV secretion system core complex digested with elastase
Authors : Rivera-Calzada, A.; Fronzes, R.; Savva, C.G.; Chandran, V.; Lian, P.W.; Laeremans, T.; Pardon, E.; Steyaert, J.; Remaut, H.; Waksman, G.; Orlova, E.V.
Deposited on : 2012-11-10
Resolution : 8.50 Å(reported)
Based on initial model : 3JQO

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

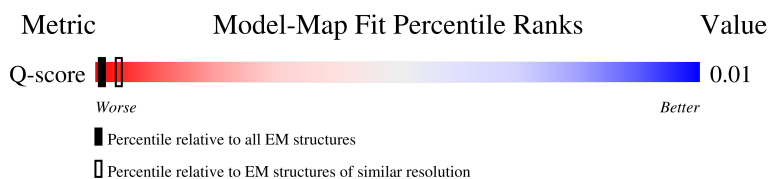
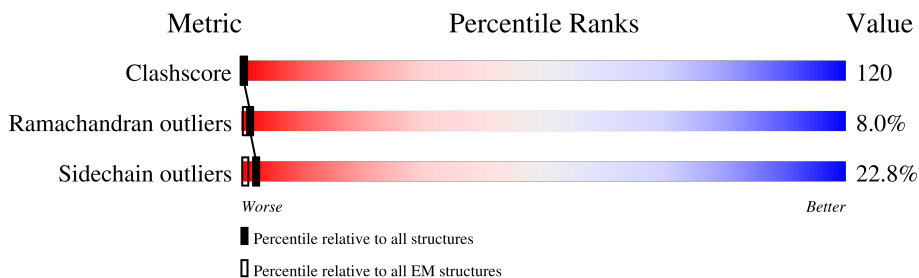
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.50 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	328 (8.00 - 9.00)

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	216	
1	D	216	
1	G	216	
1	J	216	

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Mol	Chain	Length	Quality of chain
1	M	216	
1	P	216	
1	S	216	
1	V	216	
1	Y	216	
1	b	216	
1	e	216	
1	h	216	
1	k	216	
1	n	216	
2	B	130	
2	E	130	
2	H	130	
2	K	130	
2	N	130	
2	Q	130	
2	T	130	
2	W	130	
2	Z	130	
2	c	130	
2	f	130	
2	i	130	
2	l	130	
2	o	130	
3	C	48	

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Mol	Chain	Length	Quality of chain
3	F	48	21% 21% 25% 10% • 40%
3	I	48	21% 19% 27% 10% • 40%
3	L	48	21% 21% 25% 10% • 40%
3	O	48	21% 21% 25% 10% • 40%
3	R	48	21% 21% 25% 10% • 40%
3	U	48	21% 19% 27% 10% • 40%
3	X	48	23% 21% 25% 10% • 40%
3	a	48	21% 21% 25% 10% • 40%
3	d	48	21% 21% 25% 10% • 40%
3	g	48	21% 21% 25% 10% • 40%
3	j	48	21% 21% 25% 10% • 40%
3	m	48	21% 21% 25% 10% • 40%
3	p	48	21% 21% 25% 10% • 40%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 37884 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 TRAF PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	D	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	G	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	J	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	M	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	P	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	S	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	V	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	Y	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	b	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	e	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	h	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	k	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		
1	n	197	Total	C	N	O	S	0	1
			1459	903	256	293	7		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	846	ARG	ALA	conflict	UNP Q46705
D	846	ARG	ALA	conflict	UNP Q46705

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Chain	Residue	Modelled	Actual	Comment	Reference
G	846	ARG	ALA	conflict	UNP Q46705
J	846	ARG	ALA	conflict	UNP Q46705
M	846	ARG	ALA	conflict	UNP Q46705
P	846	ARG	ALA	conflict	UNP Q46705
S	846	ARG	ALA	conflict	UNP Q46705
V	846	ARG	ALA	conflict	UNP Q46705
Y	846	ARG	ALA	conflict	UNP Q46705
b	846	ARG	ALA	conflict	UNP Q46705
e	846	ARG	ALA	conflict	UNP Q46705
h	846	ARG	ALA	conflict	UNP Q46705
k	846	ARG	ALA	conflict	UNP Q46705
n	846	ARG	ALA	conflict	UNP Q46705

- Molecule 2 is a protein called TRAO PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	E	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	H	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	K	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	N	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	Q	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	T	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	W	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	Z	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	c	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	f	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	i	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		
2	l	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	o	130	Total	C	N	O	S	0	0
			1034	648	193	190	3		

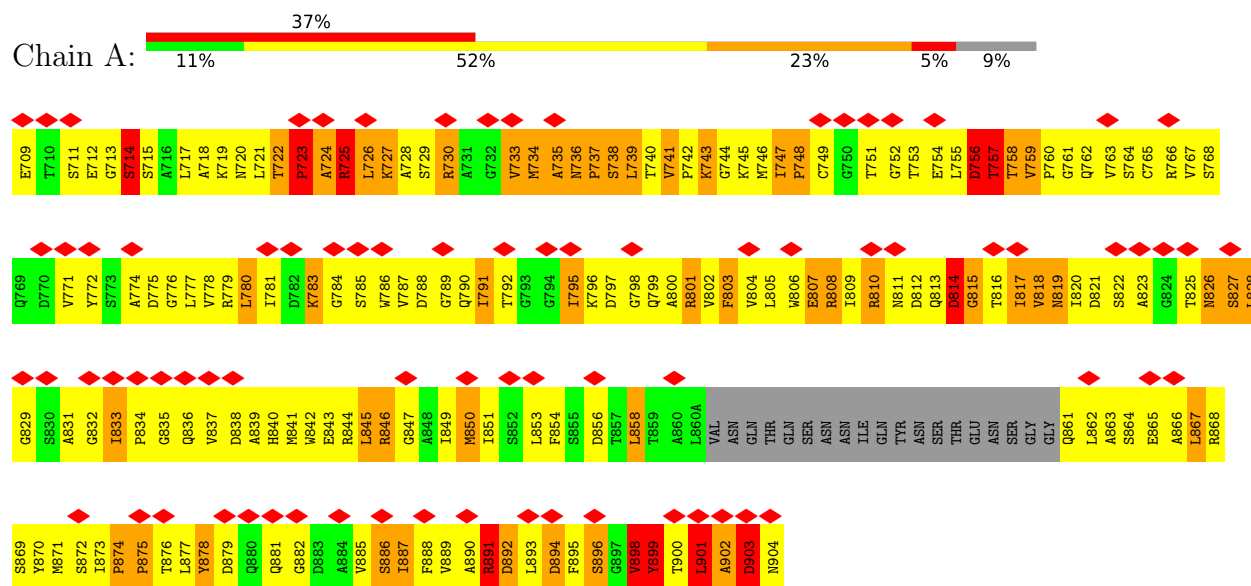
- Molecule 3 is a protein called TRAN PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	F	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	I	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	L	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	O	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	R	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	U	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	X	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	a	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	d	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	g	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	j	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	m	29	Total	C	N	O	S	0	1
			213	132	37	43	1		
3	p	29	Total	C	N	O	S	0	1
			213	132	37	43	1		

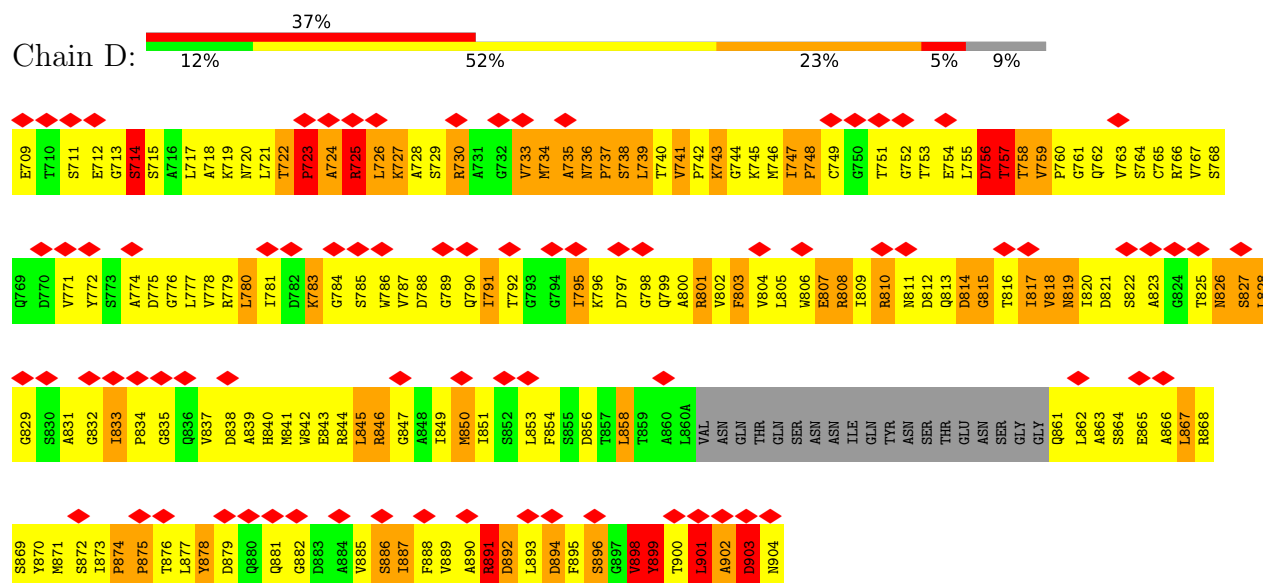
3 Residue-property plots

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.

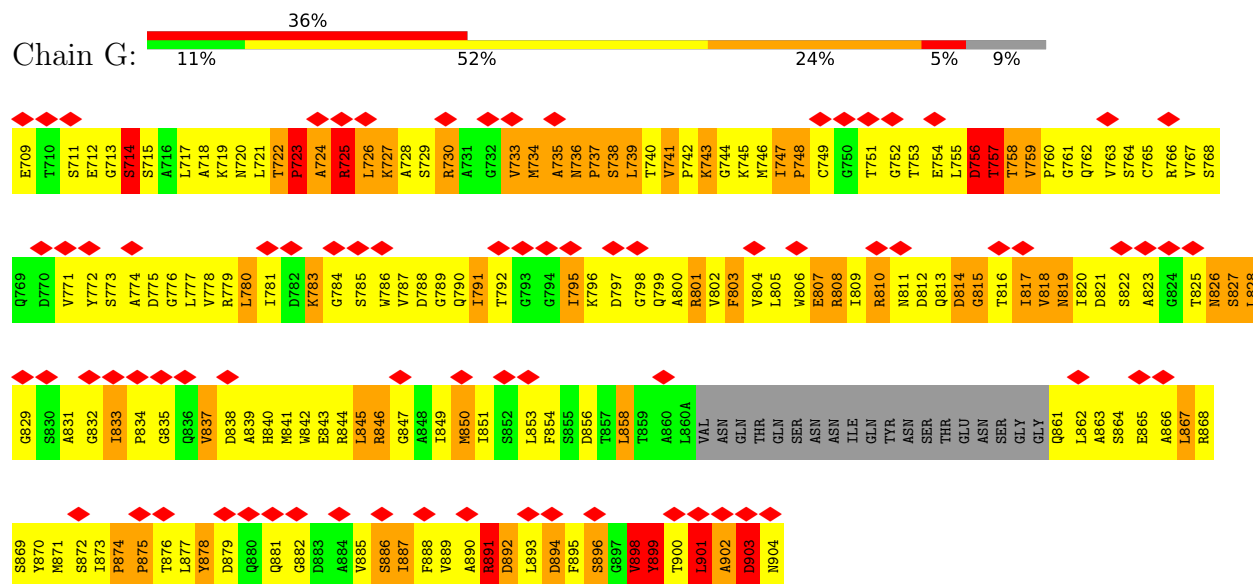
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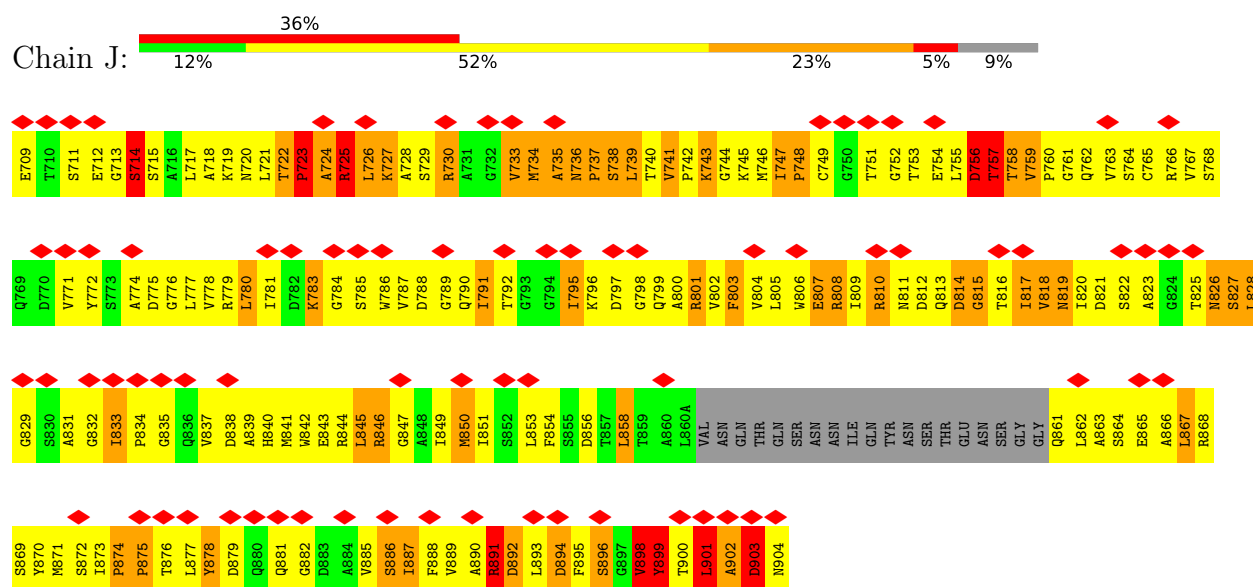
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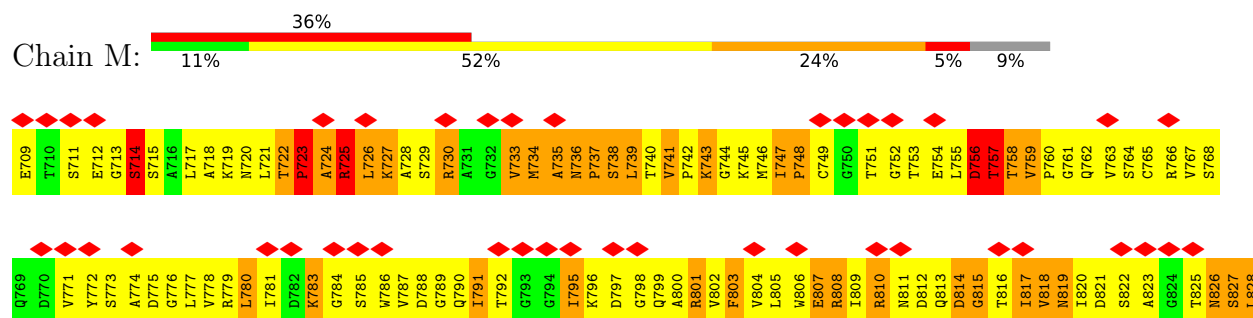
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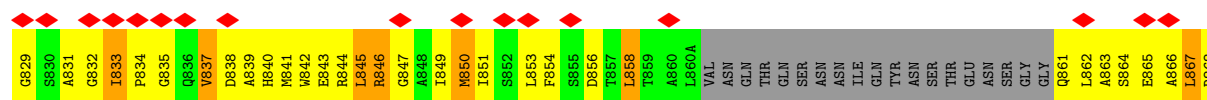


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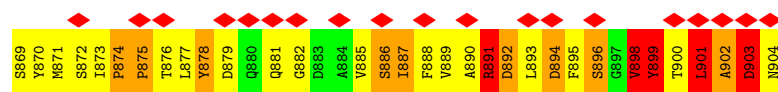
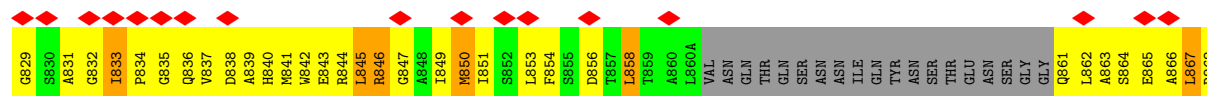
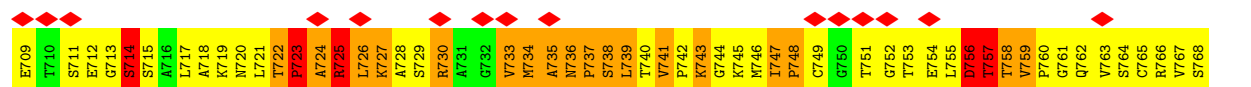
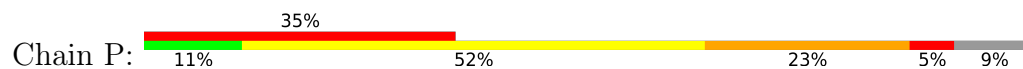


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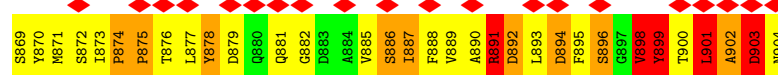
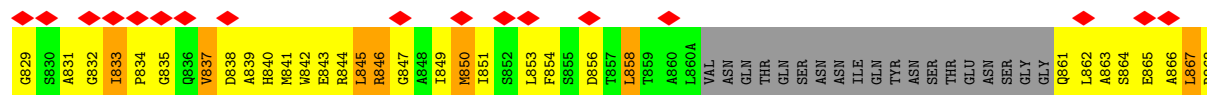
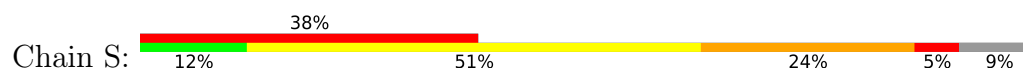




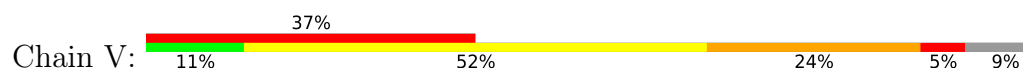
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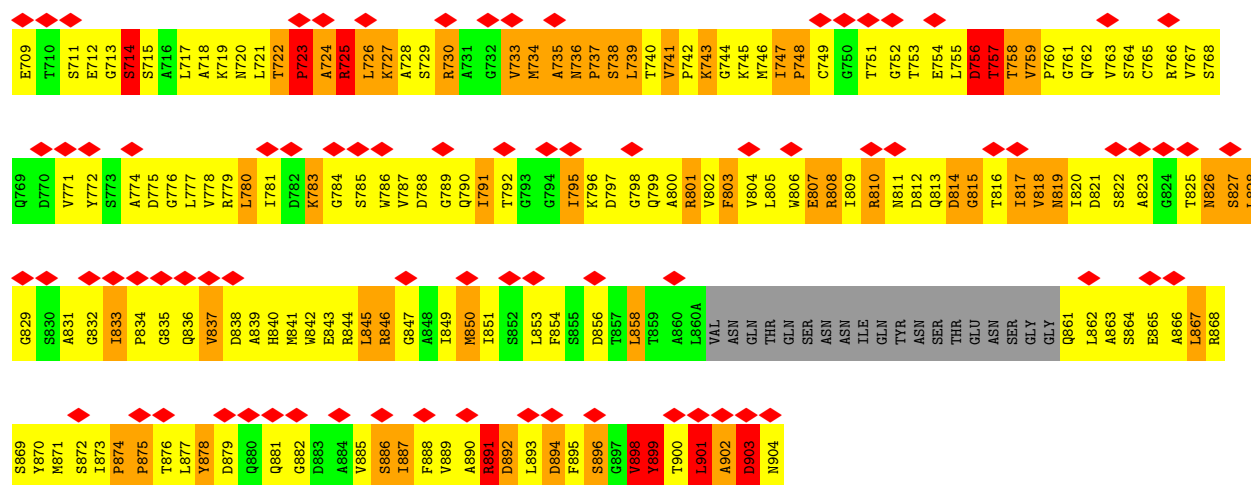


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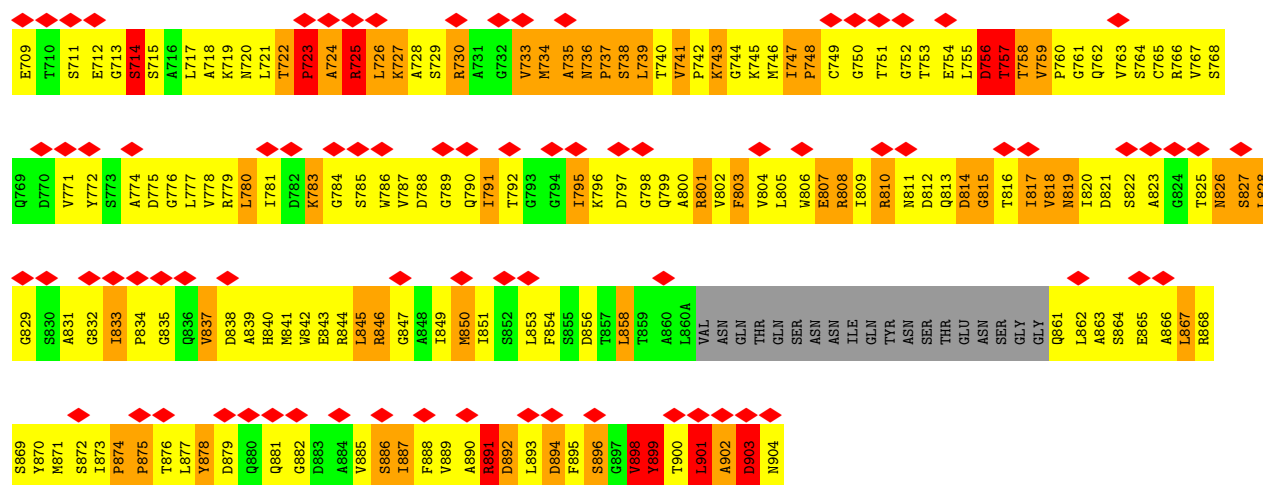
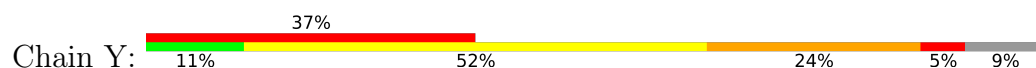


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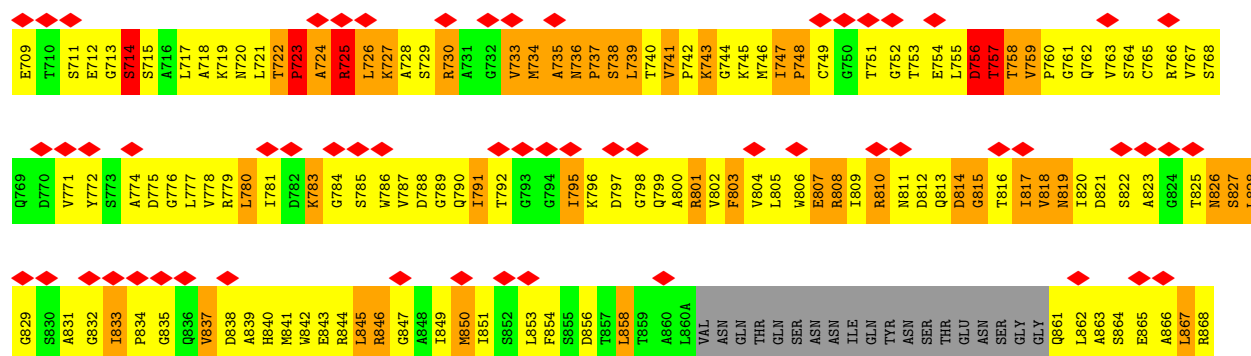
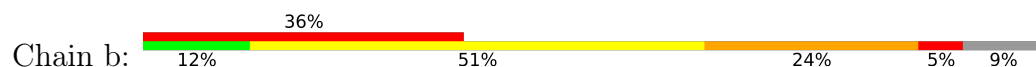


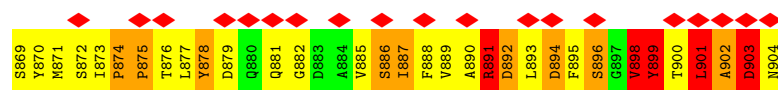


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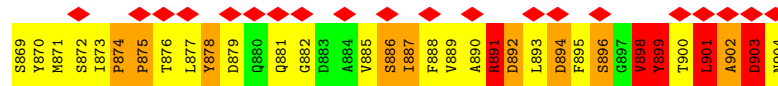
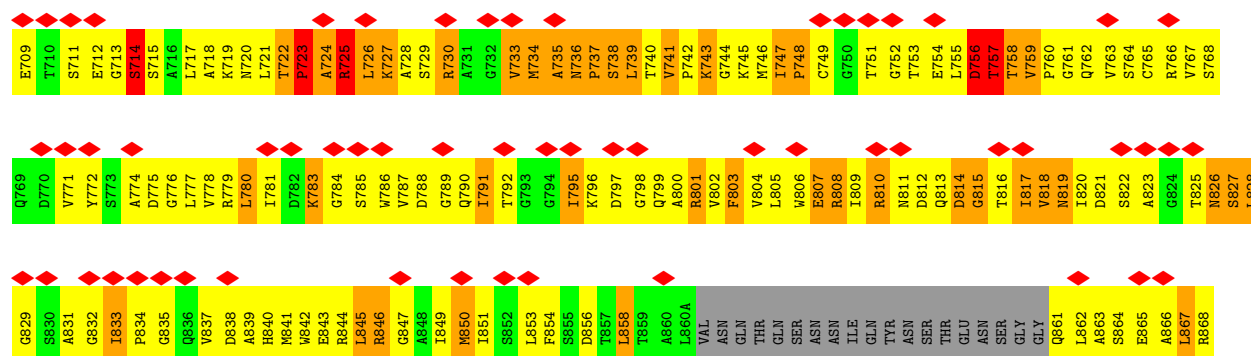
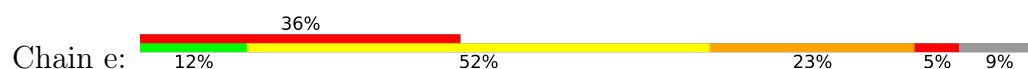


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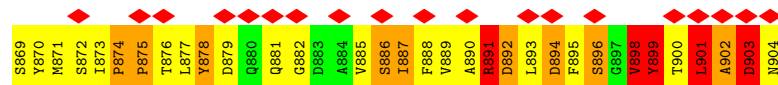
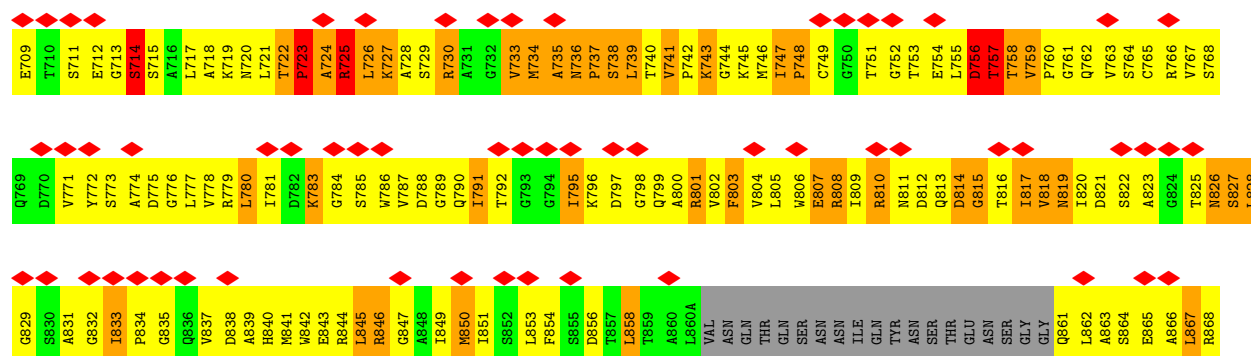
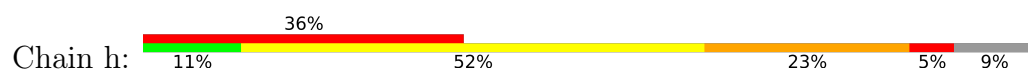




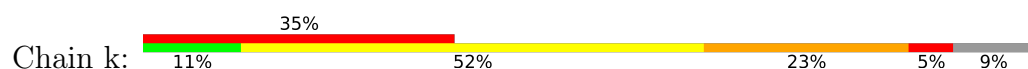
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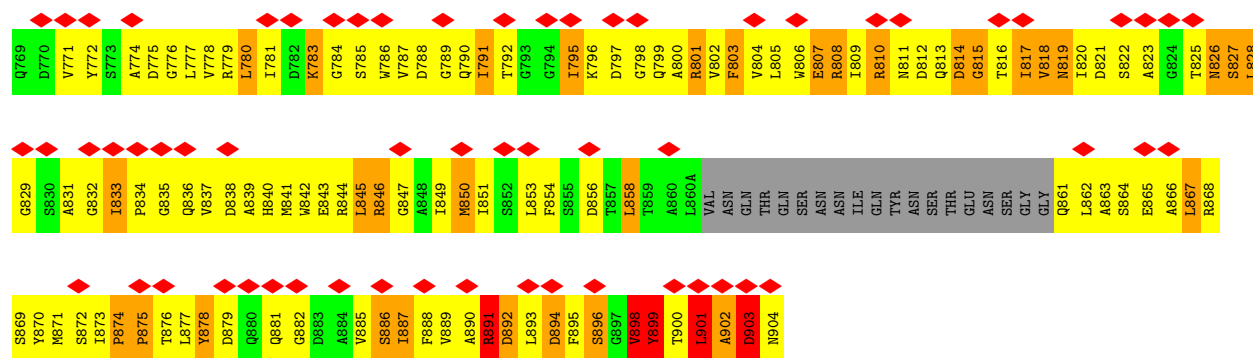


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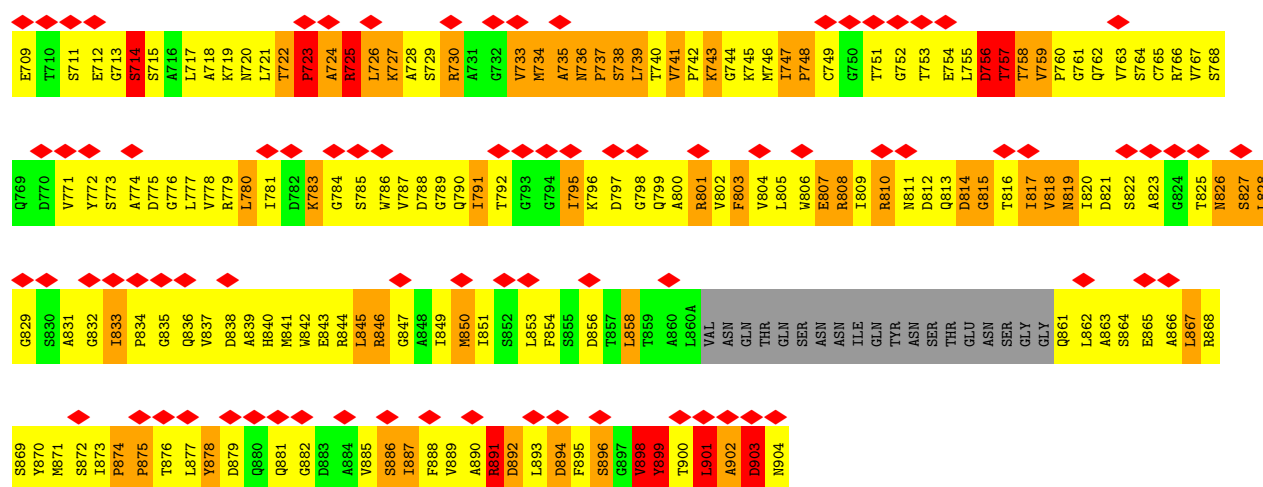
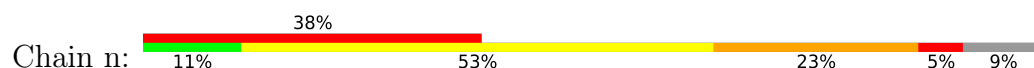


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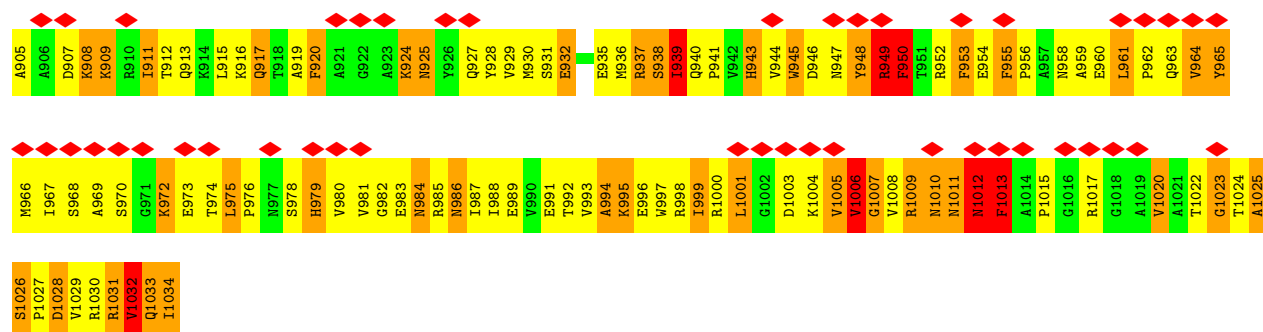
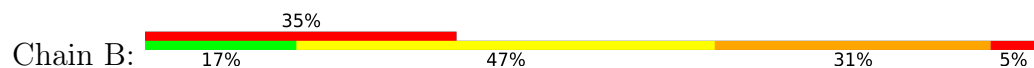




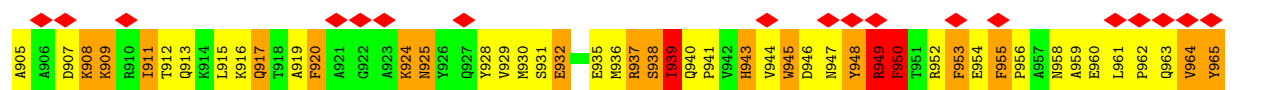
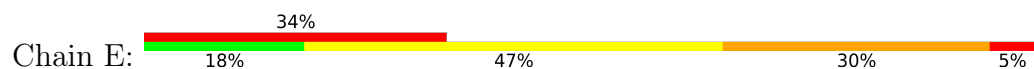
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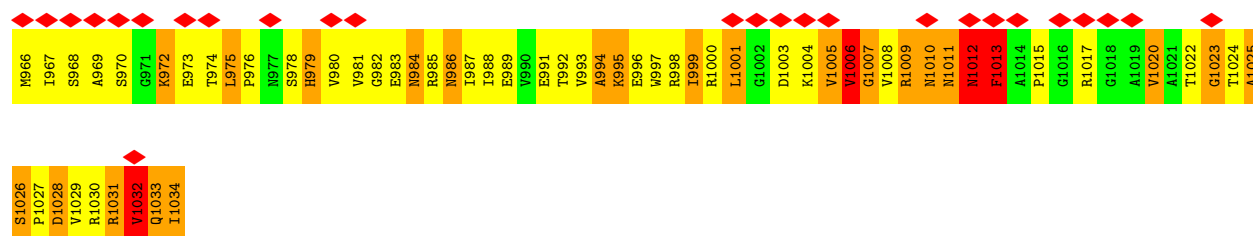


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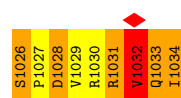
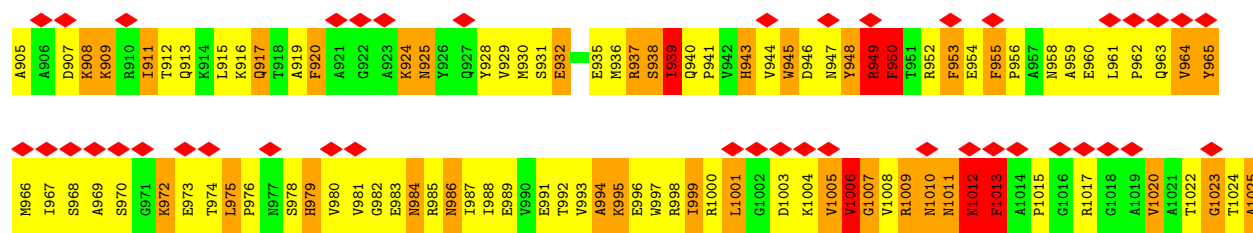
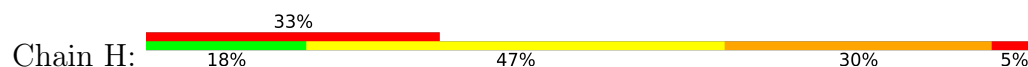


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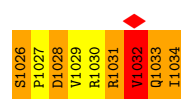
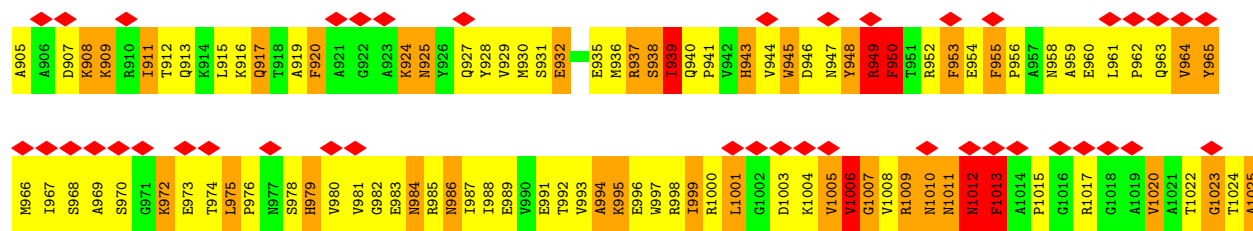
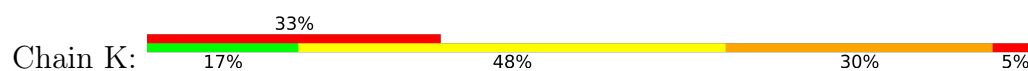




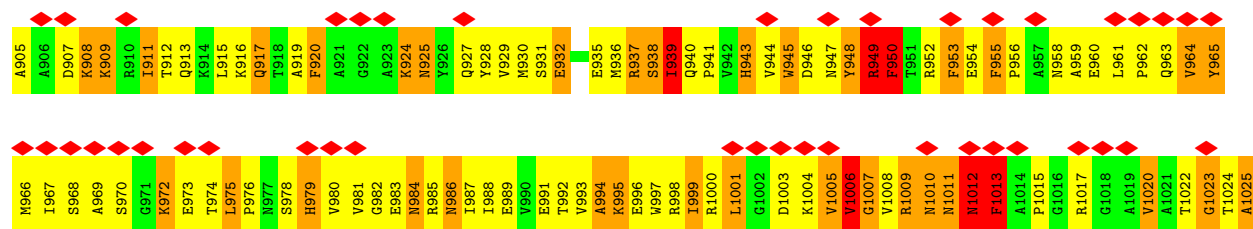
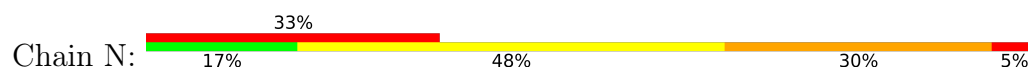
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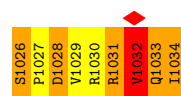


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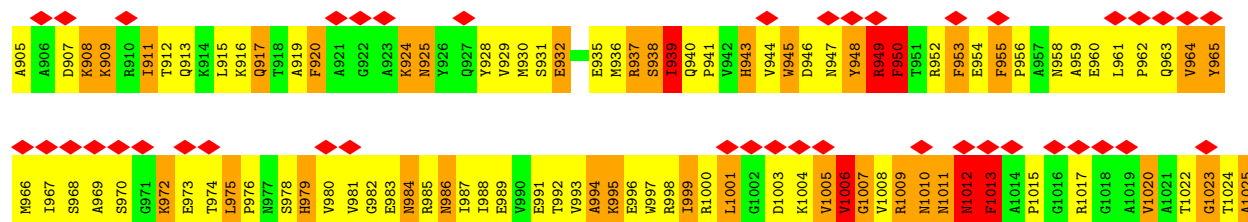
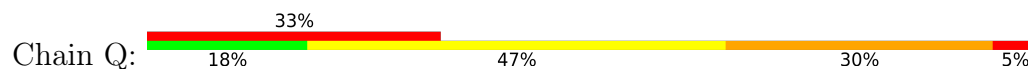


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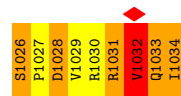
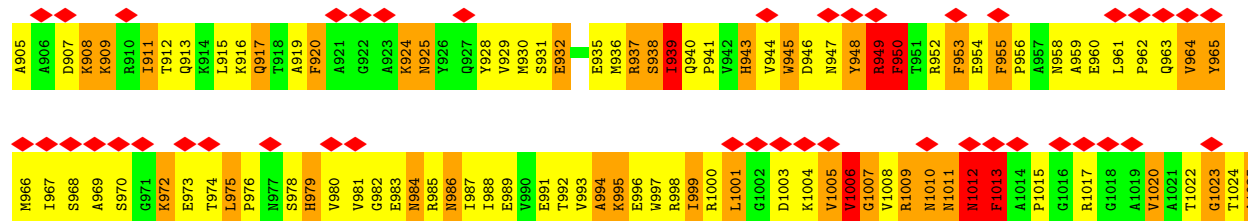
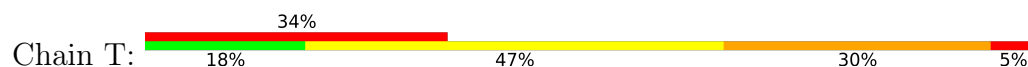




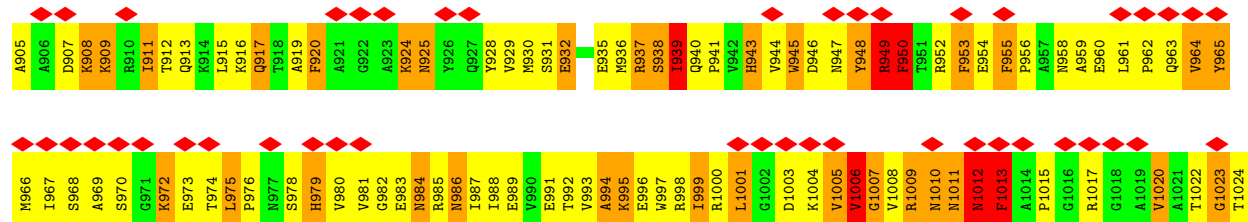
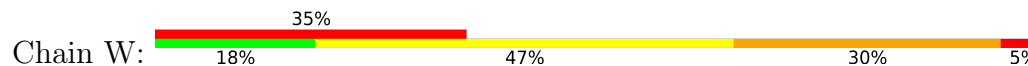
• Molecule 2: TRAO PROTEIN



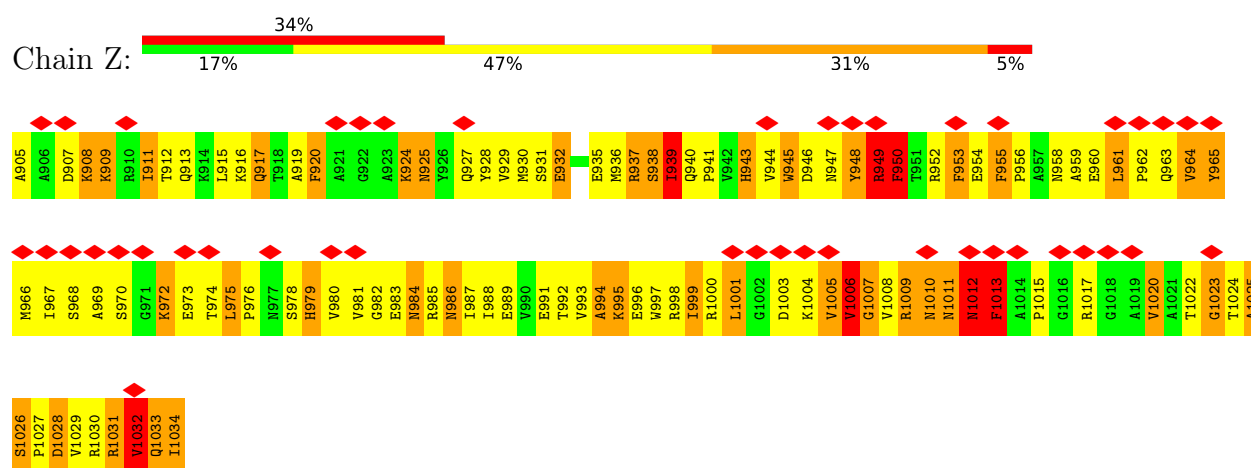
• Molecule 2: TRAO PROTEIN



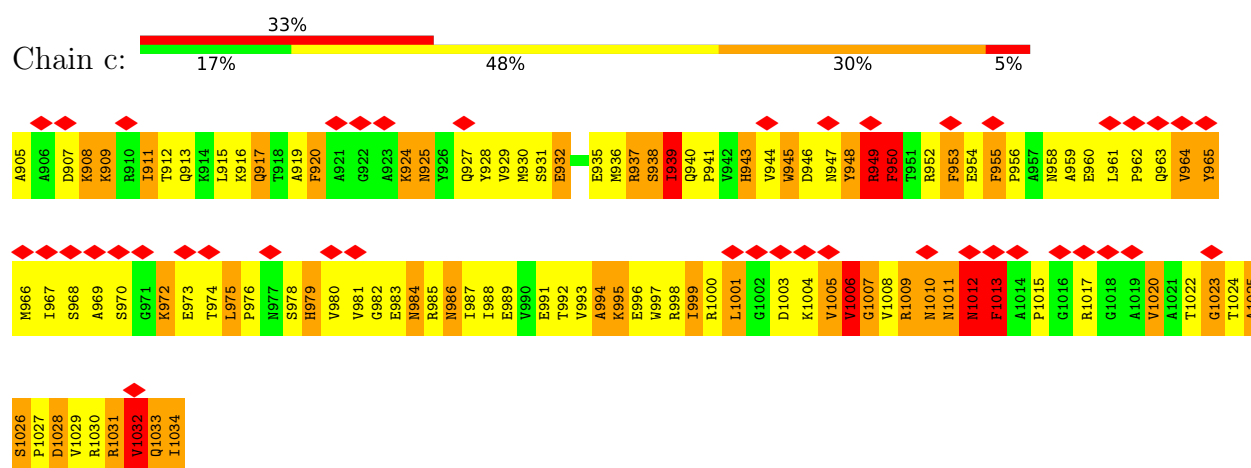
• Molecule 2: TRAO PROTEIN



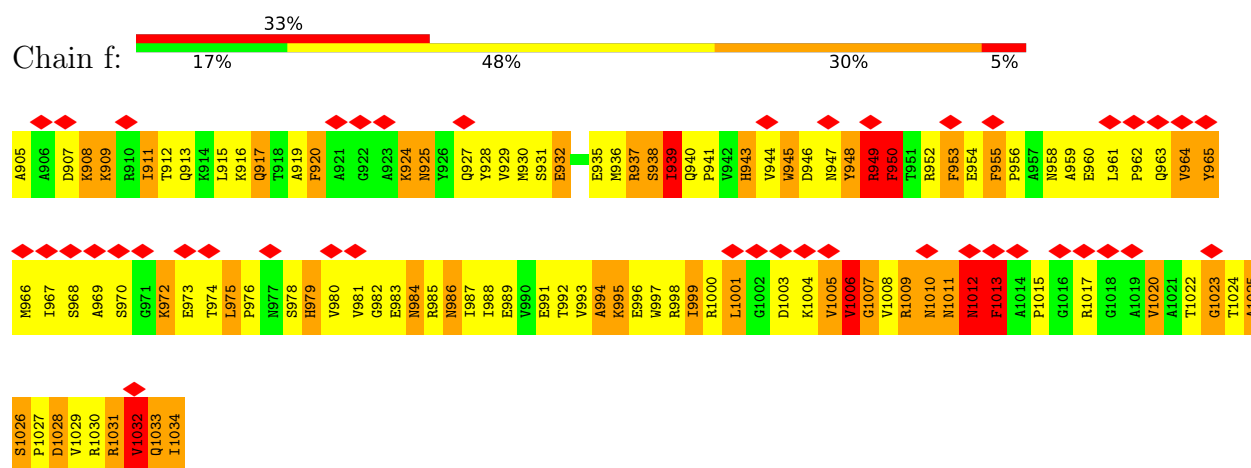
• Molecule 2: TRAO PROTEIN



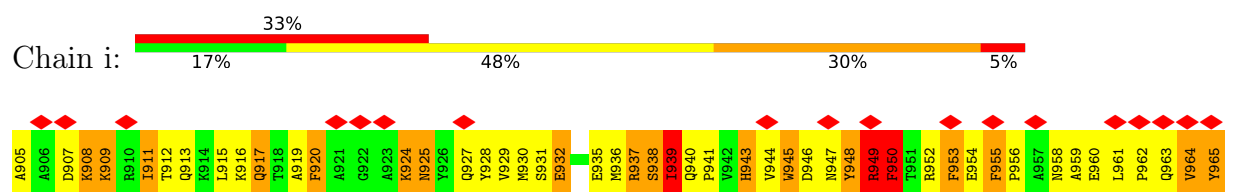
• Molecule 2: TRAO PROTEIN

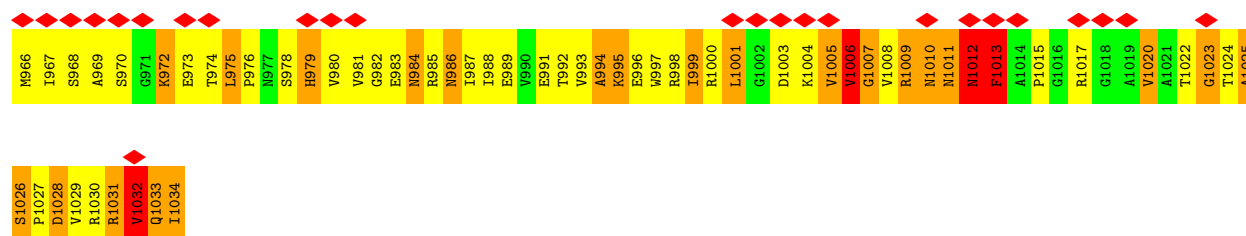


• Molecule 2: TRAO PROTEIN

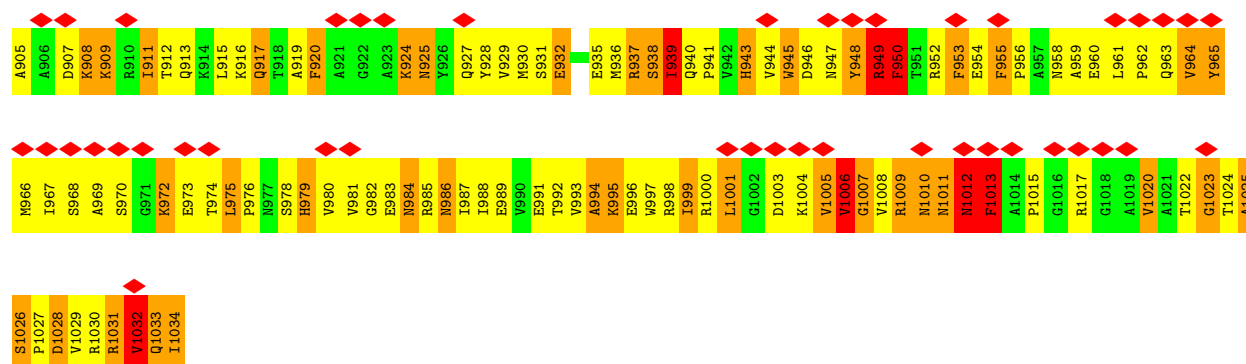
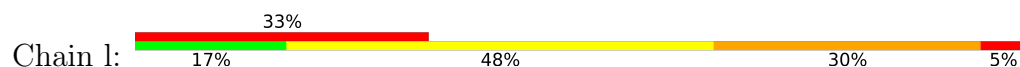


• Molecule 2: TRAO PROTEIN

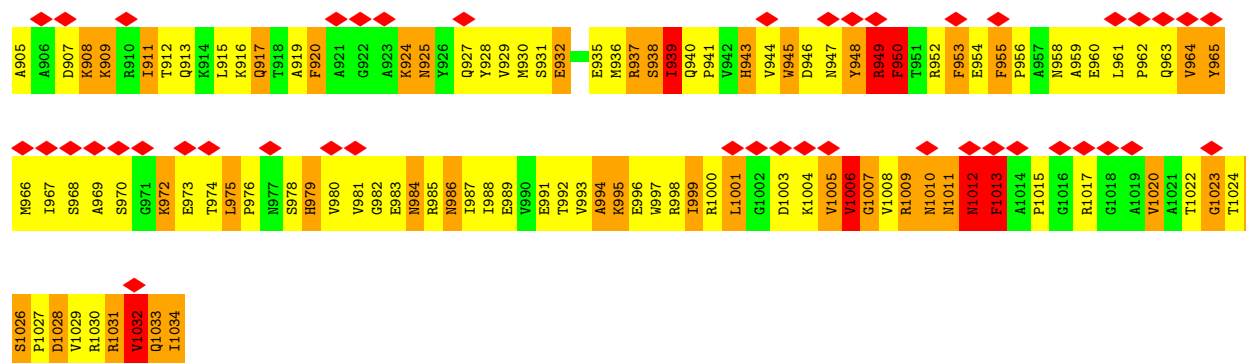
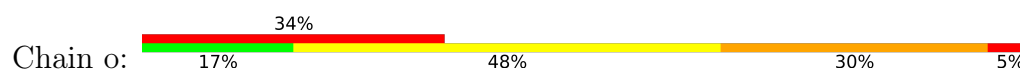




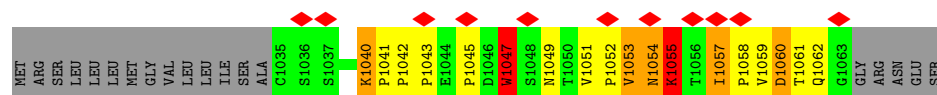
• Molecule 2: TRAO PROTEIN



• Molecule 2: TRAO PROTEIN



• Molecule 3: TRAN PROTEIN

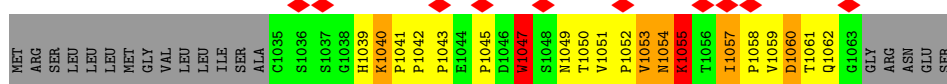


• Molecule 3: TRAN PROTEIN

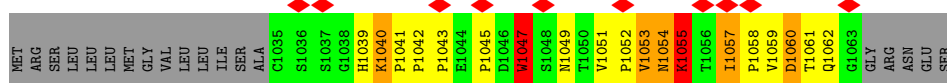




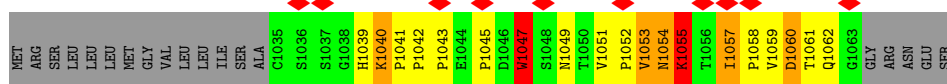
• Molecule 3: TRAN PROTEIN



• Molecule 3: TRAN PROTEIN



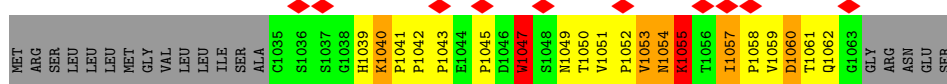
• Molecule 3: TRAN PROTEIN



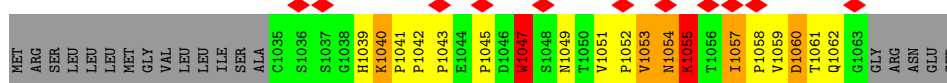
• Molecule 3: TRAN PROTEIN



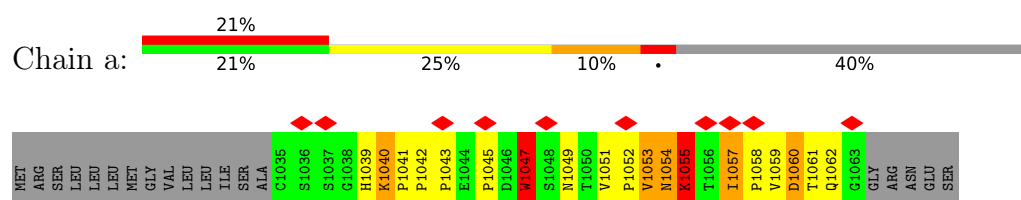
• Molecule 3: TRAN PROTEIN



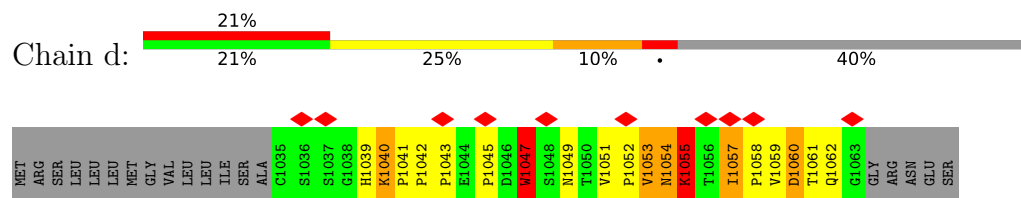
• Molecule 3: TRAN PROTEIN



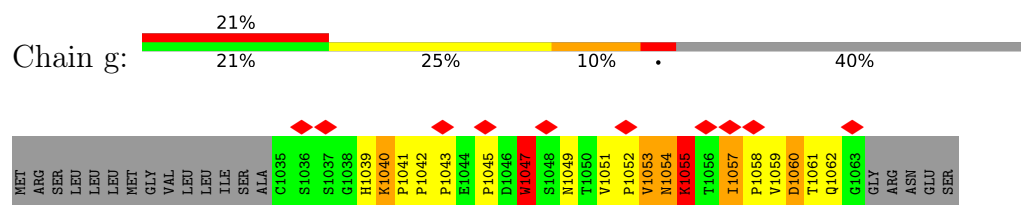
• Molecule 3: TRAN PROTEIN



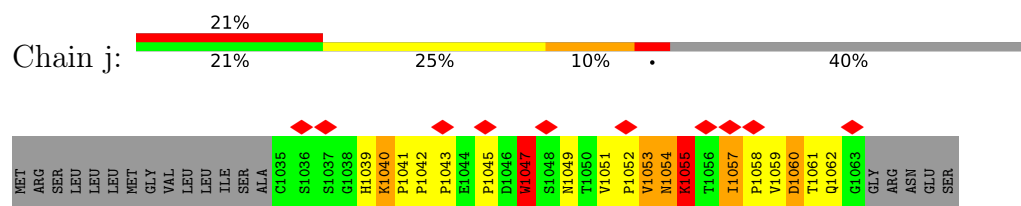
● Molecule 3: TRAN PROTEIN



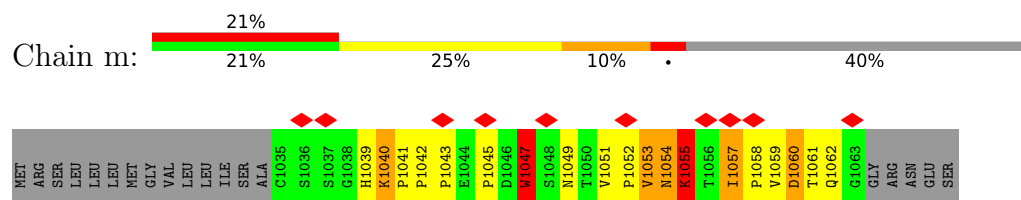
● Molecule 3: TRAN PROTEIN



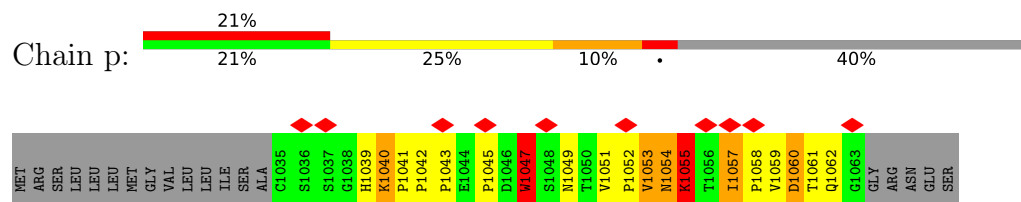
● Molecule 3: TRAN PROTEIN



● Molecule 3: TRAN PROTEIN



● Molecule 3: TRAN PROTEIN



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C14	Depositor
Number of particles used	5430	Depositor
Resolution determination method	Not provided	
CTF correction method	PHASE FLIPPING, EACH CCD IMAGE	Depositor
Microscope	FEI TECNAI 12	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	68100	Depositor
Image detector	GENERIC GATAN	Depositor
Maximum map value	5.163	Depositor
Minimum map value	-3.082	Depositor
Average map value	0.019	Depositor
Map value standard deviation	0.223	Depositor
Recommended contour level	0.23	Depositor
Map size ($\text{\AA}$)	332.8, 332.8, 332.8	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.08, 2.08, 2.08	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	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	D	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	G	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	J	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	M	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	P	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	S	1.51	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	V	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	Y	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	b	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	e	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	h	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	k	1.50	1/1480 (0.1%)	1.85	38/2007 (1.9%)
1	n	1.51	1/1480 (0.1%)	1.85	38/2007 (1.9%)
2	B	1.54	0/1055	1.79	25/1426 (1.8%)
2	E	1.54	1/1055 (0.1%)	1.79	25/1426 (1.8%)
2	H	1.54	0/1055	1.79	25/1426 (1.8%)
2	K	1.54	1/1055 (0.1%)	1.79	25/1426 (1.8%)
2	N	1.54	0/1055	1.79	25/1426 (1.8%)
2	Q	1.54	1/1055 (0.1%)	1.79	25/1426 (1.8%)
2	T	1.54	1/1055 (0.1%)	1.79	24/1426 (1.7%)
2	W	1.54	0/1055	1.79	25/1426 (1.8%)
2	Z	1.54	1/1055 (0.1%)	1.79	25/1426 (1.8%)
2	c	1.54	0/1055	1.79	25/1426 (1.8%)
2	f	1.54	1/1055 (0.1%)	1.79	25/1426 (1.8%)
2	i	1.54	0/1055	1.79	25/1426 (1.8%)
2	l	1.54	1/1055 (0.1%)	1.79	25/1426 (1.8%)
2	o	1.54	1/1055 (0.1%)	1.79	24/1426 (1.7%)
3	C	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	F	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	I	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	L	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	O	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	R	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	U	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	X	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	a	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	d	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	g	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	j	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	m	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
3	p	1.55	1/221 (0.5%)	1.76	3/307 (1.0%)
All	All	1.52	36/38584 (0.1%)	1.82	922/52360 (1.8%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	D	0	5
1	G	0	5
1	J	0	5
1	M	0	5
1	P	0	5
1	S	0	5
1	V	0	5
1	Y	0	5
1	b	0	5
1	e	0	5
1	h	0	5
1	k	0	5
1	n	0	5
2	B	0	1
2	E	0	1
2	H	0	1
2	K	0	1
2	N	0	1
2	Q	0	1
2	T	0	1
2	W	0	1
2	Z	0	1
2	c	0	1
2	f	0	1
2	i	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	l	0	1
2	o	0	1
All	All	0	84

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	R	1055	LYS	CA-C	-5.61	1.49	1.52
3	m	1055	LYS	CA-C	-5.61	1.49	1.52
3	F	1055	LYS	CA-C	-5.60	1.49	1.52
3	a	1055	LYS	CA-C	-5.60	1.49	1.52
3	I	1055	LYS	CA-C	-5.54	1.49	1.52

The worst 5 of 922 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	903	ASP	CA-CB-CG	10.21	122.81	112.60
1	e	903	ASP	CA-CB-CG	10.21	122.81	112.60
1	D	903	ASP	CA-CB-CG	10.21	122.81	112.60
1	Y	903	ASP	CA-CB-CG	10.21	122.81	112.60
1	G	903	ASP	CA-CB-CG	10.20	122.80	112.60

There are no chirality outliers.

5 of 84 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	725	ARG	Peptide
1	A	757	THR	Peptide
1	A	761	GLY	Peptide
1	A	901	LEU	Peptide
1	A	903	ASP	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	1459	0	1440	613	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1459	0	1440	606	0
1	G	1459	0	1440	608	0
1	J	1459	0	1440	606	0
1	M	1459	0	1440	607	0
1	P	1459	0	1440	611	0
1	S	1459	0	1440	608	0
1	V	1459	0	1440	604	0
1	Y	1459	0	1440	612	0
1	b	1459	0	1440	608	0
1	e	1459	0	1440	615	0
1	h	1459	0	1440	610	0
1	k	1459	0	1440	611	0
1	n	1459	0	1440	605	0
2	B	1034	0	1032	222	0
2	E	1034	0	1032	222	0
2	H	1034	0	1032	216	0
2	K	1034	0	1032	218	0
2	N	1034	0	1032	217	0
2	Q	1034	0	1032	217	0
2	T	1034	0	1032	218	0
2	W	1034	0	1032	221	0
2	Z	1034	0	1032	228	0
2	c	1034	0	1032	223	0
2	f	1034	0	1032	224	0
2	i	1034	0	1032	221	0
2	l	1034	0	1032	227	0
2	o	1034	0	1032	223	0
3	C	213	0	200	38	0
3	F	213	0	200	39	0
3	I	213	0	200	40	0
3	L	213	0	200	38	0
3	O	213	0	200	36	0
3	R	213	0	200	39	0
3	U	213	0	200	41	0
3	X	213	0	200	40	0
3	a	213	0	200	38	0
3	d	213	0	200	37	0
3	g	213	0	200	37	0
3	j	213	0	200	36	0
3	m	213	0	200	40	0
3	p	213	0	200	39	0
All	All	37884	0	37408	9029	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 120.

The worst 5 of 9029 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:P:725:ARG:CZ	1:V:808:ARG:HG3	1.33	1.48
1:Y:725:ARG:NH1	1:e:808:ARG:CG	1.77	1.47
1:e:725:ARG:NH1	1:k:808:ARG:CG	1.77	1.47
1:S:725:ARG:CZ	1:Y:808:ARG:HG3	1.33	1.46
1:S:725:ARG:NH1	1:Y:808:ARG:CG	1.77	1.46

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	D	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	G	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	J	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	M	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	P	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	S	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	V	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	Y	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	b	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	e	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	h	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	k	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
1	n	193/216 (89%)	147 (76%)	33 (17%)	13 (7%)	1	12
2	B	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	E	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	H	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	K	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	N	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	Q	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	T	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	W	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	Z	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	c	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	f	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	i	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	l	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
2	o	128/130 (98%)	88 (69%)	26 (20%)	14 (11%)	0	6
3	C	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	F	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	I	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	L	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	O	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	R	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	U	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	X	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	a	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	d	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	g	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	j	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	m	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
3	p	27/48 (56%)	20 (74%)	6 (22%)	1 (4%)	2	20
All	All	4872/5516 (88%)	3570 (73%)	910 (19%)	392 (8%)	1	9

5 of 392 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	726	LEU
1	A	814	ASP
1	A	878	TYR
1	A	899	TYR
1	A	902	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	D	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	G	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	J	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	M	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	P	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	S	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	V	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	Y	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	b	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	e	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	h	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	k	158/176 (90%)	124 (78%)	34 (22%)	1	6
1	n	158/176 (90%)	124 (78%)	34 (22%)	1	6
2	B	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	E	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	H	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	K	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	N	109/109 (100%)	81 (74%)	28 (26%)	0	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Q	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	T	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	W	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	Z	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	c	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	f	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	i	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	l	109/109 (100%)	81 (74%)	28 (26%)	0	3
2	o	109/109 (100%)	81 (74%)	28 (26%)	0	3
3	C	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	F	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	I	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	L	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	O	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	R	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	U	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	X	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	a	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	d	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	g	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	j	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	m	27/43 (63%)	22 (82%)	5 (18%)	1	8
3	p	27/43 (63%)	22 (82%)	5 (18%)	1	8
All	All	4116/4592 (90%)	3178 (77%)	938 (23%)	2	6

5 of 938 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	T	1032	VAL
1	n	801	ARG
2	Z	913	GLN
1	n	733	VAL
3	j	1040	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 199 such sidechains are listed below:

Mol	Chain	Res	Type
1	Y	813	GLN
1	e	813	GLN
2	Z	913	GLN
1	b	826	ASN
2	f	947	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2233. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 80



Y Index: 80



Z Index: 80

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: 97



Y Index: 103

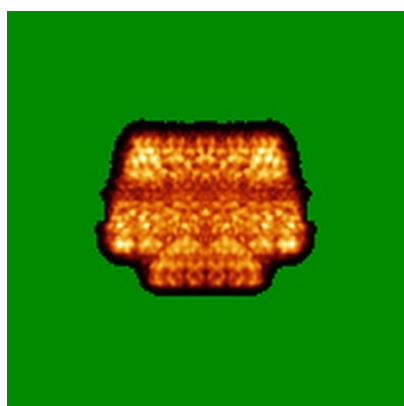


Z Index: 66

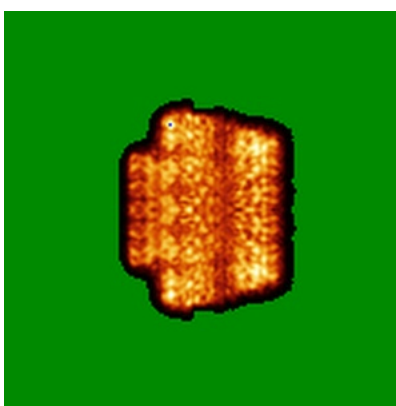
The images above show the largest variance slices of the map in three orthogonal directions.

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

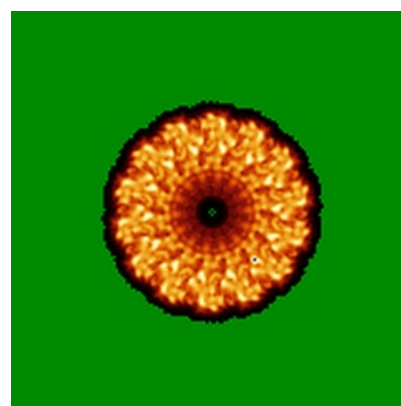
6.4.1 Primary map



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

This section was not generated.

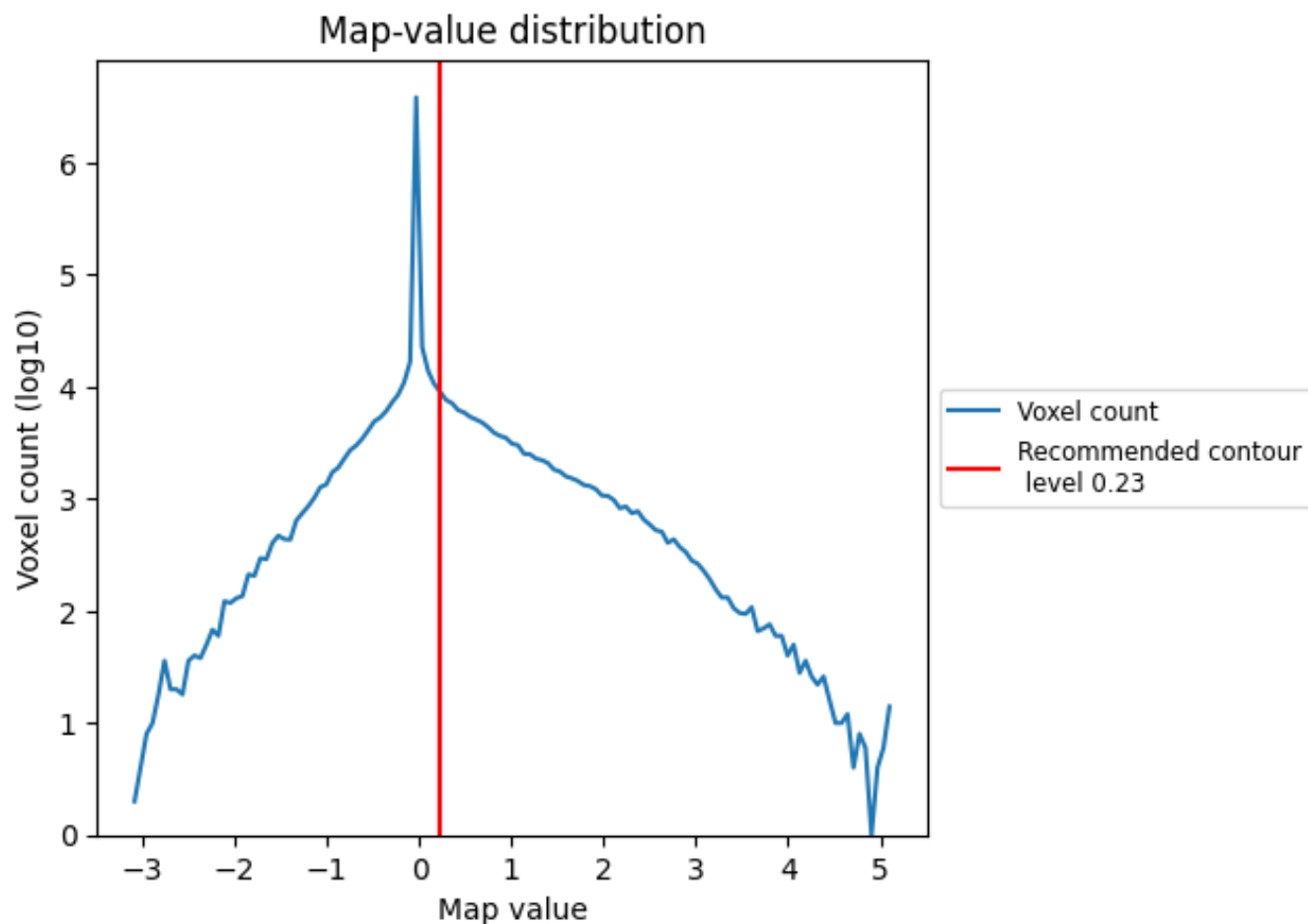
6.6 Mask visualisation

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

7 Map analysis [i](#)

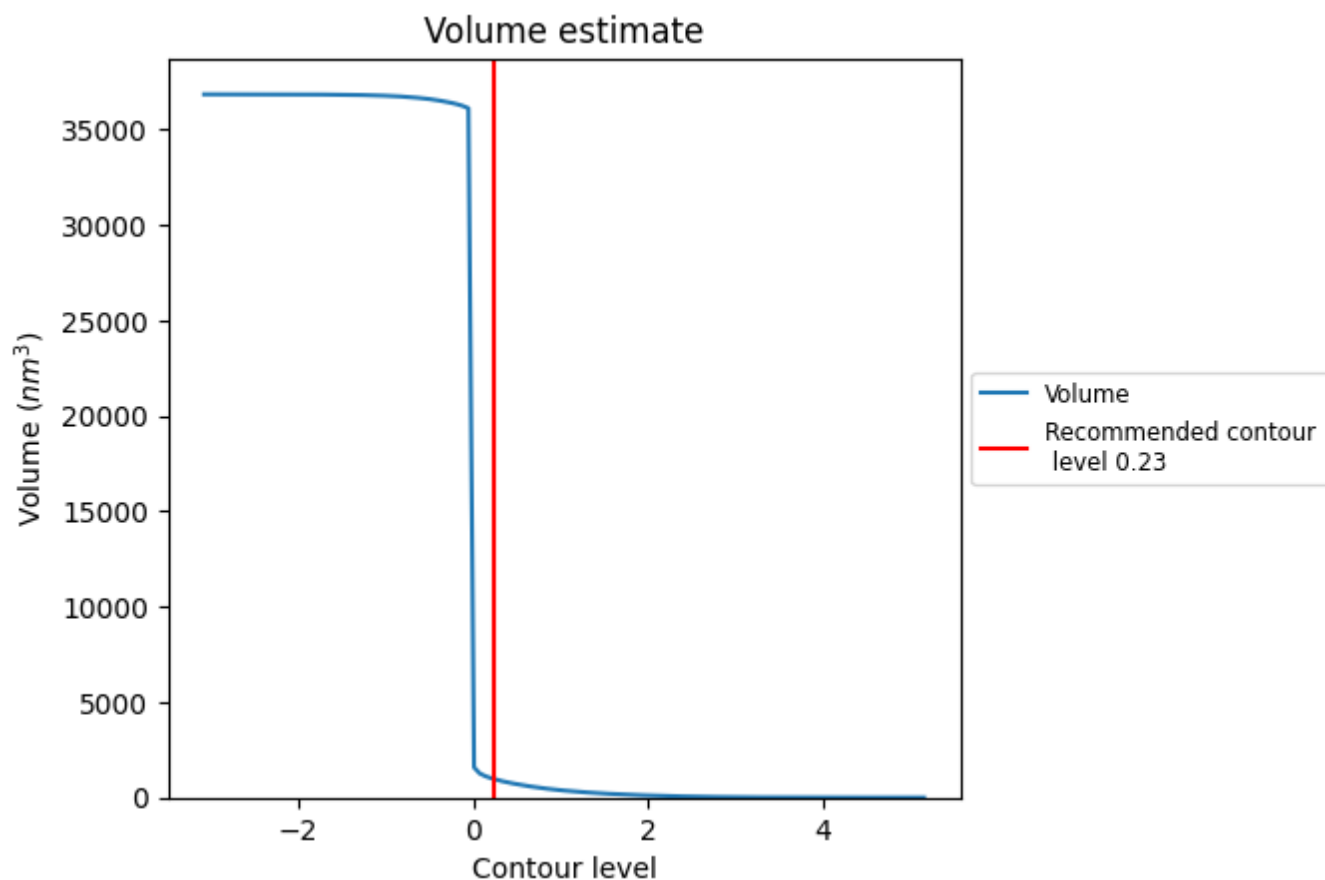
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

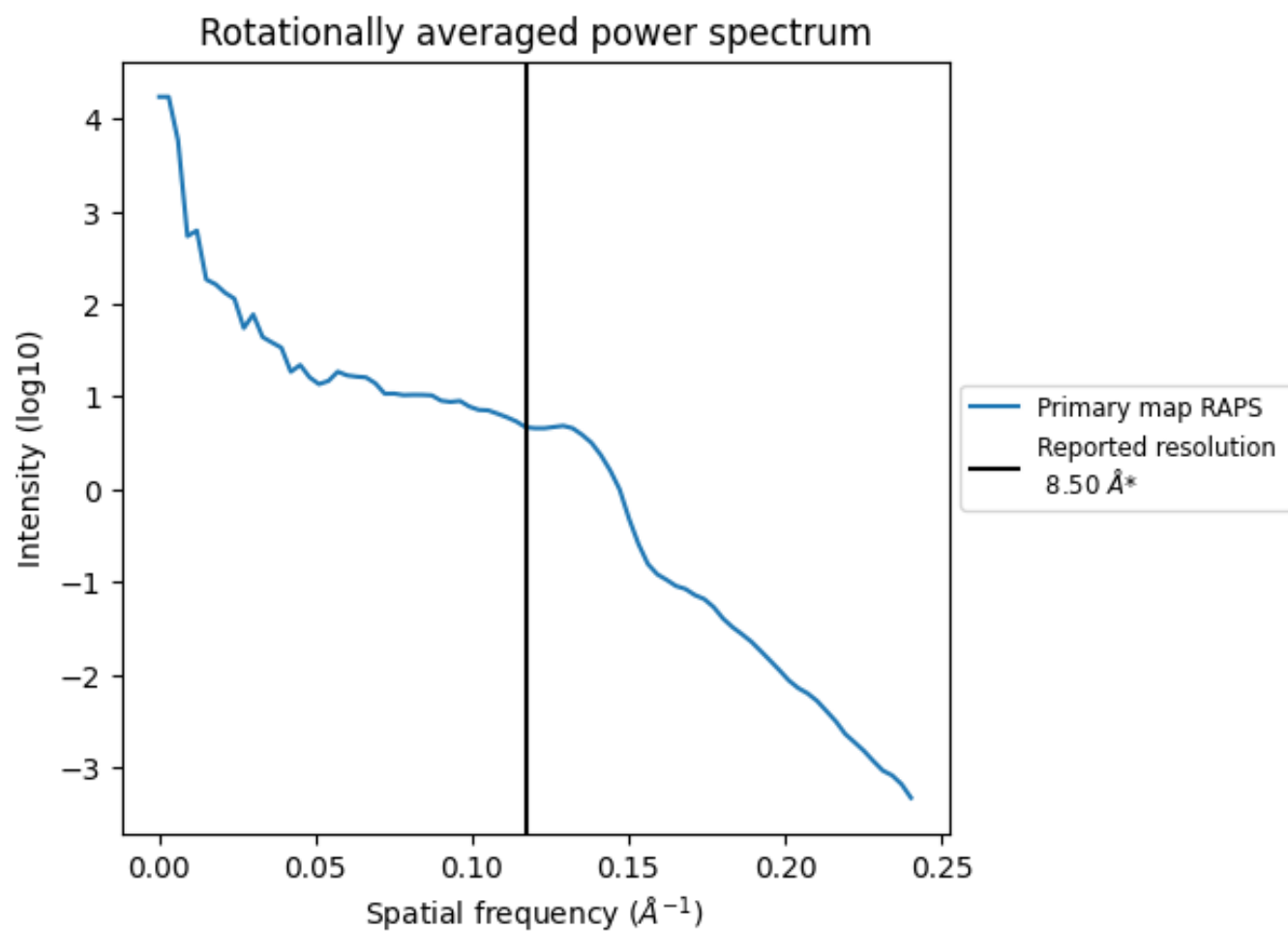
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 983 nm³; this corresponds to an approximate mass of 888 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 0.118 Å⁻¹

8 Fourier-Shell correlation

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

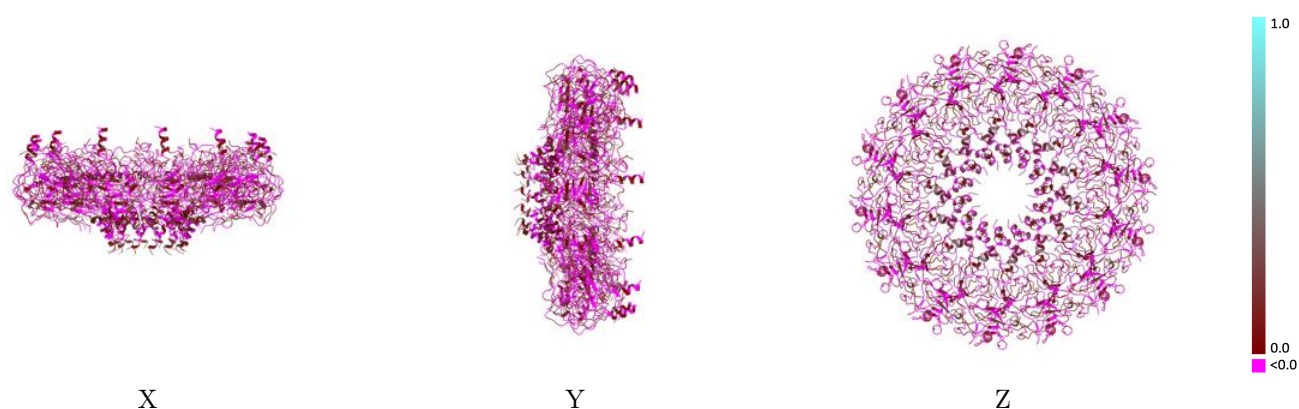
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2233 and PDB model 3ZBI. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

This section was not generated.

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

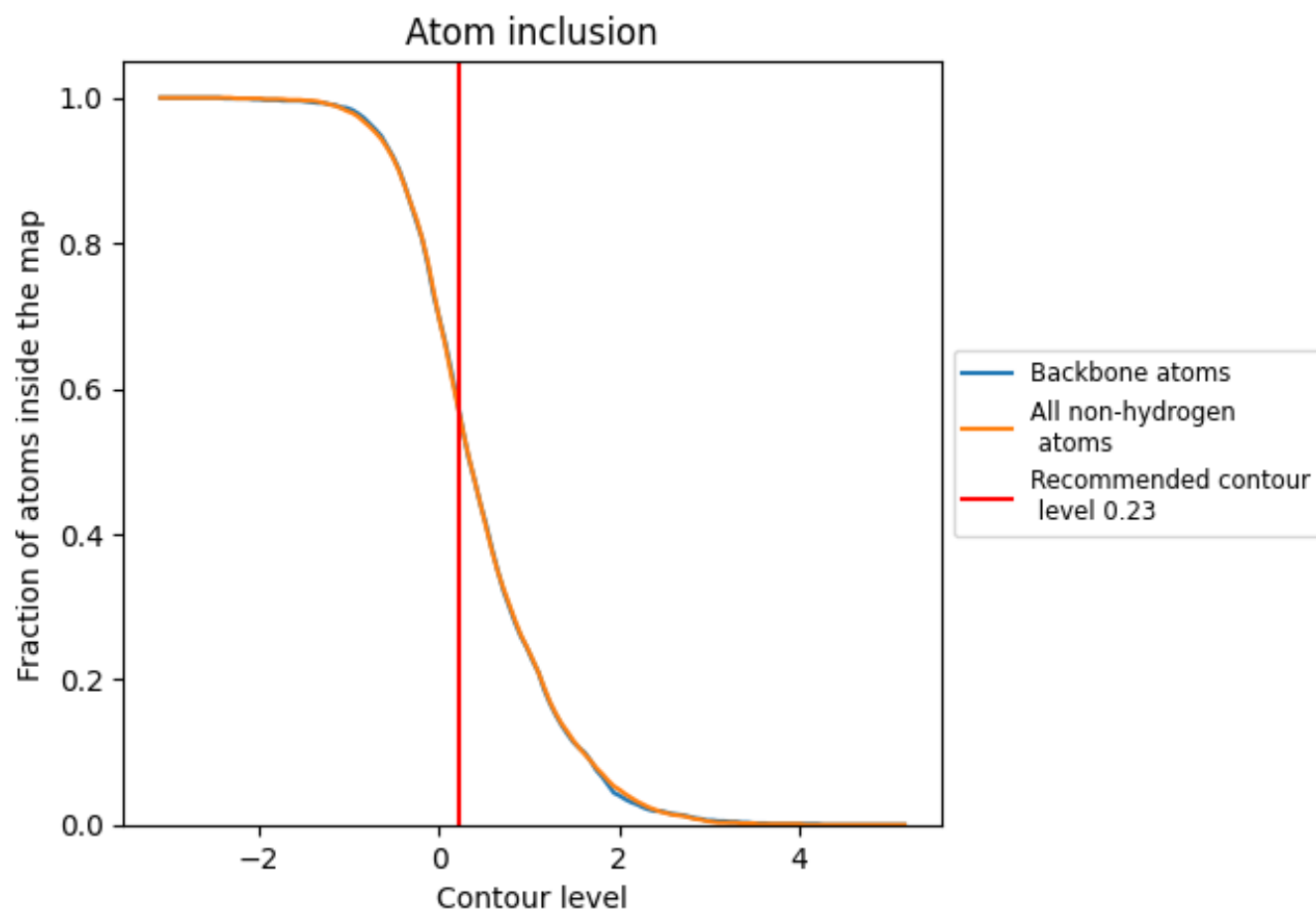


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 57% of all backbone atoms, 56% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.23) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5640	 0.0100
A	 0.5360	 0.0120
B	 0.6050	 0.0140
C	 0.5420	 -0.0210
D	 0.5340	 0.0100
E	 0.6100	 0.0150
F	 0.5520	 -0.0160
G	 0.5390	 0.0140
H	 0.6050	 0.0210
I	 0.5380	 -0.0160
J	 0.5400	 0.0090
K	 0.6060	 0.0200
L	 0.5420	 -0.0220
M	 0.5390	 0.0090
N	 0.6040	 0.0170
O	 0.5660	 -0.0150
P	 0.5440	 0.0110
Q	 0.6060	 0.0130
R	 0.5520	 -0.0220
S	 0.5320	 0.0110
T	 0.6000	 0.0160
U	 0.5380	 -0.0190
V	 0.5360	 0.0120
W	 0.6050	 0.0140
X	 0.5420	 -0.0140
Y	 0.5340	 0.0100
Z	 0.6100	 0.0130
a	 0.5520	 -0.0170
b	 0.5390	 0.0140
c	 0.6050	 0.0170
d	 0.5380	 -0.0160
e	 0.5400	 0.0110
f	 0.6060	 0.0160
g	 0.5420	 -0.0310
h	 0.5390	 0.0090



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Chain	Atom inclusion	Q-score
i	 0.6040	 0.0170
j	 0.5660	 -0.0200
k	 0.5440	 0.0110
l	 0.6060	 0.0130
m	 0.5520	 -0.0260
n	 0.5320	 0.0100
o	 0.6000	 0.0140
p	 0.5380	 -0.0200