



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 10, 2023 – 11:48 pm GMT

PDB ID : 2WGM
Title : Complete ion-coordination structure in the rotor ring of Na-dependent F-ATP synthase
Authors : Meier, T.; Pogoryelov, D.; Diederichs, K.
Deposited on : 2009-04-21
Resolution : 2.35 Å (reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

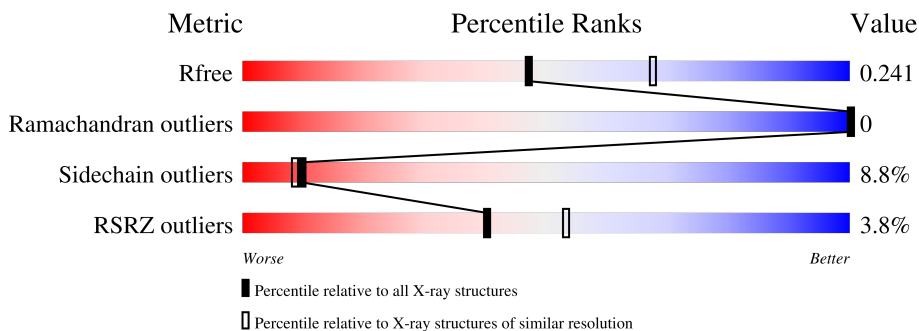
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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.



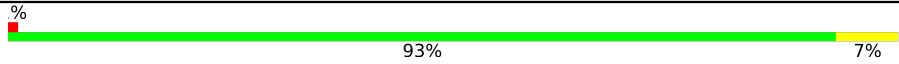
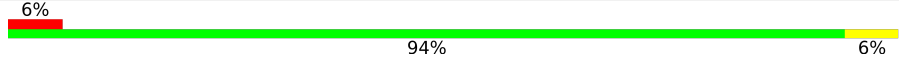
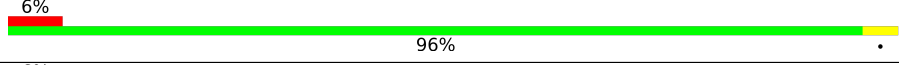
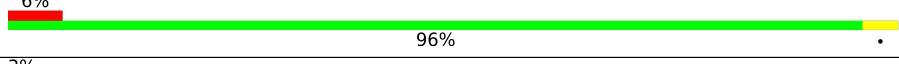
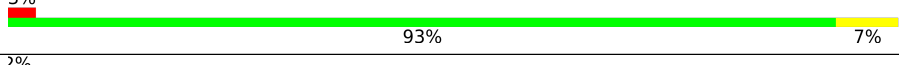
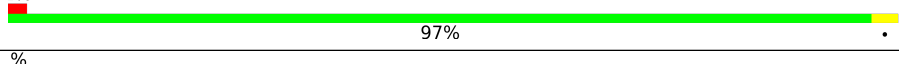
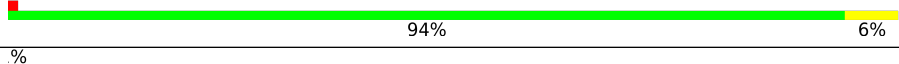
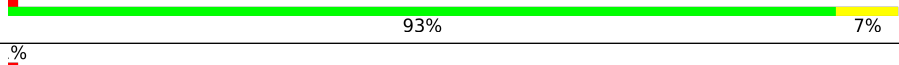
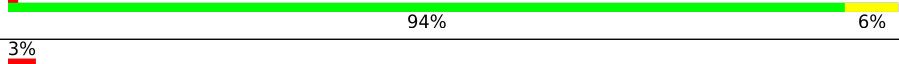
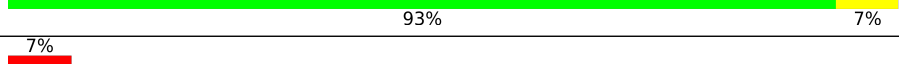
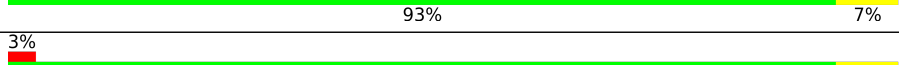
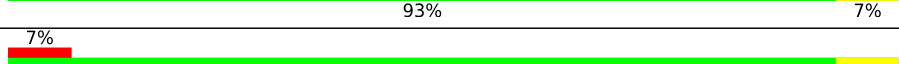
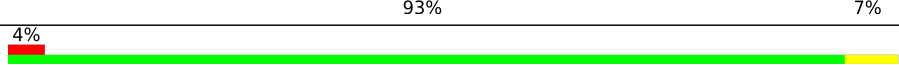
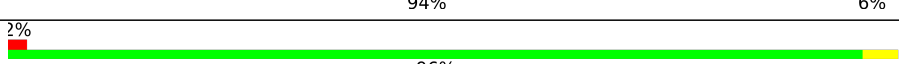
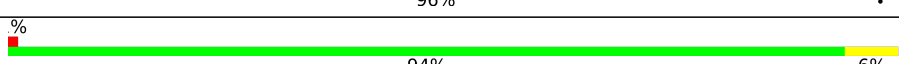
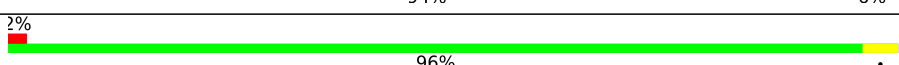
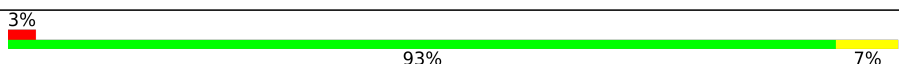
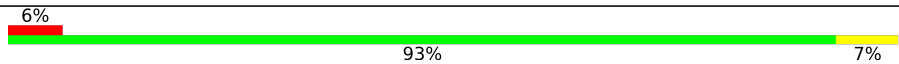
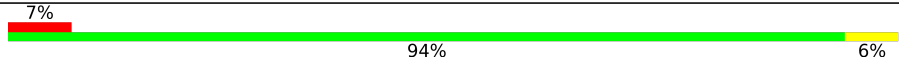
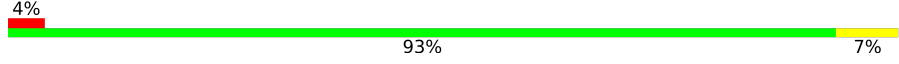
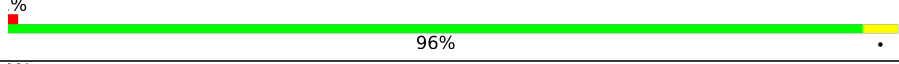
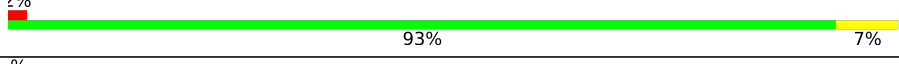
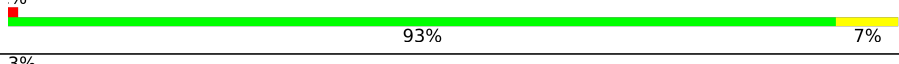
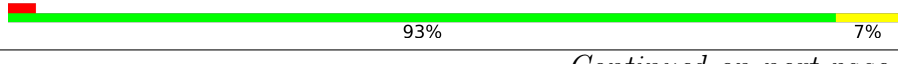

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1164 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	89	
1	B	89	
1	C	89	
1	D	89	
1	E	89	
1	F	89	

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Mol	Chain	Length	Quality of chain
1	G	89	
1	H	89	
1	I	89	
1	J	89	
1	K	89	
1	L	89	
1	M	89	
1	N	89	
1	O	89	
1	P	89	
1	Q	89	
1	R	89	
1	S	89	
1	T	89	
1	U	89	
1	V	89	
1	a	89	
1	b	89	
1	c	89	
1	d	89	
1	e	89	
1	f	89	
1	g	89	
1	h	89	
1	i	89	

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Mol	Chain	Length	Quality of chain
1	j	89	<p>4% 97% 6%</p>
1	k	89	<p>% 94% 6%</p>
1	l	89	<p>3% 96% 6%</p>
1	m	89	<p>4% 93% 7%</p>
1	n	89	<p>6% 93% 7%</p>
1	o	89	<p>6% 94% 6%</p>
1	p	89	<p>8% 94% 6%</p>
1	q	89	<p>9% 93% 7%</p>
1	r	89	<p>3% 94% 6%</p>
1	s	89	<p>3% 93% 7%</p>
1	t	89	<p>4% 96% 6%</p>
1	u	89	<p>3% 94% 6%</p>
1	v	89	<p>4% 93% 7%</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 28001 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	89	616	397	99	116	4	0	0	0
1	B	89	616	397	99	116	4	0	0	0
1	C	89	616	397	99	116	4	0	0	0
1	D	89	616	397	99	116	4	0	0	0
1	E	89	616	397	99	116	4	0	0	0
1	F	89	616	397	99	116	4	0	0	0
1	G	89	616	397	99	116	4	0	0	0
1	H	89	616	397	99	116	4	0	0	0
1	I	89	616	397	99	116	4	0	0	0
1	J	89	616	397	99	116	4	0	0	0
1	K	89	616	397	99	116	4	0	0	0
1	L	89	616	397	99	116	4	0	0	0
1	M	89	616	397	99	116	4	0	0	0
1	N	89	616	397	99	116	4	0	0	0
1	O	89	616	397	99	116	4	0	0	0
1	P	89	616	397	99	116	4	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	R	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	S	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	T	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	U	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	V	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	a	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	b	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	c	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	d	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	e	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	f	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	g	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	h	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	i	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	j	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	k	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	l	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	m	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	n	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			
1	o	89	Total	C	N	O	S	0	0	0
			616	397	99	116	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	p	89	Total 616	C 397	N 99	O 116	S 4	0	0	0
1	q	89	Total 616	C 397	N 99	O 116	S 4	0	0	0
1	r	89	Total 616	C 397	N 99	O 116	S 4	0	0	0
1	s	89	Total 616	C 397	N 99	O 116	S 4	0	0	0
1	t	89	Total 616	C 397	N 99	O 116	S 4	0	0	0
1	u	89	Total 616	C 397	N 99	O 116	S 4	0	0	0
1	v	89	Total 616	C 397	N 99	O 116	S 4	0	0	0

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Na 1	0	0
2	B	1	Total 1	Na 1	0	0
2	C	1	Total 1	Na 1	0	0
2	D	1	Total 1	Na 1	0	0
2	E	1	Total 1	Na 1	0	0
2	F	1	Total 1	Na 1	0	0
2	G	1	Total 1	Na 1	0	0
2	H	1	Total 1	Na 1	0	0
2	I	1	Total 1	Na 1	0	0
2	J	1	Total 1	Na 1	0	0
2	K	1	Total 1	Na 1	0	0
2	L	1	Total 1	Na 1	0	0

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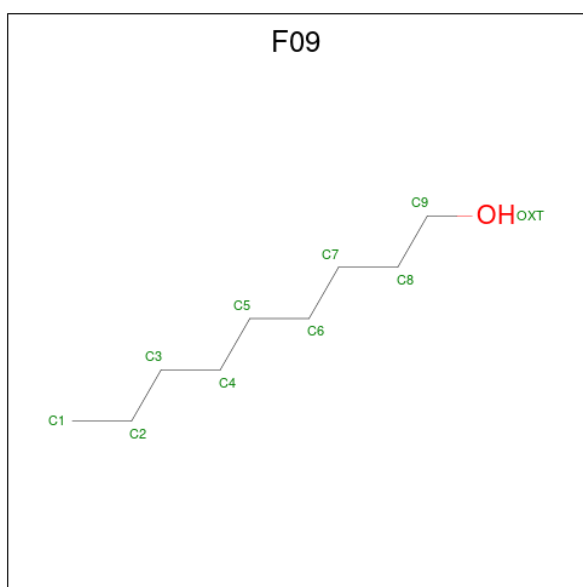
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	M	1	Total Na 1 1	0	0
2	N	1	Total Na 1 1	0	0
2	O	1	Total Na 1 1	0	0
2	P	1	Total Na 1 1	0	0
2	Q	1	Total Na 1 1	0	0
2	R	1	Total Na 1 1	0	0
2	S	1	Total Na 1 1	0	0
2	T	1	Total Na 1 1	0	0
2	U	1	Total Na 1 1	0	0
2	V	1	Total Na 1 1	0	0
2	a	1	Total Na 1 1	0	0
2	b	1	Total Na 1 1	0	0
2	c	1	Total Na 1 1	0	0
2	d	1	Total Na 1 1	0	0
2	e	1	Total Na 1 1	0	0
2	f	1	Total Na 1 1	0	0
2	g	1	Total Na 1 1	0	0
2	h	1	Total Na 1 1	0	0
2	i	1	Total Na 1 1	0	0
2	j	1	Total Na 1 1	0	0
2	k	1	Total Na 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	l	1	Total Na 1 1	0	0
2	m	1	Total Na 1 1	0	0
2	n	1	Total Na 1 1	0	0
2	o	1	Total Na 1 1	0	0
2	p	1	Total Na 1 1	0	0
2	q	1	Total Na 1 1	0	0
2	r	1	Total Na 1 1	0	0
2	s	1	Total Na 1 1	0	0
2	t	1	Total Na 1 1	0	0
2	u	1	Total Na 1 1	0	0
2	v	1	Total Na 1 1	0	0

- Molecule 3 is NONAN-1-OL (three-letter code: F09) (formula: C₉H₂₀O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	9	1		
3	B	1	Total	C	O	0	0
			10	9	1		
3	C	1	Total	C	O	0	0
			10	9	1		
3	D	1	Total	C	O	0	0
			10	9	1		
3	E	1	Total	C	O	0	0
			10	9	1		
3	F	1	Total	C	O	0	0
			10	9	1		
3	G	1	Total	C	O	0	0
			10	9	1		
3	H	1	Total	C	O	0	0
			10	9	1		
3	I	1	Total	C	O	0	0
			10	9	1		
3	J	1	Total	C	O	0	0
			10	9	1		
3	K	1	Total	C	O	0	0
			10	9	1		
3	L	1	Total	C	O	0	0
			10	9	1		
3	M	1	Total	C	O	0	0
			10	9	1		
3	N	1	Total	C	O	0	0
			10	9	1		
3	O	1	Total	C	O	0	0
			10	9	1		
3	P	1	Total	C	O	0	0
			10	9	1		
3	Q	1	Total	C	O	0	0
			10	9	1		
3	R	1	Total	C	O	0	0
			10	9	1		
3	S	1	Total	C	O	0	0
			10	9	1		
3	T	1	Total	C	O	0	0
			10	9	1		
3	U	1	Total	C	O	0	0
			10	9	1		
3	V	1	Total	C	O	0	0
			10	9	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	a	1	Total	C	O	0	0
			10	9	1		
3	b	1	Total	C	O	0	0
			10	9	1		
3	c	1	Total	C	O	0	0
			10	9	1		
3	d	1	Total	C	O	0	0
			10	9	1		
3	e	1	Total	C	O	0	0
			10	9	1		
3	f	1	Total	C	O	0	0
			10	9	1		
3	g	1	Total	C	O	0	0
			10	9	1		
3	h	1	Total	C	O	0	0
			10	9	1		
3	i	1	Total	C	O	0	0
			10	9	1		
3	j	1	Total	C	O	0	0
			10	9	1		
3	k	1	Total	C	O	0	0
			10	9	1		
3	l	1	Total	C	O	0	0
			10	9	1		
3	m	1	Total	C	O	0	0
			10	9	1		
3	n	1	Total	C	O	0	0
			10	9	1		
3	o	1	Total	C	O	0	0
			10	9	1		
3	p	1	Total	C	O	0	0
			10	9	1		
3	q	1	Total	C	O	0	0
			10	9	1		
3	r	1	Total	C	O	0	0
			10	9	1		
3	s	1	Total	C	O	0	0
			10	9	1		
3	t	1	Total	C	O	0	0
			10	9	1		
3	u	1	Total	C	O	0	0
			10	9	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	v	1	10	9	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	12	Total 12	O 12	0	0
4	B	12	Total 12	O 12	0	0
4	C	7	Total 7	O 7	0	0
4	D	9	Total 9	O 9	0	0
4	E	7	Total 7	O 7	0	0
4	F	7	Total 7	O 7	0	0
4	G	8	Total 8	O 8	0	0
4	H	8	Total 8	O 8	0	0
4	I	9	Total 9	O 9	0	0
4	J	12	Total 12	O 12	0	0
4	K	12	Total 12	O 12	0	0
4	L	11	Total 11	O 11	0	0
4	M	9	Total 9	O 9	0	0
4	N	7	Total 7	O 7	0	0
4	O	13	Total 13	O 13	0	0
4	P	9	Total 9	O 9	0	0
4	Q	9	Total 9	O 9	0	0
4	R	8	Total 8	O 8	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	S	6	Total O 6 6	0	0
4	T	9	Total O 9 9	0	0
4	U	6	Total O 6 6	0	0
4	V	9	Total O 9 9	0	0
4	a	12	Total O 12 12	0	0
4	b	10	Total O 10 10	0	0
4	c	13	Total O 13 13	0	0
4	d	13	Total O 13 13	0	0
4	e	11	Total O 11 11	0	0
4	f	11	Total O 11 11	0	0
4	g	10	Total O 10 10	0	0
4	h	11	Total O 11 11	0	0
4	i	5	Total O 5 5	0	0
4	j	10	Total O 10 10	0	0
4	k	7	Total O 7 7	0	0
4	l	11	Total O 11 11	0	0
4	m	11	Total O 11 11	0	0
4	n	8	Total O 8 8	0	0
4	o	8	Total O 8 8	0	0
4	p	9	Total O 9 9	0	0
4	q	4	Total O 4 4	0	0

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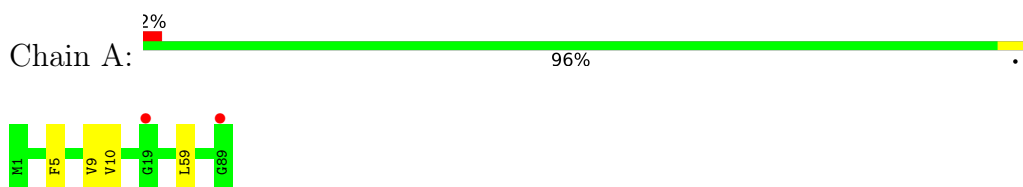
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	r	8	Total O 8 8	0	0
4	s	11	Total O 11 11	0	0
4	t	11	Total O 11 11	0	0
4	u	8	Total O 8 8	0	0
4	v	12	Total O 12 12	0	0

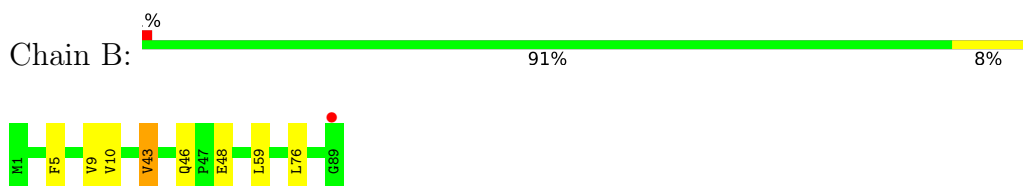
3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

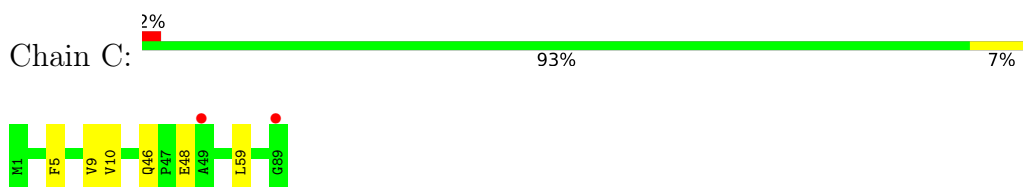
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



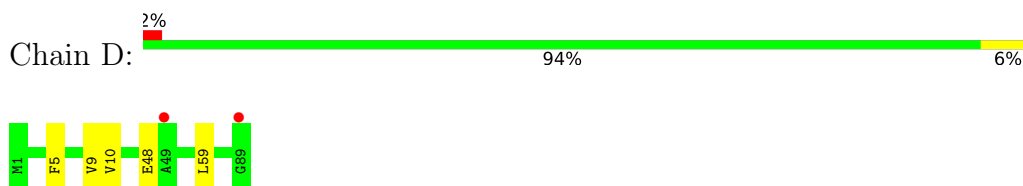
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



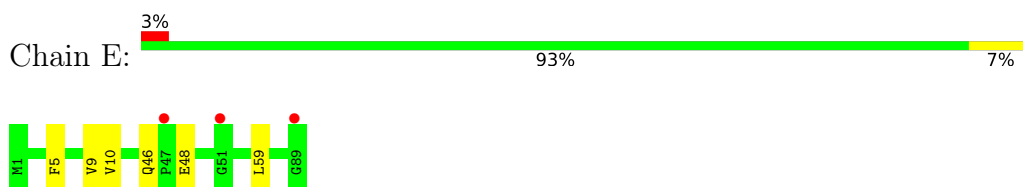
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



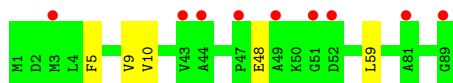
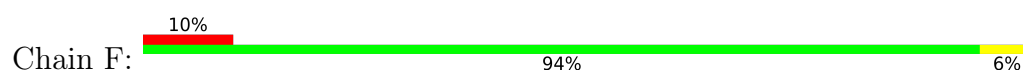
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



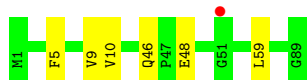
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



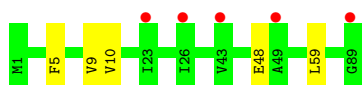
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



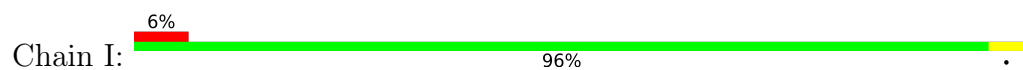
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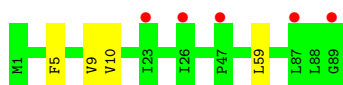
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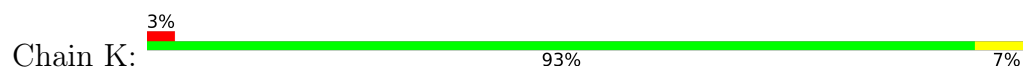
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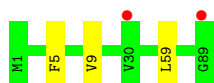
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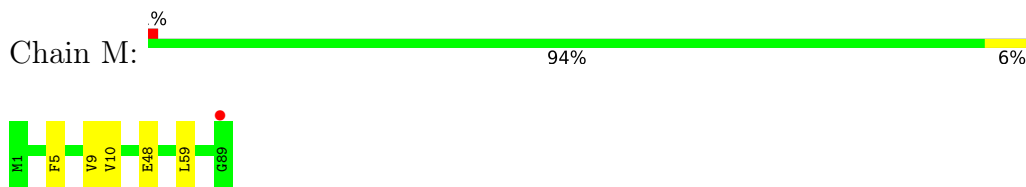
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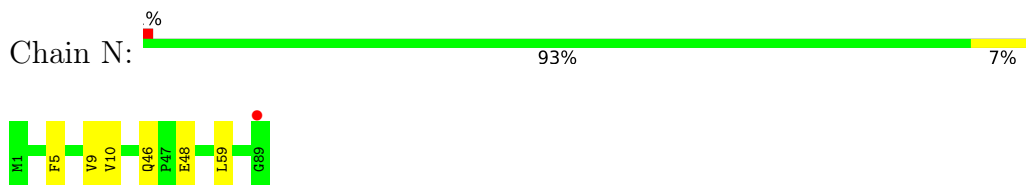
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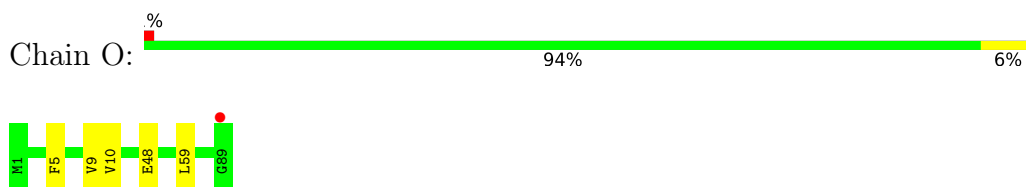
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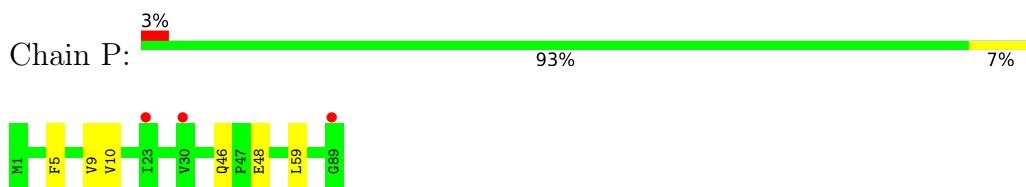
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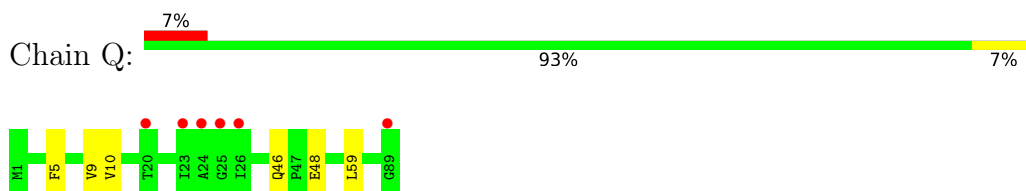
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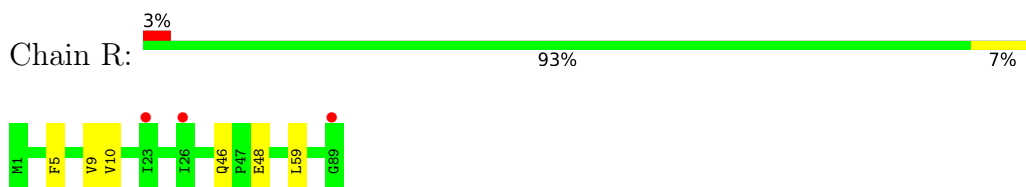
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



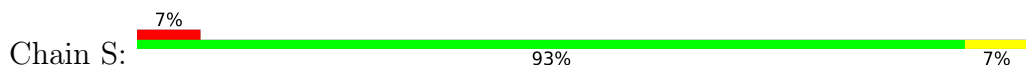
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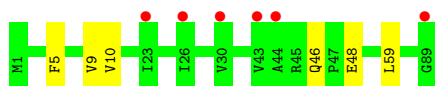


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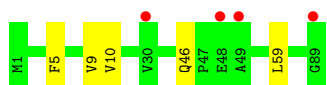
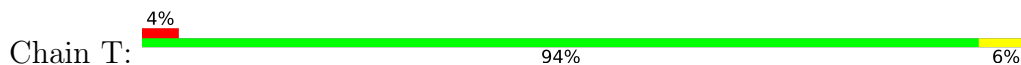


- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC

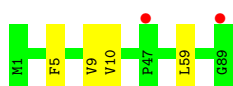




- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



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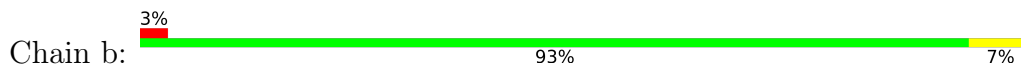
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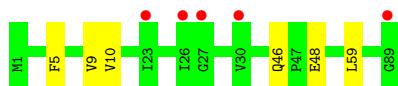
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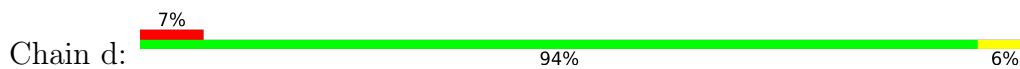
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



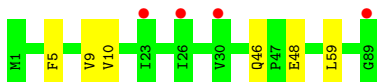
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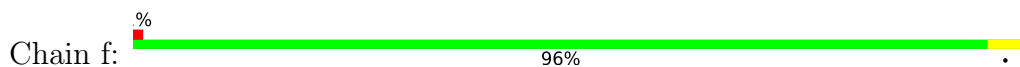
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



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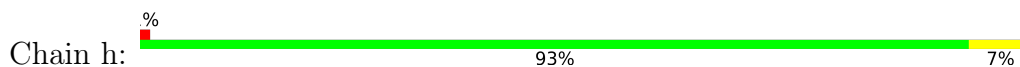
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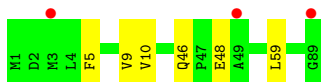
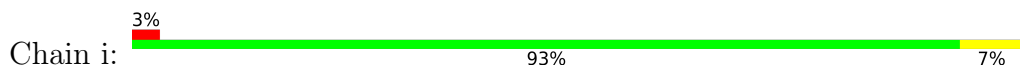
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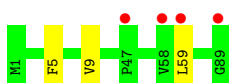
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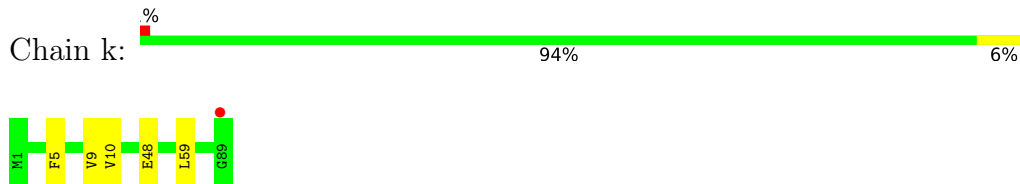
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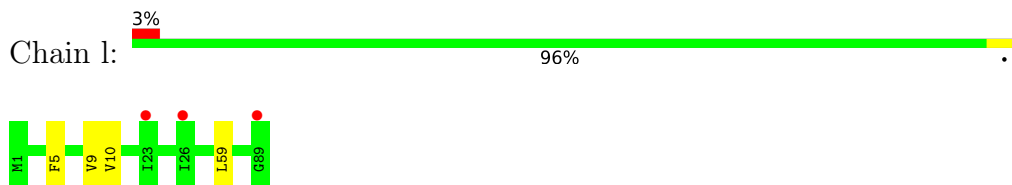
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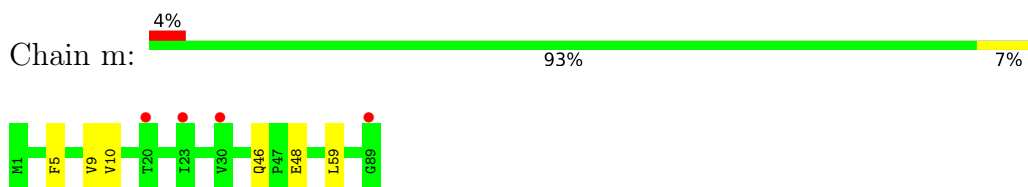
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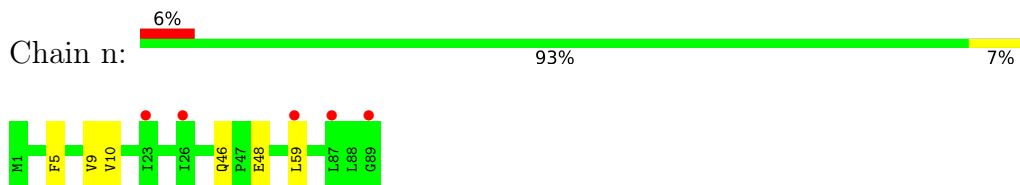
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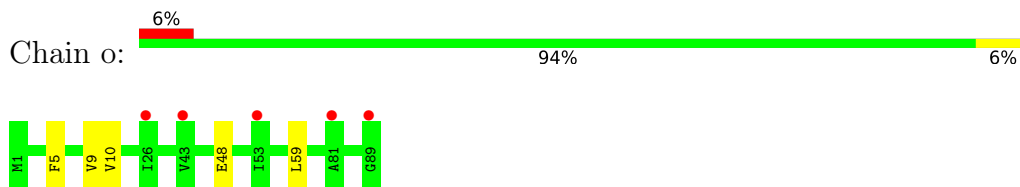
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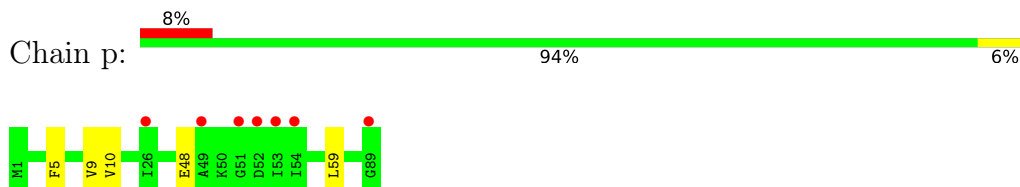
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



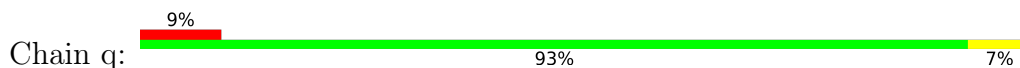
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC

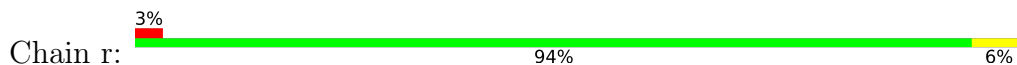


- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC





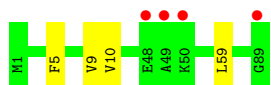
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



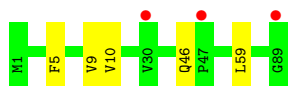
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



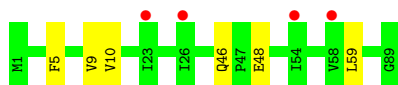
- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



- Molecule 1: ATP SYNTHASE SUBUNIT C, SODIUM ION SPECIFIC



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	146.69Å 139.28Å 151.91Å 90.00° 118.40° 90.00°	Depositor
Resolution (Å)	39.68 – 2.35 39.68 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.6 (39.68-2.35) 98.9 (39.68-2.35)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 2.34Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.220 , 0.245 0.217 , 0.241	Depositor DCC
R_{free} test set	10987 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	39.9	Xtriage
Anisotropy	0.679	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h-l,k,h 0.000 for l,k,-h-l 0.000 for h,-k,-h-l 0.000 for -h-l,-k,l 0.000 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	28001	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, F09

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	0.38	0/623	0.49	0/844
1	B	0.40	0/623	0.61	1/844 (0.1%)
1	C	0.37	0/623	0.47	0/844
1	D	0.36	0/623	0.49	0/844
1	E	0.35	0/623	0.47	0/844
1	F	0.37	0/623	0.47	0/844
1	G	0.36	0/623	0.47	0/844
1	H	0.35	0/623	0.47	0/844
1	I	0.37	0/623	0.47	0/844
1	J	0.39	0/623	0.49	0/844
1	K	0.36	0/623	0.51	0/844
1	L	0.37	0/623	0.48	0/844
1	M	0.38	0/623	0.49	0/844
1	N	0.36	0/623	0.47	0/844
1	O	0.34	0/623	0.46	0/844
1	P	0.35	0/623	0.46	0/844
1	Q	0.33	0/623	0.46	0/844
1	R	0.37	0/623	0.47	0/844
1	S	0.35	0/623	0.47	0/844
1	T	0.38	0/623	0.49	0/844
1	U	0.37	0/623	0.46	0/844
1	V	0.36	0/623	0.46	0/844
1	a	0.38	0/623	0.48	0/844
1	b	0.37	0/623	0.48	0/844
1	c	0.37	0/623	0.47	0/844
1	d	0.35	0/623	0.47	0/844
1	e	0.35	0/623	0.46	0/844
1	f	0.37	0/623	0.48	0/844
1	g	0.39	0/623	0.46	0/844
1	h	0.39	0/623	0.47	0/844
1	i	0.37	0/623	0.48	0/844
1	j	0.37	0/623	0.50	0/844

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	k	0.36	0/623	0.47	0/844
1	l	0.37	0/623	0.49	0/844
1	m	0.36	0/623	0.48	0/844
1	n	0.37	0/623	0.48	0/844
1	o	0.36	0/623	0.47	0/844
1	p	0.38	0/623	0.48	0/844
1	q	0.38	0/623	0.48	0/844
1	r	0.32	0/623	0.46	0/844
1	s	0.35	0/623	0.46	0/844
1	t	0.37	0/623	0.49	0/844
1	u	0.39	0/623	0.50	0/844
1	v	0.37	0/623	0.47	0/844
All	All	0.37	0/27412	0.48	1/37136 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	43	VAL	CG1-CB-CG2	6.05	120.58	110.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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 X-ray entries followed by that with respect to entries of similar resolution.

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	87/89 (98%)	86 (99%)	1 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	C	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	D	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	E	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	F	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	G	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	H	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	I	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
1	J	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	K	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	L	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	M	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	N	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	O	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	P	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	Q	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	R	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	S	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	T	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	U	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	V	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	a	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	b	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	c	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	d	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	e	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	f	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	g	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	h	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	i	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
1	j	87/89 (98%)	86 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	k	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	l	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	m	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	n	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	o	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
1	p	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	q	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
1	r	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
1	s	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	t	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
1	u	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
1	v	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
All	All	3828/3916 (98%)	3778 (99%)	50 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	60/60 (100%)	56 (93%)	4 (7%)	16	17
1	B	60/60 (100%)	52 (87%)	8 (13%)	4	4
1	C	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	D	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	E	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	F	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	G	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	H	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	I	60/60 (100%)	56 (93%)	4 (7%)	16	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	60/60 (100%)	56 (93%)	4 (7%)	16	17
1	K	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	L	60/60 (100%)	57 (95%)	3 (5%)	24	28
1	M	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	N	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	O	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	P	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	Q	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	R	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	S	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	T	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	U	60/60 (100%)	56 (93%)	4 (7%)	16	17
1	V	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	a	60/60 (100%)	56 (93%)	4 (7%)	16	17
1	b	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	c	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	d	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	e	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	f	60/60 (100%)	56 (93%)	4 (7%)	16	17
1	g	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	h	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	i	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	j	60/60 (100%)	57 (95%)	3 (5%)	24	28
1	k	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	l	60/60 (100%)	56 (93%)	4 (7%)	16	17
1	m	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	n	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	o	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	p	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	q	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	r	60/60 (100%)	55 (92%)	5 (8%)	11	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	s	60/60 (100%)	54 (90%)	6 (10%)	7	6
1	t	60/60 (100%)	56 (93%)	4 (7%)	16	17
1	u	60/60 (100%)	55 (92%)	5 (8%)	11	11
1	v	60/60 (100%)	54 (90%)	6 (10%)	7	6
All	All	2640/2640 (100%)	2409 (91%)	231 (9%)	10	8

5 of 231 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	V	59	LEU
1	u	9	VAL
1	f	5	PHE
1	t	59	LEU
1	q	5	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	t	46	GLN
1	i	46	GLN
1	d	46	GLN
1	U	46	GLN
1	h	46	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 88 ligands modelled in this entry, 44 are monoatomic - leaving 44 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	F09	r	314	-	9,9,9	0.36	0	8,8,8	0.73	0
3	F09	U	314	-	9,9,9	0.35	0	8,8,8	0.77	0
3	F09	a	314	-	9,9,9	0.32	0	8,8,8	0.80	0
3	F09	A	314	-	9,9,9	0.32	0	8,8,8	0.85	0
3	F09	I	314	-	9,9,9	0.33	0	8,8,8	0.82	0
3	F09	j	314	-	9,9,9	0.35	0	8,8,8	0.71	0
3	F09	F	314	-	9,9,9	0.35	0	8,8,8	0.69	0
3	F09	P	314	-	9,9,9	0.32	0	8,8,8	0.81	0
3	F09	R	314	-	9,9,9	0.31	0	8,8,8	0.80	0
3	F09	C	314	-	9,9,9	0.35	0	8,8,8	0.74	0
3	F09	l	314	-	9,9,9	0.36	0	8,8,8	0.68	0
3	F09	D	314	-	9,9,9	0.34	0	8,8,8	0.73	0
3	F09	H	314	-	9,9,9	0.34	0	8,8,8	0.74	0
3	F09	p	314	-	9,9,9	0.34	0	8,8,8	0.69	0
3	F09	t	314	-	9,9,9	0.35	0	8,8,8	0.72	0
3	F09	b	314	-	9,9,9	0.34	0	8,8,8	0.75	0
3	F09	g	314	-	9,9,9	0.34	0	8,8,8	0.81	0
3	F09	k	314	-	9,9,9	0.29	0	8,8,8	0.84	0
3	F09	m	314	-	9,9,9	0.32	0	8,8,8	0.78	0
3	F09	Q	314	-	9,9,9	0.31	0	8,8,8	0.80	0
3	F09	u	314	-	9,9,9	0.37	0	8,8,8	0.73	0
3	F09	h	314	-	9,9,9	0.29	0	8,8,8	0.80	0
3	F09	G	314	-	9,9,9	0.31	0	8,8,8	0.80	0
3	F09	O	314	-	9,9,9	0.34	0	8,8,8	0.77	0
3	F09	L	314	-	9,9,9	0.32	0	8,8,8	0.77	0
3	F09	s	314	-	9,9,9	0.32	0	8,8,8	0.80	0
3	F09	n	314	-	9,9,9	0.35	0	8,8,8	0.70	0
3	F09	S	314	-	9,9,9	0.32	0	8,8,8	0.78	0
3	F09	q	314	-	9,9,9	0.29	0	8,8,8	0.82	0
3	F09	T	314	-	9,9,9	0.33	0	8,8,8	0.75	0
3	F09	N	314	-	9,9,9	0.36	0	8,8,8	0.69	0
3	F09	c	314	-	9,9,9	0.32	0	8,8,8	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	F09	o	314	-	9,9,9	0.35	0	8,8,8	0.70	0
3	F09	f	314	-	9,9,9	0.31	0	8,8,8	0.77	0
3	F09	v	314	-	9,9,9	0.34	0	8,8,8	0.71	0
3	F09	e	314	-	9,9,9	0.37	0	8,8,8	0.65	0
3	F09	d	314	-	9,9,9	0.31	0	8,8,8	0.79	0
3	F09	B	314	-	9,9,9	0.31	0	8,8,8	0.84	0
3	F09	K	314	-	9,9,9	0.29	0	8,8,8	0.85	0
3	F09	E	314	-	9,9,9	0.32	0	8,8,8	0.81	0
3	F09	i	314	-	9,9,9	0.36	0	8,8,8	0.69	0
3	F09	V	314	-	9,9,9	0.33	0	8,8,8	0.76	0
3	F09	M	314	-	9,9,9	0.30	0	8,8,8	0.87	0
3	F09	J	314	-	9,9,9	0.33	0	8,8,8	0.78	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	F09	r	314	-	-	1/7/7/7	-
3	F09	U	314	-	-	3/7/7/7	-
3	F09	a	314	-	-	2/7/7/7	-
3	F09	A	314	-	-	4/7/7/7	-
3	F09	I	314	-	-	3/7/7/7	-
3	F09	j	314	-	-	1/7/7/7	-
3	F09	F	314	-	-	0/7/7/7	-
3	F09	P	314	-	-	2/7/7/7	-
3	F09	R	314	-	-	4/7/7/7	-
3	F09	C	314	-	-	0/7/7/7	-
3	F09	l	314	-	-	2/7/7/7	-
3	F09	D	314	-	-	1/7/7/7	-
3	F09	H	314	-	-	3/7/7/7	-
3	F09	p	314	-	-	1/7/7/7	-
3	F09	t	314	-	-	2/7/7/7	-
3	F09	b	314	-	-	2/7/7/7	-
3	F09	g	314	-	-	2/7/7/7	-
3	F09	k	314	-	-	4/7/7/7	-
3	F09	m	314	-	-	1/7/7/7	-
3	F09	Q	314	-	-	6/7/7/7	-
3	F09	u	314	-	-	0/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	F09	h	314	-	-	5/7/7/7	-
3	F09	G	314	-	-	3/7/7/7	-
3	F09	O	314	-	-	2/7/7/7	-
3	F09	L	314	-	-	3/7/7/7	-
3	F09	s	314	-	-	1/7/7/7	-
3	F09	n	314	-	-	3/7/7/7	-
3	F09	S	314	-	-	2/7/7/7	-
3	F09	q	314	-	-	2/7/7/7	-
3	F09	T	314	-	-	1/7/7/7	-
3	F09	N	314	-	-	1/7/7/7	-
3	F09	c	314	-	-	0/7/7/7	-
3	F09	o	314	-	-	2/7/7/7	-
3	F09	f	314	-	-	0/7/7/7	-
3	F09	v	314	-	-	3/7/7/7	-
3	F09	e	314	-	-	4/7/7/7	-
3	F09	d	314	-	-	3/7/7/7	-
3	F09	B	314	-	-	2/7/7/7	-
3	F09	K	314	-	-	1/7/7/7	-
3	F09	E	314	-	-	1/7/7/7	-
3	F09	i	314	-	-	3/7/7/7	-
3	F09	V	314	-	-	3/7/7/7	-
3	F09	M	314	-	-	0/7/7/7	-
3	F09	J	314	-	-	0/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 89 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L	314	F09	C2-C3-C4-C5
3	k	314	F09	C2-C3-C4-C5
3	k	314	F09	C5-C6-C7-C8
3	n	314	F09	C6-C7-C8-C9
3	R	314	F09	C2-C3-C4-C5

There are no ring outliers.

No monomer is involved in short contacts.

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 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	89/89 (100%)	0.10	2 (2%) 62 72	38, 49, 69, 115	0
1	B	89/89 (100%)	0.17	1 (1%) 80 87	38, 50, 70, 142	0
1	C	89/89 (100%)	0.02	2 (2%) 62 72	39, 51, 75, 139	0
1	D	89/89 (100%)	0.09	2 (2%) 62 72	39, 54, 75, 127	0
1	E	89/89 (100%)	0.23	3 (3%) 45 57	39, 54, 76, 124	0
1	F	89/89 (100%)	0.36	9 (10%) 7 11	39, 54, 78, 157	0
1	G	89/89 (100%)	0.02	1 (1%) 80 87	39, 52, 76, 137	0
1	H	89/89 (100%)	0.18	5 (5%) 24 35	38, 52, 77, 136	0
1	I	89/89 (100%)	0.10	5 (5%) 24 35	38, 51, 75, 143	0
1	J	89/89 (100%)	0.36	5 (5%) 24 35	37, 49, 75, 115	0
1	K	89/89 (100%)	0.19	3 (3%) 45 57	37, 49, 72, 139	0
1	L	89/89 (100%)	-0.02	2 (2%) 62 72	36, 49, 71, 136	0
1	M	89/89 (100%)	-0.08	1 (1%) 80 87	36, 49, 69, 146	0
1	N	89/89 (100%)	-0.04	1 (1%) 80 87	38, 49, 71, 152	0
1	O	89/89 (100%)	0.10	1 (1%) 80 87	37, 49, 72, 132	0
1	P	89/89 (100%)	0.03	3 (3%) 45 57	37, 50, 72, 113	0
1	Q	89/89 (100%)	0.22	6 (6%) 17 26	38, 50, 73, 121	0
1	R	89/89 (100%)	0.29	3 (3%) 45 57	38, 51, 74, 114	0
1	S	89/89 (100%)	0.27	6 (6%) 17 26	38, 51, 75, 135	0
1	T	89/89 (100%)	0.15	4 (4%) 33 46	38, 51, 75, 143	0
1	U	89/89 (100%)	-0.02	2 (2%) 62 72	38, 51, 75, 138	0
1	V	89/89 (100%)	-0.08	1 (1%) 80 87	37, 50, 74, 142	0
1	a	89/89 (100%)	0.02	2 (2%) 62 72	36, 50, 70, 115	0
1	b	89/89 (100%)	0.00	3 (3%) 45 57	37, 50, 70, 129	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	c	89/89 (100%)	0.16	5 (5%) 24 35	38, 50, 73, 138	0
1	d	89/89 (100%)	0.34	6 (6%) 17 26	36, 50, 74, 140	0
1	e	89/89 (100%)	0.25	4 (4%) 33 46	37, 50, 74, 139	0
1	f	89/89 (100%)	-0.04	1 (1%) 80 87	35, 49, 70, 123	0
1	g	89/89 (100%)	0.03	2 (2%) 62 72	36, 50, 72, 147	0
1	h	89/89 (100%)	0.04	1 (1%) 80 87	38, 50, 74, 153	0
1	i	89/89 (100%)	0.07	3 (3%) 45 57	36, 50, 75, 159	0
1	j	89/89 (100%)	0.03	4 (4%) 33 46	37, 51, 74, 105	0
1	k	89/89 (100%)	-0.12	1 (1%) 80 87	36, 50, 72, 101	0
1	l	89/89 (100%)	0.07	3 (3%) 45 57	38, 49, 70, 148	0
1	m	89/89 (100%)	-0.00	4 (4%) 33 46	37, 51, 71, 146	0
1	n	89/89 (100%)	0.16	5 (5%) 24 35	39, 53, 77, 135	0
1	o	89/89 (100%)	0.38	5 (5%) 24 35	39, 55, 76, 146	0
1	p	89/89 (100%)	0.22	7 (7%) 12 19	41, 55, 80, 142	0
1	q	89/89 (100%)	0.32	8 (8%) 9 14	41, 55, 78, 143	0
1	r	89/89 (100%)	0.12	3 (3%) 45 57	40, 53, 76, 119	0
1	s	89/89 (100%)	0.14	3 (3%) 45 57	39, 51, 74, 117	0
1	t	89/89 (100%)	0.15	4 (4%) 33 46	36, 50, 75, 151	0
1	u	89/89 (100%)	0.29	3 (3%) 45 57	38, 49, 74, 125	0
1	v	89/89 (100%)	0.22	4 (4%) 33 46	38, 49, 70, 120	0
All	All	3916/3916 (100%)	0.12	149 (3%) 40 53	35, 51, 75, 159	0

The worst 5 of 149 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	T	89	GLY	12.1
1	L	89	GLY	7.8
1	J	89	GLY	7.6
1	e	89	GLY	6.7
1	B	89	GLY	6.6

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NA	K	201	1/1	0.85	0.07	52,52,52,52	0
3	F09	k	314	10/10	0.86	0.26	59,61,72,73	0
3	F09	U	314	10/10	0.87	0.28	51,60,73,84	0
3	F09	r	314	10/10	0.88	0.32	47,62,69,70	0
3	F09	t	314	10/10	0.88	0.31	50,57,66,67	0
3	F09	p	314	10/10	0.89	0.32	58,72,74,75	0
3	F09	J	314	10/10	0.89	0.34	53,58,67,88	0
3	F09	l	314	10/10	0.89	0.37	51,61,90,95	0
3	F09	d	314	10/10	0.90	0.34	48,54,65,73	0
3	F09	F	314	10/10	0.90	0.32	41,66,82,90	0
3	F09	I	314	10/10	0.90	0.33	49,58,67,68	0
3	F09	D	314	10/10	0.91	0.37	60,72,84,89	0
2	NA	k	201	1/1	0.91	0.05	56,56,56,56	0
3	F09	m	314	10/10	0.91	0.35	60,68,74,74	0
2	NA	n	201	1/1	0.91	0.07	65,65,65,65	0
3	F09	e	314	10/10	0.91	0.35	61,66,69,75	0
3	F09	i	314	10/10	0.91	0.21	53,59,72,73	0
3	F09	b	314	10/10	0.92	0.33	51,59,73,90	0
3	F09	K	314	10/10	0.92	0.29	49,65,71,88	0
3	F09	N	314	10/10	0.92	0.33	50,59,65,70	0
3	F09	n	314	10/10	0.92	0.40	62,72,75,77	0
3	F09	o	314	10/10	0.92	0.33	46,62,85,87	0
3	F09	f	314	10/10	0.92	0.37	53,63,88,93	0
3	F09	q	314	10/10	0.92	0.40	71,75,92,93	0
3	F09	H	314	10/10	0.92	0.30	56,64,73,87	0
3	F09	s	314	10/10	0.92	0.38	52,66,75,83	0
3	F09	j	314	10/10	0.92	0.20	48,60,75,81	0
3	F09	G	314	10/10	0.93	0.27	36,64,82,83	0
3	F09	C	314	10/10	0.93	0.33	55,59,85,87	0
3	F09	O	314	10/10	0.93	0.28	42,55,64,74	0
3	F09	g	314	10/10	0.93	0.29	51,63,73,87	0
3	F09	P	314	10/10	0.93	0.37	63,68,76,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NA	m	201	1/1	0.93	0.07	57,57,57,57	0
3	F09	V	314	10/10	0.93	0.24	47,58,73,74	0
2	NA	o	201	1/1	0.93	0.07	64,64,64,64	0
3	F09	v	314	10/10	0.93	0.30	49,64,79,87	0
3	F09	Q	314	10/10	0.94	0.37	62,67,75,85	0
3	F09	R	314	10/10	0.94	0.34	59,67,72,73	0
3	F09	S	314	10/10	0.94	0.31	57,67,78,85	0
3	F09	T	314	10/10	0.94	0.23	48,64,76,82	0
2	NA	h	201	1/1	0.94	0.10	53,53,53,53	0
2	NA	u	201	1/1	0.94	0.13	50,50,50,50	0
3	F09	A	314	10/10	0.94	0.30	51,59,68,79	0
3	F09	B	314	10/10	0.94	0.23	40,66,71,76	0
2	NA	J	201	1/1	0.94	0.05	51,51,51,51	0
2	NA	H	201	1/1	0.94	0.06	57,57,57,57	0
3	F09	E	314	10/10	0.94	0.40	59,69,83,87	0
3	F09	u	314	10/10	0.94	0.40	54,60,70,76	0
2	NA	L	201	1/1	0.94	0.05	49,49,49,49	0
3	F09	h	314	10/10	0.95	0.26	58,62,70,76	0
2	NA	e	201	1/1	0.95	0.12	50,50,50,50	0
2	NA	F	201	1/1	0.95	0.06	54,54,54,54	0
2	NA	T	201	1/1	0.95	0.10	54,54,54,54	0
2	NA	V	201	1/1	0.95	0.07	47,47,47,47	0
2	NA	R	201	1/1	0.96	0.09	54,54,54,54	0
2	NA	g	201	1/1	0.96	0.08	48,48,48,48	0
2	NA	a	201	1/1	0.96	0.13	52,52,52,52	0
2	NA	p	201	1/1	0.96	0.22	63,63,63,63	0
3	F09	L	314	10/10	0.96	0.27	50,58,73,78	0
2	NA	s	201	1/1	0.96	0.08	54,54,54,54	0
2	NA	t	201	1/1	0.96	0.09	54,54,54,54	0
3	F09	c	314	10/10	0.96	0.36	53,59,69,80	0
2	NA	d	201	1/1	0.96	0.07	48,48,48,48	0
2	NA	O	201	1/1	0.97	0.09	45,45,45,45	0
2	NA	E	201	1/1	0.97	0.06	55,55,55,55	0
3	F09	a	314	10/10	0.97	0.22	47,58,73,87	0
2	NA	r	201	1/1	0.97	0.04	55,55,55,55	0
2	NA	N	201	1/1	0.97	0.07	49,49,49,49	0
2	NA	U	201	1/1	0.97	0.08	56,56,56,56	0
2	NA	f	201	1/1	0.97	0.10	54,54,54,54	0
3	F09	M	314	10/10	0.97	0.28	45,50,65,79	0
2	NA	b	201	1/1	0.98	0.10	50,50,50,50	0
2	NA	G	201	1/1	0.98	0.04	54,54,54,54	0
2	NA	A	201	1/1	0.98	0.10	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NA	I	201	1/1	0.98	0.09	48,48,48,48	0
2	NA	B	201	1/1	0.98	0.07	45,45,45,45	0
2	NA	q	201	1/1	0.98	0.07	67,67,67,67	0
2	NA	P	201	1/1	0.98	0.08	42,42,42,42	0
2	NA	i	201	1/1	0.98	0.05	46,46,46,46	0
2	NA	j	201	1/1	0.98	0.14	49,49,49,49	0
2	NA	l	201	1/1	0.99	0.09	51,51,51,51	0
2	NA	Q	201	1/1	0.99	0.05	53,53,53,53	0
2	NA	C	201	1/1	0.99	0.09	55,55,55,55	0
2	NA	v	201	1/1	0.99	0.12	45,45,45,45	0
2	NA	S	201	1/1	0.99	0.12	54,54,54,54	0
2	NA	c	201	1/1	0.99	0.07	51,51,51,51	0
2	NA	D	201	1/1	0.99	0.06	60,60,60,60	0
2	NA	M	201	1/1	0.99	0.06	44,44,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.