



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:51 AM UTC

PDB ID : 4OQ9 / pdb_00004oq9
Title : Satellite Tobacco Mosaic Virus Refined to 1.4 Å Resolution using non-crystallographic symmetry restraints
Authors : Larson, S.B.; Day, J.S.; McPherson, A.
Deposited on : 2014-02-07
Resolution : 1.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

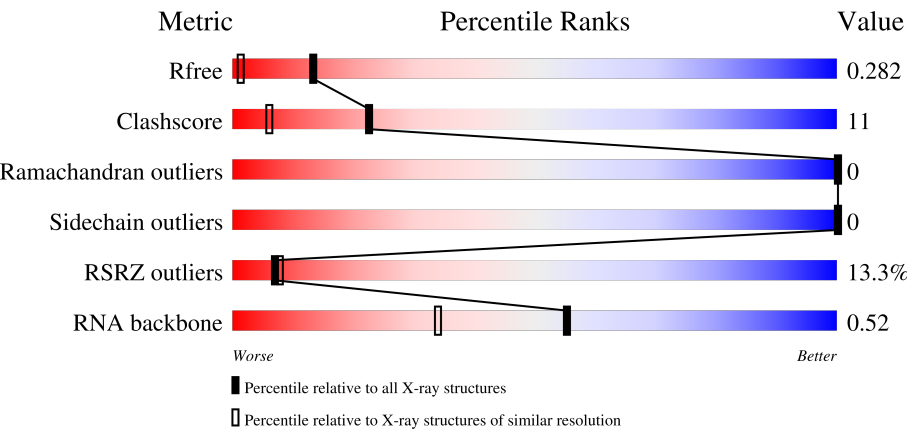
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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}	180053	1756 (1.46-1.46)
Clashscore	190562	1795 (1.46-1.46)
Ramachandran outliers	187476	1776 (1.46-1.46)
Sidechain outliers	187428	1776 (1.46-1.46)
RSRZ outliers	180081	1756 (1.46-1.46)
RNA backbone	3983	1019 (2.10-0.86)

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	159	3% 80% 11% 9%
1	B	159	% 86% . 9%
1	C	159	2% 86% 5% 9%
1	D	159	% 81% 10% 9%

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Mol	Chain	Length	Quality of chain
1	E	159	
1	F	159	
1	G	159	
1	H	159	
1	I	159	
1	J	159	
1	K	159	
1	L	159	
1	M	159	
1	N	159	
1	O	159	
2	P	10	
2	Q	10	
2	R	10	
2	S	10	
2	T	10	
2	U	10	
2	V	10	
2	W	10	
2	X	10	
2	Y	10	
2	Z	10	
2	a	10	
2	b	10	
2	c	10	

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Mol	Chain	Length	Quality of chain
2	d	10	
3	e	10	
3	f	10	
3	g	10	
3	h	10	
3	i	10	
3	j	10	
3	k	10	
3	l	10	
3	m	10	
3	n	10	
3	o	10	
3	p	10	
3	q	10	
3	r	10	
3	s	10	
4	1	2	
4	2	2	
4	3	2	
4	4	2	
4	5	2	
4	6	2	
4	7	2	
4	8	2	
4	t	2	

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Mol	Chain	Length	Quality of chain
4	u	2	100% 50% 50%
4	v	2	100% 50% 50%
4	w	2	100% 50% 50%
4	x	2	100% 50% 50%
4	y	2	100% 50% 50%
4	z	2	100% 50% 50%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 29296 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 Coat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	144	Total	C	N	O	S	0	15	0
			1201	761	213	219	8			
1	B	144	Total	C	N	O	S	0	14	0
			1191	753	210	219	9			
1	C	144	Total	C	N	O	S	0	18	0
			1204	768	210	217	9			
1	D	144	Total	C	N	O	S	0	19	0
			1223	779	215	220	9			
1	E	144	Total	C	N	O	S	0	16	0
			1211	768	214	220	9			
1	F	144	Total	C	N	O	S	0	18	0
			1216	775	214	218	9			
1	G	144	Total	C	N	O	S	0	16	0
			1198	760	210	219	9			
1	H	144	Total	C	N	O	S	0	17	0
			1205	766	210	221	8			
1	I	144	Total	C	N	O	S	0	16	0
			1201	762	210	220	9			
1	J	144	Total	C	N	O	S	0	15	0
			1190	751	210	221	8			
1	K	144	Total	C	N	O	S	0	16	0
			1198	761	209	219	9			
1	L	144	Total	C	N	O	S	0	18	0
			1209	769	212	219	9			
1	M	144	Total	C	N	O	S	0	17	0
			1201	764	210	219	8			
1	N	144	Total	C	N	O	S	0	16	0
			1198	758	211	220	9			
1	O	144	Total	C	N	O	S	0	21	0
			1221	780	212	220	9			

- Molecule 2 is a RNA chain called RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	Q	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	R	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	S	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	T	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	U	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	V	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	W	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	X	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	Y	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	Z	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	a	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	b	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	c	10	Total 221	C 100	N 50	O 61	P 10	0	10	0
2	d	10	Total 221	C 100	N 50	O 61	P 10	0	10	0

- Molecule 3 is a RNA chain called RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	e	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	f	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	g	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	h	10	Total 201	C 90	N 20	O 81	P 10	0	10	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	i	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	j	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	k	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	l	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	m	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	n	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	o	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	p	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	q	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	r	10	Total 201	C 90	N 20	O 81	P 10	0	10	0
3	s	10	Total 201	C 90	N 20	O 81	P 10	0	10	0

- Molecule 4 is a RNA chain called RNA (5'-R(P*UP*U)-3').

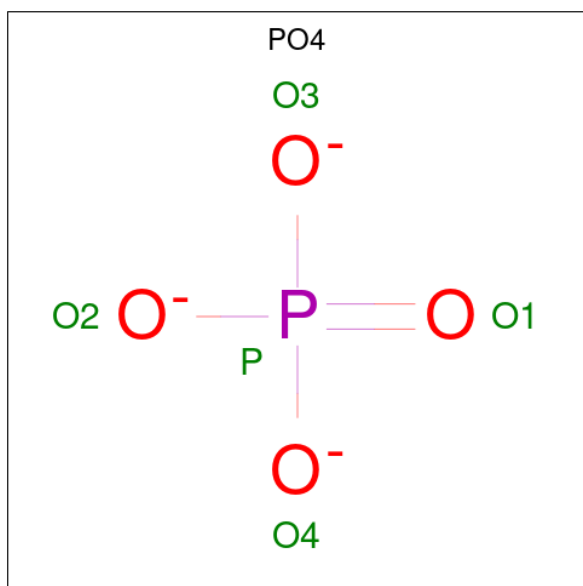
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	t	2	Total 26	C 10	N 2	O 12	P 2	0	2	0
4	u	2	Total 26	C 10	N 2	O 12	P 2	0	2	0
4	v	2	Total 26	C 10	N 2	O 12	P 2	0	2	0
4	w	2	Total 26	C 10	N 2	O 12	P 2	0	2	0
4	x	2	Total 26	C 10	N 2	O 12	P 2	0	2	0
4	y	2	Total 26	C 10	N 2	O 12	P 2	0	2	0
4	z	2	Total 26	C 10	N 2	O 12	P 2	0	2	0
4	1	2	Total 26	C 10	N 2	O 12	P 2	0	2	0

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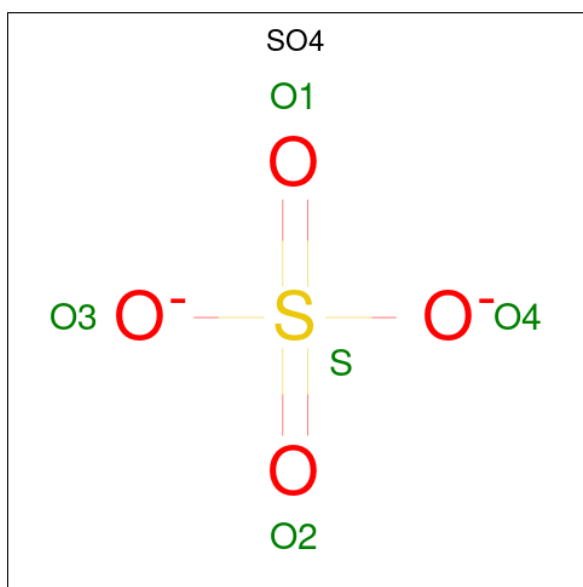
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	2	2	Total	C	N	O	P	0	2	0
			26	10	2	12	2			
4	3	2	Total	C	N	O	P	0	2	0
			26	10	2	12	2			
4	4	2	Total	C	N	O	P	0	2	0
			26	10	2	12	2			
4	5	2	Total	C	N	O	P	0	2	0
			26	10	2	12	2			
4	6	2	Total	C	N	O	P	0	2	0
			26	10	2	12	2			
4	7	2	Total	C	N	O	P	0	2	0
			26	10	2	12	2			
4	8	2	Total	C	N	O	P	0	2	0
			26	10	2	12	2			

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	1
			21	20	1		
5	H	1	Total	O	P	0	1
			21	20	1		
5	N	1	Total	O	P	0	1
			21	20	1		

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	C	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	E	1	Total	O	S	0	1
			25	20	5		
6	E	1	Total	O	S	0	0
			5	4	1		
6	F	1	Total	O	S	0	0
			5	4	1		
6	G	1	Total	O	S	0	1
			25	20	5		
6	G	1	Total	O	S	0	0
			5	4	1		
6	H	1	Total	O	S	0	0
			5	4	1		
6	I	1	Total	O	S	0	0
			5	4	1		
6	J	1	Total	O	S	0	0
			5	4	1		
6	K	1	Total	O	S	0	0
			5	4	1		
6	L	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	M	1	Total	O	S	0	1
			25	20	5		
6	M	1	Total	O	S	0	0
			5	4	1		
6	N	1	Total	O	S	0	0
			5	4	1		
6	O	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	E	1	Total 1	Mg 1	0	0
8	F	1	Total 1	Mg 1	0	0
8	K	1	Total 1	Mg 1	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	271	Total 271	O 271	0	77
9	B	267	Total 267	O 267	0	51
9	C	263	Total 263	O 263	0	43
9	D	228	Total 228	O 228	0	39
9	E	269	Total 269	O 269	0	46
9	F	259	Total 259	O 259	0	49
9	G	275	Total 275	O 275	0	49
9	H	277	Total 277	O 277	0	51
9	I	253	Total 253	O 253	0	55
9	J	279	Total 279	O 279	0	53
9	K	240	Total 240	O 240	0	60
9	L	303	Total 303	O 303	0	64
9	M	298	Total 298	O 298	0	58
9	N	254	Total 254	O 254	0	60
9	O	309	Total 309	O 309	0	70
9	P	7	Total 7	O 7	0	4

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	Q	7	Total 7	O 7	0	2
9	R	6	Total 6	O 6	0	1
9	S	8	Total 8	O 8	0	3
9	T	5	Total 5	O 5	0	1
9	U	7	Total 7	O 7	0	2
9	V	7	Total 7	O 7	0	0
9	W	6	Total 6	O 6	0	1
9	X	4	Total 4	O 4	0	2
9	Y	6	Total 6	O 6	0	1
9	Z	7	Total 7	O 7	0	2
9	a	13	Total 13	O 13	0	7
9	b	6	Total 6	O 6	0	3
9	c	6	Total 6	O 6	0	2
9	d	7	Total 7	O 7	0	2
9	e	5	Total 5	O 5	0	3
9	f	8	Total 8	O 8	0	1
9	g	9	Total 9	O 9	0	3
9	h	10	Total 10	O 10	0	2
9	i	9	Total 9	O 9	0	4
9	j	5	Total 5	O 5	0	1
9	k	9	Total 9	O 9	0	2

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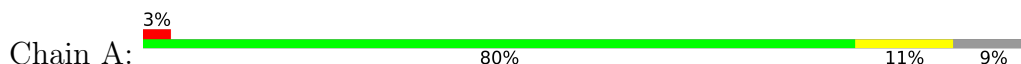
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	l	8	Total 8	O 8	0	2
9	m	10	Total 10	O 10	0	4
9	n	8	Total 8	O 8	0	3
9	o	9	Total 9	O 9	0	2
9	p	6	Total 6	O 6	0	0
9	q	10	Total 10	O 10	0	4
9	r	10	Total 10	O 10	0	3
9	s	7	Total 7	O 7	0	2
9	t	1	Total 1	O 1	0	0
9	x	2	Total 2	O 2	0	0
9	4	1	Total 1	O 1	0	0
9	6	1	Total 1	O 1	0	0
9	8	1	Total 1	O 1	0	0

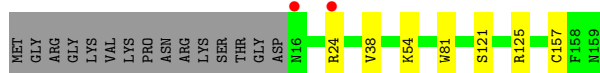
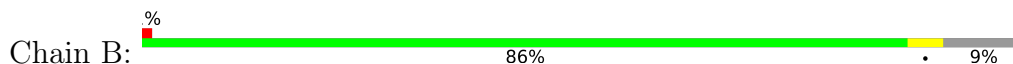
3 Residue-property plots [i](#)

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.

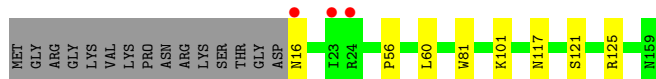
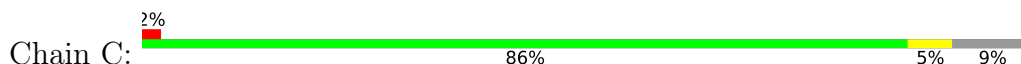
- Molecule 1: Coat protein



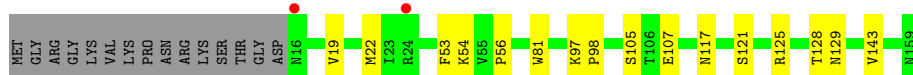
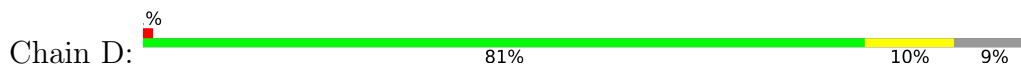
- Molecule 1: Coat protein



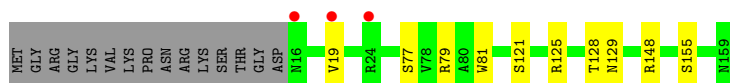
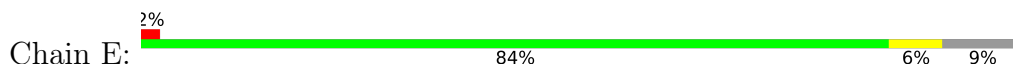
- Molecule 1: Coat protein



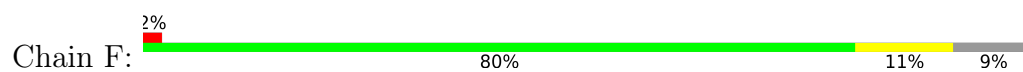
- Molecule 1: Coat protein



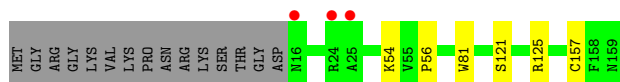
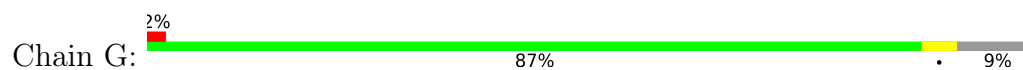
- Molecule 1: Coat protein



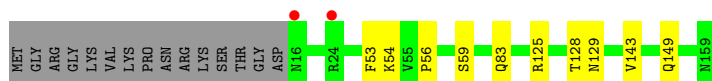
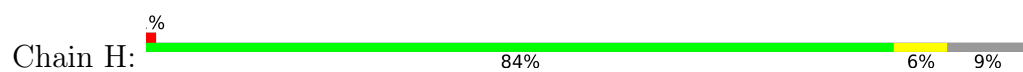
- Molecule 1: Coat protein



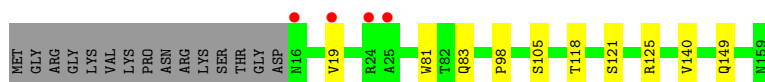
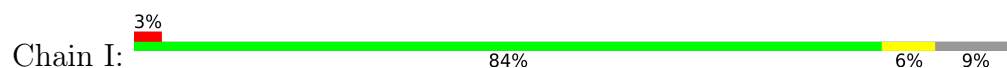
• Molecule 1: Coat protein



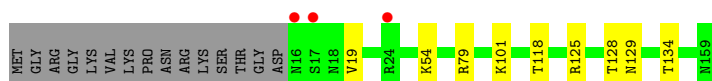
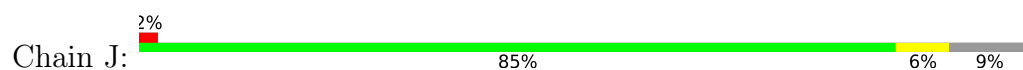
• Molecule 1: Coat protein



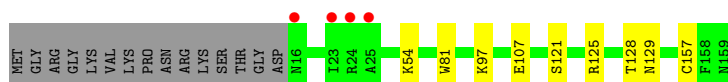
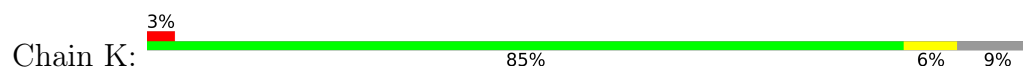
• Molecule 1: Coat protein



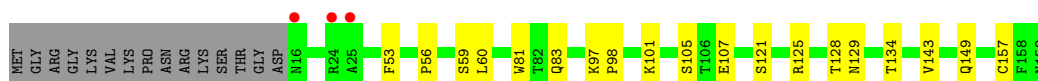
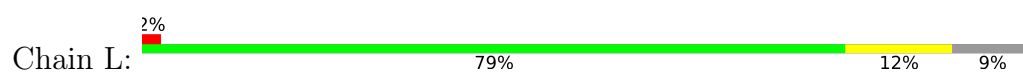
• Molecule 1: Coat protein



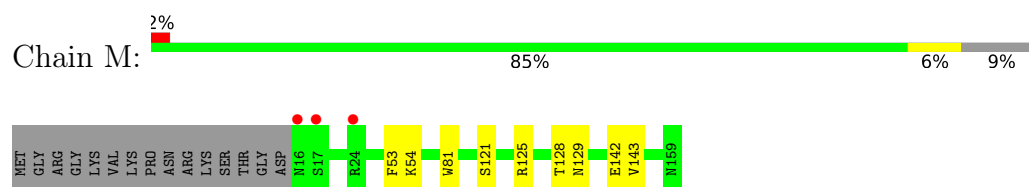
• Molecule 1: Coat protein



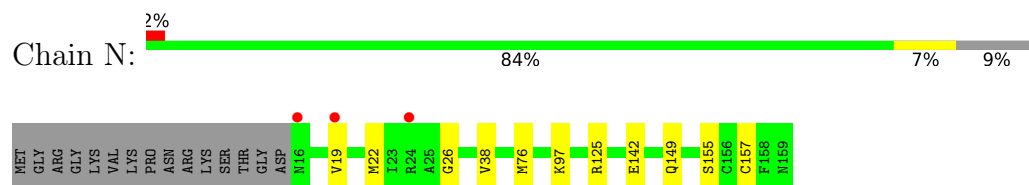
• Molecule 1: Coat protein



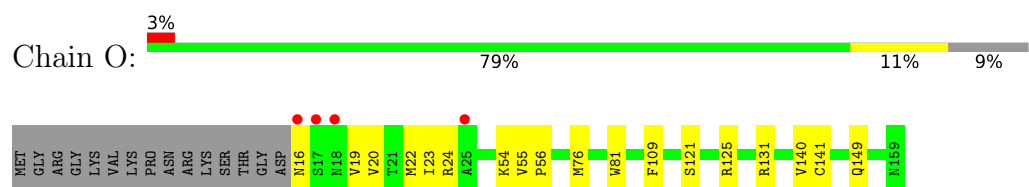
- Molecule 1: Coat protein



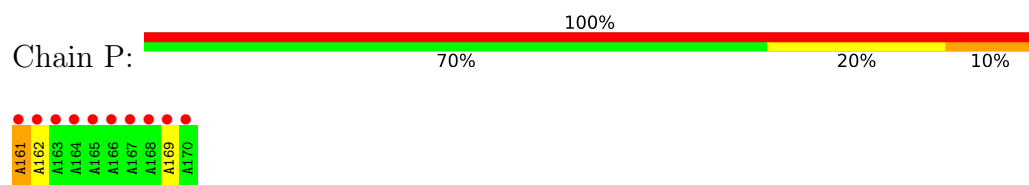
- Molecule 1: Coat protein



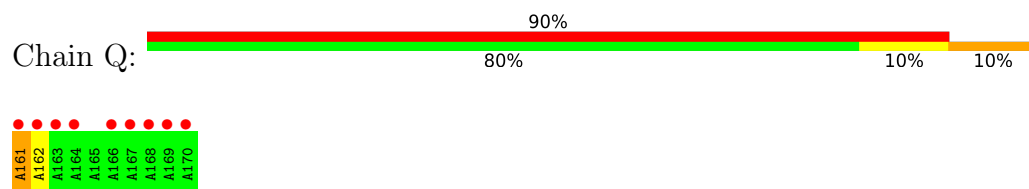
- Molecule 1: Coat protein



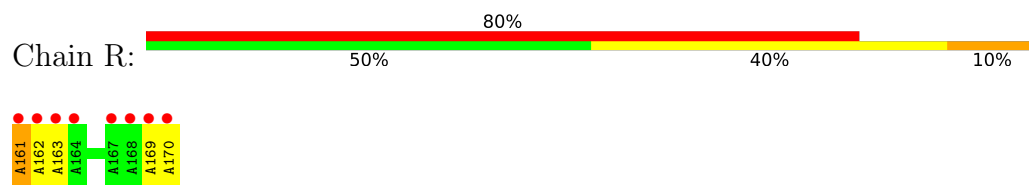
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')

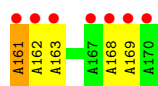


- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')

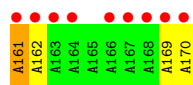


- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')

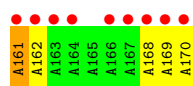
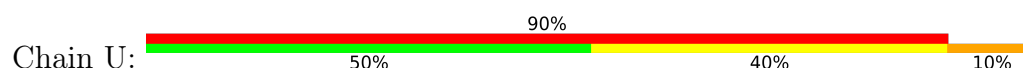




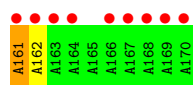
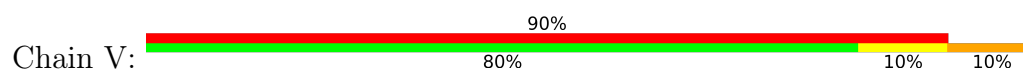
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



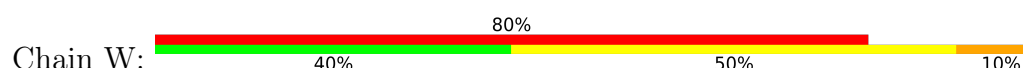
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



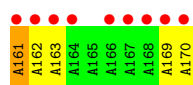
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



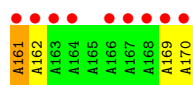
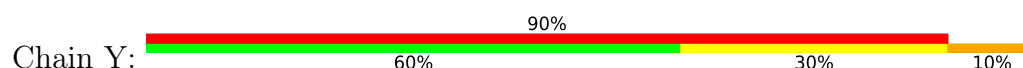
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



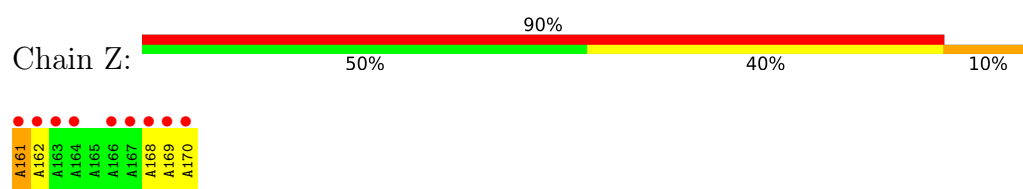
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



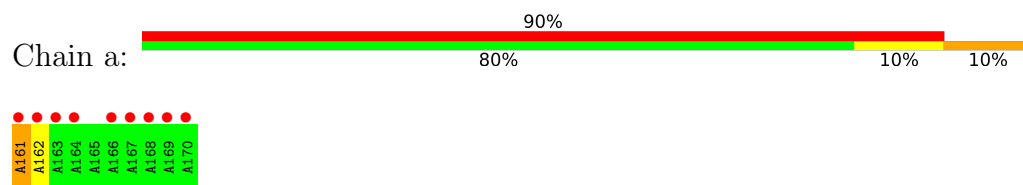
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



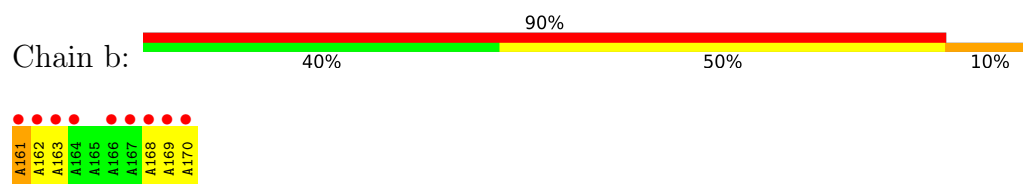
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



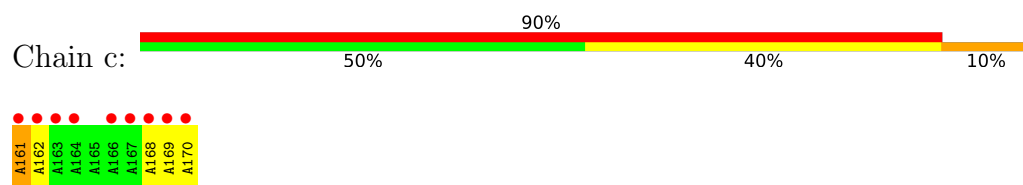
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



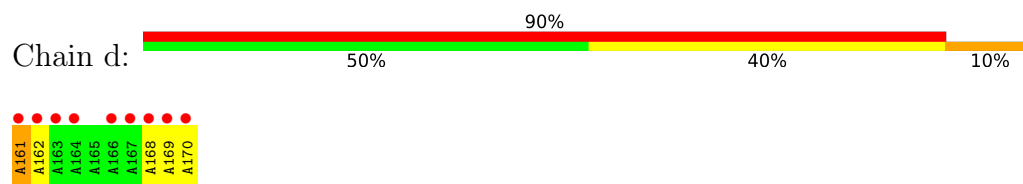
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



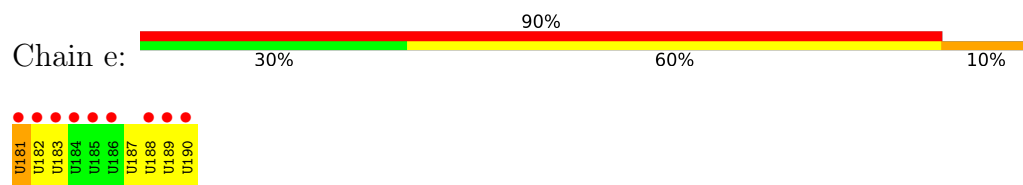
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



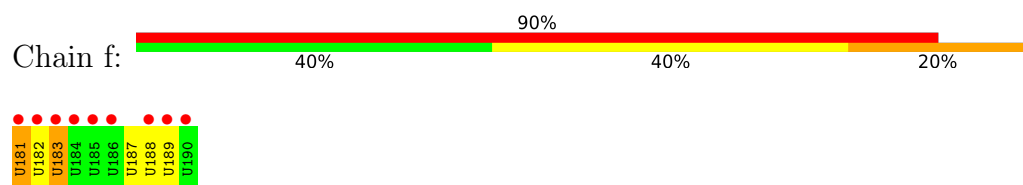
- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



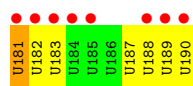
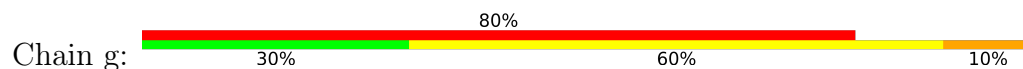
- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



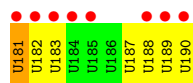
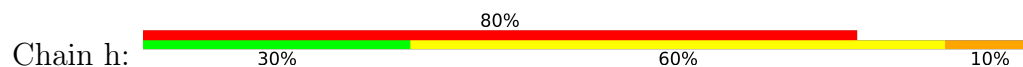
- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



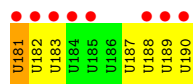
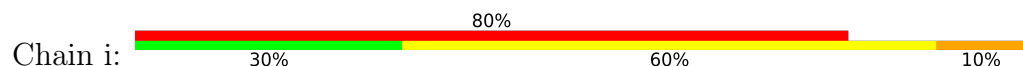
- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



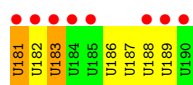
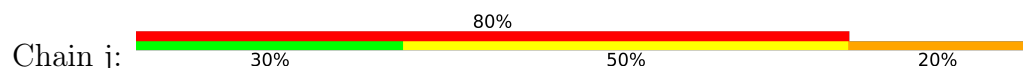
- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



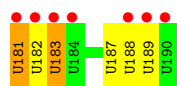
- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



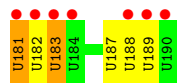
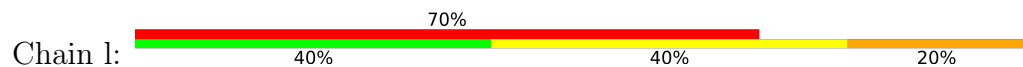
- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



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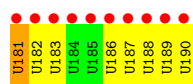


- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')

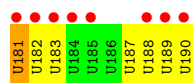
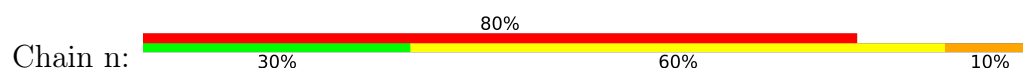


- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')

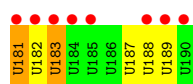
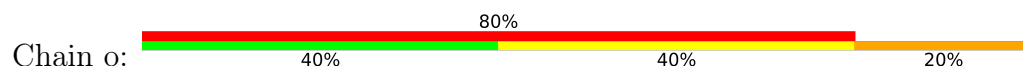




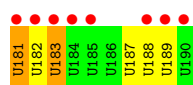
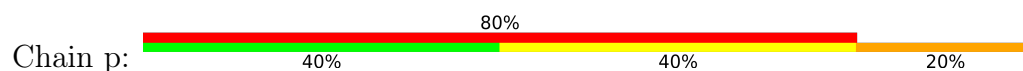
- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



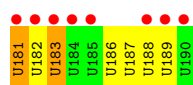
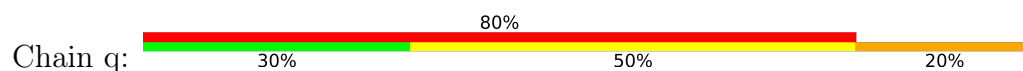
- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



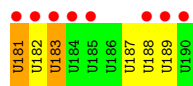
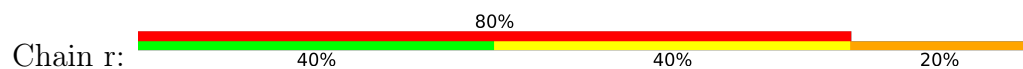
- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



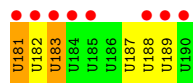
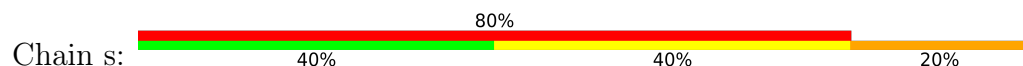
- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



- Molecule 3: RNA (5'-R(P*UP*UP*UP*UP*UP*UP*UP*UP*UP*U)-3')



- Molecule 4: RNA (5'-R(P*UP*U)-3')



- Molecule 4: RNA (5'-R(P*UP*U)-3')



- Molecule 4: RNA (5'-R(P*UP*U)-3')



- Molecule 4: RNA (5'-R(P*UP*U)-3')



- Molecule 4: RNA (5'-R(P*UP*U)-3')



- Molecule 4: RNA (5'-R(P*UP*U)-3')



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- Molecule 4: RNA (5'-R(P*UP*U)-3')



- Molecule 4: RNA (5'-R(P*UP*U)-3')



- Molecule 4: RNA (5'-R(P*UP*U)-3')





- Molecule 4: RNA (5'-R(P*UP*U)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	172.69Å 190.30Å 201.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.35 – 1.45 48.35 – 1.45	Depositor EDS
% Data completeness (in resolution range)	98.5 (48.35-1.45) 98.5 (48.35-1.45)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.44 (at 1.45Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.217 , 0.250 (Not available) , 0.282	Depositor DCC
R_{free} test set	28799 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	18.5	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 105.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	29296	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.17% 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: SO4, NA, PO4, MG

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	0.68	0/1271	0.79	0/1727
1	B	0.63	0/1251	0.76	0/1700
1	C	0.63	0/1284	0.78	0/1743
1	D	0.66	0/1309	0.75	0/1777
1	E	0.65	0/1286	0.75	0/1746
1	F	0.67	0/1303	0.78	1/1767 (0.1%)
1	G	0.61	0/1266	0.75	0/1721
1	H	0.62	0/1279	0.75	0/1740
1	I	0.66	0/1272	0.78	1/1728 (0.1%)
1	J	0.64	0/1256	0.76	0/1707
1	K	0.66	0/1273	0.80	0/1729
1	L	0.62	0/1292	0.77	0/1753
1	M	0.63	0/1274	0.77	0/1732
1	N	0.69	0/1267	0.79	0/1721
1	O	0.64	0/1306	0.75	0/1775
2	P	0.53	1/250 (0.4%)	0.88	0/386
2	Q	0.52	1/250 (0.4%)	0.86	0/386
2	R	0.53	1/250 (0.4%)	0.87	0/386
2	S	0.55	1/250 (0.4%)	0.87	0/386
2	T	0.54	1/250 (0.4%)	0.88	0/386
2	U	0.53	1/250 (0.4%)	0.86	0/386
2	V	0.54	1/250 (0.4%)	0.87	0/386
2	W	0.53	1/250 (0.4%)	0.86	0/386
2	X	0.53	1/250 (0.4%)	0.87	0/386
2	Y	0.53	1/250 (0.4%)	0.87	0/386
2	Z	0.52	1/250 (0.4%)	0.88	0/386
2	a	0.54	1/250 (0.4%)	0.88	0/386
2	b	0.54	1/250 (0.4%)	0.87	0/386
2	c	0.53	1/250 (0.4%)	0.87	0/386
2	d	0.54	1/250 (0.4%)	0.87	0/386
3	e	0.58	1/220 (0.5%)	0.92	0/336
3	f	0.57	1/220 (0.5%)	0.86	0/336

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	g	0.58	1/220 (0.5%)	0.92	0/336
3	h	0.59	1/220 (0.5%)	0.90	0/336
3	i	0.59	1/220 (0.5%)	0.91	0/336
3	j	0.58	1/220 (0.5%)	0.87	1/336 (0.3%)
3	k	0.57	1/220 (0.5%)	0.85	0/336
3	l	0.57	1/220 (0.5%)	0.86	0/336
3	m	0.59	1/220 (0.5%)	0.91	0/336
3	n	0.59	1/220 (0.5%)	0.92	0/336
3	o	0.58	1/220 (0.5%)	0.86	0/336
3	p	0.57	1/220 (0.5%)	0.86	0/336
3	q	0.56	1/220 (0.5%)	0.86	0/336
3	r	0.56	1/220 (0.5%)	0.86	0/336
3	s	0.58	1/220 (0.5%)	0.87	0/336
4	1	1.17	1/27 (3.7%)	0.89	0/38
4	2	1.20	1/27 (3.7%)	0.96	0/38
4	3	1.17	1/27 (3.7%)	0.93	0/38
4	4	1.16	1/27 (3.7%)	0.91	0/38
4	5	1.17	1/27 (3.7%)	0.84	0/38
4	6	1.17	1/27 (3.7%)	0.88	0/38
4	7	1.18	1/27 (3.7%)	0.98	0/38
4	8	1.15	1/27 (3.7%)	0.89	0/38
4	t	1.17	1/27 (3.7%)	0.90	0/38
4	u	1.18	1/27 (3.7%)	0.87	0/38
4	v	1.18	1/27 (3.7%)	0.90	0/38
4	w	1.18	1/27 (3.7%)	0.85	0/38
4	x	1.13	1/27 (3.7%)	0.86	0/38
4	y	1.16	1/27 (3.7%)	0.91	0/38
4	z	1.18	1/27 (3.7%)	0.90	0/38
All	All	0.64	45/26644 (0.2%)	0.80	3/37466 (0.0%)

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	W	161[B]	A	OP3-P	6.15	1.60	1.48
2	V	161[A]	A	OP3-P	6.10	1.60	1.48
2	T	161[A]	A	OP3-P	6.06	1.60	1.48
2	U	161[B]	A	OP3-P	6.06	1.60	1.48
2	c	161[B]	A	OP3-P	6.04	1.60	1.48
2	d	161[B]	A	OP3-P	6.04	1.60	1.48
3	m	181[A]	U	OP3-P	6.04	1.60	1.48
3	h	181[A]	U	OP3-P	6.04	1.60	1.48
2	Q	161[A]	A	OP3-P	6.03	1.60	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	s	181[B]	U	OP3-P	6.02	1.60	1.48
3	l	181[B]	U	OP3-P	6.02	1.60	1.48
2	Y	161[A]	A	OP3-P	6.01	1.60	1.48
2	R	161[A]	A	OP3-P	6.01	1.60	1.48
2	X	161[A]	A	OP3-P	6.01	1.60	1.48
2	S	161[A]	A	OP3-P	6.01	1.60	1.48
2	b	161[B]	A	OP3-P	6.01	1.60	1.48
3	f	181[B]	U	OP3-P	6.00	1.60	1.48
3	j	181[B]	U	OP3-P	6.00	1.60	1.48
3	q	181[B]	U	OP3-P	6.00	1.60	1.48
3	o	181[B]	U	OP3-P	5.98	1.60	1.48
2	P	161[A]	A	OP3-P	5.98	1.60	1.48
2	a	161[A]	A	OP3-P	5.97	1.60	1.48
3	k	181[B]	U	OP3-P	5.97	1.60	1.48
3	g	181[A]	U	OP3-P	5.96	1.60	1.48
3	p	181[B]	U	OP3-P	5.94	1.60	1.48
2	Z	161[B]	A	OP3-P	5.92	1.60	1.48
3	n	181[A]	U	OP3-P	5.91	1.60	1.48
3	r	181[B]	U	OP3-P	5.91	1.60	1.48
4	v	195[B]	U	OP3-P	5.89	1.60	1.48
3	e	181[A]	U	OP3-P	5.88	1.60	1.48
3	i	181[A]	U	OP3-P	5.86	1.60	1.48
4	w	195[B]	U	OP3-P	5.83	1.60	1.48
4	z	195[A]	U	OP3-P	5.83	1.60	1.48
4	7	195[A]	U	OP3-P	5.83	1.60	1.48
4	1	195[A]	U	OP3-P	5.81	1.60	1.48
4	t	195[B]	U	OP3-P	5.80	1.60	1.48
4	u	195[A]	U	OP3-P	5.80	1.60	1.48
4	3	195[B]	U	OP3-P	5.78	1.60	1.48
4	6	195[A]	U	OP3-P	5.78	1.60	1.48
4	y	195[A]	U	OP3-P	5.77	1.59	1.48
4	5	195[A]	U	OP3-P	5.76	1.59	1.48
4	2	195[B]	U	OP3-P	5.75	1.59	1.48
4	4	195[A]	U	OP3-P	5.72	1.59	1.48
4	x	195[B]	U	OP3-P	5.68	1.59	1.48
4	8	195[A]	U	OP3-P	5.66	1.59	1.48

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	140	VAL	CB-CA-C	-5.21	105.09	111.92
1	F	137	ALA	N-CA-C	5.11	118.61	112.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	j	186[B]	U	C1'-C2'-O2'	5.04	115.96	108.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1201	0	1240	21	0
1	B	1191	0	1224	8	0
1	C	1204	0	1262	8	0
1	D	1223	0	1283	14	0
1	E	1211	0	1260	11	0
1	F	1216	0	1280	15	0
1	G	1198	0	1238	7	0
1	H	1205	0	1250	9	0
1	I	1201	0	1245	10	0
1	J	1190	0	1219	9	0
1	K	1198	0	1247	10	0
1	L	1209	0	1266	16	0
1	M	1201	0	1248	8	0
1	N	1198	0	1236	9	0
1	O	1221	0	1276	34	0
2	P	221	0	93	3	0
2	Q	221	0	111	1	0
2	R	221	0	111	10	0
2	S	221	0	110	7	0
2	T	221	0	96	6	0
2	U	221	0	96	14	0
2	V	221	0	111	1	0
2	W	221	0	111	14	0
2	X	221	0	111	11	0
2	Y	221	0	94	7	0
2	Z	221	0	96	13	0
2	a	221	0	111	1	0
2	b	221	0	111	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	c	221	0	111	12	0
2	d	221	0	93	19	0
3	e	201	0	83	15	0
3	f	201	0	101	10	0
3	g	201	0	101	22	0
3	h	201	0	100	19	0
3	i	201	0	83	18	0
3	j	201	0	83	22	0
3	k	201	0	101	10	0
3	l	201	0	101	23	0
3	m	201	0	101	24	0
3	n	201	0	84	19	0
3	o	201	0	83	21	0
3	p	201	0	101	10	0
3	q	201	0	101	24	0
3	r	201	0	101	21	0
3	s	201	0	82	27	0
4	1	26	0	10	5	0
4	2	26	0	10	5	0
4	3	26	0	10	1	0
4	4	26	0	10	4	0
4	5	26	0	10	5	0
4	6	26	0	10	3	0
4	7	26	0	10	2	0
4	8	26	0	10	6	0
4	t	26	0	10	5	0
4	u	26	0	10	3	0
4	v	26	0	10	2	0
4	w	26	0	10	4	0
4	x	26	0	10	4	0
4	y	26	0	10	5	0
4	z	26	0	10	3	0
5	A	21	0	0	2	0
5	H	21	0	0	0	0
5	N	21	0	0	0	0
6	A	5	0	0	0	0
6	B	5	0	0	0	0
6	C	5	0	0	0	0
6	D	5	0	0	0	0
6	E	30	0	0	0	0
6	F	5	0	0	0	0
6	G	30	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	H	5	0	0	0	0
6	I	5	0	0	0	0
6	J	5	0	0	0	0
6	K	5	0	0	0	0
6	L	5	0	0	0	0
6	M	30	0	0	0	0
6	N	5	0	0	0	0
6	O	5	0	0	0	0
7	A	1	0	0	0	0
7	B	2	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
7	E	2	0	0	0	0
7	F	1	0	0	0	0
7	G	1	0	0	0	0
7	H	1	0	0	0	0
7	I	1	0	0	0	0
7	J	1	0	0	0	0
7	K	1	0	0	0	0
7	L	1	0	0	0	0
7	M	1	0	0	0	0
7	N	1	0	0	0	0
7	O	1	0	0	0	0
8	E	1	0	0	0	0
8	F	1	0	0	0	0
8	K	1	0	0	0	0
9	4	1	0	0	0	0
9	6	1	0	0	0	0
9	8	1	0	0	0	0
9	A	271	0	0	6	0
9	B	267	0	0	4	0
9	C	263	0	0	2	0
9	D	228	0	0	2	0
9	E	269	0	0	2	0
9	F	259	0	0	3	0
9	G	275	0	0	2	0
9	H	277	0	0	2	0
9	I	253	0	0	2	0
9	J	279	0	0	3	0
9	K	240	0	0	3	0
9	L	303	0	0	1	0
9	M	298	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	N	254	0	0	3	0
9	O	309	0	0	3	0
9	P	7	0	0	0	0
9	Q	7	0	0	0	0
9	R	6	0	0	0	0
9	S	8	0	0	0	0
9	T	5	0	0	0	0
9	U	7	0	0	0	0
9	V	7	0	0	1	0
9	W	6	0	0	0	0
9	X	4	0	0	0	0
9	Y	6	0	0	0	0
9	Z	7	0	0	0	0
9	a	13	0	0	0	0
9	b	6	0	0	0	0
9	c	6	0	0	0	0
9	d	7	0	0	0	0
9	e	5	0	0	0	0
9	f	8	0	0	0	0
9	g	9	0	0	0	0
9	h	10	0	0	0	0
9	i	9	0	0	0	0
9	j	5	0	0	0	0
9	k	9	0	0	0	0
9	l	8	0	0	0	0
9	m	10	0	0	1	0
9	n	8	0	0	0	0
9	o	9	0	0	0	0
9	p	6	0	0	0	0
9	q	10	0	0	1	0
9	r	10	0	0	0	0
9	s	7	0	0	0	0
9	t	1	0	0	0	0
9	x	2	0	0	0	0
All	All	29296	0	21896	487	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 11.

All (487) 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:T:170[A]:A:N6	3:i:181[A]:U:H3	1.15	1.43
2:R:170[A]:A:N6	3:g:181[A]:U:H3	1.10	1.41
2:T:170[A]:A:N6	3:i:181[A]:U:N3	1.67	1.41
2:X:170[A]:A:N6	3:m:181[A]:U:N3	1.72	1.38
2:d:170[B]:A:N1	3:s:181[B]:U:O2	1.56	1.38
2:R:170[A]:A:N6	3:g:181[A]:U:N3	1.71	1.34
2:Y:170[A]:A:N6	3:n:181[A]:U:N3	1.80	1.29
2:d:170[B]:A:C2	3:s:181[B]:U:O2	1.86	1.26
2:W:170[B]:A:N6	3:l:181[B]:U:N3	1.82	1.26
2:b:170[B]:A:N6	3:q:181[B]:U:N3	1.83	1.26
2:X:170[A]:A:N6	3:m:181[A]:U:H3	1.27	1.25
2:U:170[B]:A:N6	3:j:181[B]:U:N3	1.87	1.23
2:d:170[B]:A:N1	3:s:181[B]:U:C2	2.06	1.23
2:d:170[B]:A:N6	3:s:181[B]:U:N3	1.90	1.20
2:Z:170[B]:A:N6	3:o:181[B]:U:N3	1.88	1.19
2:Y:170[A]:A:N6	3:n:181[A]:U:H3	1.36	1.18
2:d:170[B]:A:C6	3:s:181[B]:U:C2	2.33	1.16
3:h:182[A]:U:H6	3:h:182[A]:U:O5'	1.29	1.14
3:e:182[A]:U:H6	3:e:182[A]:U:O5'	1.29	1.13
1:A:157[B]:CYS:SG	1:J:19:VAL:HG11	1.90	1.12
3:i:182[A]:U:O5'	3:i:182[A]:U:H6	1.30	1.12
2:c:170[B]:A:N6	3:r:181[B]:U:N3	1.96	1.12
3:g:182[A]:U:H6	3:g:182[A]:U:O5'	1.30	1.11
3:n:182[A]:U:H6	3:n:182[A]:U:O5'	1.34	1.10
3:m:182[A]:U:O5'	3:m:182[A]:U:H6	1.31	1.09
2:d:170[B]:A:C6	3:s:181[B]:U:N3	2.21	1.08
2:W:170[B]:A:N6	3:l:181[B]:U:H3	1.44	1.08
2:U:170[B]:A:N6	3:j:181[B]:U:H3	1.58	1.02
1:E:19:VAL:HG11	1:K:157[B]:CYS:SG	1.99	1.02
2:X:170[A]:A:C6	3:m:181[A]:U:N3	2.14	1.01
3:f:182[B]:U:H6	3:f:182[B]:U:O5'	1.46	0.99
2:d:169[B]:A:N6	3:s:181[B]:U:O4	1.96	0.99
3:q:182[B]:U:H6	3:q:182[B]:U:O5'	1.46	0.99
3:r:182[B]:U:H6	3:r:182[B]:U:O5'	1.46	0.98
2:b:170[B]:A:N6	3:q:181[B]:U:H3	1.51	0.98
2:d:170[B]:A:C6	3:s:181[B]:U:O2	2.15	0.98
3:j:182[B]:U:O5'	3:j:182[B]:U:H6	1.47	0.97
2:Z:170[B]:A:N6	3:o:181[B]:U:H3	1.57	0.97
3:s:182[B]:U:H6	3:s:182[B]:U:O5'	1.46	0.97
3:k:182[B]:U:H6	3:k:182[B]:U:O5'	1.47	0.97
3:l:182[B]:U:H6	3:l:182[B]:U:O5'	1.46	0.97
3:p:182[B]:U:H6	3:p:182[B]:U:O5'	1.47	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:19:VAL:HG11	1:G:157[B]:CYS:SG	2.04	0.96
2:c:169[B]:A:N6	3:r:181[B]:U:O4	1.99	0.96
2:b:170[B]:A:C6	3:q:181[B]:U:N3	2.31	0.96
2:U:170[B]:A:C6	3:j:181[B]:U:N3	2.34	0.96
3:o:182[B]:U:O5'	3:o:182[B]:U:H6	1.46	0.96
2:Y:170[A]:A:N6	3:n:181[A]:U:C4	2.34	0.95
3:h:182[A]:U:O5'	3:h:182[A]:U:C6	2.19	0.95
3:e:182[A]:U:O5'	3:e:182[A]:U:C6	2.19	0.95
2:c:170[B]:A:N6	3:r:181[B]:U:H3	1.63	0.94
3:i:182[A]:U:O5'	3:i:182[A]:U:C6	2.19	0.94
2:T:170[A]:A:N6	3:i:181[A]:U:C4	2.36	0.94
3:g:182[A]:U:O5'	3:g:182[A]:U:C6	2.20	0.94
2:U:169[B]:A:N6	3:j:181[B]:U:O4	2.00	0.94
3:m:182[A]:U:O5'	3:m:182[A]:U:C6	2.20	0.94
2:Z:170[B]:A:C6	3:o:181[B]:U:N3	2.36	0.93
2:b:162[B]:A:H61	3:q:188[B]:U:H3	0.97	0.92
3:n:182[A]:U:O5'	3:n:182[A]:U:C6	2.23	0.91
2:Y:170[A]:A:C6	3:n:181[A]:U:N3	2.06	0.91
2:c:162[B]:A:H61	3:r:188[B]:U:H3	1.16	0.91
2:Z:169[B]:A:N6	3:o:181[B]:U:O4	2.03	0.91
1:A:79[B]:ARG:NH2	2:d:169[B]:A:OP1	2.04	0.91
2:W:162[B]:A:H61	3:l:188[B]:U:H3	0.92	0.90
9:K:472:HOH:O	4:4:196[A]:U:C5'	2.19	0.89
9:M:475:HOH:O	4:6:196[A]:U:C5'	2.19	0.88
2:W:170[B]:A:C6	3:l:181[B]:U:N3	2.40	0.88
2:X:170[A]:A:N6	3:m:181[A]:U:C4	2.42	0.87
2:X:162[A]:A:H61	3:m:188[A]:U:H3	1.24	0.85
2:d:170[B]:A:N6	3:s:181[B]:U:H3	1.67	0.85
1:E:79[B]:ARG:NH2	2:U:169[B]:A:OP1	2.09	0.85
2:S:162[A]:A:H61	3:h:188[A]:U:H3	1.23	0.85
2:W:170[B]:A:N6	3:l:181[B]:U:C2	2.43	0.85
2:R:170[A]:A:C6	3:g:181[A]:U:N3	2.31	0.85
2:b:169[B]:A:N6	3:q:181[B]:U:O4	2.09	0.84
1:A:157[B]:CYS:SG	1:J:19:VAL:CG1	2.66	0.84
2:U:168[B]:A:N1	3:j:182[B]:U:N3	2.27	0.83
9:E:472:HOH:O	4:x:196[B]:U:C5'	2.27	0.82
2:W:162[B]:A:N6	3:l:188[B]:U:H3	1.76	0.82
2:d:168[B]:A:N1	3:s:182[B]:U:N3	2.26	0.82
1:E:19:VAL:CG1	1:K:157[B]:CYS:SG	2.68	0.81
2:d:169[B]:A:N1	3:s:181[B]:U:C4	2.49	0.81
2:R:162[A]:A:H61	3:g:188[A]:U:H3	1.26	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:168[B]:A:N1	3:o:182[B]:U:N3	2.29	0.80
2:U:170[B]:A:N6	3:j:181[B]:U:C2	2.48	0.80
9:B:475:HOH:O	4:u:196[A]:U:C5'	2.29	0.80
2:W:169[B]:A:N6	3:l:181[B]:U:O4	2.15	0.80
2:c:170[B]:A:C6	3:r:181[B]:U:N3	2.50	0.80
2:c:168[B]:A:N1	3:r:182[B]:U:N3	2.26	0.78
2:b:162[B]:A:N6	3:q:188[B]:U:H3	1.80	0.78
1:D:19:VAL:CG1	1:G:157[B]:CYS:SG	2.72	0.77
1:J:79[B]:ARG:NH2	2:Z:169[B]:A:OP1	2.16	0.77
2:c:170[B]:A:N6	3:r:181[B]:U:C2	2.52	0.77
1:O:55:VAL:HB	1:O:140[B]:VAL:HG12	1.66	0.76
2:d:170[B]:A:N6	3:s:181[B]:U:C4	2.53	0.76
9:D:467:HOH:O	4:w:196[B]:U:C5'	2.33	0.76
3:q:182[B]:U:O5'	3:q:182[B]:U:C6	2.37	0.76
1:I:19:VAL:HG11	1:L:157[B]:CYS:SG	2.26	0.76
2:Z:170[B]:A:N6	3:o:181[B]:U:C2	2.51	0.75
1:B:157[B]:CYS:SG	1:N:19:VAL:HG11	2.27	0.74
9:A:661:HOH:O	4:t:196[B]:U:C5'	2.36	0.74
1:F:53:PHE:HB3	1:F:143[B]:VAL:CG1	2.18	0.73
3:k:182[B]:U:O5'	3:k:182[B]:U:C6	2.38	0.73
2:b:170[B]:A:N6	3:q:181[B]:U:C2	2.48	0.73
9:F:467:HOH:O	4:y:196[A]:U:C5'	2.35	0.72
2:b:168[B]:A:N1	3:q:182[B]:U:N3	2.31	0.72
3:f:182[B]:U:O5'	3:f:182[B]:U:C6	2.37	0.72
3:l:182[B]:U:O5'	3:l:182[B]:U:C6	2.37	0.72
9:O:483:HOH:O	4:8:196[A]:U:C5'	2.37	0.72
3:j:182[B]:U:O5'	3:j:182[B]:U:C6	2.38	0.72
2:S:162[A]:A:N6	3:h:188[A]:U:H3	1.88	0.72
3:r:182[B]:U:O5'	3:r:182[B]:U:C6	2.37	0.71
9:G:486:HOH:O	4:z:196[A]:U:C5'	2.38	0.71
2:P:169[A]:A:N6	3:e:181[A]:U:O4	2.24	0.71
2:R:170[A]:A:N6	3:g:181[A]:U:C4	2.57	0.70
3:s:182[B]:U:O5'	3:s:182[B]:U:C6	2.37	0.70
9:J:355:HOH:O	1:K:128[B]:THR:HG22	1.89	0.70
2:R:170[A]:A:N6	3:g:181[A]:U:C2	2.56	0.70
1:D:54:LYS:O	1:D:56[B]:PRO:HD3	1.92	0.70
3:p:182[B]:U:O5'	3:p:182[B]:U:C6	2.38	0.70
3:o:182[B]:U:O5'	3:o:182[B]:U:C6	2.37	0.69
1:D:53:PHE:HB3	1:D:143[B]:VAL:CG1	2.22	0.69
2:X:169[A]:A:N6	3:m:181[A]:U:O4	2.25	0.69
2:d:169[B]:A:N1	3:s:181[B]:U:N3	2.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:h:188[A]:U:H2'	3:h:189[A]:U:C6	2.28	0.68
3:i:188[A]:U:H2'	3:i:189[A]:U:C6	2.29	0.67
1:A:128[B]:THR:HG22	9:A:768:HOH:O	1.94	0.67
1:O:54:LYS:O	1:O:56[B]:PRO:HD3	1.93	0.67
2:d:169[B]:A:C6	3:s:181[B]:U:O4	2.48	0.67
3:h:182[A]:U:C5	3:h:182[A]:U:OP2	2.48	0.67
3:e:188[A]:U:H2'	3:e:189[A]:U:C6	2.30	0.66
3:e:182[A]:U:OP2	3:e:182[A]:U:C5	2.48	0.66
3:m:188[A]:U:H2'	3:m:189[A]:U:C6	2.30	0.66
3:n:188[A]:U:H2'	3:n:189[A]:U:C6	2.30	0.66
3:g:188[A]:U:H2'	3:g:189[A]:U:C6	2.31	0.66
3:i:182[A]:U:C5	3:i:182[A]:U:OP2	2.49	0.66
1:H:54:LYS:HE2	9:H:520:HOH:O	1.96	0.66
2:b:170[B]:A:N6	3:q:181[B]:U:C4	2.63	0.66
2:c:169[B]:A:N1	3:r:181[B]:U:N3	2.44	0.66
3:g:182[A]:U:C5	3:g:182[A]:U:OP2	2.49	0.66
3:k:188[B]:U:H2'	3:k:189[B]:U:C6	2.30	0.66
3:j:188[B]:U:H2'	3:j:189[B]:U:C6	2.32	0.65
3:f:188[B]:U:H2'	3:f:189[B]:U:C6	2.31	0.65
3:o:188[B]:U:H2'	3:o:189[B]:U:C6	2.31	0.65
1:B:54:LYS:HE2	9:B:525:HOH:O	1.96	0.65
3:q:188[B]:U:H2'	3:q:189[B]:U:C6	2.32	0.65
3:l:188[B]:U:H2'	3:l:189[B]:U:C6	2.32	0.65
3:p:188[B]:U:H2'	3:p:189[B]:U:C6	2.32	0.65
3:m:182[A]:U:C5	3:m:182[A]:U:OP2	2.50	0.65
3:s:188[B]:U:H2'	3:s:189[B]:U:C6	2.32	0.64
3:r:188[B]:U:H2'	3:r:189[B]:U:C6	2.32	0.64
2:S:169[A]:A:N6	3:h:181[A]:U:O4	2.29	0.64
2:U:169[B]:A:N1	3:j:181[B]:U:N3	2.46	0.64
1:E:128[B]:THR:HG22	9:F:349:HOH:O	1.98	0.64
2:W:168[B]:A:N1	3:l:182[B]:U:N3	2.38	0.64
2:S:161[A]:A:O2'	2:S:162[A]:A:H5'	1.99	0.63
2:U:169[B]:A:N1	3:j:181[B]:U:C4	2.66	0.63
1:F:157[B]:CYS:SG	1:O:19:VAL:HG11	2.39	0.63
2:U:170[B]:A:N6	3:j:181[B]:U:C4	2.66	0.63
9:N:465:HOH:O	4:7:196[A]:U:C5'	2.47	0.62
3:h:182[A]:U:OP2	3:h:182[A]:U:H5	1.83	0.62
3:p:181[B]:U:O5'	3:p:181[B]:U:H6	1.83	0.62
1:O:55:VAL:HB	1:O:140[B]:VAL:CG1	2.29	0.62
1:M:53:PHE:HB3	1:M:143[B]:VAL:CG1	2.29	0.62
3:l:181[B]:U:H6	3:l:181[B]:U:O5'	1.83	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:e:182[A]:U:OP2	3:e:182[A]:U:H5	1.83	0.62
2:Z:170[B]:A:N6	3:o:181[B]:U:C4	2.68	0.61
3:q:181[B]:U:H6	3:q:181[B]:U:O5'	1.83	0.61
3:n:182[A]:U:C5	3:n:182[A]:U:OP2	2.53	0.61
1:D:53:PHE:HB3	1:D:143[B]:VAL:HG12	1.82	0.61
1:J:101[B]:LYS:HE3	1:J:134:THR:HG22	1.83	0.61
3:m:182[A]:U:OP2	3:m:182[A]:U:H5	1.84	0.61
2:Z:169[B]:A:N1	3:o:181[B]:U:N3	2.49	0.61
3:k:181[B]:U:O5'	3:k:181[B]:U:H6	1.84	0.61
1:H:53:PHE:HB3	1:H:143[B]:VAL:CG1	2.31	0.60
3:o:181[B]:U:H6	3:o:181[B]:U:O5'	1.83	0.60
3:j:181[B]:U:H6	3:j:181[B]:U:O5'	1.84	0.60
2:Z:169[B]:A:N1	3:o:181[B]:U:C4	2.69	0.60
1:G:54:LYS:O	1:G:56[B]:PRO:HD3	2.01	0.60
1:O:140[B]:VAL:HG13	1:O:141:CYS:SG	2.41	0.60
3:i:182[A]:U:OP2	3:i:182[A]:U:H5	1.83	0.60
1:L:53:PHE:HB3	1:L:143[B]:VAL:CG1	2.32	0.59
3:m:181[A]:U:C6	3:m:181[A]:U:H3'	2.38	0.59
1:F:53:PHE:HB3	1:F:143[B]:VAL:HG12	1.83	0.59
3:r:181[B]:U:H6	3:r:181[B]:U:O5'	1.84	0.59
1:L:125:ARG:HD2	4:5:195[A]:U:OP3	2.03	0.59
3:f:181[B]:U:H6	3:f:181[B]:U:O5'	1.84	0.59
3:k:188[B]:U:H2'	3:k:189[B]:U:H6	1.68	0.59
3:s:181[B]:U:O5'	3:s:181[B]:U:H6	1.85	0.59
3:g:182[A]:U:OP2	3:g:182[A]:U:H5	1.83	0.59
2:W:163[B]:A:H61	3:l:187[B]:U:H3	1.51	0.59
1:O:76[B]:MET:HG3	1:O:131:ARG:CZ	2.33	0.58
3:e:181[A]:U:C6	3:e:181[A]:U:H3'	2.38	0.58
3:g:181[A]:U:H3'	3:g:181[A]:U:C6	2.38	0.58
3:i:181[A]:U:H3'	3:i:181[A]:U:C6	2.38	0.58
1:O:140[B]:VAL:HG13	1:O:141:CYS:N	2.18	0.58
3:f:188[B]:U:H2'	3:f:189[B]:U:H6	1.69	0.58
3:h:181[A]:U:C6	3:h:181[A]:U:H3'	2.38	0.58
3:j:188[B]:U:H2'	3:j:189[B]:U:H6	1.69	0.58
9:L:5177:HOH:O	4:5:196[A]:U:C5'	2.51	0.58
3:p:181[B]:U:C5	3:p:181[B]:U:OP2	2.57	0.58
2:b:169[B]:A:N1	3:q:181[B]:U:C4	2.73	0.57
1:O:149[B]:GLN:NE2	9:O:535[B]:HOH:O	2.37	0.57
3:p:188[B]:U:H2'	3:p:189[B]:U:H6	1.69	0.57
9:H:475:HOH:O	4:1:196[A]:U:C5'	2.52	0.57
3:n:181[A]:U:H3'	3:n:181[A]:U:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:170[A]:A:C6	3:i:181[A]:U:N3	2.08	0.57
3:m:186[A]:U:OP1	9:m:209:HOH:O	2.17	0.57
1:J:128[B]:THR:HG22	9:K:351:HOH:O	2.05	0.57
2:S:163[A]:A:H61	3:h:187[A]:U:H3	1.52	0.57
2:c:169[B]:A:N1	3:r:181[B]:U:C4	2.72	0.57
2:d:168[B]:A:N6	3:s:182[B]:U:O4	2.37	0.57
1:G:54:LYS:HE2	9:G:508:HOH:O	2.05	0.56
3:o:188[B]:U:H2'	3:o:189[B]:U:H6	1.69	0.56
2:R:163[A]:A:H61	3:g:187[A]:U:H3	1.53	0.56
3:j:181[B]:U:C5	3:j:181[B]:U:OP2	2.58	0.56
3:l:181[B]:U:C5	3:l:181[B]:U:OP2	2.58	0.56
3:s:181[B]:U:C6	3:s:181[B]:U:H3'	2.41	0.56
2:X:163[A]:A:H61	3:m:187[A]:U:H3	1.53	0.56
2:Y:169[A]:A:N1	3:n:181[A]:U:C4	2.73	0.56
2:b:163[B]:A:H61	3:q:187[B]:U:H3	1.51	0.56
3:n:182[A]:U:OP2	3:n:182[A]:U:H5	1.88	0.56
3:r:188[B]:U:H2'	3:r:189[B]:U:H6	1.69	0.56
1:A:98:PRO:HD2	1:A:105[A]:SER:OG	2.05	0.56
1:F:125:ARG:HE	4:y:195[A]:U:H3'	1.71	0.56
1:I:125:ARG:HE	4:2:195[B]:U:H3'	1.71	0.56
2:X:169[A]:A:N1	3:m:181[A]:U:C4	2.74	0.56
1:D:125:ARG:HE	4:w:195[B]:U:H3'	1.70	0.56
1:M:53:PHE:HB3	1:M:143[B]:VAL:HG12	1.87	0.56
3:o:181[B]:U:C6	3:o:181[B]:U:H3'	2.41	0.56
3:q:181[B]:U:C5	3:q:181[B]:U:OP2	2.59	0.56
3:q:188[B]:U:H2'	3:q:189[B]:U:H6	1.69	0.55
3:f:181[B]:U:C5	3:f:181[B]:U:OP2	2.59	0.55
3:l:188[B]:U:H2'	3:l:189[B]:U:H6	1.69	0.55
1:B:24:ARG:HD2	9:B:541:HOH:O	2.06	0.55
1:O:125:ARG:HD2	4:8:195[A]:U:OP3	2.06	0.55
1:H:128[B]:THR:HG23	1:H:129:ASN:N	2.20	0.55
3:l:181[B]:U:C6	3:l:181[B]:U:H3'	2.41	0.55
3:o:181[B]:U:C5	3:o:181[B]:U:OP2	2.59	0.55
3:k:181[B]:U:C5	3:k:181[B]:U:OP2	2.59	0.55
3:k:181[B]:U:H3'	3:k:181[B]:U:C6	2.42	0.55
3:f:181[B]:U:H3'	3:f:181[B]:U:C6	2.42	0.55
1:I:19:VAL:CG1	1:L:157[B]:CYS:SG	2.95	0.55
3:r:181[B]:U:C5	3:r:181[B]:U:OP2	2.60	0.54
2:Y:169[A]:A:N6	3:n:181[A]:U:O4	2.40	0.54
2:d:170[B]:A:N6	3:s:181[B]:U:C2	2.60	0.54
3:s:181[B]:U:C5	3:s:181[B]:U:OP2	2.60	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118[B]:THR:HG21	9:A:706[B]:HOH:O	2.06	0.54
1:K:125:ARG:HE	4:4:195[A]:U:H3'	1.72	0.54
2:S:169[A]:A:N1	3:h:181[A]:U:C4	2.75	0.54
3:q:181[B]:U:C6	3:q:181[B]:U:H3'	2.41	0.54
4:y:195[A]:U:OP3	4:y:196[A]:U:C5'	2.56	0.54
1:B:38:VAL:HG22	1:B:157[B]:CYS:SG	2.48	0.54
1:D:22[A]:MET:HE2	9:V:207:HOH:O	2.07	0.54
3:p:181[B]:U:H3'	3:p:181[B]:U:C6	2.42	0.54
1:O:76[B]:MET:HG2	1:O:131:ARG:NH1	2.23	0.54
3:r:181[B]:U:H3'	3:r:181[B]:U:C6	2.43	0.53
1:K:54:LYS:HE2	9:K:523:HOH:O	2.06	0.53
2:b:169[B]:A:N1	3:q:181[B]:U:N3	2.55	0.53
3:j:181[B]:U:C6	3:j:181[B]:U:H3'	2.43	0.53
3:i:181[A]:U:C6	3:i:181[A]:U:C3'	2.92	0.53
2:c:168[B]:A:N6	3:r:182[B]:U:O4	2.38	0.53
3:g:181[A]:U:C5	3:g:181[A]:U:OP2	2.62	0.53
3:l:183[B]:U:H6	3:l:183[B]:U:O5'	1.91	0.53
3:o:183[B]:U:H6	3:o:183[B]:U:O5'	1.91	0.53
2:Z:168[B]:A:N6	3:o:182[B]:U:O4	2.39	0.53
3:j:183[B]:U:H6	3:j:183[B]:U:O5'	1.92	0.53
3:s:188[B]:U:H2'	3:s:189[B]:U:H6	1.70	0.53
1:O:125:ARG:HE	4:8:195[A]:U:H3'	1.73	0.53
3:g:181[A]:U:C6	3:g:181[A]:U:C3'	2.92	0.53
3:m:181[A]:U:C6	3:m:181[A]:U:C3'	2.92	0.53
1:E:125:ARG:HE	4:x:195[B]:U:H3'	1.74	0.53
1:L:97[B]:LYS:HG3	1:L:107:GLU:O	2.09	0.53
3:f:183[B]:U:H6	3:f:183[B]:U:O5'	1.91	0.53
3:p:183[B]:U:H6	3:p:183[B]:U:O5'	1.92	0.53
3:q:183[B]:U:H6	3:q:183[B]:U:O5'	1.92	0.53
1:O:76[B]:MET:HG3	1:O:131:ARG:HD3	1.91	0.52
3:k:183[B]:U:H6	3:k:183[B]:U:O5'	1.92	0.52
1:E:77:SER:OG	1:E:155[C]:SER:OG	2.27	0.52
3:r:183[B]:U:H6	3:r:183[B]:U:O5'	1.92	0.52
2:T:161[A]:A:O2'	2:T:162[A]:A:H5'	2.10	0.52
3:h:181[A]:U:C6	3:h:181[A]:U:C3'	2.92	0.52
3:e:181[A]:U:C5	3:e:181[A]:U:OP2	2.63	0.52
3:s:183[B]:U:O5'	3:s:183[B]:U:H6	1.92	0.52
1:L:128[B]:THR:HG23	1:L:129:ASN:N	2.25	0.52
3:e:181[A]:U:C6	3:e:181[A]:U:C3'	2.92	0.52
3:e:181[A]:U:O5'	3:e:181[A]:U:H6	1.93	0.52
1:A:128[B]:THR:CG2	9:A:768:HOH:O	2.54	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:125:ARG:HE	4:1:195[A]:U:H3'	1.75	0.51
1:I:98:PRO:HD2	1:I:105[A]:SER:OG	2.11	0.51
2:P:169[A]:A:N1	3:e:181[A]:U:C4	2.77	0.51
1:H:56:PRO:HG2	1:H:59[B]:SER:OG	2.10	0.51
1:O:76[B]:MET:CG	1:O:131:ARG:NH1	2.74	0.51
2:P:161[A]:A:O2'	2:P:162[A]:A:H5'	2.11	0.51
1:A:81:TRP:CD1	1:A:121:SER:HB3	2.46	0.51
3:s:181[B]:U:C6	3:s:181[B]:U:C3'	2.94	0.51
1:G:125:ARG:HE	4:z:195[A]:U:H3'	1.76	0.51
2:U:168[B]:A:N6	3:j:182[B]:U:O4	2.40	0.51
3:g:181[A]:U:O5'	3:g:181[A]:U:H6	1.93	0.51
3:l:181[B]:U:C6	3:l:181[B]:U:C3'	2.94	0.50
3:n:181[A]:U:C6	3:n:181[A]:U:C3'	2.94	0.50
1:L:53:PHE:HB3	1:L:143[B]:VAL:HG12	1.92	0.50
3:m:181[A]:U:C5	3:m:181[A]:U:OP2	2.64	0.50
2:R:161[A]:A:O2'	2:R:162[A]:A:H5'	2.12	0.50
1:A:128[B]:THR:HG23	1:A:129:ASN:N	2.26	0.50
3:k:181[B]:U:C6	3:k:181[B]:U:C3'	2.95	0.50
1:N:149[B]:GLN:NE2	9:N:547[B]:HOH:O	2.44	0.50
1:E:128[B]:THR:HG23	1:E:129:ASN:N	2.26	0.50
2:W:170[B]:A:N6	3:l:181[B]:U:C4	2.72	0.50
2:Q:161[A]:A:O2'	2:Q:162[A]:A:H5'	2.12	0.49
2:T:169[A]:A:N6	3:i:181[A]:U:O4	2.44	0.49
2:Y:161[A]:A:O2'	2:Y:162[A]:A:H5'	2.12	0.49
3:i:181[A]:U:H6	3:i:181[A]:U:O5'	1.96	0.49
3:o:181[B]:U:C6	3:o:181[B]:U:C3'	2.95	0.49
3:g:181[A]:U:H3'	3:g:181[A]:U:H6	1.77	0.49
3:h:181[A]:U:C5	3:h:181[A]:U:OP2	2.65	0.49
4:y:195[A]:U:P	4:y:196[A]:U:C5'	3.00	0.49
3:h:181[A]:U:H6	3:h:181[A]:U:O5'	1.95	0.49
1:I:125:ARG:HG3	4:2:195[B]:U:OP3	2.13	0.49
3:p:181[B]:U:C6	3:p:181[B]:U:C3'	2.95	0.49
3:r:181[B]:U:C6	3:r:181[B]:U:C3'	2.96	0.49
1:A:125:ARG:HE	4:t:195[B]:U:H3'	1.78	0.49
2:b:168[B]:A:N6	3:q:182[B]:U:O4	2.41	0.49
3:m:181[A]:U:H6	3:m:181[A]:U:O5'	1.95	0.49
3:i:181[A]:U:OP2	3:i:181[A]:U:C5	2.65	0.49
2:Z:161[B]:A:O2'	2:Z:162[B]:A:H5'	2.12	0.48
1:I:125:ARG:HD2	4:2:195[B]:U:OP3	2.14	0.48
2:U:162[B]:A:N6	3:j:188[B]:U:N3	2.61	0.48
2:V:161[A]:A:O2'	2:V:162[A]:A:H5'	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:f:181[B]:U:C6	3:f:181[B]:U:C3'	2.96	0.48
1:N:125:ARG:HE	4:7:195[A]:U:H3'	1.78	0.48
2:a:161[A]:A:O2'	2:a:162[A]:A:H5'	2.12	0.48
3:q:181[B]:U:C6	3:q:181[B]:U:C3'	2.95	0.48
1:A:125:ARG:HD2	4:t:195[B]:U:OP3	2.14	0.48
2:X:161[A]:A:O2'	2:X:162[A]:A:H5'	2.13	0.48
1:A:98:PRO:HG2	1:O:20[B]:VAL:HG11	1.94	0.48
1:O:23[B]:ILE:HD12	4:t:195[B]:U:OP1	2.13	0.48
3:h:181[A]:U:H3'	3:h:181[A]:U:H6	1.78	0.48
3:e:181[A]:U:H3'	3:e:181[A]:U:H6	1.77	0.48
2:U:169[B]:A:C6	3:j:181[B]:U:O4	2.66	0.48
3:j:181[B]:U:C6	3:j:181[B]:U:C3'	2.96	0.48
1:F:30:LYS:HB2	1:O:22[B]:MET:SD	2.54	0.48
2:W:168[B]:A:N6	3:l:182[B]:U:O4	2.45	0.48
3:e:188[A]:U:H2'	3:e:189[A]:U:H6	1.78	0.47
1:M:125:ARG:HD2	4:6:195[A]:U:OP3	2.14	0.47
1:O:16:ASN:ND2	9:O:305:HOH:O	2.48	0.47
1:C:125:ARG:HE	4:v:195[B]:U:H3'	1.78	0.47
2:b:161[B]:A:O2'	2:b:162[B]:A:H5'	2.15	0.47
2:c:161[B]:A:O2'	2:c:162[B]:A:H5'	2.14	0.47
3:n:181[A]:U:C5	3:n:181[A]:U:OP2	2.67	0.47
9:B:476:HOH:O	1:N:22[A]:MET:HE2	2.14	0.47
1:K:128[B]:THR:HG23	1:K:129:ASN:N	2.29	0.47
2:W:161[B]:A:O2'	2:W:162[B]:A:H5'	2.14	0.47
1:J:128[B]:THR:HG23	1:J:129:ASN:N	2.30	0.47
2:d:161[B]:A:O2'	2:d:162[B]:A:H5'	2.15	0.47
3:i:181[A]:U:H3'	3:i:181[A]:U:H6	1.77	0.47
1:I:81:TRP:CD1	1:I:121:SER:HB3	2.49	0.47
3:h:188[A]:U:H2'	3:h:189[A]:U:H6	1.77	0.47
1:F:54[A]:LYS:HE2	9:F:497:HOH:O	2.15	0.46
1:O:125:ARG:HG3	4:8:195[A]:U:OP3	2.15	0.46
3:h:182[A]:U:H6	3:h:182[A]:U:C5'	2.24	0.46
1:A:23[B]:ILE:HD11	1:O:125:ARG:HB2	1.97	0.46
1:D:97[B]:LYS:NZ	9:D:349:HOH:O	2.48	0.46
1:L:125:ARG:HE	4:5:195[A]:U:H3'	1.79	0.46
1:O:125:ARG:CG	4:8:195[A]:U:OP3	2.63	0.46
2:U:161[B]:A:O2'	2:U:162[B]:A:H5'	2.15	0.46
1:N:76[A]:MET:HE3	1:N:155[A]:SER:OG	2.15	0.46
3:n:181[A]:U:H3'	3:n:181[A]:U:H6	1.78	0.46
3:n:181[A]:U:H6	3:n:181[A]:U:O5'	1.98	0.46
1:I:125:ARG:CG	4:2:195[B]:U:OP3	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:169[A]:A:N6	3:g:181[A]:U:O4	2.47	0.46
3:h:187[A]:U:H2'	3:h:188[A]:U:O4'	2.15	0.46
3:q:186[B]:U:OP2	9:q:210[B]:HOH:O	2.21	0.46
1:H:125:ARG:HG3	4:l:195[A]:U:OP3	2.15	0.46
1:K:81:TRP:CD1	1:K:121:SER:HB3	2.51	0.46
1:M:128[B]:THR:HG23	1:M:129:ASN:N	2.30	0.46
1:O:125:ARG:CD	4:8:195[A]:U:OP3	2.64	0.46
2:W:169[B]:A:N1	3:l:181[B]:U:N3	2.64	0.46
3:e:187[A]:U:H2'	3:e:188[A]:U:O4'	2.16	0.46
1:F:53:PHE:HB3	1:F:143[B]:VAL:HG13	1.97	0.46
1:D:125:ARG:HG3	4:w:195[B]:U:OP3	2.15	0.46
3:i:187[A]:U:H2'	3:i:188[A]:U:O4'	2.16	0.46
1:F:101[B]:LYS:NZ	1:F:134:THR:HG22	2.30	0.45
1:N:26:GLY:N	9:N:517[B]:HOH:O	2.24	0.45
1:O:140[B]:VAL:CG1	1:O:141:CYS:N	2.78	0.45
3:m:181[A]:U:H3'	3:m:181[A]:U:H6	1.77	0.45
3:n:187[A]:U:H2'	3:n:188[A]:U:O4'	2.16	0.45
9:I:470:HOH:O	4:2:196[B]:U:C5'	2.63	0.45
1:L:56:PRO:HG2	1:L:59[B]:SER:OG	2.17	0.45
2:R:162[A]:A:N6	3:g:188[A]:U:H3	2.04	0.45
2:d:169[B]:A:N1	3:s:181[B]:U:O4	2.45	0.45
3:i:182[A]:U:H6	3:i:182[A]:U:C5'	2.24	0.45
1:D:81:TRP:CD1	1:D:121:SER:HB3	2.52	0.45
1:M:54[B]:LYS:NZ	1:M:142:GLU:OE1	2.46	0.45
3:g:187[A]:U:H2'	3:g:188[A]:U:O4'	2.16	0.45
3:n:188[A]:U:H2'	3:n:189[A]:U:H6	1.80	0.45
1:E:125:ARG:HG3	4:x:195[B]:U:OP3	2.16	0.45
3:e:182[A]:U:H6	3:e:182[A]:U:C5'	2.24	0.45
1:L:81:TRP:CD1	1:L:121:SER:HB3	2.52	0.45
3:n:182[A]:U:H6	3:n:182[A]:U:C5'	2.27	0.45
1:F:125:ARG:HG3	4:y:195[A]:U:OP3	2.17	0.45
2:Z:169[B]:A:C6	3:o:181[B]:U:O4	2.68	0.45
3:m:187[A]:U:H2'	3:m:188[A]:U:O4'	2.16	0.45
1:B:125:ARG:HE	4:u:195[A]:U:H3'	1.83	0.44
1:C:125:ARG:HD2	4:v:195[B]:U:OP3	2.18	0.44
1:G:125:ARG:HG3	4:z:195[A]:U:OP3	2.17	0.44
1:C:101[A]:LYS:NZ	9:C:419:HOH:O	2.50	0.44
1:O:76[B]:MET:HE2	1:O:76[B]:MET:HB2	1.83	0.44
1:G:81:TRP:CD1	1:G:121:SER:HB3	2.53	0.44
1:C:81:TRP:CD1	1:C:121:SER:HB3	2.53	0.43
3:i:188[A]:U:H2'	3:i:189[A]:U:H6	1.79	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:m:182[A]:U:H6	3:m:182[A]:U:C5'	2.25	0.43
2:X:162[A]:A:N6	3:m:188[A]:U:H3	2.03	0.43
1:B:81:TRP:CD1	1:B:121:SER:HB3	2.54	0.43
1:K:97[B]:LYS:HG3	1:K:107:GLU:O	2.19	0.43
1:L:101[B]:LYS:HE3	1:L:134:THR:HG22	2.01	0.43
1:L:125:ARG:CD	4:5:195[A]:U:OP3	2.66	0.43
1:O:81:TRP:CD1	1:O:121:SER:HB3	2.53	0.43
3:g:182[A]:U:H6	3:g:182[A]:U:C5'	2.24	0.43
1:E:148[C]:ARG:HD2	9:E:305:HOH:O	2.19	0.43
2:S:168[A]:A:C2'	2:S:169[A]:A:H5'	2.49	0.43
1:A:97:LYS:NZ	9:A:711[B]:HOH:O	2.51	0.43
1:O:76[B]:MET:HG3	1:O:131:ARG:CD	2.48	0.43
1:F:81:TRP:CD1	1:F:121:SER:HB3	2.53	0.43
1:F:128[B]:THR:HG23	1:F:129:ASN:N	2.33	0.43
3:m:188[A]:U:H2'	3:m:189[A]:U:H6	1.80	0.43
1:F:98:PRO:HD2	1:F:105[A]:SER:OG	2.19	0.43
1:O:76[B]:MET:CG	1:O:131:ARG:CZ	2.97	0.43
1:N:97[A]:LYS:HB3	1:N:142:GLU:HB2	2.01	0.42
1:F:83:GLN:HG2	1:F:149[B]:GLN:HG2	2.01	0.42
1:F:30:LYS:CB	1:O:22[B]:MET:SD	3.07	0.42
1:F:30:LYS:HG3	1:O:24:ARG:HG2	2.01	0.42
1:H:128[B]:THR:CG2	1:H:129:ASN:N	2.82	0.42
4:w:195[B]:U:OP3	4:w:196[B]:U:C5'	2.67	0.42
5:A:201[C]:PO4:O1	1:D:117:ASN:ND2	2.50	0.42
3:g:188[A]:U:H2'	3:g:189[A]:U:H6	1.80	0.42
1:E:125:ARG:HD2	4:x:195[B]:U:OP3	2.20	0.42
1:H:125:ARG:HD2	4:1:195[A]:U:OP3	2.20	0.42
1:E:81:TRP:CD1	1:E:121:SER:HB3	2.55	0.42
1:J:118[B]:THR:HG21	9:J:308[B]:HOH:O	2.19	0.42
2:c:169[B]:A:C6	3:r:181[B]:U:O4	2.70	0.42
4:1:195[A]:U:OP3	4:1:196[A]:U:C5'	2.68	0.42
2:W:169[B]:A:N1	3:l:181[B]:U:C4	2.88	0.42
1:C:16:ASN:HB3	9:C:540:HOH:O	2.19	0.42
1:D:98:PRO:HD2	1:D:105[A]:SER:OG	2.20	0.42
1:D:128[B]:THR:HG23	1:D:129:ASN:N	2.34	0.42
1:J:125:ARG:HD2	4:3:195[B]:U:OP3	2.19	0.42
3:o:187[B]:U:H2'	3:o:188[B]:U:O4'	2.20	0.42
3:p:187[B]:U:H2'	3:p:188[B]:U:O4'	2.20	0.42
1:I:83:GLN:HG2	1:I:149[B]:GLN:HG2	2.01	0.41
1:L:60[B]:LEU:N	1:L:60[B]:LEU:HD12	2.35	0.41
3:q:187[B]:U:H2'	3:q:188[B]:U:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:ARG:HB2	1:O:23[B]:ILE:HD11	2.02	0.41
1:D:97[B]:LYS:HG3	1:D:107:GLU:O	2.19	0.41
1:K:125:ARG:HD2	4:4:195[A]:U:OP3	2.20	0.41
1:O:76[B]:MET:HG3	1:O:131:ARG:NE	2.34	0.41
3:j:187[B]:U:H2'	3:j:188[B]:U:O4'	2.20	0.41
1:A:109:PHE:CE1	1:O:20[B]:VAL:HG12	2.55	0.41
1:M:125:ARG:HE	4:6:195[A]:U:H3'	1.85	0.41
1:B:157[B]:CYS:SG	1:N:19:VAL:CG1	3.03	0.41
3:l:187[B]:U:H2'	3:l:188[B]:U:O4'	2.20	0.41
1:A:29:PRO:HD3	1:O:81:TRP:CZ2	2.56	0.41
5:A:201[B]:PO4:O1	1:C:117:ASN:ND2	2.52	0.41
1:K:125:ARG:HG3	4:4:195[A]:U:OP3	2.20	0.41
1:L:98:PRO:HD2	1:L:105[A]:SER:OG	2.20	0.41
1:M:81:TRP:CD1	1:M:121:SER:HB3	2.56	0.41
2:X:169[A]:A:N1	3:m:181[A]:U:N3	2.69	0.41
3:f:187[B]:U:H2'	3:f:188[B]:U:O4'	2.20	0.41
3:h:182[A]:U:C6	3:h:182[A]:U:P	3.13	0.41
3:s:187[B]:U:H2'	3:s:188[B]:U:O4'	2.20	0.41
1:A:105[B]:SER:HB3	1:A:107:GLU:OE2	2.20	0.41
1:I:118[B]:THR:HG21	9:I:544:HOH:O	2.21	0.41
1:L:125:ARG:CG	4:5:195[A]:U:OP3	2.69	0.41
1:N:38:VAL:HG22	1:N:157[B]:CYS:SG	2.61	0.41
3:k:187[B]:U:H2'	3:k:188[B]:U:O4'	2.20	0.41
1:L:83:GLN:HG2	1:L:149[B]:GLN:HG2	2.03	0.40
1:B:125:ARG:HG3	4:u:195[A]:U:OP3	2.21	0.40
1:H:83:GLN:HG2	1:H:149[B]:GLN:HG2	2.02	0.40
1:A:22[B]:MET:CE	1:O:109:PHE:HD2	2.34	0.40
1:J:54:LYS:HE2	9:J:501:HOH:O	2.21	0.40
3:r:187[B]:U:H2'	3:r:188[B]:U:O4'	2.21	0.40
1:A:16:ASN:ND2	9:A:769:HOH:O	2.55	0.40
1:A:125:ARG:HG3	4:t:195[B]:U:OP3	2.22	0.40

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 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	158/159 (99%)	153 (97%)	5 (3%)	0	100	100
1	B	156/159 (98%)	152 (97%)	4 (3%)	0	100	100
1	C	160/159 (101%)	156 (98%)	4 (2%)	0	100	100
1	D	163/159 (102%)	159 (98%)	4 (2%)	0	100	100
1	E	160/159 (101%)	156 (98%)	4 (2%)	0	100	100
1	F	162/159 (102%)	157 (97%)	5 (3%)	0	100	100
1	G	158/159 (99%)	154 (98%)	4 (2%)	0	100	100
1	H	160/159 (101%)	156 (98%)	4 (2%)	0	100	100
1	I	159/159 (100%)	153 (96%)	6 (4%)	0	100	100
1	J	157/159 (99%)	152 (97%)	5 (3%)	0	100	100
1	K	159/159 (100%)	155 (98%)	4 (2%)	0	100	100
1	L	161/159 (101%)	156 (97%)	5 (3%)	0	100	100
1	M	159/159 (100%)	154 (97%)	5 (3%)	0	100	100
1	N	158/159 (99%)	154 (98%)	4 (2%)	0	100	100
1	O	163/159 (102%)	158 (97%)	5 (3%)	0	100	100
All	All	2393/2385 (100%)	2325 (97%)	68 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	144/140 (103%)	144 (100%)	0	100	100
1	B	142/140 (101%)	142 (100%)	0	100	100
1	C	146/140 (104%)	146 (100%)	0	100	100
1	D	149/140 (106%)	149 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	146/140 (104%)	146 (100%)	0	100	100
1	F	148/140 (106%)	148 (100%)	0	100	100
1	G	144/140 (103%)	144 (100%)	0	100	100
1	H	146/140 (104%)	146 (100%)	0	100	100
1	I	145/140 (104%)	145 (100%)	0	100	100
1	J	143/140 (102%)	143 (100%)	0	100	100
1	K	145/140 (104%)	145 (100%)	0	100	100
1	L	147/140 (105%)	147 (100%)	0	100	100
1	M	145/140 (104%)	145 (100%)	0	100	100
1	N	144/140 (103%)	144 (100%)	0	100	100
1	O	149/140 (106%)	149 (100%)	0	100	100
All	All	2183/2100 (104%)	2183 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	ASN
1	A	132	GLN
1	B	89	ASN
1	B	132	GLN
1	C	18	ASN
1	C	89	ASN
1	D	89	ASN
1	E	89	ASN
1	F	18	ASN
1	F	89	ASN
1	F	132	GLN
1	G	89	ASN
1	G	132	GLN
1	H	89	ASN
1	J	89	ASN
1	J	132	GLN
1	K	18	ASN
1	K	132	GLN
1	L	18	ASN
1	L	89	ASN

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Mol	Chain	Res	Type
1	L	132	GLN
1	M	18	ASN
1	M	48	GLN
1	M	89	ASN
1	N	89	ASN
1	O	89	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	P	9/10 (90%)	0	0
2	Q	9/10 (90%)	0	0
2	R	9/10 (90%)	0	0
2	S	9/10 (90%)	0	0
2	T	9/10 (90%)	0	0
2	U	9/10 (90%)	0	0
2	V	9/10 (90%)	0	0
2	W	9/10 (90%)	0	0
2	X	9/10 (90%)	0	0
2	Y	9/10 (90%)	0	0
2	Z	9/10 (90%)	0	0
2	a	9/10 (90%)	0	0
2	b	9/10 (90%)	0	0
2	c	9/10 (90%)	0	0
2	d	9/10 (90%)	0	0
3	e	9/10 (90%)	2 (22%)	0
3	f	9/10 (90%)	1 (11%)	0
3	g	9/10 (90%)	2 (22%)	0
3	h	9/10 (90%)	2 (22%)	0
3	i	9/10 (90%)	2 (22%)	0
3	j	9/10 (90%)	1 (11%)	0
3	k	9/10 (90%)	1 (11%)	0
3	l	9/10 (90%)	1 (11%)	0
3	m	9/10 (90%)	2 (22%)	0
3	n	9/10 (90%)	2 (22%)	0
3	o	9/10 (90%)	1 (11%)	0
3	p	9/10 (90%)	1 (11%)	0
3	q	9/10 (90%)	1 (11%)	0
3	r	9/10 (90%)	1 (11%)	0
3	s	9/10 (90%)	1 (11%)	0
4	l	0/2	-	-

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	2	0/2	-	-
4	3	0/2	-	-
4	4	0/2	-	-
4	5	0/2	-	-
4	6	0/2	-	-
4	7	0/2	-	-
4	8	0/2	-	-
4	t	0/2	-	-
4	u	0/2	-	-
4	v	0/2	-	-
4	w	0/2	-	-
4	x	0/2	-	-
4	y	0/2	-	-
4	z	0/2	-	-
All	All	270/330 (81%)	21 (7%)	0

All (21) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	e	183[A]	U
3	e	190[A]	U
3	f	183[B]	U
3	g	183[A]	U
3	g	190[A]	U
3	h	183[A]	U
3	h	190[A]	U
3	i	183[A]	U
3	i	190[A]	U
3	j	183[B]	U
3	k	183[B]	U
3	l	183[B]	U
3	m	183[A]	U
3	m	190[A]	U
3	n	183[A]	U
3	n	190[A]	U
3	o	183[B]	U
3	p	183[B]	U
3	q	183[B]	U
3	r	183[B]	U
3	s	183[B]	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 65 ligands modelled in this entry, 20 are monoatomic - leaving 45 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	$\# Z > 2$
6	SO4	M	201[D]	-	4,4,4	0.23	0	6,6,6	0.21	0
6	SO4	G	201[C]	-	4,4,4	0.22	0	6,6,6	0.12	0
6	SO4	D	201	-	4,4,4	0.23	0	6,6,6	0.23	0
6	SO4	G	201[E]	-	4,4,4	0.23	0	6,6,6	0.13	0
6	SO4	E	201[D]	-	4,4,4	0.24	0	6,6,6	0.13	0
6	SO4	M	201[B]	-	4,4,4	0.23	0	6,6,6	0.13	0
6	SO4	B	201	-	4,4,4	0.23	0	6,6,6	0.13	0
6	SO4	I	201	-	4,4,4	0.22	0	6,6,6	0.22	0
6	SO4	E	202	-	4,4,4	0.22	0	6,6,6	0.21	0
6	SO4	E	201[B]	-	4,4,4	0.24	0	6,6,6	0.17	0
5	PO4	N	201[A]	-	4,4,4	1.04	0	6,6,6	0.68	0
6	SO4	G	201[D]	-	4,4,4	0.22	0	6,6,6	0.12	0
6	SO4	F	201	-	4,4,4	0.28	0	6,6,6	0.08	0
6	SO4	N	202	-	4,4,4	0.22	0	6,6,6	0.13	0
5	PO4	A	201[A]	8	4,4,4	0.95	0	6,6,6	0.54	0
5	PO4	N	201[C]	8	4,4,4	0.96	0	6,6,6	0.55	0
6	SO4	O	201	-	4,4,4	0.22	0	6,6,6	0.21	0
5	PO4	H	201[A]	8	4,4,4	1.10	0	6,6,6	0.36	0
5	PO4	N	201[E]	8	4,4,4	1.11	0	6,6,6	0.58	0
6	SO4	G	201[B]	-	4,4,4	0.22	0	6,6,6	0.20	0
5	PO4	A	201[C]	8	4,4,4	0.97	0	6,6,6	0.56	0
6	SO4	K	201	-	4,4,4	0.23	0	6,6,6	0.18	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PO4	A	201[E]	8	4,4,4	1.05	0	6,6,6	0.58	0
5	PO4	H	201[C]	8	4,4,4	1.03	0	6,6,6	0.67	0
5	PO4	H	201[E]	8	4,4,4	1.07	0	6,6,6	0.86	0
6	SO4	C	201	-	4,4,4	0.23	0	6,6,6	0.18	0
6	SO4	J	201	-	4,4,4	0.21	0	6,6,6	0.19	0
5	PO4	N	201[D]	8	4,4,4	0.95	0	6,6,6	0.35	0
6	SO4	M	201[A]	-	4,4,4	0.21	0	6,6,6	0.24	0
6	SO4	H	202	-	4,4,4	0.23	0	6,6,6	0.12	0
5	PO4	A	201[D]	8	4,4,4	0.98	0	6,6,6	0.73	0
5	PO4	N	201[B]	8	4,4,4	1.02	0	6,6,6	0.49	0
6	SO4	M	201[C]	-	4,4,4	0.23	0	6,6,6	0.10	0
5	PO4	H	201[D]	8	4,4,4	1.06	0	6,6,6	0.59	0
6	SO4	E	201[A]	-	4,4,4	0.23	0	6,6,6	0.17	0
6	SO4	M	201[E]	-	4,4,4	0.23	0	6,6,6	0.12	0
6	SO4	A	202	-	4,4,4	0.22	0	6,6,6	0.13	0
5	PO4	A	201[B]	8	4,4,4	0.91	0	6,6,6	0.54	0
6	SO4	G	202	-	4,4,4	0.21	0	6,6,6	0.11	0
6	SO4	E	201[C]	-	4,4,4	0.22	0	6,6,6	0.14	0
5	PO4	H	201[B]	8	4,4,4	1.02	0	6,6,6	0.63	0
6	SO4	M	202	-	4,4,4	0.22	0	6,6,6	0.11	0
6	SO4	E	201[E]	-	4,4,4	0.23	0	6,6,6	0.14	0
6	SO4	G	201[A]	-	4,4,4	0.24	0	6,6,6	0.19	0
6	SO4	L	201	-	4,4,4	0.24	0	6,6,6	0.13	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	201[C]	PO4	1	0
5	A	201[B]	PO4	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	144/159 (90%)	0.37	5 (3%)	47	49	13, 26, 31, 62	15 (10%)
1	B	144/159 (90%)	0.25	2 (1%)	73	77	14, 26, 33, 62	14 (9%)
1	C	144/159 (90%)	0.26	3 (2%)	63	66	14, 26, 32, 62	18 (12%)
1	D	144/159 (90%)	0.28	2 (1%)	73	77	13, 26, 32, 62	19 (13%)
1	E	144/159 (90%)	0.21	3 (2%)	63	66	12, 26, 32, 62	16 (11%)
1	F	144/159 (90%)	0.27	3 (2%)	63	66	13, 26, 32, 62	18 (12%)
1	G	144/159 (90%)	0.22	3 (2%)	63	66	14, 26, 33, 62	16 (11%)
1	H	144/159 (90%)	0.25	2 (1%)	73	77	13, 26, 33, 62	17 (11%)
1	I	144/159 (90%)	0.38	4 (2%)	55	57	13, 26, 32, 62	16 (11%)
1	J	144/159 (90%)	0.29	3 (2%)	63	66	14, 26, 31, 62	15 (10%)
1	K	144/159 (90%)	0.36	4 (2%)	55	57	12, 26, 33, 62	16 (11%)
1	L	144/159 (90%)	0.31	3 (2%)	63	66	14, 26, 33, 62	18 (12%)
1	M	144/159 (90%)	0.29	3 (2%)	63	66	12, 26, 33, 62	17 (11%)
1	N	144/159 (90%)	0.34	3 (2%)	63	66	14, 26, 31, 62	16 (11%)
1	O	144/159 (90%)	0.33	4 (2%)	55	57	13, 25, 31, 62	21 (14%)
2	P	10/10 (100%)	4.05	10 (100%)	0	0	18, 54, 86, 89	10 (100%)
2	Q	10/10 (100%)	3.75	9 (90%)	0	0	18, 54, 86, 89	10 (100%)
2	R	10/10 (100%)	3.52	8 (80%)	0	0	18, 54, 86, 89	10 (100%)
2	S	10/10 (100%)	3.32	7 (70%)	0	0	13, 53, 93, 94	10 (100%)
2	T	10/10 (100%)	4.21	9 (90%)	0	0	18, 54, 86, 89	10 (100%)
2	U	10/10 (100%)	4.27	9 (90%)	0	0	16, 56, 88, 95	10 (100%)
2	V	10/10 (100%)	3.56	9 (90%)	0	0	18, 54, 86, 89	10 (100%)
2	W	10/10 (100%)	3.65	8 (80%)	0	0	16, 56, 88, 95	10 (100%)
2	X	10/10 (100%)	3.50	9 (90%)	0	0	18, 54, 86, 89	10 (100%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	Y	10/10 (100%)	4.00	9 (90%) 0 0	18, 54, 86, 89	10 (100%)
2	Z	10/10 (100%)	4.35	9 (90%) 0 0	16, 56, 88, 95	10 (100%)
2	a	10/10 (100%)	3.93	9 (90%) 0 0	18, 54, 86, 89	10 (100%)
2	b	10/10 (100%)	4.03	9 (90%) 0 0	16, 56, 88, 95	10 (100%)
2	c	10/10 (100%)	3.87	9 (90%) 0 0	16, 56, 88, 95	10 (100%)
2	d	10/10 (100%)	4.24	9 (90%) 0 0	16, 56, 88, 95	10 (100%)
3	e	10/10 (100%)	3.78	9 (90%) 0 0	17, 55, 90, 99	10 (100%)
3	f	10/10 (100%)	3.46	9 (90%) 0 0	18, 55, 94, 100	10 (100%)
3	g	10/10 (100%)	3.43	8 (80%) 0 0	17, 55, 90, 99	10 (100%)
3	h	10/10 (100%)	3.32	8 (80%) 0 0	17, 55, 90, 99	10 (100%)
3	i	10/10 (100%)	3.76	8 (80%) 0 0	17, 55, 90, 99	10 (100%)
3	j	10/10 (100%)	3.98	8 (80%) 0 0	17, 55, 94, 100	10 (100%)
3	k	10/10 (100%)	3.25	7 (70%) 0 0	18, 55, 94, 100	10 (100%)
3	l	10/10 (100%)	3.23	7 (70%) 0 0	18, 55, 94, 100	10 (100%)
3	m	10/10 (100%)	3.67	10 (100%) 0 0	17, 55, 90, 99	10 (100%)
3	n	10/10 (100%)	3.83	8 (80%) 0 0	17, 55, 90, 99	10 (100%)
3	o	10/10 (100%)	3.68	8 (80%) 0 0	18, 55, 94, 100	10 (100%)
3	p	10/10 (100%)	3.47	8 (80%) 0 0	18, 55, 94, 100	10 (100%)
3	q	10/10 (100%)	3.18	8 (80%) 0 0	18, 55, 94, 100	10 (100%)
3	r	10/10 (100%)	3.18	8 (80%) 0 0	17, 55, 94, 100	10 (100%)
3	s	10/10 (100%)	3.93	8 (80%) 0 0	18, 55, 94, 100	10 (100%)
4	1	2/2 (100%)	5.57	2 (100%) 0 0	29, 29, 29, 49	2 (100%)
4	2	2/2 (100%)	5.32	2 (100%) 0 0	26, 26, 26, 50	2 (100%)
4	3	2/2 (100%)	6.95	2 (100%) 0 0	29, 29, 29, 49	2 (100%)
4	4	2/2 (100%)	6.66	2 (100%) 0 0	30, 30, 30, 48	2 (100%)
4	5	2/2 (100%)	5.72	2 (100%) 0 0	31, 31, 31, 51	2 (100%)
4	6	2/2 (100%)	5.81	2 (100%) 0 0	28, 28, 28, 48	2 (100%)
4	7	2/2 (100%)	6.21	2 (100%) 0 0	26, 26, 26, 48	2 (100%)
4	8	2/2 (100%)	5.55	2 (100%) 0 0	27, 27, 27, 49	2 (100%)
4	t	2/2 (100%)	6.09	2 (100%) 0 0	30, 30, 30, 51	2 (100%)
4	u	2/2 (100%)	6.20	2 (100%) 0 0	30, 30, 30, 50	2 (100%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
4	v	2/2 (100%)	6.38	2 (100%) 0 0	31, 31, 31, 50	2 (100%)
4	w	2/2 (100%)	6.26	2 (100%) 0 0	35, 35, 35, 49	2 (100%)
4	x	2/2 (100%)	6.23	2 (100%) 0 0	32, 32, 32, 50	2 (100%)
4	y	2/2 (100%)	6.29	2 (100%) 0 0	35, 35, 35, 49	2 (100%)
4	z	2/2 (100%)	6.53	2 (100%) 0 0	30, 30, 30, 51	2 (100%)
All	All	2490/2715 (91%)	0.78	331 (13%) 7 8	12, 26, 65, 100	582 (23%)

All (331) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	4	195[A]	U	8.7
4	3	195[B]	U	8.0
4	8	195[A]	U	7.7
4	z	195[A]	U	7.7
4	7	195[A]	U	7.7
2	U	168[B]	A	7.4
4	u	195[A]	U	7.3
4	w	195[B]	U	7.3
4	1	195[A]	U	7.3
4	y	195[A]	U	7.2
4	t	195[B]	U	7.1
2	T	168[A]	A	7.0
4	x	195[B]	U	7.0
4	v	195[B]	U	6.9
4	6	195[A]	U	6.8
4	5	195[A]	U	6.8
4	2	195[B]	U	6.6
2	Z	168[B]	A	6.6
2	Y	168[A]	A	6.3
4	3	196[B]	U	5.9
4	v	196[B]	U	5.9
2	a	168[A]	A	5.7
2	c	168[B]	A	5.7
2	Z	169[B]	A	5.6
2	Z	170[B]	A	5.5
4	x	196[B]	U	5.5
2	Z	161[B]	A	5.5
2	P	168[A]	A	5.4
4	z	196[A]	U	5.4
2	U	169[B]	A	5.4

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Mol	Chain	Res	Type	RSRZ
2	d	168[B]	A	5.4
4	y	196[A]	U	5.4
3	e	184[A]	U	5.3
3	j	184[B]	U	5.3
3	n	184[A]	U	5.3
4	w	196[B]	U	5.3
2	U	170[B]	A	5.2
2	d	161[B]	A	5.2
3	j	183[B]	U	5.2
3	o	184[B]	U	5.2
3	s	183[B]	U	5.2
2	U	167[B]	A	5.2
2	R	168[A]	A	5.2
2	d	170[B]	A	5.2
3	j	188[B]	U	5.1
3	s	184[B]	U	5.1
4	t	196[B]	U	5.1
2	W	168[B]	A	5.1
2	c	163[B]	A	5.1
4	u	196[A]	U	5.1
2	T	170[A]	A	5.1
2	b	168[B]	A	5.1
3	i	184[A]	U	5.0
2	Q	170[A]	A	5.0
2	d	162[B]	A	5.0
2	d	169[B]	A	5.0
3	n	190[A]	U	5.0
3	o	183[B]	U	5.0
2	c	170[B]	A	5.0
2	T	163[A]	A	5.0
2	T	169[A]	A	5.0
2	V	168[A]	A	5.0
2	S	168[A]	A	4.9
2	Y	169[A]	A	4.9
2	P	163[A]	A	4.9
2	P	166[A]	A	4.9
2	S	170[A]	A	4.9
2	V	163[A]	A	4.9
2	b	170[B]	A	4.9
2	c	162[B]	A	4.9
3	g	183[A]	U	4.8
3	i	189[A]	U	4.8

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Mol	Chain	Res	Type	RSRZ
3	j	190[B]	U	4.8
4	6	196[A]	U	4.8
2	T	167[A]	A	4.8
2	Q	168[A]	A	4.8
2	S	163[A]	A	4.8
2	Y	162[A]	A	4.8
3	p	188[B]	U	4.8
4	7	196[A]	U	4.8
2	a	170[A]	A	4.8
2	d	166[B]	A	4.8
3	s	185[B]	U	4.7
2	W	163[B]	A	4.7
2	b	169[B]	A	4.7
3	g	190[A]	U	4.7
3	s	189[B]	U	4.7
2	S	161[A]	A	4.7
4	5	196[A]	U	4.7
2	a	169[A]	A	4.6
3	f	190[B]	U	4.6
3	l	183[B]	U	4.6
3	o	188[B]	U	4.6
3	h	183[A]	U	4.6
3	m	190[A]	U	4.6
4	4	196[A]	U	4.6
2	Q	163[A]	A	4.6
2	S	162[A]	A	4.6
2	S	169[A]	A	4.6
2	V	170[A]	A	4.6
2	W	170[B]	A	4.6
3	e	190[A]	U	4.6
3	g	188[A]	U	4.6
3	i	183[A]	U	4.6
3	k	190[B]	U	4.6
2	Q	161[A]	A	4.6
3	e	182[A]	U	4.6
3	i	188[A]	U	4.6
2	P	169[A]	A	4.5
2	R	163[A]	A	4.5
2	W	162[B]	A	4.5
2	Y	170[A]	A	4.5
2	R	170[A]	A	4.5
2	T	162[A]	A	4.5

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Mol	Chain	Res	Type	RSRZ
2	Z	167[B]	A	4.5
2	a	162[A]	A	4.5
2	R	162[A]	A	4.5
2	W	169[B]	A	4.5
2	a	163[A]	A	4.5
2	b	161[B]	A	4.5
2	b	162[B]	A	4.5
2	b	166[B]	A	4.5
2	c	169[B]	A	4.5
3	k	183[B]	U	4.5
2	U	162[B]	A	4.4
2	d	167[B]	A	4.4
2	X	170[A]	A	4.4
3	i	190[A]	U	4.4
3	m	189[A]	U	4.4
3	n	189[A]	U	4.4
2	P	170[A]	A	4.4
2	X	168[A]	A	4.4
3	l	190[B]	U	4.4
3	p	184[B]	U	4.4
2	Y	161[A]	A	4.3
2	Y	163[A]	A	4.3
2	Z	162[B]	A	4.3
3	f	183[B]	U	4.3
3	r	188[B]	U	4.3
1	G	16	ASN	4.3
2	Q	169[A]	A	4.3
2	U	163[B]	A	4.3
2	V	161[A]	A	4.3
2	V	169[A]	A	4.3
3	h	182[A]	U	4.3
3	l	189[B]	U	4.3
3	o	190[B]	U	4.3
3	p	190[B]	U	4.2
3	s	188[B]	U	4.2
2	a	161[A]	A	4.2
1	B	16	ASN	4.2
1	E	16	ASN	4.2
3	l	182[B]	U	4.2
3	n	182[A]	U	4.2
3	r	190[B]	U	4.2
2	P	161[A]	A	4.2

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Mol	Chain	Res	Type	RSRZ
3	l	181[B]	U	4.2
2	W	161[B]	A	4.2
2	c	161[B]	A	4.2
3	e	183[A]	U	4.2
3	h	190[A]	U	4.2
3	j	182[B]	U	4.2
2	R	161[A]	A	4.1
3	e	189[A]	U	4.1
3	n	183[A]	U	4.1
3	s	181[B]	U	4.1
3	e	181[A]	U	4.1
3	i	182[A]	U	4.1
3	j	189[B]	U	4.1
3	p	183[B]	U	4.1
3	r	183[B]	U	4.1
2	U	161[B]	A	4.1
2	V	162[A]	A	4.1
3	j	185[B]	U	4.1
3	k	188[B]	U	4.1
3	p	189[B]	U	4.1
2	Q	162[A]	A	4.0
2	b	167[B]	A	4.0
3	g	182[A]	U	4.0
3	n	188[A]	U	4.0
3	p	182[B]	U	4.0
2	Z	166[B]	A	4.0
3	f	189[B]	U	4.0
3	l	188[B]	U	4.0
4	2	196[B]	U	4.0
2	T	161[A]	A	4.0
2	Y	167[A]	A	4.0
3	i	181[A]	U	4.0
3	o	182[B]	U	4.0
3	q	190[B]	U	4.0
3	r	182[B]	U	4.0
3	f	181[B]	U	3.9
3	h	181[A]	U	3.9
2	X	163[A]	A	3.9
2	X	169[A]	A	3.9
3	m	181[A]	U	3.9
3	n	181[A]	U	3.9
3	n	185[A]	U	3.9

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Mol	Chain	Res	Type	RSRZ
1	K	16	ASN	3.9
2	P	167[A]	A	3.9
3	f	182[B]	U	3.9
3	m	182[A]	U	3.9
3	m	184[A]	U	3.9
3	m	188[A]	U	3.9
4	l	196[A]	U	3.9
2	X	162[A]	A	3.9
2	c	167[B]	A	3.9
1	D	16	ASN	3.9
1	O	16	ASN	3.9
3	e	185[A]	U	3.8
3	f	188[B]	U	3.8
2	R	169[A]	A	3.8
2	Z	163[B]	A	3.8
3	h	184[A]	U	3.8
3	q	183[B]	U	3.8
3	q	184[B]	U	3.8
2	P	162[A]	A	3.8
3	g	189[A]	U	3.8
3	o	185[B]	U	3.8
3	s	182[B]	U	3.8
2	X	161[A]	A	3.8
2	a	164[A]	A	3.8
3	j	181[B]	U	3.8
3	o	181[B]	U	3.8
3	s	190[B]	U	3.8
3	k	189[B]	U	3.7
3	q	182[B]	U	3.7
2	U	166[B]	A	3.7
1	N	16	ASN	3.7
3	h	188[A]	U	3.7
3	k	181[B]	U	3.7
3	r	181[B]	U	3.7
2	b	163[B]	A	3.6
3	g	181[A]	U	3.6
3	m	183[A]	U	3.6
3	o	189[B]	U	3.6
3	q	188[B]	U	3.6
3	h	189[A]	U	3.6
3	k	182[B]	U	3.6
3	p	181[B]	U	3.6

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Mol	Chain	Res	Type	RSRZ
3	q	189[B]	U	3.6
2	W	167[B]	A	3.6
1	L	16	ASN	3.6
2	a	167[A]	A	3.5
3	q	181[B]	U	3.5
1	O	25	ALA	3.5
1	A	16	ASN	3.5
1	H	16	ASN	3.4
3	f	184[B]	U	3.4
3	k	184[B]	U	3.4
3	r	189[B]	U	3.4
3	g	184[A]	U	3.4
1	L	24	ARG	3.4
1	F	16	ASN	3.4
1	C	24	ARG	3.4
1	K	24	ARG	3.4
4	8	196[A]	U	3.4
1	J	16	ASN	3.3
2	d	163[B]	A	3.3
2	X	164[A]	A	3.3
3	r	184[B]	U	3.3
1	A	23[A]	ILE	3.3
2	Q	166[A]	A	3.3
3	e	188[A]	U	3.2
1	N	24	ARG	3.2
3	m	186[A]	U	3.2
1	I	25	ALA	3.2
2	Q	167[A]	A	3.1
2	T	166[A]	A	3.1
1	M	16	ASN	3.1
1	M	24	ARG	3.1
1	C	16	ASN	3.0
2	Y	166[A]	A	3.0
3	i	185[A]	U	3.0
1	A	24	ARG	2.9
2	b	164[B]	A	2.9
2	X	167[A]	A	2.8
2	R	167[A]	A	2.8
2	X	166[A]	A	2.8
3	m	185[A]	U	2.8
3	q	185[B]	U	2.7
1	D	24	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
2	d	164[B]	A	2.7
3	l	184[B]	U	2.7
2	V	167[A]	A	2.7
2	Y	164[A]	A	2.7
2	Z	164[B]	A	2.7
1	A	17	SER	2.6
2	Q	164[A]	A	2.6
2	R	164[A]	A	2.6
1	I	16	ASN	2.6
2	W	164[B]	A	2.6
1	H	24	ARG	2.6
2	U	164[B]	A	2.6
1	O	17	SER	2.5
2	T	164[A]	A	2.5
3	f	185[B]	U	2.5
3	m	187[A]	U	2.5
1	M	17	SER	2.5
2	V	166[A]	A	2.5
1	O	18[A]	ASN	2.4
2	V	164[A]	A	2.4
1	F	24	ARG	2.4
1	J	24	ARG	2.4
1	I	19	VAL	2.4
3	r	185[B]	U	2.4
3	p	185[B]	U	2.3
2	c	164[B]	A	2.3
3	g	185[A]	U	2.3
1	B	24	ARG	2.3
3	f	186[B]	U	2.3
2	a	166[A]	A	2.3
3	e	186[A]	U	2.3
2	P	164[A]	A	2.2
2	P	165[A]	A	2.2
1	K	25	ALA	2.2
1	L	25	ALA	2.2
1	J	17	SER	2.2
1	I	24	ARG	2.2
3	h	185[A]	U	2.2
2	c	166[B]	A	2.2
1	K	23	ILE	2.1
1	A	19	VAL	2.1
1	E	19	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	N	19	VAL	2.1
1	G	24	ARG	2.1
1	E	24	ARG	2.1
1	C	23	ILE	2.1
1	F	17	SER	2.1
1	G	25	ALA	2.0
2	S	167[A]	A	2.0

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 oligosaccharides 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
7	NA	B	202	1/1	0.68	0.20	97,97,97,97	1
6	SO4	G	201[B]	5/5	0.69	0.18	48,49,57,57	5
6	SO4	G	201[C]	5/5	0.69	0.18	31,42,53,55	5
6	SO4	G	201[D]	5/5	0.69	0.18	59,60,64,65	5
6	SO4	G	201[E]	5/5	0.69	0.18	54,57,58,62	5
6	SO4	G	201[A]	5/5	0.69	0.18	35,39,43,44	5
7	NA	E	205	1/1	0.71	0.25	100,100,100,100	0
6	SO4	E	201[A]	5/5	0.73	0.19	33,40,54,55	5
6	SO4	E	201[B]	5/5	0.73	0.19	45,49,51,56	5
6	SO4	E	201[C]	5/5	0.73	0.19	42,45,48,51	5
6	SO4	E	201[D]	5/5	0.73	0.19	48,49,54,54	5
6	SO4	E	201[E]	5/5	0.73	0.19	43,44,54,55	5
6	SO4	B	201	5/5	0.73	0.20	83,99,106,111	0
6	SO4	M	202	5/5	0.74	0.19	77,92,97,101	0
6	SO4	H	202	5/5	0.78	0.25	105,106,111,119	0
7	NA	C	202[B]	1/1	0.79	0.21	47,47,47,47	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	SO4	K	201	5/5	0.79	0.21	109,116,122,125	0
6	SO4	L	201	5/5	0.80	0.17	87,95,100,107	0
6	SO4	A	202	5/5	0.80	0.21	94,102,108,117	0
6	SO4	I	201	5/5	0.80	0.23	92,103,107,112	0
6	SO4	J	201	5/5	0.80	0.16	58,80,86,89	0
6	SO4	G	202	5/5	0.80	0.17	91,100,107,110	0
6	SO4	N	202	5/5	0.81	0.23	119,121,122,130	0
6	SO4	D	201	5/5	0.81	0.16	61,81,90,97	0
6	SO4	M	201[A]	5/5	0.82	0.19	19,40,44,47	5
6	SO4	M	201[B]	5/5	0.82	0.19	72,73,76,76	5
6	SO4	M	201[C]	5/5	0.82	0.19	58,60,61,64	5
6	SO4	M	201[D]	5/5	0.82	0.19	33,40,48,50	5
6	SO4	M	201[E]	5/5	0.82	0.19	71,72,75,76	5
6	SO4	O	201	5/5	0.83	0.15	56,78,78,89	0
6	SO4	C	201	5/5	0.84	0.15	75,86,89,98	0
6	SO4	E	202	5/5	0.84	0.15	77,87,90,101	0
7	NA	L	202	1/1	0.85	0.36	80,80,80,80	1
7	NA	K	203[B]	1/1	0.86	0.20	43,43,43,43	1
7	NA	N	203[A]	1/1	0.86	0.30	79,79,79,79	1
7	NA	M	203[B]	1/1	0.90	0.13	41,41,41,41	1
7	NA	D	202	1/1	0.90	0.36	103,103,103,103	0
7	NA	B	203	1/1	0.91	0.24	101,101,101,101	0
6	SO4	F	201	5/5	0.91	0.10	58,68,75,85	0
8	MG	E	203	1/1	0.91	0.14	74,74,74,74	0
7	NA	I	202[A]	1/1	0.92	0.20	52,52,52,52	1
7	NA	O	202[B]	1/1	0.92	0.16	47,47,47,47	1
7	NA	A	203[A]	1/1	0.92	0.12	46,46,46,46	1
8	MG	K	202	1/1	0.93	0.14	70,70,70,70	0
7	NA	E	204	1/1	0.94	0.18	64,64,64,64	0
7	NA	F	203	1/1	0.95	0.16	67,67,67,67	0
7	NA	H	203	1/1	0.95	0.21	61,61,61,61	0
8	MG	F	202	1/1	0.96	0.07	56,56,56,56	0
7	NA	G	203	1/1	0.96	0.13	66,66,66,66	0
7	NA	J	202[A]	1/1	0.97	0.13	45,45,45,45	1
5	PO4	H	201[A]	5/5	1.00	0.06	16,26,30,38	4
5	PO4	H	201[B]	5/5	1.00	0.06	19,20,30,30	4
5	PO4	H	201[C]	5/5	1.00	0.06	17,25,30,33	4
5	PO4	H	201[D]	5/5	1.00	0.06	20,23,32,33	4
5	PO4	H	201[E]	5/5	1.00	0.06	19,21,27,29	4
5	PO4	N	201[A]	5/5	1.00	0.07	25,26,30,35	4
5	PO4	N	201[B]	5/5	1.00	0.07	17,22,32,35	4
5	PO4	N	201[C]	5/5	1.00	0.07	25,28,29,31	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	PO4	N	201[D]	5/5	1.00	0.07	19,21,32,34	4
5	PO4	N	201[E]	5/5	1.00	0.07	22,25,30,35	4
5	PO4	A	201[A]	5/5	1.00	0.05	22,25,26,32	4
5	PO4	A	201[B]	5/5	1.00	0.05	24,25,29,30	4
5	PO4	A	201[C]	5/5	1.00	0.05	21,26,32,34	4
5	PO4	A	201[D]	5/5	1.00	0.05	26,26,28,35	4
5	PO4	A	201[E]	5/5	1.00	0.05	19,26,31,32	4

6.5 Other polymers [i](#)

There are no such residues in this entry.