



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 11, 2024 – 08:00 AM EST

PDB ID : 3CC4  
Title : Co-crystal Structure of Anisomycin Bound to the 50S Ribosomal Subunit  
Authors : Blaha, G.; Gurel, G.  
Deposited on : 2008-02-24  
Resolution : 2.70 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
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

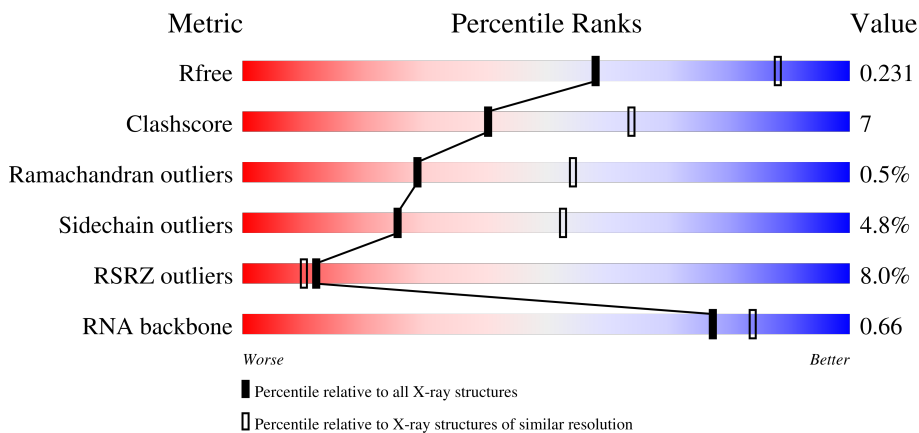
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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.



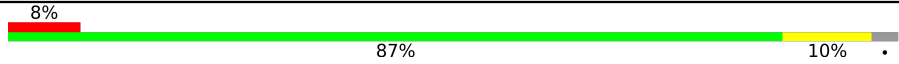
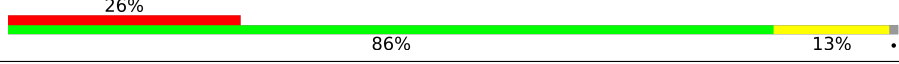
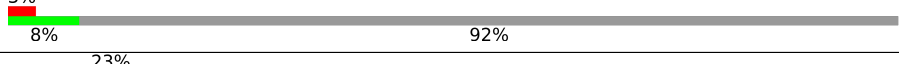


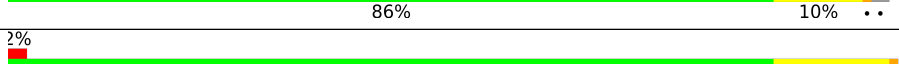
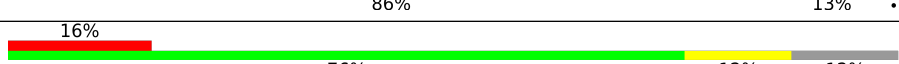
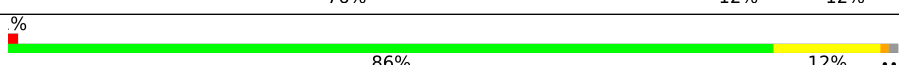
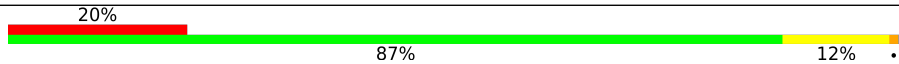
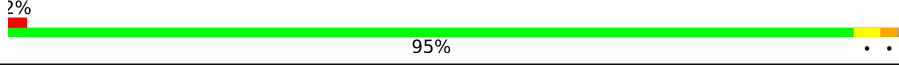

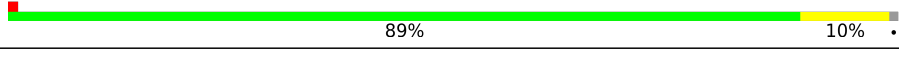
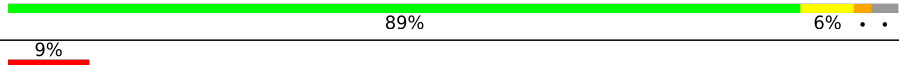

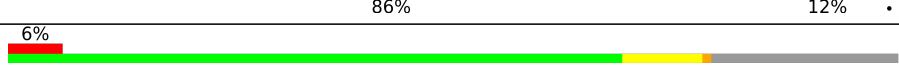










Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)
RNA backbone	3102	1159 (3.00-2.40)

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  $\geq 3$ , 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	240	 9% 84% 14% ..
2	B	338	 3% 87% 12% .
3	C	246	 % 83% 14% .
4	D	177	 40% 66% 14% 21%

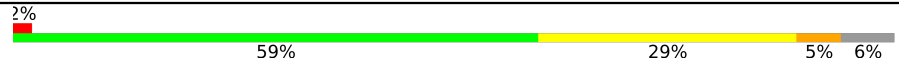

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Mol	Chain	Length	Quality of chain
5	E	178	
6	F	120	
7	G	348	
8	H	177	
9	I	162	
10	J	145	
11	K	132	
12	L	165	
13	M	196	
14	N	187	
15	O	116	
16	P	149	
17	Q	96	
18	R	155	
19	S	85	
20	T	120	
21	U	67	
22	V	71	
23	W	154	
24	X	92	
25	Y	241	
26	Z	116	
27	1	57	
28	2	50	
29	3	92	

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Mol	Chain	Length	Quality of chain
30	0	2923	
31	9	122	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
32	MG	0	8069	-	-	-	X
32	MG	A	8051	-	-	-	X
34	SR	0	8933	-	-	-	X
34	SR	0	8947	-	-	-	X
34	SR	0	8957	-	-	-	X
34	SR	0	8976	-	-	-	X
34	SR	0	8982	-	-	-	X
34	SR	0	8986	-	-	-	X
34	SR	0	8994	-	-	-	X
34	SR	0	8996	-	-	-	X
34	SR	0	9006	-	-	-	X
34	SR	B	8987	-	-	-	X
35	NA	0	8512	-	-	-	X
35	NA	0	8522	-	-	-	X
35	NA	0	8546	-	-	-	X
35	NA	0	8549	-	-	-	X
35	NA	0	8553	-	-	-	X
35	NA	0	8554	-	-	-	X
35	NA	0	8555	-	-	-	X
35	NA	0	8560	-	-	-	X
35	NA	0	8561	-	-	-	X
35	NA	0	8562	-	-	-	X
35	NA	0	8573	-	-	-	X
35	NA	9	8572	-	-	-	X
35	NA	S	8510	-	-	-	X

## 2 Entry composition [i](#)

There are 39 unique types of molecules in this entry. The entry contains 99135 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 50S ribosomal protein L2P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	237	1753	1072	352	324	5	0	0	0

- Molecule 2 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	337	2625	1616	493	511	5	0	0	0

- Molecule 3 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	246	1860	1130	345	384	1	0	0	0

- Molecule 4 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	140	1094	685	195	210	4	0	0	0

- Molecule 5 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	172	1357	840	224	289	4	0	0	0

- Molecule 6 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	F	119	890	551	141	197	1	0	0	0

- Molecule 7 is a protein called 50S ribosomal protein L10E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	G	29	240	149	39	51	1	0	0	0

- Molecule 8 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	H	160	1282	798	240	238	6	0	0	0

- Molecule 9 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
9	I	70	519	323	81	114	1	0	0	0

- Molecule 10 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	J	142	1120	696	199	222	3	0	0	0

- Molecule 11 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
11	K	132	994	609	189	192	4	0	0	0

- Molecule 12 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
12	L	145	1118	670	222	226	0	0	0

- Molecule 13 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
13	M	194	1558	943	333	281	1	0	0	0

- Molecule 14 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
14	N	186	1445	895	262	286	2	0	0	0

- Molecule 15 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
15	O	115	865	529	161	175	0	0	0

- Molecule 16 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
16	P	143	1136	683	229	224	0	0	0

- Molecule 17 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
17	Q	95	735	450	141	144	0	0	0

- Molecule 18 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
18	R	150	1149	713	209	223	4	0	0	0

- Molecule 19 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
19	S	81	641	389	111	138	3	0	0	0

- Molecule 20 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
20	T	119	950	568	180	202	0	0	0

- Molecule 21 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	53	Total	C	N	O	S	0	0	0
			410	244	75	86	5			

- Molecule 22 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	65	Total	C	N	O	S	0	0	0
			499	304	94	100	1			

- Molecule 23 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	W	154	Total	C	N	O	S	0	0	0
			1196	737	209	244	6			

- Molecule 24 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	X	82	Total	C	N	O	S	0	0	0
			654	402	129	122	1			

- Molecule 25 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	Y	142	Total	C	N	O	0	0	0
			1130	686	228	216			

- Molecule 26 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Z	73	Total	C	N	O	S	0	0	0
			573	343	113	112	5			

- Molecule 27 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 28 is a protein called 50S ribosomal protein L39e.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

- Molecule 29 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 30 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	0	2754	Total	C	N	O	P	0	0	0
			59021	26349	10873	19054	2745			

- Molecule 31 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	9	122	Total	C	N	O	P	0	0	0
			2599	1160	471	847	121			

- Molecule 32 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	A	1	Total	Mg	0	0
			1	1		
32	B	1	Total	Mg	0	0
			1	1		
32	K	1	Total	Mg	0	0
			1	1		
32	T	1	Total	Mg	0	0
			1	1		
32	Y	1	Total	Mg	0	0
			1	1		
32	0	87	Total	Mg	0	0
			87	87		
32	9	1	Total	Mg	0	0
			1	1		

- Molecule 33 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
33	A	1	Total Cl 1 1	0	0
33	B	1	Total Cl 1 1	0	0
33	J	3	Total Cl 3 3	0	0
33	L	1	Total Cl 1 1	0	0
33	M	1	Total Cl 1 1	0	0
33	N	1	Total Cl 1 1	0	0
33	O	1	Total Cl 1 1	0	0
33	R	1	Total Cl 1 1	0	0
33	Y	1	Total Cl 1 1	0	0
33	3	1	Total Cl 1 1	0	0
33	0	10	Total Cl 10 10	0	0

- Molecule 34 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	A	3	Total Sr 3 3	0	0
34	B	2	Total Sr 2 2	0	0
34	F	1	Total Sr 1 1	0	0
34	H	1	Total Sr 1 1	0	0
34	R	1	Total Sr 1 1	0	0
34	S	1	Total Sr 1 1	0	0
34	1	2	Total Sr 2 2	0	0
34	3	2	Total Sr 2 2	0	0
34	0	92	Total Sr 92 92	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	9	3	Total 3	Sr 3	0	0

- Molecule 35 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	B	1	Total 1	Na 1	0	0
35	C	1	Total 1	Na 1	0	0
35	J	1	Total 1	Na 1	0	0
35	M	1	Total 1	Na 1	0	0
35	Q	1	Total 1	Na 1	0	0
35	R	1	Total 1	Na 1	0	0
35	S	1	Total 1	Na 1	0	0
35	0	66	Total 66	Na 66	0	0
35	9	2	Total 2	Na 2	0	0

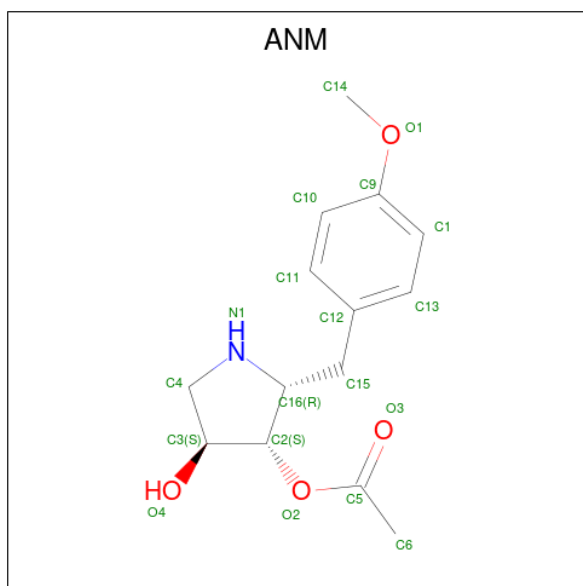
- Molecule 36 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	O	1	Total 1	Cd 1	0	0
36	U	1	Total 1	Cd 1	0	0
36	Z	1	Total 1	Cd 1	0	0
36	1	1	Total 1	Cd 1	0	0
36	3	1	Total 1	Cd 1	0	0

- Molecule 37 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
37	0	2	Total K 2 2	0	0

- Molecule 38 is ANISOMYCIN (three-letter code: ANM) (formula: C<sub>14</sub>H<sub>19</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
38	0	1	19	14	1	4	0	0

- Molecule 39 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
39	A	110	Total O 110 110	0	0
39	B	140	Total O 140 140	0	0
39	C	163	Total O 163 163	0	0
39	D	46	Total O 46 46	0	0
39	E	44	Total O 44 44	0	0
39	F	26	Total O 26 26	0	0
39	G	17	Total O 17 17	0	0
39	H	67	Total O 67 67	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
39	I	6	Total 6	O 6	0	0
39	J	49	Total 49	O 49	0	0
39	K	56	Total 56	O 56	0	0
39	L	85	Total 85	O 85	0	0
39	M	121	Total 121	O 121	0	0
39	N	61	Total 61	O 61	0	0
39	O	44	Total 44	O 44	0	0
39	P	62	Total 62	O 62	0	0
39	Q	48	Total 48	O 48	0	0
39	R	78	Total 78	O 78	0	0
39	S	32	Total 32	O 32	0	0
39	T	39	Total 39	O 39	0	0
39	U	27	Total 27	O 27	0	0
39	V	13	Total 13	O 13	0	0
39	W	65	Total 65	O 65	0	0
39	X	23	Total 23	O 23	0	0
39	Y	92	Total 92	O 92	0	0
39	Z	31	Total 31	O 31	0	0
39	1	48	Total 48	O 48	0	0
39	2	38	Total 38	O 38	0	0
39	3	66	Total 66	O 66	0	0

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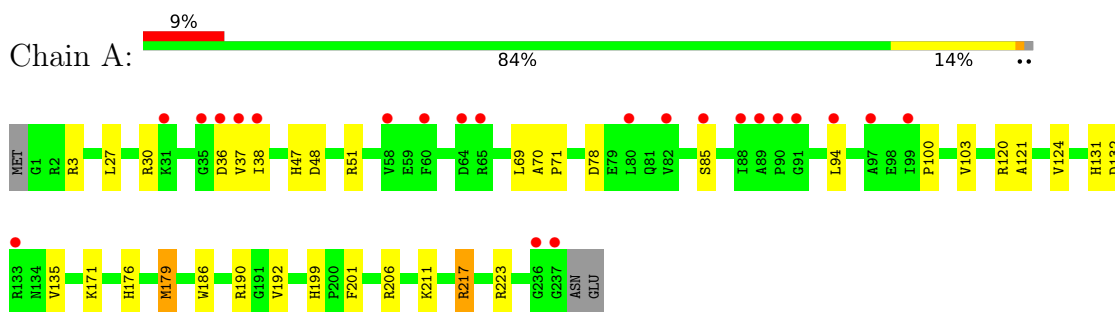
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
39	0	5972	Total 5972	O 5972	0	0
39	9	147	Total 147	O 147	0	0

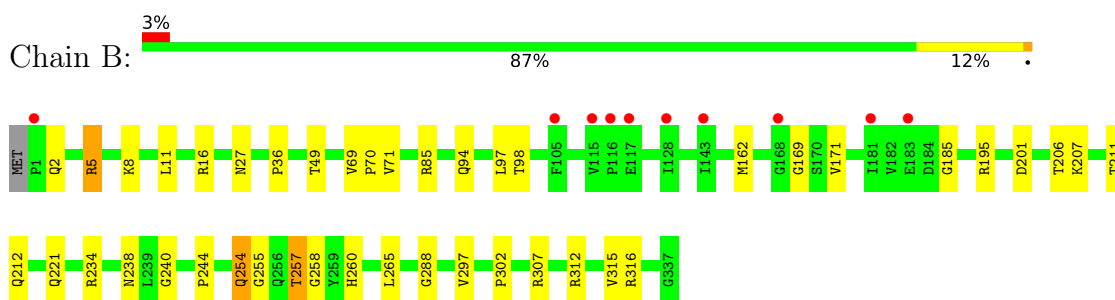
### 3 Residue-property plots [i](#)

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.

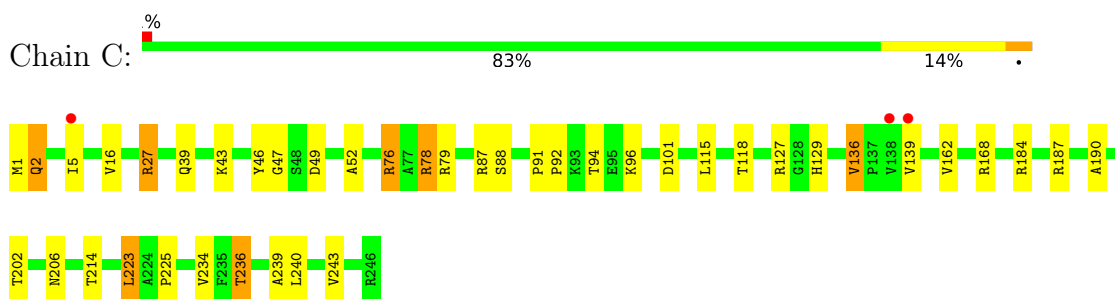
- Molecule 1: 50S ribosomal protein L2P



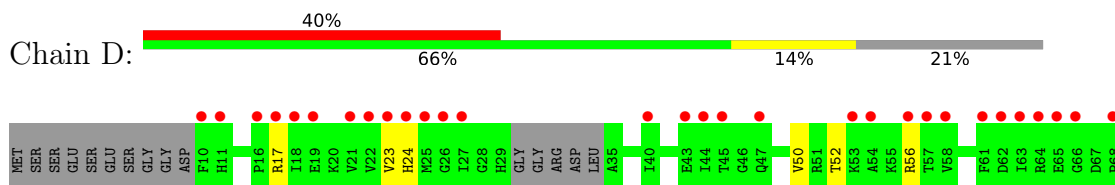
- Molecule 2: 50S ribosomal protein L3P

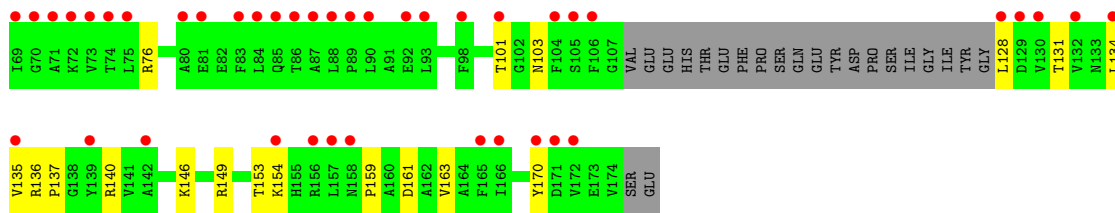


- Molecule 3: 50S ribosomal protein L4P

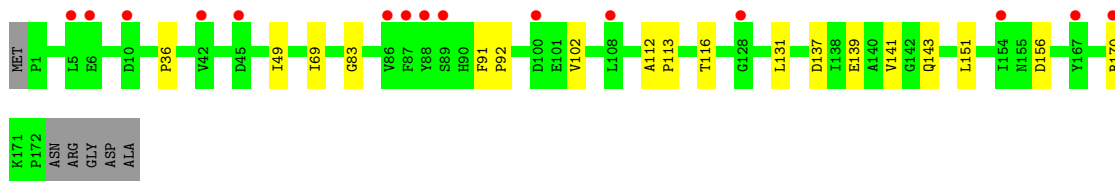
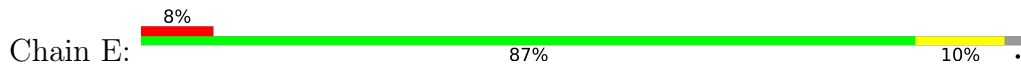


- Molecule 4: 50S ribosomal protein L5P

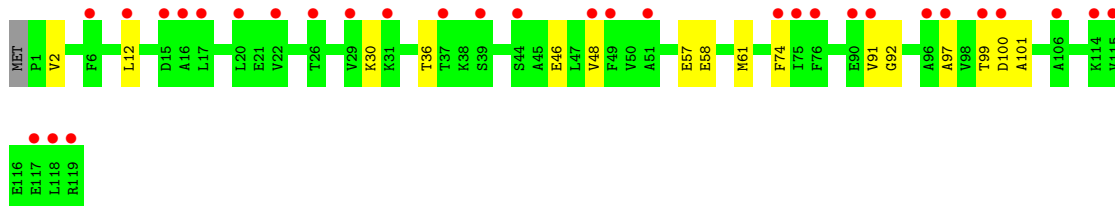
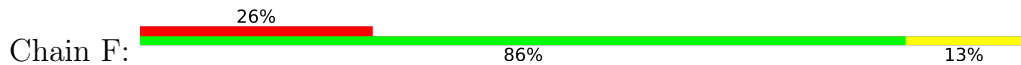




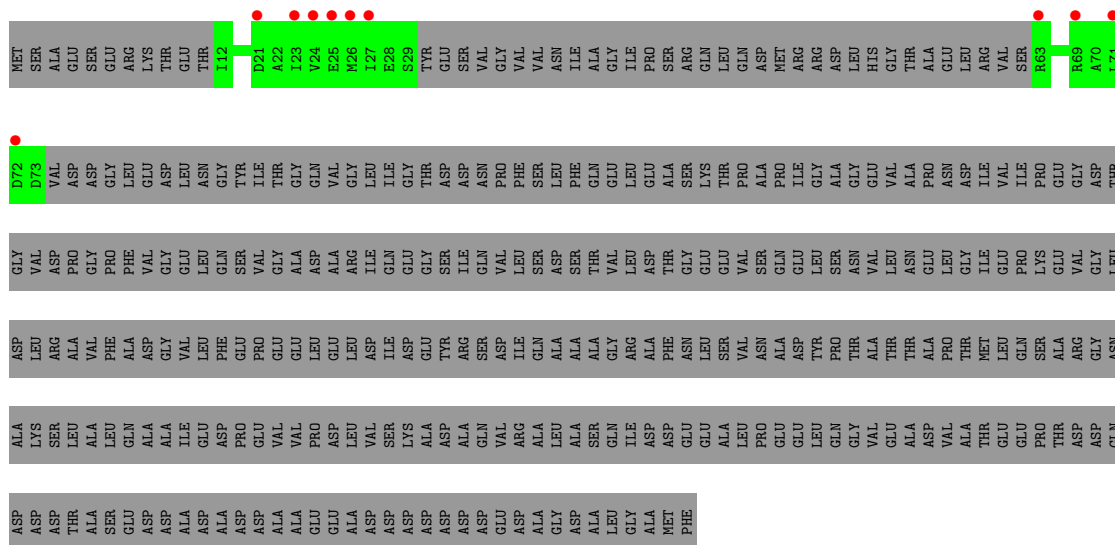
• Molecule 5: 50S ribosomal protein L6P



• Molecule 6: 50S ribosomal protein L7Ae

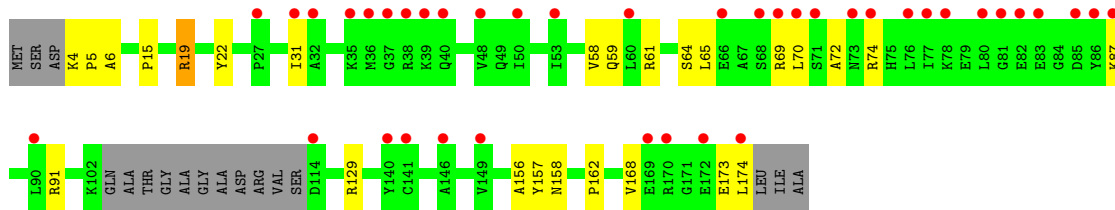
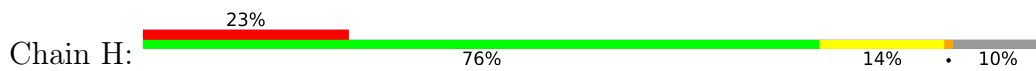


• Molecule 7: 50S ribosomal protein L10E

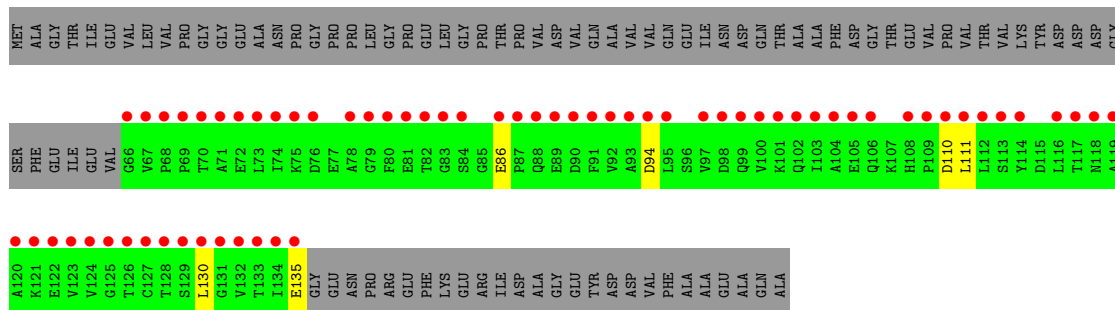
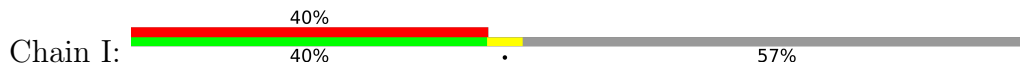


• Molecule 8: 50S ribosomal protein L10e

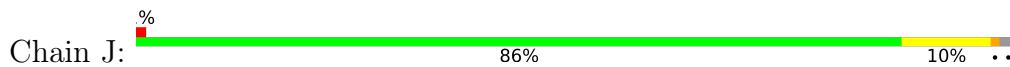




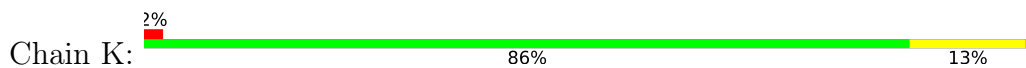
- Molecule 9: 50S ribosomal protein L11P



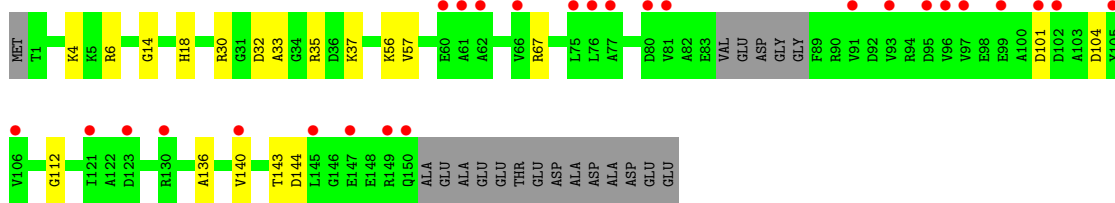
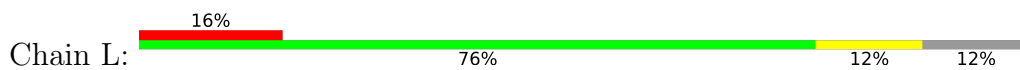
- Molecule 10: 50S ribosomal protein L13P



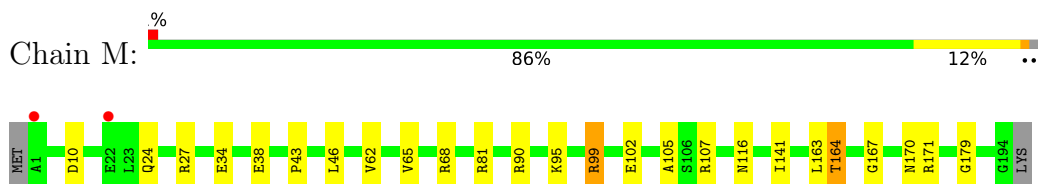
- Molecule 11: 50S ribosomal protein L14P



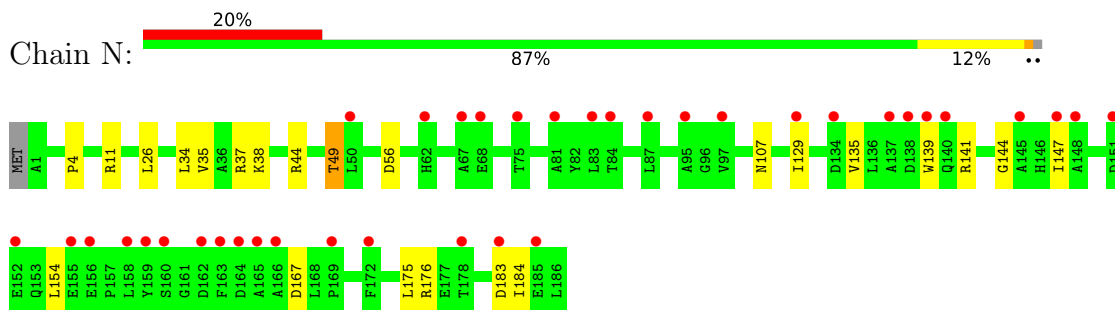
- Molecule 12: 50S ribosomal protein L15P



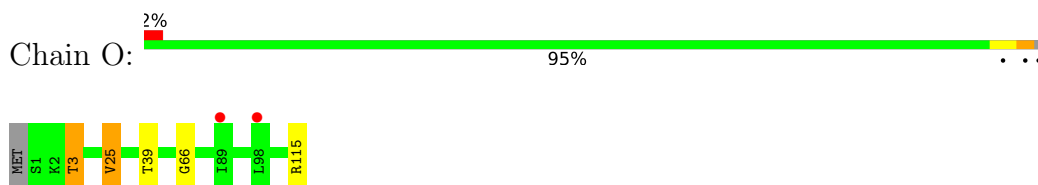
- Molecule 13: 50S ribosomal protein L15e



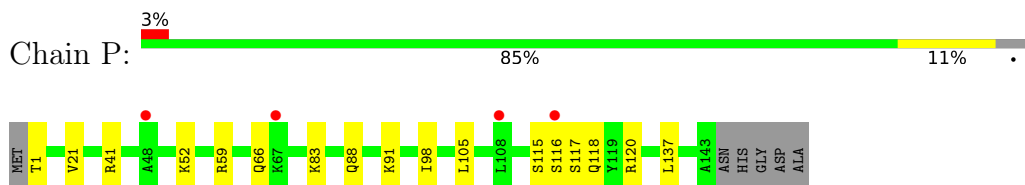
- Molecule 14: 50S ribosomal protein L18P



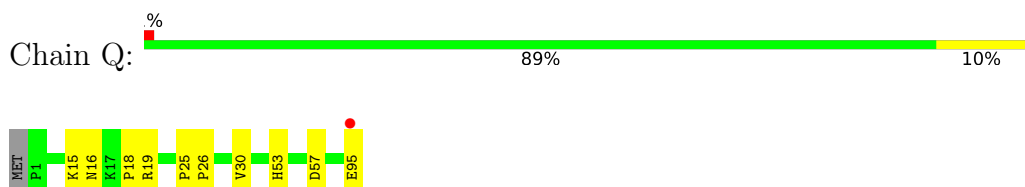
- Molecule 15: 50S ribosomal protein L18e



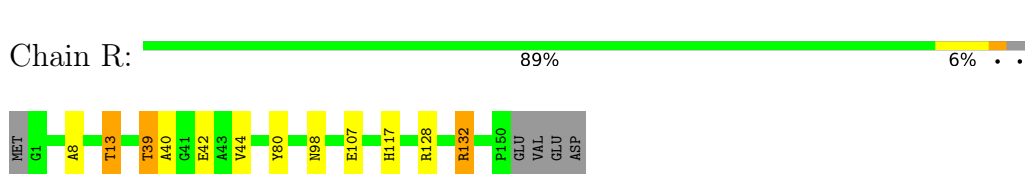
- Molecule 16: 50S ribosomal protein L19e



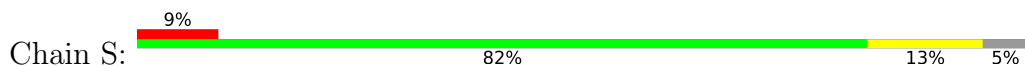
- Molecule 17: 50S ribosomal protein L21e



- Molecule 18: 50S ribosomal protein L22P

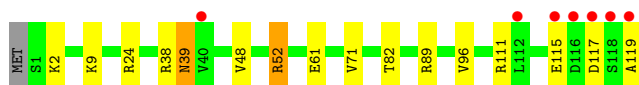
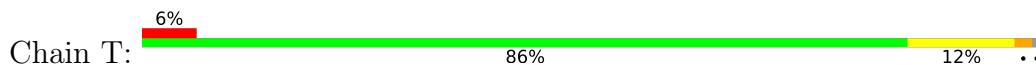


- Molecule 19: 50S ribosomal protein L23P

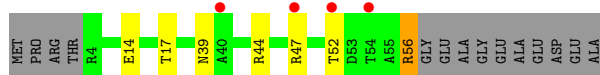




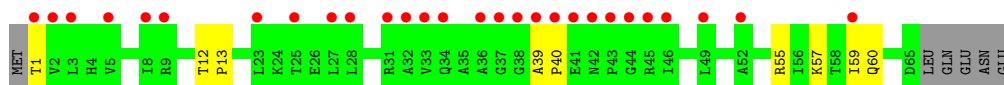
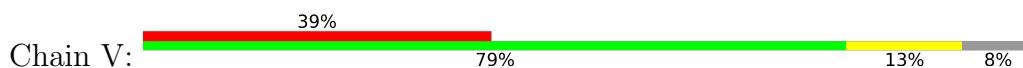
- Molecule 20: 50S ribosomal protein L24P



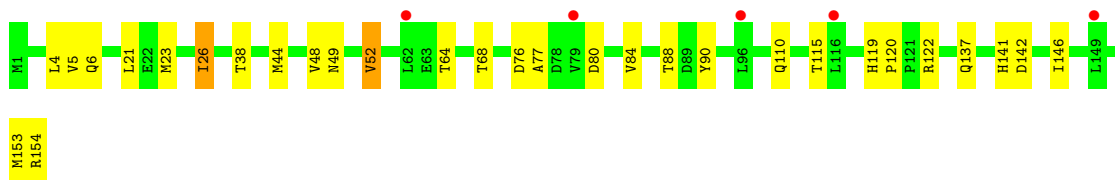
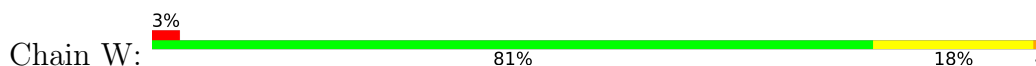
- Molecule 21: 50S ribosomal protein L24e



- Molecule 22: 50S ribosomal protein L29P



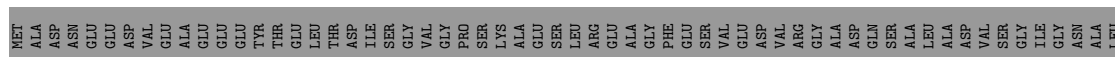
- Molecule 23: 50S ribosomal protein L30P

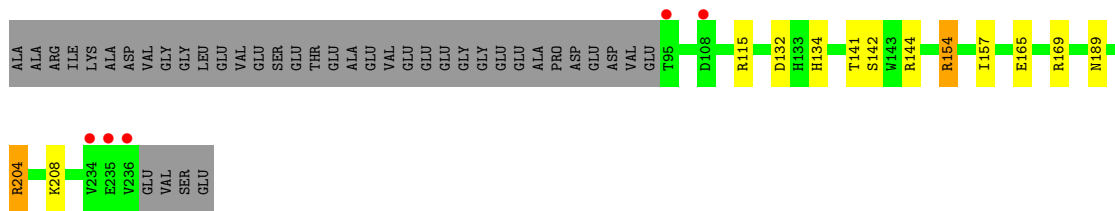


- Molecule 24: 50S ribosomal protein L31e

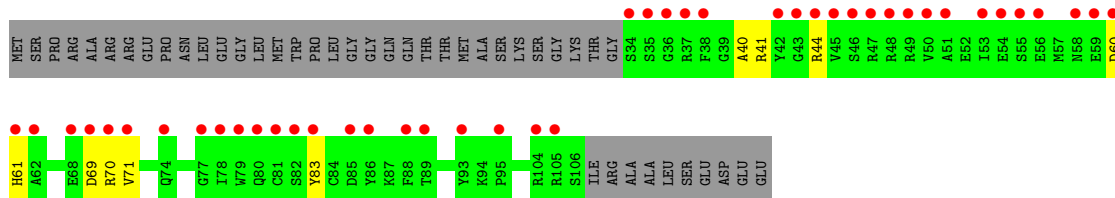


- Molecule 25: 50S ribosomal protein L32e

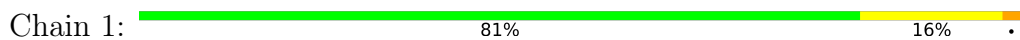




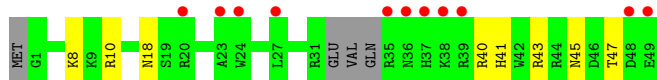
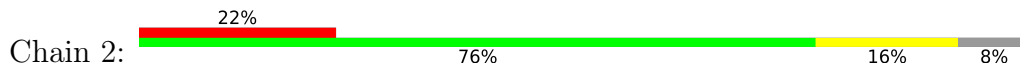
• Molecule 26: 50S ribosomal protein L37Ae



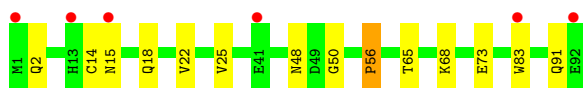
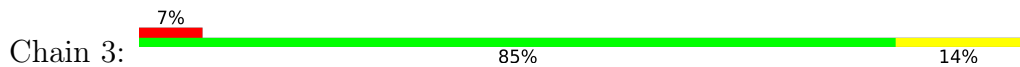
• Molecule 27: 50S ribosomal protein L37e



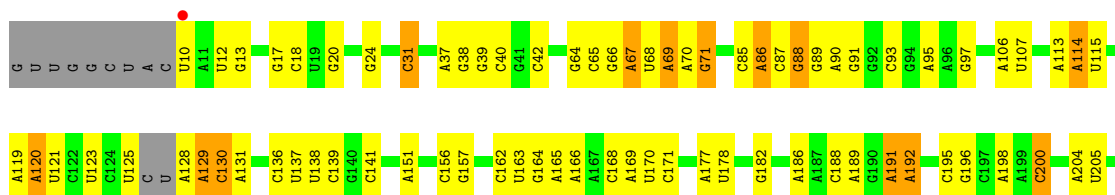
• Molecule 28: 50S ribosomal protein L39e

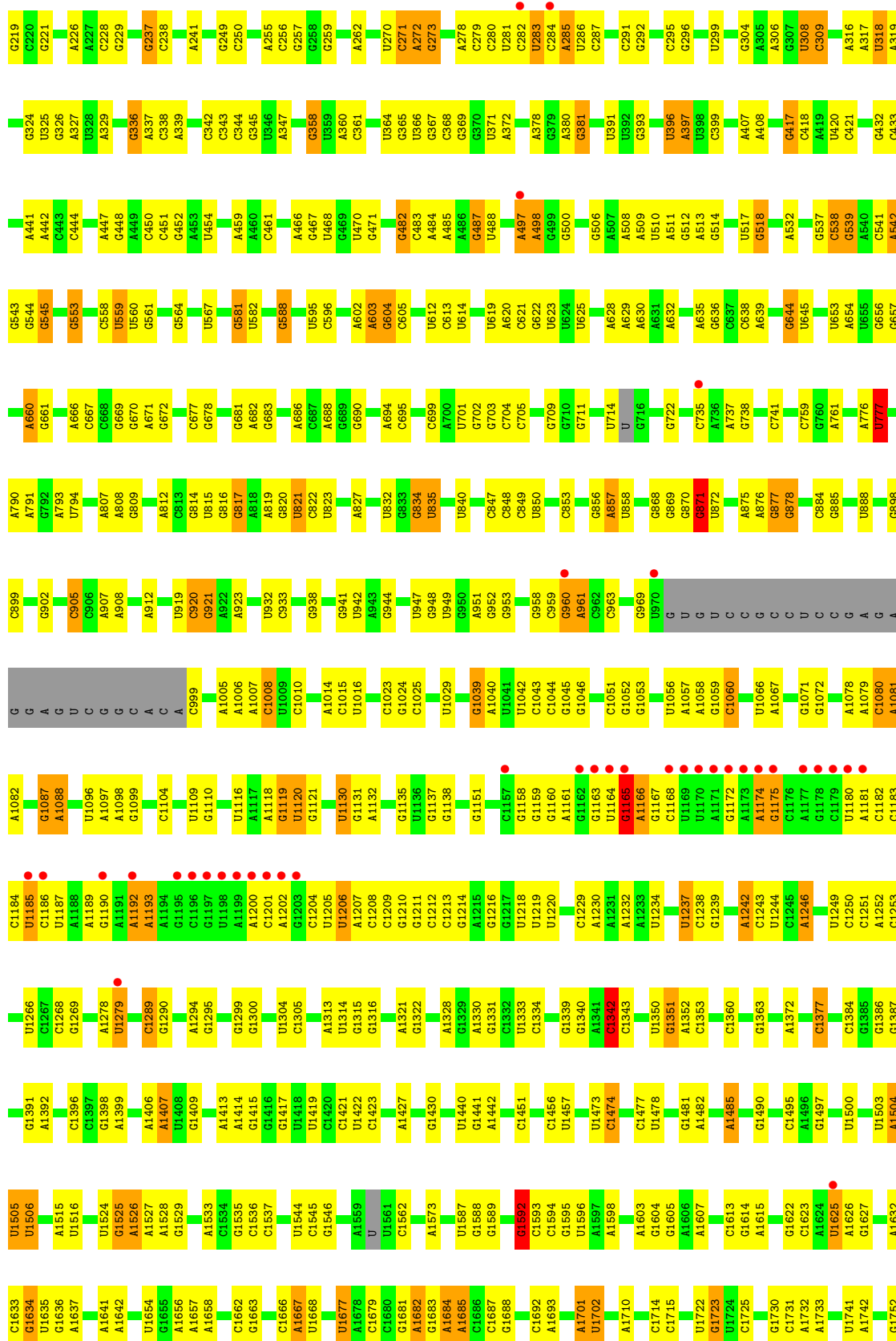


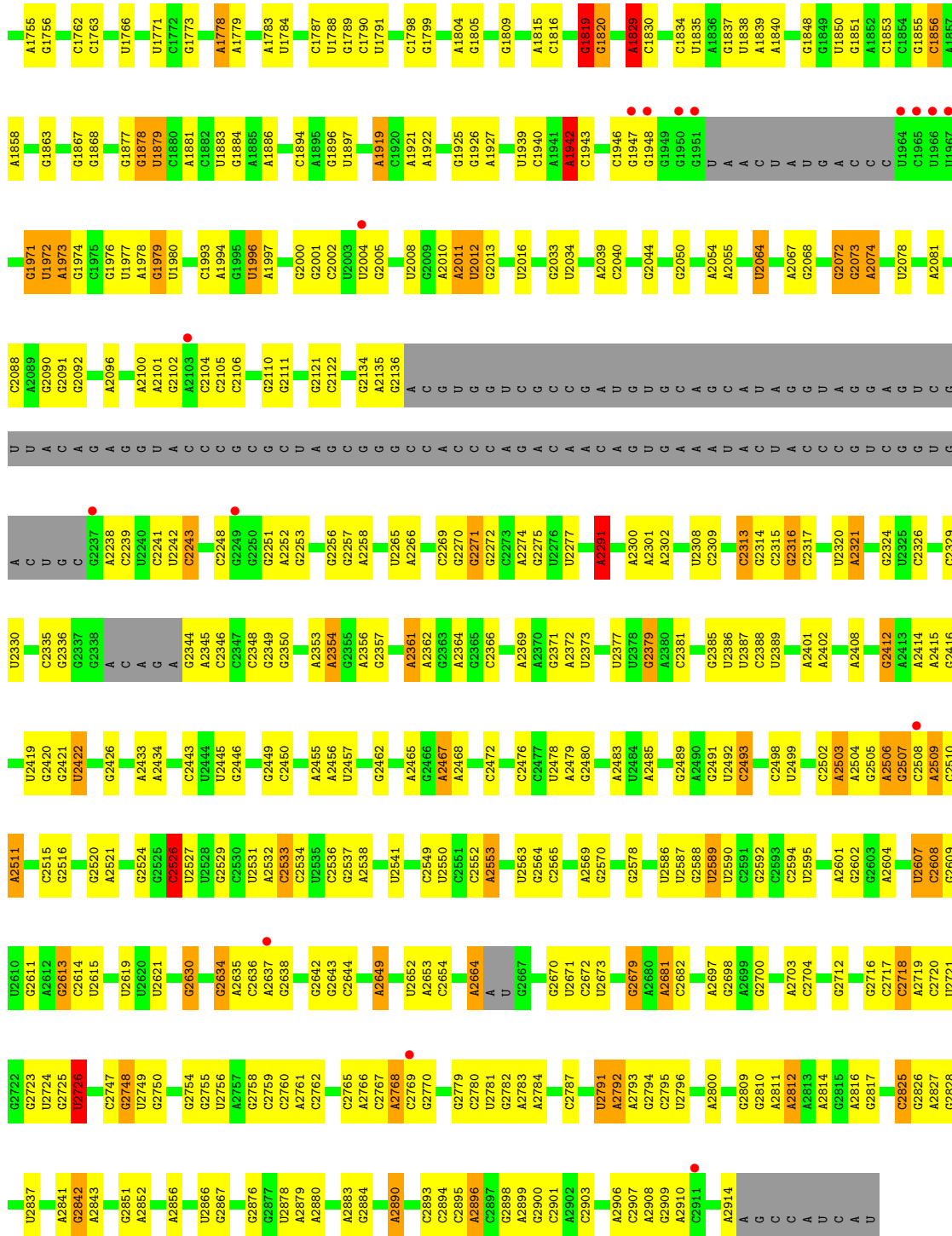
• Molecule 29: 50S ribosomal protein L44E



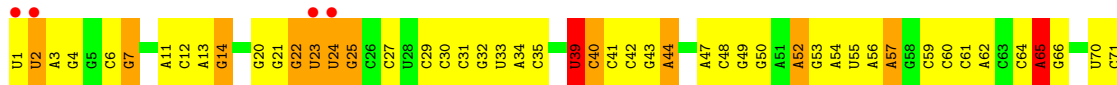
• Molecule 30: 23S ribosomal RNA

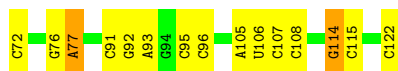






• Molecule 31: 5S ribosomal RNA





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	211.78Å 299.08Å 573.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.85 – 2.70 85.45 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.9 (49.85-2.70) 96.9 (85.45-2.40)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.00 (at 2.40Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.202 , 0.244 0.191 , 0.231	Depositor DCC
$R_{free}$ test set	6547 reflections (0.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.7	Xtrriage
Anisotropy	0.174	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 63.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	99135	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.56% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, UR3, OMG, PSU, NA, ANM, SR, 1MA, CL, OMU, CD, K

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	0.51	0/1786	0.78	0/2408
2	B	0.53	0/2690	0.78	0/3652
3	C	0.54	0/1885	0.77	0/2552
4	D	0.65	0/1111	0.71	1/1498 (0.1%)
5	E	0.60	0/1382	0.68	0/1880
6	F	0.54	0/901	0.71	0/1224
7	G	0.51	0/241	0.67	0/324
8	H	0.60	0/1302	0.79	0/1743
9	I	0.59	0/526	0.62	0/716
10	J	0.61	0/1136	0.72	0/1530
11	K	0.51	0/1004	0.80	0/1351
12	L	0.49	0/1130	0.76	0/1509
13	M	0.51	0/1582	0.77	0/2116
14	N	0.55	0/1474	0.77	0/1999
15	O	0.47	0/874	0.73	1/1181 (0.1%)
16	P	0.52	0/1147	0.67	0/1528
17	Q	0.49	0/749	0.77	0/1005
18	R	0.54	0/1172	0.74	0/1578
19	S	0.54	0/648	0.67	0/875
20	T	0.46	0/958	0.76	1/1289 (0.1%)
21	U	0.57	0/417	0.71	0/562
22	V	0.44	0/502	0.67	0/675
23	W	0.52	0/1219	0.78	1/1655 (0.1%)
24	X	0.52	0/664	0.72	0/895
25	Y	0.52	0/1146	0.74	0/1536
26	Z	0.69	0/584	0.74	0/781
27	1	0.55	0/438	0.75	0/578
28	2	0.45	0/401	0.70	0/529
29	3	0.59	0/771	0.70	0/1024
30	0	0.37	0/65958	0.68	15/102869 (0.0%)
31	9	0.32	0/2904	0.69	1/4526 (0.0%)
All	All	0.43	0/98702	0.70	20/147588 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
23	W	0	1
30	0	0	42
31	9	0	2
All	All	0	45

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	4	LEU	CA-CB-CG	7.59	132.77	115.30
30	0	1942	A	C5'-C4'-C3'	6.82	126.92	116.00
30	0	871	G	C5'-C4'-O4'	-6.64	101.13	109.10
30	0	1504	A	N9-C1'-C2'	5.91	121.68	114.00
30	0	2726	U	N1-C1'-C2'	5.85	121.60	114.00
31	9	39	U	N1-C1'-C2'	5.84	121.59	114.00
30	0	1504	A	C1'-O4'-C4'	-5.62	105.40	109.90
15	O	66	GLY	N-CA-C	5.61	127.11	113.10
30	0	1592	G	N9-C1'-C2'	5.49	121.14	114.00
30	0	1819	G	C5'-C4'-C3'	5.49	124.78	116.00
30	0	2467	A	C1'-O4'-C4'	-5.47	105.52	109.90
20	T	52	ARG	N-CA-C	5.42	125.64	111.00
30	0	1829	A	N9-C1'-C2'	-5.39	106.08	112.00
30	0	2313	C	C5'-C4'-O4'	5.32	115.48	109.10
30	0	1120	U	C5'-C4'-C3'	-5.21	107.66	116.00
4	D	170	TYR	N-CA-C	5.14	124.87	111.00
30	0	1165	G	C1'-O4'-C4'	-5.12	105.80	109.90
30	0	777	U	O4'-C1'-N1	5.12	112.29	108.20
30	0	2316	G	C5'-C4'-C3'	-5.09	107.86	116.00
30	0	2291	A	N9-C1'-C2'	5.05	120.56	114.00

There are no chirality outliers.

All (45) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	0	1039	G	Sidechain
30	0	1078	A	Sidechain
30	0	1237	U	Sidechain

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>Group</b>
30	0	1342	C	Sidechain
30	0	1351	G	Sidechain
30	0	1417	G	Sidechain
30	0	1430	G	Sidechain
30	0	1677	U	Sidechain
30	0	1702	U	Sidechain
30	0	1809	G	Sidechain
30	0	1829	A	Sidechain
30	0	1848	G	Sidechain
30	0	1863	G	Sidechain
30	0	1867	G	Sidechain
30	0	1877	G	Sidechain
30	0	1878	G	Sidechain
30	0	1972	U	Sidechain
30	0	1993	C	Sidechain
30	0	221	G	Sidechain
30	0	2308	U	Sidechain
30	0	2316	G	Sidechain
30	0	2412	G	Sidechain
30	0	2465	A	Sidechain
30	0	2493	C	Sidechain
30	0	2503	A	Sidechain
30	0	2506	A	Sidechain
30	0	2526	C	Sidechain
30	0	2552	C	Sidechain
30	0	2607	U	Sidechain
30	0	2630	G	Sidechain
30	0	2679	G	Sidechain
30	0	270	U	Sidechain
30	0	2726	U	Sidechain
30	0	2842	G	Sidechain
30	0	391	U	Sidechain
30	0	396	U	Sidechain
30	0	471	G	Sidechain
30	0	482	G	Sidechain
30	0	518	G	Sidechain
30	0	619	U	Sidechain
30	0	817	G	Sidechain
30	0	888	U	Sidechain
31	9	39	U	Sidechain
31	9	65	A	Sidechain
23	W	90	TYR	Sidechain

## 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	1753	0	1766	21	0
2	B	2625	0	2533	29	0
3	C	1860	0	1813	22	0
4	D	1094	0	1085	11	0
5	E	1357	0	1266	10	0
6	F	890	0	843	8	0
7	G	240	0	231	0	0
8	H	1282	0	1292	18	0
9	I	519	0	500	4	0
10	J	1120	0	1098	14	0
11	K	994	0	1027	11	0
12	L	1118	0	1076	12	0
13	M	1558	0	1573	19	0
14	N	1445	0	1401	16	0
15	O	865	0	873	4	0
16	P	1136	0	1123	11	0
17	Q	735	0	729	6	0
18	R	1149	0	1122	11	0
19	S	641	0	605	5	0
20	T	950	0	924	8	0
21	U	410	0	364	3	0
22	V	499	0	511	4	0
23	W	1196	0	1137	22	0
24	X	654	0	653	11	0
25	Y	1130	0	1133	13	0
26	Z	573	0	532	6	0
27	1	431	0	426	10	0
28	2	396	0	413	5	0
29	3	755	0	729	7	0
30	0	59021	0	29812	846	0
31	9	2599	0	1325	64	0
32	0	87	0	0	0	0
32	9	1	0	0	0	0
32	A	1	0	0	0	0
32	B	1	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	Y	1	0	0	0	0
33	0	10	0	0	0	0
33	3	1	0	0	0	0
33	A	1	0	0	0	0
33	B	1	0	0	0	0
33	J	3	0	0	1	0
33	L	1	0	0	0	0
33	M	1	0	0	0	0
33	N	1	0	0	0	0
33	O	1	0	0	0	0
33	R	1	0	0	0	0
33	Y	1	0	0	0	0
34	0	92	0	0	0	0
34	1	2	0	0	0	0
34	3	2	0	0	0	0
34	9	3	0	0	0	0
34	A	3	0	0	0	0
34	B	2	0	0	0	0
34	F	1	0	0	0	0
34	H	1	0	0	0	0
34	R	1	0	0	0	0
34	S	1	0	0	0	0
35	0	66	0	0	0	0
35	9	2	0	0	0	0
35	B	1	0	0	0	0
35	C	1	0	0	0	0
35	J	1	0	0	0	0
35	M	1	0	0	0	0
35	Q	1	0	0	0	0
35	R	1	0	0	0	0
35	S	1	0	0	0	0
36	1	1	0	0	0	0
36	3	1	0	0	0	0
36	O	1	0	0	0	0
36	U	1	0	0	0	0
36	Z	1	0	0	0	0
37	0	2	0	0	0	0
38	0	19	0	19	5	0
39	0	5972	0	0	121	0
39	1	48	0	0	0	0
39	2	38	0	0	0	0
39	3	66	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
39	9	147	0	0	5	0
39	A	110	0	0	4	0
39	B	140	0	0	5	0
39	C	163	0	0	2	0
39	D	46	0	0	0	0
39	E	44	0	0	0	0
39	F	26	0	0	0	0
39	G	17	0	0	0	0
39	H	67	0	0	3	0
39	I	6	0	0	1	0
39	J	49	0	0	1	0
39	K	56	0	0	0	0
39	L	85	0	0	2	0
39	M	121	0	0	1	0
39	N	61	0	0	1	0
39	O	44	0	0	0	0
39	P	62	0	0	0	0
39	Q	48	0	0	0	0
39	R	78	0	0	0	0
39	S	32	0	0	0	0
39	T	39	0	0	0	0
39	U	27	0	0	0	0
39	V	13	0	0	0	0
39	W	65	0	0	2	0
39	X	23	0	0	1	0
39	Y	92	0	0	3	0
39	Z	31	0	0	1	0
All	All	99135	0	59934	1085	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 7.

All (1085) 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)
30:0:1160:G:H5'	30:0:1161:A:H5'	1.22	1.16
31:9:76:G:H3'	31:9:77:A:H5''	1.34	1.02
15:O:3:THR:HG22	30:0:656:G:H5'	1.43	1.00
30:0:871:G:H5'	30:0:871:G:H8	1.27	0.98
30:0:871:G:H5'	30:0:871:G:C8	1.98	0.97
30:0:2717:C:H2'	30:0:2718:C:H5''	1.46	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:171:ARG:HD3	30:0:156:C:H5''	1.44	0.96
10:J:82:THR:HG23	30:0:1242:A:H5'	1.47	0.96
30:0:2717:C:C2'	30:0:2718:C:H5''	1.97	0.94
8:H:59:GLN:HE21	8:H:129:ARG:HE	1.15	0.93
2:B:221:GLN:HE22	11:K:42:ASN:HD22	1.13	0.93
14:N:37:ARG:NH1	31:9:6:C:H5''	1.83	0.93
31:9:56:A:H2'	31:9:57:A:H5''	1.48	0.92
30:0:542:A:H5'	30:0:542:A:H8	1.35	0.91
30:0:870:G:H2'	30:0:871:G:H5''	1.53	0.90
23:W:21:LEU:HD21	23:W:48:VAL:HG11	1.54	0.90
16:P:115:SER:H	16:P:118:GLN:HE21	1.20	0.89
30:0:1474:C:H5'	30:0:1474:C:H6	1.37	0.89
30:0:1116:U:HO2'	30:0:1118:A:H2	0.87	0.87
30:0:1160:G:H5'	30:0:1161:A:C5'	2.04	0.87
30:0:1160:G:C5'	30:0:1161:A:H5'	2.03	0.86
30:0:2506:A:HO2'	30:0:2507:G:H8	0.89	0.86
30:0:2812:A:H2	30:0:2814:A:H62	1.24	0.85
30:0:1667:A:H5'	30:0:1667:A:H8	1.42	0.85
30:0:1603:A:H5'	30:0:1605:G:O4'	1.75	0.85
30:0:1118:A:H62	30:0:1244:U:H3	1.25	0.84
30:0:1701:A:H4'	30:0:1702:U:H5''	1.56	0.84
11:K:10:GLN:H	11:K:10:GLN:HE21	1.25	0.83
30:0:2586:U:H3	30:0:2592:G:H22	1.21	0.83
39:N:8843:HOH:O	31:9:49:G:H5''	1.77	0.83
30:0:381:G:H5''	39:0:4352:HOH:O	1.77	0.83
30:0:1835:U:H5	30:0:1840:A:N7	1.76	0.83
3:C:5:ILE:HD11	3:C:16:VAL:HG23	1.61	0.82
30:0:541:C:H2'	30:0:542:A:H5''	1.61	0.82
30:0:559:U:H6	30:0:559:U:H5'	1.45	0.81
30:0:545:G:H5'	30:0:545:G:H8	1.44	0.81
30:0:2533:C:H6	30:0:2533:C:H5'	1.46	0.81
30:0:1979:G:H2'	39:0:3320:HOH:O	1.82	0.79
30:0:2291:A:C8	30:0:2309:C:H5'	2.18	0.78
30:0:871:G:H8	30:0:871:G:C5'	1.96	0.78
30:0:2908:A:H2'	30:0:2909:G:O4'	1.83	0.78
30:0:506:G:H22	30:0:509:A:C5'	1.97	0.78
38:0:2924:ANM:H151	38:0:2924:ANM:H63	1.63	0.78
30:0:1300:G:H1'	39:0:4716:HOH:O	1.82	0.77
13:M:102:GLU:OE1	13:M:164:THR:HG21	1.85	0.77
30:0:1205:U:H2'	30:0:1206:U:H5''	1.66	0.77
30:0:506:G:H22	30:0:509:A:H5''	1.50	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:853:C:H3'	39:0:4586:HOH:O	1.83	0.77
30:0:541:C:C2'	30:0:542:A:H5''	2.15	0.76
30:0:1666:C:O2'	30:0:1667:A:H5''	1.86	0.75
28:2:41:HIS:H	28:2:45:ASN:HD22	1.34	0.75
31:9:29:C:H2'	31:9:30:C:H5'	1.68	0.75
30:0:1116:U:H3	30:0:1246:A:H62	1.34	0.75
3:C:27:ARG:NH2	30:0:657:G:OP1	2.20	0.75
30:0:1118:A:H3'	30:0:1118:A:C8	2.22	0.75
30:0:1118:A:H3'	30:0:1118:A:H8	1.51	0.75
30:0:2506:A:O2'	30:0:2507:G:H8	1.69	0.75
30:0:182:G:H5'	39:0:5189:HOH:O	1.86	0.74
31:9:14:G:H5'	31:9:14:G:H8	1.51	0.74
30:0:1474:C:H5'	30:0:1474:C:C6	2.22	0.74
13:M:163:LEU:HD21	30:0:188:C:H5''	1.71	0.73
30:0:1120:U:H5'	30:0:1121:G:OP2	1.89	0.73
30:0:1209:C:H2'	30:0:1210:G:H8	1.53	0.73
18:R:98:ASN:HD21	30:0:500:G:H21	1.34	0.73
22:V:1:THR:HB	30:0:93:C:H5''	1.70	0.73
30:0:877:G:H5'	30:0:878:G:OP1	1.90	0.72
30:0:1166:A:H61	30:0:1180:U:H3	1.35	0.72
30:0:544:G:H2'	30:0:545:G:H5''	1.72	0.72
30:0:1973:A:H5'	30:0:1973:A:H8	1.55	0.72
31:9:56:A:C2'	31:9:57:A:H5''	2.20	0.72
30:0:282:C:H1'	30:0:368:C:N4	2.04	0.72
23:W:137:GLN:HE21	23:W:141:HIS:HE1	1.37	0.71
30:0:1189:A:H1'	30:0:1209:C:O4'	1.90	0.71
30:0:1206:U:H6	30:0:1206:U:H5'	1.53	0.71
31:9:92:G:H2'	31:9:93:A:C8	2.26	0.71
10:J:52:GLN:NE2	30:0:1119:G:H2'	2.05	0.71
30:0:1878:G:H1'	39:0:6168:HOH:O	1.91	0.71
30:0:2491:G:H1'	39:0:6923:HOH:O	1.91	0.70
30:0:2534:C:H1'	39:0:3522:HOH:O	1.91	0.70
3:C:184:ARG:NH2	30:0:450:C:OP1	2.24	0.70
30:0:1741:U:H5'	30:0:1742:A:OP1	1.91	0.70
30:0:1183:C:H2'	39:0:6292:HOH:O	1.91	0.70
2:B:5:ARG:HH11	2:B:8:LYS:HE2	1.56	0.70
30:0:281:U:H2'	30:0:282:C:O4'	1.91	0.70
1:A:211:LYS:HB2	39:A:9075:HOH:O	1.91	0.69
30:0:1701:A:H5'	39:0:6332:HOH:O	1.92	0.69
28:2:43:ARG:HH22	30:0:1684:A:H1'	1.57	0.69
30:0:823:U:H3'	39:0:4481:HOH:O	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:116:SER:O	30:0:1593:C:H5'	1.92	0.69
2:B:206:THR:HG21	30:0:2716:G:H5''	1.72	0.69
30:0:2851:G:O2'	30:0:2852:A:H5'	1.92	0.69
30:0:541:C:H2'	30:0:542:A:C5'	2.23	0.69
30:0:1159:G:H21	30:0:1189:A:H8	1.39	0.69
31:9:39:U:H1'	31:9:44:A:H61	1.57	0.68
30:0:870:G:C2'	30:0:871:G:H5''	2.21	0.68
30:0:1527:A:H1'	30:0:1528:A:C8	2.29	0.68
30:0:2533:C:H5'	30:0:2533:C:C6	2.27	0.68
30:0:12:U:H2'	30:0:13:G:H5'	1.75	0.68
5:E:143:GLN:HE21	30:0:2780:C:H1'	1.58	0.68
3:C:139:VAL:HG13	39:C:8643:HOH:O	1.92	0.68
30:0:1119:G:N2	30:0:1246:A:C2	2.58	0.68
30:0:2769:C:C2'	30:0:2770:G:H5'	2.23	0.68
18:R:8:ALA:HB1	18:R:13:THR:HG21	1.75	0.67
30:0:603:A:H5''	30:0:604:G:OP1	1.94	0.67
30:0:681:G:N3	30:0:681:G:H5'	2.09	0.67
30:0:2783:A:H3'	39:0:5264:HOH:O	1.93	0.67
30:0:1641:A:H2'	30:0:1642:A:H5'	1.76	0.67
30:0:1205:U:H2'	30:0:1206:U:C5'	2.24	0.67
30:0:1666:C:C2'	30:0:1667:A:H5''	2.25	0.67
24:X:37:LEU:HD13	24:X:85:VAL:HG21	1.78	0.66
30:0:2538:A:H8	38:0:2924:ANM:H61	1.61	0.65
21:U:39:ASN:ND2	21:U:44:ARG:HH11	1.93	0.65
30:0:558:C:C2'	30:0:559:U:H5''	2.26	0.65
30:0:1701:A:H4'	30:0:1702:U:C5'	2.23	0.65
30:0:1377:C:H6	30:0:1377:C:H5'	1.61	0.65
30:0:1667:A:H5'	30:0:1667:A:C8	2.29	0.65
30:0:2613:G:O2'	30:0:2614:C:H5'	1.96	0.65
11:K:39:GLY:HA2	39:0:5253:HOH:O	1.97	0.65
10:J:52:GLN:HE22	30:0:1119:G:H8	1.43	0.65
12:L:136:ALA:HB3	39:L:8874:HOH:O	1.96	0.65
30:0:2073:G:H5''	39:0:3853:HOH:O	1.95	0.65
30:0:2827:A:H2'	30:0:2828:G:O4'	1.97	0.65
18:R:128:ARG:NH2	30:0:2054:A:N3	2.44	0.65
31:9:23:U:O2'	31:9:24:U:H4'	1.96	0.65
30:0:119:A:H2'	30:0:120:A:H5''	1.78	0.65
2:B:238:ASN:HD22	2:B:240:GLY:H	1.44	0.64
30:0:2005:G:OP2	30:0:2005:G:H3'	1.97	0.64
30:0:2766:A:H5'	39:0:9579:HOH:O	1.96	0.64
30:0:1183:C:N4	30:0:1184:C:H41	1.95	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2578:G:H5'	30:0:2578:G:H8	1.62	0.64
30:0:2765:C:H4'	39:0:5557:HOH:O	1.98	0.64
30:0:542:A:H5'	30:0:542:A:C8	2.24	0.64
30:0:545:G:H5'	30:0:545:G:C8	2.29	0.64
2:B:212:GLN:HA	30:0:1733:A:H4'	1.80	0.64
25:Y:204:ARG:HH22	30:0:553:G:P	2.21	0.64
30:0:1947:G:H2'	30:0:1948:G:H8	1.62	0.64
23:W:88:THR:HG23	23:W:110:GLN:HE21	1.62	0.64
30:0:2637:A:H5'	39:0:9282:HOH:O	1.96	0.64
26:Z:60:ASP:HB3	26:Z:69:ASP:HB3	1.80	0.64
30:0:1701:A:H5''	30:0:1702:U:H3'	1.79	0.64
30:0:2635:A:O2'	30:0:2636:C:H5'	1.98	0.64
30:0:2756:U:H3	30:0:2896:A:H2	1.45	0.63
30:0:871:G:C8	30:0:871:G:C5'	2.73	0.63
30:0:2878:U:H2'	30:0:2879:A:O4'	1.97	0.63
30:0:1189:A:H3'	39:0:7737:HOH:O	1.97	0.63
30:0:2502:C:C2'	30:0:2503:A:H5'	2.28	0.63
30:0:2717:C:O2'	30:0:2718:C:H5''	1.98	0.63
30:0:1116:U:O2'	30:0:1118:A:H2	1.70	0.63
30:0:544:G:C2'	30:0:545:G:H5''	2.28	0.63
4:D:154:LYS:H	4:D:154:LYS:HD2	1.63	0.62
30:0:2426:G:H1'	39:0:6139:HOH:O	1.97	0.62
8:H:59:GLN:NE2	8:H:129:ARG:HE	1.92	0.62
30:0:1165:G:H4'	30:0:1174:A:O2'	1.99	0.62
1:A:223:ARG:NH1	30:0:2270:G:H4'	2.15	0.62
30:0:90:A:H2'	30:0:91:G:O4'	1.98	0.62
30:0:1166:A:H1'	30:0:1192:A:C2	2.34	0.62
30:0:1205:U:C2'	30:0:1206:U:H5''	2.30	0.62
30:0:2004:U:H4'	39:0:5340:HOH:O	1.99	0.62
1:A:223:ARG:HH12	30:0:2270:G:H4'	1.65	0.62
30:0:1666:C:H2'	30:0:1667:A:C5'	2.29	0.62
30:0:2679:G:H2'	30:0:2681:A:OP2	1.99	0.62
30:0:2896:A:H5''	39:0:6146:HOH:O	1.99	0.62
29:3:25:VAL:HG22	29:3:68:LYS:HG3	1.82	0.62
30:0:1184:C:H1'	39:0:7526:HOH:O	1.99	0.62
31:9:7:G:H5'	39:9:9098:HOH:O	2.00	0.62
8:H:19:ARG:HH12	30:0:1008:C:H5''	1.65	0.62
30:0:832:U:OP2	39:0:7839:HOH:O	2.16	0.62
25:Y:169:ARG:HD2	30:0:1328:A:OP1	2.00	0.61
31:9:20:G:O2'	31:9:21:G:H5'	1.99	0.61
23:W:154:ARG:NH1	30:0:588:G:O6	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1441:G:O2'	30:0:1442:A:H5'	1.99	0.61
30:0:123:U:H5'	39:0:6705:HOH:O	2.00	0.61
6:F:91:VAL:HG12	6:F:92:GLY:H	1.64	0.61
20:T:52:ARG:HD2	30:0:317:A:H5''	1.82	0.61
20:T:24:ARG:HH21	20:T:39:ASN:HD22	1.48	0.61
30:0:1666:C:H2'	30:0:1667:A:H5'	1.83	0.61
30:0:2768:A:H2'	30:0:2769:C:O4'	2.00	0.61
3:C:115:LEU:HD13	3:C:223:LEU:HD21	1.82	0.61
30:0:1189:A:H1'	30:0:1209:C:C1'	2.30	0.61
11:K:29:LEU:HB3	11:K:55:VAL:HG11	1.81	0.61
30:0:69:A:H5'	30:0:69:A:C8	2.36	0.61
30:0:282:C:O2'	30:0:283:U:H5'	2.00	0.61
30:0:2717:C:H2'	30:0:2718:C:C5'	2.26	0.61
11:K:87:ARG:NH2	30:0:2720:C:O2	2.34	0.60
12:L:56:LYS:HE3	30:0:2443:C:H1'	1.83	0.60
29:3:48:ASN:HD21	30:0:2468:A:H61	1.49	0.60
30:0:848:C:H5'	39:0:7329:HOH:O	2.00	0.60
2:B:212:GLN:HB2	2:B:257:THR:HG21	1.83	0.60
31:9:14:G:H5'	31:9:14:G:C8	2.35	0.60
30:0:558:C:O2'	30:0:559:U:H5''	2.02	0.60
30:0:1209:C:H2'	30:0:1210:G:C8	2.36	0.60
30:0:1819:G:H2'	30:0:1820:G:H4'	1.81	0.60
18:R:39:THR:HG22	18:R:42:GLU:H	1.67	0.60
30:0:1278:A:H4'	30:0:1279:U:C4	2.37	0.60
30:0:2502:C:H2'	30:0:2503:A:H5'	1.83	0.60
30:0:2587:OMU:H2'	30:0:2589:U:H5''	1.84	0.60
31:9:39:U:H3'	31:9:40:C:H5''	1.84	0.60
13:M:24:GLN:NE2	13:M:27:ARG:HH11	1.99	0.60
30:0:905:C:H3'	39:0:5219:HOH:O	2.00	0.60
30:0:2241:C:O2'	30:0:2242:U:H5'	2.01	0.59
30:0:2563:U:H2'	30:0:2565:C:O5'	2.01	0.59
13:M:99:ARG:HH21	13:M:170:ASN:HD22	1.50	0.59
14:N:144:GLY:O	14:N:147:ILE:HG22	2.02	0.59
30:0:920:C:H5''	30:0:921:G:O5'	2.02	0.59
30:0:1372:A:H3'	39:0:7247:HOH:O	2.02	0.59
30:0:2064:U:H5'	30:0:2652:U:H4'	1.85	0.59
30:0:447:A:O2'	30:0:448:G:H5'	2.03	0.59
30:0:2507:G:H2'	30:0:2510:C:H42	1.67	0.59
30:0:2638:G:H5'	39:0:4962:HOH:O	2.02	0.59
30:0:2851:G:C2'	30:0:2852:A:H5'	2.32	0.58
30:0:2748:G:H5'	39:0:7599:HOH:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:969:G:H1	30:0:999:C:H42	1.50	0.58
30:0:69:A:H5'	30:0:69:A:H8	1.68	0.58
30:0:1182:C:H1'	30:0:1192:A:H8	1.69	0.58
9:I:86:GLU:HG2	30:0:1180:U:H4'	1.86	0.58
30:0:1681:G:H5''	30:0:1682:A:H5'	1.84	0.58
31:9:29:C:C2'	31:9:30:C:H5'	2.34	0.58
30:0:292:G:H2'	30:0:358:G:N2	2.19	0.58
30:0:316:A:N3	30:0:336:G:O2'	2.36	0.58
30:0:2769:C:H2'	30:0:2770:G:H5'	1.85	0.57
30:0:2816:A:H5''	30:0:2817:G:H5'	1.86	0.57
31:9:71:C:H2'	31:9:72:C:H6	1.69	0.57
30:0:506:G:H22	30:0:509:A:H5'	1.70	0.57
30:0:2372:A:H2'	30:0:2373:U:C6	2.39	0.57
30:0:1201:C:H5''	39:0:6282:HOH:O	2.03	0.57
30:0:1632:A:H2'	30:0:1633:C:H5'	1.86	0.57
31:9:76:G:C3'	31:9:77:A:H5''	2.20	0.57
30:0:558:C:H2'	30:0:559:U:C5'	2.33	0.57
30:0:2372:A:H2'	30:0:2373:U:H6	1.69	0.57
10:J:45:VAL:HG11	10:J:121:LEU:HD22	1.85	0.57
8:H:6:ALA:HA	8:H:61:ARG:HH12	1.70	0.57
30:0:1947:G:H2'	30:0:1948:G:C8	2.40	0.57
16:P:115:SER:H	16:P:118:GLN:NE2	1.98	0.57
8:H:15:PRO:HG3	30:0:1053:G:OP1	2.05	0.57
30:0:2529:G:H3'	39:0:7241:HOH:O	2.05	0.57
30:0:2712:G:H5'	39:0:5253:HOH:O	2.05	0.57
14:N:37:ARG:NH1	31:9:6:C:OP1	2.34	0.56
30:0:2795:C:O2'	30:0:2796:U:H5'	2.05	0.56
16:P:105:LEU:HD21	16:P:137:LEU:HD11	1.87	0.56
30:0:2769:C:H2'	30:0:2770:G:O4'	2.05	0.56
31:9:64:C:C2'	31:9:65:A:H5'	2.34	0.56
30:0:317:A:H5'	39:0:3798:HOH:O	2.05	0.56
30:0:2301:A:H5''	30:0:2302:A:H5'	1.86	0.56
5:E:143:GLN:NE2	30:0:2779:G:H21	2.03	0.56
30:0:1080:C:H4'	30:0:1081:A:OP1	2.05	0.56
30:0:1118:A:C8	30:0:1118:A:C3'	2.85	0.56
30:0:1835:U:C5	30:0:1840:A:N7	2.66	0.56
11:K:66:ARG:HH22	30:0:1994:A:P	2.28	0.56
30:0:1116:U:O2'	30:0:1118:A:C2	2.52	0.56
30:0:2505:G:O2'	30:0:2506:A:H5'	2.05	0.56
19:S:51:GLN:HE21	19:S:53:ASN:HD21	1.53	0.56
30:0:1175:G:H1'	30:0:1193:A:H2'	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1790:C:H2'	30:0:1791:U:H6	1.71	0.56
30:0:625:U:H5''	30:0:1044:C:N4	2.21	0.56
28:2:10:ARG:NH2	30:0:121:U:OP2	2.36	0.56
30:0:441:A:H1'	30:0:442:A:N7	2.21	0.56
30:0:711:G:H1'	39:0:7152:HOH:O	2.06	0.56
30:0:1406:A:H4'	30:0:1407:A:H5''	1.87	0.56
30:0:2700:G:H3'	39:0:3609:HOH:O	2.06	0.56
31:9:39:U:H1'	31:9:44:A:N6	2.20	0.56
3:C:127:ARG:NH2	3:C:225:PRO:HG2	2.21	0.55
30:0:1377:C:H5'	30:0:1377:C:C6	2.41	0.55
30:0:1972:U:H2'	30:0:1973:A:C5'	2.36	0.55
30:0:2748:G:H1'	39:0:7956:HOH:O	2.06	0.55
30:0:644:G:N3	30:0:644:G:H5'	2.20	0.55
30:0:1187:U:O2'	30:0:1189:A:H2	1.89	0.55
30:0:2472:C:O2'	30:0:2634:G:H4'	2.07	0.55
30:0:2670:G:O2'	30:0:2671:U:H5'	2.06	0.55
11:K:32:ILE:HD11	11:K:56:SER:HB3	1.88	0.55
30:0:907:A:H4'	30:0:1328:A:C2	2.41	0.55
10:J:88:PRO:HD3	30:0:1104:C:H4'	1.87	0.55
23:W:137:GLN:HE21	23:W:141:HIS:CE1	2.22	0.55
30:0:2768:A:H5''	39:0:4460:HOH:O	2.06	0.55
30:0:138:U:H5''	30:0:139:C:OP2	2.07	0.55
30:0:669:G:O2'	30:0:670:G:H5'	2.06	0.55
30:0:2769:C:O2'	30:0:2770:G:H5'	2.07	0.55
14:N:4:PRO:HB2	30:0:1010:C:H4'	1.88	0.55
29:3:2:GLN:HE21	29:3:91:GLN:HE21	1.54	0.55
30:0:602:A:O2'	30:0:605:C:H4'	2.07	0.54
3:C:76:ARG:HG2	3:C:78:ARG:NH1	2.22	0.54
30:0:2718:C:H5'	30:0:2718:C:H6	1.72	0.54
5:E:139:GLU:OE2	30:0:2781:U:H1'	2.05	0.54
30:0:272:A:H3'	39:0:7588:HOH:O	2.07	0.54
30:0:595:U:H2'	30:0:596:C:H6	1.72	0.54
4:D:146:LYS:NZ	14:N:107:ASN:HD21	2.05	0.54
23:W:64:THR:O	23:W:68:THR:HG22	2.07	0.54
30:0:1625:U:H4'	39:0:4699:HOH:O	2.06	0.54
30:0:1666:C:C2'	30:0:1667:A:C5'	2.85	0.54
30:0:1682:A:H5''	39:0:9470:HOH:O	2.06	0.54
30:0:1174:A:C5	30:0:1201:C:H4'	2.43	0.54
30:0:1741:U:O2'	30:0:2723:G:H4'	2.07	0.54
31:9:49:G:O2'	31:9:50:G:H5'	2.08	0.54
10:J:18:ILE:HD13	30:0:1244:U:OP1	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1130:U:H2'	30:0:1131:G:O4'	2.07	0.54
23:W:88:THR:HG23	23:W:110:GLN:NE2	2.23	0.54
21:U:56:ARG:NH2	30:0:2890:A:H1'	2.22	0.53
30:0:1528:A:H2'	30:0:1529:G:O4'	2.08	0.53
30:0:1634:G:H3'	39:0:3923:HOH:O	2.06	0.53
30:0:2419:U:H5''	30:0:2420:G:H5'	1.90	0.53
30:0:2769:C:H2'	30:0:2770:G:C5'	2.38	0.53
1:A:199:HIS:HE1	30:0:1881:A:OP1	1.89	0.53
9:I:111:LEU:HD23	30:0:1163:G:H4'	1.89	0.53
23:W:84:VAL:HG12	39:W:6679:HOH:O	2.07	0.53
25:Y:132:ASP:OD2	30:0:621:C:H5'	2.08	0.53
30:0:1289:C:O2'	30:0:1290:G:H5'	2.09	0.53
30:0:1477:C:H5'	30:0:1868:G:C5'	2.38	0.53
30:0:2420:G:O2'	30:0:2421:G:H5'	2.08	0.53
31:9:54:A:O2'	31:9:55:U:H5'	2.08	0.53
10:J:69:TYR:CE1	30:0:2081:A:H4'	2.43	0.53
14:N:37:ARG:NH1	31:9:6:C:C5'	2.67	0.53
29:3:48:ASN:ND2	29:3:50:GLY:H	2.06	0.53
30:0:821:U:H2'	30:0:822:C:H6	1.74	0.53
30:0:1058:A:H2'	30:0:1060:C:H5''	1.89	0.53
30:0:380:A:H2'	39:0:7284:HOH:O	2.09	0.53
30:0:2265:U:H2'	30:0:2266:A:C8	2.44	0.53
30:0:2768:A:O2'	30:0:2769:C:H5'	2.08	0.53
30:0:272:A:H5'	30:0:273:G:OP2	2.09	0.53
30:0:671:A:O2'	30:0:672:G:H2'	2.09	0.53
30:0:899:C:H5'	39:0:3228:HOH:O	2.08	0.53
17:Q:95:GLU:HA	30:0:949:U:H4'	1.90	0.53
30:0:31:C:H2'	39:0:7745:HOH:O	2.08	0.53
30:0:1641:A:C2'	30:0:1642:A:H5'	2.39	0.53
31:9:64:C:H2'	31:9:65:A:H5'	1.90	0.53
30:0:2346:C:H6	30:0:2346:C:O5'	1.92	0.53
29:3:65:THR:HB	29:3:83:TRP:H	1.73	0.53
10:J:52:GLN:HE22	30:0:1119:G:H2'	1.71	0.53
22:V:55:ARG:O	22:V:59:ILE:HG12	2.09	0.53
30:0:1456:C:H2'	30:0:1457:U:C6	2.44	0.53
30:0:2526:C:H5'	30:0:2526:C:C6	2.44	0.53
30:0:558:C:H2'	30:0:559:U:H5''	1.90	0.52
30:0:952:G:N3	30:0:2302:A:H2'	2.24	0.52
30:0:1279:U:H2'	30:0:1279:U:O2	2.08	0.52
30:0:2251:G:H2'	30:0:2252:A:C8	2.44	0.52
30:0:17:G:H2'	30:0:18:C:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:2:U:OP2	31:9:3:A:H5'	2.09	0.52
39:Z:8706:HOH:O	30:0:1886:A:H4'	2.10	0.52
30:0:10:U:O4	30:0:532:A:OP2	2.28	0.52
30:0:849:C:H1'	39:0:6667:HOH:O	2.10	0.52
30:0:2787:C:H5	39:0:4665:HOH:O	1.92	0.52
39:I:1549:HOH:O	30:0:1180:U:H1'	2.08	0.52
30:0:482:G:H4'	30:0:508:A:N1	2.24	0.52
30:0:814:G:H4'	39:0:3158:HOH:O	2.09	0.52
30:0:2353:A:H4'	30:0:2354:A:O5'	2.09	0.52
11:K:87:ARG:HG3	30:0:2721:U:H4'	1.92	0.52
30:0:304:G:H1'	30:0:347:A:N6	2.24	0.52
30:0:343:C:O2'	30:0:344:C:H5'	2.08	0.52
30:0:1766:U:O2	30:0:1778:A:H5'	2.10	0.52
1:A:48:ASP:HB3	39:A:9064:HOH:O	2.08	0.52
3:C:76:ARG:HH22	30:0:1363:G:P	2.32	0.52
8:H:72:ALA:HB2	8:H:156:ALA:HB2	1.92	0.52
30:0:468:U:H3'	39:0:7628:HOH:O	2.10	0.52
30:0:1118:A:H8	30:0:1119:G:H5''	1.73	0.52
3:C:236:THR:HG22	3:C:239:ALA:H	1.75	0.52
12:L:6:ARG:HD3	30:0:1299:G:O6	2.09	0.52
15:O:3:THR:CG2	30:0:656:G:H5'	2.30	0.52
20:T:52:ARG:O	30:0:317:A:OP1	2.27	0.52
4:D:146:LYS:HZ1	14:N:38:LYS:HE2	1.75	0.52
30:0:88:G:H2'	30:0:89:G:C8	2.44	0.52
30:0:1314:U:H2'	39:0:5916:HOH:O	2.08	0.52
30:0:2010:A:H2'	39:0:6002:HOH:O	2.09	0.52
2:B:307:ARG:HG3	2:B:307:ARG:HH11	1.75	0.52
30:0:1714:C:O2'	30:0:1715:C:H5'	2.10	0.52
30:0:2320:U:H4'	30:0:2321:A:O4'	2.10	0.52
30:0:2538:A:C8	38:0:2924:ANM:H61	2.44	0.52
30:0:1250:C:O2'	30:0:1251:C:H5'	2.10	0.51
30:0:1506:U:H6	30:0:1506:U:H5'	1.74	0.51
30:0:280:C:H2'	30:0:281:U:O4'	2.10	0.51
30:0:1972:U:H2'	30:0:1973:A:H5''	1.92	0.51
30:0:2748:G:H2'	39:0:7599:HOH:O	2.10	0.51
31:9:12:C:H5'	31:9:70:U:O4'	2.10	0.51
30:0:2111:G:H1'	39:0:9050:HOH:O	2.10	0.51
30:0:512:G:O3'	30:0:513:A:H8	1.94	0.51
30:0:1131:G:C6	30:0:1230:A:C4	2.98	0.51
30:0:2783:A:H2'	30:0:2784:A:C8	2.46	0.51
4:D:103:ASN:HD22	4:D:134:LEU:H	1.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:57:LYS:HA	22:V:60:GLN:HE21	1.75	0.51
23:W:80:ASP:O	23:W:84:VAL:HG23	2.11	0.51
30:0:1333:U:H2'	30:0:1334:C:C6	2.46	0.51
1:A:199:HIS:HD2	1:A:201:PHE:H	1.58	0.51
4:D:76:ARG:NE	31:9:44:A:O4'	2.42	0.51
30:0:1014:A:H2'	30:0:1015:C:H5'	1.92	0.51
30:0:1132:A:N6	30:0:1229:C:H2'	2.25	0.51
30:0:1189:A:O2'	30:0:1208:C:H2'	2.10	0.51
30:0:1268:C:O2'	30:0:1269:G:H5'	2.11	0.51
30:0:2604:A:H5'	39:0:5833:HOH:O	2.10	0.51
12:L:18:HIS:HD2	30:0:902:G:N7	2.09	0.51
12:L:143:THR:HG22	12:L:144:ASP:H	1.76	0.51
30:0:136:C:H2'	30:0:137:U:O4'	2.11	0.51
30:0:794:U:H3	30:0:819:A:H61	1.57	0.51
30:0:820:G:O2'	30:0:856:G:H4'	2.11	0.51
30:0:1249:U:H2'	30:0:1250:C:C6	2.45	0.51
30:0:2243:C:H5''	39:0:3776:HOH:O	2.11	0.51
2:B:201:ASP:HB2	2:B:312:ARG:HD2	1.91	0.51
30:0:2344:G:N3	30:0:2344:G:H2'	2.25	0.51
31:9:54:A:H2	39:9:9064:HOH:O	1.93	0.51
25:Y:144:ARG:NH1	30:0:905:C:OP1	2.43	0.51
30:0:1755:A:H2'	30:0:1756:G:O4'	2.10	0.51
13:M:24:GLN:HE21	13:M:27:ARG:HH11	1.57	0.50
18:R:117:HIS:HD2	30:0:20:G:H21	1.59	0.50
30:0:67:A:H5''	30:0:69:A:C8	2.46	0.50
30:0:182:G:H5''	39:0:3749:HOH:O	2.11	0.50
30:0:1211:G:O2'	30:0:1212:C:H5'	2.11	0.50
30:0:2385:G:H2'	30:0:2386:U:C6	2.46	0.50
14:N:141:ARG:NH2	31:9:48:C:H4'	2.26	0.50
24:X:30:MET:HG2	30:0:1384:C:H5'	1.93	0.50
30:0:396:U:O2'	30:0:418:C:H4'	2.12	0.50
30:0:1667:A:H2'	30:0:1668:U:C6	2.46	0.50
30:0:71:G:H5''	39:0:3940:HOH:O	2.10	0.50
30:0:1015:C:H2'	30:0:1016:U:C6	2.46	0.50
30:0:1200:A:H3'	39:0:5796:HOH:O	2.10	0.50
30:0:407:A:H5'	39:0:6070:HOH:O	2.10	0.50
30:0:1940:C:H4'	39:0:7406:HOH:O	2.10	0.50
8:H:168:VAL:HG13	39:H:9008:HOH:O	2.11	0.50
11:K:74:VAL:HG12	11:K:75:ARG:HG3	1.92	0.50
14:N:11:ARG:HD3	31:9:114:G:O6	2.11	0.50
23:W:6:GLN:HB2	23:W:26:ILE:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1172:G:H5''	39:0:7316:HOH:O	2.11	0.50
30:0:1596:U:H2'	30:0:1598:A:OP2	2.11	0.50
23:W:21:LEU:HD22	23:W:26:ILE:HD11	1.92	0.50
30:0:271:C:H41	30:0:378:A:H2	1.58	0.50
30:0:396:U:H1'	39:0:7686:HOH:O	2.09	0.50
30:0:969:G:H1	30:0:999:C:N4	2.10	0.50
30:0:1778:A:H2'	30:0:1779:A:H5'	1.93	0.50
30:0:125:U:H2'	39:0:3792:HOH:O	2.10	0.50
30:0:1185:U:H2'	30:0:1186:C:C6	2.46	0.50
30:0:1925:G:O2'	30:0:1926:G:H5'	2.12	0.50
30:0:2252:A:C5	30:0:2253:G:H1'	2.46	0.50
27:1:12:ASN:O	30:0:1415:G:H5'	2.11	0.50
30:0:485:A:N3	30:0:487:G:H5''	2.27	0.50
30:0:1819:G:H2'	30:0:1820:G:C5'	2.42	0.50
30:0:1972:U:C2'	30:0:1973:A:H5''	2.42	0.50
30:0:2415:A:H2'	30:0:2416:G:H5'	1.94	0.50
31:9:95:C:O2'	31:9:96:C:H5'	2.12	0.50
30:0:255:A:H2'	30:0:256:C:C6	2.46	0.50
30:0:559:U:H5'	30:0:559:U:C6	2.36	0.50
30:0:2104:C:O2	30:0:2485:A:N1	2.45	0.50
1:A:121:ALA:O	1:A:124:VAL:HG22	2.12	0.49
30:0:1562:C:H2'	30:0:1562:C:O2	2.12	0.49
1:A:192:VAL:HG12	39:A:9054:HOH:O	2.11	0.49
30:0:564:G:H1'	39:0:6359:HOH:O	2.12	0.49
30:0:2498:C:O2'	30:0:2499:U:H5'	2.12	0.49
12:L:14:GLY:O	30:0:1295:G:H5''	2.12	0.49
31:9:52:A:H2'	31:9:53:G:O4'	2.12	0.49
31:9:92:G:H2'	31:9:93:A:H8	1.76	0.49
8:H:31:ILE:HG23	39:H:9028:HOH:O	2.13	0.49
30:0:1350:U:H4'	39:0:5156:HOH:O	2.12	0.49
30:0:2256:G:O2'	30:0:2257:G:H5'	2.12	0.49
30:0:2300:A:H4'	30:0:2301:A:O5'	2.13	0.49
28:2:8:LYS:NZ	30:0:1677:U:OP2	2.38	0.49
30:0:660:A:H4'	30:0:661:G:O5'	2.13	0.49
30:0:1181:A:N1	30:0:1192:A:O2'	2.44	0.49
30:0:249:G:O2'	30:0:250:C:H5'	2.13	0.49
30:0:958:G:H2'	30:0:959:C:C6	2.47	0.49
30:0:1419:U:H2'	30:0:1685:A:C2	2.47	0.49
39:B:9096:HOH:O	30:0:2672:C:H1'	2.12	0.49
5:E:116:THR:HG22	5:E:151:LEU:HD22	1.95	0.49
6:F:91:VAL:HG11	30:0:262:A:OP2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:120:A:N3	30:0:120:A:H2'	2.28	0.49
30:0:1894:C:N4	30:0:1939:U:H2'	2.27	0.49
30:0:2508:C:H2'	39:0:6808:HOH:O	2.12	0.49
30:0:2756:U:N3	30:0:2896:A:H2	2.08	0.49
30:0:2825:C:H4'	30:0:2826:G:O5'	2.13	0.49
31:9:34:A:H2'	31:9:35:C:O4'	2.12	0.49
31:9:35:C:H5''	39:9:9077:HOH:O	2.12	0.49
2:B:221:GLN:HE22	11:K:42:ASN:ND2	1.94	0.49
30:0:1135:G:H5'	39:0:5971:HOH:O	2.13	0.49
30:0:1838:U:O2'	30:0:2644:C:H5'	2.13	0.49
30:0:2758:G:H2'	30:0:2759:C:C6	2.48	0.49
31:9:61:C:H2'	31:9:62:A:H8	1.77	0.49
24:X:74:ALA:HB2	24:X:85:VAL:HG13	1.95	0.49
30:0:459:A:H5''	39:0:9053:HOH:O	2.13	0.49
30:0:1046:G:N3	30:0:1082:A:H2	2.11	0.49
30:0:1632:A:C2'	30:0:1633:C:H5'	2.43	0.49
30:0:1919:A:H4'	39:0:4884:HOH:O	2.12	0.49
30:0:2248:C:H3'	39:0:5478:HOH:O	2.13	0.49
2:B:288:GLY:HA2	30:0:2898:G:H4'	1.95	0.49
4:D:159:PRO:O	4:D:163:VAL:HG23	2.13	0.49
23:W:48:VAL:HG12	23:W:52:VAL:HB	1.94	0.49
30:0:64:G:H2'	30:0:65:C:O4'	2.13	0.49
30:0:567:U:OP1	39:0:5320:HOH:O	2.19	0.49
30:0:1603:A:H5''	30:0:1605:G:H5'	1.95	0.49
5:E:137:ASP:O	5:E:141:VAL:HG23	2.12	0.48
8:H:70:LEU:O	8:H:74:ARG:HB2	2.13	0.48
30:0:1189:A:H1'	30:0:1209:C:H1'	1.94	0.48
30:0:2649:A:H5'	30:0:2649:A:H8	1.77	0.48
2:B:16:ARG:NH1	39:B:9082:HOH:O	2.45	0.48
9:I:130:LEU:HD21	30:0:1167:G:H4'	1.95	0.48
39:Y:8908:HOH:O	30:0:1330:A:H5''	2.12	0.48
30:0:1044:C:H5	39:0:6654:HOH:O	1.94	0.48
30:0:1946:C:H2'	30:0:1971:G:C8	2.48	0.48
30:0:2090:G:H2'	30:0:2091:G:C8	2.48	0.48
13:M:164:THR:HG22	13:M:167:GLY:H	1.78	0.48
30:0:1441:G:H1'	39:0:7823:HOH:O	2.11	0.48
31:9:114:G:H2'	31:9:115:C:C6	2.49	0.48
14:N:44:ARG:NH1	31:9:4:G:H21	2.11	0.48
30:0:324:G:O2'	30:0:325:U:H5'	2.13	0.48
30:0:1119:G:N2	30:0:1246:A:N1	2.61	0.48
25:Y:142:SER:OG	30:0:1331:G:OP2	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:432:G:O2'	30:0:433:C:H5'	2.14	0.48
30:0:558:C:H2'	30:0:559:U:H5'	1.95	0.48
30:0:947:U:O2'	30:0:948:G:H5'	2.13	0.48
20:T:38:ARG:HH21	30:0:306:A:P	2.37	0.48
6:F:91:VAL:HG12	6:F:92:GLY:N	2.29	0.48
18:R:40:ALA:O	18:R:44:VAL:HG23	2.13	0.48
30:0:42:C:H1'	39:0:4709:HOH:O	2.13	0.48
30:0:318:U:H5'	30:0:339:A:C2	2.49	0.48
30:0:932:U:H2'	30:0:933:C:C6	2.49	0.48
30:0:1819:G:H2'	30:0:1820:G:C4'	2.44	0.48
6:F:2:VAL:HG22	6:F:57:GLU:OE1	2.14	0.48
8:H:6:ALA:HA	8:H:61:ARG:NH1	2.28	0.48
30:0:2011:A:H4'	30:0:2012:U:O5'	2.14	0.48
30:0:2361:A:H2'	30:0:2362:A:C8	2.49	0.48
30:0:2608:C:H2'	39:0:7867:HOH:O	2.14	0.48
24:X:43:VAL:HG22	24:X:76:ARG:NH1	2.29	0.48
30:0:1066:U:H2'	30:0:1067:A:C8	2.49	0.48
30:0:1183:C:H42	30:0:1184:C:H41	1.61	0.48
30:0:2000:G:O2'	30:0:2001:G:H5'	2.14	0.48
1:A:47:HIS:HD2	30:0:1654:U:H2'	1.78	0.47
8:H:6:ALA:HB3	30:0:2521:A:OP2	2.14	0.47
16:P:41:ARG:HH22	30:0:1500:U:P	2.37	0.47
27:1:28:HIS:HE1	30:0:776:A:OP1	1.97	0.47
30:0:622:G:O2'	30:0:623:U:H5'	2.14	0.47
30:0:1087:G:H4'	30:0:1088:A:OP1	2.14	0.47
30:0:1206:U:H2'	30:0:1207:A:O4'	2.13	0.47
30:0:1613:C:H2'	30:0:1614:G:O4'	2.14	0.47
30:0:1855:G:H4'	30:0:1856:C:O5'	2.13	0.47
30:0:2135:A:O2'	30:0:2136:G:H5'	2.14	0.47
30:0:790:A:H1'	30:0:1710:A:H2'	1.96	0.47
30:0:2649:A:H5'	30:0:2649:A:C8	2.50	0.47
1:A:51:ARG:NH1	1:A:120:ARG:O	2.47	0.47
2:B:5:ARG:NH1	2:B:8:LYS:HE2	2.27	0.47
5:E:49:ILE:HD11	5:E:69:ILE:HD12	1.95	0.47
30:0:24:G:N2	30:0:518:G:H1'	2.29	0.47
30:0:635:A:H2'	30:0:636:G:H5''	1.95	0.47
30:0:2329:C:O2'	30:0:2330:U:H5'	2.13	0.47
30:0:2526:C:O2'	30:0:2527:U:H5'	2.14	0.47
30:0:2755:G:H1'	39:0:4715:HOH:O	2.14	0.47
2:B:244:PRO:HB3	30:0:1234:U:N3	2.28	0.47
14:N:49:THR:HG22	14:N:56:ASP:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:14:GLU:O	21:U:17:THR:HB	2.15	0.47
30:0:961:A:H4'	39:0:6826:HOH:O	2.14	0.47
30:0:1166:A:OP1	30:0:1174:A:H4'	2.14	0.47
30:0:1926:G:H2'	30:0:1927:A:C8	2.50	0.47
30:0:2842:G:H2'	30:0:2843:A:H5'	1.95	0.47
30:0:677:C:O2'	30:0:678:G:H5'	2.15	0.47
30:0:1181:A:C2'	30:0:1182:C:H5'	2.45	0.47
30:0:1342:C:C2'	30:0:1343:C:H5'	2.45	0.47
30:0:1603:A:H5'	30:0:1605:G:C4'	2.44	0.47
31:9:107:C:O2'	31:9:108:C:H5'	2.14	0.47
13:M:95:LYS:HE2	30:0:157:G:H4'	1.97	0.47
16:P:83:LYS:HG2	30:0:793:A:H5''	1.97	0.47
20:T:38:ARG:NH1	39:0:6736:HOH:O	2.47	0.47
23:W:23:MET:O	30:0:1025:C:H5'	2.15	0.47
29:3:15:ASN:O	30:0:2408:A:H4'	2.15	0.47
30:0:368:C:H2'	30:0:369:G:H5'	1.97	0.47
30:0:1535:G:H2'	30:0:1536:C:C6	2.50	0.47
30:0:1622:G:H2'	30:0:1623:C:H5'	1.97	0.47
30:0:1829:A:H2'	30:0:1830:C:H5'	1.97	0.47
30:0:2064:U:H5'	30:0:2652:U:O3'	2.15	0.47
30:0:2105:C:H2'	30:0:2106:C:C6	2.49	0.47
31:9:39:U:HO2'	31:9:42:C:H5	1.57	0.47
27:1:16:HIS:HD2	30:0:470:U:O2'	1.97	0.47
30:0:560:U:H2'	30:0:561:G:H8	1.79	0.47
30:0:714:U:H3'	39:0:6997:HOH:O	2.15	0.47
30:0:2414:A:H2'	30:0:2415:A:C8	2.50	0.47
30:0:170:U:H2'	30:0:171:C:H5'	1.95	0.47
30:0:653:U:H2'	30:0:654:A:C8	2.49	0.47
30:0:920:C:H4'	30:0:921:G:C2	2.49	0.47
30:0:1016:U:H1'	39:0:3685:HOH:O	2.13	0.47
30:0:1588:G:C6	30:0:1589:G:N1	2.83	0.47
30:0:1662:C:H2'	30:0:1663:G:O4'	2.15	0.47
3:C:118:THR:O	3:C:136:VAL:HG13	2.15	0.47
8:H:22:TYR:CZ	30:0:1007:A:H2'	2.49	0.47
13:M:99:ARG:HD2	13:M:167:GLY:HA2	1.97	0.47
17:Q:15:LYS:HD3	30:0:2364:A:H5''	1.97	0.47
30:0:255:A:H2'	30:0:256:C:H6	1.80	0.47
30:0:1406:A:H4'	30:0:1407:A:C5'	2.45	0.47
30:0:1595:G:O2'	30:0:1596:U:H5'	2.15	0.47
30:0:1815:A:H2'	30:0:1816:C:O4'	2.15	0.47
2:B:211:THR:HG21	39:0:7515:HOH:O	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:141:ARG:HH21	31:9:48:C:H4'	1.79	0.46
26:Z:40:ALA:HA	30:0:1773:G:C8	2.51	0.46
30:0:299:U:H5'	39:0:7395:HOH:O	2.16	0.46
30:0:2064:U:H4'	30:0:2653:A:OP1	2.14	0.46
17:Q:19:ARG:HH21	31:9:11:A:P	2.37	0.46
30:0:256:C:H2'	30:0:257:G:O4'	2.15	0.46
30:0:559:U:H2'	30:0:560:U:O4'	2.15	0.46
30:0:704:C:H2'	30:0:705:C:H6	1.80	0.46
30:0:951:A:O2'	30:0:952:G:H5'	2.15	0.46
30:0:960:G:C2'	30:0:960:G:N3	2.78	0.46
30:0:1515:A:H2'	30:0:1516:U:C6	2.50	0.46
17:Q:26:PRO:O	17:Q:30:VAL:HG23	2.15	0.46
20:T:111:ARG:HB3	20:T:119:ALA:HB2	1.97	0.46
30:0:595:U:H2'	30:0:596:C:C6	2.49	0.46
30:0:834:G:H3'	30:0:835:U:H4'	1.98	0.46
30:0:1592:G:H2'	30:0:1593:C:C6	2.51	0.46
30:0:1603:A:C5'	30:0:1605:G:H5'	2.45	0.46
23:W:6:GLN:HB2	23:W:26:ILE:CD1	2.45	0.46
30:0:192:A:H5'	39:0:7700:HOH:O	2.16	0.46
30:0:1057:A:H1'	30:0:2492:U:O2'	2.15	0.46
30:0:2072:G:C6	30:0:2533:C:H1'	2.51	0.46
30:0:2909:G:H2'	30:0:2910:A:H8	1.80	0.46
19:S:33:SER:O	19:S:37:VAL:HG23	2.15	0.46
23:W:21:LEU:HD22	23:W:26:ILE:CD1	2.44	0.46
30:0:694:A:H2'	30:0:695:C:H5'	1.97	0.46
30:0:1137:G:H1'	39:0:3907:HOH:O	2.15	0.46
30:0:2781:U:C2'	30:0:2782:G:H5'	2.45	0.46
14:N:34:LEU:HD22	14:N:129:ILE:HD13	1.98	0.46
30:0:12:U:C2'	30:0:13:G:H5'	2.46	0.46
30:0:821:U:H3'	39:0:3796:HOH:O	2.15	0.46
30:0:1118:A:C8	30:0:1119:G:H5''	2.51	0.46
30:0:1973:A:H5'	30:0:1973:A:C8	2.42	0.46
30:0:645:U:O2	30:0:761:A:H2	1.98	0.46
30:0:702:G:O2'	30:0:703:G:H5'	2.16	0.46
30:0:1158:G:O2'	30:0:1159:G:H5'	2.16	0.46
30:0:1218:U:H2'	30:0:1219:U:C6	2.51	0.46
30:0:1804:A:H2'	30:0:1805:G:C8	2.50	0.46
30:0:2361:A:H5'	30:0:2361:A:H8	1.81	0.46
30:0:2531:U:O2'	30:0:2532:A:H5'	2.15	0.46
27:1:21:ARG:HD2	27:1:37:CYS:SG	2.55	0.46
30:0:407:A:H2'	30:0:408:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1060:C:H6	30:0:1060:C:H5'	1.81	0.46
30:0:1614:G:H2'	39:0:4660:HOH:O	2.16	0.46
30:0:1771:U:O2'	30:0:1773:G:N7	2.48	0.46
30:0:2445:U:H2'	30:0:2446:G:C8	2.50	0.46
30:0:2879:A:H2'	30:0:2880:A:O4'	2.16	0.46
30:0:2894:C:O2'	30:0:2895:C:H5'	2.15	0.46
30:0:2900:G:H2'	30:0:2901:C:O4'	2.16	0.46
2:B:238:ASN:HD22	2:B:240:GLY:N	2.11	0.46
6:F:58:GLU:CD	13:M:27:ARG:HH22	2.19	0.46
30:0:113:A:OP2	30:0:114:A:H2'	2.15	0.46
30:0:807:A:O2'	30:0:808:A:H5'	2.16	0.46
1:A:179:MET:HG2	1:A:186:TRP:HB2	1.97	0.46
39:C:8656:HOH:O	30:0:2100:A:H5'	2.15	0.46
16:P:59:ARG:HH22	16:P:66:GLN:HE22	1.64	0.46
26:Z:70:ARG:HD3	26:Z:83:TYR:HB2	1.97	0.46
28:2:40:ARG:HD2	28:2:47:THR:HG22	1.97	0.46
30:0:538:C:H5''	30:0:539:G:C8	2.50	0.46
30:0:612:U:H2'	30:0:613:C:C6	2.51	0.46
8:H:174:LEU:HD21	30:0:1220:U:H4'	1.97	0.45
30:0:876:A:H2'	30:0:876:A:N3	2.31	0.45
30:0:1641:A:H2'	30:0:1642:A:C5'	2.44	0.45
30:0:1657:A:H2'	30:0:1658:A:C8	2.51	0.45
30:0:1972:U:H2'	30:0:1973:A:H5'	1.98	0.45
30:0:2421:G:H3'	30:0:2422:U:C5'	2.46	0.45
30:0:2509:A:OP2	30:0:2510:C:H5	1.97	0.45
30:0:2852:A:H5''	39:0:5266:HOH:O	2.17	0.45
8:H:64:SER:OG	30:0:2520:G:H5'	2.16	0.45
30:0:95:A:H5''	30:0:97:G:O4'	2.16	0.45
30:0:319:A:H4'	30:0:338:C:C4	2.52	0.45
30:0:960:G:N3	30:0:960:G:H3'	2.31	0.45
30:0:1056:U:H2'	30:0:1057:A:O4'	2.16	0.45
30:0:1413:A:H2'	30:0:1414:A:O4'	2.16	0.45
30:0:2326:C:H4'	30:0:2412:G:C4'	2.47	0.45
3:C:168:ARG:NH2	3:C:190:ALA:O	2.49	0.45
11:K:55:VAL:HG12	11:K:56:SER:N	2.32	0.45
14:N:35:VAL:HG11	31:9:6:C:H4'	1.97	0.45
15:O:25:VAL:HG13	30:0:709:G:O2'	2.16	0.45
25:Y:115:ARG:HH21	30:0:1266:U:H4'	1.82	0.45
30:0:629:A:H2'	30:0:630:A:O4'	2.16	0.45
30:0:1201:C:H2'	30:0:1202:A:H5'	1.99	0.45
30:0:2314:G:C2'	30:0:2315:C:H5'	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:ARG:HB2	39:A:9064:HOH:O	2.17	0.45
10:J:127:ILE:HG22	33:J:8801:CL:CL	2.53	0.45
18:R:39:THR:HG23	18:R:107:GLU:O	2.17	0.45
30:0:281:U:O2'	30:0:282:C:H5'	2.16	0.45
30:0:1485:A:H8	39:0:9975:HOH:O	1.99	0.45
30:0:1592:G:O2'	30:0:1593:C:O5'	2.34	0.45
30:0:1787:C:H4'	30:0:2883:A:O4'	2.17	0.45
30:0:1973:A:H2'	30:0:1974:G:O4'	2.16	0.45
30:0:2766:A:O2'	30:0:2767:C:H5'	2.16	0.45
38:0:2924:ANM:H62	38:0:2924:ANM:H2	1.87	0.45
31:9:13:A:O2'	31:9:14:G:H5''	2.17	0.45
31:9:24:U:H3'	31:9:25:G:H5'	1.97	0.45
8:H:69:ARG:HD3	39:H:9028:HOH:O	2.16	0.45
30:0:17:G:H2'	30:0:18:C:H6	1.81	0.45
30:0:812:A:H1'	39:0:3988:HOH:O	2.16	0.45
30:0:1304:U:H2'	30:0:1305:C:C6	2.52	0.45
30:0:1497:G:H4'	30:0:1627:G:O2'	2.16	0.45
30:0:2781:U:H2'	30:0:2782:G:H5'	1.98	0.45
6:F:48:VAL:HG23	6:F:74:PHE:HB3	1.99	0.45
27:1:8:GLN:HE22	27:1:11:LYS:HZ2	1.65	0.45
30:0:777:U:H4'	30:0:777:U:OP2	2.16	0.45
30:0:1391:G:H2'	30:0:1392:A:H5'	1.99	0.45
30:0:2589:U:H2'	30:0:2590:U:C6	2.52	0.45
30:0:2758:G:H2'	30:0:2759:C:H6	1.82	0.45
31:9:49:G:H2'	31:9:50:G:O4'	2.17	0.45
3:C:88:SER:HB3	3:C:91:PRO:HB3	1.99	0.45
30:0:295:C:H2'	30:0:296:G:O4'	2.15	0.45
30:0:366:U:H2'	30:0:367:G:O4'	2.16	0.45
30:0:1160:G:HO2'	30:0:1190:G:H8	1.64	0.45
30:0:1181:A:H2'	30:0:1182:C:H5'	1.98	0.45
30:0:1333:U:H2'	30:0:1334:C:H6	1.82	0.45
30:0:1398:G:H2'	30:0:1399:A:C8	2.51	0.45
30:0:1503:U:H2'	30:0:1504:A:O4'	2.16	0.45
30:0:2387:U:H2'	30:0:2388:C:C6	2.51	0.45
30:0:2883:A:H2'	30:0:2884:G:O4'	2.17	0.45
13:M:43:PRO:HG3	13:M:62:VAL:HG21	1.97	0.45
30:0:308:U:H5'	30:0:309:C:OP1	2.16	0.45
30:0:1015:C:H2'	30:0:1016:U:H6	1.80	0.45
30:0:2456:A:H2'	30:0:2457:U:C6	2.52	0.45
2:B:94:GLN:O	30:0:2673:U:H4'	2.17	0.45
4:D:140:ARG:HB3	31:9:29:C:H5''	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:107:ARG:NH1	39:M:8871:HOH:O	2.49	0.45
30:0:168:C:H6	30:0:168:C:O5'	2.00	0.45
30:0:847:C:H4'	39:0:3779:HOH:O	2.16	0.45
30:0:1427:A:H61	30:0:1440:U:C1'	2.30	0.45
30:0:2401:A:H2'	30:0:2402:A:C8	2.52	0.45
3:C:127:ARG:HD3	3:C:129:HIS:HE1	1.82	0.45
13:M:34:GLU:HB3	13:M:38:GLU:HG3	1.97	0.45
24:X:43:VAL:HG12	24:X:44:ASP:N	2.32	0.45
30:0:291:C:H2'	30:0:292:G:O4'	2.17	0.45
30:0:397:A:O2'	30:0:417:G:N3	2.37	0.45
30:0:2509:A:H2'	30:0:2510:C:O4'	2.17	0.45
30:0:2594:C:O2'	30:0:2595:U:H5'	2.16	0.45
1:A:36:ASP:O	1:A:38:ILE:N	2.44	0.44
2:B:234:ARG:NH2	30:0:2039:A:OP2	2.51	0.44
2:B:254:GLN:HG2	2:B:255:GLY:N	2.32	0.44
19:S:11:THR:H	19:S:14:ALA:HB3	1.80	0.44
30:0:638:C:H2'	30:0:639:A:C8	2.53	0.44
30:0:907:A:H2'	30:0:908:A:H8	1.80	0.44
30:0:2371:G:H5'	39:0:5043:HOH:O	2.17	0.44
30:0:2510:C:H5'	30:0:2511:A:OP2	2.18	0.44
30:0:2607:U:H4'	39:0:9455:HOH:O	2.16	0.44
31:9:22:G:H5'	31:9:23:U:OP1	2.17	0.44
23:W:44:MET:CE	30:0:944:G:H21	2.31	0.44
30:0:1204:C:H2'	30:0:1205:U:O4'	2.17	0.44
30:0:2866:U:H4'	30:0:2867:G:H5'	1.99	0.44
1:A:100:PRO:HG2	1:A:103:VAL:HG21	1.99	0.44
1:A:206:ARG:NH2	30:0:2630:G:O6	2.50	0.44
25:Y:154:ARG:NH2	30:0:1071:G:H4'	2.32	0.44
30:0:737:A:H2'	30:0:738:G:O4'	2.17	0.44
30:0:821:U:H2'	30:0:822:C:C6	2.53	0.44
30:0:1167:G:H2'	30:0:1168:C:C6	2.51	0.44
30:0:1878:G:O2'	30:0:1879:U:C6	2.68	0.44
30:0:1942:A:H3'	39:0:7406:HOH:O	2.17	0.44
30:0:2524:G:H21	30:0:2526:C:N4	2.16	0.44
4:D:135:VAL:HG22	4:D:136:ARG:H	1.82	0.44
30:0:168:C:H5'	30:0:2277:U:OP1	2.17	0.44
30:0:690:G:H4'	30:0:741:C:O2	2.17	0.44
30:0:960:G:N3	30:0:960:G:H2'	2.31	0.44
30:0:1594:C:O2'	30:0:1607:A:H4'	2.17	0.44
30:0:1878:G:O2'	30:0:1879:U:P	2.74	0.44
12:L:30:ARG:NH2	39:L:8818:HOH:O	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:1:5:THR:HG23	30:0:1688:G:O2'	2.18	0.44
30:0:1996:U:O2'	30:0:1997:A:H5'	2.17	0.44
30:0:2754:G:H2'	30:0:2755:G:O4'	2.17	0.44
3:C:115:LEU:O	3:C:118:THR:HB	2.18	0.44
12:L:33:ALA:HB2	30:0:165:A:H5''	2.00	0.44
12:L:57:VAL:HG21	30:0:2443:C:H5'	1.99	0.44
25:Y:165:GLU:HB3	39:Y:8889:HOH:O	2.17	0.44
29:3:73:GLU:HB3	39:3:9051:HOH:O	2.17	0.44
30:0:454:U:H5''	39:0:7834:HOH:O	2.17	0.44
30:0:2421:G:H3'	30:0:2422:U:H5''	2.00	0.44
31:9:3:A:OP2	31:9:25:G:N2	2.51	0.44
1:A:132:ASP:HB3	1:A:135:VAL:H	1.82	0.44
30:0:128:A:O2'	30:0:129:A:H5'	2.17	0.44
30:0:162:C:H2'	30:0:163:U:H5'	1.99	0.44
30:0:666:A:H2'	30:0:667:C:O4'	2.18	0.44
30:0:951:A:C2'	30:0:952:G:H5'	2.48	0.44
30:0:1252:A:H2'	30:0:1253:C:O4'	2.18	0.44
30:0:1477:C:H5'	30:0:1868:G:H5''	2.00	0.44
30:0:1683:G:C2	30:0:1693:A:O4'	2.71	0.44
30:0:2092:G:H2'	30:0:2613:G:OP1	2.18	0.44
30:0:2256:G:C2'	30:0:2257:G:H5'	2.48	0.44
30:0:2899:A:O2'	30:0:2900:G:H5'	2.18	0.44
4:D:131:THR:HG21	30:0:2348:C:H1'	1.99	0.44
30:0:71:G:H8	39:0:3940:HOH:O	2.00	0.44
30:0:137:U:OP1	30:0:259:G:O2'	2.36	0.44
30:0:542:A:H2'	30:0:543:G:O4'	2.18	0.44
30:0:1165:G:H1'	30:0:1174:A:H1'	1.98	0.44
30:0:1172:G:H1'	39:0:5007:HOH:O	2.17	0.44
30:0:1422:U:H2'	30:0:1423:C:C6	2.52	0.44
30:0:2379:G:N7	30:0:2408:A:N1	2.65	0.44
30:0:2809:G:H2'	30:0:2810:G:O4'	2.18	0.44
30:0:138:U:OP2	30:0:139:C:H5	2.00	0.44
30:0:920:C:H5'	30:0:921:G:C4	2.53	0.44
30:0:1130:U:H5'	39:0:7729:HOH:O	2.17	0.44
30:0:1592:G:H2'	30:0:1593:C:H6	1.83	0.44
30:0:2039:A:H2'	30:0:2040:C:C6	2.52	0.44
1:A:70:ALA:HA	1:A:71:PRO:HD3	1.90	0.43
2:B:315:VAL:HG23	2:B:316:ARG:HG2	2.00	0.43
8:H:74:ARG:NH1	30:0:2504:A:H4'	2.33	0.43
30:0:466:A:H2'	30:0:467:G:O4'	2.18	0.43
30:0:484:A:N1	30:0:506:G:H4'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:941:G:C5	30:0:942:U:C4	3.06	0.43
30:0:1421:C:O2'	30:0:1422:U:H5'	2.17	0.43
30:0:1790:C:H2'	30:0:1791:U:C6	2.52	0.43
30:0:2326:C:H4'	30:0:2412:G:H4'	2.00	0.43
30:0:2703:A:H2'	30:0:2704:C:H6	1.83	0.43
31:9:91:C:H2'	31:9:92:G:O4'	2.18	0.43
3:C:47:GLY:HA2	3:C:92:PRO:HB2	2.00	0.43
18:R:128:ARG:NH2	30:0:2054:A:C2	2.83	0.43
30:0:558:C:C2'	30:0:559:U:C5'	2.92	0.43
30:0:1762:C:H2'	30:0:1763:C:H6	1.84	0.43
30:0:2088:C:H1'	30:0:2841:A:N1	2.33	0.43
30:0:2533:C:H6	30:0:2533:C:C5'	2.24	0.43
30:0:2578:G:H5'	30:0:2578:G:C8	2.49	0.43
16:P:1:THR:O	30:0:1396:C:H1'	2.18	0.43
19:S:17:ASP:HB3	19:S:23:LYS:HB2	2.00	0.43
30:0:371:U:H2'	30:0:372:A:H8	1.83	0.43
30:0:2765:C:H2'	30:0:2766:A:C8	2.54	0.43
13:M:171:ARG:CD	30:0:156:C:H5''	2.31	0.43
16:P:88:GLN:HE22	30:0:1799:G:H21	1.65	0.43
16:P:120:ARG:HD2	30:0:1594:C:OP2	2.19	0.43
18:R:132:ARG:NH2	30:0:2055:A:H4'	2.33	0.43
23:W:119:HIS:HE1	39:0:9570:HOH:O	2.01	0.43
27:1:8:GLN:HE22	27:1:11:LYS:NZ	2.16	0.43
30:0:603:A:H1'	30:0:605:C:C2	2.53	0.43
30:0:1377:C:H1'	39:0:9041:HOH:O	2.18	0.43
30:0:1504:A:H5'	39:0:4450:HOH:O	2.19	0.43
30:0:1544:U:H2'	30:0:1545:C:C6	2.54	0.43
30:0:1837:G:H3'	39:0:7851:HOH:O	2.18	0.43
30:0:2569:A:H2'	30:0:2570:G:O5'	2.18	0.43
5:E:112:ALA:HA	5:E:113:PRO:HD3	1.88	0.43
13:M:171:ARG:NH2	30:0:189:A:OP1	2.52	0.43
30:0:191:A:C4	30:0:237:G:N7	2.87	0.43
30:0:417:G:P	39:0:7478:HOH:O	2.75	0.43
30:0:790:A:H2'	30:0:791:A:O4'	2.18	0.43
30:0:1039:G:H2'	30:0:1040:A:O4'	2.19	0.43
30:0:1042:U:O2'	30:0:1043:C:H5'	2.18	0.43
30:0:1138:G:H4'	39:0:5749:HOH:O	2.18	0.43
30:0:1213:C:O2'	30:0:1214:G:H5'	2.18	0.43
30:0:1788:U:O2'	30:0:1789:G:H5'	2.19	0.43
30:0:2072:G:H3'	30:0:2073:G:C5'	2.49	0.43
30:0:2274:A:O2'	30:0:2275:G:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:2697:A:H2'	30:0:2698:G:O4'	2.18	0.43
30:0:2791:U:H1'	30:0:2792:A:H5''	2.00	0.43
31:9:33:U:H2'	39:9:9068:HOH:O	2.19	0.43
12:L:37:LYS:NZ	30:0:919:U:O3'	2.50	0.43
24:X:15:ARG:NH1	30:0:2896:A:OP1	2.52	0.43
25:Y:208:LYS:O	30:0:1313:A:H5'	2.18	0.43
26:Z:61:HIS:HB2	26:Z:71:VAL:HB	1.99	0.43
30:0:271:C:H4'	30:0:272:A:OP1	2.18	0.43
30:0:364:U:H2'	30:0:365:G:O4'	2.19	0.43
30:0:407:A:H8	39:0:4495:HOH:O	2.00	0.43
30:0:497:A:H2'	30:0:498:A:C5'	2.49	0.43
30:0:1096:U:O2'	30:0:1097:A:H5'	2.18	0.43
2:B:297:VAL:HG23	39:B:9071:HOH:O	2.17	0.43
30:0:37:A:H2'	30:0:38:G:C8	2.53	0.43
30:0:195:C:H2'	30:0:196:G:H5'	2.00	0.43
30:0:603:A:H4'	30:0:604:G:O5'	2.18	0.43
30:0:722:G:H22	30:0:938:G:P	2.41	0.43
30:0:1477:C:O2'	30:0:1478:U:H5'	2.18	0.43
30:0:1921:A:O2'	30:0:1922:A:H5'	2.19	0.43
30:0:2653:A:H2'	30:0:2654:C:C6	2.54	0.43
18:R:98:ASN:ND2	30:0:500:G:H21	2.10	0.43
24:X:43:VAL:HG12	24:X:44:ASP:H	1.83	0.43
30:0:488:U:H2'	39:0:4037:HOH:O	2.18	0.43
30:0:517:U:H1'	39:0:7636:HOH:O	2.19	0.43
30:0:815:U:O2'	30:0:1598:A:H4'	2.18	0.43
30:0:1926:G:H2'	30:0:1927:A:H8	1.84	0.43
30:0:2039:A:H4'	30:0:2760:C:O2'	2.19	0.43
31:9:47:A:C2	31:9:48:C:C2	3.07	0.43
2:B:36:PRO:HG3	2:B:169:GLY:H	1.83	0.43
10:J:52:GLN:NE2	30:0:1119:G:H8	2.13	0.43
30:0:1278:A:H4'	30:0:1279:U:N3	2.34	0.43
30:0:1481:G:H2'	30:0:1482:A:O4'	2.19	0.43
30:0:1634:G:H2'	30:0:1635:U:C6	2.54	0.43
30:0:2001:G:O2'	30:0:2002:C:H5'	2.18	0.43
30:0:2256:G:H2'	30:0:2257:G:C5'	2.49	0.43
5:E:83:GLY:HA3	5:E:170:ARG:HE	1.83	0.43
22:V:39:ALA:N	22:V:40:PRO:HD2	2.34	0.43
25:Y:141:THR:HG23	39:Y:8884:HOH:O	2.18	0.43
30:0:65:C:O2'	30:0:66:G:H5'	2.19	0.43
30:0:238:C:H4'	30:0:287:C:OP1	2.19	0.43
30:0:285:A:H2'	30:0:286:U:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1342:C:O2'	30:0:1343:C:H5'	2.19	0.43
30:0:1451:C:H5'	30:0:1505:U:C5	2.54	0.43
1:A:217:ARG:NH2	30:0:1853:C:O2'	2.52	0.42
27:1:42:SER:HB3	30:0:1473:U:O4'	2.18	0.42
30:0:420:U:H2'	30:0:421:C:C6	2.54	0.42
30:0:2121:G:O2'	30:0:2122:C:H5'	2.19	0.42
2:B:207:LYS:HG3	30:0:2717:C:OP1	2.18	0.42
3:C:46:TYR:CE1	30:0:450:C:H4'	2.53	0.42
13:M:90:ARG:NH2	30:0:2266:A:OP2	2.51	0.42
23:W:5:VAL:HG11	23:W:153:MET:HE3	2.00	0.42
30:0:1490:G:H4'	30:0:1533:A:OP1	2.18	0.42
30:0:1762:C:H2'	30:0:1763:C:C6	2.54	0.42
30:0:1834:C:H2'	30:0:1840:A:N6	2.34	0.42
30:0:2515:C:H2'	30:0:2516:G:O4'	2.19	0.42
30:0:2672:C:H2'	30:0:2673:U:C6	2.53	0.42
30:0:85:C:H5''	30:0:86:A:OP2	2.19	0.42
30:0:164:G:H3'	39:0:3671:HOH:O	2.18	0.42
30:0:204:A:C2'	30:0:205:U:H5'	2.49	0.42
30:0:255:A:H2'	30:0:256:C:O4'	2.19	0.42
30:0:1187:U:H2'	39:0:6950:HOH:O	2.18	0.42
30:0:2526:C:H5'	30:0:2526:C:H6	1.84	0.42
30:0:2793:A:H2'	30:0:2794:G:H5'	2.01	0.42
31:9:59:C:H2'	31:9:60:C:C6	2.54	0.42
23:W:115:THR:HG23	39:W:5420:HOH:O	2.18	0.42
30:0:952:G:H4'	39:0:4063:HOH:O	2.18	0.42
30:0:1159:G:H1	30:0:1208:C:H42	1.68	0.42
30:0:2324:G:N2	30:0:2377:U:H1'	2.34	0.42
30:0:2433:A:H2'	30:0:2434:A:C8	2.54	0.42
30:0:2906:A:H5'	30:0:2907:C:O4'	2.19	0.42
10:J:52:GLN:NE2	30:0:1119:G:C8	2.87	0.42
17:Q:53:HIS:CD2	30:0:2389:U:H4'	2.54	0.42
25:Y:134:HIS:CD2	25:Y:134:HIS:H	2.37	0.42
30:0:661:G:C5	30:0:686:A:C2	3.08	0.42
30:0:1339:G:C6	30:0:1340:G:N1	2.87	0.42
30:0:1427:A:H61	30:0:1440:U:H1'	1.84	0.42
30:0:1850:U:H2'	30:0:1851:G:H8	1.84	0.42
30:0:1942:A:O2'	30:0:1943:C:H5'	2.20	0.42
30:0:2614:C:O2'	30:0:2615:U:H5'	2.20	0.42
23:W:44:MET:HE2	30:0:944:G:H21	1.84	0.42
25:Y:169:ARG:HD3	30:0:1328:A:C8	2.55	0.42
30:0:1079:A:H4'	30:0:2078:U:H5'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1622:G:C2'	30:0:1623:C:H5'	2.49	0.42
30:0:1839:A:H5'	30:0:2643:G:H4'	2.01	0.42
31:9:56:A:C3'	31:9:57:A:H5''	2.49	0.42
30:0:129:A:O2'	30:0:131:A:OP1	2.37	0.42
30:0:204:A:H2'	30:0:205:U:H5'	2.01	0.42
30:0:278:A:H2'	30:0:279:C:O4'	2.20	0.42
30:0:451:C:O2'	30:0:452:G:H5'	2.19	0.42
30:0:1386:G:O2'	30:0:1387:G:H5'	2.19	0.42
1:A:190:ARG:HD2	30:0:1884:G:O6	2.20	0.42
3:C:96:LYS:NZ	30:0:1351:G:OP1	2.39	0.42
10:J:41:ALA:HB3	39:J:5907:HOH:O	2.20	0.42
12:L:30:ARG:HD3	30:0:164:G:H4'	2.01	0.42
17:Q:25:PRO:HA	17:Q:26:PRO:HD3	1.88	0.42
30:0:1525:G:H5'	30:0:1526:A:OP2	2.19	0.42
30:0:1682:A:H2'	39:0:9817:HOH:O	2.20	0.42
30:0:2269:C:C2'	30:0:2270:G:H5'	2.50	0.42
31:9:27:C:H1'	39:9:9053:HOH:O	2.17	0.42
2:B:258:GLY:H	2:B:260:HIS:CE1	2.38	0.42
30:0:816:G:C6	30:0:817:G:N1	2.88	0.42
30:0:1052:G:N3	30:0:1052:G:H2'	2.35	0.42
30:0:1058:A:H2'	30:0:1060:C:C5'	2.50	0.42
30:0:1186:C:H42	30:0:1190:G:H22	1.68	0.42
30:0:1243:C:H3'	39:0:4869:HOH:O	2.20	0.42
30:0:1537:C:H1'	39:0:6638:HOH:O	2.19	0.42
30:0:2672:C:H2'	30:0:2673:U:H6	1.85	0.42
3:C:79:ARG:O	3:C:87:ARG:HG2	2.20	0.42
5:E:143:GLN:HE21	30:0:2780:C:C1'	2.28	0.42
10:J:74:ARG:NH1	10:J:105:LEU:HD11	2.35	0.42
10:J:82:THR:CG2	30:0:1242:A:H5'	2.34	0.42
24:X:23:HIS:HE1	30:0:2044:G:OP1	2.02	0.42
30:0:39:G:N2	30:0:444:C:C2	2.88	0.42
30:0:200:C:H2'	39:0:3470:HOH:O	2.19	0.42
30:0:304:G:H1'	30:0:347:A:H61	1.84	0.42
30:0:567:U:H6	30:0:567:U:O5'	2.02	0.42
30:0:1023:C:O2'	30:0:1024:G:H5'	2.20	0.42
30:0:1406:A:H5'	30:0:1407:A:C8	2.55	0.42
30:0:1477:C:C5'	30:0:1868:G:H5''	2.49	0.42
30:0:1544:U:H2'	30:0:1545:C:H6	1.85	0.42
30:0:1883:U:H5'	30:0:2012:U:OP2	2.19	0.42
30:0:2356:A:H2'	30:0:2357:G:O4'	2.19	0.42
30:0:2724:U:H2'	30:0:2725:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:80:TYR:O	30:0:2050:G:H5''	2.20	0.41
30:0:360:A:H2'	30:0:361:C:O4'	2.19	0.41
30:0:821:U:H5''	39:0:3074:HOH:O	2.20	0.41
30:0:1098:A:H2'	30:0:1099:G:O4'	2.20	0.41
30:0:1587:U:H2'	30:0:1588:G:O4'	2.20	0.41
30:0:1679:C:H5'	39:0:9335:HOH:O	2.20	0.41
30:0:1856:C:H5'	30:0:1858:A:O4'	2.20	0.41
30:0:1878:G:O2'	30:0:1879:U:OP2	2.37	0.41
30:0:2134:G:N2	30:0:2242:U:C2	2.88	0.41
30:0:2335:C:H2'	30:0:2336:G:C8	2.55	0.41
30:0:2842:G:C2'	30:0:2843:A:H5'	2.50	0.41
31:9:60:C:O2'	31:9:61:C:H5'	2.19	0.41
3:C:39:GLN:O	3:C:43:LYS:HD3	2.20	0.41
4:D:103:ASN:ND2	4:D:134:LEU:H	2.17	0.41
4:D:146:LYS:HZ1	14:N:107:ASN:HD21	1.68	0.41
24:X:10:VAL:HG23	24:X:72:VAL:HG12	2.03	0.41
25:Y:134:HIS:HE1	30:0:538:C:OP2	2.02	0.41
30:0:68:U:O2'	30:0:69:A:H5''	2.20	0.41
30:0:177:A:H2'	30:0:178:U:O4'	2.20	0.41
30:0:344:C:H2'	30:0:345:G:O4'	2.20	0.41
30:0:2506:A:O2'	30:0:2507:G:O5'	2.38	0.41
30:0:2664:A:H8	30:0:2664:A:OP1	2.02	0.41
2:B:5:ARG:HE	2:B:5:ARG:HB3	1.69	0.41
8:H:4:LYS:HA	8:H:5:PRO:HD3	1.96	0.41
24:X:25:ARG:HD2	39:X:5356:HOH:O	2.19	0.41
30:0:1615:A:H4'	39:0:5927:HOH:O	2.20	0.41
31:9:1:U:H5''	31:9:3:A:OP1	2.20	0.41
2:B:69:VAL:HA	2:B:70:PRO:HD3	1.93	0.41
2:B:238:ASN:HD21	30:0:2609:G:N2	2.18	0.41
2:B:302:PRO:HA	30:0:2717:C:H5'	2.02	0.41
20:T:9:LYS:HD3	39:0:3781:HOH:O	2.20	0.41
23:W:122:ARG:HH12	23:W:154:ARG:N	2.19	0.41
30:0:308:U:C4	30:0:342:C:H1'	2.55	0.41
30:0:1315:G:H4'	30:0:1316:G:OP2	2.20	0.41
30:0:2073:G:C6	30:0:2489:G:H4'	2.55	0.41
30:0:2366:C:H6	30:0:2366:C:O5'	2.03	0.41
38:0:2924:ANM:H63	38:0:2924:ANM:C15	2.43	0.41
31:9:31:C:H2'	31:9:32:G:O4'	2.21	0.41
30:0:241:A:C2	30:0:378:A:H4'	2.55	0.41
30:0:932:U:H2'	30:0:933:C:H6	1.86	0.41
30:0:1636:G:O2'	30:0:1637:A:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:9:105:A:H2'	31:9:106:U:O4'	2.21	0.41
6:F:36:THR:HG23	6:F:97:ALA:HB2	2.03	0.41
30:0:1205:U:C2'	30:0:1206:U:C5'	2.95	0.41
30:0:2379:G:H5'	30:0:2381:C:O4'	2.21	0.41
30:0:2506:A:O2'	30:0:2507:G:P	2.79	0.41
30:0:2672:C:O2'	30:0:2673:U:H5'	2.20	0.41
30:0:2781:U:H2'	30:0:2782:G:C5'	2.50	0.41
31:9:29:C:H2'	31:9:30:C:C5'	2.45	0.41
19:S:37:VAL:O	19:S:41:VAL:HG23	2.21	0.41
30:0:326:G:O2'	30:0:327:A:H5'	2.20	0.41
30:0:612:U:H2'	30:0:613:C:H6	1.85	0.41
30:0:963:C:O2	30:0:1005:A:N1	2.54	0.41
30:0:1377:C:H2'	30:0:1723:G:O6	2.21	0.41
30:0:1603:A:H5''	30:0:1604:G:H3'	2.03	0.41
30:0:1896:G:C6	30:0:1897:U:C4	3.09	0.41
30:0:2349:G:O2'	30:0:2350:G:H5'	2.20	0.41
30:0:2455:A:H2'	30:0:2456:A:O4'	2.20	0.41
31:9:23:U:C2'	31:9:24:U:H4'	2.51	0.41
15:O:39:THR:O	15:O:115:ARG:NH2	2.54	0.41
26:Z:41:ARG:HH12	30:0:821:U:H4'	1.86	0.41
30:0:629:A:C2	30:0:2074:A:C2	3.09	0.41
30:0:1495:C:H1'	30:0:1573:A:H1'	2.03	0.41
30:0:2238:A:O2'	30:0:2239:C:H5'	2.21	0.41
31:9:24:U:H3'	31:9:25:G:C5'	2.51	0.41
31:9:39:U:H3'	31:9:40:C:C5'	2.50	0.41
1:A:171:LYS:HB2	30:0:820:G:C5	2.56	0.41
2:B:85:ARG:NH1	39:B:9096:HOH:O	2.53	0.41
2:B:254:GLN:NE2	39:B:9055:HOH:O	2.54	0.41
3:C:49:ASP:HB3	3:C:52:ALA:HB2	2.02	0.41
13:M:163:LEU:CD2	30:0:188:C:H5''	2.45	0.41
20:T:2:LYS:HG2	30:0:447:A:OP1	2.21	0.41
27:1:9:GLY:HA2	30:0:1687:C:O2	2.21	0.41
30:0:682:A:H2'	30:0:683:G:O4'	2.20	0.41
30:0:1321:A:H2'	30:0:1322:G:C8	2.56	0.41
30:0:1829:A:C2'	30:0:1830:C:H5'	2.50	0.41
30:0:1976:G:O2'	30:0:1977:U:H5'	2.21	0.41
30:0:2067:A:H2'	30:0:2068:G:O4'	2.21	0.41
30:0:2271:G:H2'	30:0:2271:G:N3	2.36	0.41
30:0:2837:U:H2'	39:0:6892:HOH:O	2.21	0.41
30:0:2896:A:N3	30:0:2896:A:H2'	2.36	0.41
1:A:176:HIS:CD2	30:0:857:A:H4'	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:206:ASN:HB2	30:0:329:A:OP2	2.21	0.41
5:E:91:PHE:HA	5:E:92:PRO:HD3	1.88	0.41
30:0:581:G:O2'	30:0:582:U:H5'	2.20	0.41
30:0:1398:G:O2'	30:0:1399:A:H5'	2.21	0.41
30:0:1783:A:O2'	30:0:1784:U:H5'	2.21	0.41
30:0:2016:U:H6	30:0:2016:U:O5'	2.03	0.41
30:0:2553:A:N3	30:0:2553:A:H2'	2.35	0.41
13:M:179:GLY:O	30:0:399:C:H5'	2.22	0.40
16:P:117:SER:HB3	30:0:1593:C:OP1	2.21	0.40
30:0:130:C:H2'	39:0:3186:HOH:O	2.21	0.40
30:0:226:A:H1'	30:0:393:G:C5	2.56	0.40
30:0:827:A:H1'	39:0:6263:HOH:O	2.20	0.40
30:0:1165:G:H4'	30:0:1174:A:HO2'	1.86	0.40
30:0:2385:G:H2'	30:0:2386:U:H6	1.83	0.40
30:0:2493:C:H2'	30:0:2493:C:O2	2.21	0.40
30:0:2549:C:H2'	30:0:2550:U:O4'	2.22	0.40
30:0:2642:G:H2'	30:0:2643:G:O4'	2.21	0.40
9:I:110:ASP:O	30:0:1163:G:H5'	2.21	0.40
12:L:67:ARG:HB2	12:L:112:GLY:HA3	2.04	0.40
13:M:65:VAL:HG21	13:M:105:ALA:HB2	2.04	0.40
30:0:228:C:H2'	30:0:229:G:H5'	2.03	0.40
30:0:613:C:H2'	30:0:614:U:H6	1.87	0.40
30:0:912:A:C4	30:0:1294:A:C2	3.09	0.40
30:0:1185:U:H5'	39:0:7526:HOH:O	2.21	0.40
30:0:1268:C:H2'	30:0:1269:G:H8	1.86	0.40
30:0:1972:U:C2'	30:0:1973:A:C5'	2.99	0.40
30:0:2449:G:H2'	30:0:2450:C:O4'	2.21	0.40
30:0:2812:A:C2	30:0:2814:A:N6	2.75	0.40
6:F:30:LYS:HE2	6:F:99:THR:HG21	2.04	0.40
14:N:147:ILE:HD11	31:9:50:G:OP1	2.22	0.40
26:Z:41:ARG:NH1	30:0:821:U:H4'	2.37	0.40
30:0:106:A:H2'	30:0:107:U:O4'	2.22	0.40
30:0:849:C:O2'	30:0:850:U:H5'	2.21	0.40
30:0:876:A:N3	30:0:876:A:C2'	2.85	0.40
30:0:2419:U:H5''	30:0:2420:G:C5'	2.51	0.40
3:C:1:MET:HG2	3:C:2:GLN:H	1.87	0.40
23:W:21:LEU:HD23	23:W:21:LEU:HA	1.86	0.40
27:1:16:HIS:CD2	30:0:470:U:O2'	2.73	0.40
30:0:39:G:H2'	30:0:40:C:O4'	2.22	0.40
30:0:441:A:O5'	30:0:441:A:H8	2.04	0.40
30:0:1080:C:H6	30:0:1080:C:O5'	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:0:1299:G:N2	39:0:4716:HOH:O	2.54	0.40
30:0:1545:C:H2'	30:0:1546:G:O4'	2.22	0.40
30:0:1762:C:O2'	30:0:1763:C:H5'	2.21	0.40
30:0:2291:A:N9	30:0:2309:C:H5'	2.35	0.40
8:H:158:ASN:ND2	30:0:2502:C:H4'	2.36	0.40
24:X:15:ARG:NH2	30:0:2856:A:OP1	2.55	0.40
30:0:396:U:HO2'	30:0:397:A:P	2.45	0.40
30:0:483:C:C4	30:0:484:A:C6	3.10	0.40
30:0:877:G:C5'	30:0:878:G:OP1	2.65	0.40
30:0:1051:C:H2'	30:0:1052:G:O4'	2.21	0.40
30:0:1119:G:C5	30:0:1243:C:C4	3.10	0.40
30:0:2478:U:O2'	30:0:2479:A:H5'	2.21	0.40
30:0:2893:C:O2'	30:0:2894:C:H5'	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	235/240 (98%)	220 (94%)	13 (6%)	2 (1%)	17	40
2	B	335/338 (99%)	314 (94%)	19 (6%)	2 (1%)	25	50
3	C	244/246 (99%)	229 (94%)	15 (6%)	0	100	100
4	D	134/177 (76%)	121 (90%)	11 (8%)	2 (2%)	10	26
5	E	170/178 (96%)	159 (94%)	11 (6%)	0	100	100
6	F	117/120 (98%)	110 (94%)	4 (3%)	3 (3%)	5	13
7	G	25/348 (7%)	25 (100%)	0	0	100	100
8	H	156/177 (88%)	148 (95%)	7 (4%)	1 (1%)	25	50
9	I	68/162 (42%)	60 (88%)	8 (12%)	0	100	100
10	J	140/145 (97%)	131 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	K	130/132 (98%)	123 (95%)	6 (5%)	1 (1%)	19	43
12	L	141/165 (86%)	134 (95%)	7 (5%)	0	100	100
13	M	192/196 (98%)	188 (98%)	4 (2%)	0	100	100
14	N	184/187 (98%)	174 (95%)	5 (3%)	5 (3%)	5	12
15	O	113/116 (97%)	112 (99%)	1 (1%)	0	100	100
16	P	141/149 (95%)	139 (99%)	2 (1%)	0	100	100
17	Q	93/96 (97%)	88 (95%)	5 (5%)	0	100	100
18	R	148/155 (96%)	143 (97%)	5 (3%)	0	100	100
19	S	79/85 (93%)	76 (96%)	3 (4%)	0	100	100
20	T	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
21	U	51/67 (76%)	50 (98%)	1 (2%)	0	100	100
22	V	63/71 (89%)	61 (97%)	2 (3%)	0	100	100
23	W	152/154 (99%)	148 (97%)	2 (1%)	2 (1%)	12	30
24	X	80/92 (87%)	76 (95%)	4 (5%)	0	100	100
25	Y	140/241 (58%)	139 (99%)	1 (1%)	0	100	100
26	Z	71/116 (61%)	64 (90%)	6 (8%)	1 (1%)	11	28
27	1	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
28	2	42/50 (84%)	42 (100%)	0	0	100	100
29	3	90/92 (98%)	87 (97%)	2 (2%)	1 (1%)	14	34
All	All	3705/4472 (83%)	3524 (95%)	161 (4%)	20 (0%)	29	54

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	37	VAL
14	N	154	LEU
14	N	184	ILE
14	N	183	ASP
1	A	27	LEU
4	D	56	ARG
8	H	19	ARG
14	N	139	TRP
14	N	167	ASP
23	W	77	ALA
2	B	2	GLN

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Mol	Chain	Res	Type
6	F	100	ASP
6	F	101	ALA
11	K	127	ALA
2	B	185	GLY
4	D	137	PRO
23	W	49	ASN
26	Z	44	ARG
6	F	61	MET
29	3	56	PRO

### 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	179/182 (98%)	170 (95%)	9 (5%)	24	51
2	B	282/283 (100%)	269 (95%)	13 (5%)	27	54
3	C	193/193 (100%)	177 (92%)	16 (8%)	11	25
4	D	117/148 (79%)	107 (92%)	10 (8%)	10	24
5	E	152/156 (97%)	148 (97%)	4 (3%)	46	75
6	F	93/94 (99%)	91 (98%)	2 (2%)	52	79
7	G	27/282 (10%)	27 (100%)	0	100	100
8	H	134/145 (92%)	127 (95%)	7 (5%)	23	49
9	I	58/130 (45%)	56 (97%)	2 (3%)	37	66
10	J	118/121 (98%)	110 (93%)	8 (7%)	16	36
11	K	106/106 (100%)	99 (93%)	7 (7%)	16	38
12	L	113/127 (89%)	107 (95%)	6 (5%)	22	48
13	M	158/160 (99%)	150 (95%)	8 (5%)	24	50
14	N	149/150 (99%)	144 (97%)	5 (3%)	37	66
15	O	93/94 (99%)	91 (98%)	2 (2%)	52	79
16	P	113/117 (97%)	109 (96%)	4 (4%)	36	65
17	Q	79/80 (99%)	76 (96%)	3 (4%)	33	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	R	117/122 (96%)	114 (97%)	3 (3%)	46	75
19	S	71/74 (96%)	69 (97%)	2 (3%)	43	73
20	T	105/106 (99%)	96 (91%)	9 (9%)	10	24
21	U	44/53 (83%)	41 (93%)	3 (7%)	16	36
22	V	51/57 (90%)	49 (96%)	2 (4%)	32	61
23	W	130/130 (100%)	123 (95%)	7 (5%)	22	47
24	X	66/74 (89%)	59 (89%)	7 (11%)	6	15
25	Y	120/196 (61%)	116 (97%)	4 (3%)	38	67
26	Z	60/94 (64%)	60 (100%)	0	100	100
27	1	46/47 (98%)	45 (98%)	1 (2%)	52	79
28	2	42/46 (91%)	41 (98%)	1 (2%)	49	77
29	3	79/79 (100%)	75 (95%)	4 (5%)	24	50
All	All	3095/3646 (85%)	2946 (95%)	149 (5%)	25	53

All (149) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	30	ARG
1	A	69	LEU
1	A	78	ASP
1	A	85	SER
1	A	94	LEU
1	A	131	HIS
1	A	179	MET
1	A	217	ARG
2	B	5	ARG
2	B	11	LEU
2	B	27	ASN
2	B	49	THR
2	B	71	VAL
2	B	97	LEU
2	B	98	THR
2	B	162	MET
2	B	171	VAL
2	B	195	ARG
2	B	254	GLN
2	B	257	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	B	265	LEU
3	C	2	GLN
3	C	27	ARG
3	C	76	ARG
3	C	78	ARG
3	C	94	THR
3	C	101	ASP
3	C	136	VAL
3	C	162	VAL
3	C	187	ARG
3	C	202	THR
3	C	214	THR
3	C	223	LEU
3	C	234	VAL
3	C	236	THR
3	C	240	LEU
3	C	243	VAL
4	D	17	ARG
4	D	23	VAL
4	D	24	HIS
4	D	50	VAL
4	D	52	THR
4	D	101	THR
4	D	128	LEU
4	D	149	ARG
4	D	153	THR
4	D	161	ASP
5	E	36	PRO
5	E	102	VAL
5	E	131	LEU
5	E	156	ASP
6	F	12	LEU
6	F	46	GLU
8	H	58	VAL
8	H	65	LEU
8	H	87	LYS
8	H	91	ARG
8	H	157	TYR
8	H	162	PRO
8	H	173	GLU
9	I	94	ASP
9	I	135	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
10	J	28	GLU
10	J	47	THR
10	J	52	GLN
10	J	74	ARG
10	J	79	PHE
10	J	107	ASN
10	J	130	VAL
10	J	131	THR
11	K	7	ASP
11	K	10	GLN
11	K	49	LEU
11	K	62	PRO
11	K	98	VAL
11	K	107	THR
11	K	119	GLN
12	L	4	LYS
12	L	32	ASP
12	L	35	ARG
12	L	101	ASP
12	L	104	ASP
12	L	140	VAL
13	M	10	ASP
13	M	46	LEU
13	M	68	ARG
13	M	81	ARG
13	M	99	ARG
13	M	116	ASN
13	M	141	ILE
13	M	164	THR
14	N	26	LEU
14	N	49	THR
14	N	135	VAL
14	N	175	LEU
14	N	176	ARG
15	O	3	THR
15	O	25	VAL
16	P	21	VAL
16	P	52	LYS
16	P	91	LYS
16	P	98	ILE
17	Q	16	ASN
17	Q	18	PRO

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
17	Q	57	ASP
18	R	13	THR
18	R	39	THR
18	R	132	ARG
19	S	10	VAL
19	S	81	ILE
20	T	39	ASN
20	T	48	VAL
20	T	61	GLU
20	T	71	VAL
20	T	82	THR
20	T	89	ARG
20	T	96	VAL
20	T	115	GLU
20	T	117	ASP
21	U	47	ARG
21	U	52	THR
21	U	56	ARG
22	V	12	THR
22	V	13	PRO
23	W	26	ILE
23	W	38	THR
23	W	52	VAL
23	W	76	ASP
23	W	120	PRO
23	W	142	ASP
23	W	146	ILE
24	X	15	ARG
24	X	49	ARG
24	X	52	PRO
24	X	72	VAL
24	X	79	GLU
24	X	80	GLU
24	X	82	GLU
25	Y	154	ARG
25	Y	157	ILE
25	Y	189	ASN
25	Y	204	ARG
27	1	21	ARG
28	2	18	ASN
29	3	14	CYS
29	3	18	GLN

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Mol	Chain	Res	Type
29	3	22	VAL
29	3	56	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (64) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	199	HIS
2	B	27	ASN
2	B	145	HIS
2	B	238	ASN
2	B	260	HIS
2	B	332	ASN
3	C	73	GLN
3	C	129	HIS
4	D	103	ASN
5	E	143	GLN
7	G	64	ASN
8	H	34	HIS
8	H	59	GLN
8	H	62	HIS
10	J	52	GLN
10	J	107	ASN
11	K	10	GLN
11	K	42	ASN
11	K	44	HIS
12	L	18	HIS
12	L	41	HIS
12	L	42	ASN
13	M	24	GLN
13	M	58	GLN
13	M	137	ASN
13	M	170	ASN
14	N	107	ASN
14	N	140	GLN
16	P	50	GLN
16	P	66	GLN
16	P	88	GLN
16	P	118	GLN
17	Q	16	ASN
17	Q	40	HIS
18	R	22	GLN

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Mol	Chain	Res	Type
18	R	94	ASN
18	R	98	ASN
18	R	117	HIS
18	R	122	GLN
18	R	123	GLN
19	S	9	HIS
19	S	44	GLN
19	S	51	GLN
20	T	39	ASN
21	U	39	ASN
22	V	60	GLN
23	W	12	ASN
23	W	110	GLN
23	W	119	HIS
23	W	125	HIS
23	W	141	HIS
24	X	23	HIS
25	Y	119	GLN
25	Y	133	HIS
25	Y	134	HIS
25	Y	189	ASN
27	1	8	GLN
27	1	16	HIS
27	1	28	HIS
28	2	41	HIS
28	2	45	ASN
29	3	2	GLN
29	3	48	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	0	2745/2923 (93%)	232 (8%)	28 (1%)
31	9	121/122 (99%)	17 (14%)	1 (0%)
All	All	2866/3045 (94%)	249 (8%)	29 (1%)

All (249) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	0	31	C
30	0	67	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
30	0	69	A
30	0	70	A
30	0	71	G
30	0	86	A
30	0	87	C
30	0	88	G
30	0	114	A
30	0	115	U
30	0	120	A
30	0	130	C
30	0	141	C
30	0	151	A
30	0	166	A
30	0	186	A
30	0	191	A
30	0	192	A
30	0	198	A
30	0	200	C
30	0	219	G
30	0	237	G
30	0	271	C
30	0	272	A
30	0	273	G
30	0	283	U
30	0	284	C
30	0	285	A
30	0	308	U
30	0	309	C
30	0	318	U
30	0	336	G
30	0	337	A
30	0	358	G
30	0	381	G
30	0	397	A
30	0	417	G
30	0	461	C
30	0	487	G
30	0	497	A
30	0	498	A
30	0	510	U
30	0	511	A
30	0	514	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
30	0	537	G
30	0	538	C
30	0	539	G
30	0	542	A
30	0	545	G
30	0	553	G
30	0	559	U
30	0	581	G
30	0	588	G
30	0	604	G
30	0	620	A
30	0	632	A
30	0	644	G
30	0	660	A
30	0	688	A
30	0	701	U
30	0	735	C
30	0	759	C
30	0	777	U
30	0	809	G
30	0	821	U
30	0	835	U
30	0	840	U
30	0	857	A
30	0	858	U
30	0	868	G
30	0	869	G
30	0	871	G
30	0	872	U
30	0	875	A
30	0	877	G
30	0	878	G
30	0	884	C
30	0	885	G
30	0	898	G
30	0	905	C
30	0	920	C
30	0	921	G
30	0	923	A
30	0	953	G
30	0	960	G
30	0	961	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
30	0	1006	A
30	0	1008	C
30	0	1029	U
30	0	1045	G
30	0	1059	G
30	0	1060	C
30	0	1072	G
30	0	1081	A
30	0	1087	G
30	0	1088	A
30	0	1109	U
30	0	1110	G
30	0	1119	G
30	0	1130	U
30	0	1151	G
30	0	1164	U
30	0	1165	G
30	0	1166	A
30	0	1174	A
30	0	1175	G
30	0	1185	U
30	0	1192	A
30	0	1193	A
30	0	1206	U
30	0	1216	G
30	0	1237	U
30	0	1238	C
30	0	1239	G
30	0	1242	A
30	0	1279	U
30	0	1289	C
30	0	1342	C
30	0	1353	C
30	0	1360	C
30	0	1377	C
30	0	1407	A
30	0	1409	G
30	0	1474	C
30	0	1485	A
30	0	1505	U
30	0	1506	U
30	0	1524	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
30	0	1525	G
30	0	1526	A
30	0	1592	G
30	0	1625	U
30	0	1626	A
30	0	1634	G
30	0	1656	A
30	0	1667	A
30	0	1682	A
30	0	1684	A
30	0	1685	A
30	0	1692	C
30	0	1701	A
30	0	1722	U
30	0	1723	G
30	0	1725	C
30	0	1730	G
30	0	1731	C
30	0	1732	A
30	0	1752	G
30	0	1778	A
30	0	1798	C
30	0	1819	G
30	0	1820	G
30	0	1829	A
30	0	1856	C
30	0	1879	U
30	0	1919	A
30	0	1942	A
30	0	1971	G
30	0	1973	A
30	0	1978	A
30	0	1979	G
30	0	1980	U
30	0	1996	U
30	0	2008	U
30	0	2011	A
30	0	2012	U
30	0	2013	G
30	0	2033	G
30	0	2034	U
30	0	2064	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
30	0	2072	G
30	0	2073	G
30	0	2074	A
30	0	2096	A
30	0	2101	A
30	0	2102	G
30	0	2110	G
30	0	2243	C
30	0	2258	A
30	0	2271	G
30	0	2272	G
30	0	2291	A
30	0	2317	C
30	0	2321	A
30	0	2345	A
30	0	2354	A
30	0	2361	A
30	0	2369	A
30	0	2379	G
30	0	2422	U
30	0	2462	G
30	0	2467	A
30	0	2476	C
30	0	2480	G
30	0	2483	A
30	0	2507	G
30	0	2509	A
30	0	2511	A
30	0	2533	C
30	0	2537	G
30	0	2541	U
30	0	2553	A
30	0	2564	G
30	0	2589	U
30	0	2601	A
30	0	2602	G
30	0	2608	C
30	0	2611	G
30	0	2613	G
30	0	2634	G
30	0	2649	A
30	0	2664	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
30	0	2681	A
30	0	2682	C
30	0	2719	A
30	0	2726	U
30	0	2747	C
30	0	2748	G
30	0	2749	U
30	0	2750	G
30	0	2762	C
30	0	2768	A
30	0	2792	A
30	0	2800	A
30	0	2811	A
30	0	2812	A
30	0	2825	C
30	0	2876	G
30	0	2890	A
30	0	2896	A
30	0	2903	C
30	0	2914	A
31	9	2	U
31	9	7	G
31	9	14	G
31	9	22	G
31	9	23	U
31	9	24	U
31	9	25	G
31	9	40	C
31	9	41	C
31	9	43	G
31	9	44	A
31	9	52	A
31	9	57	A
31	9	66	G
31	9	77	A
31	9	114	G
31	9	122	C

All (29) RNA pucker outliers are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
30	0	69	A

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Mol	Chain	Res	Type
30	0	129	A
30	0	169	A
30	0	603	A
30	0	699	C
30	0	834	G
30	0	857	A
30	0	871	G
30	0	877	G
30	0	1080	C
30	0	1232	A
30	0	1237	U
30	0	1246	A
30	0	1352	A
30	0	1377	C
30	0	1684	A
30	0	1692	C
30	0	1856	C
30	0	1942	A
30	0	2313	C
30	0	2467	A
30	0	2526	C
30	0	2536	C
30	0	2649	A
30	0	2718	C
30	0	2726	U
30	0	2761	A
30	0	2791	U
31	9	65	A

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

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
30	OMU	0	2587	30	19,22,23	0.27	0	26,31,34	0.44	0
30	PSU	0	2621	30	18,21,22	1.36	2 (11%)	22,30,33	1.20	3 (13%)
30	OMG	0	2588	30	18,26,27	1.03	2 (11%)	19,38,41	0.73	1 (5%)
30	1MA	0	628	30,35	16,25,26	1.36	3 (18%)	18,37,40	1.17	2 (11%)
30	UR3	0	2619	30	19,22,23	0.39	0	26,32,35	0.65	1 (3%)

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
30	OMU	0	2587	30	-	0/9/27/28	0/2/2/2
30	PSU	0	2621	30	-	0/7/25/26	0/2/2/2
30	OMG	0	2588	30	-	0/5/27/28	0/3/3/3
30	1MA	0	628	30,35	-	0/3/25/26	0/3/3/3
30	UR3	0	2619	30	-	0/7/25/26	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	0	2621	PSU	C2-N1	4.32	1.42	1.36
30	0	628	1MA	C2-N3	3.41	1.33	1.29
30	0	2621	PSU	C6-C5	2.73	1.38	1.35
30	0	628	1MA	C6-N6	2.67	1.34	1.27
30	0	2588	OMG	C8-N7	-2.53	1.30	1.35
30	0	2588	OMG	C5-C6	-2.49	1.42	1.47
30	0	628	1MA	C8-N7	-2.09	1.31	1.35

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	2621	PSU	C6-C5-C4	2.97	120.28	118.20
30	0	628	1MA	N1-C2-N3	2.87	129.37	126.02
30	0	2621	PSU	O2-C2-N1	2.68	125.75	122.79
30	0	2621	PSU	C6-N1-C2	-2.62	120.00	122.68
30	0	628	1MA	C5-C6-N1	2.50	117.62	113.90
30	0	2619	UR3	C4-N3-C2	2.35	126.78	124.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	0	2588	OMG	O6-C6-C5	2.21	128.68	124.37

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	0	2587	OMU	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 306 ligands modelled in this entry, 305 are monoatomic - leaving 1 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	$\# Z  > 2$
38	ANM	0	2924	37	20,20,20	0.47	0	22,27,27	1.97	6 (27%)

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	ANM	0	2924	37	-	4/10/23/23	0/2/2/2

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	0	2924	ANM	O2-C5-C6	5.23	120.72	111.09
38	0	2924	ANM	C4-C3-C2	-3.85	98.31	103.29
38	0	2924	ANM	C2-O2-C5	-3.75	111.92	117.72
38	0	2924	ANM	C3-C2-C16	-3.01	99.95	104.29
38	0	2924	ANM	C14-O1-C9	-2.79	111.46	117.51
38	0	2924	ANM	O2-C5-O3	-2.07	118.84	122.96

There are no chirality outliers.

All (4) torsion outliers are listed below:

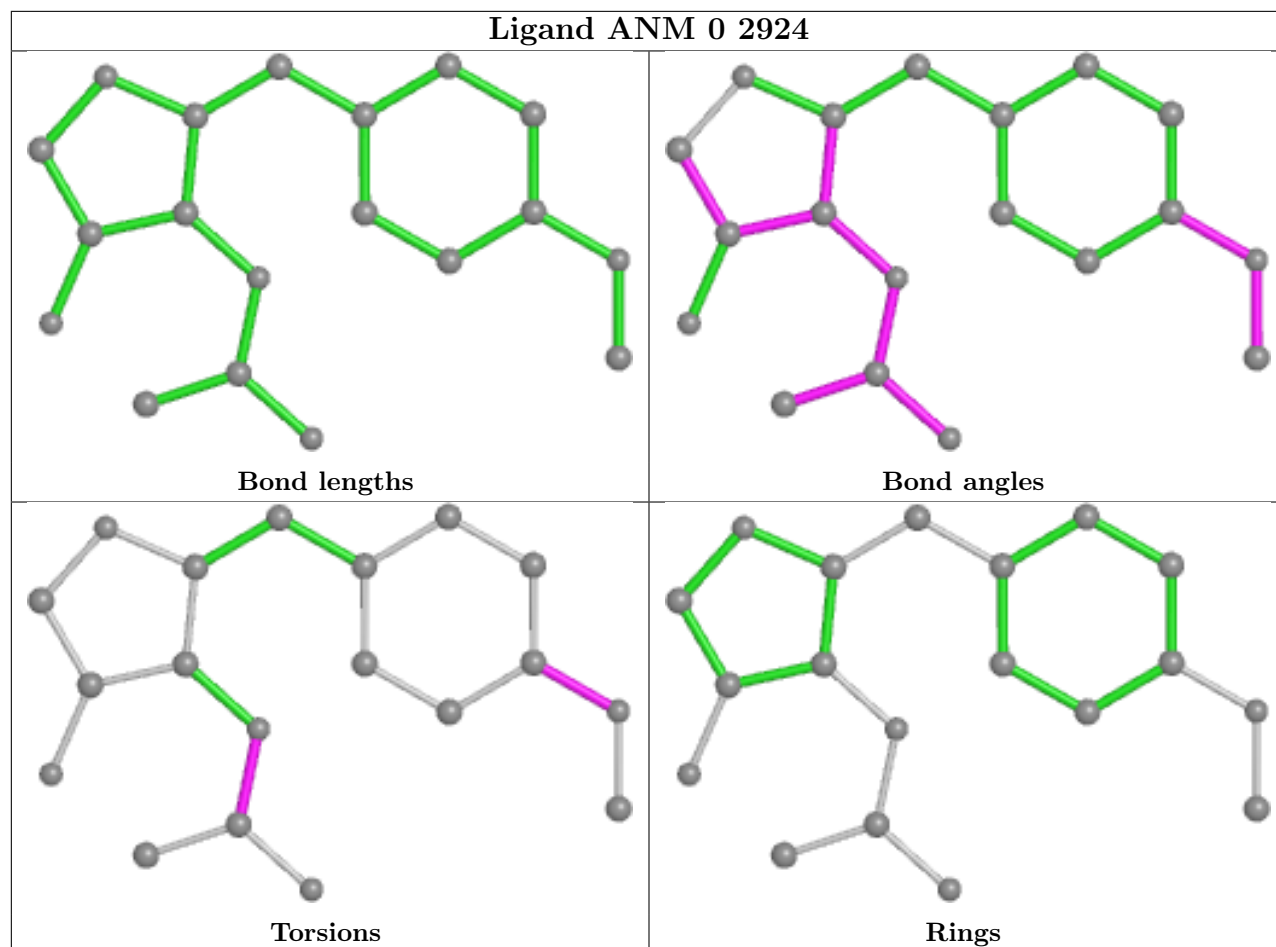
Mol	Chain	Res	Type	Atoms
38	0	2924	ANM	C6-C5-O2-C2
38	0	2924	ANM	O3-C5-O2-C2
38	0	2924	ANM	C10-C9-O1-C14
38	0	2924	ANM	C1-C9-O1-C14

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	0	2924	ANM	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	237/240 (98%)	0.63	22 (9%) 8 6	24, 49, 88, 107	0
2	B	337/338 (99%)	0.37	10 (2%) 50 51	27, 53, 82, 95	0
3	C	246/246 (100%)	0.29	3 (1%) 79 80	21, 42, 65, 78	0
4	D	140/177 (79%)	2.48	71 (50%) 0 0	61, 99, 124, 134	0
5	E	172/178 (96%)	0.70	15 (8%) 10 8	44, 69, 88, 94	0
6	F	119/120 (99%)	1.32	31 (26%) 0 0	43, 69, 99, 114	0
7	G	29/348 (8%)	1.76	10 (34%) 0 0	77, 95, 103, 106	0
8	H	160/177 (90%)	1.29	40 (25%) 0 0	44, 61, 96, 101	0
9	I	70/162 (43%)	5.14	65 (92%) 0 0	131, 146, 163, 164	0
10	J	142/145 (97%)	0.31	2 (1%) 75 77	35, 50, 71, 91	0
11	K	132/132 (100%)	0.15	2 (1%) 73 76	32, 49, 72, 77	0
12	L	145/165 (87%)	0.94	27 (18%) 1 1	25, 63, 109, 125	0
13	M	194/196 (98%)	0.12	2 (1%) 82 83	28, 40, 56, 62	0
14	N	186/187 (99%)	1.13	37 (19%) 1 0	42, 64, 112, 121	0
15	O	115/116 (99%)	0.50	2 (1%) 70 72	33, 53, 69, 80	0
16	P	143/149 (95%)	0.42	4 (2%) 53 54	38, 53, 67, 74	0
17	Q	95/96 (98%)	0.28	1 (1%) 80 82	34, 45, 62, 73	0
18	R	150/155 (96%)	0.14	0 100 100	30, 43, 63, 71	0
19	S	81/85 (95%)	0.91	8 (9%) 7 5	42, 56, 79, 90	0
20	T	119/120 (99%)	0.65	7 (5%) 22 21	35, 54, 84, 109	0
21	U	53/67 (79%)	0.62	4 (7%) 14 12	40, 56, 78, 84	0
22	V	65/71 (91%)	2.56	28 (43%) 0 0	52, 73, 117, 123	0
23	W	154/154 (100%)	0.54	5 (3%) 47 48	33, 49, 65, 75	0
24	X	82/92 (89%)	0.86	12 (14%) 2 1	43, 60, 85, 101	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	Y	142/241 (58%)	0.18	5 (3%) 44 44	22, 41, 64, 89	0
26	Z	73/116 (62%)	2.49	44 (60%) 0 0	58, 76, 89, 100	0
27	1	56/57 (98%)	0.04	0 100 100	24, 30, 36, 43	0
28	2	46/50 (92%)	1.02	11 (23%) 0 0	34, 60, 91, 101	0
29	3	92/92 (100%)	0.70	6 (6%) 18 17	36, 59, 72, 86	0
30	0	2749/2923 (94%)	-0.32	56 (2%) 65 67	18, 43, 87, 165	0
31	9	122/122 (100%)	-0.29	4 (3%) 46 46	34, 65, 86, 145	0
All	All	6646/7517 (88%)	0.31	534 (8%) 12 10	18, 50, 99, 165	0

All (534) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
22	V	39	ALA	14.6
22	V	1	THR	12.8
22	V	40	PRO	12.0
9	I	74	ILE	11.8
14	N	166	ALA	10.8
4	D	63	ILE	10.8
9	I	97	VAL	10.4
9	I	70	THR	9.8
9	I	72	GLU	9.0
9	I	66	GLY	8.9
9	I	132	VAL	8.9
9	I	128	THR	8.9
4	D	57	THR	8.5
9	I	100	VAL	8.5
26	Z	35	SER	8.4
22	V	43	PRO	8.3
31	9	1	U	7.9
9	I	91	PHE	7.9
9	I	108	HIS	7.9
26	Z	58	ASN	7.7
9	I	99	GLN	7.7
9	I	71	ALA	7.6
4	D	90	LEU	7.4
22	V	37	GLY	7.1
9	I	79	GLY	7.1
9	I	117	THR	7.0
9	I	102	GLN	7.0
9	I	104	ALA	6.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
9	I	106	GLN	6.7
9	I	98	ASP	6.6
20	T	119	ALA	6.5
9	I	109	PRO	6.5
4	D	10	PHE	6.5
9	I	80	PHE	6.4
9	I	111	LEU	6.2
30	0	1198	U	6.2
4	D	134	LEU	6.2
4	D	18	ILE	6.2
9	I	112	LEU	6.1
4	D	85	GLN	6.1
19	S	81	ILE	6.1
4	D	64	ARG	6.0
9	I	127	CYS	6.0
9	I	78	ALA	5.9
22	V	38	GLY	5.8
1	A	237	GLY	5.8
26	Z	46	SER	5.8
9	I	88	GLN	5.7
30	0	1172	G	5.7
9	I	73	LEU	5.7
9	I	105	GLU	5.6
4	D	89	PRO	5.6
26	Z	45	VAL	5.6
1	A	37	VAL	5.5
4	D	44	ILE	5.5
22	V	41	GLU	5.4
6	F	49	PHE	5.4
9	I	103	ILE	5.4
9	I	130	LEU	5.4
9	I	113	SER	5.4
9	I	120	ALA	5.3
4	D	40	ILE	5.3
9	I	69	PRO	5.3
4	D	88	LEU	5.1
4	D	128	LEU	5.1
30	0	1199	A	5.1
26	Z	44	ARG	5.1
26	Z	104	ARG	5.1
4	D	75	LEU	5.1
9	I	116	LEU	5.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	Y	235	GLU	4.9
4	D	69	ILE	4.9
9	I	76	ASP	4.8
9	I	86	GLU	4.8
9	I	121	LYS	4.8
4	D	104	PHE	4.8
22	V	36	ALA	4.7
26	Z	34	SER	4.7
9	I	94	ASP	4.6
9	I	82	THR	4.6
4	D	130	VAL	4.6
9	I	83	GLY	4.5
9	I	92	VAL	4.5
30	0	1202	A	4.5
8	H	77	ILE	4.5
9	I	93	ALA	4.5
4	D	61	PHE	4.5
24	X	88	GLU	4.5
12	L	60	GLU	4.4
5	E	45	ASP	4.4
9	I	133	THR	4.4
4	D	56	ARG	4.4
6	F	75	ILE	4.4
26	Z	78	ILE	4.4
30	0	735	C	4.4
26	Z	49	ARG	4.3
9	I	110	ASP	4.3
19	S	76	GLU	4.3
7	G	23	ILE	4.3
14	N	155	GLU	4.3
26	Z	69	ASP	4.3
8	H	76	LEU	4.3
9	I	75	LYS	4.3
9	I	118	ASN	4.3
4	D	157	LEU	4.2
14	N	160	SER	4.2
4	D	27	ILE	4.2
9	I	131	GLY	4.2
26	Z	55	SER	4.2
30	0	1171	A	4.2
12	L	106	VAL	4.2
4	D	84	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
26	Z	82	SER	4.1
30	0	1169	U	4.1
30	0	1163	G	4.1
24	X	7	GLU	4.1
8	H	40	GLN	4.1
22	V	2	VAL	4.1
9	I	67	VAL	4.1
4	D	106	PHE	4.1
8	H	141	CYS	4.1
4	D	26	GLY	4.0
30	0	970	U	4.0
8	H	86	TYR	4.0
14	N	152	GLU	4.0
24	X	74	ALA	4.0
30	0	1173	A	4.0
26	Z	60	ASP	4.0
26	Z	83	TYR	4.0
4	D	23	VAL	4.0
26	Z	50	VAL	4.0
31	9	24	U	3.9
26	Z	62	ALA	3.9
28	2	20	ARG	3.9
28	2	49	GLU	3.9
9	I	126	THR	3.9
28	2	39	ARG	3.8
4	D	58	VAL	3.8
6	F	17	LEU	3.8
24	X	71	ARG	3.8
24	X	77	PHE	3.8
3	C	139	VAL	3.8
14	N	165	ALA	3.7
22	V	3	LEU	3.7
4	D	22	VAL	3.7
24	X	80	GLU	3.7
9	I	123	VAL	3.7
4	D	70	GLY	3.7
4	D	92	GLU	3.7
4	D	24	HIS	3.7
4	D	170	TYR	3.7
10	J	70	PHE	3.6
30	0	282	C	3.6
22	V	46	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
4	D	62	ASP	3.6
8	H	81	GLY	3.6
30	0	1170	U	3.6
12	L	96	VAL	3.5
8	H	37	GLY	3.5
12	L	75	LEU	3.5
5	E	108	LEU	3.5
21	U	47	ARG	3.5
6	F	99	THR	3.5
9	I	119	ALA	3.5
7	G	27	ILE	3.5
26	Z	61	HIS	3.4
9	I	124	VAL	3.4
20	T	118	SER	3.4
22	V	32	ALA	3.4
30	0	1177	A	3.4
30	0	1181	A	3.4
26	Z	54	GLU	3.4
26	Z	53	ILE	3.4
14	N	172	PHE	3.4
6	F	106	ALA	3.4
4	D	154	LYS	3.4
4	D	25	MET	3.4
26	Z	68	GLU	3.3
1	A	94	LEU	3.3
8	H	70	LEU	3.3
4	D	68	PRO	3.3
7	G	26	MET	3.3
22	V	44	GLY	3.3
9	I	68	PRO	3.3
4	D	19	GLU	3.3
6	F	91	VAL	3.3
26	Z	42	TYR	3.3
7	G	71	LEU	3.3
8	H	174	LEU	3.3
4	D	158	ASN	3.3
1	A	99	ILE	3.3
4	D	87	ALA	3.3
8	H	35	LYS	3.3
4	D	86	THR	3.2
5	E	87	PHE	3.2
12	L	105	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
26	Z	79	TRP	3.2
8	H	140	TYR	3.2
22	V	33	VAL	3.2
12	L	80	ASP	3.2
9	I	84	SER	3.2
1	A	58	VAL	3.2
12	L	81	VAL	3.2
9	I	114	TYR	3.2
4	D	73	VAL	3.2
4	D	101	THR	3.2
28	2	37	HIS	3.2
1	A	90	PRO	3.2
28	2	27	LEU	3.2
25	Y	108	ASP	3.1
2	B	181	ILE	3.1
11	K	118	ALA	3.1
4	D	47	GLN	3.1
9	I	89	GLU	3.1
9	I	90	ASP	3.1
30	0	10	U	3.1
6	F	12	LEU	3.1
8	H	73	ASN	3.1
20	T	116	ASP	3.1
4	D	165	PHE	3.1
8	H	82	GLU	3.1
12	L	145	LEU	3.1
14	N	83	LEU	3.1
29	3	15	ASN	3.1
14	N	62	HIS	3.1
4	D	45	THR	3.1
4	D	43	GLU	3.1
5	E	154	ILE	3.1
29	3	13	HIS	3.1
30	0	1186	C	3.1
4	D	171	ASP	3.1
8	H	85	ASP	3.1
30	0	1951	G	3.1
28	2	23	ALA	3.1
30	0	1200	A	3.1
4	D	129	ASP	3.1
9	I	81	GLU	3.1
1	A	35	GLY	3.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
19	S	77	VAL	3.0
26	Z	48	ARG	3.0
14	N	159	TYR	3.0
9	I	122	GLU	3.0
28	2	35	ARG	3.0
22	V	59	ILE	3.0
30	0	2637	A	3.0
8	H	38	ARG	3.0
30	0	1203	G	3.0
12	L	91	VAL	3.0
14	N	138	ASP	3.0
22	V	8	ILE	3.0
4	D	98	PHE	3.0
4	D	93	LEU	3.0
28	2	36	ASN	3.0
24	X	85	VAL	3.0
22	V	52	ALA	3.0
12	L	99	GLU	3.0
26	Z	43	GLY	3.0
8	H	53	ILE	2.9
26	Z	38	PHE	2.9
30	0	497	A	2.9
14	N	145	ALA	2.9
30	0	1947	G	2.9
14	N	158	LEU	2.9
30	0	1178	G	2.9
22	V	45	ARG	2.9
26	Z	47	ARG	2.9
6	F	26	THR	2.9
9	I	95	LEU	2.9
4	D	65	GLU	2.9
1	A	31	LYS	2.9
6	F	20	LEU	2.9
6	F	29	VAL	2.9
7	G	24	VAL	2.9
30	0	1279	U	2.9
20	T	117	ASP	2.9
28	2	48	ASP	2.9
6	F	119	ARG	2.9
9	I	129	SER	2.9
30	0	2769	C	2.9
9	I	101	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
4	D	74	THR	2.9
1	A	38	ILE	2.8
24	X	10	VAL	2.8
5	E	100	ASP	2.8
12	L	150	GLN	2.8
30	0	1168	C	2.8
8	H	78	LYS	2.8
19	S	78	ALA	2.8
8	H	69	ARG	2.8
5	E	10	ASP	2.8
3	C	138	VAL	2.8
8	H	169	GLU	2.8
10	J	92	GLN	2.8
19	S	20	PHE	2.8
24	X	72	VAL	2.8
14	N	147	ILE	2.8
14	N	163	PHE	2.8
30	0	1197	G	2.8
30	0	1948	G	2.8
8	H	114	ASP	2.7
14	N	164	ASP	2.7
1	A	91	GLY	2.7
30	0	1165	G	2.7
4	D	11	HIS	2.7
8	H	36	MET	2.7
1	A	65	ARG	2.7
26	Z	89	THR	2.7
6	F	44	SER	2.7
30	0	1190	G	2.7
30	0	1164	U	2.7
22	V	34	GLN	2.7
4	D	135	VAL	2.7
6	F	97	ALA	2.7
4	D	139	TYR	2.7
30	0	1180	U	2.7
4	D	132	VAL	2.7
8	H	66	GLU	2.7
12	L	149	ARG	2.7
26	Z	93	TYR	2.7
5	E	170	ARG	2.7
1	A	64	ASP	2.7
6	F	90	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
17	Q	95	GLU	2.7
26	Z	70	ARG	2.7
14	N	169	PRO	2.7
14	N	178	THR	2.7
1	A	236	GLY	2.6
6	F	16	ALA	2.6
4	D	156	ARG	2.6
25	Y	95	THR	2.6
14	N	67	ALA	2.6
14	N	95	ALA	2.6
1	A	82	VAL	2.6
1	A	60	PHE	2.6
22	V	31	ARG	2.6
24	X	73	ARG	2.6
7	G	21	ASP	2.6
1	A	85	SER	2.6
4	D	66	GLY	2.6
9	I	125	GLY	2.6
8	H	39	LYS	2.6
12	L	97	VAL	2.6
26	Z	56	GLU	2.6
22	V	49	LEU	2.6
31	9	23	U	2.6
30	0	1965	C	2.6
8	H	172	GLU	2.6
26	Z	59	GLU	2.6
1	A	80	LEU	2.6
31	9	2	U	2.6
29	3	41	GLU	2.6
2	B	116	PRO	2.6
24	X	82	GLU	2.6
4	D	17	ARG	2.6
14	N	139	TRP	2.6
19	S	80	ARG	2.6
22	V	42	ASN	2.6
8	H	48	VAL	2.6
4	D	83	PHE	2.6
30	0	1964	U	2.6
12	L	121	ILE	2.6
4	D	71	ALA	2.6
8	H	83	GLU	2.6
4	D	166	ILE	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
13	M	1	ALA	2.5
14	N	81	ALA	2.5
23	W	62	LEU	2.5
26	Z	81	CYS	2.5
6	F	51	ALA	2.5
8	H	50	ILE	2.5
14	N	97	VAL	2.5
16	P	67	LYS	2.5
19	S	45	TYR	2.5
22	V	23	LEU	2.5
29	3	92	GLU	2.5
2	B	105	PHE	2.5
8	H	68	SER	2.5
6	F	114	LYS	2.5
8	H	74	ARG	2.5
8	H	27	PRO	2.5
2	B	143	ILE	2.5
6	F	96	ALA	2.5
21	U	54	THR	2.5
8	H	149	VAL	2.5
25	Y	236	VAL	2.5
4	D	105	SER	2.5
29	3	1	MET	2.5
4	D	172	VAL	2.5
6	F	6	PHE	2.5
14	N	68	GLU	2.4
30	0	1966	U	2.4
4	D	16	PRO	2.4
22	V	25	THR	2.4
30	0	1179	C	2.4
22	V	5	VAL	2.4
14	N	183	ASP	2.4
8	H	146	ALA	2.4
6	F	115	VAL	2.4
9	I	135	GLU	2.4
26	Z	36	GLY	2.4
30	0	2237	G	2.4
30	0	1192	A	2.4
26	Z	77	GLY	2.4
4	D	142	ALA	2.4
20	T	112	LEU	2.4
1	A	88	ILE	2.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
7	G	72	ASP	2.4
8	H	31	ILE	2.4
6	F	74	PHE	2.4
14	N	140	GLN	2.4
25	Y	234	VAL	2.4
26	Z	80	GLN	2.3
14	N	87	LEU	2.3
12	L	147	GLU	2.3
12	L	62	ALA	2.3
30	0	284	C	2.3
8	H	170	ARG	2.3
26	Z	37	ARG	2.3
12	L	66	VAL	2.3
26	Z	85	ASP	2.3
8	H	71	SER	2.3
14	N	185	GLU	2.3
26	Z	86	TYR	2.3
30	0	1185	U	2.3
3	C	5	ILE	2.3
30	0	1196	C	2.3
30	0	1174	A	2.3
4	D	53	LYS	2.3
6	F	48	VAL	2.3
6	F	117	GLU	2.3
14	N	137	ALA	2.3
30	0	1967	U	2.3
23	W	79	VAL	2.3
30	0	2508	C	2.3
1	A	133	ARG	2.3
14	N	84	THR	2.3
30	0	1625	U	2.3
30	0	1162	G	2.3
5	E	5	LEU	2.3
16	P	108	LEU	2.3
26	Z	51	ALA	2.3
1	A	36	ASP	2.3
12	L	102	ASP	2.3
2	B	168	GLY	2.3
19	S	15	MET	2.3
23	W	96	LEU	2.3
30	0	1950	G	2.3
4	D	54	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
12	L	101	ASP	2.3
14	N	162	ASP	2.3
30	0	2004	U	2.2
5	E	88	TYR	2.2
26	Z	105	ARG	2.2
26	Z	74	GLN	2.2
6	F	118	LEU	2.2
23	W	116	LEU	2.2
30	0	960	G	2.2
6	F	39	SER	2.2
8	H	60	LEU	2.2
22	V	27	LEU	2.2
1	A	89	ALA	2.2
6	F	15	ASP	2.2
2	B	183	GLU	2.2
4	D	81	GLU	2.2
6	F	22	VAL	2.2
9	I	134	ILE	2.2
5	E	89	SER	2.2
7	G	69	ARG	2.2
12	L	130	ARG	2.2
8	H	80	LEU	2.2
5	E	6	GLU	2.2
24	X	9	VAL	2.2
5	E	128	GLY	2.2
6	F	100	ASP	2.2
12	L	77	ALA	2.2
6	F	37	THR	2.2
4	D	21	VAL	2.2
20	T	40	VAL	2.2
26	Z	95	PRO	2.2
2	B	115	VAL	2.1
5	E	86	VAL	2.1
15	O	89	ILE	2.1
2	B	117	GLU	2.1
13	M	22	GLU	2.1
14	N	156	GLU	2.1
30	0	1157	C	2.1
16	P	48	ALA	2.1
21	U	52	THR	2.1
30	0	2103	A	2.1
26	Z	71	VAL	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
12	L	123	ASP	2.1
22	V	9	ARG	2.1
1	A	97	ALA	2.1
14	N	75	THR	2.1
2	B	128	ILE	2.1
5	E	42	VAL	2.1
16	P	116	SER	2.1
26	Z	88	PHE	2.1
14	N	134	ASP	2.1
15	O	98	LEU	2.1
8	H	87	LYS	2.1
7	G	63	ARG	2.1
12	L	95	ASP	2.1
8	H	90	LEU	2.1
12	L	76	LEU	2.1
2	B	1	PRO	2.1
14	N	129	ILE	2.1
4	D	80	ALA	2.1
21	U	40	ALA	2.1
30	0	1175	G	2.1
30	0	1195	G	2.1
12	L	140	VAL	2.1
4	D	72	LYS	2.1
6	F	31	LYS	2.1
12	L	61	ALA	2.1
14	N	148	ALA	2.1
6	F	76	PHE	2.1
30	0	2249	G	2.0
14	N	50	LEU	2.0
23	W	149	LEU	2.0
12	L	93	VAL	2.0
30	0	1201	C	2.0
20	T	115	GLU	2.0
14	N	151	ASP	2.0
28	2	24	TRP	2.0
29	3	83	TRP	2.0
9	I	87	PRO	2.0
30	0	2911	C	2.0
11	K	109	LEU	2.0
7	G	25	GLU	2.0
5	E	167	TYR	2.0
8	H	32	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
28	2	38	LYS	2.0
22	V	28	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
30	1MA	0	628	23/24	0.98	0.18	25,28,29,31	0
30	OMU	0	2587	21/22	0.98	0.15	31,33,35,37	0
30	OMG	0	2588	24/25	0.98	0.15	27,30,33,35	0
30	UR3	0	2619	21/22	0.98	0.17	30,34,36,39	0
30	PSU	0	2621	20/21	0.98	0.16	22,26,34,34	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
34	SR	9	8978	1/1	0.09	0.14	144,144,144,144	0
34	SR	0	9006	1/1	0.15	1.95	200,200,200,200	0
34	SR	0	8955	1/1	0.16	0.35	200,200,200,200	0
34	SR	0	8957	1/1	0.29	0.75	200,200,200,200	0
35	NA	S	8510	1/1	0.35	0.43	79,79,79,79	0
35	NA	9	8572	1/1	0.38	0.43	76,76,76,76	0
34	SR	0	8976	1/1	0.40	0.45	186,186,186,186	0
32	MG	0	8089	1/1	0.43	0.17	48,48,48,48	0
34	SR	0	8919	1/1	0.47	0.24	178,178,178,178	0
34	SR	0	8922	1/1	0.48	0.37	159,159,159,159	0
34	SR	0	8996	1/1	0.50	0.82	200,200,200,200	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
34	SR	0	8986	1/1	0.51	1.96	200,200,200,200	0
34	SR	0	8947	1/1	0.54	0.47	200,200,200,200	0
34	SR	0	8959	1/1	0.54	0.26	169,169,169,169	0
34	SR	A	8977	1/1	0.54	0.17	172,172,172,172	0
34	SR	0	8979	1/1	0.56	0.29	194,194,194,194	0
35	NA	0	8546	1/1	0.57	1.03	95,95,95,95	0
34	SR	0	8994	1/1	0.60	0.60	190,190,190,190	0
34	SR	9	9003	1/1	0.61	0.10	162,162,162,162	0
34	SR	0	8983	1/1	0.64	0.23	164,164,164,164	0
34	SR	0	8934	1/1	0.64	0.13	90,90,90,90	0
34	SR	0	8984	1/1	0.65	0.10	128,128,128,128	0
34	SR	0	8924	1/1	0.65	0.13	145,145,145,145	0
34	SR	0	8989	1/1	0.67	0.39	187,187,187,187	0
35	NA	0	8522	1/1	0.67	0.52	78,78,78,78	0
34	SR	S	8961	1/1	0.67	0.10	114,114,114,114	0
35	NA	0	8573	1/1	0.67	0.63	69,69,69,69	0
34	SR	B	8987	1/1	0.67	0.69	200,200,200,200	0
32	MG	0	8069	1/1	0.69	0.57	47,47,47,47	0
35	NA	0	8561	1/1	0.69	0.83	74,74,74,74	0
34	SR	0	8993	1/1	0.70	0.17	168,168,168,168	0
34	SR	0	8944	1/1	0.70	0.26	185,185,185,185	0
34	SR	0	8971	1/1	0.70	0.17	170,170,170,170	0
34	SR	0	8916	1/1	0.71	0.15	118,118,118,118	0
35	NA	0	8557	1/1	0.72	0.15	67,67,67,67	0
35	NA	0	8512	1/1	0.72	0.51	43,43,43,43	0
35	NA	0	8571	1/1	0.72	0.32	83,83,83,83	0
32	MG	0	8092	1/1	0.72	0.15	61,61,61,61	0
34	SR	0	8969	1/1	0.72	0.39	150,150,150,150	0
35	NA	0	8553	1/1	0.73	0.41	79,79,79,79	0
32	MG	0	8050	1/1	0.73	0.18	37,37,37,37	0
35	NA	0	8554	1/1	0.74	0.76	65,65,65,65	0
35	NA	0	8549	1/1	0.74	0.42	81,81,81,81	0
35	NA	M	8539	1/1	0.74	0.25	41,41,41,41	0
32	MG	0	8040	1/1	0.75	0.34	83,83,83,83	0
34	SR	0	8956	1/1	0.75	0.14	142,142,142,142	0
34	SR	0	8960	1/1	0.75	0.11	145,145,145,145	0
34	SR	0	8982	1/1	0.76	0.85	180,180,180,180	0
34	SR	0	8949	1/1	0.76	0.20	110,110,110,110	0
34	SR	0	8933	1/1	0.76	0.52	138,138,138,138	0
35	NA	0	8555	1/1	0.77	0.74	54,54,54,54	0
35	NA	0	8533	1/1	0.77	0.25	63,63,63,63	0
34	SR	0	8963	1/1	0.77	0.12	133,133,133,133	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
34	SR	0	8990	1/1	0.77	0.22	118,118,118,118	0
34	SR	0	8953	1/1	0.77	0.24	160,160,160,160	0
32	MG	A	8051	1/1	0.77	0.50	81,81,81,81	0
35	NA	0	8531	1/1	0.78	0.16	40,40,40,40	0
34	SR	0	8981	1/1	0.78	0.23	167,167,167,167	0
35	NA	0	8560	1/1	0.78	0.46	69,69,69,69	0
32	MG	0	8062	1/1	0.78	0.23	34,34,34,34	0
35	NA	0	8562	1/1	0.78	0.85	69,69,69,69	0
35	NA	0	8568	1/1	0.78	0.39	47,47,47,47	0
35	NA	0	8511	1/1	0.78	0.33	59,59,59,59	0
34	SR	9	8980	1/1	0.78	0.27	182,182,182,182	0
34	SR	0	9002	1/1	0.78	0.15	184,184,184,184	0
34	SR	0	8914	1/1	0.79	0.34	118,118,118,118	0
34	SR	0	8917	1/1	0.79	0.18	119,119,119,119	0
32	MG	0	8079	1/1	0.80	0.24	47,47,47,47	0
34	SR	0	8988	1/1	0.80	0.08	163,163,163,163	0
34	SR	0	8938	1/1	0.80	0.08	159,159,159,159	0
35	NA	9	8543	1/1	0.80	0.08	70,70,70,70	0
34	SR	0	8974	1/1	0.80	0.29	166,166,166,166	0
32	MG	0	8031	1/1	0.81	0.20	61,61,61,61	0
34	SR	0	8951	1/1	0.81	0.07	146,146,146,146	0
32	MG	0	8063	1/1	0.81	0.28	72,72,72,72	0
34	SR	0	8997	1/1	0.81	0.64	184,184,184,184	0
34	SR	0	8958	1/1	0.81	0.11	108,108,108,108	0
34	SR	0	8939	1/1	0.82	0.18	152,152,152,152	0
35	NA	0	8565	1/1	0.82	0.54	62,62,62,62	0
32	MG	0	8024	1/1	0.82	0.57	85,85,85,85	0
32	MG	0	8088	1/1	0.82	0.16	37,37,37,37	0
34	SR	0	8998	1/1	0.82	0.41	173,173,173,173	0
35	NA	0	8575	1/1	0.82	0.34	94,94,94,94	0
34	SR	0	8991	1/1	0.82	0.23	191,191,191,191	0
34	SR	0	8948	1/1	0.82	0.17	102,102,102,102	0
34	SR	0	9000	1/1	0.83	0.17	159,159,159,159	0
34	SR	0	8966	1/1	0.83	0.08	110,110,110,110	0
35	NA	0	8506	1/1	0.83	0.25	47,47,47,47	0
34	SR	0	8995	1/1	0.83	0.19	136,136,136,136	0
34	SR	0	9007	1/1	0.83	0.39	200,200,200,200	0
34	SR	0	8973	1/1	0.83	0.10	137,137,137,137	0
34	SR	0	8928	1/1	0.83	0.20	138,138,138,138	0
34	SR	0	8975	1/1	0.83	0.11	134,134,134,134	0
37	K	0	8401	1/1	0.83	0.41	81,81,81,81	0
35	NA	0	8505	1/1	0.84	0.57	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
34	SR	0	9001	1/1	0.84	0.24	169,169,169,169	0
32	MG	0	8072	1/1	0.84	0.28	52,52,52,52	0
32	MG	0	8080	1/1	0.84	0.28	57,57,57,57	0
35	NA	0	8567	1/1	0.85	0.43	78,78,78,78	0
32	MG	0	8043	1/1	0.85	0.15	49,49,49,49	0
32	MG	0	8030	1/1	0.85	0.37	55,55,55,55	0
35	NA	Q	8540	1/1	0.85	0.22	60,60,60,60	0
34	SR	0	8910	1/1	0.85	0.12	97,97,97,97	0
32	MG	0	8016	1/1	0.85	0.33	49,49,49,49	0
34	SR	0	8941	1/1	0.85	0.19	115,115,115,115	0
32	MG	0	8006	1/1	0.85	0.21	30,30,30,30	0
35	NA	0	8501	1/1	0.86	0.20	39,39,39,39	0
32	MG	0	8038	1/1	0.86	0.12	58,58,58,58	0
32	MG	B	8042	1/1	0.86	0.12	50,50,50,50	0
34	SR	0	8945	1/1	0.86	0.11	99,99,99,99	0
32	MG	0	8055	1/1	0.86	0.27	38,38,38,38	0
35	NA	0	8518	1/1	0.86	0.41	79,79,79,79	0
32	MG	0	8071	1/1	0.86	0.27	55,55,55,55	0
34	SR	0	9004	1/1	0.86	0.42	200,200,200,200	0
34	SR	0	8926	1/1	0.86	0.12	115,115,115,115	0
35	NA	0	8504	1/1	0.87	0.28	26,26,26,26	0
34	SR	0	8942	1/1	0.87	0.15	121,121,121,121	0
35	NA	0	8525	1/1	0.87	0.12	69,69,69,69	0
34	SR	0	8970	1/1	0.87	0.07	131,131,131,131	0
35	NA	0	8556	1/1	0.87	0.50	44,44,44,44	0
35	NA	0	8574	1/1	0.87	0.43	53,53,53,53	0
34	SR	A	8930	1/1	0.87	0.08	116,116,116,116	0
35	NA	0	8542	1/1	0.87	0.41	42,42,42,42	0
35	NA	0	8502	1/1	0.87	0.34	67,67,67,67	0
35	NA	0	8548	1/1	0.87	0.37	57,57,57,57	0
34	SR	B	8950	1/1	0.88	0.19	108,108,108,108	0
35	NA	0	8523	1/1	0.88	0.26	48,48,48,48	0
32	MG	0	8044	1/1	0.88	0.12	33,33,33,33	0
32	MG	0	8081	1/1	0.88	0.24	54,54,54,54	0
34	SR	0	8920	1/1	0.88	0.12	124,124,124,124	0
35	NA	0	8509	1/1	0.88	0.34	64,64,64,64	0
34	SR	0	8964	1/1	0.88	0.08	126,126,126,126	0
32	MG	0	8085	1/1	0.88	0.28	80,80,80,80	0
32	MG	0	8066	1/1	0.88	0.22	52,52,52,52	0
32	MG	0	8075	1/1	0.89	0.08	45,45,45,45	0
35	NA	J	8538	1/1	0.89	0.20	56,56,56,56	0
35	NA	0	8530	1/1	0.89	0.27	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
34	SR	0	8908	1/1	0.89	0.18	107,107,107,107	0
35	NA	0	8508	1/1	0.89	0.23	37,37,37,37	0
34	SR	0	8909	1/1	0.89	0.14	94,94,94,94	0
35	NA	0	8544	1/1	0.89	0.30	64,64,64,64	0
35	NA	R	8532	1/1	0.89	0.18	53,53,53,53	0
34	SR	0	8967	1/1	0.89	0.11	133,133,133,133	0
34	SR	0	8968	1/1	0.89	0.10	143,143,143,143	0
35	NA	0	8519	1/1	0.89	0.42	39,39,39,39	0
35	NA	0	8520	1/1	0.89	0.18	54,54,54,54	0
35	NA	0	8521	1/1	0.89	0.29	61,61,61,61	0
32	MG	0	8039	1/1	0.89	0.33	69,69,69,69	0
35	NA	0	8514	1/1	0.90	0.28	42,42,42,42	0
32	MG	0	8083	1/1	0.90	0.15	56,56,56,56	0
34	SR	0	8911	1/1	0.90	0.08	78,78,78,78	0
34	SR	0	8992	1/1	0.90	0.24	123,123,123,123	0
34	SR	0	9008	1/1	0.90	0.14	90,90,90,90	0
35	NA	0	8545	1/1	0.90	0.30	37,37,37,37	0
32	MG	T	8057	1/1	0.90	0.15	57,57,57,57	0
32	MG	0	8073	1/1	0.90	0.14	76,76,76,76	0
36	CD	O	8705	1/1	0.90	0.06	124,124,124,124	0
32	MG	0	8037	1/1	0.90	0.22	83,83,83,83	0
35	NA	0	8559	1/1	0.91	0.23	75,75,75,75	0
32	MG	0	8008	1/1	0.91	0.19	25,25,25,25	0
32	MG	0	8059	1/1	0.91	0.09	36,36,36,36	0
34	SR	0	8965	1/1	0.91	0.12	120,120,120,120	0
32	MG	0	8077	1/1	0.91	0.16	32,32,32,32	0
34	SR	H	8972	1/1	0.92	0.20	130,130,130,130	0
32	MG	0	8076	1/1	0.92	0.22	35,35,35,35	0
34	SR	0	8923	1/1	0.92	0.19	101,101,101,101	0
32	MG	0	8020	1/1	0.92	0.20	54,54,54,54	0
33	CL	0	8817	1/1	0.92	0.12	53,53,53,53	0
35	NA	B	8552	1/1	0.92	0.34	56,56,56,56	0
35	NA	C	8503	1/1	0.92	0.28	37,37,37,37	0
35	NA	0	8563	1/1	0.92	0.37	60,60,60,60	0
35	NA	0	8564	1/1	0.92	0.19	65,65,65,65	0
34	SR	A	8929	1/1	0.92	0.27	131,131,131,131	0
35	NA	0	8529	1/1	0.93	0.09	37,37,37,37	0
32	MG	0	8036	1/1	0.93	0.12	49,49,49,49	0
33	CL	0	8805	1/1	0.93	0.15	59,59,59,59	0
32	MG	0	8010	1/1	0.93	0.17	26,26,26,26	0
32	MG	0	8078	1/1	0.93	0.37	51,51,51,51	0
34	SR	0	8936	1/1	0.93	0.13	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
32	MG	0	8047	1/1	0.93	0.44	49,49,49,49	0
32	MG	0	8068	1/1	0.93	0.09	47,47,47,47	0
32	MG	0	8049	1/1	0.93	0.37	55,55,55,55	0
32	MG	0	8017	1/1	0.93	0.19	56,56,56,56	0
34	SR	0	8943	1/1	0.93	0.08	95,95,95,95	0
34	SR	0	8921	1/1	0.93	0.12	92,92,92,92	0
32	MG	0	8033	1/1	0.93	0.11	45,45,45,45	0
32	MG	0	8056	1/1	0.93	0.20	42,42,42,42	0
34	SR	0	8985	1/1	0.93	0.12	110,110,110,110	0
36	CD	Z	8703	1/1	0.93	0.06	81,81,81,81	0
32	MG	0	8034	1/1	0.93	0.11	32,32,32,32	0
37	K	0	8402	1/1	0.93	0.17	64,64,64,64	0
32	MG	0	8070	1/1	0.94	0.17	45,45,45,45	0
34	SR	0	8918	1/1	0.94	0.14	79,79,79,79	0
32	MG	0	8091	1/1	0.94	0.07	42,42,42,42	0
34	SR	F	9005	1/1	0.94	0.06	136,136,136,136	0
32	MG	0	8053	1/1	0.94	0.16	61,61,61,61	0
35	NA	0	8541	1/1	0.94	0.34	53,53,53,53	0
34	SR	0	8962	1/1	0.94	0.26	167,167,167,167	0
33	CL	A	8809	1/1	0.94	0.15	57,57,57,57	0
34	SR	3	8999	1/1	0.94	0.08	95,95,95,95	0
35	NA	0	8569	1/1	0.94	0.26	53,53,53,53	0
35	NA	0	8570	1/1	0.94	0.17	49,49,49,49	0
35	NA	0	8516	1/1	0.94	0.23	30,30,30,30	0
35	NA	0	8547	1/1	0.94	0.42	54,54,54,54	0
35	NA	0	8517	1/1	0.94	0.32	30,30,30,30	0
33	CL	O	8808	1/1	0.94	0.17	61,61,61,61	0
35	NA	0	8550	1/1	0.94	0.25	54,54,54,54	0
32	MG	0	8029	1/1	0.94	0.18	39,39,39,39	0
32	MG	0	8064	1/1	0.94	0.27	38,38,38,38	0
32	MG	0	8007	1/1	0.94	0.30	26,26,26,26	0
32	MG	0	8012	1/1	0.94	0.23	21,21,21,21	0
32	MG	0	8061	1/1	0.94	0.39	37,37,37,37	0
33	CL	Y	8820	1/1	0.95	0.11	38,38,38,38	0
32	MG	0	8018	1/1	0.95	0.24	38,38,38,38	0
32	MG	0	8084	1/1	0.95	0.18	31,31,31,31	0
33	CL	0	8822	1/1	0.95	0.25	68,68,68,68	0
32	MG	K	8054	1/1	0.95	0.16	39,39,39,39	0
32	MG	0	8067	1/1	0.95	0.28	34,34,34,34	0
32	MG	0	8045	1/1	0.95	0.17	32,32,32,32	0
34	SR	0	8946	1/1	0.95	0.16	108,108,108,108	0
35	NA	0	8528	1/1	0.95	0.20	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
32	MG	0	8035	1/1	0.95	0.10	44,44,44,44	0
32	MG	0	8048	1/1	0.95	0.28	28,28,28,28	0
32	MG	0	8093	1/1	0.95	0.11	29,29,29,29	0
32	MG	9	8074	1/1	0.95	0.13	67,67,67,67	0
35	NA	0	8535	1/1	0.95	0.25	52,52,52,52	0
35	NA	0	8537	1/1	0.95	0.12	34,34,34,34	0
32	MG	0	8032	1/1	0.95	0.09	40,40,40,40	0
34	SR	0	8954	1/1	0.95	0.08	105,105,105,105	0
35	NA	0	8507	1/1	0.95	0.30	45,45,45,45	0
34	SR	0	8927	1/1	0.95	0.15	167,167,167,167	0
33	CL	J	8801	1/1	0.95	0.13	62,62,62,62	0
34	SR	0	8931	1/1	0.95	0.11	108,108,108,108	0
33	CL	J	8821	1/1	0.95	0.15	56,56,56,56	0
33	CL	L	8810	1/1	0.95	0.09	49,49,49,49	0
35	NA	0	8515	1/1	0.95	0.23	33,33,33,33	0
32	MG	0	8041	1/1	0.95	0.33	24,24,24,24	0
38	ANM	0	2924	19/19	0.95	0.22	31,37,40,40	0
33	CL	0	8815	1/1	0.96	0.11	57,57,57,57	0
33	CL	0	8816	1/1	0.96	0.19	60,60,60,60	0
32	MG	0	8058	1/1	0.96	0.12	23,23,23,23	0
35	NA	0	8524	1/1	0.96	0.26	45,45,45,45	0
35	NA	0	8558	1/1	0.96	0.26	44,44,44,44	0
32	MG	0	8023	1/1	0.96	0.18	22,22,22,22	0
35	NA	0	8526	1/1	0.96	0.09	32,32,32,32	0
35	NA	0	8527	1/1	0.96	0.26	52,52,52,52	0
32	MG	0	8060	1/1	0.96	0.10	42,42,42,42	0
32	MG	0	8001	1/1	0.96	0.20	25,25,25,25	0
32	MG	0	8014	1/1	0.96	0.22	30,30,30,30	0
32	MG	0	8019	1/1	0.96	0.30	24,24,24,24	0
35	NA	0	8566	1/1	0.96	0.29	37,37,37,37	0
32	MG	0	8011	1/1	0.96	0.29	23,23,23,23	0
35	NA	0	8534	1/1	0.96	0.28	32,32,32,32	0
32	MG	0	8087	1/1	0.96	0.20	42,42,42,42	0
35	NA	0	8536	1/1	0.96	0.12	50,50,50,50	0
33	CL	N	8807	1/1	0.96	0.14	61,61,61,61	0
32	MG	0	8022	1/1	0.96	0.21	29,29,29,29	0
34	SR	1	8913	1/1	0.96	0.09	85,85,85,85	0
34	SR	3	8932	1/1	0.96	0.13	73,73,73,73	0
32	MG	0	8046	1/1	0.96	0.16	28,28,28,28	0
34	SR	0	8901	1/1	0.96	0.16	58,58,58,58	0
34	SR	0	8902	1/1	0.96	0.15	69,69,69,69	0
32	MG	0	8090	1/1	0.96	0.13	54,54,54,54	0

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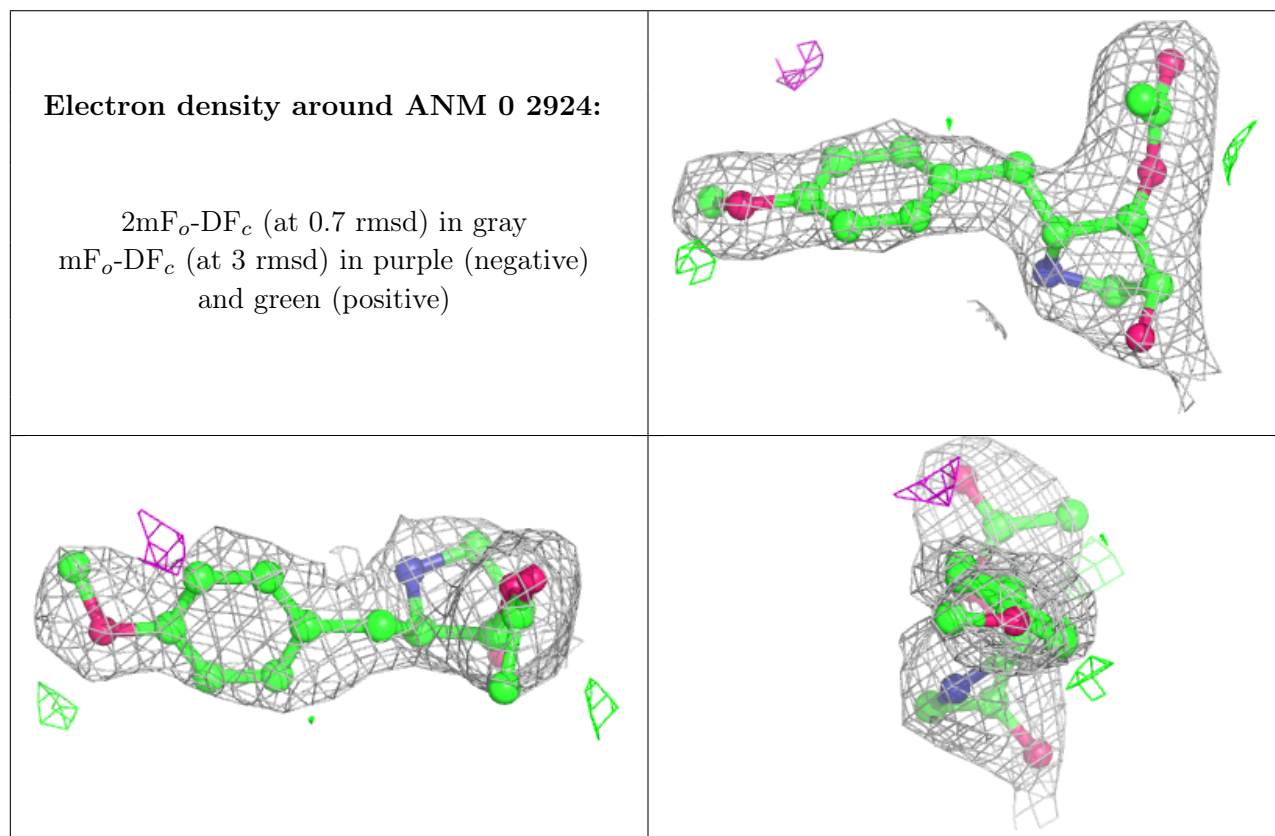
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
34	SR	0	8937	1/1	0.96	0.21	100,100,100,100	0
33	CL	0	8811	1/1	0.96	0.11	53,53,53,53	0
33	CL	0	8814	1/1	0.96	0.17	47,47,47,47	0
32	MG	0	8082	1/1	0.97	0.33	48,48,48,48	0
32	MG	0	8065	1/1	0.97	0.13	33,33,33,33	0
32	MG	0	8003	1/1	0.97	0.19	30,30,30,30	0
33	CL	0	8813	1/1	0.97	0.07	48,48,48,48	0
34	SR	0	8935	1/1	0.97	0.11	79,79,79,79	0
34	SR	R	8912	1/1	0.97	0.16	84,84,84,84	0
35	NA	0	8551	1/1	0.97	0.23	46,46,46,46	0
32	MG	0	8004	1/1	0.97	0.24	25,25,25,25	0
35	NA	0	8513	1/1	0.97	0.27	44,44,44,44	0
32	MG	0	8025	1/1	0.97	0.13	24,24,24,24	0
34	SR	1	8952	1/1	0.97	0.12	79,79,79,79	0
34	SR	0	8940	1/1	0.97	0.10	85,85,85,85	0
33	CL	J	8802	1/1	0.97	0.15	60,60,60,60	0
32	MG	0	8027	1/1	0.97	0.14	34,34,34,34	0
32	MG	0	8013	1/1	0.97	0.08	26,26,26,26	0
33	CL	M	8818	1/1	0.97	0.15	37,37,37,37	0
32	MG	0	8009	1/1	0.97	0.26	21,21,21,21	0
32	MG	Y	8086	1/1	0.97	0.11	39,39,39,39	0
32	MG	0	8052	1/1	0.98	0.11	40,40,40,40	0
34	SR	0	8925	1/1	0.98	0.12	90,90,90,90	0
32	MG	0	8002	1/1	0.98	0.17	22,22,22,22	0
33	CL	0	8812	1/1	0.98	0.11	48,48,48,48	0
32	MG	0	8021	1/1	0.98	0.13	32,32,32,32	0
32	MG	0	8026	1/1	0.98	0.14	31,31,31,31	0
32	MG	0	8015	1/1	0.98	0.19	27,27,27,27	0
34	SR	0	8903	1/1	0.98	0.20	53,53,53,53	0
32	MG	0	8005	1/1	0.98	0.30	26,26,26,26	0
33	CL	3	8804	1/1	0.98	0.05	54,54,54,54	0
33	CL	0	8803	1/1	0.98	0.07	46,46,46,46	0
32	MG	0	8028	1/1	0.99	0.26	22,22,22,22	0
33	CL	R	8806	1/1	0.99	0.17	43,43,43,43	0
33	CL	B	8819	1/1	0.99	0.12	46,46,46,46	0
34	SR	0	8904	1/1	0.99	0.20	52,52,52,52	0
36	CD	U	8701	1/1	0.99	0.12	58,58,58,58	0
34	SR	0	8905	1/1	0.99	0.26	57,57,57,57	0
36	CD	1	8702	1/1	0.99	0.08	57,57,57,57	0
36	CD	3	8704	1/1	0.99	0.09	66,66,66,66	0
34	SR	0	8915	1/1	0.99	0.06	117,117,117,117	0
34	SR	0	8906	1/1	0.99	0.21	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
34	SR	0	8907	1/1	0.99	0.32	76,76,76,76	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.