



Full wwPDB EM Validation Report ⓘ

Sep 17, 2026 – 01:11 AM EDT

PDB ID : 6V39 / pdb_00006v39
EMDB ID : EMD-21030
Title : Cryo-EM structure of the Acinetobacter baumannii Ribosome: 70S with P-site tRNA
Authors : Morgan, C.E.; Yu, E.W.
Deposited on : 2019-11-25
Resolution : 3.04 Å(reported)
Based on initial model : 5AFI

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

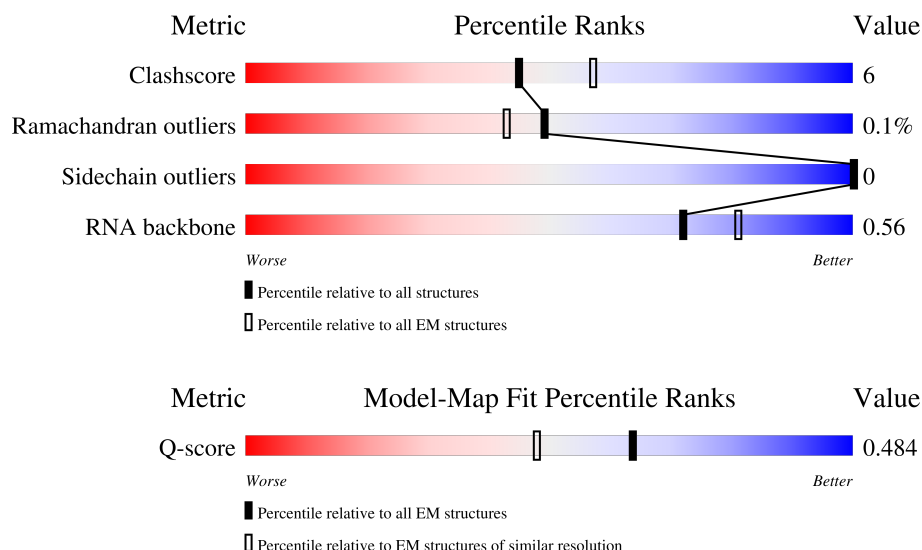
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.04 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13952 (2.54 - 3.54)

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

Mol	Chain	Length	Quality of chain
1	0	51	
2	1	44	
3	2	64	

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Mol	Chain	Length	Quality of chain
4	3	38	
5	AN1	2918	
6	B	115	
7	C	274	
8	D	212	
9	E	200	
10	F	178	
11	G	177	
12	H	148	
13	I	142	
14	J	122	
15	K	146	
16	L	137	
17	M	125	
18	N	116	
19	O	122	
20	P	119	
21	Q	103	
22	R	109	
23	S	106	
24	T	105	
25	U	98	
26	V	85	
27	W	78	
28	X	65	

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Mol	Chain	Length	Quality of chain
29	Y	58	
30	Z	61	
31	sN1	1544	
32	b	250	
33	c	250	
34	d	208	
35	e	165	
36	f	127	
37	g	156	
38	h	131	
39	i	128	
40	j	103	
41	k	128	
42	l	124	
43	m	118	
44	n	101	
45	o	89	
46	p	101	
47	q	85	
48	r	75	
49	s	91	
50	t	88	
51	u	71	
52	v	77	
53	w	3	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 141897 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	51	Total	C	N	O	S	0	0
			427	274	77	73	3		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	44	Total	C	N	O	S	0	0
			363	222	85	54	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			509	319	110	76	4		

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			295	179	64	48	4		

- Molecule 5 is a RNA chain called 23s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AN1	2892	Total	C	N	O	P	0	0
			62023	27689	11345	20098	2891		

- Molecule 6 is a RNA chain called 5s ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	115	Total	C	N	O	P	0	0
			2450	1095	440	800	115		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	270	Total	C	N	O	S	0	0
			2096	1291	434	363	8		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	211	Total	C	N	O	S	0	0
			1572	972	297	300	3		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	186	Total	C	N	O	S	0	0
			1419	893	265	257	4		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	175	Total	C	N	O	S	0	0
			1381	877	247	249	8		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	174	Total	C	N	O	S	0	0
			1318	832	236	249	1		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	60	Total	C	N	O	S	0	0
			458	287	84	86	1		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	142	Total	C	N	O	S	0	0
			1125	718	200	203	4		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	122	Total	C	N	O	S	0	0
			946	592	180	169	5		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	146	Total	C	N	O	S	0	0
			1089	673	215	200	1		

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	137	Total	C	N	O	S	0	0
			1087	687	210	185	5		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	119	Total	C	N	O	S	0	0
			942	590	186	163	3		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	114	Total	C	N	O	S	0	0
			857	528	173	155	1		

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	O	117	Total	C	N	O	0	0
			919	578	177	164		

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	117	Total	C	N	O	S	0	0
			934	589	197	146	2		

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	103	Total	C	N	O	S	0	0
			807	506	155	143	3		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	109	Total	C	N	O	S	0	0
			826	514	158	150	4		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	90	Total	C	N	O		0	0
			702	447	127	128			

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	100	Total	C	N	O		0	0
			749	465	139	145			

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	97	Total	C	N	O	S	0	0
			760	477	143	139	1		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	80	Total	C	N	O	S	0	0
			598	370	115	111	2		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	77	Total	C	N	O	S	0	0
			632	395	130	105	2		

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	62	Total	C	N	O	S	0	0
			498	308	96	93	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	58	Total	C	N	O	S	0	0
			463	286	88	85	4		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	55	Total	C	N	O	S	0	0
			456	271	102	82	1		

- Molecule 31 is a RNA chain called 16s Ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	sN1	1528	Total	C	N	O	P	0	0
			32782	14631	5994	10630	1527		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	225	Total	C	N	O	S	0	0
			1769	1110	328	325	6		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	215	Total	C	N	O	S	0	0
			1690	1065	318	299	8		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	207	Total	C	N	O	S	0	0
			1631	1017	313	299	2		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	155	Total	C	N	O	S	0	0
			1129	700	217	207	5		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	94	Total	C	N	O	S	0	0
			793	499	147	143	4		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	141	Total	C	N	O	S	0	0
			1111	696	210	199	6		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	130	Total	C	N	O	S	0	0
			985	615	177	187	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	127	Total	C	N	O	S	0	0
			995	621	198	175	1		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	100	Total	C	N	O	S	0	0
			801	500	150	148	3		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	117	Total	C	N	O	S	0	0
			862	535	167	159	1		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	122	Total	C	N	O	S	0	0
			945	580	193	167	5		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	115	Total	C	N	O	S	0	0
			903	558	184	158	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	100	Total	C	N	O	S	0	0
			792	493	158	137	4		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	88	Total	C	N	O	S	0	0
			705	434	144	126	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	83	Total	C	N	O	S	0	0
			649	406	129	113	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	80	Total	C	N	O	S	0	0
			630	396	118	115	1		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	r	53	Total	C	N	O	0	0
			438	282	75	81		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	82	Total	C	N	O	S	0	0
			646	412	125	107	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	85	Total	C	N	O	S	0	0
			658	406	138	112	2		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	u	21	Total	C	N	O	0	0
			182	115	37	30		

- Molecule 52 is a RNA chain called tRNA-met.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	v	77	Total	C	N	O	P	S	0	0
			1636	733	291	535	76	1		

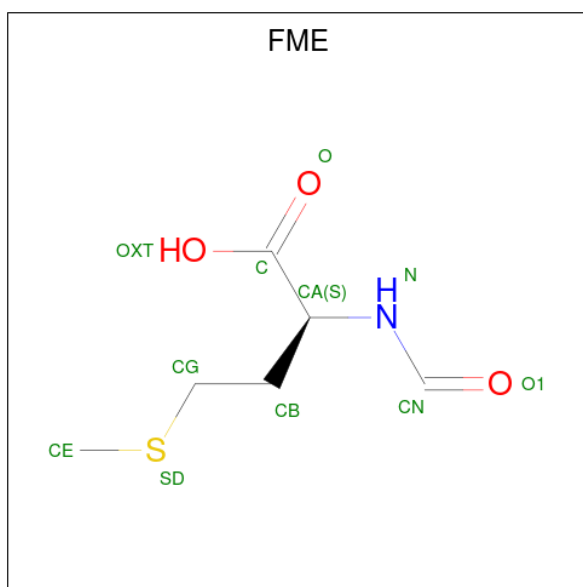
- Molecule 53 is a RNA chain called mRNA 5'-AUG-3'.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	3	Total	C	N	O	P	0	0
			65	29	12	21	3		

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
54	3	1	Total	Zn	0
			1	1	

- Molecule 55 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



Mol	Chain	Residues	Atoms					AltConf
55	AN1	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	AN1	59	Total	Mg	0
			59	59	
56	sN1	55	Total	Mg	0
			55	55	

- Molecule 57 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
57	AN1	1	Total	Na	0
			1	1	

- Molecule 58 is water.

Mol	Chain	Residues	Atoms		AltConf
58	1	1	Total	O	0
			1	1	
58	AN1	193	Total	O	0
			193	193	
58	B	1	Total	O	0
			1	1	

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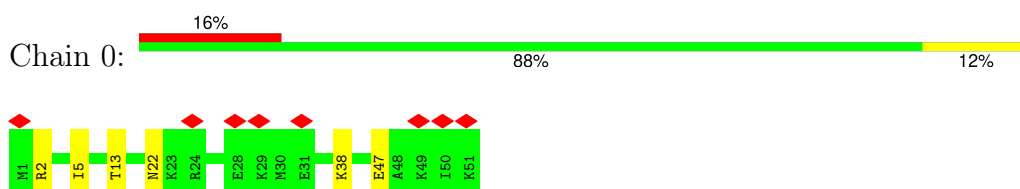
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Mol	Chain	Residues	Atoms		AltConf
58	C	2	Total 2	O 2	0
58	D	2	Total 2	O 2	0
58	K	2	Total 2	O 2	0
58	Z	1	Total 1	O 1	0
58	sN1	63	Total 63	O 63	0
58	h	1	Total 1	O 1	0
58	j	1	Total 1	O 1	0
58	m	1	Total 1	O 1	0
58	q	1	Total 1	O 1	0
58	s	3	Total 3	O 3	0
58	t	1	Total 1	O 1	0

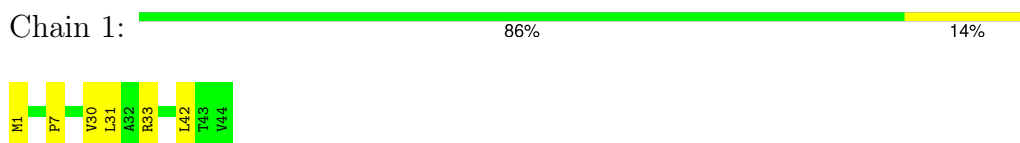
3 Residue-property plots [i](#)

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 atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

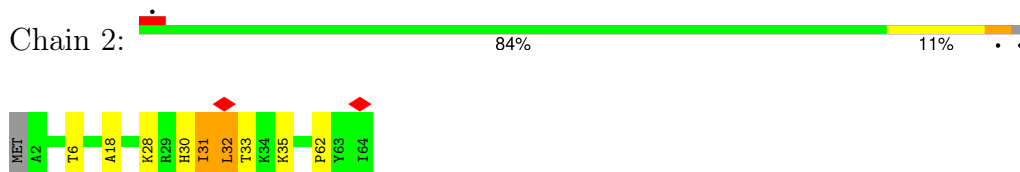
- Molecule 1: 50S ribosomal protein L33



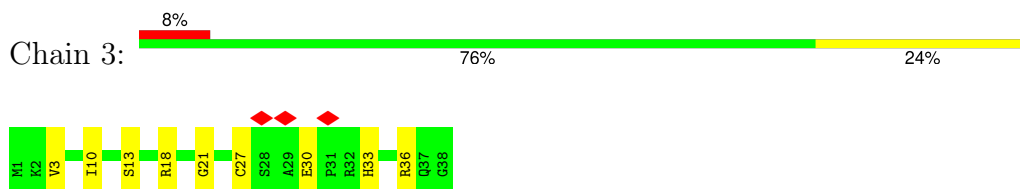
- Molecule 2: 50S ribosomal protein L34



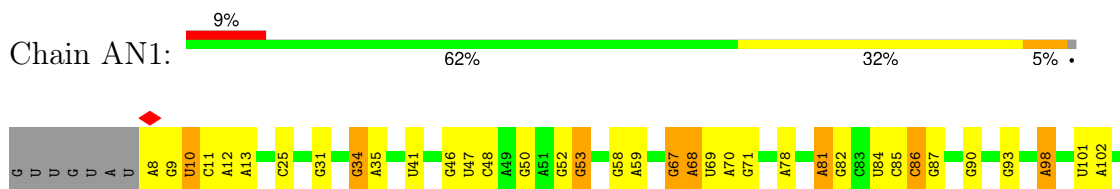
- Molecule 3: 50S ribosomal protein L35

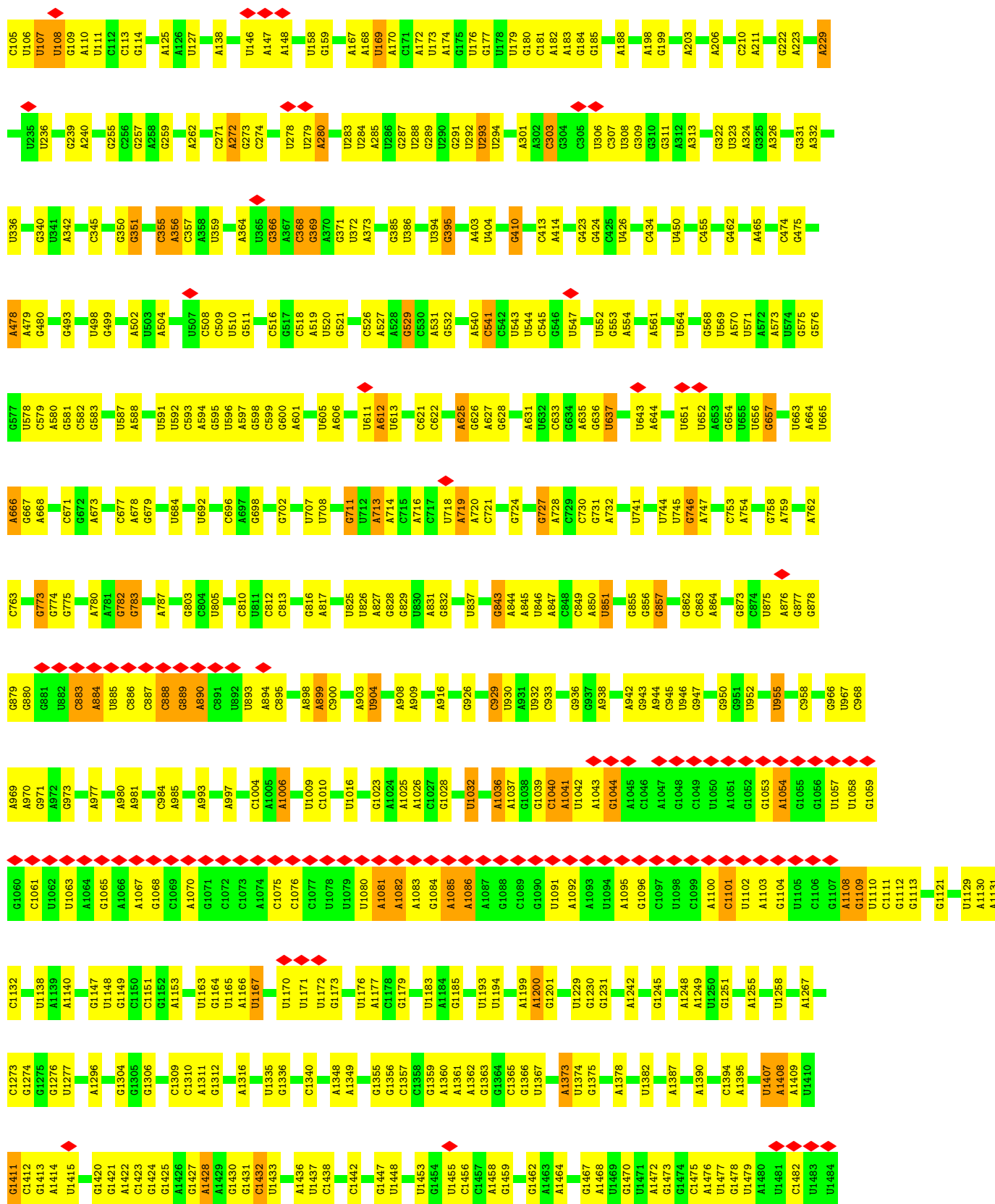


- Molecule 4: 50S ribosomal protein L36

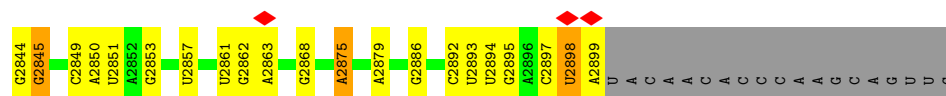


- Molecule 5: 23S ribosomal RNA





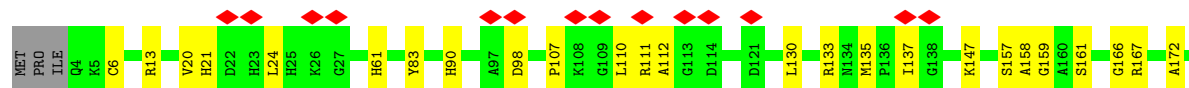
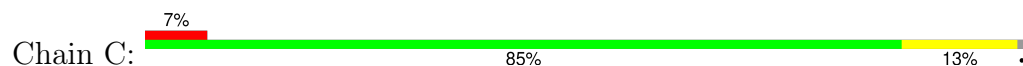




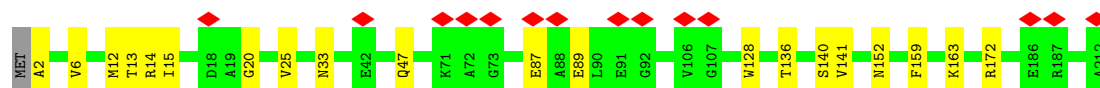
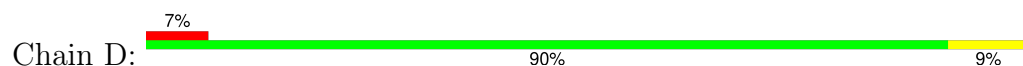
• Molecule 6: 5s ribosomal RNA



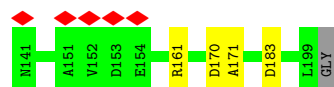
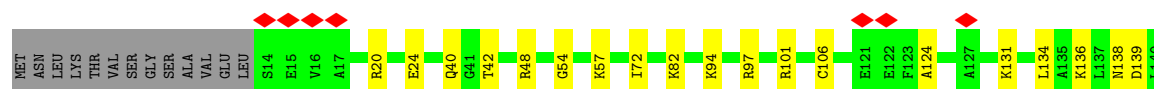
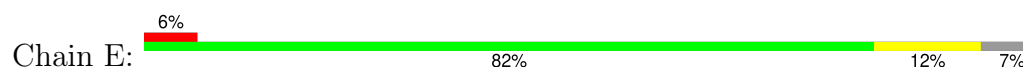
• Molecule 7: 50S ribosomal protein L2



• Molecule 8: 50S ribosomal protein L3

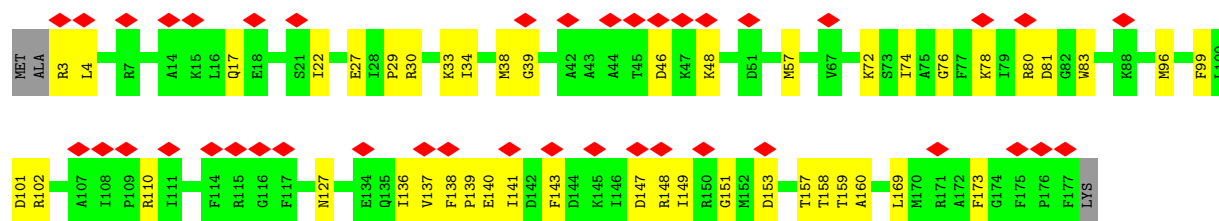


• Molecule 9: 50S ribosomal protein L4

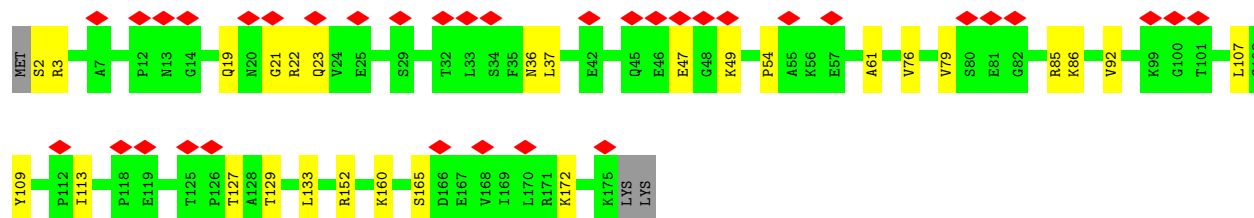
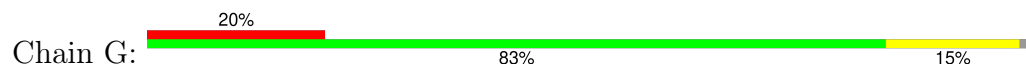


• Molecule 10: 50S ribosomal protein L5

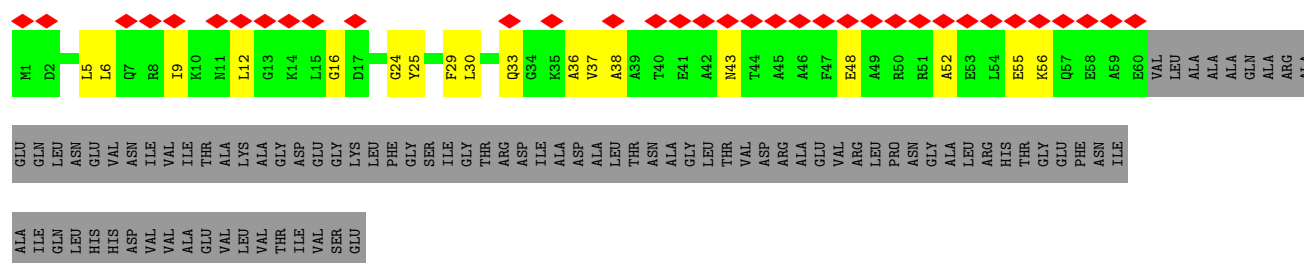




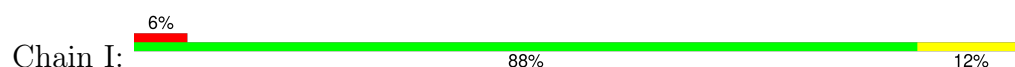
• Molecule 11: 50S ribosomal protein L6



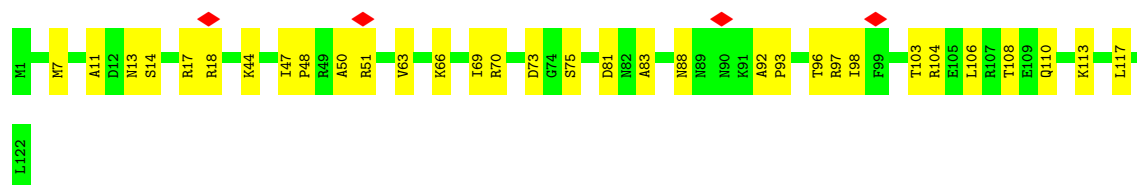
• Molecule 12: 50S ribosomal protein L9



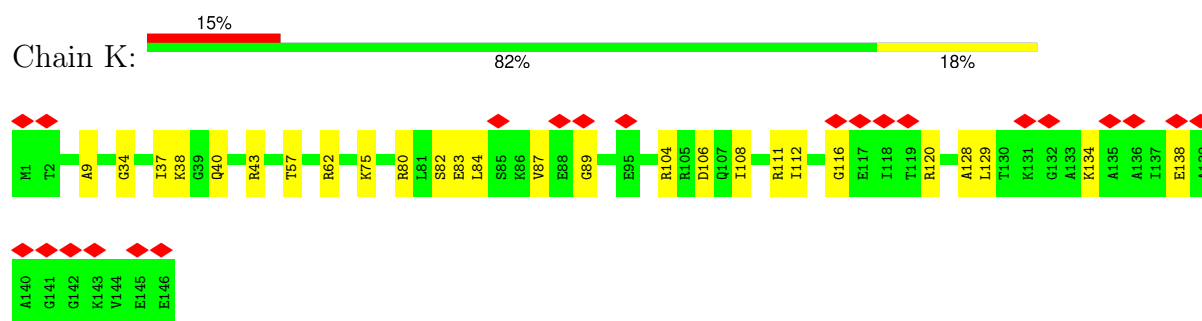
• Molecule 13: 50S ribosomal protein L13



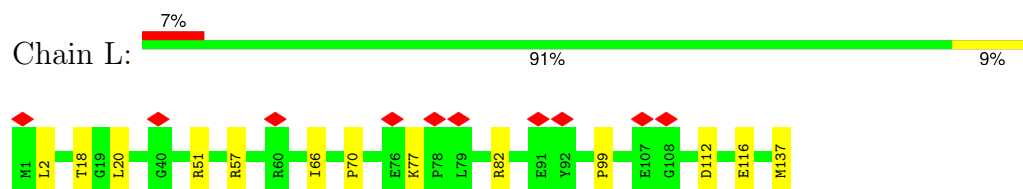
• Molecule 14: 50S ribosomal protein L14



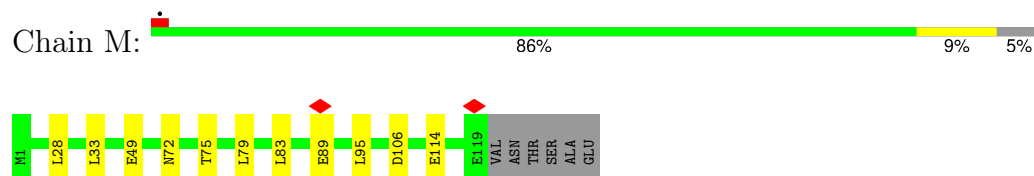
• Molecule 15: 50S ribosomal protein L15



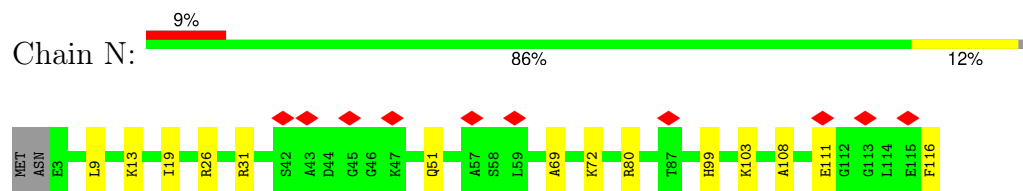
- Molecule 16: 50S ribosomal protein L16



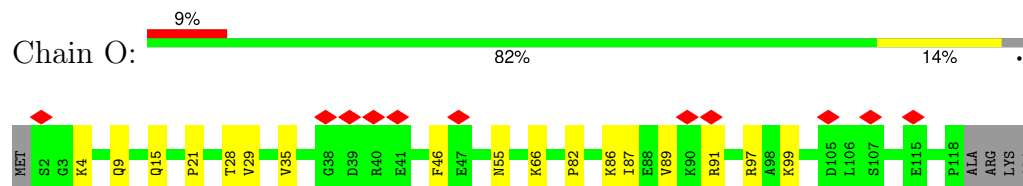
- Molecule 17: 50S ribosomal protein L17



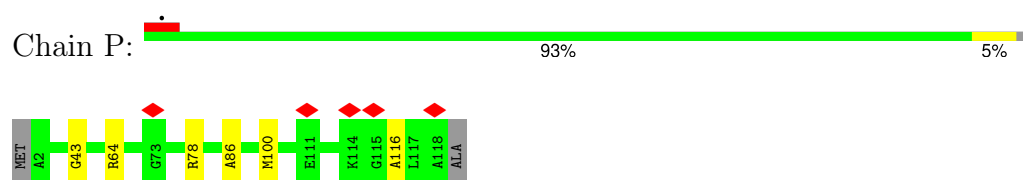
- Molecule 18: 50S ribosomal protein L18



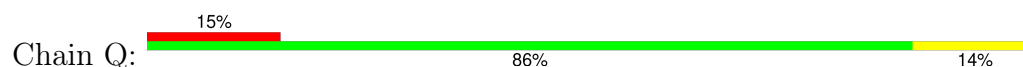
- Molecule 19: 50S ribosomal protein L19

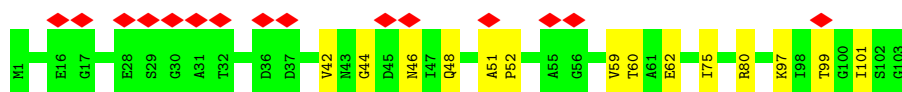


- Molecule 20: 50S ribosomal protein L20

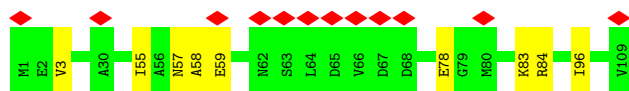
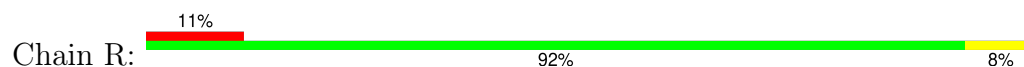


- Molecule 21: 50S ribosomal protein L21

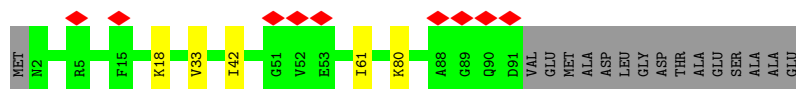




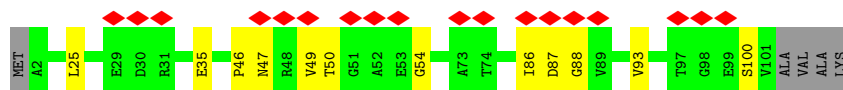
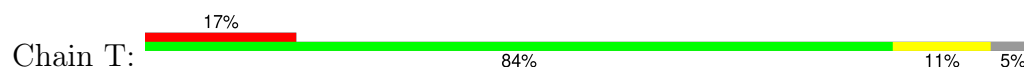
- Molecule 22: 50S ribosomal protein L22



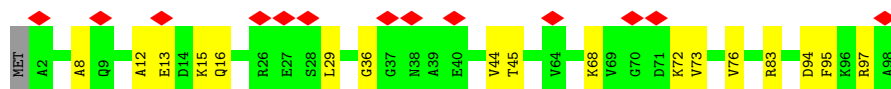
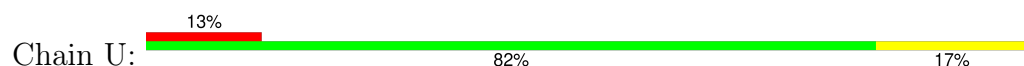
- Molecule 23: 50S ribosomal protein L23



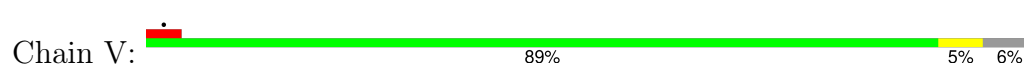
- Molecule 24: 50S ribosomal protein L24



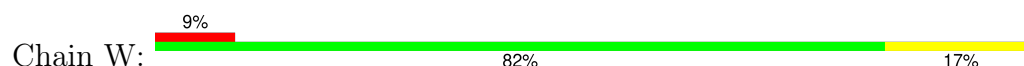
- Molecule 25: 50S ribosomal protein L25



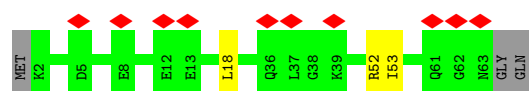
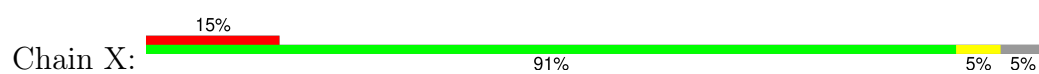
- Molecule 26: 50S ribosomal protein L27



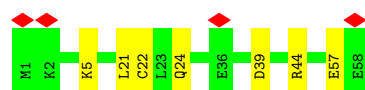
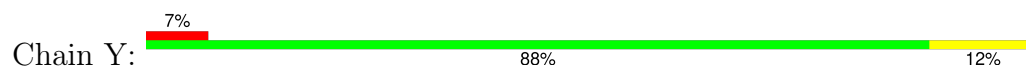
- Molecule 27: 50S ribosomal protein L28



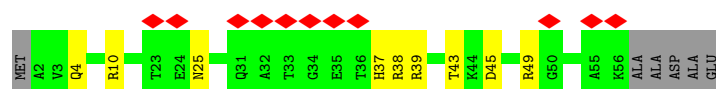
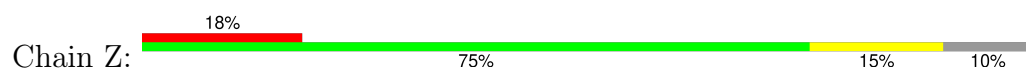
- Molecule 28: 50S ribosomal protein L29



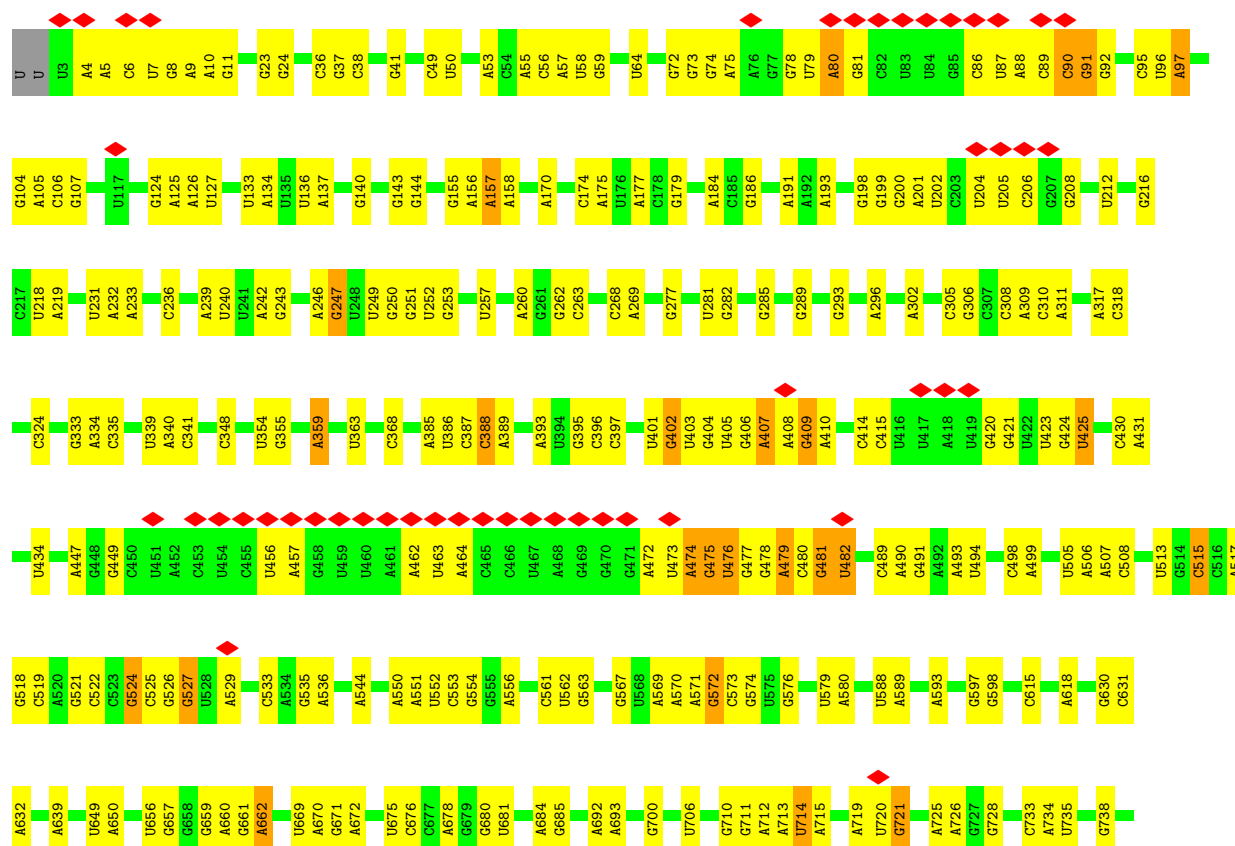
- Molecule 29: 50S ribosomal protein L30

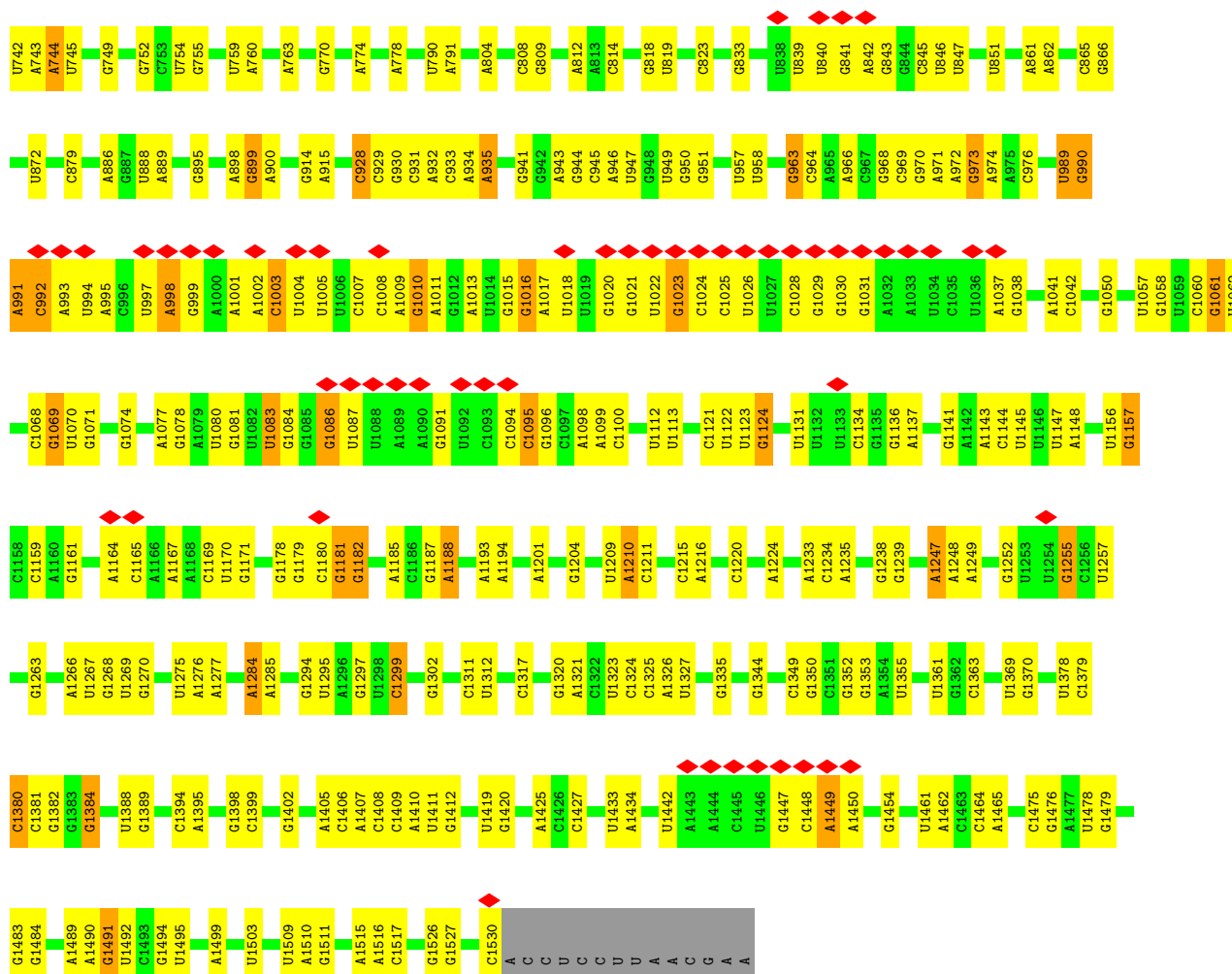


- Molecule 30: 50S ribosomal protein L32



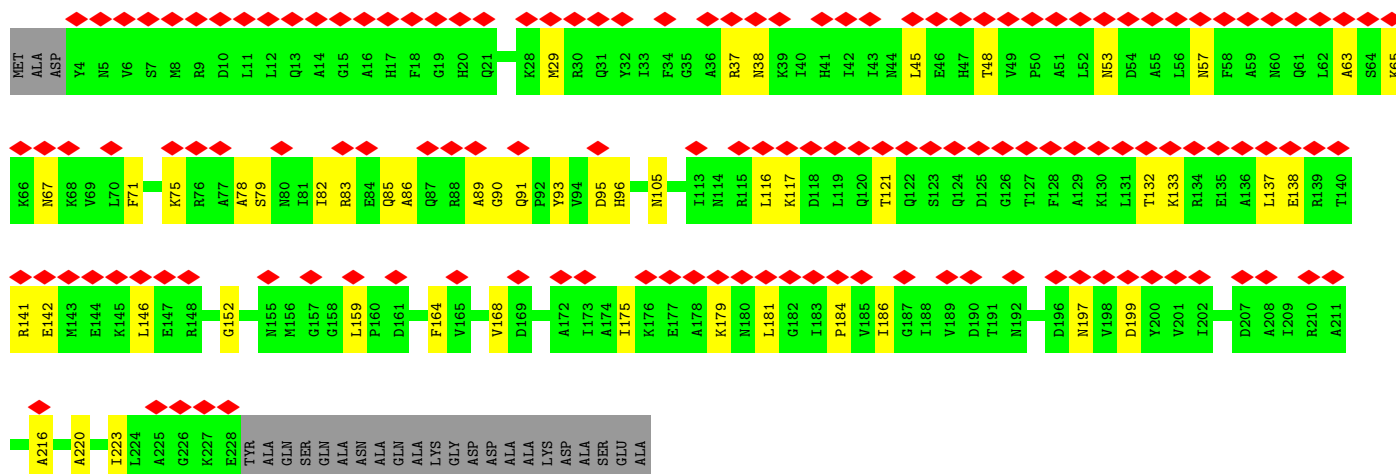
- Molecule 31: 16s Ribosomal RNA





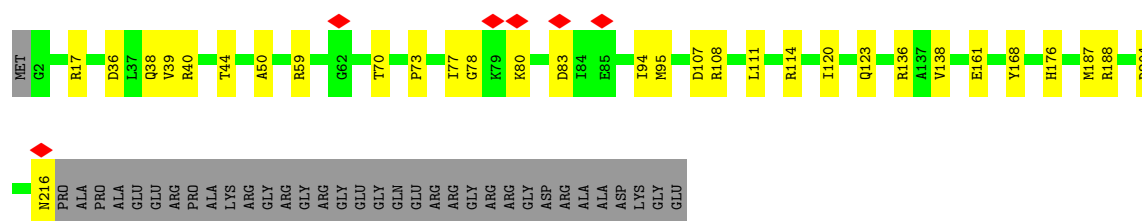
• Molecule 32: 30S ribosomal protein S2

Chain b:



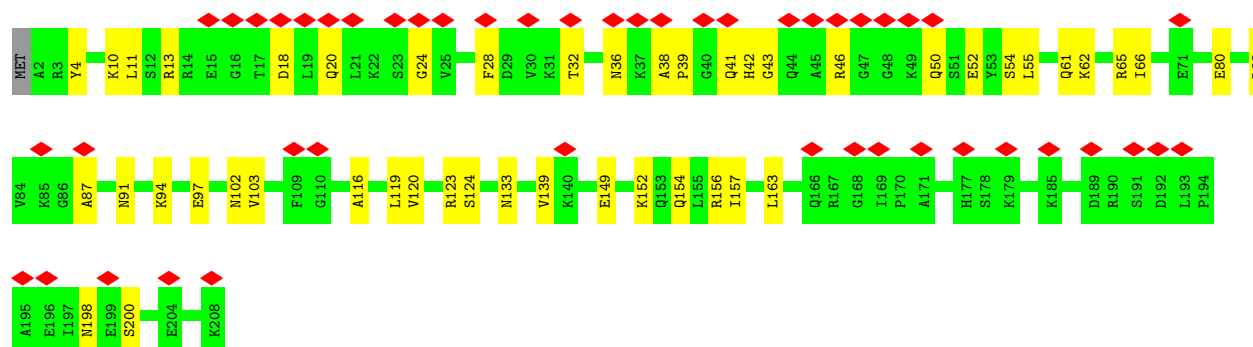
• Molecule 33: 30S ribosomal protein S3

Chain c: 



- Molecule 34: 30S ribosomal protein S4

Chain d: 



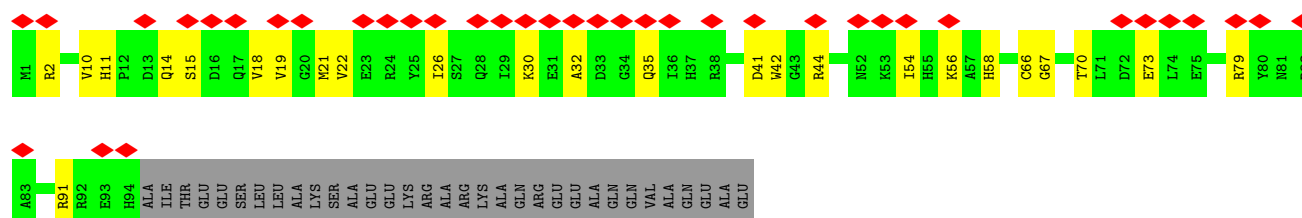
- Molecule 35: 30S ribosomal protein S5

Chain e: 



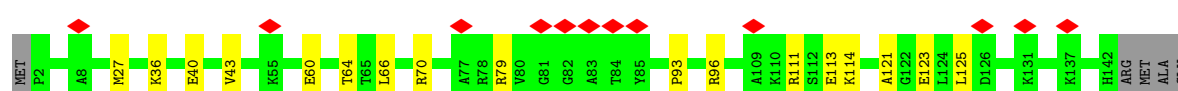
- Molecule 36: 30S ribosomal protein S6

Chain f: 



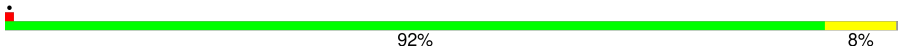
- Molecule 37: 30S ribosomal protein S7

Chain g: 



ALA
ASN
LYS
ALA
PHE
SER
HIS
TYR
ARG
PHE

- Molecule 38: 30S ribosomal protein S8

Chain h:  92% 8%

MET S2 M3 R15 N16 K22 A37 E43 V49 E55 Y66 I102 S131

- Molecule 39: 30S ribosomal protein S9

Chain i:  88% 11%

MET A2 Y5 R10 K11 T14 L19 K25 D60 L61 T82 D89 L96 R104 D105 R117 R128

- Molecule 40: 30S ribosomal protein S10

Chain j:  13% 72% 25%

MET SER N3 Q4 R7 I8 R16 A22 V26 E27 R31 V36 C37 G38 M42 H56 V57 N58 K59 D63 E66 I67 R68 K71 R72 L73 I74 T80 D81 K82 T83 V84 D85 K89 L90 D91 L92 A101 L102 GLY

- Molecule 41: 30S ribosomal protein S11

Chain k:  17% 66% 25% 9%

MET ALA ASP THR ARG LYS VAL T12 R13 S16 E17 G18 V19 A20 H21 T32 T33 T34 D35 R36 Q37 G38 G50 F51 R52 R55 T58 P59 F60 V64 E67 V68 K71 L74 D75 L78 R79 N80 L81 D82 V83 L84 R92 A98

L99 G100 A101 V102 G103 Y104 K105 I106 N107 S108 T109 T110 D111 N118 G119 K125 V128

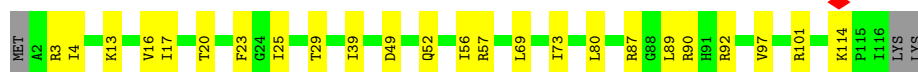
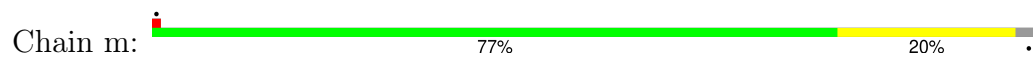
- Molecule 42: 30S ribosomal protein S12

Chain l:  19% 83% 15%

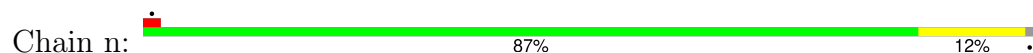
MET A2 L15 V16 E17 K18 L24 C27 R30 C34 T35 R36 T41 P42 K43 K44 P45 M46 S47 A48 M49 R50 R51 V52 C53 R54 G60 F61 E62 E70 H73 L74 Q75 E76 H77 G85 R86 V87 K88 D89 L90 P91 G92 H95 R99 G100 S101 L102

D109 R114 Y117 K123 LYS

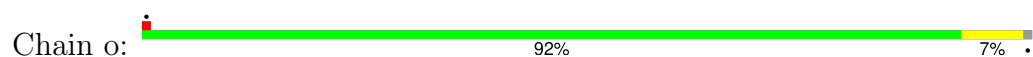
- Molecule 43: 30S ribosomal protein S13



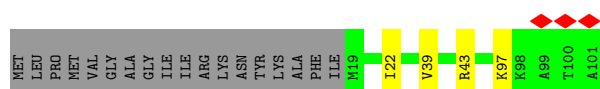
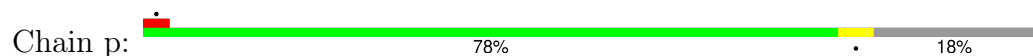
- Molecule 44: 30S ribosomal protein S14



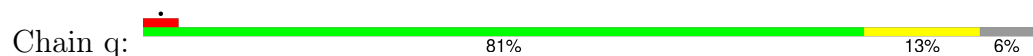
- Molecule 45: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S16



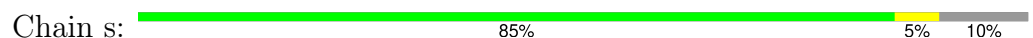
- Molecule 47: 30S ribosomal protein S17



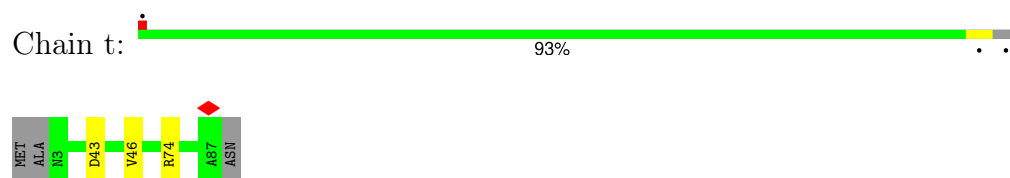
- Molecule 48: 30S ribosomal protein S18



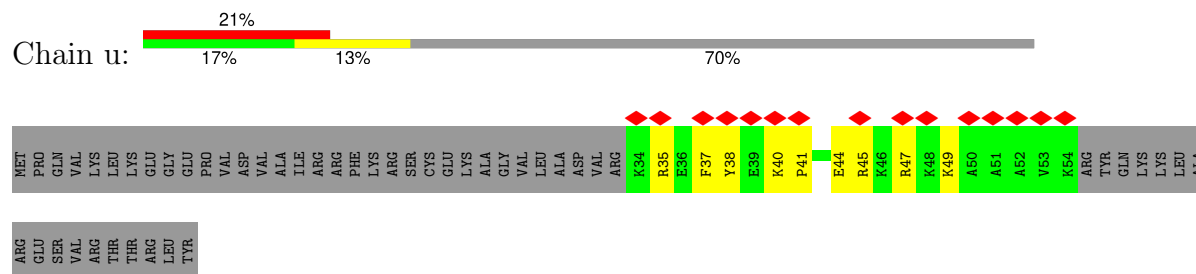
- Molecule 49: 30S ribosomal protein S19



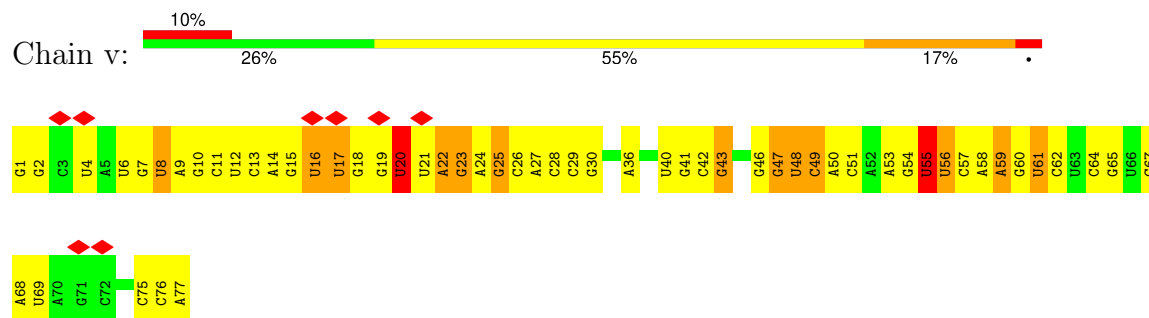
- Molecule 50: 30S ribosomal protein S20



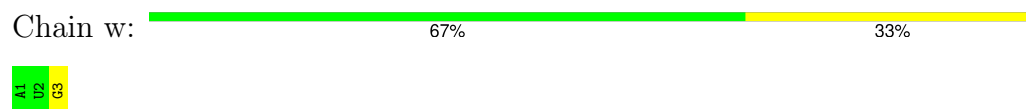
- Molecule 51: 30S ribosomal protein S21



- Molecule 52: tRNA-met



- Molecule 53: mRNA 5'-AUG-3'



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24306	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.512	Depositor
Minimum map value	-1.632	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.091	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	544.768, 544.768, 544.768	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.064, 1.064, 1.064	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UR3, MA6, OMG, 6MZ, FME, ZN, PSU, 2MA, MG, 4OC, 5MU, 4SU, OMU, H2U, 3TD, 5MC, NA, 7MG, 2MG

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	0	0.13	0/434	0.33	0/573
2	1	0.13	0/367	0.36	0/481
3	2	0.14	0/515	0.44	0/678
4	3	0.16	0/296	0.50	0/389
5	AN1	0.10	0/69101	0.23	0/107780
6	B	0.09	0/2739	0.21	0/4266
7	C	0.13	0/2136	0.35	0/2869
8	D	0.13	0/1590	0.31	0/2142
9	E	0.11	0/1440	0.30	0/1944
10	F	0.15	0/1401	0.43	0/1877
11	G	0.13	0/1337	0.36	0/1807
12	H	0.15	0/461	0.42	0/616
13	I	0.13	0/1151	0.32	0/1551
14	J	0.13	0/956	0.35	0/1286
15	K	0.13	0/1097	0.38	0/1461
16	L	0.12	0/1104	0.31	0/1475
17	M	0.15	0/956	0.38	0/1282
18	N	0.12	0/865	0.31	0/1156
19	O	0.13	0/931	0.33	0/1249
20	P	0.13	0/947	0.31	0/1262
21	Q	0.14	0/818	0.37	0/1094
22	R	0.13	0/831	0.32	0/1113
23	S	0.12	0/708	0.31	0/947
24	T	0.14	0/753	0.39	0/1010
25	U	0.13	0/770	0.34	0/1036
26	V	0.12	0/606	0.31	0/810
27	W	0.12	0/642	0.31	0/856
28	X	0.11	0/499	0.29	0/662
29	Y	0.13	0/468	0.34	0/624
30	Z	0.12	0/462	0.33	0/615
31	sN1	0.09	1/36476 (0.0%)	0.20	0/56895

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	b	0.15	0/1799	0.41	0/2429
33	c	0.11	0/1714	0.31	0/2304
34	d	0.11	0/1653	0.32	0/2213
35	e	0.12	0/1141	0.33	0/1537
36	f	0.12	0/808	0.38	0/1089
37	g	0.11	0/1127	0.31	0/1511
38	h	0.12	0/993	0.31	0/1331
39	i	0.13	0/1006	0.36	0/1346
40	j	0.15	0/811	0.38	0/1096
41	k	0.13	0/878	0.37	0/1189
42	l	0.14	0/958	0.42	0/1284
43	m	0.14	0/913	0.41	0/1226
44	n	0.11	0/803	0.30	0/1071
45	o	0.10	0/715	0.28	0/958
46	p	0.10	0/660	0.31	0/886
47	q	0.12	0/637	0.34	0/858
48	r	0.11	0/445	0.33	0/601
49	s	0.11	0/664	0.34	0/897
50	t	0.13	0/664	0.28	0/885
51	u	0.24	0/184	0.37	0/240
52	v	0.17	1/1739 (0.1%)	0.27	0/2709
53	w	0.08	0/72	0.16	0/110
All	All	0.11	2/153241 (0.0%)	0.26	0/229576

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	v	8	4SU	O3'-P	5.37	1.61	1.56
31	sN1	1495	UR3	O3'-P	5.02	1.61	1.56

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	427	0	462	4	0
2	1	363	0	401	5	0
3	2	509	0	566	8	0
4	3	295	0	327	6	0
5	AN1	62023	0	31191	563	0
6	B	2450	0	1241	39	0
7	C	2096	0	2157	27	0
8	D	1572	0	1610	16	0
9	E	1419	0	1464	19	0
10	F	1381	0	1433	35	0
11	G	1318	0	1373	16	0
12	H	458	0	480	11	0
13	I	1125	0	1148	12	0
14	J	946	0	1007	20	0
15	K	1089	0	1159	16	0
16	L	1087	0	1162	8	0
17	M	942	0	987	7	0
18	N	857	0	899	9	0
19	O	919	0	973	14	0
20	P	934	0	997	5	0
21	Q	807	0	842	9	0
22	R	826	0	894	6	0
23	S	702	0	756	3	0
24	T	749	0	797	8	0
25	U	760	0	783	12	0
26	V	598	0	600	3	0
27	W	632	0	667	9	0
28	X	498	0	537	2	0
29	Y	463	0	488	4	0
30	Z	456	0	448	7	0
31	sN1	32782	0	16505	333	0
32	b	1769	0	1787	33	0
33	c	1690	0	1774	20	0
34	d	1631	0	1691	28	0
35	e	1129	0	1174	11	0
36	f	793	0	788	15	0
37	g	1111	0	1163	10	0
38	h	985	0	1047	7	0
39	i	995	0	1053	12	0
40	j	801	0	832	18	0
41	k	862	0	877	24	0
42	l	945	0	996	12	0
43	m	903	0	962	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	n	792	0	833	9	0
45	o	705	0	712	6	0
46	p	649	0	660	3	0
47	q	630	0	678	8	0
48	r	438	0	456	7	0
49	s	646	0	663	4	0
50	t	658	0	710	2	0
51	u	182	0	198	9	0
52	v	1636	0	831	40	0
53	w	65	0	33	1	0
54	3	1	0	0	0	0
55	AN1	10	0	10	0	0
56	AN1	59	0	0	0	0
56	sN1	55	0	0	0	0
57	AN1	1	0	0	0	0
58	1	1	0	0	0	0
58	AN1	193	0	0	2	0
58	B	1	0	0	0	0
58	C	2	0	0	0	0
58	D	2	0	0	0	0
58	K	2	0	0	0	0
58	Z	1	0	0	0	0
58	h	1	0	0	0	0
58	j	1	0	0	0	0
58	m	1	0	0	0	0
58	q	1	0	0	0	0
58	s	3	0	0	0	0
58	sN1	63	0	0	1	0
58	t	1	0	0	0	0
All	All	141897	0	94282	1398	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 6.

All (1398) 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)
5:AN1:1462:G:H1	5:AN1:1520:A:N6	1.44	1.12
31:sN1:1442:U:H3	31:sN1:1454:G:H1	1.08	1.02
6:B:70:G:H21	6:B:101:A:H62	0.97	0.97
6:B:70:G:N2	6:B:101:A:H62	1.64	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:sN1:1069:G:O6	31:sN1:1081:G:N2	1.99	0.95
52:v:15:G:H22	52:v:49:C:N4	1.65	0.95
52:v:15:G:N2	52:v:49:C:H42	1.64	0.95
6:B:70:G:H21	6:B:101:A:N6	1.69	0.89
6:B:2:C:O2	6:B:113:G:N2	2.06	0.87
31:sN1:1157:G:N7	31:sN1:1179:G:N2	2.22	0.87
31:sN1:657:G:N1	31:sN1:743:A:N6	2.22	0.87
5:AN1:2096:G:H1	5:AN1:2185:U:H3	0.87	0.86
31:sN1:1069:G:C6	31:sN1:1081:G:N2	2.46	0.84
5:AN1:1846:G:N2	5:AN1:1888:C:O2	2.10	0.82
43:m:49:ASP:H	43:m:52:GLN:HE21	1.22	0.82
31:sN1:1083:U:H3	31:sN1:1096:G:H1	0.84	0.79
31:sN1:1157:G:O6	31:sN1:1179:G:N1	2.17	0.78
5:AN1:873:G:N2	5:AN1:900:C:O2	2.14	0.77
6:B:18:G:N1	6:B:61:C:N3	2.29	0.77
31:sN1:991:A:N6	31:sN1:995:A:N6	2.33	0.77
5:AN1:1595:A:H5''	5:AN1:1596:A:H5'	1.65	0.76
42:l:44:LYS:HD2	42:l:45:PRO:HD2	1.68	0.76
52:v:15:G:N1	52:v:49:C:N3	2.35	0.75
31:sN1:257:U:OP2	50:t:74:ARG:NH2	2.20	0.74
5:AN1:52:G:H5''	5:AN1:53:G:H5'	1.69	0.74
5:AN1:875:U:O2	5:AN1:898:A:N7	2.21	0.74
31:sN1:991:A:C6	31:sN1:995:A:N6	2.57	0.73
5:AN1:293:U:H3	5:AN1:351:G:H1	1.35	0.73
5:AN1:2112:G:O6	5:AN1:2166:A:N6	2.21	0.73
5:AN1:1036:A:H61	5:AN1:1113:G:H1	1.35	0.73
5:AN1:873:G:N1	5:AN1:900:C:N3	2.31	0.73
6:B:18:G:N2	6:B:61:C:O2	2.16	0.73
31:sN1:657:G:C6	31:sN1:743:A:N6	2.57	0.73
52:v:16:U:OP1	52:v:20:H2U:N3	2.22	0.72
31:sN1:473:U:H2'	31:sN1:474:A:H8	1.55	0.71
5:AN1:2734:A:N1	5:AN1:2762:G:O6	2.23	0.71
5:AN1:1862:A:H61	5:AN1:1871:G:H2'	1.55	0.71
13:I:17:VAL:HG13	13:I:137:PRO:HB2	1.71	0.71
5:AN1:879:G:O6	5:AN1:893:U:O2	2.08	0.70
31:sN1:1074:G:N2	31:sN1:1077:A:OP2	2.21	0.70
5:AN1:1108:A:H2'	5:AN1:1109:G:H4'	1.73	0.70
10:F:158:THR:HG22	10:F:160:ALA:H	1.57	0.70
10:F:80:ARG:HE	10:F:81:ASP:H	1.41	0.69
10:F:143:PHE:HB2	43:m:3:ARG:HH22	1.57	0.69
5:AN1:322:G:N7	9:E:131:LYS:NZ	2.40	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:198:A:H3'	5:AN1:199:G:H21	1.57	0.69
31:sN1:72:G:N2	31:sN1:95:C:O2	2.19	0.69
31:sN1:662:A:N7	31:sN1:721:G:O6	2.25	0.69
5:AN1:829:G:O2'	15:K:40:GLN:NE2	2.26	0.69
24:T:47:ASN:HD22	24:T:50:THR:HG23	1.58	0.69
31:sN1:293:G:N2	31:sN1:296:A:OP2	2.25	0.69
31:sN1:1069:G:O6	31:sN1:1081:G:C2	2.46	0.69
5:AN1:884:A:H61	43:m:89:LEU:HD11	1.59	0.68
41:k:125:LYS:HG2	51:u:35:ARG:HD2	1.75	0.68
5:AN1:2804:A:O2'	5:AN1:2886:G:O6	2.12	0.68
31:sN1:177:A:O2'	31:sN1:179:G:N1	2.27	0.67
5:AN1:1846:G:N1	5:AN1:1888:C:N3	2.35	0.67
6:B:28:C:H1'	6:B:55:A:H61	1.59	0.67
52:v:7:G:O6	52:v:50:A:N6	2.26	0.67
6:B:2:C:N3	6:B:113:G:N1	2.30	0.67
31:sN1:991:A:N6	31:sN1:995:A:H61	1.92	0.67
5:AN1:843:G:O2'	5:AN1:845:A:N7	2.27	0.67
31:sN1:670:A:H2'	31:sN1:671:G:C8	2.30	0.67
31:sN1:1159:C:H42	31:sN1:1171:G:H1	1.43	0.67
5:AN1:364:A:OP2	5:AN1:424:G:O2'	2.13	0.66
5:AN1:1750:C:H5	19:O:97:ARG:HH11	1.42	0.66
10:F:74:ILE:HG22	10:F:76:GLY:H	1.60	0.66
31:sN1:420:G:H2'	31:sN1:421:G:C8	2.31	0.66
31:sN1:1406:C:H2'	31:sN1:1407:A:H8	1.61	0.66
14:J:97:ARG:NH1	31:sN1:335:C:OP2	2.29	0.66
5:AN1:1749:G:N2	5:AN1:1752:G:OP2	2.27	0.66
5:AN1:2159:U:OP1	5:AN1:2161:C:N4	2.29	0.66
31:sN1:671:G:H2'	31:sN1:672:A:H8	1.61	0.66
4:3:10:ILE:HD12	5:AN1:2473:U:H3	1.60	0.65
5:AN1:744:U:H1'	5:AN1:746:G:H21	1.61	0.65
5:AN1:1528:G:O2'	5:AN1:1536:A:N1	2.27	0.65
5:AN1:280:A:H2	5:AN1:364:A:H62	1.45	0.65
41:k:58:THR:HG22	41:k:60:PHE:H	1.61	0.65
9:E:124:ALA:O	9:E:136:LYS:NZ	2.30	0.65
31:sN1:75:A:N1	31:sN1:92:G:O6	2.29	0.65
5:AN1:2123:G:N2	5:AN1:2158:G:O6	2.30	0.65
10:F:148:ARG:NH1	10:F:149:ILE:O	2.30	0.64
5:AN1:1775:U:OP2	5:AN1:1780:A:N6	2.27	0.64
5:AN1:2077:C:H2'	5:AN1:2078:A:H8	1.62	0.64
5:AN1:2107:U:O2	5:AN1:2111:G:N2	2.31	0.64
31:sN1:721:G:OP1	31:sN1:851:U:O2'	2.15	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:879:G:H2'	5:AN1:880:G:H8	1.62	0.64
5:AN1:2468:G:N2	5:AN1:2469:U:O2'	2.30	0.64
31:sN1:991:A:C5	31:sN1:995:A:N6	2.66	0.64
5:AN1:410:G:OP2	5:AN1:2402:U:O2'	2.14	0.64
31:sN1:1113:U:O2	31:sN1:1181:G:O6	2.16	0.64
47:q:25:LEU:HD11	47:q:42:SER:HB2	1.79	0.64
5:AN1:2449:A:H3'	5:AN1:2450:G:H21	1.62	0.64
32:b:37:ARG:HG3	32:b:38:ASN:H	1.62	0.64
5:AN1:1844:A:H4'	5:AN1:1845:G:H8	1.62	0.64
14:J:88:ASN:HD21	14:J:92:ALA:HB3	1.62	0.64
1:O:13:THR:HB	1:O:38:LYS:HD3	1.80	0.63
5:AN1:2743:G:H21	5:AN1:2753:A:H62	1.45	0.63
31:sN1:231:U:H2'	31:sN1:232:A:H8	1.64	0.63
5:AN1:2130:A:H62	5:AN1:2153:G:H4'	1.63	0.63
31:sN1:710:G:H2'	31:sN1:711:G:C8	2.34	0.63
31:sN1:808:C:O2'	31:sN1:898:A:N1	2.32	0.63
2:1:30:VAL:HG22	2:1:33:ARG:HH11	1.62	0.63
5:AN1:70:A:H61	5:AN1:98:A:H61	1.46	0.63
7:C:6:CYS:SG	7:C:13:ARG:NH2	2.72	0.63
31:sN1:1010:G:N2	31:sN1:1013:A:OP2	2.32	0.63
25:U:68:LYS:HG2	25:U:73:VAL:HG22	1.81	0.63
5:AN1:973:G:HO2'	5:AN1:1153:A:HO2'	1.47	0.63
5:AN1:1413:G:N2	5:AN1:1577:A:OP2	2.31	0.63
41:k:71:LYS:HA	41:k:74:LEU:HD12	1.80	0.63
7:C:107:PRO:HD2	7:C:110:LEU:HD22	1.80	0.63
6:B:108:C:H2'	6:B:109:G:H8	1.64	0.62
31:sN1:899:G:H2'	31:sN1:900:A:H8	1.64	0.62
31:sN1:1201:A:H1'	33:c:188:ARG:HH22	1.64	0.62
5:AN1:885:U:O2	43:m:92:ARG:NE	2.32	0.62
36:f:44:ARG:HD2	36:f:56:LYS:HE2	1.81	0.62
5:AN1:1258:U:O2	30:Z:4:GLN:NE2	2.32	0.62
31:sN1:79:U:O4	31:sN1:80:A:N6	2.33	0.62
31:sN1:410:A:OP2	31:sN1:424:G:N2	2.31	0.62
40:j:36:VAL:HG22	40:j:38:GLY:H	1.64	0.62
5:AN1:176:U:H2'	5:AN1:177:G:H8	1.65	0.62
33:c:17:ARG:NH1	33:c:216:ASN:OD1	2.33	0.62
5:AN1:2861:U:OP2	5:AN1:2862:G:O2'	2.18	0.62
7:C:161:SER:HB3	7:C:194:GLU:HG3	1.82	0.61
4:3:13:SER:OG	4:3:27:CYS:SG	2.57	0.61
31:sN1:733:C:H2'	31:sN1:734:A:H8	1.65	0.61
5:AN1:499:G:N1	5:AN1:502:A:OP2	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:625:A:H5''	15:K:80:ARG:HH21	1.66	0.61
32:b:71:PHE:HD2	32:b:82:ILE:HD11	1.65	0.61
43:m:39:ILE:HD11	43:m:52:GLN:HB2	1.82	0.61
34:d:38:ALA:HB3	34:d:43:GLY:HA3	1.81	0.61
39:i:104:ARG:NH1	39:i:105:ASP:O	2.34	0.61
31:sN1:473:U:H2'	31:sN1:474:A:C8	2.35	0.61
5:AN1:1306:G:OP2	5:AN1:1306:G:N2	2.30	0.61
15:K:82:SER:HB3	15:K:116:GLY:HA3	1.82	0.61
10:F:46:ASP:HB2	10:F:48:LYS:HG2	1.83	0.61
31:sN1:1016:G:H2'	31:sN1:1017:A:C8	2.35	0.61
5:AN1:2879:A:OP2	30:Z:49:ARG:NH1	2.34	0.61
5:AN1:1647:G:O2'	17:M:106:ASP:OD2	2.17	0.60
8:D:2:ALA:N	8:D:89:GLU:OE1	2.34	0.60
31:sN1:535:G:H2'	31:sN1:536:A:H8	1.65	0.60
5:AN1:1533:U:N3	5:AN1:1534:G:N3	2.45	0.60
48:r:37:GLY:O	48:r:63:ARG:NH1	2.33	0.60
31:sN1:657:G:N1	31:sN1:743:A:C6	2.70	0.60
5:AN1:2130:A:OP2	5:AN1:2152:G:N1	2.35	0.60
31:sN1:425:U:OP2	34:d:13:ARG:NH2	2.34	0.60
3:2:30:HIS:O	3:2:32:LEU:N	2.35	0.60
5:AN1:2111:G:O2'	5:AN1:2113:A:N7	2.31	0.60
5:AN1:2116:G:H5''	5:AN1:2164:G:H22	1.65	0.60
5:AN1:2734:A:H2	5:AN1:2762:G:H1	1.47	0.60
31:sN1:1009:A:N6	31:sN1:1015:G:O6	2.35	0.60
43:m:3:ARG:O	43:m:57:ARG:NH2	2.34	0.60
10:F:80:ARG:NH2	52:v:57:C:OP2	2.34	0.60
29:Y:39:ASP:OD1	29:Y:44:ARG:NH1	2.32	0.60
31:sN1:711:G:H2'	31:sN1:712:A:C8	2.37	0.60
6:B:18:G:O6	6:B:61:C:N4	2.34	0.60
31:sN1:1016:G:H2'	31:sN1:1017:A:H8	1.66	0.60
31:sN1:156:A:N6	31:sN1:339:U:O2'	2.35	0.60
31:sN1:1068:C:OP1	35:e:53:ARG:NH1	2.31	0.60
52:v:15:G:N2	52:v:49:C:N4	2.31	0.60
5:AN1:846:U:H2'	5:AN1:847:A:H8	1.66	0.60
31:sN1:670:A:H2'	31:sN1:671:G:H8	1.66	0.60
5:AN1:12:A:H2'	5:AN1:13:A:C8	2.37	0.59
8:D:6:VAL:H	8:D:33:ASN:HD21	1.48	0.59
25:U:12:ALA:H	25:U:15:LYS:HE3	1.66	0.59
31:sN1:6:C:H2'	31:sN1:7:U:H2'	1.84	0.59
5:AN1:1111:C:H2'	5:AN1:1112:G:H8	1.67	0.59
5:AN1:1713:U:H3	5:AN1:1739:G:H1	1.49	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:46:U:OP2	18:N:31:ARG:NH2	2.35	0.59
5:AN1:878:G:H2'	5:AN1:879:G:H8	1.67	0.59
5:AN1:1535:U:H2'	5:AN1:1536:A:H8	1.68	0.59
9:E:97:ARG:HG2	9:E:101:ARG:HE	1.67	0.59
31:sN1:104:G:N7	58:sN1:1708:HOH:O	2.32	0.59
31:sN1:239:A:H4'	31:sN1:240:U:H3'	1.84	0.59
31:sN1:669:U:OP1	36:f:79:ARG:NH1	2.35	0.59
31:sN1:678:A:H61	31:sN1:706:U:H3	1.50	0.59
31:sN1:997:U:O4	31:sN1:998:A:N6	2.36	0.59
16:L:20:LEU:HD23	16:L:99:PRO:HG2	1.85	0.59
40:j:26:VAL:HG13	40:j:36:VAL:HG11	1.83	0.59
5:AN1:844:A:N6	5:AN1:929:C:O2'	2.35	0.59
10:F:3:ARG:NH1	10:F:101:ASP:OD2	2.35	0.59
5:AN1:84:U:OP1	28:X:52:ARG:NH2	2.36	0.59
31:sN1:252:U:H2'	31:sN1:253:G:H8	1.67	0.59
5:AN1:303:C:H5''	5:AN1:336:U:H2'	1.85	0.59
5:AN1:587:U:H2'	5:AN1:588:A:H8	1.68	0.59
22:R:3:VAL:HG21	22:R:58:ALA:HB2	1.84	0.59
31:sN1:719:A:OP2	51:u:45:ARG:NH2	2.36	0.59
32:b:65:LYS:HB2	32:b:67:ASN:HD21	1.67	0.59
5:AN1:1717:G:N2	5:AN1:1734:G:O2'	2.35	0.58
5:AN1:2123:G:H2'	5:AN1:2124:G:C8	2.38	0.58
5:AN1:2109:U:O4	5:AN1:2163:U:O2'	2.20	0.58
12:H:5:LEU:HB2	12:H:16:GLY:HA2	1.85	0.58
20:P:64:ARG:NH1	20:P:100:MET:SD	2.76	0.58
34:d:87:ALA:O	34:d:91:ASN:ND2	2.36	0.58
5:AN1:2287:U:H2'	5:AN1:2288:G:C8	2.37	0.58
5:AN1:2769:U:OP1	8:D:172:ARG:NH1	2.37	0.58
31:sN1:657:G:H1	31:sN1:743:A:N6	2.00	0.58
33:c:39:VAL:HG21	33:c:95:MET:HE3	1.83	0.58
5:AN1:1911:3TD:N1	5:AN1:1938:C:O2	2.37	0.58
10:F:110:ARG:HD3	10:F:137:VAL:HB	1.85	0.58
31:sN1:1083:U:O4	31:sN1:1096:G:O6	2.21	0.58
14:J:66:LYS:HE2	14:J:81:ASP:HA	1.84	0.58
31:sN1:517:A:H62	31:sN1:526:G:N2	2.01	0.58
52:v:40:U:H2'	52:v:41:G:H8	1.68	0.58
40:j:56:HIS:CD2	40:j:57:VAL:HG13	2.38	0.58
21:Q:51:ALA:HB3	21:Q:52:PRO:HD3	1.86	0.58
15:K:89:GLY:O	15:K:120:ARG:NH2	2.37	0.58
5:AN1:168:A:H3'	5:AN1:169:U:H5''	1.85	0.57
5:AN1:510:U:H4'	5:AN1:1230:G:H4'	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:b:138:GLU:OE1	32:b:141:ARG:NH2	2.37	0.57
5:AN1:1041:A:O2'	5:AN1:1108:A:N6	2.37	0.57
5:AN1:167:A:N3	5:AN1:2204:C:O2'	2.37	0.57
43:m:16:VAL:O	43:m:20:THR:HG23	2.04	0.57
7:C:230:HIS:HD2	7:C:232:HIS:H	1.52	0.57
3:2:6:THR:HG22	3:2:62:PRO:HD2	1.86	0.57
34:d:10:LYS:HD2	34:d:39:PRO:HB3	1.87	0.57
7:C:159:GLY:O	7:C:177:ARG:NH2	2.38	0.57
10:F:38:MET:HE1	10:F:57:MET:HB2	1.86	0.57
31:sN1:333:G:H2'	31:sN1:334:A:H8	1.69	0.57
31:sN1:661:G:OP1	48:r:53:ARG:NH2	2.38	0.57
34:d:198:ASN:OD1	34:d:200:SER:OG	2.18	0.57
39:i:10:ARG:HG3	39:i:11:LYS:HG2	1.86	0.57
5:AN1:474:C:O2	5:AN1:478:A:N6	2.38	0.57
5:AN1:1111:C:H2'	5:AN1:1112:G:C8	2.38	0.57
5:AN1:1535:U:H2'	5:AN1:1536:A:C8	2.39	0.57
5:AN1:184:G:H3'	5:AN1:185:G:H8	1.70	0.57
6:B:12:U:OP2	6:B:68:C:O2'	2.22	0.56
25:U:76:VAL:HG12	25:U:97:ARG:HA	1.87	0.56
31:sN1:354:U:H2'	31:sN1:355:G:H8	1.70	0.56
5:AN1:1083:A:H1'	5:AN1:1100:A:H61	1.69	0.56
5:AN1:1432:C:HO2'	5:AN1:1512:G:HO2'	1.52	0.56
5:AN1:2242:G:H2'	5:AN1:2243:A:H8	1.70	0.56
52:v:55:5MU:O2'	52:v:56:PSU:O4'	2.20	0.56
5:AN1:1081:A:O3'	5:AN1:1102:U:O2'	2.24	0.56
5:AN1:1487:G:H5''	5:AN1:1488:C:H5''	1.88	0.56
32:b:45:LEU:HA	32:b:48:THR:HG22	1.86	0.56
33:c:78:GLY:O	33:c:80:LYS:NZ	2.35	0.56
34:d:36:ASN:HA	34:d:46:ARG:HH11	1.69	0.56
39:i:25:LYS:NZ	39:i:60:ASP:OD2	2.36	0.56
5:AN1:1587:U:H2'	5:AN1:1588:A:H8	1.70	0.56
29:Y:5:LYS:HB2	29:Y:57:GLU:HG2	1.87	0.56
50:t:43:ASP:HB3	50:t:46:VAL:HG22	1.87	0.56
5:AN1:35:A:N6	5:AN1:511:G:O2'	2.38	0.56
14:J:69:ILE:HD11	14:J:103:THR:HG21	1.87	0.56
31:sN1:397:C:O2'	31:sN1:618:A:N3	2.36	0.56
36:f:15:SER:O	36:f:19:VAL:HG23	2.04	0.56
10:F:138:PHE:O	10:F:140:GLU:N	2.39	0.56
16:L:112:ASP:O	16:L:116:GLU:HG3	2.06	0.56
5:AN1:1589:C:H2'	5:AN1:1590:A:H8	1.70	0.56
5:AN1:1844:A:H4'	5:AN1:1845:G:C8	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:L:51:ARG:HG3	16:L:66:ILE:HD11	1.88	0.56
31:sN1:550:A:H2'	31:sN1:551:A:H8	1.71	0.56
44:n:64:CYS:HB3	44:n:68:GLY:H	1.70	0.56
5:AN1:2324:A:H2'	5:AN1:2325:A:C8	2.41	0.56
17:M:79:LEU:HD12	17:M:83:LEU:HD12	1.86	0.56
5:AN1:31:G:O2'	22:R:78:GLU:O	2.24	0.55
5:AN1:86:C:H2'	5:AN1:87:G:H8	1.72	0.55
5:AN1:1462:G:N2	5:AN1:1520:A:N1	2.43	0.55
5:AN1:1662:A:H61	5:AN1:1992:C:H42	1.53	0.55
7:C:135:MET:O	7:C:167:ARG:NH1	2.36	0.55
33:c:36:ASP:OD2	33:c:59:ARG:NH1	2.37	0.55
40:j:42:MET:HB2	40:j:71:LYS:HB3	1.88	0.55
5:AN1:294:U:H3	5:AN1:350:G:H22	1.52	0.55
5:AN1:1713:U:O2	5:AN1:1739:G:N2	2.37	0.55
5:AN1:2387:G:O2'	5:AN1:2420:C:N4	2.36	0.55
10:F:127:ASN:HD22	10:F:157:THR:HA	1.71	0.55
10:F:78:LYS:HD3	52:v:57:C:H1'	1.88	0.55
31:sN1:9:A:H5'	35:e:123:LEU:HD11	1.89	0.55
31:sN1:72:G:N1	31:sN1:95:C:N3	2.40	0.55
31:sN1:1406:C:H2'	31:sN1:1407:A:C8	2.42	0.55
34:d:52:GLU:HA	34:d:55:LEU:HD12	1.89	0.55
5:AN1:719:A:H2'	5:AN1:720:A:H8	1.72	0.55
5:AN1:2577:G:N2	5:AN1:2577:G:OP2	2.40	0.55
31:sN1:518:G:O2'	31:sN1:533:C:O2'	2.22	0.55
35:e:156:ARG:NH1	38:h:43:GLU:OE2	2.39	0.55
5:AN1:597:A:H2'	5:AN1:598:G:H8	1.71	0.55
5:AN1:673:A:OP1	9:E:57:LYS:NZ	2.38	0.55
31:sN1:973:G:OP2	31:sN1:1355:U:O2'	2.24	0.55
31:sN1:1024:C:N4	31:sN1:1031:G:O6	2.40	0.55
31:sN1:1247:A:H2'	31:sN1:1248:A:C8	2.41	0.55
31:sN1:1410:A:H2	31:sN1:1484:G:H22	1.55	0.55
5:AN1:1042:U:H4'	5:AN1:1044:G:H1'	1.89	0.55
31:sN1:715:A:H5'	41:k:118:ASN:HD21	1.71	0.55
31:sN1:1078:G:OP2	35:e:51:LYS:NZ	2.37	0.55
15:K:80:ARG:HB2	15:K:83:GLU:HG3	1.88	0.55
23:S:33:VAL:HG21	23:S:42:ILE:HG12	1.89	0.55
12:H:30:LEU:HB3	12:H:36:ALA:HB3	1.89	0.55
31:sN1:1447:G:N2	31:sN1:1449:A:O2'	2.40	0.55
5:AN1:1425:G:H1	5:AN1:1561:U:H3	1.53	0.55
5:AN1:2242:G:H2'	5:AN1:2243:A:C8	2.42	0.55
5:AN1:2528:G:N2	5:AN1:2659:G:O2'	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:N:51:GLN:O	18:N:80:ARG:NH2	2.39	0.55
31:sN1:133:U:H2'	31:sN1:134:A:H8	1.71	0.55
31:sN1:649:U:O4	31:sN1:749:G:O2'	2.22	0.55
5:AN1:342:A:O2'	9:E:161:ARG:NH1	2.40	0.54
20:P:43:GLY:HA3	21:Q:75:ILE:HD12	1.89	0.54
30:Z:25:ASN:OD1	30:Z:38:ARG:NH2	2.36	0.54
6:B:16:A:H1'	6:B:65:G:N2	2.22	0.54
8:D:140:SER:OG	8:D:141:VAL:N	2.34	0.54
31:sN1:1284:A:H2	31:sN1:1350:G:H1'	1.71	0.54
5:AN1:1842:G:H2'	5:AN1:1843:A:C8	2.42	0.54
5:AN1:2639:G:H2'	5:AN1:2640:A:H8	1.71	0.54
24:T:93:VAL:HA	24:T:100:SER:HA	1.90	0.54
34:d:61:GLN:OE1	34:d:65:ARG:NH1	2.38	0.54
36:f:18:VAL:O	36:f:22:VAL:HG23	2.06	0.54
5:AN1:85:C:HO2'	5:AN1:86:C:H6	1.55	0.54
5:AN1:711:G:H8	5:AN1:716:A:H62	1.56	0.54
5:AN1:955:U:O2'	6:B:86:U:O4	2.18	0.54
5:AN1:2637:A:H5''	13:I:78:THR:HG21	1.90	0.54
12:H:55:GLU:HG3	12:H:56:LYS:HD3	1.88	0.54
31:sN1:143:G:H2'	31:sN1:144:G:C8	2.42	0.54
31:sN1:475:G:O2'	31:sN1:476:U:OP1	2.22	0.54
31:sN1:680:G:N2	41:k:38:GLY:O	2.41	0.54
31:sN1:1144:C:HO2'	39:i:5:TYR:HH	1.46	0.54
49:s:16:PHE:O	49:s:20:GLU:HG2	2.08	0.54
5:AN1:579:C:H2'	5:AN1:580:A:H8	1.73	0.54
5:AN1:876:A:H3'	5:AN1:877:G:H8	1.71	0.54
31:sN1:202:U:O2	31:sN1:208:G:O6	2.26	0.54
31:sN1:657:G:C2	31:sN1:743:A:C6	2.96	0.54
33:c:38:GLN:HB3	33:c:94:ILE:HD11	1.88	0.54
34:d:97:GLU:HA	34:d:102:ASN:HD22	1.72	0.54
36:f:66:CYS:SG	36:f:67:GLY:N	2.81	0.54
5:AN1:520:U:H2'	5:AN1:521:G:H8	1.72	0.54
5:AN1:719:A:H2'	5:AN1:720:A:C8	2.42	0.54
5:AN1:741:U:O2'	5:AN1:1657:U:OP1	2.25	0.54
11:G:22:ARG:HB3	11:G:23:GLN:NE2	2.23	0.54
31:sN1:1263:G:N2	31:sN1:1266:A:OP2	2.30	0.54
5:AN1:1311:A:H2'	5:AN1:1312:G:H8	1.72	0.54
14:J:14:SER:HA	14:J:51:ARG:HH21	1.72	0.54
31:sN1:1071:G:H1'	32:b:105:ASN:HD21	1.72	0.54
31:sN1:1381:C:H2'	31:sN1:1382:G:C8	2.43	0.54
32:b:79:SER:HB2	32:b:83:ARG:HH11	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:l:7:PRO:HB2	5:AN1:1304:G:H4'	1.90	0.54
5:AN1:552:U:H2'	5:AN1:553:G:O4'	2.07	0.54
6:B:108:C:O2'	6:B:109:G:OP1	2.26	0.54
31:sN1:1037:A:H2'	31:sN1:1038:G:C8	2.42	0.54
31:sN1:1344:G:O6	39:i:10:ARG:NH2	2.41	0.54
31:sN1:1461:U:H2'	31:sN1:1462:A:H8	1.73	0.54
5:AN1:12:A:H2'	5:AN1:13:A:H8	1.73	0.54
31:sN1:1323:U:H2'	31:sN1:1324:C:H6	1.73	0.54
41:k:12:THR:OG1	41:k:13:ARG:N	2.38	0.54
5:AN1:849:C:H2'	5:AN1:850:A:H8	1.72	0.54
10:F:136:ILE:HG13	10:F:138:PHE:HD1	1.73	0.54
31:sN1:969:C:OP2	40:j:59:LYS:NZ	2.40	0.54
5:AN1:570:A:OP2	21:Q:80:ARG:NH2	2.41	0.53
5:AN1:1902:G:O6	5:AN1:1914:A:N6	2.41	0.53
31:sN1:1147:U:O4	31:sN1:1148:A:N6	2.41	0.53
31:sN1:1267:U:H2'	31:sN1:1268:G:H8	1.72	0.53
43:m:39:ILE:HD12	43:m:56:ILE:HD11	1.90	0.53
5:AN1:579:C:H2'	5:AN1:580:A:C8	2.43	0.53
5:AN1:1920:C:H2'	5:AN1:1921:C:C6	2.43	0.53
19:O:4:LYS:O	19:O:9:GLN:NE2	2.42	0.53
31:sN1:720:U:H3'	31:sN1:721:G:H5''	1.90	0.53
48:r:39:ILE:HD11	48:r:59:ILE:HG21	1.91	0.53
5:AN1:527:A:H5'	13:I:113:PRO:HG3	1.89	0.53
5:AN1:1006:A:N3	5:AN1:1151:C:O2'	2.38	0.53
38:h:43:GLU:HG2	38:h:102:ILE:HD13	1.91	0.53
52:v:17:U:O5'	52:v:61:U:O2'	2.25	0.53
3:2:28:LYS:HA	3:2:32:LEU:HD11	1.90	0.53
31:sN1:934:A:O2'	31:sN1:935:A:H8	1.91	0.53
52:v:36:A:C6	53:w:3:G:C6	2.96	0.53
5:AN1:1054:A:N6	5:AN1:1084:G:OP2	2.41	0.53
14:J:93:PRO:HD2	14:J:113:LYS:HD2	1.89	0.53
31:sN1:96:U:O2'	31:sN1:97:A:N7	2.40	0.53
31:sN1:1144:C:O2'	39:i:5:TYR:OH	2.22	0.53
44:n:33:ASN:O	44:n:41:ARG:NH1	2.41	0.53
3:2:18:ALA:HB2	5:AN1:626:G:H5'	1.90	0.53
5:AN1:93:G:O2'	5:AN1:111:U:O2'	2.23	0.53
5:AN1:2254:C:O2'	5:AN1:2423:C:OP2	2.26	0.53
12:H:48:GLU:O	12:H:52:ALA:HB3	2.09	0.53
31:sN1:200:G:H3'	31:sN1:201:A:H8	1.73	0.53
5:AN1:323:U:O3'	9:E:161:ARG:NH1	2.41	0.53
5:AN1:877:G:H2'	5:AN1:878:G:H8	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:1310:C:H2'	5:AN1:1311:A:H8	1.73	0.53
5:AN1:2111:G:H4'	5:AN1:2113:A:H62	1.73	0.53
5:AN1:1025:A:H2'	5:AN1:1026:A:C8	2.44	0.53
5:AN1:1065:G:N2	5:AN1:1092:A:O2'	2.41	0.53
5:AN1:1080:U:O2'	5:AN1:1082:A:N7	2.37	0.53
31:sN1:74:G:H2'	31:sN1:75:A:C8	2.43	0.53
31:sN1:1252:G:O2'	31:sN1:1255:G:N3	2.36	0.53
51:u:41:PRO:HA	51:u:44:GLU:HG2	1.91	0.53
31:sN1:1299:C:OP1	43:m:13:LYS:NZ	2.35	0.53
32:b:75:LYS:HB2	32:b:78:ALA:HB3	1.91	0.53
43:m:90:ARG:HB2	43:m:97:VAL:HG22	1.90	0.53
52:v:8:4SU:H5	52:v:14:A:N7	2.24	0.53
5:AN1:909:A:H8	5:AN1:2273:G:H21	1.56	0.53
39:i:25:LYS:N	39:i:60:ASP:OD1	2.39	0.53
5:AN1:1103:A:N6	5:AN1:1104:G:O6	2.43	0.52
16:L:137:MET:O	25:U:83:ARG:NH1	2.43	0.52
31:sN1:1083:U:O2	31:sN1:1096:G:N2	2.33	0.52
5:AN1:1467:G:O6	5:AN1:1468:A:N6	2.43	0.52
5:AN1:1589:C:H2'	5:AN1:1590:A:C8	2.45	0.52
8:D:15:ILE:HG23	19:O:15:GLN:HE22	1.74	0.52
9:E:183:ASP:OD1	9:E:183:ASP:N	2.40	0.52
13:I:20:ALA:HA	13:I:23:LYS:HD2	1.91	0.52
31:sN1:333:G:H2'	31:sN1:334:A:C8	2.43	0.52
31:sN1:89:C:O2'	31:sN1:90:C:OP2	2.27	0.52
31:sN1:1069:G:H2'	31:sN1:1070:U:C6	2.45	0.52
15:K:84:LEU:O	15:K:87:VAL:HG12	2.09	0.52
15:K:111:ARG:HG2	15:K:128:ALA:HB3	1.90	0.52
15:K:134:LYS:O	15:K:138:GLU:HG2	2.10	0.52
5:AN1:627:A:N3	5:AN1:637:U:O2'	2.42	0.52
5:AN1:877:G:H2'	5:AN1:878:G:C8	2.44	0.52
14:J:108:THR:HG22	14:J:110:GLN:H	1.74	0.52
31:sN1:449:G:H1	31:sN1:476:U:H3	1.56	0.52
52:v:29:C:H2'	52:v:30:G:C8	2.45	0.52
5:AN1:575:G:O2'	5:AN1:1249:A:OP1	2.28	0.52
5:AN1:862:G:H2'	5:AN1:863:C:C6	2.45	0.52
5:AN1:876:A:H3'	5:AN1:877:G:C8	2.45	0.52
5:AN1:1004:C:OP1	13:I:37:ARG:NH1	2.41	0.52
5:AN1:2587:C:H2'	5:AN1:2588:G:H8	1.74	0.52
15:K:112:ILE:HB	15:K:129:LEU:HD23	1.92	0.52
31:sN1:481:G:H4'	31:sN1:482:U:H3'	1.91	0.52
5:AN1:1359:G:N7	27:W:2:SER:N	2.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:1430:G:H2'	5:AN1:1431:G:C8	2.44	0.52
5:AN1:2093:U:H2'	5:AN1:2094:U:C6	2.44	0.52
10:F:99:PHE:HD1	10:F:102:ARG:HH11	1.58	0.52
31:sN1:91:G:H2'	31:sN1:92:G:H8	1.73	0.52
31:sN1:888:U:H2'	31:sN1:889:A:H8	1.75	0.52
37:g:60:GLU:O	37:g:64:THR:HG23	2.09	0.52
5:AN1:1040:C:O2	5:AN1:1109:G:N2	2.43	0.52
5:AN1:1412:C:H3'	5:AN1:1413:G:H8	1.75	0.52
5:AN1:2125:C:H2'	5:AN1:2155:G:H22	1.74	0.52
11:G:54:PRO:HB3	11:G:61:ALA:HB1	1.90	0.52
21:Q:62:GLU:HG3	21:Q:97:LYS:HB3	1.92	0.52
31:sN1:1294:G:N2	37:g:114:LYS:O	2.43	0.52
31:sN1:1409:C:H2'	31:sN1:1410:A:C8	2.44	0.52
41:k:19:VAL:HG12	41:k:82:ASP:HB2	1.91	0.52
52:v:68:A:H2'	52:v:69:U:C6	2.45	0.52
5:AN1:184:G:OP2	5:AN1:184:G:N2	2.25	0.52
5:AN1:718:U:O2'	5:AN1:719:A:H8	1.92	0.52
5:AN1:1273:C:H2'	5:AN1:1274:G:H8	1.75	0.52
5:AN1:2225:U:H2'	5:AN1:2226:G:H8	1.74	0.52
5:AN1:2694:U:H2'	5:AN1:2695:G:C8	2.44	0.52
18:N:69:ALA:HA	18:N:72:LYS:HE3	1.91	0.52
19:O:29:VAL:HG12	19:O:89:VAL:HA	1.92	0.52
36:f:18:VAL:HA	36:f:21:MET:HB2	1.92	0.52
5:AN1:2095:U:H2'	5:AN1:2096:G:H8	1.74	0.52
10:F:17:GLN:NE2	10:F:22:ILE:O	2.43	0.52
31:sN1:763:A:OP2	31:sN1:809:G:N2	2.43	0.52
5:AN1:1430:G:H2'	5:AN1:1431:G:H8	1.75	0.51
5:AN1:2639:G:H2'	5:AN1:2640:A:C8	2.45	0.51
35:e:71:ILE:HD12	35:e:144:ARG:HB3	1.92	0.51
41:k:19:VAL:N	41:k:34:THR:O	2.43	0.51
5:AN1:1310:C:O2'	5:AN1:1387:A:N3	2.39	0.51
5:AN1:2063:G:H1	5:AN1:2439:U:H3	1.58	0.51
5:AN1:2373:A:O2'	18:N:116:PHE:OXT	2.23	0.51
13:I:26:GLY:O	13:I:30:THR:HG23	2.10	0.51
37:g:27:MET:HG2	37:g:43:VAL:HG21	1.92	0.51
5:AN1:1053:G:H21	5:AN1:1101:C:H41	1.58	0.51
9:E:134:LEU:O	9:E:138:ASN:ND2	2.43	0.51
5:AN1:107:U:OP1	5:AN1:108:U:O2'	2.19	0.51
5:AN1:1348:A:H2'	5:AN1:1349:A:H8	1.75	0.51
5:AN1:2830:G:H2'	5:AN1:2875:A:H61	1.74	0.51
27:W:62:LEU:HD12	27:W:66:LYS:HD3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:b:116:LEU:HD12	32:b:146:LEU:HB3	1.91	0.51
5:AN1:1506:U:H2'	5:AN1:1507:G:H8	1.75	0.51
5:AN1:2287:U:H2'	5:AN1:2288:G:H8	1.76	0.51
32:b:138:GLU:O	32:b:142:GLU:HG2	2.10	0.51
52:v:15:G:O6	52:v:49:C:O2	2.28	0.51
5:AN1:636:G:H2'	5:AN1:637:U:C6	2.46	0.51
5:AN1:1427:G:H2'	5:AN1:1428:A:C8	2.46	0.51
31:sN1:80:A:H2'	31:sN1:81:G:C8	2.46	0.51
31:sN1:710:G:H2'	31:sN1:711:G:H8	1.76	0.51
31:sN1:1081:G:H1'	31:sN1:1100:C:H41	1.75	0.51
34:d:28:PHE:O	34:d:32:THR:HG22	2.10	0.51
5:AN1:1442:C:O2'	5:AN1:1542:A:N3	2.42	0.51
5:AN1:1462:G:H1	5:AN1:1520:A:H61	0.65	0.51
5:AN1:2067:A:H2'	5:AN1:2068:C:C6	2.46	0.51
6:B:26:C:H2'	6:B:27:A:C8	2.46	0.51
31:sN1:155:G:N2	31:sN1:158:A:OP2	2.43	0.51
31:sN1:191:A:N3	31:sN1:218:U:O2'	2.38	0.51
31:sN1:475:G:HO2'	31:sN1:476:U:P	2.31	0.51
41:k:16:SER:O	41:k:16:SER:OG	2.26	0.51
5:AN1:413:C:H2'	5:AN1:414:A:C8	2.46	0.51
5:AN1:837:U:H3	5:AN1:936:G:H1	1.59	0.51
5:AN1:2026:6MZ:H2	5:AN1:2495:C:H5''	1.92	0.51
18:N:19:ILE:HG21	18:N:26:ARG:HB3	1.93	0.51
31:sN1:576:G:O2'	45:o:54:ARG:NH1	2.37	0.51
31:sN1:693:A:OP1	41:k:52:ARG:NH2	2.44	0.51
41:k:18:GLY:HA2	41:k:35:ASP:HA	1.92	0.51
42:l:54:ARG:HD2	42:l:62:GLU:HG2	1.92	0.51
5:AN1:109:G:H4'	5:AN1:110:A:H5'	1.93	0.51
5:AN1:879:G:N2	5:AN1:893:U:O2'	2.35	0.51
5:AN1:1524:A:H62	5:AN1:1539:G:H21	1.58	0.51
5:AN1:2894:U:O2'	13:I:134:ALA:O	2.29	0.51
31:sN1:1087:U:O2'	31:sN1:1167:A:O2'	2.27	0.51
5:AN1:493:G:H21	22:R:57:ASN:HD21	1.59	0.51
5:AN1:878:G:H2'	5:AN1:879:G:C8	2.44	0.51
6:B:6:C:O3'	18:N:26:ARG:NH2	2.41	0.51
31:sN1:733:C:H2'	31:sN1:734:A:C8	2.46	0.51
31:sN1:1483:G:H2'	31:sN1:1484:G:C8	2.45	0.51
34:d:24:GLY:HA3	34:d:163:LEU:HD23	1.93	0.51
34:d:103:VAL:HG21	34:d:139:VAL:HG21	1.92	0.51
37:g:113:GLU:HG3	37:g:114:LYS:H	1.76	0.51
1:0:22:ASN:ND2	5:AN1:2281:C:OP1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:2448:C:H2'	5:AN1:2449:A:H8	1.76	0.50
11:G:107:LEU:HB3	11:G:152:ARG:HD3	1.92	0.50
31:sN1:991:A:H8	31:sN1:994:U:C2	2.30	0.50
41:k:51:PHE:HD2	41:k:55:ARG:HB3	1.76	0.50
44:n:2:ALA:N	44:n:67:THR:O	2.44	0.50
5:AN1:67:G:O2'	5:AN1:68:A:O5'	2.27	0.50
5:AN1:2892:C:H2'	5:AN1:2893:U:C6	2.47	0.50
31:sN1:1086:G:N2	31:sN1:1167:A:O5'	2.44	0.50
33:c:50:ALA:O	33:c:70:THR:OG1	2.29	0.50
1:O:2:ARG:NE	5:AN1:2281:C:OP2	2.32	0.50
7:C:199:GLU:HG3	7:C:202:LEU:HD12	1.93	0.50
11:G:23:GLN:HA	11:G:36:ASN:HA	1.94	0.50
20:P:86:ALA:HB2	20:P:116:ALA:HB2	1.93	0.50
31:sN1:250:G:O6	31:sN1:269:A:N6	2.45	0.50
31:sN1:631:C:H2'	31:sN1:632:A:H8	1.75	0.50
37:g:93:PRO:HA	37:g:96:ARG:HD3	1.94	0.50
43:m:4:ILE:HG23	43:m:57:ARG:HG3	1.93	0.50
5:AN1:1567:A:OP1	7:C:61:HIS:NE2	2.38	0.50
5:AN1:2563:G:H2'	5:AN1:2564:A:C8	2.47	0.50
5:AN1:665:U:H2'	5:AN1:666:A:O4'	2.11	0.50
5:AN1:1478:G:H2'	5:AN1:1479:U:C6	2.46	0.50
5:AN1:1523:A:N7	5:AN1:1539:G:N2	2.59	0.50
5:AN1:2468:G:N2	5:AN1:2471:C:OP2	2.45	0.50
5:AN1:628:G:N2	5:AN1:631:A:OP2	2.33	0.50
5:AN1:875:U:H2'	5:AN1:876:A:H8	1.77	0.50
5:AN1:2315:U:H2'	5:AN1:2317:G:H1	1.75	0.50
5:AN1:2591:G:N2	5:AN1:2594:A:OP2	2.33	0.50
5:AN1:2849:C:H2'	5:AN1:2850:A:H8	1.77	0.50
7:C:24:LEU:HD13	7:C:83:TYR:HB2	1.93	0.50
31:sN1:588:U:H2'	31:sN1:589:A:H8	1.74	0.50
31:sN1:712:A:H2'	31:sN1:713:A:C8	2.47	0.50
32:b:95:ASP:OD1	32:b:96:HIS:N	2.44	0.50
5:AN1:696:C:O2'	5:AN1:732:A:N6	2.44	0.50
5:AN1:720:A:H2'	5:AN1:721:C:C6	2.47	0.50
5:AN1:1373:A:O2'	5:AN1:1375:G:OP2	2.29	0.50
13:I:21:THR:HG23	13:I:61:GLN:HG2	1.92	0.50
15:K:75:LYS:HB3	15:K:108:ILE:HG12	1.94	0.50
31:sN1:552:U:H2'	31:sN1:553:C:C6	2.46	0.50
31:sN1:720:U:O4'	51:u:49:LYS:HE3	2.11	0.50
31:sN1:1320:G:H2'	31:sN1:1321:A:C8	2.46	0.50
33:c:111:LEU:O	33:c:204:ARG:NH2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:k:67:GLU:O	41:k:71:LYS:HG2	2.12	0.50
51:u:40:LYS:N	51:u:41:PRO:HD2	2.27	0.50
31:sN1:535:G:H2'	31:sN1:536:A:C8	2.46	0.50
34:d:116:ALA:O	34:d:120:VAL:HG23	2.12	0.50
39:i:89:ASP:N	39:i:89:ASP:OD1	2.44	0.50
5:AN1:413:C:H2'	5:AN1:414:A:H8	1.76	0.49
5:AN1:1095:A:H2'	5:AN1:1096:G:H8	1.77	0.49
6:B:38:U:N3	6:B:42:G:OP2	2.43	0.49
25:U:36:GLY:HA3	25:U:97:ARG:HB2	1.94	0.49
32:b:159:LEU:HD13	32:b:181:LEU:HD21	1.94	0.49
5:AN1:34:G:H22	5:AN1:511:G:H2'	1.77	0.49
5:AN1:887:C:H3'	5:AN1:888:C:H5''	1.92	0.49
5:AN1:1199:A:H4'	5:AN1:1200:A:H5'	1.92	0.49
5:AN1:2472:A:H61	5:AN1:2525:G:H2'	1.77	0.49
11:G:19:GLN:HG3	11:G:21:GLY:H	1.76	0.49
31:sN1:476:U:H2'	31:sN1:477:G:C8	2.48	0.49
31:sN1:1475:C:H2'	31:sN1:1476:G:H8	1.76	0.49
33:c:120:ILE:HA	33:c:123:GLN:HE21	1.76	0.49
5:AN1:1846:G:H2'	5:AN1:1847:U:C6	2.47	0.49
21:Q:59:VAL:HG22	21:Q:101:ILE:HG23	1.94	0.49
40:j:85:ASP:O	40:j:89:LYS:HG3	2.12	0.49
41:k:17:GLU:HA	41:k:80:ASN:HB2	1.95	0.49
5:AN1:2533:U:H2'	5:AN1:2534:C:H6	1.76	0.49
26:V:11:LYS:O	26:V:14:ARG:NH1	2.45	0.49
31:sN1:260:A:O2'	47:q:67:PRO:O	2.28	0.49
31:sN1:998:A:N1	31:sN1:1037:A:N6	2.59	0.49
52:v:42:C:H2'	52:v:43:G:C8	2.48	0.49
5:AN1:2212:G:H2'	5:AN1:2213:G:H8	1.78	0.49
5:AN1:2311:C:O2'	5:AN1:2312:G:H8	1.95	0.49
6:B:55:A:O2'	10:F:27:GLU:OE2	2.26	0.49
9:E:97:ARG:HD3	9:E:101:ARG:HH21	1.76	0.49
31:sN1:571:A:HO2'	31:sN1:879:C:HO2'	1.58	0.49
31:sN1:990:G:N7	31:sN1:1210:A:N6	2.60	0.49
33:c:114:ARG:HH11	33:c:187:MET:HE1	1.77	0.49
47:q:32:HIS:HD2	47:q:35:TYR:H	1.59	0.49
52:v:1:G:H2'	52:v:2:G:H8	1.77	0.49
5:AN1:879:G:H2'	5:AN1:880:G:C8	2.46	0.49
5:AN1:879:G:C6	5:AN1:893:U:O2	2.65	0.49
5:AN1:1798:A:H2'	5:AN1:1799:A:C8	2.48	0.49
6:B:12:U:O3'	6:B:104:U:O2'	2.31	0.49
28:X:18:LEU:HB2	28:X:53:ILE:HG21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:sN1:414:C:H2'	31:sN1:415:C:C6	2.47	0.49
34:d:62:LYS:O	34:d:66:ILE:HG13	2.12	0.49
5:AN1:2092:C:H42	5:AN1:2189:G:H1	1.58	0.49
12:H:38:ALA:O	12:H:43:ASN:ND2	2.43	0.49
31:sN1:1145:U:H4'	39:i:14:THR:HG21	1.95	0.49
31:sN1:1285:A:N3	31:sN1:1349:C:O2'	2.38	0.49
31:sN1:1464:C:H2'	31:sN1:1465:A:C8	2.48	0.49
52:v:8:4SU:H1'	52:v:22:A:N1	2.27	0.49
6:B:27:A:H2'	6:B:28:C:C6	2.48	0.49
31:sN1:659:G:H2'	31:sN1:660:A:C8	2.48	0.49
5:AN1:1075:C:O2'	5:AN1:1085:A:OP1	2.29	0.49
7:C:20:VAL:HG23	7:C:21:HIS:H	1.78	0.49
31:sN1:252:U:H2'	31:sN1:253:G:C8	2.47	0.49
31:sN1:671:G:H2'	31:sN1:672:A:C8	2.44	0.49
5:AN1:2200:G:OP2	7:C:147:LYS:NZ	2.40	0.48
31:sN1:249:U:H2'	31:sN1:250:G:C8	2.48	0.48
5:AN1:1743:A:H2'	5:AN1:1744:C:C6	2.48	0.48
5:AN1:2096:G:O6	5:AN1:2185:U:O4	2.32	0.48
6:B:68:C:H2'	6:B:69:U:H6	1.78	0.48
40:j:7:ARG:HB3	40:j:101:ALA:HB3	1.95	0.48
41:k:64:VAL:O	41:k:68:VAL:HG23	2.13	0.48
46:p:22:ILE:HG12	46:p:39:VAL:HG22	1.94	0.48
5:AN1:90:G:O2'	5:AN1:109:G:N2	2.45	0.48
5:AN1:889:G:O2'	5:AN1:890:A:N7	2.41	0.48
5:AN1:1421:G:OP2	5:AN1:1422:A:O2'	2.29	0.48
5:AN1:2229:U:H2'	5:AN1:2230:G:C8	2.48	0.48
40:j:80:THR:O	40:j:83:THR:OG1	2.29	0.48
42:l:34:CYS:O	42:l:77:HIS:N	2.45	0.48
5:AN1:1878:U:H2'	5:AN1:1879:U:C6	2.48	0.48
5:AN1:1879:U:H2'	5:AN1:1880:G:O4'	2.13	0.48
5:AN1:2114:U:H3	5:AN1:2140:G:H1'	1.77	0.48
11:G:109:TYR:OH	11:G:152:ARG:NH1	2.46	0.48
19:O:86:LYS:NZ	19:O:87:ILE:H	2.11	0.48
31:sN1:1311:C:H2'	31:sN1:1312:U:C6	2.48	0.48
5:AN1:1962:A:N3	5:AN1:2588:G:O2'	2.41	0.48
31:sN1:588:U:H2'	31:sN1:589:A:C8	2.49	0.48
5:AN1:1506:U:H2'	5:AN1:1507:G:C8	2.48	0.48
5:AN1:2147:C:O2	5:AN1:2148:C:N4	2.46	0.48
7:C:133:ARG:HB3	7:C:186:VAL:HG22	1.96	0.48
11:G:86:LYS:HG3	11:G:165:SER:OG	2.14	0.48
31:sN1:58:U:H2'	31:sN1:59:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:sN1:1068:C:H2'	31:sN1:1069:G:H8	1.78	0.48
34:d:119:LEU:O	34:d:124:SER:OG	2.30	0.48
34:d:154:GLN:HE21	34:d:157:ILE:HG13	1.78	0.48
5:AN1:462:G:N2	5:AN1:465:A:OP2	2.29	0.48
5:AN1:2088:U:H5''	12:H:24:GLY:HA3	1.95	0.48
10:F:29:PRO:HB2	10:F:169:LEU:HD12	1.95	0.48
31:sN1:472:A:H2'	31:sN1:473:U:C6	2.49	0.48
5:AN1:2093:U:H2'	5:AN1:2094:U:H6	1.79	0.48
5:AN1:2196:C:OP2	27:W:37:ARG:NH2	2.46	0.48
31:sN1:1411:U:H2'	31:sN1:1412:G:H8	1.78	0.48
40:j:3:ASN:CG	40:j:4:GLN:H	2.21	0.48
40:j:22:ALA:O	40:j:26:VAL:HG23	2.13	0.48
43:m:16:VAL:HG13	43:m:17:ILE:HD12	1.95	0.48
52:v:29:C:H2'	52:v:30:G:H8	1.77	0.48
52:v:53:A:H2'	52:v:54:G:C8	2.48	0.48
5:AN1:1591:C:H2'	5:AN1:1592:A:C8	2.49	0.48
5:AN1:1683:C:H2'	5:AN1:1684:C:H6	1.79	0.48
5:AN1:2543:A:H2'	5:AN1:2544:U:C6	2.49	0.48
31:sN1:73:G:H2'	31:sN1:74:G:C8	2.49	0.48
31:sN1:251:G:H2'	31:sN1:252:U:C6	2.49	0.48
31:sN1:1080:U:O2'	31:sN1:1099:A:OP2	2.32	0.48
34:d:123:ARG:HG2	34:d:133:ASN:HB3	1.94	0.48
47:q:69:SER:OG	47:q:70:LYS:N	2.46	0.48
52:v:12:U:O2	52:v:25:G:N2	2.42	0.48
5:AN1:70:A:H61	5:AN1:98:A:N6	2.12	0.48
5:AN1:671:C:OP1	9:E:48:ARG:NH2	2.45	0.48
5:AN1:1276:G:H2'	5:AN1:1277:U:C6	2.49	0.48
5:AN1:2323:A:H2'	5:AN1:2324:A:C8	2.48	0.48
10:F:30:ARG:H	10:F:159:THR:HG22	1.78	0.48
13:I:34:ARG:HH22	13:I:40:HIS:HB3	1.79	0.48
25:U:94:ASP:OD1	25:U:94:ASP:N	2.46	0.48
31:sN1:198:G:H2'	31:sN1:199:G:C8	2.48	0.48
31:sN1:928:C:O2	31:sN1:1384:G:N1	2.47	0.48
31:sN1:1112:U:H3	31:sN1:1182:G:H1	1.61	0.48
37:g:36:LYS:O	37:g:40:GLU:HG3	2.13	0.48
52:v:28:C:H2'	52:v:29:C:C6	2.49	0.48
5:AN1:71:G:N7	58:AN1:3141:HOH:O	2.35	0.47
5:AN1:2119:G:H1'	5:AN1:2172:A:C2	2.49	0.47
5:AN1:2533:U:H2'	5:AN1:2534:C:C6	2.49	0.47
31:sN1:246:A:H4'	31:sN1:247:G:H5'	1.96	0.47
31:sN1:971:A:OP1	44:n:69:ARG:NH2	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:sN1:1020:G:H2'	31:sN1:1021:G:C8	2.49	0.47
7:C:230:HIS:CD2	7:C:232:HIS:H	2.31	0.47
31:sN1:386:U:H2'	31:sN1:387:C:C6	2.49	0.47
31:sN1:498:C:H2'	31:sN1:499:A:H8	1.79	0.47
5:AN1:158:U:H2'	5:AN1:159:G:H8	1.79	0.47
5:AN1:1025:A:H2'	5:AN1:1026:A:H8	1.79	0.47
5:AN1:1794:U:OP2	7:C:273:VAL:HG21	2.14	0.47
16:L:2:LEU:HB2	16:L:70:PRO:HD2	1.94	0.47
25:U:8:ALA:HB1	25:U:44:VAL:HB	1.95	0.47
27:W:38:PHE:HE2	27:W:51:LEU:HD21	1.78	0.47
31:sN1:943:A:H2'	31:sN1:944:G:C8	2.48	0.47
41:k:21:HIS:CE1	41:k:84:LEU:HD12	2.49	0.47
41:k:78:LEU:HB3	41:k:104:TYR:HE1	1.80	0.47
4:3:3:VAL:HG22	4:3:36:ARG:HD2	1.96	0.47
4:3:30:GLU:HB2	4:3:33:HIS:ND1	2.30	0.47
5:AN1:86:C:H2'	5:AN1:87:G:C8	2.49	0.47
5:AN1:587:U:H2'	5:AN1:588:A:C8	2.47	0.47
5:AN1:1912:A:OP1	5:AN1:1959:U:O2'	2.24	0.47
5:AN1:2049:G:H5'	8:D:152:ASN:O	2.14	0.47
5:AN1:2526:A:N7	11:G:172:LYS:NZ	2.63	0.47
9:E:54:GLY:HA2	9:E:72:ILE:HG12	1.97	0.47
31:sN1:998:A:H2'	31:sN1:999:G:C8	2.49	0.47
31:sN1:1405:A:H61	31:sN1:1489:A:H61	1.60	0.47
43:m:25:ILE:HG23	43:m:29:THR:HG23	1.96	0.47
47:q:50:GLU:CD	47:q:50:GLU:H	2.22	0.47
3:2:32:LEU:HD23	3:2:35:LYS:HZ3	1.80	0.47
5:AN1:636:G:H2'	5:AN1:637:U:H6	1.80	0.47
5:AN1:1311:A:H2'	5:AN1:1312:G:C8	2.50	0.47
5:AN1:2483:G:H2'	5:AN1:2484:G:H8	1.78	0.47
5:AN1:2811:C:H1'	30:Z:39:ARG:HH21	1.80	0.47
17:M:28:LEU:HD21	17:M:95:LEU:HD21	1.97	0.47
31:sN1:498:C:H2'	31:sN1:499:A:C8	2.49	0.47
31:sN1:754:U:H2'	31:sN1:755:G:O4'	2.15	0.47
31:sN1:941:G:N1	31:sN1:1335:G:OP2	2.38	0.47
31:sN1:1269:U:H2'	31:sN1:1270:G:C8	2.49	0.47
31:sN1:1327:U:H4'	43:m:23:PHE:CE2	2.50	0.47
41:k:36:ARG:NH2	41:k:82:ASP:OD2	2.47	0.47
52:v:54:G:N1	52:v:55:5MU:O4	2.48	0.47
5:AN1:278:U:H3	5:AN1:366:G:H22	1.63	0.47
5:AN1:372:U:H2'	5:AN1:373:A:H8	1.80	0.47
5:AN1:720:A:H2'	5:AN1:721:C:H6	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:816:G:N1	5:AN1:1183:U:OP2	2.35	0.47
5:AN1:1356:G:H2'	5:AN1:1357:C:H6	1.79	0.47
5:AN1:1382:U:H5'	5:AN1:1464:A:H1'	1.97	0.47
5:AN1:1767:C:H2'	5:AN1:1768:A:H8	1.80	0.47
5:AN1:1862:A:H2'	5:AN1:1863:G:C8	2.50	0.47
7:C:111:ARG:HE	7:C:112:ALA:H	1.63	0.47
21:Q:46:ASN:HD21	21:Q:48:GLN:HG3	1.80	0.47
31:sN1:157:A:H2'	31:sN1:158:A:C8	2.50	0.47
31:sN1:249:U:H2'	31:sN1:250:G:H8	1.77	0.47
32:b:53:ASN:O	32:b:57:ASN:ND2	2.48	0.47
32:b:65:LYS:HB2	32:b:67:ASN:ND2	2.29	0.47
35:e:14:LEU:HD21	35:e:17:VAL:HG23	1.97	0.47
35:e:131:ASN:HD22	35:e:134:ASN:H	1.62	0.47
38:h:2:SER:OG	38:h:3:MET:N	2.47	0.47
52:v:68:A:H2'	52:v:69:U:H6	1.78	0.47
5:AN1:698:G:O2'	5:AN1:1630:A:N3	2.44	0.47
5:AN1:2169:A:H2'	5:AN1:2170:C:C5	2.50	0.47
6:B:26:C:H2'	6:B:27:A:H8	1.79	0.47
5:AN1:2107:U:O4'	5:AN1:2114:U:O2'	2.33	0.47
5:AN1:2229:U:H2'	5:AN1:2230:G:H8	1.80	0.47
5:AN1:2324:A:H2'	5:AN1:2325:A:H8	1.80	0.47
9:E:24:GLU:OE2	15:K:9:ALA:N	2.40	0.47
14:J:47:ILE:HG23	14:J:50:ALA:HB2	1.97	0.47
31:sN1:1379:C:H1'	37:g:79:ARG:HH22	1.80	0.47
36:f:70:THR:O	36:f:73:GLU:HG2	2.14	0.47
37:g:121:ALA:O	37:g:125:LEU:HG	2.15	0.47
2:l:1:MET:N	5:AN1:1617:G:H21	2.13	0.47
5:AN1:1521:G:H2'	5:AN1:1522:C:C6	2.49	0.47
31:sN1:232:A:H2'	31:sN1:233:A:C8	2.50	0.47
31:sN1:424:G:H5''	34:d:10:LYS:HE3	1.95	0.47
31:sN1:1017:A:H2'	31:sN1:1018:U:C6	2.50	0.47
33:c:73:PRO:O	33:c:77:ILE:HG12	2.14	0.47
5:AN1:805:U:OP2	15:K:43:ARG:NH2	2.46	0.46
5:AN1:2694:U:H2'	5:AN1:2695:G:H8	1.81	0.46
31:sN1:80:A:N1	31:sN1:88:A:H1'	2.30	0.46
31:sN1:1269:U:H2'	31:sN1:1270:G:H8	1.79	0.46
36:f:26:ILE:HG22	36:f:30:LYS:HG2	1.96	0.46
47:q:60:VAL:HG12	47:q:79:VAL:HG22	1.96	0.46
52:v:42:C:O2'	52:v:43:G:OP1	2.31	0.46
33:c:123:GLN:OE1	33:c:136:ARG:NH1	2.48	0.46
35:e:40:ASP:HB3	35:e:44:ARG:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:v:24:A:H2'	52:v:25:G:C8	2.50	0.46
5:AN1:849:C:H2'	5:AN1:850:A:C8	2.49	0.46
5:AN1:1356:G:H2'	5:AN1:1357:C:C6	2.50	0.46
5:AN1:2055:A:H2'	5:AN1:2499:2MA:HM23	1.98	0.46
5:AN1:2843:U:H2'	5:AN1:2844:G:O4'	2.15	0.46
11:G:76:VAL:HA	11:G:79:VAL:HG12	1.97	0.46
31:sN1:250:G:O2'	47:q:19:ASP:O	2.33	0.46
31:sN1:305:C:H2'	31:sN1:306:G:H8	1.79	0.46
32:b:37:ARG:HG3	32:b:38:ASN:N	2.30	0.46
45:o:4:THR:OG1	45:o:5:ASN:N	2.49	0.46
5:AN1:1602:C:O2'	5:AN1:1608:A:N1	2.44	0.46
5:AN1:2060:C:H2'	5:AN1:2061:C:C6	2.50	0.46
5:AN1:2072:U:OP2	5:AN1:2234:G:N2	2.40	0.46
5:AN1:2787:A:O2'	5:AN1:2788:G:H8	1.98	0.46
6:B:61:C:H2'	6:B:62:U:C6	2.50	0.46
7:C:98:ASP:N	7:C:98:ASP:OD2	2.44	0.46
14:J:7:MET:HE1	14:J:44:LYS:HG3	1.97	0.46
17:M:72:ASN:ND2	17:M:75:THR:OG1	2.49	0.46
31:sN1:657:G:C2	31:sN1:743:A:N1	2.83	0.46
31:sN1:934:A:O2'	31:sN1:935:A:O5'	2.32	0.46
31:sN1:1325:C:C2	31:sN1:1326:A:C8	3.03	0.46
2:1:1:MET:H2	5:AN1:1617:G:H21	1.63	0.46
5:AN1:582:C:N4	5:AN1:583:G:O6	2.49	0.46
5:AN1:605:U:H2'	5:AN1:606:A:H8	1.81	0.46
5:AN1:970:A:H5'	5:AN1:1183:U:H1'	1.97	0.46
5:AN1:2469:U:O2'	5:AN1:2471:C:OP2	2.24	0.46
10:F:34:ILE:HD12	10:F:96:MET:HB2	1.98	0.46
10:F:140:GLU:HG2	10:F:141:ILE:N	2.31	0.46
15:K:104:ARG:NH1	15:K:106:ASP:OD1	2.49	0.46
22:R:55:ILE:O	22:R:59:GLU:HG2	2.15	0.46
31:sN1:23:G:H2'	31:sN1:24:G:H8	1.80	0.46
31:sN1:553:C:H2'	31:sN1:554:G:C8	2.50	0.46
31:sN1:1004:U:H2'	31:sN1:1005:U:C6	2.50	0.46
5:AN1:596:U:H2'	5:AN1:597:A:C8	2.51	0.46
10:F:4:LEU:HD13	10:F:173:PHE:HD2	1.81	0.46
15:K:37:ILE:HG22	15:K:38:LYS:H	1.80	0.46
19:O:21:PRO:HD3	19:O:86:LYS:HZ1	1.81	0.46
31:sN1:199:G:HO2'	31:sN1:200:G:H8	1.64	0.46
31:sN1:692:A:H2'	31:sN1:693:A:C8	2.51	0.46
31:sN1:933:C:C4	31:sN1:934:A:N7	2.84	0.46
31:sN1:1478:U:H2'	31:sN1:1479:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:c:40:ARG:O	33:c:44:THR:HG23	2.16	0.46
52:v:40:U:H2'	52:v:41:G:C8	2.48	0.46
3:2:30:HIS:O	3:2:32:LEU:HG	2.16	0.46
3:2:30:HIS:C	3:2:32:LEU:H	2.20	0.46
5:AN1:529:G:N7	58:AN1:3143:HOH:O	2.36	0.46
5:AN1:597:A:H2'	5:AN1:598:G:C8	2.50	0.46
5:AN1:916:A:N3	6:B:78:U:O2'	2.45	0.46
5:AN1:2484:G:H2'	5:AN1:2485:U:C6	2.51	0.46
11:G:47:GLU:HG2	11:G:49:LYS:H	1.81	0.46
31:sN1:407:A:N7	31:sN1:409:G:N2	2.54	0.46
31:sN1:423:U:H5''	34:d:10:LYS:HE2	1.98	0.46
31:sN1:1057:U:OP1	44:n:85:ARG:NH2	2.48	0.46
31:sN1:1057:U:H2'	31:sN1:1058:G:H8	1.81	0.46
3:2:31:ILE:O	3:2:33:THR:N	2.49	0.46
5:AN1:511:G:OP1	5:AN1:1229:U:O2'	2.34	0.46
5:AN1:713:A:N3	45:o:40:GLN:NE2	2.64	0.46
5:AN1:1938:C:OP2	5:AN1:1939:U:O2'	2.26	0.46
6:B:81:G:O6	6:B:91:A:N6	2.49	0.46
31:sN1:1068:C:H2'	31:sN1:1069:G:C8	2.51	0.46
32:b:220:ALA:O	32:b:223:ILE:HG22	2.16	0.46
5:AN1:181:C:H2'	5:AN1:182:A:H8	1.81	0.46
5:AN1:1348:A:H2'	5:AN1:1349:A:C8	2.50	0.46
5:AN1:1793:C:HO2'	7:C:257:THR:HG1	1.63	0.46
14:J:110:GLN:O	14:J:113:LYS:NZ	2.48	0.46
5:AN1:884:A:N6	43:m:89:LEU:HD11	2.29	0.46
5:AN1:886:C:H1'	43:m:92:ARG:NH1	2.31	0.46
5:AN1:898:A:H3'	5:AN1:899:A:H8	1.81	0.46
18:N:99:HIS:HA	18:N:103:LYS:HE2	1.98	0.46
31:sN1:661:G:H22	31:sN1:738:G:H1	1.63	0.46
31:sN1:989:U:H1'	31:sN1:990:G:OP2	2.16	0.46
31:sN1:1510:A:H2'	31:sN1:1511:G:C8	2.51	0.46
5:AN1:2674:A:H2'	5:AN1:2675:A:C8	2.51	0.45
31:sN1:74:G:H2'	31:sN1:75:A:H8	1.81	0.45
31:sN1:991:A:H62	31:sN1:995:A:N6	2.08	0.45
31:sN1:1215:C:H2'	31:sN1:1216:A:C8	2.51	0.45
48:r:29:LEU:O	48:r:33:ILE:HG12	2.16	0.45
5:AN1:2096:G:N2	5:AN1:2185:U:O2	2.34	0.45
5:AN1:2169:A:H2'	5:AN1:2170:C:C6	2.51	0.45
31:sN1:597:G:H2'	31:sN1:598:G:H8	1.81	0.45
31:sN1:1069:G:H2'	31:sN1:1070:U:H6	1.80	0.45
31:sN1:1159:C:H42	31:sN1:1171:G:H22	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:f:14:GLN:O	36:f:18:VAL:HG23	2.16	0.45
42:l:102:LEU:H	42:l:102:LEU:HD12	1.80	0.45
5:AN1:1472:A:N6	5:AN1:1510:G:O2'	2.47	0.45
5:AN1:1500:A:O2'	5:AN1:1502:U:O4'	2.27	0.45
5:AN1:2683:U:H2'	5:AN1:2684:G:O4'	2.16	0.45
16:L:57:ARG:NH2	16:L:116:GLU:OE2	2.49	0.45
24:T:47:ASN:ND2	24:T:50:THR:HG23	2.28	0.45
31:sN1:388:C:C2	31:sN1:389:A:C8	3.05	0.45
31:sN1:403:U:H2'	31:sN1:404:G:H8	1.81	0.45
5:AN1:1719:U:O4	5:AN1:1734:G:N2	2.48	0.45
5:AN1:1869:G:H2'	5:AN1:1870:C:C6	2.51	0.45
5:AN1:2806:A:H62	5:AN1:2886:G:H21	1.64	0.45
5:AN1:498:U:H2'	5:AN1:499:G:O4'	2.16	0.45
5:AN1:831:A:H2'	5:AN1:832:G:C8	2.52	0.45
5:AN1:1767:C:H2'	5:AN1:1768:A:C8	2.52	0.45
5:AN1:2499:2MA:O2'	5:AN1:2501:G:OP2	2.35	0.45
5:AN1:2674:A:H2'	5:AN1:2675:A:H8	1.82	0.45
8:D:13:THR:OG1	8:D:14:ARG:N	2.49	0.45
17:M:33:LEU:HD13	17:M:114:GLU:HB3	1.99	0.45
27:W:15:GLY:HA3	27:W:29:PHE:HE1	1.81	0.45
31:sN1:268:C:H2'	31:sN1:269:A:C8	2.52	0.45
31:sN1:386:U:H2'	31:sN1:387:C:H6	1.81	0.45
31:sN1:743:A:H2'	31:sN1:744:A:C8	2.51	0.45
31:sN1:1381:C:H2'	31:sN1:1382:G:H8	1.80	0.45
32:b:86:ALA:O	32:b:90:GLY:N	2.50	0.45
39:i:82:THR:HG23	39:i:96:LEU:HD13	1.98	0.45
41:k:21:HIS:HB2	41:k:32:THR:HG23	1.99	0.45
52:v:25:G:H2'	52:v:26:C:O4'	2.17	0.45
5:AN1:52:G:H2'	5:AN1:222:G:C5	2.51	0.45
5:AN1:272:A:N1	5:AN1:426:U:O2'	2.47	0.45
5:AN1:727:G:OP1	7:C:13:ARG:HG2	2.17	0.45
5:AN1:844:A:H1'	5:AN1:846:U:C4	2.52	0.45
31:sN1:680:G:H2'	31:sN1:681:U:C6	2.51	0.45
31:sN1:1363:C:OP1	39:i:117:ARG:NH1	2.50	0.45
32:b:117:LYS:O	32:b:121:THR:HG23	2.17	0.45
38:h:22:LYS:O	38:h:66:TYR:OH	2.28	0.45
5:AN1:306:U:H2'	5:AN1:307:C:C6	2.51	0.45
5:AN1:673:A:N3	5:AN1:2439:U:O2'	2.43	0.45
5:AN1:2077:C:H2'	5:AN1:2078:A:C8	2.47	0.45
5:AN1:2325:A:H2'	5:AN1:2326:G:C8	2.51	0.45
22:R:84:ARG:HB2	22:R:96:ILE:HB	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:1923:A:H2'	5:AN1:1924:A:C8	2.52	0.45
5:AN1:2021:C:H2'	5:AN1:2022:U:C6	2.52	0.45
5:AN1:2137:A:H2	5:AN1:2138:A:H62	1.65	0.45
5:AN1:2622:C:H2'	5:AN1:2623:G:H8	1.82	0.45
11:G:2:SER:OG	11:G:3:ARG:N	2.50	0.45
31:sN1:402:G:H2'	31:sN1:403:U:H6	1.81	0.45
31:sN1:1491:G:H2'	31:sN1:1492:U:O4'	2.16	0.45
32:b:37:ARG:CG	32:b:38:ASN:H	2.30	0.45
5:AN1:475:G:N1	5:AN1:478:A:OP2	2.48	0.45
5:AN1:1361:A:OP1	27:W:2:SER:OG	2.32	0.45
5:AN1:1365:C:H2'	5:AN1:1366:G:O4'	2.17	0.45
5:AN1:1588:A:H2'	5:AN1:1589:C:H6	1.81	0.45
5:AN1:2894:U:H2'	5:AN1:2895:G:C8	2.52	0.45
9:E:170:ASP:OD1	9:E:171:ALA:N	2.48	0.45
13:I:45:THR:HG22	20:P:64:ARG:HH21	1.82	0.45
40:j:85:ASP:OD1	40:j:85:ASP:N	2.45	0.45
43:m:114:LYS:HE2	43:m:114:LYS:HB3	1.70	0.45
4:3:18:ARG:HE	4:3:21:GLY:HA2	1.80	0.45
5:AN1:516:C:OP2	30:Z:10:ARG:NH2	2.50	0.45
5:AN1:1176:U:H2'	5:AN1:1177:A:C8	2.52	0.45
5:AN1:1335:U:OP1	23:S:18:LYS:NZ	2.48	0.45
5:AN1:2456:U:C2	5:AN1:2457:A:C8	3.05	0.45
5:AN1:2645:C:H2'	5:AN1:2646:U:H6	1.82	0.45
6:B:54:G:H4'	6:B:55:A:H8	1.82	0.45
8:D:128:TRP:CD1	8:D:163:LYS:HB3	2.52	0.45
11:G:127:THR:HG23	11:G:129:THR:H	1.80	0.45
31:sN1:232:A:H2'	31:sN1:233:A:H8	1.82	0.45
36:f:11:HIS:CE1	36:f:54:ILE:HD12	2.52	0.45
5:AN1:67:G:N1	5:AN1:81:A:C6	2.85	0.44
5:AN1:966:G:H2'	5:AN1:967:U:C6	2.52	0.44
23:S:61:ILE:HG12	23:S:80:LYS:HG3	1.99	0.44
30:Z:43:THR:HG22	30:Z:45:ASP:H	1.83	0.44
31:sN1:1215:C:H2'	31:sN1:1216:A:H8	1.82	0.44
34:d:91:ASN:HA	34:d:94:LYS:HD3	1.98	0.44
47:q:32:HIS:CD2	47:q:35:TYR:H	2.35	0.44
5:AN1:8:A:N6	5:AN1:2899:A:N3	2.66	0.44
5:AN1:9:G:H2'	5:AN1:10:U:C6	2.53	0.44
5:AN1:229:A:N1	5:AN1:240:A:H5''	2.32	0.44
5:AN1:239:G:H8	5:AN1:239:G:OP2	2.00	0.44
5:AN1:293:U:O4	5:AN1:351:G:O6	2.35	0.44
5:AN1:1413:G:H1	5:AN1:1576:U:H3'	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:2468:G:H5''	5:AN1:2469:U:H2'	1.98	0.44
5:AN1:2736:A:H2'	5:AN1:2737:A:C8	2.52	0.44
10:F:147:ASP:OD2	10:F:147:ASP:N	2.50	0.44
31:sN1:36:C:H2'	31:sN1:37:G:H8	1.83	0.44
31:sN1:714:U:H4'	41:k:118:ASN:ND2	2.33	0.44
31:sN1:865:C:H2'	31:sN1:866:G:O4'	2.18	0.44
40:j:92:LEU:H	40:j:92:LEU:HD23	1.82	0.44
48:r:25:ASP:OD1	48:r:25:ASP:N	2.50	0.44
52:v:6:U:H2'	52:v:7:G:C8	2.51	0.44
5:AN1:568:G:H2'	5:AN1:2026:6MZ:N7	2.31	0.44
5:AN1:578:U:H2'	5:AN1:579:C:C6	2.52	0.44
5:AN1:1437:U:H2'	5:AN1:1438:C:C6	2.53	0.44
5:AN1:1437:U:H2'	5:AN1:1438:C:H6	1.82	0.44
5:AN1:2110:A:H3'	5:AN1:2111:G:H8	1.82	0.44
5:AN1:2301:U:H5	10:F:153:ASP:HB2	1.82	0.44
5:AN1:2379:G:O2'	5:AN1:2380:U:OP1	2.32	0.44
10:F:33:LYS:HB3	10:F:157:THR:HB	1.99	0.44
12:H:6:LEU:HD11	12:H:37:VAL:HG13	1.98	0.44
25:U:72:LYS:HE3	25:U:72:LYS:HB3	1.84	0.44
31:sN1:1464:C:H2'	31:sN1:1465:A:H8	1.81	0.44
5:AN1:1068:G:N3	5:AN1:1086:A:O2'	2.38	0.44
5:AN1:1394:C:H2'	5:AN1:1395:A:H8	1.83	0.44
5:AN1:1591:C:H2'	5:AN1:1592:A:H8	1.80	0.44
5:AN1:2594:A:H5''	7:C:234:GLY:HA3	2.00	0.44
6:B:110:C:H2'	6:B:111:C:H6	1.82	0.44
19:O:86:LYS:HZ2	19:O:87:ILE:H	1.65	0.44
31:sN1:498:C:OP1	42:l:114:ARG:NH2	2.49	0.44
5:AN1:287:G:H2'	5:AN1:288:U:C6	2.53	0.44
5:AN1:580:A:H2'	5:AN1:581:G:C8	2.52	0.44
5:AN1:753:C:H2'	5:AN1:754:A:H8	1.83	0.44
5:AN1:1164:G:H2'	5:AN1:1165:U:C6	2.53	0.44
5:AN1:1436:A:H2'	5:AN1:1437:U:C6	2.53	0.44
5:AN1:2158:G:H2'	5:AN1:2159:U:O4'	2.18	0.44
10:F:17:GLN:HA	10:F:22:ILE:HD12	1.99	0.44
31:sN1:58:U:H2'	31:sN1:59:G:C8	2.53	0.44
31:sN1:385:A:H3'	31:sN1:386:U:H6	1.83	0.44
31:sN1:1170:U:H2'	31:sN1:1171:G:C8	2.53	0.44
32:b:91:GLN:HE21	32:b:223:ILE:HG12	1.83	0.44
52:v:23:G:H2'	52:v:24:A:C8	2.52	0.44
4:3:10:ILE:HG21	4:3:33:HIS:CD2	2.52	0.44
11:G:36:ASN:OD1	11:G:37:LEU:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:T:86:ILE:HG22	24:T:87:ASP:H	1.82	0.44
31:sN1:310:C:H2'	31:sN1:311:A:C8	2.52	0.44
32:b:63:ALA:HB2	32:b:223:ILE:HD12	1.99	0.44
33:c:216:ASN:HB3	40:j:16:ARG:HD2	2.00	0.44
51:u:49:LYS:C	51:u:49:LYS:HD3	2.42	0.44
5:AN1:678:A:H2'	5:AN1:679:G:C8	2.52	0.44
5:AN1:2304:G:O2'	5:AN1:2306:A:OP2	2.27	0.44
5:AN1:2622:C:H2'	5:AN1:2623:G:C8	2.53	0.44
5:AN1:2784:C:H2'	5:AN1:2785:C:C6	2.53	0.44
5:AN1:2815:C:H2'	5:AN1:2817:A:N7	2.33	0.44
7:C:199:GLU:HG2	7:C:202:LEU:HB2	2.00	0.44
11:G:109:TYR:HD2	11:G:113:ILE:HD11	1.82	0.44
14:J:47:ILE:HG13	14:J:48:PRO:HD2	2.00	0.44
25:U:76:VAL:HB	25:U:95:PHE:HB3	1.99	0.44
31:sN1:490:A:H2'	31:sN1:491:G:C8	2.53	0.44
5:AN1:1424:G:H2'	5:AN1:1425:G:H8	1.82	0.44
5:AN1:1726:C:H1'	5:AN1:1727:G:C6	2.53	0.44
5:AN1:1792:U:H2'	5:AN1:1793:C:C6	2.53	0.44
6:B:87:A:H2'	16:L:18:THR:HG22	1.99	0.44
7:C:232:HIS:CE1	7:C:244:PRO:HA	2.53	0.44
12:H:25:TYR:HE1	12:H:29:PHE:HD1	1.65	0.44
31:sN1:1003:C:H2'	31:sN1:1004:U:C6	2.53	0.44
31:sN1:1060:C:OP2	31:sN1:1061:G:O2'	2.35	0.44
32:b:184:PRO:HA	32:b:199:ASP:OD1	2.18	0.44
52:v:28:C:H2'	52:v:29:C:H6	1.82	0.44
5:AN1:518:C:H2'	5:AN1:519:A:H8	1.81	0.44
5:AN1:1166:A:H2'	5:AN1:1167:U:O4'	2.18	0.44
5:AN1:1919:U:H4'	52:v:12:U:O2'	2.17	0.44
5:AN1:2113:A:H2	5:AN1:2166:A:N6	2.16	0.44
5:AN1:2295:G:H2'	5:AN1:2296:C:C6	2.53	0.44
6:B:64:A:N6	6:B:105:C:H2'	2.32	0.44
31:sN1:136:U:H2'	31:sN1:137:A:H8	1.82	0.44
31:sN1:317:A:H2'	31:sN1:318:C:H6	1.83	0.44
31:sN1:1388:U:H2'	31:sN1:1389:G:C8	2.52	0.44
32:b:164:PHE:HD1	32:b:186:ILE:HG13	1.83	0.44
5:AN1:25:C:O2'	5:AN1:552:U:OP1	2.35	0.43
5:AN1:2401:G:O2'	5:AN1:2407:A:N6	2.50	0.43
5:AN1:2841:U:H5''	19:O:55:ASN:O	2.18	0.43
31:sN1:991:A:H4'	31:sN1:992:C:O5'	2.18	0.43
32:b:93:TYR:O	32:b:152:GLY:HA3	2.18	0.43
49:s:64:GLU:CD	49:s:64:GLU:H	2.25	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:46:G:H2'	5:AN1:47:U:C6	2.53	0.43
5:AN1:753:C:H2'	5:AN1:754:A:C8	2.53	0.43
11:G:92:VAL:HG12	11:G:160:LYS:NZ	2.33	0.43
12:H:9:ILE:HD12	12:H:12:LEU:HD23	2.00	0.43
32:b:85:GLN:HG2	32:b:216:ALA:HB1	1.98	0.43
34:d:80:GLU:OE2	34:d:83:ARG:NH1	2.50	0.43
5:AN1:173:U:H2'	5:AN1:174:A:H8	1.83	0.43
5:AN1:520:U:H2'	5:AN1:521:G:C8	2.52	0.43
5:AN1:580:A:H2'	5:AN1:581:G:H8	1.84	0.43
5:AN1:898:A:H3'	5:AN1:899:A:C8	2.54	0.43
5:AN1:2467:A:H2'	5:AN1:2468:G:C4	2.53	0.43
9:E:134:LEU:HG	9:E:138:ASN:HD21	1.83	0.43
31:sN1:281:U:H2'	31:sN1:282:G:C8	2.53	0.43
31:sN1:395:G:H2'	31:sN1:396:C:C6	2.53	0.43
31:sN1:914:G:H2'	31:sN1:915:A:C8	2.53	0.43
31:sN1:1002:A:H3'	31:sN1:1003:C:C6	2.53	0.43
31:sN1:1478:U:H2'	31:sN1:1479:G:H8	1.83	0.43
41:k:98:ALA:O	41:k:102:VAL:HG23	2.18	0.43
5:AN1:631:A:O2'	5:AN1:2400:U:OP1	2.36	0.43
5:AN1:873:G:O6	5:AN1:900:C:N4	2.34	0.43
5:AN1:1942:U:H2'	5:AN1:1943:C:H6	1.83	0.43
5:AN1:2696:A:H2'	5:AN1:2697:C:C6	2.54	0.43
7:C:20:VAL:HG23	7:C:21:HIS:N	2.33	0.43
31:sN1:1022:U:H4'	31:sN1:1023:G:O4'	2.18	0.43
36:f:2:ARG:HD3	36:f:91:ARG:HE	1.82	0.43
52:v:9:A:H2'	52:v:11:C:H5	1.83	0.43
5:AN1:148:A:N6	5:AN1:1593:G:O2'	2.26	0.43
5:AN1:903:A:H3'	5:AN1:904:U:H5''	2.00	0.43
5:AN1:1193:U:H2'	5:AN1:1194:U:C6	2.53	0.43
15:K:57:THR:O	15:K:62:ARG:NH1	2.52	0.43
32:b:168:VAL:HG13	32:b:175:ILE:HG13	1.99	0.43
34:d:149:GLU:HA	34:d:152:LYS:HD2	2.01	0.43
5:AN1:1919:U:H2'	5:AN1:1920:C:C6	2.54	0.43
5:AN1:1942:U:H2'	5:AN1:1943:C:C6	2.53	0.43
5:AN1:2448:C:H2'	5:AN1:2449:A:C8	2.53	0.43
5:AN1:2633:U:H2'	5:AN1:2634:G:O4'	2.19	0.43
16:L:77:LYS:NZ	16:L:82:ARG:O	2.51	0.43
21:Q:42:VAL:HG12	21:Q:44:GLY:H	1.83	0.43
31:sN1:80:A:H2'	31:sN1:81:G:H8	1.83	0.43
31:sN1:401:U:H3'	31:sN1:402:G:H5'	2.00	0.43
32:b:132:THR:OG1	32:b:133:LYS:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:394:U:O2'	5:AN1:395:G:N7	2.45	0.43
5:AN1:707:U:H2'	5:AN1:708:U:C6	2.54	0.43
5:AN1:1662:A:H61	5:AN1:1992:C:N4	2.17	0.43
5:AN1:2262:A:H4'	5:AN1:2263:A:N3	2.34	0.43
18:N:9:LEU:O	18:N:13:LYS:HG3	2.18	0.43
31:sN1:8:G:O2'	31:sN1:9:A:H5''	2.18	0.43
31:sN1:462:A:H2'	31:sN1:464:A:C8	2.53	0.43
31:sN1:833:G:H1	31:sN1:847:U:H3	1.65	0.43
31:sN1:1509:U:H2'	31:sN1:1510:A:C8	2.53	0.43
33:c:83:ASP:OD1	33:c:83:ASP:N	2.47	0.43
35:e:114:LEU:HD13	35:e:122:VAL:HG11	2.00	0.43
5:AN1:826:U:H2'	5:AN1:827:A:C8	2.53	0.43
5:AN1:1623:C:H2'	5:AN1:1624:A:O4'	2.18	0.43
9:E:82:LYS:HE2	9:E:82:LYS:HB3	1.84	0.43
31:sN1:430:C:H2'	31:sN1:431:A:C8	2.54	0.43
31:sN1:1011:A:H2	31:sN1:1216:A:H1'	1.82	0.43
31:sN1:1405:A:C5	31:sN1:1491:G:N1	2.86	0.43
34:d:4:TYR:CE1	34:d:11:LEU:HD11	2.54	0.43
42:l:24:LEU:HA	42:l:30:ARG:HD2	2.01	0.43
51:u:37:PHE:HD2	51:u:41:PRO:HD3	1.84	0.43
5:AN1:1568:A:H2'	5:AN1:1569:A:C8	2.52	0.43
5:AN1:1634:G:H2'	5:AN1:1635:A:C8	2.54	0.43
6:B:22:G:O2'	6:B:25:C:N4	2.52	0.43
7:C:21:HIS:ND1	7:C:90:HIS:HE1	2.17	0.43
14:J:70:ARG:HD2	14:J:70:ARG:HA	1.81	0.43
29:Y:21:LEU:HD23	29:Y:24:GLN:HE21	1.83	0.43
31:sN1:725:A:H2'	31:sN1:726:A:C8	2.54	0.43
33:c:138:VAL:HG21	33:c:168:TYR:HD2	1.83	0.43
34:d:11:LEU:HD23	34:d:65:ARG:NE	2.34	0.43
35:e:103:GLY:H	35:e:121:ASN:HD22	1.66	0.43
41:k:18:GLY:H	41:k:78:LEU:HD11	1.84	0.43
5:AN1:182:A:H2'	5:AN1:183:A:C8	2.54	0.43
5:AN1:368:C:H4'	5:AN1:369:G:H5'	2.01	0.43
5:AN1:1862:A:H2	5:AN1:1872:A:H8	1.67	0.43
10:F:80:ARG:HG3	10:F:81:ASP:H	1.84	0.43
10:F:136:ILE:HG13	10:F:138:PHE:CD1	2.53	0.43
11:G:85:ARG:HB3	11:G:133:LEU:HB2	2.01	0.43
14:J:63:VAL:HG12	14:J:106:LEU:HD11	2.01	0.43
31:sN1:734:A:H2'	31:sN1:735:U:H6	1.84	0.43
31:sN1:1530:C:H41	51:u:47:ARG:HH11	1.67	0.43
49:s:39:MET:HE2	49:s:39:MET:HB2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:5:ILE:HD12	1:O:47:GLU:HG3	2.01	0.42
5:AN1:2070:U:H2'	5:AN1:2071:U:C6	2.54	0.42
5:AN1:2463:C:H2'	5:AN1:2464:A:O4'	2.19	0.42
5:AN1:2798:U:H2'	5:AN1:2799:C:H6	1.84	0.42
6:B:62:U:H2'	6:B:63:U:C5	2.54	0.42
6:B:66:C:H2'	6:B:67:G:O4'	2.18	0.42
19:O:46:PHE:CZ	19:O:66:LYS:HD2	2.54	0.42
31:sN1:489:C:H2'	31:sN1:490:A:C8	2.53	0.42
31:sN1:631:C:H2'	31:sN1:632:A:C8	2.53	0.42
5:AN1:11:C:H2'	5:AN1:12:A:C8	2.54	0.42
5:AN1:1436:A:H2'	5:AN1:1437:U:H6	1.84	0.42
5:AN1:2174:C:C2	5:AN1:2175:C:H5	2.37	0.42
5:AN1:2275:G:N7	26:V:14:ARG:NH2	2.66	0.42
5:AN1:2301:U:H3	10:F:39:GLY:H	1.66	0.42
5:AN1:2387:G:HO2'	5:AN1:2420:C:N4	2.17	0.42
5:AN1:2519:G:O2'	5:AN1:2760:A:O2'	2.31	0.42
6:B:108:C:H2'	6:B:109:G:C8	2.49	0.42
14:J:51:ARG:H	14:J:51:ARG:HD3	1.84	0.42
31:sN1:519:C:H41	42:l:50:ARG:HH11	1.66	0.42
31:sN1:861:A:H2'	31:sN1:862:A:C8	2.54	0.42
31:sN1:1141:G:N2	31:sN1:1143:A:H62	2.16	0.42
39:i:19:LEU:HD12	39:i:61:LEU:HD21	2.02	0.42
40:j:7:ARG:HD2	40:j:73:LEU:HD11	2.01	0.42
5:AN1:591:U:H2'	5:AN1:592:U:C6	2.54	0.42
5:AN1:746:G:H5'	5:AN1:747:A:OP2	2.19	0.42
5:AN1:758:G:H2'	5:AN1:759:A:O4'	2.18	0.42
5:AN1:1255:A:OP1	22:R:83:LYS:NZ	2.46	0.42
5:AN1:1359:G:N2	5:AN1:1362:A:OP2	2.41	0.42
31:sN1:715:A:H5'	41:k:118:ASN:ND2	2.34	0.42
31:sN1:1187:G:H5'	33:c:176:HIS:CE1	2.54	0.42
40:j:66:GLU:OE2	40:j:68:ARG:NE	2.47	0.42
5:AN1:946:U:H2'	5:AN1:947:G:H8	1.84	0.42
5:AN1:1163:U:H2'	5:AN1:1164:G:H8	1.84	0.42
5:AN1:1475:C:H2'	5:AN1:1476:A:C8	2.55	0.42
5:AN1:2043:C:H2'	5:AN1:2044:G:H8	1.84	0.42
5:AN1:2498:G:H5''	5:AN1:2499:2MA:H5''	2.02	0.42
14:J:13:ASN:HD21	14:J:96:THR:HG1	1.63	0.42
31:sN1:124:G:H2'	31:sN1:125:A:C8	2.54	0.42
31:sN1:899:G:H2'	31:sN1:900:A:C8	2.51	0.42
31:sN1:1113:U:C2	31:sN1:1181:G:O6	2.72	0.42
44:n:15:LYS:HE2	44:n:15:LYS:HB2	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:86:C:C2	5:AN1:87:G:C8	3.06	0.42
5:AN1:677:C:H2'	5:AN1:678:A:H8	1.83	0.42
5:AN1:1810:G:OP2	5:AN1:1811:A:O2'	2.28	0.42
25:U:29:LEU:HD13	25:U:45:THR:HG21	2.02	0.42
31:sN1:405:U:H2'	31:sN1:406:G:O4'	2.19	0.42
31:sN1:770:G:O6	31:sN1:804:A:N6	2.53	0.42
31:sN1:943:A:H2'	31:sN1:944:G:H8	1.84	0.42
31:sN1:1011:A:C2	31:sN1:1216:A:H1'	2.54	0.42
31:sN1:1433:U:O4	31:sN1:1434:A:N6	2.52	0.42
35:e:39:GLY:HA3	35:e:116:ALA:HB1	2.00	0.42
42:l:85:GLY:HA3	42:l:96:HIS:CD2	2.54	0.42
5:AN1:569:U:H3'	21:Q:80:ARG:NH2	2.34	0.42
5:AN1:850:A:H2'	5:AN1:851:U:C6	2.55	0.42
6:B:68:C:H2'	6:B:69:U:C6	2.55	0.42
7:C:130:LEU:HB2	7:C:135:MET:HE2	2.02	0.42
8:D:159:PHE:HB3	13:I:81:PRO:HG3	2.00	0.42
31:sN1:518:G:H1	31:sN1:525:C:H42	1.67	0.42
33:c:107:ASP:OD1	33:c:108:ARG:N	2.53	0.42
34:d:50:GLN:HG3	34:d:54:SER:HB3	2.02	0.42
42:l:99:ARG:HG3	42:l:117:TYR:HA	2.01	0.42
5:AN1:812:C:H2'	5:AN1:813:C:H6	1.85	0.42
5:AN1:984:C:O2'	5:AN1:997:A:N3	2.43	0.42
5:AN1:1411:G:H2'	5:AN1:1412:C:C6	2.54	0.42
6:B:28:C:H2'	6:B:29:C:O4'	2.20	0.42
27:W:37:ARG:HG3	27:W:48:ARG:HG3	2.02	0.42
27:W:71:LEU:HD22	27:W:76:GLN:HE22	1.85	0.42
31:sN1:576:G:HO2'	45:o:54:ARG:HH12	1.63	0.42
31:sN1:1419:U:H2'	31:sN1:1420:G:C8	2.55	0.42
40:j:63:ASP:OD2	44:n:85:ARG:NH1	2.52	0.42
48:r:27:ASP:OD1	48:r:28:THR:N	2.52	0.42
5:AN1:292:U:H2'	5:AN1:293:U:C6	2.55	0.42
5:AN1:307:C:H2'	5:AN1:308:U:C6	2.55	0.42
5:AN1:1924:A:H2'	5:AN1:1925:G:O4'	2.19	0.42
5:AN1:2587:C:H2'	5:AN1:2588:G:C8	2.54	0.42
5:AN1:2835:G:O2'	17:M:49:GLU:OE1	2.35	0.42
8:D:87:GLU:OE2	8:D:87:GLU:N	2.48	0.42
14:J:104:ARG:CZ	19:O:35:VAL:HG21	2.50	0.42
31:sN1:37:G:H2'	31:sN1:38:C:C6	2.55	0.42
5:AN1:657:G:O2'	9:E:94:LYS:O	2.38	0.42
5:AN1:1394:C:H2'	5:AN1:1395:A:C8	2.54	0.42
5:AN1:1420:G:H2'	5:AN1:1421:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:2098:C:H2'	5:AN1:2099:C:O4'	2.19	0.42
5:AN1:2743:G:N2	5:AN1:2753:A:H62	2.15	0.42
12:H:48:GLU:O	12:H:52:ALA:CB	2.68	0.42
24:T:46:PRO:HD3	24:T:54:GLY:HA3	2.01	0.42
24:T:87:ASP:OD1	24:T:88:GLY:N	2.52	0.42
31:sN1:78:G:H2'	31:sN1:90:C:H42	1.85	0.42
31:sN1:456:U:H2'	31:sN1:457:A:H8	1.84	0.42
31:sN1:759:U:H2'	31:sN1:760:A:C8	2.55	0.42
31:sN1:929:C:H2'	31:sN1:930:G:C8	2.54	0.42
31:sN1:1238:G:H2'	31:sN1:1239:G:H8	1.85	0.42
31:sN1:1311:C:H2'	31:sN1:1312:U:H6	1.84	0.42
32:b:133:LYS:O	32:b:137:LEU:HG	2.19	0.42
5:AN1:1355:G:N7	5:AN1:1356:G:C8	2.88	0.42
5:AN1:1407:U:O4	5:AN1:1408:A:N6	2.53	0.42
5:AN1:1681:U:H2'	5:AN1:1682:A:C8	2.55	0.42
5:AN1:2805:A:H2'	5:AN1:2806:A:C8	2.55	0.42
8:D:15:ILE:HG23	19:O:15:GLN:NE2	2.35	0.42
25:U:68:LYS:HB2	25:U:68:LYS:HE2	1.78	0.42
31:sN1:174:C:H2'	31:sN1:175:A:H8	1.84	0.42
31:sN1:552:U:H2'	31:sN1:553:C:H6	1.84	0.42
31:sN1:991:A:H8	31:sN1:994:U:N3	2.17	0.42
31:sN1:1002:A:H5''	31:sN1:1003:C:C5	2.55	0.42
32:b:29:MET:HE2	32:b:29:MET:HB3	1.79	0.42
32:b:179:LYS:HD2	32:b:197:ASN:HD21	1.85	0.42
2:1:31:LEU:HD22	2:1:42:LEU:HG	2.01	0.41
5:AN1:35:A:H61	5:AN1:511:G:H1'	1.84	0.41
5:AN1:519:A:H2'	5:AN1:520:U:C6	2.55	0.41
5:AN1:663:U:H2'	5:AN1:664:A:H8	1.85	0.41
5:AN1:1408:A:H2'	5:AN1:1409:A:C8	2.55	0.41
5:AN1:1588:A:H2'	5:AN1:1589:C:C6	2.55	0.41
5:AN1:1665:G:O2'	5:AN1:1987:U:O4	2.37	0.41
5:AN1:2149:A:H2'	5:AN1:2150:G:C8	2.54	0.41
5:AN1:2176:U:H2'	5:AN1:2177:G:C8	2.55	0.41
5:AN1:2192:C:H2'	5:AN1:2193:U:C6	2.55	0.41
5:AN1:2657:G:OP2	5:AN1:2657:G:H8	2.02	0.41
7:C:167:ARG:HA	7:C:172:ALA:HA	2.01	0.41
31:sN1:242:A:N6	31:sN1:277:G:C2	2.88	0.41
31:sN1:456:U:H2'	31:sN1:457:A:C8	2.55	0.41
31:sN1:675:U:H2'	31:sN1:676:C:H6	1.85	0.41
44:n:87:THR:HG22	44:n:93:VAL:HG23	2.02	0.41
5:AN1:981:A:N3	5:AN1:981:A:H2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:1458:A:H2'	5:AN1:1459:G:C8	2.55	0.41
8:D:47:GLN:HE22	8:D:87:GLU:HG3	1.85	0.41
31:sN1:1188:A:H8	31:sN1:1188:A:OP2	2.03	0.41
31:sN1:1369:U:H2'	31:sN1:1370:G:O4'	2.21	0.41
31:sN1:1407:A:H2'	31:sN1:1408:C:C6	2.55	0.41
52:v:59:A:N3	52:v:61:U:H5''	2.35	0.41
5:AN1:593:C:H2'	5:AN1:594:A:H8	1.85	0.41
5:AN1:1310:C:H2'	5:AN1:1311:A:C8	2.54	0.41
5:AN1:1560:U:H2'	5:AN1:1561:U:C6	2.55	0.41
5:AN1:2643:U:H2'	5:AN1:2644:G:H8	1.84	0.41
5:AN1:2727:G:H2'	5:AN1:2728:G:C8	2.56	0.41
7:C:157:SER:OG	7:C:158:ALA:N	2.53	0.41
8:D:15:ILE:HD12	8:D:25:VAL:HG11	2.01	0.41
9:E:20:ARG:NH2	9:E:106:CYS:SG	2.93	0.41
25:U:13:GLU:OE2	25:U:16:GLN:NE2	2.54	0.41
31:sN1:55:A:H2'	31:sN1:56:C:O4'	2.20	0.41
31:sN1:945:C:H2'	31:sN1:946:A:H8	1.85	0.41
31:sN1:1169:C:H2'	31:sN1:1170:U:C6	2.56	0.41
31:sN1:1201:A:N3	33:c:188:ARG:NH1	2.61	0.41
31:sN1:1220:C:P	49:s:78:ARG:HH21	2.44	0.41
31:sN1:1379:C:C2	31:sN1:1380:C:H5	2.39	0.41
32:b:89:ALA:HB1	32:b:223:ILE:HG21	2.02	0.41
36:f:42:TRP:CZ2	48:r:24:LYS:HE2	2.55	0.41
37:g:66:LEU:O	37:g:70:ARG:HG3	2.19	0.41
52:v:24:A:H2'	52:v:25:G:N7	2.34	0.41
5:AN1:1462:G:N1	5:AN1:1520:A:N6	2.25	0.41
5:AN1:1844:A:H5''	5:AN1:1845:G:OP1	2.20	0.41
24:T:25:LEU:HD21	24:T:35:GLU:HB3	2.02	0.41
26:V:37:ILE:HG22	26:V:38:VAL:HG23	2.01	0.41
31:sN1:656:U:OP1	45:o:8:ARG:NH1	2.53	0.41
31:sN1:734:A:H2'	31:sN1:735:U:C6	2.56	0.41
31:sN1:947:U:OP2	43:m:101:ARG:HD2	2.20	0.41
34:d:41:GLN:HG3	34:d:42:HIS:CD2	2.55	0.41
36:f:41:ASP:OD1	36:f:58:HIS:NE2	2.51	0.41
41:k:83:VAL:O	41:k:84:LEU:HD23	2.20	0.41
52:v:10:G:C2	52:v:27:A:H1'	2.55	0.41
5:AN1:519:A:H2'	5:AN1:520:U:H6	1.84	0.41
5:AN1:1798:A:H2'	5:AN1:1799:A:H8	1.85	0.41
5:AN1:1989:U:H4'	8:D:136:THR:OG1	2.20	0.41
6:B:101:A:H2'	6:B:102:A:O4'	2.20	0.41
18:N:108:ALA:O	18:N:111:GLU:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:sN1:198:G:H2'	31:sN1:199:G:H8	1.84	0.41
31:sN1:479:A:H2'	31:sN1:480:C:O4'	2.21	0.41
31:sN1:872:U:O2'	38:h:15:ARG:NH1	2.48	0.41
31:sN1:1352:G:H2'	31:sN1:1353:G:C8	2.55	0.41
5:AN1:184:G:H3'	5:AN1:185:G:C8	2.52	0.41
5:AN1:308:U:H2'	5:AN1:309:G:O4'	2.20	0.41
5:AN1:309:G:N2	5:AN1:311:G:H3'	2.36	0.41
5:AN1:540:A:H2'	5:AN1:541:C:C6	2.55	0.41
5:AN1:1482:C:N4	5:AN1:1498:G:H1	2.19	0.41
5:AN1:2845:G:H1'	5:AN1:2862:G:H21	1.86	0.41
8:D:20:GLY:HA2	19:O:82:PRO:HD2	2.02	0.41
27:W:63:GLY:O	27:W:67:VAL:HG23	2.20	0.41
31:sN1:562:U:OP2	31:sN1:563:G:O2'	2.32	0.41
31:sN1:579:U:H2'	31:sN1:580:A:H8	1.84	0.41
31:sN1:1086:G:H2'	31:sN1:1087:U:O4'	2.21	0.41
36:f:10:VAL:HG23	36:f:58:HIS:HB3	2.03	0.41
42:l:43:LYS:HE3	42:l:43:LYS:HB2	1.85	0.41
45:o:39:LEU:HD23	45:o:39:LEU:HA	1.89	0.41
5:AN1:47:U:H2'	5:AN1:48:C:C6	2.55	0.41
5:AN1:611:U:H5''	5:AN1:612:A:C8	2.55	0.41
5:AN1:664:A:H2'	5:AN1:665:U:C6	2.55	0.41
5:AN1:944:A:H2'	5:AN1:945:C:C6	2.55	0.41
5:AN1:1828:C:H2'	5:AN1:1829:C:O4'	2.21	0.41
5:AN1:1912:A:H5''	5:AN1:1959:U:O2	2.20	0.41
5:AN1:2239:U:H2'	5:AN1:2240:U:C6	2.56	0.41
5:AN1:2306:A:H2'	5:AN1:2307:A:H5''	2.02	0.41
5:AN1:2842:G:H2'	5:AN1:2843:U:C6	2.56	0.41
9:E:136:LYS:HA	9:E:139:ASP:OD2	2.20	0.41
12:H:33:GLN:OE1	12:H:33:GLN:N	2.54	0.41
24:T:47:ASN:HD21	24:T:49:VAL:HB	1.85	0.41
31:sN1:742:U:H2'	31:sN1:743:A:C8	2.56	0.41
40:j:8:ILE:HB	40:j:74:ILE:HB	2.02	0.41
51:u:38:TYR:C	51:u:40:LYS:H	2.29	0.41
5:AN1:179:U:H2'	5:AN1:180:G:H8	1.85	0.41
5:AN1:181:C:H2'	5:AN1:182:A:C8	2.56	0.41
5:AN1:199:G:N2	5:AN1:199:G:OP2	2.54	0.41
5:AN1:210:C:OP2	5:AN1:211:A:O2'	2.34	0.41
5:AN1:932:U:H2'	5:AN1:933:C:C6	2.55	0.41
5:AN1:1273:C:H2'	5:AN1:1274:G:C8	2.55	0.41
5:AN1:1559:C:H2'	5:AN1:1560:U:C6	2.56	0.41
5:AN1:2106:G:O5'	5:AN1:2114:U:H2'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:2287:U:OP1	5:AN1:2376:U:O2'	2.38	0.41
6:B:37:U:H2'	6:B:38:U:C6	2.56	0.41
8:D:12:MET:HE2	8:D:12:MET:HB3	1.99	0.41
14:J:73:ASP:OD1	14:J:75:SER:OG	2.38	0.41
17:M:89:GLU:CD	17:M:89:GLU:H	2.29	0.41
31:sN1:976:C:O2	44:n:59:ARG:HG2	2.21	0.41
31:sN1:1057:U:O2'	40:j:58:ASN:ND2	2.54	0.41
43:m:69:LEU:O	43:m:73:ILE:HG23	2.21	0.41
5:AN1:8:A:H61	5:AN1:2898:U:H3	1.67	0.41
5:AN1:158:U:H2'	5:AN1:159:G:C8	2.56	0.41
5:AN1:301:A:N1	5:AN1:324:A:O2'	2.39	0.41
5:AN1:1016:U:OP1	5:AN1:1032:U:O2'	2.36	0.41
5:AN1:1108:A:H8	5:AN1:1109:G:H4'	1.85	0.41
5:AN1:1475:C:H2'	5:AN1:1476:A:H8	1.86	0.41
5:AN1:2130:A:C6	5:AN1:2154:A:H5'	2.55	0.41
5:AN1:2172:A:O2'	5:AN1:2173:C:O4'	2.22	0.41
5:AN1:2207:G:N3	5:AN1:2207:G:H2'	2.35	0.41
5:AN1:2484:G:H2'	5:AN1:2485:U:H6	1.85	0.41
5:AN1:2641:U:H3'	5:AN1:2642:C:C5'	2.51	0.41
5:AN1:2734:A:N1	5:AN1:2762:G:C6	2.89	0.41
9:E:40:GLN:HG2	9:E:42:THR:HG23	2.03	0.41
20:P:78:ARG:HD3	20:P:78:ARG:HA	1.79	0.41
31:sN1:359:A:N6	42:l:27:CYS:SG	2.94	0.41
31:sN1:823:C:O2	38:h:16:ASN:ND2	2.53	0.41
31:sN1:949:U:H2'	31:sN1:950:G:H8	1.86	0.41
31:sN1:1178:G:H1'	31:sN1:1179:G:C4	2.56	0.41
31:sN1:1233:A:H2'	31:sN1:1234:C:C6	2.55	0.41
32:b:181:LEU:HD12	32:b:181:LEU:HA	1.93	0.41
34:d:18:ASP:OD1	34:d:20:GLN:NE2	2.54	0.41
46:p:97:LYS:HE3	46:p:97:LYS:HB2	1.83	0.41
5:AN1:67:G:H2'	5:AN1:68:A:N7	2.36	0.41
5:AN1:1138:U:OP2	13:I:65:THR:OG1	2.39	0.41
5:AN1:1355:G:C6	5:AN1:1367:U:C2	3.08	0.41
5:AN1:1517:G:OP2	5:AN1:1518:A:O2'	2.28	0.41
5:AN1:1524:A:H62	5:AN1:1539:G:N2	2.18	0.41
5:AN1:1860:U:H2'	5:AN1:1861:U:C6	2.56	0.41
5:AN1:1905:C:OP1	52:v:69:U:O2'	2.39	0.41
5:AN1:2572:G:H5'	5:AN1:2574:G:N7	2.36	0.41
5:AN1:2655:G:N2	5:AN1:2658:A:OP2	2.54	0.41
5:AN1:2753:A:H2'	5:AN1:2754:A:H5''	2.02	0.41
10:F:80:ARG:HB3	10:F:83:TRP:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:J:11:ALA:HB2	14:J:83:ALA:HB1	2.02	0.41
14:J:98:ILE:HD12	14:J:117:LEU:HB3	2.03	0.41
19:O:99:LYS:HA	19:O:99:LYS:HD3	1.85	0.41
31:sN1:218:U:H2'	31:sN1:219:A:C8	2.56	0.41
31:sN1:1015:G:C2	31:sN1:1016:G:C6	3.09	0.41
31:sN1:1284:A:H2'	31:sN1:1285:A:C8	2.56	0.41
34:d:154:GLN:NE2	34:d:156:ARG:HE	2.19	0.41
5:AN1:113:C:H2'	5:AN1:114:G:H8	1.87	0.40
5:AN1:182:A:H2'	5:AN1:183:A:H8	1.87	0.40
5:AN1:599:C:H2'	5:AN1:600:G:O4'	2.22	0.40
5:AN1:621:C:H2'	5:AN1:622:C:H6	1.86	0.40
5:AN1:849:C:H5'	29:Y:22:CYS:SG	2.61	0.40
5:AN1:984:C:H2'	5:AN1:985:A:O4'	2.21	0.40
5:AN1:2172:A:H2'	5:AN1:2173:C:C6	2.55	0.40
5:AN1:2301:U:H2'	5:AN1:2302:C:C6	2.56	0.40
5:AN1:2645:C:H2'	5:AN1:2646:U:C6	2.56	0.40
31:sN1:242:A:H62	31:sN1:277:G:N2	2.19	0.40
31:sN1:403:U:H2'	31:sN1:404:G:C8	2.56	0.40
31:sN1:754:U:OP1	31:sN1:819:U:O2'	2.39	0.40
37:g:111:ARG:HD3	37:g:123:GLU:HB2	2.01	0.40
52:v:1:G:H2'	52:v:2:G:C8	2.55	0.40
5:AN1:85:C:C2	5:AN1:86:C:C5	3.09	0.40
5:AN1:326:A:H61	5:AN1:340:G:H2'	1.86	0.40
5:AN1:575:G:H2'	5:AN1:576:G:C8	2.56	0.40
5:AN1:856:G:H3'	5:AN1:857:G:C8	2.56	0.40
5:AN1:1147:G:H2'	5:AN1:1148:U:C6	2.56	0.40
5:AN1:1680:G:H2'	5:AN1:1681:U:C6	2.56	0.40
5:AN1:1878:U:H2'	5:AN1:1879:U:H6	1.86	0.40
5:AN1:2102:A:N1	5:AN1:2180:A:N6	2.69	0.40
10:F:80:ARG:H	10:F:83:TRP:HD1	1.69	0.40
14:J:17:ARG:HG2	14:J:18:ARG:HG3	2.03	0.40
31:sN1:106:C:O2'	46:p:43:ARG:O	2.39	0.40
31:sN1:1094:C:H2'	31:sN1:1095:C:C6	2.56	0.40
38:h:37:ALA:HB1	38:h:49:VAL:HG21	2.03	0.40
5:AN1:113:C:H2'	5:AN1:114:G:C8	2.56	0.40
5:AN1:173:U:H2'	5:AN1:174:A:C8	2.56	0.40
5:AN1:355:C:O2'	5:AN1:356:A:H2'	2.20	0.40
5:AN1:730:C:H2'	5:AN1:731:G:O4'	2.21	0.40
5:AN1:773:G:OP1	5:AN1:775:G:O2'	2.37	0.40
5:AN1:782:G:H5'	5:AN1:783:G:OP1	2.21	0.40
5:AN1:1850:A:H4'	5:AN1:2229:U:H4'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN1:2312:G:H2'	5:AN1:2313:C:C6	2.56	0.40
5:AN1:2485:U:H2'	5:AN1:2486:G:O4'	2.22	0.40
5:AN1:2791:C:H2'	5:AN1:2792:U:C6	2.56	0.40
10:F:38:MET:HG3	10:F:151:GLY:O	2.21	0.40
10:F:80:ARG:H	10:F:83:TRP:CD1	2.40	0.40
10:F:137:VAL:O	10:F:137:VAL:HG12	2.21	0.40
30:Z:37:HIS:ND1	30:Z:38:ARG:O	2.54	0.40
31:sN1:515:C:H2'	31:sN1:527:G:N2	2.37	0.40
31:sN1:572:G:O2'	31:sN1:818:G:H5'	2.21	0.40
31:sN1:895:G:N2	31:sN1:898:A:OP2	2.50	0.40
31:sN1:1095:C:H2'	31:sN1:1096:G:C8	2.55	0.40
36:f:32:ALA:HB3	36:f:35:GLN:NE2	2.37	0.40
42:l:52:VAL:HG21	42:l:90:LEU:HD23	2.04	0.40
5:AN1:1185:G:H5'	15:K:34:GLY:HA2	2.04	0.40
5:AN1:1561:U:H2'	5:AN1:1562:C:C6	2.56	0.40
5:AN1:2647:C:H2'	5:AN1:2648:C:C6	2.57	0.40
6:B:63:U:H2'	6:B:64:A:O4'	2.22	0.40
31:sN1:308:C:H2'	31:sN1:309:A:H8	1.86	0.40
31:sN1:475:G:H2'	31:sN1:476:U:C6	2.57	0.40
31:sN1:845:C:H2'	31:sN1:846:U:H6	1.87	0.40
5:AN1:880:G:C6	5:AN1:893:U:H1'	2.57	0.40
5:AN1:880:G:H22	5:AN1:893:U:H4'	1.86	0.40
5:AN1:883:C:H5'	5:AN1:884:A:OP2	2.22	0.40
5:AN1:968:C:H2'	5:AN1:969:A:O4'	2.21	0.40
5:AN1:1792:U:H2'	5:AN1:1793:C:H6	1.87	0.40
5:AN1:1858:G:H1	5:AN1:1876:U:H3	1.68	0.40
5:AN1:2070:U:H2'	5:AN1:2071:U:H6	1.87	0.40
5:AN1:2188:G:H2'	5:AN1:2189:G:H8	1.86	0.40
5:AN1:2834:G:C4	5:AN1:2835:G:C8	3.09	0.40
7:C:137:ILE:HD11	7:C:166:GLY:HA2	2.04	0.40
10:F:72:LYS:HD2	10:F:72:LYS:HA	1.78	0.40
19:O:28:THR:HG22	19:O:91:ARG:HB3	2.04	0.40
21:Q:60:THR:OG1	21:Q:99:THR:OG1	2.28	0.40
31:sN1:231:U:H2'	31:sN1:232:A:C8	2.51	0.40
31:sN1:529:A:N6	33:c:161:GLU:OE1	2.55	0.40
31:sN1:1123:U:O2'	31:sN1:1124:G:P	2.78	0.40
31:sN1:1187:G:H4'	31:sN1:1188:A:OP2	2.22	0.40
31:sN1:1268:G:H2'	31:sN1:1269:U:C6	2.57	0.40
32:b:133:LYS:HE3	32:b:133:LYS:HB3	1.89	0.40
43:m:80:LEU:HD21	43:m:87:ARG:HE	1.86	0.40
52:v:47:G:H3'	52:v:48:U:C6	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	49/51 (96%)	47 (96%)	2 (4%)	0	100	100
2	1	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
3	2	61/64 (95%)	54 (88%)	5 (8%)	2 (3%)	3	15
4	3	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
7	C	268/274 (98%)	259 (97%)	9 (3%)	0	100	100
8	D	209/212 (99%)	205 (98%)	4 (2%)	0	100	100
9	E	184/200 (92%)	184 (100%)	0	0	100	100
10	F	173/178 (97%)	158 (91%)	14 (8%)	1 (1%)	21	53
11	G	172/177 (97%)	167 (97%)	5 (3%)	0	100	100
12	H	58/148 (39%)	53 (91%)	5 (9%)	0	100	100
13	I	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
14	J	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
15	K	144/146 (99%)	141 (98%)	3 (2%)	0	100	100
16	L	135/137 (98%)	135 (100%)	0	0	100	100
17	M	117/125 (94%)	117 (100%)	0	0	100	100
18	N	112/116 (97%)	111 (99%)	1 (1%)	0	100	100
19	O	115/122 (94%)	112 (97%)	3 (3%)	0	100	100
20	P	115/119 (97%)	114 (99%)	1 (1%)	0	100	100
21	Q	101/103 (98%)	94 (93%)	7 (7%)	0	100	100
22	R	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
23	S	88/106 (83%)	88 (100%)	0	0	100	100
24	T	98/105 (93%)	97 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	U	95/98 (97%)	94 (99%)	1 (1%)	0	100	100
26	V	78/85 (92%)	77 (99%)	1 (1%)	0	100	100
27	W	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
28	X	60/65 (92%)	60 (100%)	0	0	100	100
29	Y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
30	Z	53/61 (87%)	51 (96%)	2 (4%)	0	100	100
32	b	223/250 (89%)	216 (97%)	7 (3%)	0	100	100
33	c	213/250 (85%)	205 (96%)	8 (4%)	0	100	100
34	d	205/208 (99%)	201 (98%)	4 (2%)	0	100	100
35	e	153/165 (93%)	153 (100%)	0	0	100	100
36	f	92/127 (72%)	88 (96%)	4 (4%)	0	100	100
37	g	139/156 (89%)	138 (99%)	1 (1%)	0	100	100
38	h	128/131 (98%)	123 (96%)	5 (4%)	0	100	100
39	i	125/128 (98%)	123 (98%)	2 (2%)	0	100	100
40	j	98/103 (95%)	94 (96%)	4 (4%)	0	100	100
41	k	115/128 (90%)	110 (96%)	5 (4%)	0	100	100
42	l	120/124 (97%)	113 (94%)	7 (6%)	0	100	100
43	m	113/118 (96%)	110 (97%)	3 (3%)	0	100	100
44	n	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
45	o	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
46	p	81/101 (80%)	80 (99%)	1 (1%)	0	100	100
47	q	78/85 (92%)	76 (97%)	2 (3%)	0	100	100
48	r	51/75 (68%)	51 (100%)	0	0	100	100
49	s	80/91 (88%)	79 (99%)	1 (1%)	0	100	100
50	t	83/88 (94%)	82 (99%)	1 (1%)	0	100	100
51	u	19/71 (27%)	17 (90%)	2 (10%)	0	100	100
All	All	5361/5872 (91%)	5223 (97%)	135 (2%)	3 (0%)	49	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	31	ILE
3	2	32	LEU

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Mol	Chain	Res	Type
10	F	139	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/47 (100%)	47 (100%)	0	100	100
2	1	36/36 (100%)	36 (100%)	0	100	100
3	2	52/53 (98%)	52 (100%)	0	100	100
4	3	33/33 (100%)	33 (100%)	0	100	100
7	C	216/220 (98%)	216 (100%)	0	100	100
8	D	166/167 (99%)	166 (100%)	0	100	100
9	E	144/155 (93%)	144 (100%)	0	100	100
10	F	145/147 (99%)	145 (100%)	0	100	100
11	G	139/142 (98%)	139 (100%)	0	100	100
12	H	45/112 (40%)	45 (100%)	0	100	100
13	I	118/118 (100%)	118 (100%)	0	100	100
14	J	103/103 (100%)	103 (100%)	0	100	100
15	K	108/108 (100%)	108 (100%)	0	100	100
16	L	113/113 (100%)	113 (100%)	0	100	100
17	M	96/101 (95%)	96 (100%)	0	100	100
18	N	83/85 (98%)	83 (100%)	0	100	100
19	O	99/102 (97%)	99 (100%)	0	100	100
20	P	85/86 (99%)	85 (100%)	0	100	100
21	Q	84/84 (100%)	84 (100%)	0	100	100
22	R	88/88 (100%)	88 (100%)	0	100	100
23	S	76/87 (87%)	76 (100%)	0	100	100
24	T	82/85 (96%)	82 (100%)	0	100	100
25	U	79/80 (99%)	79 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	V	60/64 (94%)	60 (100%)	0	100	100
27	W	69/70 (99%)	69 (100%)	0	100	100
28	X	54/56 (96%)	54 (100%)	0	100	100
29	Y	54/54 (100%)	54 (100%)	0	100	100
30	Z	47/50 (94%)	47 (100%)	0	100	100
32	b	185/200 (92%)	185 (100%)	0	100	100
33	c	175/198 (88%)	175 (100%)	0	100	100
34	d	170/171 (99%)	170 (100%)	0	100	100
35	e	113/120 (94%)	113 (100%)	0	100	100
36	f	86/111 (78%)	86 (100%)	0	100	100
37	g	116/128 (91%)	116 (100%)	0	100	100
38	h	108/109 (99%)	108 (100%)	0	100	100
39	i	99/100 (99%)	99 (100%)	0	100	100
40	j	89/91 (98%)	89 (100%)	0	100	100
41	k	88/98 (90%)	88 (100%)	0	100	100
42	l	104/106 (98%)	104 (100%)	0	100	100
43	m	95/98 (97%)	95 (100%)	0	100	100
44	n	81/82 (99%)	81 (100%)	0	100	100
45	o	71/72 (99%)	71 (100%)	0	100	100
46	p	63/77 (82%)	63 (100%)	0	100	100
47	q	72/76 (95%)	72 (100%)	0	100	100
48	r	47/66 (71%)	47 (100%)	0	100	100
49	s	70/78 (90%)	70 (100%)	0	100	100
50	t	65/67 (97%)	65 (100%)	0	100	100
51	u	18/62 (29%)	18 (100%)	0	100	100
All	All	4436/4756 (93%)	4436 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (108) such sidechains are listed below:

Mol	Chain	Res	Type
2	1	16	HIS

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Mol	Chain	Res	Type
3	2	30	HIS
3	2	50	HIS
7	C	4	GLN
7	C	48	HIS
7	C	58	HIS
7	C	60	GLN
7	C	90	HIS
7	C	117	GLN
7	C	200	ASN
7	C	230	HIS
7	C	250	GLN
8	D	47	GLN
8	D	108	GLN
8	D	137	HIS
9	E	61	GLN
9	E	96	ASN
9	E	138	ASN
10	F	127	ASN
11	G	74	ASN
11	G	106	ASN
11	G	143	GLN
13	I	40	HIS
13	I	77	HIS
13	I	95	HIS
13	I	135	GLN
15	K	40	GLN
15	K	71	GLN
16	L	22	HIS
16	L	110	ASN
17	M	72	ASN
19	O	13	ASN
19	O	15	GLN
19	O	59	ASN
19	O	78	GLN
20	P	11	HIS
20	P	44	GLN
21	Q	46	ASN
21	Q	48	GLN
21	Q	87	GLN
22	R	57	ASN
22	R	60	HIS
23	S	2	ASN

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Mol	Chain	Res	Type
23	S	29	GLN
24	T	47	ASN
25	U	16	GLN
25	U	58	ASN
25	U	84	HIS
27	W	6	GLN
28	X	24	ASN
29	Y	24	GLN
30	Z	41	HIS
32	b	5	ASN
32	b	13	GLN
32	b	47	HIS
32	b	67	ASN
32	b	80	ASN
32	b	96	HIS
32	b	105	ASN
32	b	111	GLN
32	b	114	ASN
32	b	155	ASN
32	b	170	HIS
32	b	197	ASN
33	c	6	HIS
33	c	18	HIS
33	c	19	ASN
34	d	42	HIS
34	d	44	GLN
34	d	73	GLN
34	d	102	ASN
34	d	154	GLN
34	d	159	ASN
35	e	120	HIS
35	e	121	ASN
35	e	131	ASN
36	f	3	HIS
36	f	11	HIS
36	f	35	GLN
37	g	32	GLN
38	h	53	GLN
38	h	86	GLN
39	i	48	GLN
39	i	79	HIS
40	j	56	HIS

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Mol	Chain	Res	Type
40	j	58	ASN
41	k	21	HIS
41	k	27	ASN
41	k	28	ASN
41	k	80	ASN
41	k	117	HIS
42	l	72	HIS
43	m	8	ASN
43	m	12	ASN
43	m	52	GLN
43	m	105	ASN
44	n	8	ASN
44	n	54	ASN
45	o	37	ASN
45	o	42	HIS
46	p	44	ASN
47	q	32	HIS
48	r	36	ASN
48	r	54	GLN
49	s	52	HIS
50	t	13	GLN
50	t	70	ASN
50	t	80	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	sN1	1527/1544 (98%)	213 (13%)	0
5	AN1	2891/2918 (99%)	490 (16%)	8 (0%)
52	v	76/77 (98%)	29 (38%)	0
53	w	2/3 (66%)	0	0
6	B	114/115 (99%)	20 (17%)	1 (0%)
All	All	4610/4657 (98%)	752 (16%)	9 (0%)

All (752) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	AN1	10	U
5	AN1	34	G
5	AN1	41	U
5	AN1	50	G

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Mol	Chain	Res	Type
5	AN1	53	G
5	AN1	58	G
5	AN1	59	A
5	AN1	67	G
5	AN1	68	A
5	AN1	69	U
5	AN1	78	A
5	AN1	81	A
5	AN1	82	G
5	AN1	86	C
5	AN1	98	A
5	AN1	101	U
5	AN1	102	A
5	AN1	105	C
5	AN1	106	U
5	AN1	107	U
5	AN1	108	U
5	AN1	125	A
5	AN1	127	U
5	AN1	138	A
5	AN1	146	U
5	AN1	147	A
5	AN1	169	U
5	AN1	170	A
5	AN1	172	A
5	AN1	188	A
5	AN1	203	A
5	AN1	206	A
5	AN1	223	A
5	AN1	229	A
5	AN1	236	U
5	AN1	255	G
5	AN1	257	G
5	AN1	259	G
5	AN1	262	A
5	AN1	271	C
5	AN1	272	A
5	AN1	273	G
5	AN1	274	C
5	AN1	279	U
5	AN1	280	A
5	AN1	283	U

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Mol	Chain	Res	Type
5	AN1	284	U
5	AN1	285	A
5	AN1	289	G
5	AN1	291	G
5	AN1	293	U
5	AN1	303	C
5	AN1	313	A
5	AN1	331	G
5	AN1	332	A
5	AN1	345	C
5	AN1	351	G
5	AN1	356	A
5	AN1	357	C
5	AN1	359	U
5	AN1	366	G
5	AN1	369	G
5	AN1	371	G
5	AN1	385	G
5	AN1	386	U
5	AN1	395	G
5	AN1	403	A
5	AN1	404	U
5	AN1	410	G
5	AN1	423	G
5	AN1	434	C
5	AN1	450	U
5	AN1	455	C
5	AN1	479	A
5	AN1	480	G
5	AN1	504	A
5	AN1	508	C
5	AN1	509	C
5	AN1	526	C
5	AN1	529	G
5	AN1	531	A
5	AN1	532	G
5	AN1	541	C
5	AN1	543	U
5	AN1	544	U
5	AN1	545	C
5	AN1	547	U
5	AN1	554	A

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Mol	Chain	Res	Type
5	AN1	561	A
5	AN1	564	U
5	AN1	571	U
5	AN1	573	A
5	AN1	595	G
5	AN1	601	A
5	AN1	612	A
5	AN1	613	U
5	AN1	625	A
5	AN1	633	C
5	AN1	635	A
5	AN1	637	U
5	AN1	643	U
5	AN1	644	A
5	AN1	651	U
5	AN1	652	U
5	AN1	654	G
5	AN1	656	U
5	AN1	657	G
5	AN1	666	A
5	AN1	667	G
5	AN1	668	A
5	AN1	684	U
5	AN1	692	U
5	AN1	702	G
5	AN1	711	G
5	AN1	713	A
5	AN1	714	A
5	AN1	719	A
5	AN1	724	G
5	AN1	727	G
5	AN1	728	A
5	AN1	745	U
5	AN1	746	G
5	AN1	762	A
5	AN1	763	C
5	AN1	773	G
5	AN1	774	G
5	AN1	780	A
5	AN1	782	G
5	AN1	783	G
5	AN1	787	A

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Mol	Chain	Res	Type
5	AN1	803	G
5	AN1	810	C
5	AN1	817	A
5	AN1	825	U
5	AN1	828	G
5	AN1	843	G
5	AN1	851	U
5	AN1	855	G
5	AN1	857	G
5	AN1	864	A
5	AN1	883	C
5	AN1	884	A
5	AN1	888	C
5	AN1	889	G
5	AN1	890	A
5	AN1	894	A
5	AN1	895	C
5	AN1	899	A
5	AN1	904	U
5	AN1	908	A
5	AN1	926	G
5	AN1	929	C
5	AN1	930	U
5	AN1	938	A
5	AN1	942	A
5	AN1	943	G
5	AN1	950	G
5	AN1	955	U
5	AN1	958	C
5	AN1	971	G
5	AN1	977	A
5	AN1	980	A
5	AN1	993	A
5	AN1	1006	A
5	AN1	1009	U
5	AN1	1010	C
5	AN1	1023	G
5	AN1	1028	G
5	AN1	1032	U
5	AN1	1036	A
5	AN1	1037	A
5	AN1	1039	G

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Mol	Chain	Res	Type
5	AN1	1040	C
5	AN1	1041	A
5	AN1	1043	A
5	AN1	1044	G
5	AN1	1054	A
5	AN1	1057	U
5	AN1	1058	U
5	AN1	1059	G
5	AN1	1061	C
5	AN1	1063	U
5	AN1	1067	A
5	AN1	1070	A
5	AN1	1076	C
5	AN1	1081	A
5	AN1	1082	A
5	AN1	1085	A
5	AN1	1086	A
5	AN1	1091	U
5	AN1	1101	C
5	AN1	1108	A
5	AN1	1109	G
5	AN1	1110	U
5	AN1	1121	G
5	AN1	1129	U
5	AN1	1130	A
5	AN1	1131	A
5	AN1	1132	C
5	AN1	1140	A
5	AN1	1149	G
5	AN1	1167	U
5	AN1	1170	U
5	AN1	1171	U
5	AN1	1172	U
5	AN1	1173	G
5	AN1	1179	G
5	AN1	1200	A
5	AN1	1201	G
5	AN1	1231	G
5	AN1	1242	A
5	AN1	1245	G
5	AN1	1248	A
5	AN1	1251	G

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Mol	Chain	Res	Type
5	AN1	1267	A
5	AN1	1296	A
5	AN1	1309	C
5	AN1	1316	A
5	AN1	1336	G
5	AN1	1340	C
5	AN1	1360	A
5	AN1	1363	G
5	AN1	1373	A
5	AN1	1374	U
5	AN1	1378	A
5	AN1	1390	A
5	AN1	1407	U
5	AN1	1408	A
5	AN1	1411	G
5	AN1	1414	A
5	AN1	1415	U
5	AN1	1423	C
5	AN1	1428	A
5	AN1	1432	C
5	AN1	1433	U
5	AN1	1447	G
5	AN1	1448	U
5	AN1	1453	U
5	AN1	1455	U
5	AN1	1456	C
5	AN1	1470	G
5	AN1	1473	G
5	AN1	1477	U
5	AN1	1485	A
5	AN1	1501	C
5	AN1	1502	U
5	AN1	1504	U
5	AN1	1505	A
5	AN1	1509	U
5	AN1	1510	G
5	AN1	1520	A
5	AN1	1530	A
5	AN1	1531	C
5	AN1	1534	G
5	AN1	1539	G
5	AN1	1540	C

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Mol	Chain	Res	Type
5	AN1	1541	G
5	AN1	1542	A
5	AN1	1544	G
5	AN1	1545	U
5	AN1	1564	A
5	AN1	1567	A
5	AN1	1574	U
5	AN1	1583	C
5	AN1	1605	G
5	AN1	1606	A
5	AN1	1616	A
5	AN1	1642	C
5	AN1	1645	U
5	AN1	1646	U
5	AN1	1672	G
5	AN1	1673	C
5	AN1	1691	U
5	AN1	1712	U
5	AN1	1713	U
5	AN1	1714	G
5	AN1	1717	G
5	AN1	1718	A
5	AN1	1725	U
5	AN1	1726	C
5	AN1	1731	C
5	AN1	1746	G
5	AN1	1760	G
5	AN1	1769	A
5	AN1	1776	A
5	AN1	1780	A
5	AN1	1796	C
5	AN1	1797	A
5	AN1	1798	A
5	AN1	1805	A
5	AN1	1812	C
5	AN1	1825	A
5	AN1	1829	C
5	AN1	1844	A
5	AN1	1855	U
5	AN1	1866	U
5	AN1	1871	G
5	AN1	1872	A

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Mol	Chain	Res	Type
5	AN1	1885	A
5	AN1	1895	A
5	AN1	1899	G
5	AN1	1902	G
5	AN1	1905	C
5	AN1	1907	PSU
5	AN1	1909	A
5	AN1	1910	C
5	AN1	1911	3TD
5	AN1	1915	A
5	AN1	1917	G
5	AN1	1918	G
5	AN1	1925	G
5	AN1	1926	G
5	AN1	1932	A
5	AN1	1933	A
5	AN1	1934	A
5	AN1	1936	U
5	AN1	1950	G
5	AN1	1951	U
5	AN1	1958	C
5	AN1	1960	G
5	AN1	1963	C
5	AN1	1966	A
5	AN1	1967	U
5	AN1	1968	G
5	AN1	1978	U
5	AN1	1987	U
5	AN1	1989	U
5	AN1	1993	C
5	AN1	2018	U
5	AN1	2019	C
5	AN1	2025	G
5	AN1	2026	6MZ
5	AN1	2027	A
5	AN1	2029	A
5	AN1	2030	U
5	AN1	2039	C
5	AN1	2051	C
5	AN1	2052	G
5	AN1	2056	A
5	AN1	2057	G

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Mol	Chain	Res	Type
5	AN1	2058	A
5	AN1	2065	7MG
5	AN1	2089	G
5	AN1	2092	C
5	AN1	2104	U
5	AN1	2106	G
5	AN1	2107	U
5	AN1	2108	G
5	AN1	2111	G
5	AN1	2112	G
5	AN1	2113	A
5	AN1	2114	U
5	AN1	2115	A
5	AN1	2116	G
5	AN1	2117	G
5	AN1	2119	G
5	AN1	2120	G
5	AN1	2121	G
5	AN1	2122	A
5	AN1	2123	G
5	AN1	2127	U
5	AN1	2128	U
5	AN1	2129	G
5	AN1	2133	C
5	AN1	2142	U
5	AN1	2143	A
5	AN1	2145	U
5	AN1	2146	U
5	AN1	2148	C
5	AN1	2149	A
5	AN1	2152	G
5	AN1	2153	G
5	AN1	2154	A
5	AN1	2157	C
5	AN1	2158	G
5	AN1	2167	A
5	AN1	2168	U
5	AN1	2169	A
5	AN1	2171	C
5	AN1	2172	A
5	AN1	2174	C
5	AN1	2178	G

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Mol	Chain	Res	Type
5	AN1	2194	A
5	AN1	2200	G
5	AN1	2207	G
5	AN1	2221	A
5	AN1	2222	C
5	AN1	2234	G
5	AN1	2235	G
5	AN1	2261	U
5	AN1	2275	G
5	AN1	2279	U
5	AN1	2283	A
5	AN1	2284	A
5	AN1	2301	U
5	AN1	2304	G
5	AN1	2305	A
5	AN1	2308	U
5	AN1	2312	G
5	AN1	2314	G
5	AN1	2316	A
5	AN1	2321	A
5	AN1	2323	A
5	AN1	2346	C
5	AN1	2355	C
5	AN1	2357	A
5	AN1	2378	G
5	AN1	2379	G
5	AN1	2380	U
5	AN1	2381	C
5	AN1	2399	C
5	AN1	2408	A
5	AN1	2418	C
5	AN1	2425	G
5	AN1	2426	A
5	AN1	2427	U
5	AN1	2429	A
5	AN1	2431	A
5	AN1	2437	U
5	AN1	2443	G
5	AN1	2444	A
5	AN1	2446	A
5	AN1	2455	A
5	AN1	2468	G

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Mol	Chain	Res	Type
5	AN1	2469	U
5	AN1	2470	U
5	AN1	2472	A
5	AN1	2473	U
5	AN1	2474	A
5	AN1	2487	U
5	AN1	2494	C
5	AN1	2498	G
5	AN1	2499	2MA
5	AN1	2501	G
5	AN1	2503	C
5	AN1	2514	A
5	AN1	2516	C
5	AN1	2525	G
5	AN1	2530	A
5	AN1	2543	A
5	AN1	2548	OMU
5	AN1	2550	U
5	AN1	2562	A
5	AN1	2563	G
5	AN1	2568	A
5	AN1	2574	G
5	AN1	2598	A
5	AN1	2599	G
5	AN1	2605	U
5	AN1	2606	C
5	AN1	2607	C
5	AN1	2609	U
5	AN1	2611	U
5	AN1	2625	U
5	AN1	2635	A
5	AN1	2642	C
5	AN1	2657	G
5	AN1	2661	A
5	AN1	2685	U
5	AN1	2686	A
5	AN1	2710	G
5	AN1	2722	U
5	AN1	2730	A
5	AN1	2744	A
5	AN1	2753	A
5	AN1	2754	A

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Mol	Chain	Res	Type
5	AN1	2761	A
5	AN1	2774	A
5	AN1	2776	A
5	AN1	2787	A
5	AN1	2788	G
5	AN1	2793	U
5	AN1	2794	U
5	AN1	2796	U
5	AN1	2797	G
5	AN1	2800	C
5	AN1	2804	A
5	AN1	2816	G
5	AN1	2817	A
5	AN1	2829	U
5	AN1	2831	A
5	AN1	2845	G
5	AN1	2851	U
5	AN1	2853	G
5	AN1	2857	U
5	AN1	2863	A
5	AN1	2868	G
5	AN1	2875	A
5	AN1	2897	C
5	AN1	2898	U
6	B	2	C
6	B	10	C
6	B	11	A
6	B	14	G
6	B	15	C
6	B	22	G
6	B	23	A
6	B	31	G
6	B	32	A
6	B	39	C
6	B	40	C
6	B	42	G
6	B	44	A
6	B	50	A
6	B	86	U
6	B	87	A
6	B	105	C
6	B	106	A

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Mol	Chain	Res	Type
6	B	108	C
6	B	109	G
31	sN1	4	A
31	sN1	5	A
31	sN1	10	A
31	sN1	11	G
31	sN1	41	G
31	sN1	49	C
31	sN1	50	U
31	sN1	53	A
31	sN1	57	A
31	sN1	64	U
31	sN1	80	A
31	sN1	86	C
31	sN1	87	U
31	sN1	90	C
31	sN1	91	G
31	sN1	97	A
31	sN1	105	A
31	sN1	107	G
31	sN1	126	A
31	sN1	127	U
31	sN1	140	G
31	sN1	157	A
31	sN1	170	A
31	sN1	184	A
31	sN1	186	G
31	sN1	193	A
31	sN1	204	U
31	sN1	205	U
31	sN1	206	C
31	sN1	212	U
31	sN1	216	G
31	sN1	236	C
31	sN1	243	G
31	sN1	247	G
31	sN1	262	G
31	sN1	263	C
31	sN1	285	G
31	sN1	289	G
31	sN1	302	A
31	sN1	324	C

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Mol	Chain	Res	Type
31	sN1	340	A
31	sN1	341	C
31	sN1	348	C
31	sN1	359	A
31	sN1	363	U
31	sN1	368	C
31	sN1	388	C
31	sN1	393	A
31	sN1	402	G
31	sN1	407	A
31	sN1	408	A
31	sN1	409	G
31	sN1	425	U
31	sN1	434	U
31	sN1	447	A
31	sN1	463	U
31	sN1	474	A
31	sN1	475	G
31	sN1	476	U
31	sN1	478	G
31	sN1	479	A
31	sN1	481	G
31	sN1	482	U
31	sN1	493	A
31	sN1	494	U
31	sN1	505	U
31	sN1	506	A
31	sN1	507	A
31	sN1	508	C
31	sN1	515	C
31	sN1	521	G
31	sN1	522	C
31	sN1	524	7MG
31	sN1	527	G
31	sN1	544	A
31	sN1	556	A
31	sN1	561	C
31	sN1	567	G
31	sN1	569	A
31	sN1	570	A
31	sN1	572	G
31	sN1	573	C

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Mol	Chain	Res	Type
31	sN1	574	G
31	sN1	593	A
31	sN1	615	C
31	sN1	630	G
31	sN1	639	A
31	sN1	650	A
31	sN1	662	A
31	sN1	684	A
31	sN1	685	G
31	sN1	700	G
31	sN1	714	U
31	sN1	721	G
31	sN1	728	G
31	sN1	744	A
31	sN1	745	U
31	sN1	752	G
31	sN1	774	A
31	sN1	778	A
31	sN1	790	U
31	sN1	791	A
31	sN1	812	A
31	sN1	814	C
31	sN1	839	U
31	sN1	840	U
31	sN1	841	G
31	sN1	842	A
31	sN1	843	G
31	sN1	886	A
31	sN1	899	G
31	sN1	928	C
31	sN1	931	C
31	sN1	932	A
31	sN1	935	A
31	sN1	951	G
31	sN1	957	U
31	sN1	958	U
31	sN1	963	2MG
31	sN1	966	A
31	sN1	968	G
31	sN1	970	G
31	sN1	972	A
31	sN1	973	G

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Mol	Chain	Res	Type
31	sN1	974	A
31	sN1	989	U
31	sN1	990	G
31	sN1	991	A
31	sN1	992	C
31	sN1	993	A
31	sN1	998	A
31	sN1	1001	A
31	sN1	1003	C
31	sN1	1007	C
31	sN1	1008	C
31	sN1	1010	G
31	sN1	1016	G
31	sN1	1023	G
31	sN1	1025	C
31	sN1	1026	U
31	sN1	1028	C
31	sN1	1029	G
31	sN1	1030	G
31	sN1	1041	A
31	sN1	1042	C
31	sN1	1050	G
31	sN1	1061	G
31	sN1	1062	U
31	sN1	1069	G
31	sN1	1083	U
31	sN1	1084	G
31	sN1	1086	G
31	sN1	1091	G
31	sN1	1095	C
31	sN1	1098	A
31	sN1	1121	C
31	sN1	1122	U
31	sN1	1124	G
31	sN1	1131	U
31	sN1	1134	C
31	sN1	1136	G
31	sN1	1137	A
31	sN1	1156	U
31	sN1	1157	G
31	sN1	1161	G
31	sN1	1164	A

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Mol	Chain	Res	Type
31	sN1	1165	C
31	sN1	1180	C
31	sN1	1181	G
31	sN1	1182	G
31	sN1	1185	A
31	sN1	1188	A
31	sN1	1193	A
31	sN1	1194	A
31	sN1	1209	U
31	sN1	1210	A
31	sN1	1211	C
31	sN1	1224	A
31	sN1	1235	A
31	sN1	1247	A
31	sN1	1249	A
31	sN1	1255	G
31	sN1	1257	U
31	sN1	1275	U
31	sN1	1276	A
31	sN1	1277	A
31	sN1	1284	A
31	sN1	1295	U
31	sN1	1297	G
31	sN1	1299	C
31	sN1	1302	G
31	sN1	1317	C
31	sN1	1361	U
31	sN1	1378	U
31	sN1	1380	C
31	sN1	1384	G
31	sN1	1394	C
31	sN1	1395	A
31	sN1	1398	G
31	sN1	1402	G
31	sN1	1425	A
31	sN1	1427	C
31	sN1	1448	C
31	sN1	1449	A
31	sN1	1450	A
31	sN1	1490	A
31	sN1	1491	G
31	sN1	1494	G

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Mol	Chain	Res	Type
31	sN1	1499	A
31	sN1	1503	U
31	sN1	1517	C
31	sN1	1526	G
31	sN1	1527	G
52	v	4	U
52	v	13	C
52	v	16	U
52	v	17	U
52	v	18	G
52	v	19	G
52	v	20	H2U
52	v	21	U
52	v	22	A
52	v	23	G
52	v	25	G
52	v	43	G
52	v	46	G
52	v	47	G
52	v	48	U
52	v	49	C
52	v	51	C
52	v	55	5MU
52	v	58	A
52	v	59	A
52	v	60	G
52	v	61	U
52	v	62	C
52	v	64	C
52	v	65	G
52	v	67	C
52	v	75	C
52	v	76	C
52	v	77	A

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	AN1	355	C
5	AN1	356	A
5	AN1	368	C
5	AN1	478	A

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Mol	Chain	Res	Type
5	AN1	782	G
5	AN1	1538	A
5	AN1	2170	C
5	AN1	2379	G
6	B	108	C

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

28 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
5	5MU	AN1	1935	5	19,22,23	4.99	7 (36%)	27,32,35	3.64	9 (33%)
5	7MG	AN1	2065	5	23,26,27	3.54	10 (43%)	27,39,42	2.15	9 (33%)
31	7MG	sN1	524	31	23,26,27	3.63	11 (47%)	27,39,42	2.18	9 (33%)
5	OMU	AN1	2548	5	19,22,23	3.10	8 (42%)	25,31,34	1.81	4 (16%)
52	H2U	v	20	52	18,21,22	3.21	4 (22%)	19,30,33	1.33	3 (15%)
5	2MG	AN1	2441	5	23,26,27	2.89	8 (34%)	33,38,41	2.21	11 (33%)
31	2MG	sN1	963	31	23,26,27	2.91	8 (34%)	33,38,41	2.23	10 (30%)
5	2MA	AN1	2499	5,56	22,25,26	3.98	9 (40%)	32,37,40	2.75	11 (34%)
5	6MZ	AN1	2026	5	22,25,26	2.47	4 (18%)	29,36,39	3.41	13 (44%)
31	MA6	sN1	1515	31	23,26,27	1.38	4 (17%)	33,38,41	3.31	12 (36%)
31	5MC	sN1	964	31	19,22,23	3.90	8 (42%)	26,32,35	0.97	2 (7%)
31	MA6	sN1	1516	31	23,26,27	1.38	4 (17%)	33,38,41	3.29	12 (36%)
5	PSU	AN1	2576	5	18,21,22	1.10	1 (5%)	21,30,33	1.89	5 (23%)
52	4SU	v	8	52	18,21,22	4.47	8 (44%)	25,30,33	2.25	5 (20%)
31	UR3	sN1	1495	31	19,22,23	2.94	6 (31%)	26,32,35	1.61	3 (11%)
5	PSU	AN1	2500	5	18,21,22	1.15	1 (5%)	21,30,33	1.90	4 (19%)
52	PSU	v	56	52	18,21,22	1.13	1 (5%)	21,30,33	1.71	4 (19%)
31	PSU	sN1	513	31	18,21,22	1.16	1 (5%)	21,30,33	1.63	4 (19%)
5	PSU	AN1	952	5	18,21,22	1.12	1 (5%)	21,30,33	1.91	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
52	5MU	v	55	52	19,22,23	5.05	7 (36%)	27,32,35	3.75	9 (33%)
5	3TD	AN1	1911	5	19,22,23	4.32	7 (36%)	23,32,35	1.81	3 (13%)
5	PSU	AN1	1907	5	18,21,22	1.14	1 (5%)	21,30,33	1.87	4 (19%)
5	PSU	AN1	2601	5	18,21,22	1.10	1 (5%)	21,30,33	1.93	5 (23%)
5	PSU	AN1	1913	5	18,21,22	1.12	1 (5%)	21,30,33	1.83	5 (23%)
5	PSU	AN1	2453	5	18,21,22	1.11	1 (5%)	21,30,33	1.94	6 (28%)
31	4OC	sN1	1399	31	20,23,24	3.21	8 (40%)	25,32,35	0.88	1 (4%)
5	OMG	AN1	2247	52,5	23,26,27	2.35	8 (34%)	32,38,41	1.84	8 (25%)
31	2MG	sN1	1204	31	23,26,27	2.90	8 (34%)	33,38,41	2.20	11 (33%)

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
5	5MU	AN1	1935	5	-	0/7/25/26	0/2/2/2
5	7MG	AN1	2065	5	-	0/7/37/38	0/3/3/3
31	7MG	sN1	524	31	-	3/7/37/38	0/3/3/3
5	OMU	AN1	2548	5	-	2/9/27/28	0/2/2/2
52	H2U	v	20	52	-	4/7/38/39	0/2/2/2
5	2MG	AN1	2441	5	-	1/9/27/28	0/3/3/3
31	2MG	sN1	963	31	-	0/9/27/28	0/3/3/3
5	2MA	AN1	2499	5,56	-	1/7/25/26	0/3/3/3
5	6MZ	AN1	2026	5	-	2/9/27/28	0/3/3/3
31	MA6	sN1	1515	31	-	3/11/29/30	0/3/3/3
31	5MC	sN1	964	31	-	0/7/25/26	0/2/2/2
31	MA6	sN1	1516	31	-	4/11/29/30	0/3/3/3
5	PSU	AN1	2576	5	-	0/7/25/26	0/2/2/2
52	4SU	v	8	52	-	4/7/25/26	0/2/2/2
31	UR3	sN1	1495	31	-	0/7/25/26	0/2/2/2
5	PSU	AN1	2500	5	-	0/7/25/26	0/2/2/2
52	PSU	v	56	52	-	2/7/25/26	0/2/2/2
31	PSU	sN1	513	31	-	0/7/25/26	0/2/2/2
5	PSU	AN1	952	5	-	0/7/25/26	0/2/2/2
52	5MU	v	55	52	-	6/7/25/26	0/2/2/2
5	3TD	AN1	1911	5	-	3/7/25/26	0/2/2/2
5	PSU	AN1	1907	5	-	1/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PSU	AN1	2601	5	-	0/7/25/26	0/2/2/2
5	PSU	AN1	1913	5	-	2/7/25/26	0/2/2/2
5	PSU	AN1	2453	5	-	0/7/25/26	0/2/2/2
31	4OC	sN1	1399	31	-	2/9/29/30	0/2/2/2
5	OMG	AN1	2247	52,5	-	0/9/27/28	0/3/3/3
31	2MG	sN1	1204	31	-	0/9/27/28	0/3/3/3

All (146) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AN1	1911	3TD	C6-C5	12.81	1.49	1.35
5	AN1	2499	2MA	C4-N3	12.19	1.50	1.34
52	v	55	5MU	C2-N1	11.66	1.56	1.38
5	AN1	1935	5MU	C2-N1	11.58	1.56	1.38
52	v	55	5MU	C6-N1	11.24	1.57	1.38
5	AN1	1935	5MU	C6-N1	10.96	1.56	1.38
5	AN1	1935	5MU	C4-C5	10.24	1.61	1.44
52	v	55	5MU	C4-C5	10.19	1.61	1.44
52	v	20	H2U	C2-N1	10.17	1.49	1.35
5	AN1	1911	3TD	C2-N1	10.09	1.49	1.37
5	AN1	2026	6MZ	C6-N6	10.06	1.45	1.34
52	v	8	4SU	C2-N1	9.99	1.54	1.38
31	sN1	964	5MC	C6-C5	9.17	1.49	1.34
31	sN1	524	7MG	C8-N9	8.67	1.51	1.45
52	v	8	4SU	C4-N3	8.65	1.46	1.37
5	AN1	2065	7MG	C8-N9	8.43	1.51	1.45
31	sN1	963	2MG	C2-N3	7.72	1.46	1.32
31	sN1	1204	2MG	C2-N3	7.71	1.46	1.32
5	AN1	2441	2MG	C2-N3	7.60	1.46	1.32
5	AN1	2499	2MA	C2-N3	7.43	1.46	1.34
52	v	55	5MU	C4-N3	-7.35	1.25	1.38
31	sN1	1495	UR3	C2-N1	7.32	1.48	1.38
5	AN1	2548	OMU	C2-N1	7.31	1.49	1.38
52	v	8	4SU	C5-C4	7.30	1.51	1.42
5	AN1	1935	5MU	C4-N3	-7.29	1.25	1.38
31	sN1	1399	4OC	C4-N3	7.22	1.44	1.32
31	sN1	524	7MG	C5-N7	7.12	1.44	1.35
52	v	8	4SU	C2-N3	7.04	1.50	1.38
5	AN1	2499	2MA	C6-N1	7.02	1.44	1.35
5	AN1	2065	7MG	C5-N7	7.00	1.44	1.35
31	sN1	964	5MC	C5-C4	6.99	1.49	1.44
5	AN1	2548	OMU	C2-N3	6.96	1.50	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	sN1	964	5MC	C4-N3	6.90	1.45	1.34
31	sN1	1495	UR3	C6-C5	6.79	1.50	1.35
31	sN1	963	2MG	C4-N3	6.78	1.49	1.34
31	sN1	1204	2MG	C4-N3	6.66	1.49	1.34
5	AN1	2441	2MG	C4-N3	6.66	1.49	1.34
5	AN1	1935	5MU	C6-C5	6.65	1.45	1.34
52	v	55	5MU	C6-C5	6.64	1.45	1.34
52	v	20	H2U	C2-N3	6.57	1.49	1.38
52	v	8	4SU	C6-C5	6.55	1.50	1.35
5	AN1	2247	OMG	C4-N3	6.41	1.48	1.34
31	sN1	1399	4OC	C6-C5	6.33	1.49	1.35
31	sN1	1399	4OC	C2-N3	6.33	1.48	1.36
31	sN1	964	5MC	C2-N3	6.30	1.48	1.36
5	AN1	2499	2MA	C2-N1	6.05	1.44	1.34
5	AN1	1911	3TD	C6-N1	6.04	1.46	1.36
31	sN1	524	7MG	C2-N3	5.91	1.47	1.33
31	sN1	524	7MG	C4-N3	5.84	1.47	1.34
31	sN1	963	2MG	C2-N2	5.80	1.45	1.33
31	sN1	1204	2MG	C2-N2	5.77	1.45	1.33
5	AN1	2065	7MG	C2-N3	5.77	1.47	1.33
5	AN1	2441	2MG	C2-N2	5.75	1.45	1.33
5	AN1	2065	7MG	C4-N3	5.73	1.47	1.34
31	sN1	1495	UR3	C2-N3	5.68	1.50	1.39
5	AN1	2548	OMU	C6-C5	5.67	1.48	1.35
5	AN1	2247	OMG	C2-N3	5.43	1.46	1.33
31	sN1	524	7MG	C4-N9	5.28	1.44	1.37
5	AN1	1911	3TD	C2-N3	5.21	1.49	1.38
52	v	20	H2U	C4-N3	5.02	1.46	1.37
31	sN1	524	7MG	C2-N2	5.02	1.45	1.34
5	AN1	2065	7MG	C2-N2	4.89	1.45	1.34
31	sN1	1204	2MG	C2-N1	4.87	1.44	1.36
52	v	8	4SU	C4-S4	-4.84	1.60	1.68
31	sN1	963	2MG	C2-N1	4.83	1.44	1.36
5	AN1	2065	7MG	C4-N9	4.82	1.43	1.37
5	AN1	2441	2MG	C2-N1	4.80	1.44	1.36
31	sN1	1399	4OC	C4-N4	4.79	1.45	1.36
5	AN1	2499	2MA	C5-C6	4.73	1.54	1.41
31	sN1	964	5MC	C6-N1	4.54	1.45	1.38
31	sN1	964	5MC	C4-N4	4.42	1.45	1.34
5	AN1	2548	OMU	C4-N3	4.38	1.46	1.38
31	sN1	964	5MC	C2-N1	4.37	1.49	1.40
31	sN1	1399	4OC	C2-N1	4.33	1.49	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AN1	2247	OMG	C2-N2	4.09	1.43	1.34
52	v	56	PSU	C6-C5	3.96	1.39	1.35
31	sN1	1515	MA6	C6-N6	3.95	1.47	1.36
31	sN1	1516	MA6	C6-N6	3.93	1.47	1.36
31	sN1	513	PSU	C6-C5	3.93	1.39	1.35
31	sN1	524	7MG	C2-N1	3.91	1.47	1.37
5	AN1	2065	7MG	C2-N1	3.90	1.47	1.37
5	AN1	1913	PSU	C6-C5	3.84	1.39	1.35
5	AN1	1907	PSU	C6-C5	3.81	1.39	1.35
5	AN1	2500	PSU	C6-C5	3.77	1.39	1.35
5	AN1	952	PSU	C6-C5	3.67	1.39	1.35
31	sN1	524	7MG	C5-C6	3.65	1.52	1.43
31	sN1	1399	4OC	C5-C4	3.65	1.49	1.41
5	AN1	2601	PSU	C6-C5	3.62	1.39	1.35
5	AN1	2065	7MG	C5-C6	3.56	1.52	1.43
5	AN1	2576	PSU	C6-C5	3.53	1.39	1.35
5	AN1	2453	PSU	C6-C5	3.52	1.39	1.35
5	AN1	2499	2MA	C6-N6	-3.37	1.25	1.34
31	sN1	1495	UR3	C6-N1	3.37	1.46	1.38
31	sN1	1399	4OC	C6-N1	3.33	1.46	1.38
52	v	55	5MU	O4-C4	-3.28	1.17	1.23
5	AN1	2065	7MG	C6-N1	3.28	1.45	1.38
31	sN1	524	7MG	C6-N1	3.28	1.45	1.38
5	AN1	2441	2MG	C5-N7	-2.94	1.33	1.39
5	AN1	2548	OMU	O4-C4	-2.89	1.18	1.24
5	AN1	1911	3TD	C4-N3	2.89	1.46	1.40
31	sN1	963	2MG	C5-N7	-2.88	1.33	1.39
5	AN1	2548	OMU	C6-N1	2.86	1.44	1.38
5	AN1	1935	5MU	O4-C4	-2.86	1.18	1.23
31	sN1	1204	2MG	C5-N7	-2.86	1.33	1.39
5	AN1	2026	6MZ	C5-C4	-2.85	1.34	1.39
5	AN1	2026	6MZ	C5-N7	-2.83	1.33	1.39
52	v	8	4SU	C6-N1	2.82	1.44	1.38
31	sN1	1516	MA6	C5-C4	-2.82	1.34	1.39
31	sN1	1515	MA6	C5-C4	-2.80	1.34	1.39
31	sN1	964	5MC	O2-C2	-2.79	1.18	1.23
52	v	8	4SU	O2-C2	-2.66	1.18	1.23
5	AN1	2247	OMG	C5-N7	-2.64	1.33	1.39
31	sN1	1495	UR3	C4-N3	2.63	1.45	1.40
31	sN1	1399	4OC	O2-C2	-2.61	1.18	1.23
5	AN1	2247	OMG	C6-N1	2.61	1.43	1.38
5	AN1	2247	OMG	C5-C6	2.60	1.54	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AN1	2065	7MG	O6-C6	-2.58	1.18	1.23
5	AN1	2499	2MA	C5-N7	-2.55	1.34	1.39
5	AN1	2441	2MG	O6-C6	-2.54	1.18	1.23
31	sN1	524	7MG	O6-C6	-2.54	1.18	1.23
31	sN1	963	2MG	C5-C6	2.51	1.53	1.44
52	v	20	H2U	O2-C2	-2.51	1.18	1.23
31	sN1	963	2MG	O6-C6	-2.50	1.18	1.23
5	AN1	1935	5MU	O2-C2	-2.49	1.18	1.23
31	sN1	1204	2MG	C5-C6	2.49	1.53	1.44
31	sN1	1204	2MG	O6-C6	-2.48	1.18	1.23
5	AN1	2441	2MG	C5-C6	2.47	1.53	1.44
5	AN1	2247	OMG	O6-C6	-2.46	1.18	1.23
5	AN1	2247	OMG	C2-N1	2.45	1.43	1.37
5	AN1	1911	3TD	O2-C2	-2.45	1.18	1.23
5	AN1	2548	OMU	C5-C4	2.43	1.49	1.43
5	AN1	2548	OMU	O2-C2	-2.42	1.18	1.23
52	v	55	5MU	O2-C2	-2.42	1.18	1.23
31	sN1	963	2MG	C6-N1	2.39	1.43	1.38
31	sN1	1204	2MG	C6-N1	2.38	1.43	1.38
5	AN1	2026	6MZ	C8-N9	-2.37	1.33	1.37
5	AN1	2441	2MG	C6-N1	2.36	1.43	1.38
31	sN1	1515	MA6	C5-N7	-2.31	1.34	1.39
31	sN1	1516	MA6	C5-N7	-2.30	1.34	1.39
31	sN1	1495	UR3	C5-C4	2.30	1.49	1.43
5	AN1	2499	2MA	C4-N9	-2.23	1.33	1.37
5	AN1	2499	2MA	C8-N7	2.18	1.35	1.31
31	sN1	1515	MA6	C8-N9	-2.08	1.34	1.37
5	AN1	1911	3TD	O4-C4	-2.07	1.18	1.23
31	sN1	524	7MG	C5-C4	2.06	1.44	1.37
31	sN1	1516	MA6	C8-N9	-2.06	1.34	1.37

All (186) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	v	55	5MU	C5-C4-N3	12.65	126.32	115.32
31	sN1	1515	MA6	N1-C6-N6	-12.22	101.97	116.86
31	sN1	1516	MA6	N1-C6-N6	-12.06	102.16	116.86
5	AN1	1935	5MU	C5-C4-N3	11.90	125.67	115.32
5	AN1	2026	6MZ	C4-N9-C1'	-9.90	103.47	126.63
5	AN1	2026	6MZ	C1'-N9-C8	9.73	148.69	127.09
5	AN1	1935	5MU	C5-C6-N1	-9.69	112.79	123.31
52	v	55	5MU	C5-C6-N1	-9.59	112.89	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	sN1	1515	MA6	C5-C6-N6	8.09	138.13	125.33
31	sN1	1516	MA6	C5-C6-N6	8.06	138.09	125.33
52	v	8	4SU	C4-N3-C2	-7.53	120.09	127.31
5	AN1	2499	2MA	C1'-N9-C8	-7.49	110.47	127.09
31	sN1	963	2MG	C2-N3-C4	6.78	120.49	112.00
5	AN1	2441	2MG	C2-N3-C4	6.55	120.19	112.00
31	sN1	1204	2MG	C2-N3-C4	6.49	120.12	112.00
5	AN1	2499	2MA	N9-C8-N7	-5.89	105.58	113.94
5	AN1	2499	2MA	C5-C4-N3	-5.62	121.26	127.18
31	sN1	1515	MA6	N1-C2-N3	-5.61	120.08	128.58
31	sN1	1516	MA6	N1-C2-N3	-5.61	120.09	128.58
5	AN1	2548	OMU	C4-N3-C2	-5.61	119.65	126.61
31	sN1	963	2MG	C5-C4-N3	-5.57	119.52	128.39
31	sN1	1495	UR3	C4-N3-C2	-5.57	120.10	124.58
5	AN1	1911	3TD	N1-C2-N3	5.51	120.13	116.13
5	AN1	2026	6MZ	C5-C4-N3	-5.37	119.32	126.72
5	AN1	2441	2MG	C5-C4-N3	-5.35	119.87	128.39
5	AN1	2026	6MZ	N1-C2-N3	-5.31	120.54	128.58
31	sN1	1204	2MG	C5-C4-N3	-5.21	120.09	128.39
52	v	8	4SU	C5-C4-N3	5.14	119.54	114.75
52	v	55	5MU	C4-N3-C2	-5.14	120.60	127.34
52	v	55	5MU	O4-C4-C5	-5.13	119.05	124.92
5	AN1	2499	2MA	C4-N9-C8	5.08	111.07	105.74
5	AN1	2499	2MA	C4-N9-C1'	5.06	138.46	126.63
31	sN1	524	7MG	C5-C6-N1	5.00	119.73	110.94
5	AN1	2065	7MG	C5-C6-N1	4.98	119.71	110.94
5	AN1	2453	PSU	C4-N3-C2	-4.96	119.54	126.37
5	AN1	1935	5MU	O4-C4-C5	-4.91	119.31	124.92
5	AN1	2247	OMG	C5-C4-N3	-4.90	120.59	128.39
5	AN1	2601	PSU	C4-N3-C2	-4.89	119.64	126.37
5	AN1	1935	5MU	C4-N3-C2	-4.86	120.97	127.34
31	sN1	1515	MA6	C5-C4-N3	-4.78	120.13	126.72
31	sN1	1516	MA6	C5-C4-N3	-4.78	120.14	126.72
5	AN1	952	PSU	C4-N3-C2	-4.76	119.81	126.37
5	AN1	2601	PSU	N1-C2-N3	4.76	120.19	115.17
5	AN1	952	PSU	N1-C2-N3	4.76	120.19	115.17
5	AN1	2500	PSU	N1-C2-N3	4.76	120.19	115.17
5	AN1	2500	PSU	C4-N3-C2	-4.75	119.83	126.37
5	AN1	2576	PSU	N1-C2-N3	4.73	120.16	115.17
5	AN1	2453	PSU	N1-C2-N3	4.72	120.15	115.17
5	AN1	2576	PSU	C4-N3-C2	-4.72	119.87	126.37
5	AN1	1907	PSU	N1-C2-N3	4.68	120.11	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	AN1	1907	PSU	C4-N3-C2	-4.68	119.93	126.37
52	v	55	5MU	N3-C2-N1	4.67	120.97	114.89
5	AN1	1913	PSU	N1-C2-N3	4.60	120.02	115.17
31	sN1	524	7MG	C2-N3-C4	4.58	120.19	112.30
5	AN1	1913	PSU	C4-N3-C2	-4.56	120.08	126.37
5	AN1	2247	OMG	C2-N3-C4	4.55	120.13	112.30
5	AN1	2065	7MG	C2-N3-C4	4.53	120.10	112.30
5	AN1	1935	5MU	N3-C2-N1	4.52	120.78	114.89
5	AN1	1911	3TD	C4-N3-C2	-4.38	119.97	124.61
31	sN1	1516	MA6	N9-C8-N7	-4.34	107.78	113.94
52	v	56	PSU	N1-C2-N3	4.29	119.69	115.17
31	sN1	1515	MA6	N9-C8-N7	-4.29	107.85	113.94
5	AN1	2499	2MA	N3-C4-N9	4.28	132.43	126.99
52	v	56	PSU	C4-N3-C2	-4.22	120.55	126.37
31	sN1	963	2MG	C2-N1-C6	-4.22	119.45	124.55
5	AN1	2441	2MG	C2-N1-C6	-4.19	119.49	124.55
31	sN1	513	PSU	C4-N3-C2	-4.19	120.60	126.37
31	sN1	524	7MG	C5-C4-N3	-4.18	120.29	128.13
31	sN1	1204	2MG	C2-N1-C6	-4.14	119.54	124.55
5	AN1	2065	7MG	C5-C4-N3	-4.07	120.50	128.13
31	sN1	513	PSU	N1-C2-N3	4.04	119.43	115.17
5	AN1	1935	5MU	C5M-C5-C6	-3.96	117.49	122.85
5	AN1	2026	6MZ	C4-C5-C6	3.95	120.06	116.78
31	sN1	524	7MG	C4-C5-N7	3.91	109.99	105.38
31	sN1	1516	MA6	C4-C5-C6	3.88	119.93	115.91
5	AN1	2026	6MZ	N9-C8-N7	-3.87	108.44	113.94
52	v	8	4SU	N3-C2-N1	3.87	119.93	114.89
5	AN1	2548	OMU	N3-C2-N1	3.84	119.89	114.89
5	AN1	1935	5MU	C5M-C5-C4	3.82	122.86	118.78
31	sN1	1515	MA6	C4-C5-C6	3.81	119.85	115.91
52	v	55	5MU	C5M-C5-C4	3.75	122.79	118.78
5	AN1	2065	7MG	C4-C5-N7	3.70	109.74	105.38
31	sN1	1495	UR3	C5-C4-N3	3.68	119.88	115.04
5	AN1	2548	OMU	C5-C4-N3	3.62	119.87	114.80
52	v	55	5MU	C5M-C5-C6	-3.61	117.96	122.85
31	sN1	963	2MG	N9-C4-N3	3.46	132.88	125.95
5	AN1	2499	2MA	C5-N7-C8	3.46	108.88	103.45
5	AN1	2026	6MZ	N3-C4-N9	3.45	133.04	127.17
31	sN1	1516	MA6	C2-N1-C6	3.43	120.21	111.83
5	AN1	2026	6MZ	C2-N3-C4	3.42	120.18	111.83
31	sN1	1515	MA6	C2-N1-C6	3.40	120.12	111.83
5	AN1	2499	2MA	N3-C2-N1	-3.34	119.88	125.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	v	8	4SU	C5-C4-S4	-3.32	120.51	124.31
31	sN1	963	2MG	N1-C2-N2	3.31	119.94	116.56
5	AN1	2441	2MG	N1-C2-N2	3.31	119.94	116.56
31	sN1	1515	MA6	C2-N3-C4	3.31	119.91	111.83
31	sN1	1516	MA6	C2-N3-C4	3.30	119.88	111.83
31	sN1	1204	2MG	N1-C2-N2	3.27	119.89	116.56
5	AN1	2065	7MG	C5-C4-N9	3.26	110.50	106.33
5	AN1	2441	2MG	N9-C4-N3	3.21	132.37	125.95
5	AN1	2247	OMG	N9-C8-N7	-3.17	107.51	113.40
31	sN1	1204	2MG	N9-C4-N3	3.09	132.13	125.95
52	v	20	H2U	C5-C6-N1	3.07	120.81	111.52
31	sN1	524	7MG	C5-C4-N9	3.03	110.22	106.33
31	sN1	964	5MC	C5-C6-N1	-3.01	120.04	123.31
52	v	20	H2U	N3-C2-N1	3.00	119.66	116.65
5	AN1	2548	OMU	O4-C4-C5	-2.95	120.08	125.16
52	v	55	5MU	O4-C4-N3	-2.92	114.63	120.11
31	sN1	1516	MA6	C5-N7-C8	2.91	108.03	103.45
31	sN1	1204	2MG	N9-C8-N7	-2.90	108.02	113.40
5	AN1	2441	2MG	N9-C8-N7	-2.90	108.02	113.40
31	sN1	1515	MA6	N3-C4-N9	2.89	132.09	127.17
31	sN1	1515	MA6	C5-N7-C8	2.89	107.99	103.45
31	sN1	1516	MA6	N3-C4-N9	2.88	132.06	127.17
5	AN1	2453	PSU	O2-C2-N1	-2.87	119.83	122.79
31	sN1	524	7MG	O6-C6-C5	-2.85	120.63	127.62
5	AN1	1913	PSU	O2-C2-N1	-2.82	119.88	122.79
5	AN1	2065	7MG	C2-N1-C6	-2.81	120.01	125.11
5	AN1	952	PSU	O2-C2-N1	-2.80	119.90	122.79
5	AN1	2065	7MG	O6-C6-C5	-2.80	120.74	127.62
5	AN1	2026	6MZ	C5-N7-C8	2.80	107.85	103.45
31	sN1	524	7MG	C2-N1-C6	-2.78	120.06	125.11
5	AN1	2576	PSU	O2-C2-N1	-2.78	119.92	122.79
31	sN1	963	2MG	N9-C8-N7	-2.78	108.25	113.40
5	AN1	1907	PSU	O2-C2-N1	-2.77	119.94	122.79
31	sN1	524	7MG	N9-C4-N3	2.76	129.50	125.46
52	v	20	H2U	C5-C4-N3	2.75	119.61	116.69
31	sN1	963	2MG	C5-C6-N1	2.72	120.19	113.25
5	AN1	1935	5MU	O4-C4-N3	-2.71	115.03	120.11
31	sN1	1204	2MG	C5-C6-N1	2.70	120.13	113.25
5	AN1	2500	PSU	O2-C2-N1	-2.70	120.00	122.79
5	AN1	2441	2MG	C5-C6-N1	2.66	120.04	113.25
5	AN1	2247	OMG	N9-C4-N3	2.61	131.17	125.95
5	AN1	2247	OMG	C2-N1-C6	-2.61	120.38	125.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	AN1	2601	PSU	O2-C2-N1	-2.60	120.11	122.79
5	AN1	1911	3TD	C6-C5-C4	2.55	119.90	118.19
52	v	55	5MU	O2-C2-N1	-2.52	119.52	122.80
31	sN1	963	2MG	O6-C6-C5	-2.51	119.92	126.53
5	AN1	2441	2MG	O6-C6-C5	-2.50	119.93	126.53
52	v	8	4SU	C1'-N1-C2	2.50	122.08	117.59
31	sN1	1516	MA6	C4-N9-C8	2.49	108.35	105.74
5	AN1	2500	PSU	C6-N1-C2	-2.49	120.38	122.69
31	sN1	1204	2MG	O6-C6-C5	-2.49	119.96	126.53
5	AN1	2576	PSU	C6-N1-C2	-2.49	120.38	122.69
5	AN1	1913	PSU	C6-N1-C2	-2.46	120.40	122.69
5	AN1	952	PSU	C6-N1-C2	-2.46	120.41	122.69
31	sN1	1515	MA6	C4-N9-C8	2.44	108.30	105.74
5	AN1	1935	5MU	O2-C2-N1	-2.43	119.63	122.80
52	v	56	PSU	C6-N1-C2	-2.42	120.44	122.69
5	AN1	2247	OMG	C5-C6-N1	2.42	119.41	113.25
5	AN1	2065	7MG	N9-C4-N3	2.41	129.00	125.46
5	AN1	2247	OMG	C8-N7-C5	2.41	108.56	104.26
5	AN1	1907	PSU	C6-N1-C2	-2.40	120.47	122.69
5	AN1	2026	6MZ	C5-C6-N1	2.38	120.71	118.15
31	sN1	1204	2MG	C1'-N9-C4	-2.38	119.47	126.49
31	sN1	524	7MG	N9-C8-N7	2.36	106.71	103.37
5	AN1	2601	PSU	C6-N1-C2	-2.27	120.58	122.69
5	AN1	2065	7MG	N9-C8-N7	2.27	106.59	103.37
31	sN1	1495	UR3	C6-N1-C2	-2.25	119.96	121.80
31	sN1	1516	MA6	C4-C5-N7	-2.23	108.03	110.58
52	v	56	PSU	O2-C2-N1	-2.21	120.51	122.79
31	sN1	1399	4OC	C6-C5-C4	2.20	119.65	117.00
31	sN1	1515	MA6	C4-C5-N7	-2.18	108.08	110.58
31	sN1	513	PSU	C6-N1-C2	-2.17	120.67	122.69
5	AN1	2499	2MA	CM2-C2-N1	2.17	120.38	117.13
5	AN1	2441	2MG	C1'-N9-C4	-2.17	120.07	126.49
31	sN1	963	2MG	N1-C2-N3	-2.17	120.03	123.68
5	AN1	2499	2MA	N6-C6-N1	2.16	119.94	117.03
31	sN1	1204	2MG	N1-C2-N3	-2.15	120.06	123.68
5	AN1	2453	PSU	C6-N1-C2	-2.13	120.72	122.69
5	AN1	2499	2MA	C4-C5-N7	-2.13	108.15	110.58
5	AN1	2453	PSU	C6-C5-C4	2.13	119.61	118.17
31	sN1	1204	2MG	C8-N7-C5	2.11	108.01	104.26
5	AN1	2441	2MG	C8-N7-C5	2.10	108.00	104.26
5	AN1	2247	OMG	C4-C5-N7	-2.09	107.35	110.67
5	AN1	2441	2MG	N1-C2-N3	-2.09	120.16	123.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	AN1	2026	6MZ	C9-N6-C6	-2.08	120.92	122.85
31	sN1	513	PSU	O4'-C1'-C2'	2.07	108.01	105.15
5	AN1	1913	PSU	O4'-C1'-C2'	2.07	108.01	105.15
5	AN1	2026	6MZ	C4-C5-N7	-2.06	108.22	110.58
31	sN1	963	2MG	C8-N7-C5	2.05	107.91	104.26
31	sN1	964	5MC	CM5-C5-C6	-2.04	120.09	122.85
5	AN1	2601	PSU	C6-C5-C4	2.04	119.55	118.17
5	AN1	2453	PSU	O4'-C1'-C2'	2.03	107.96	105.15
5	AN1	2576	PSU	O4'-C1'-C2'	2.03	107.96	105.15
5	AN1	2026	6MZ	C4-N9-C8	2.00	107.84	105.74

There are no chirality outliers.

All (40) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	AN1	1911	3TD	O4'-C4'-C5'-O5'
5	AN1	1913	PSU	O4'-C1'-C5-C6
5	AN1	2548	OMU	O4'-C4'-C5'-O5'
31	sN1	1515	MA6	C5-C6-N6-C9
52	v	8	4SU	O4'-C1'-N1-C2
52	v	8	4SU	O4'-C1'-N1-C6
52	v	55	5MU	C2'-C1'-N1-C6
52	v	56	PSU	C2'-C1'-C5-C4
52	v	56	PSU	C2'-C1'-C5-C6
5	AN1	1911	3TD	C3'-C4'-C5'-O5'
5	AN1	2548	OMU	C3'-C4'-C5'-O5'
31	sN1	524	7MG	C3'-C4'-C5'-O5'
52	v	55	5MU	C2'-C1'-N1-C2
31	sN1	1399	4OC	O4'-C4'-C5'-O5'
52	v	20	H2U	O4'-C4'-C5'-O5'
52	v	20	H2U	C3'-C4'-C5'-O5'
31	sN1	1515	MA6	N1-C6-N6-C9
5	AN1	2026	6MZ	O4'-C4'-C5'-O5'
5	AN1	2026	6MZ	C3'-C4'-C5'-O5'
52	v	55	5MU	C3'-C4'-C5'-O5'
52	v	55	5MU	O4'-C4'-C5'-O5'
5	AN1	2499	2MA	O4'-C4'-C5'-O5'
31	sN1	524	7MG	O4'-C4'-C5'-O5'
52	v	8	4SU	C3'-C4'-C5'-O5'
52	v	8	4SU	O4'-C4'-C5'-O5'
31	sN1	1516	MA6	C5-C6-N6-C10
5	AN1	1911	3TD	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
31	sN1	524	7MG	C4'-C5'-O5'-P
52	v	55	5MU	O4'-C1'-N1-C2
31	sN1	1399	4OC	C3'-C4'-C5'-O5'
5	AN1	1907	PSU	C4'-C5'-O5'-P
31	sN1	1516	MA6	C3'-C4'-C5'-O5'
31	sN1	1515	MA6	C5-C6-N6-C10
52	v	55	5MU	O4'-C1'-N1-C6
5	AN1	2441	2MG	C3'-C4'-C5'-O5'
52	v	20	H2U	C2'-C1'-N1-C6
5	AN1	1913	PSU	O4'-C4'-C5'-O5'
52	v	20	H2U	C2'-C1'-N1-C2
31	sN1	1516	MA6	N1-C6-N6-C10
31	sN1	1516	MA6	O4'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
52	v	20	H2U	1	0
5	AN1	2499	2MA	3	0
5	AN1	2026	6MZ	2	0
52	v	8	4SU	2	0
52	v	56	PSU	1	0
52	v	55	5MU	2	0
5	AN1	1911	3TD	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 117 ligands modelled in this entry, 116 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
55	FME	AN1	3001	-	8,9,10	0.99	0	8,9,11	0.90	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	FME	AN1	3001	-	-	3/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	AN1	3001	FME	O1-CN-N-CA
55	AN1	3001	FME	C-CA-CB-CG
55	AN1	3001	FME	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

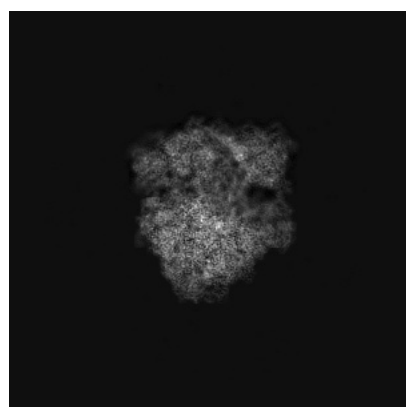
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21030. These allow visual inspection of the internal detail of the map and identification of artifacts.

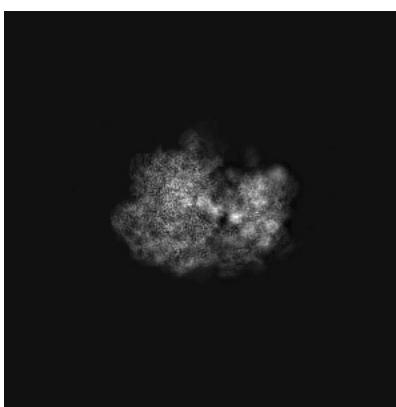
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

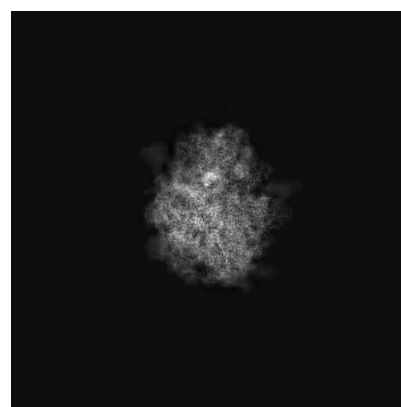
6.1.1 Primary map



X



Y

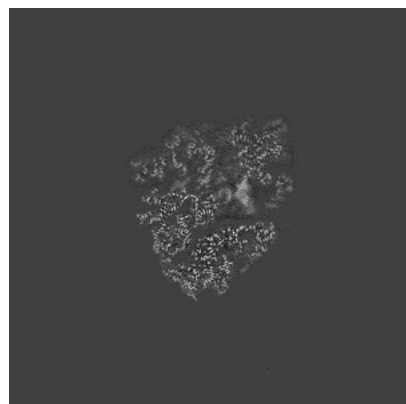


Z

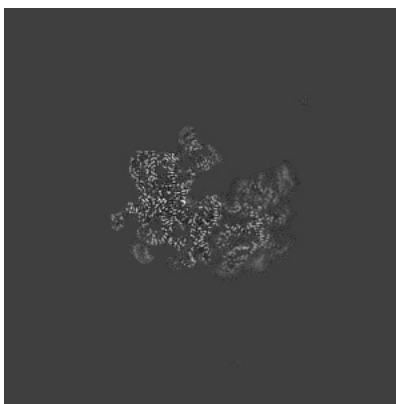
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

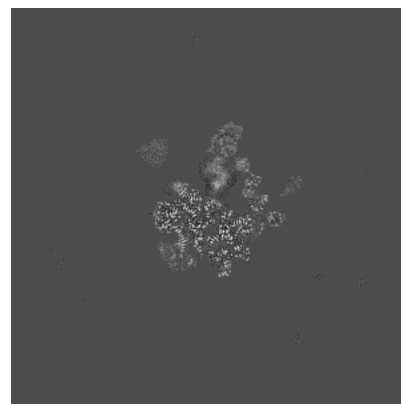
6.2.1 Primary map



X Index: 256



Y Index: 256

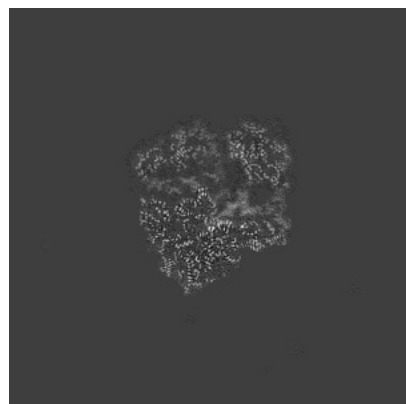


Z Index: 256

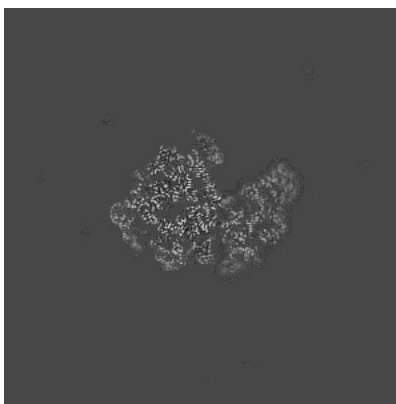
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

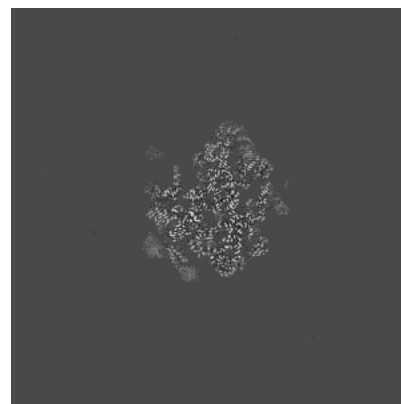
6.3.1 Primary map



X Index: 264



Y Index: 240

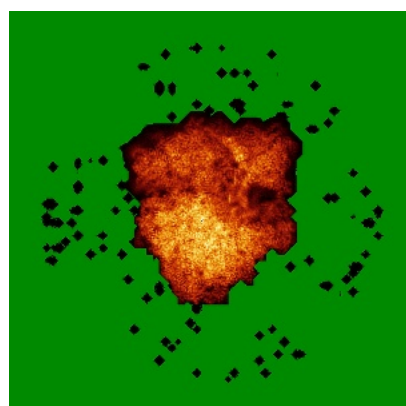


Z Index: 227

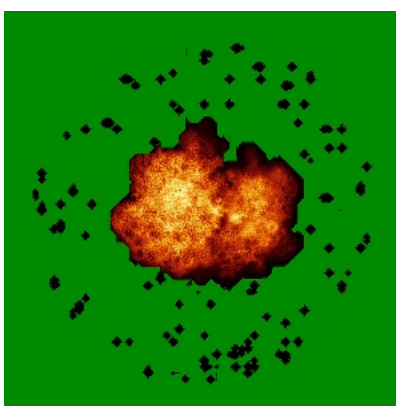
The images above show the largest variance slices of the map in three orthogonal directions.

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

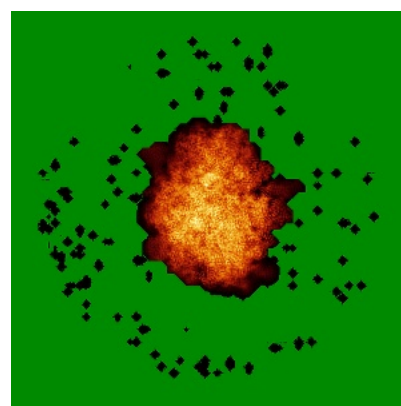
6.4.1 Primary map



X



Y

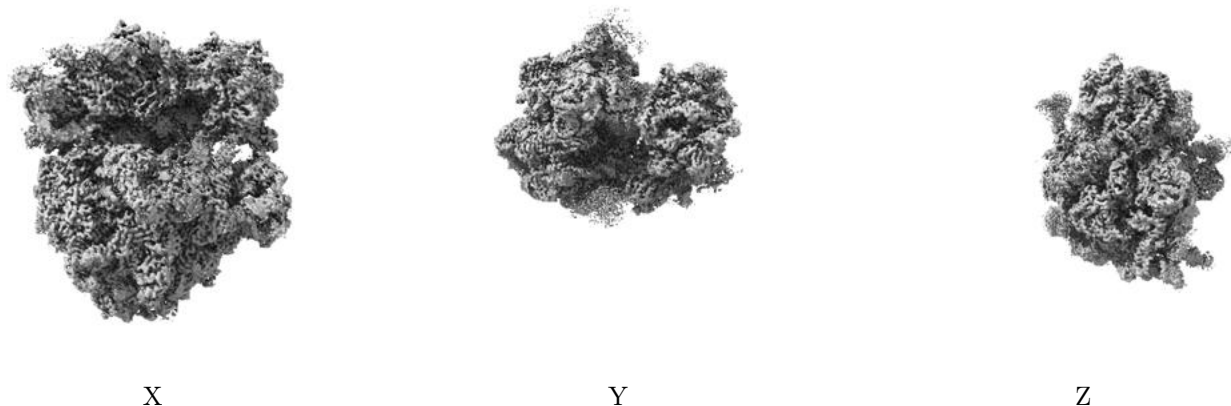


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

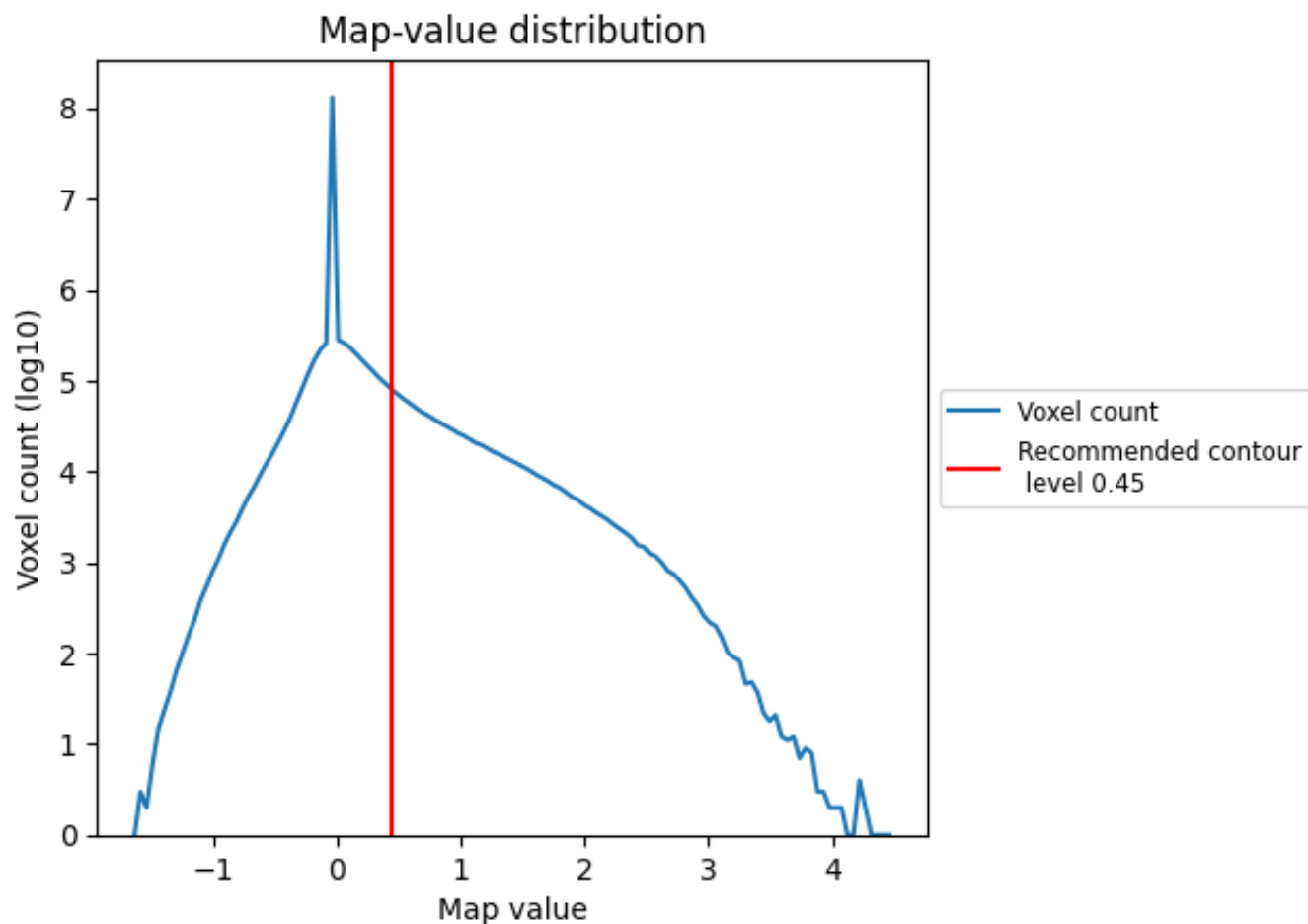
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

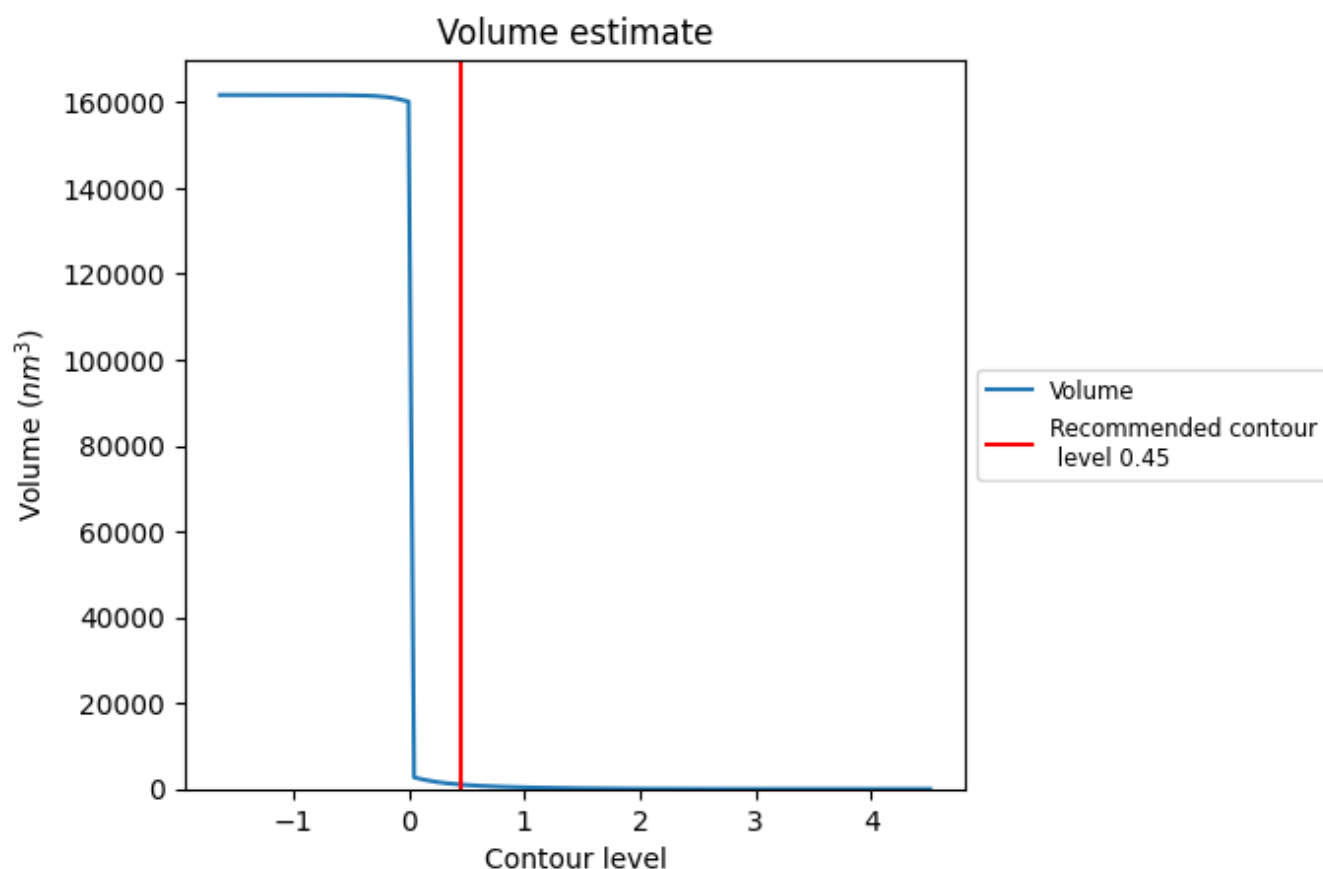
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

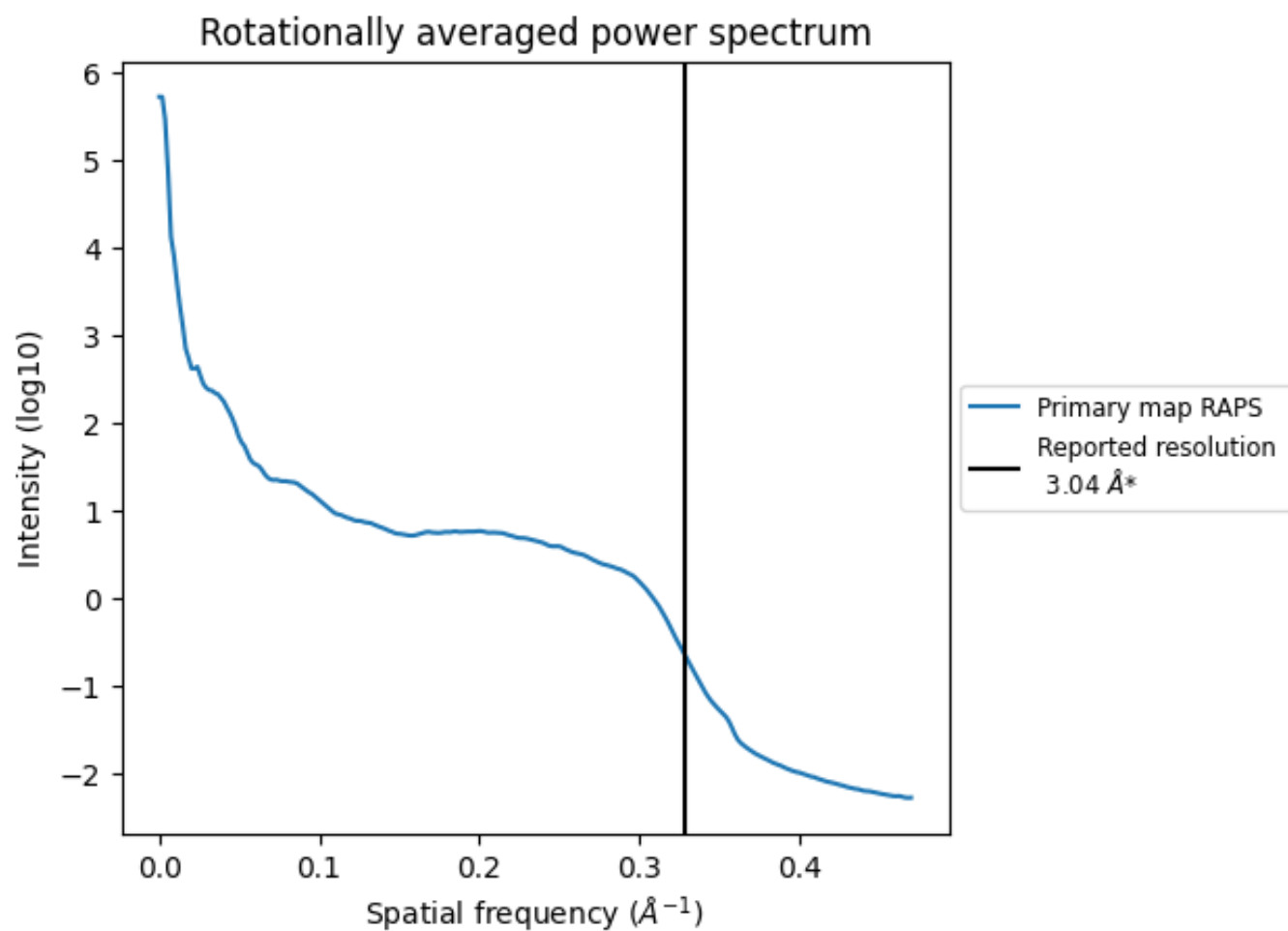
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1023 nm^3 ; this corresponds to an approximate mass of 924 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.329 Å⁻¹

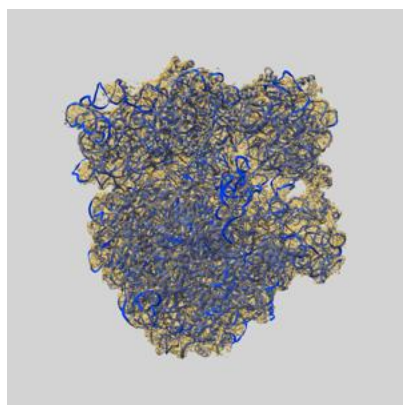
8 Fourier-Shell correlation ⓘ

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

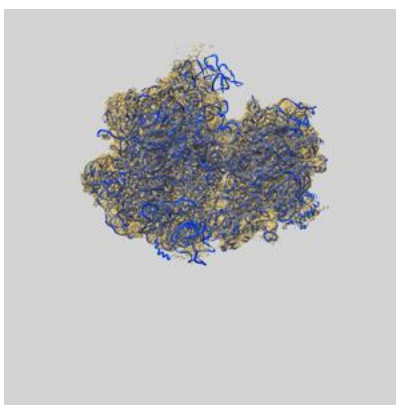
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21030 and PDB model 6V39. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

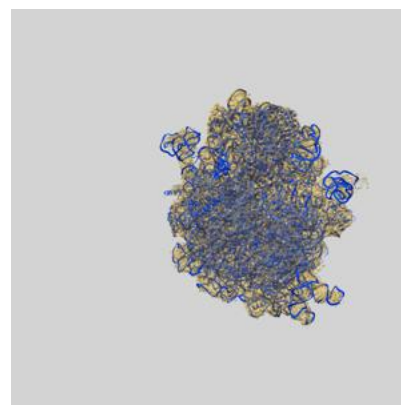
9.1 Map-model overlay [i](#)



X



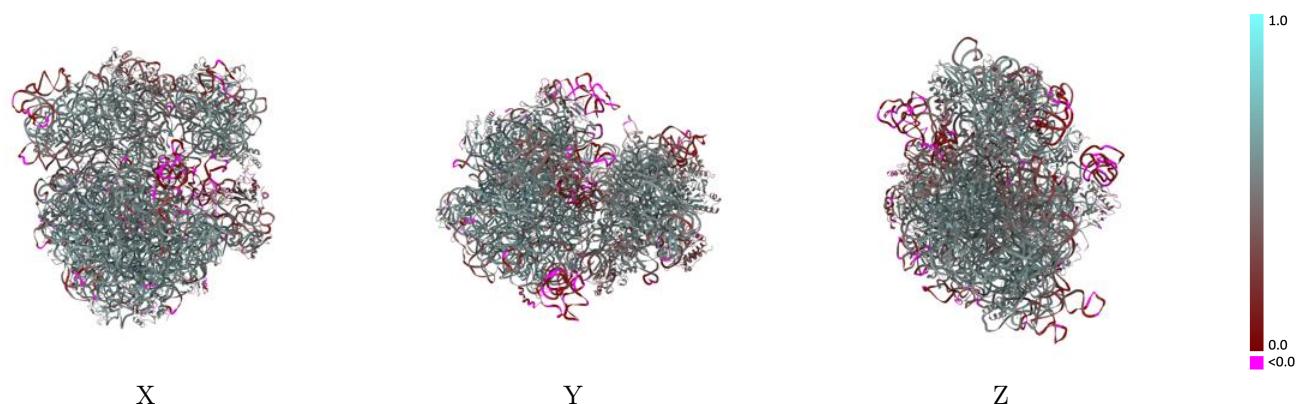
Y



Z

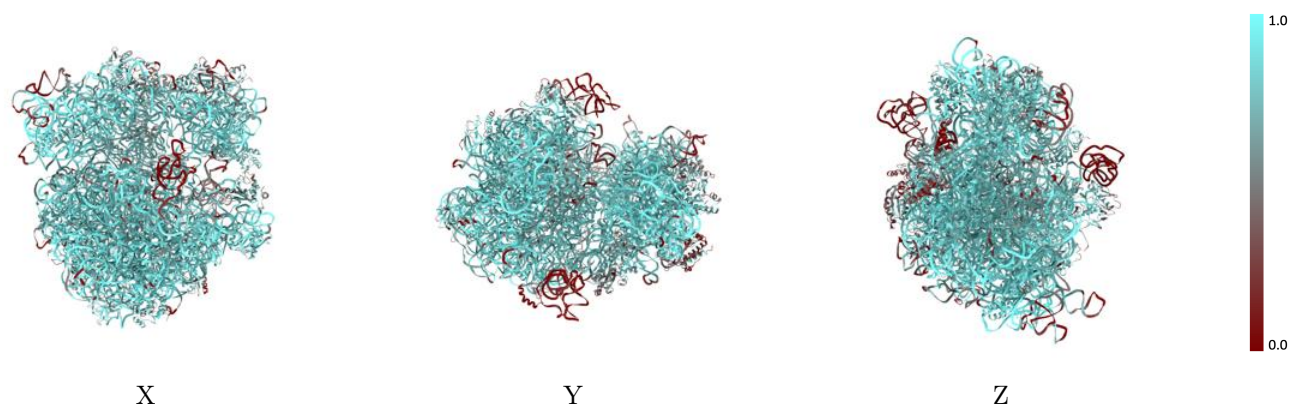
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



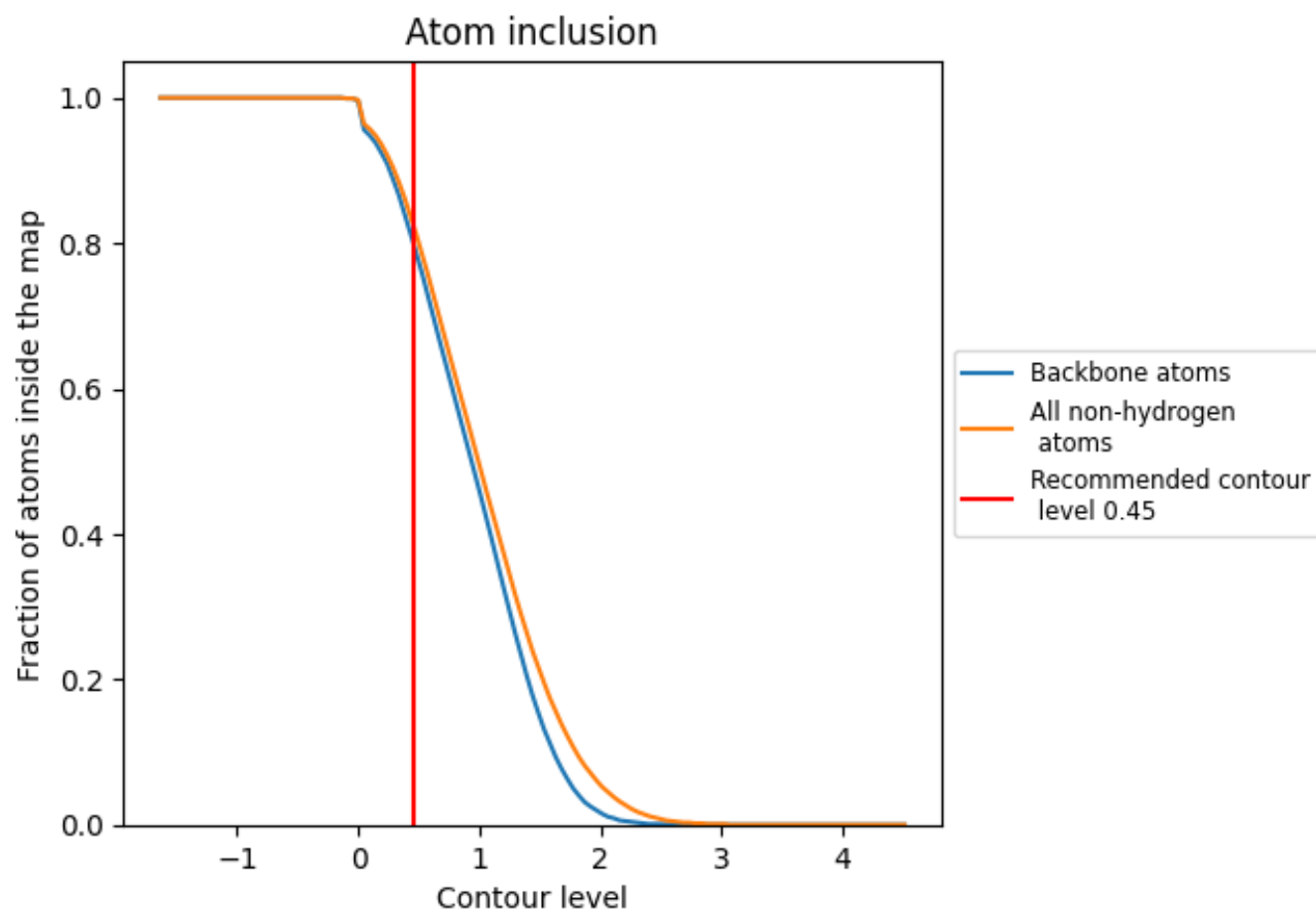
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8280	 0.4840
0	 0.7220	 0.4830
1	 0.9270	 0.6020
2	 0.8670	 0.5560
3	 0.8150	 0.4980
AN1	 0.8580	 0.4980
B	 0.8540	 0.4270
C	 0.8510	 0.5470
D	 0.8650	 0.5480
E	 0.8440	 0.5340
F	 0.5660	 0.2930
G	 0.6270	 0.3870
H	 0.3410	 0.2940
I	 0.8590	 0.5390
J	 0.8510	 0.5460
K	 0.7990	 0.5010
L	 0.8110	 0.5150
M	 0.9170	 0.5820
N	 0.8000	 0.4650
O	 0.8050	 0.5050
P	 0.9070	 0.5650
Q	 0.8160	 0.5080
R	 0.7970	 0.5200
S	 0.7700	 0.5020
T	 0.6830	 0.4360
U	 0.7680	 0.4900
V	 0.8990	 0.5670
W	 0.8190	 0.5330
X	 0.6720	 0.4230
Y	 0.8480	 0.5280
Z	 0.7860	 0.5100
b	 0.3210	 0.3450
c	 0.7760	 0.5010
d	 0.5800	 0.3910
e	 0.8180	 0.5110



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Chain	Atom inclusion	Q-score
f	 0.4910	 0.3610
g	 0.7150	 0.4250
h	 0.8440	 0.5420
i	 0.8550	 0.5390
j	 0.7190	 0.5010
k	 0.5970	 0.4050
l	 0.6000	 0.4670
m	 0.8120	 0.4960
n	 0.8160	 0.5410
o	 0.8300	 0.5100
p	 0.8530	 0.5470
q	 0.7890	 0.5240
r	 0.7120	 0.4740
s	 0.8560	 0.5250
sN1	 0.8740	 0.4730
t	 0.8590	 0.5210
u	 0.3200	 0.4040
v	 0.8250	 0.2140
w	 1.0000	 0.4340