



Full wwPDB EM Validation Report ⓘ

Jun 26, 2026 – 02:06 AM EDT

PDB ID : 7UVW / pdb_00007uvw
EMDB ID : EMD-26818
Title : A. baumannii ribosome: 70S with E-site tRNA
Authors : Morgan, C.E.; Yu, E.W.
Deposited on : 2022-05-02
Resolution : 2.37 Å(reported)

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:

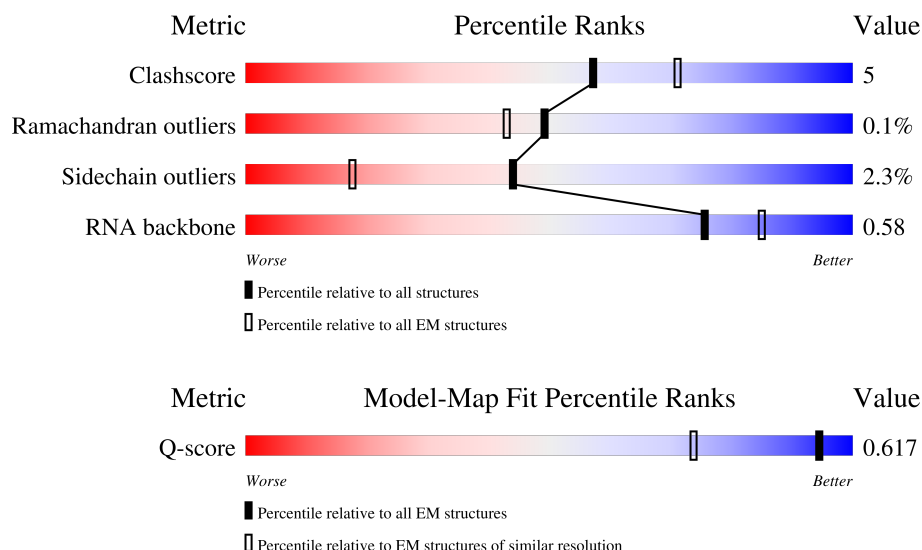
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.37 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	4742 (1.87 - 2.87)

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	

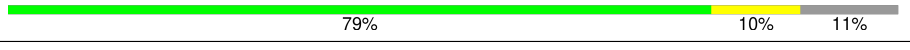
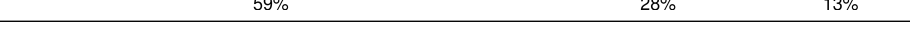
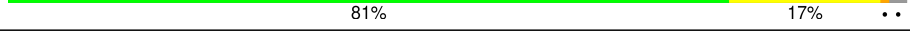
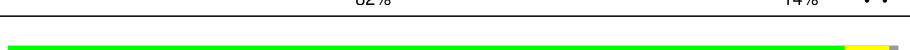
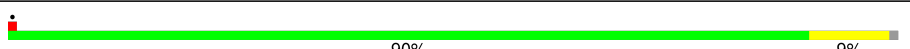
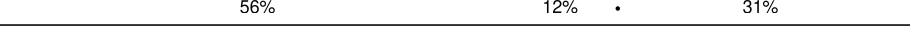
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Mol	Chain	Length	Quality of chain
4	3	38	
5	A	2918	
6	B	115	
7	C	274	
8	D	212	
9	E	200	
10	F	178	
11	G	177	
12	H	148	
13	I	142	
14	J	122	
15	K	146	
16	L	137	
17	M	125	
18	N	116	
19	O	122	
20	P	119	
21	Q	103	
22	R	109	
23	S	106	
24	T	105	
25	U	98	
26	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	a	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 54 unique types of molecules in this entry. The entry contains 138233 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	A	2719	Total	C	N	O	P	0	0
			58332	26037	10679	18897	2719		

- 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	272	Total	C	N	O	S	0	0
			2111	1302	436	365	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	200	Total	C	N	O	S	0	0
			1516	952	281	278	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	174	Total	C	N	O	S	0	0
			1370	871	243	248	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	144	Total	C	N	O	S	0	0
			1071	663	213	195			

- 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	116	Total	C	N	O	S	0	0
			873	537	176	158	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	117	Total	C	N	O	S	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	91	Total	C	N	O	S	0	0
			710	452	128	129	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	103	Total	C	N	O		0	0
			766	476	142	148			

- 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	76	Total	C	N	O	S	0	0
			577	358	111	106	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	60	Total	C	N	O	S	0	0
			486	302	93	90	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	57	Total	C	N	O	S	0	0
			455	281	87	84	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	54	Total	C	N	O	S	0	0
			447	265	100	81	1		

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

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1007	U	C	conflict	GB 1211343212
a	1034	C	U	conflict	GB 1211343212

- 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	104	Total	C	N	O	S	0	0
			867	546	158	159	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	136	Total	C	N	O	S	0	0
			1073	671	201	194	7		

- 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	126	Total	C	N	O	S	0	0
			991	618	197	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	82	Total	C	N	O	S	0	0
			644	403	128	112	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	79	Total	C	N	O	S	0	0
			621	390	116	114	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
48	r	52	Total	C	N	O	0	0
			426	273	74	79		

- 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	86	Total	C	N	O	S	0	0
			663	409	139	113	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	63	Total	C	N	O	S	0	0
			522	327	105	89	1		

- 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.

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

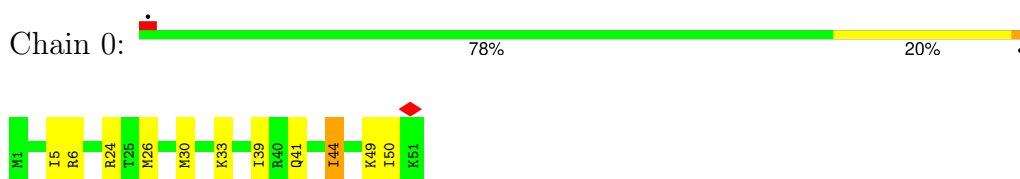
- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

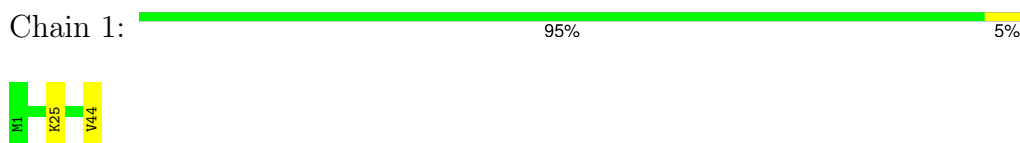
3 Residue-property plots [i](#)

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.

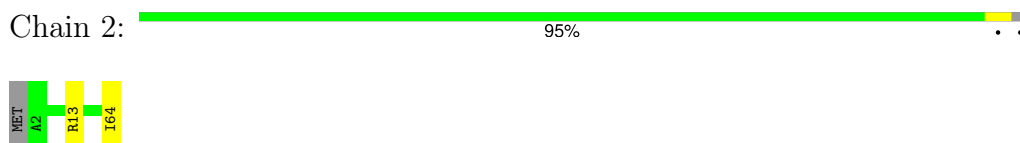
- Molecule 1: 50S ribosomal protein L33



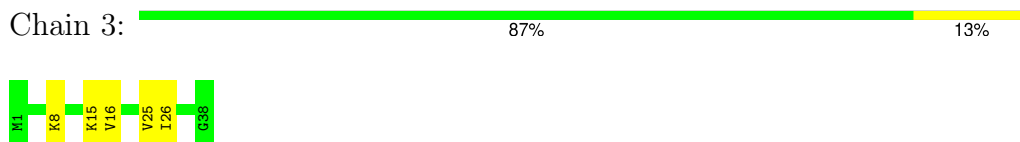
- Molecule 2: 50S ribosomal protein L34



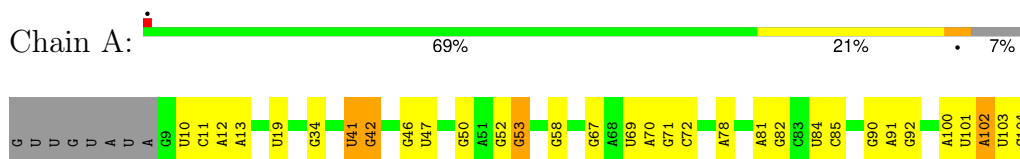
- Molecule 3: 50S ribosomal protein L35



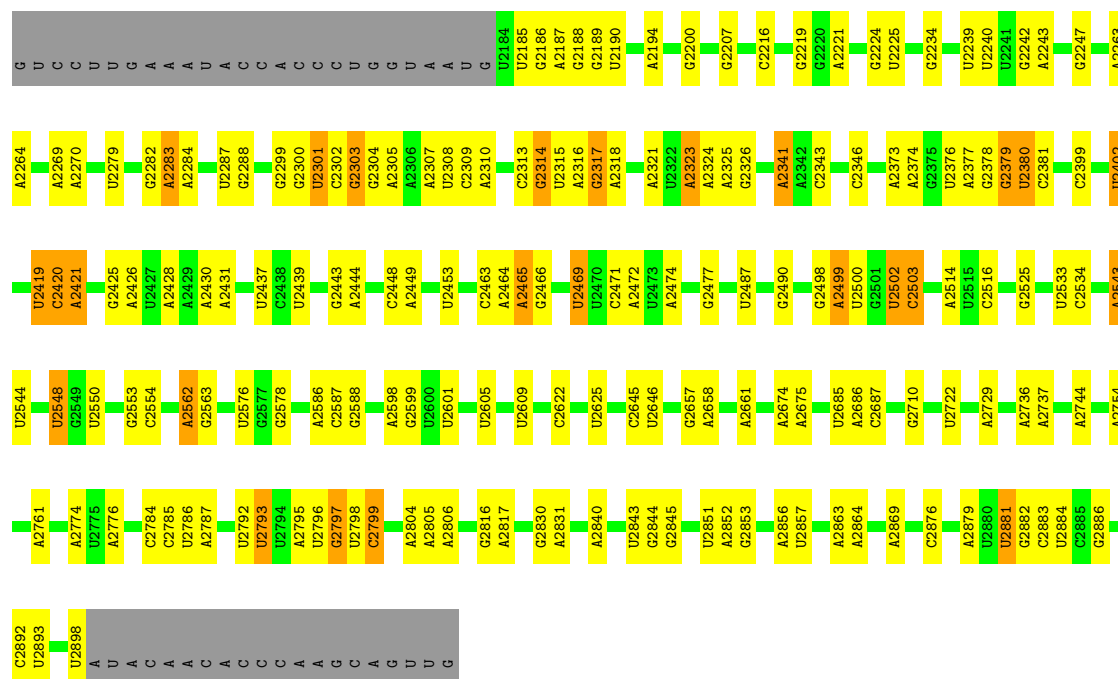
- Molecule 4: 50S ribosomal protein L36



- Molecule 5: 23s ribosomal RNA

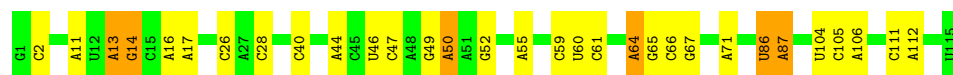






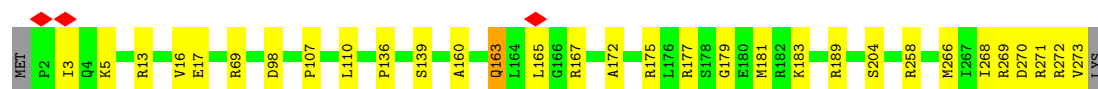
- Molecule 6: 5s ribosomal RNA

Chain B: 73% 22% 5%



- Molecule 7: 50S ribosomal protein L2

Chain C: 88% 11% .



- Molecule 8: 50S ribosomal protein L3

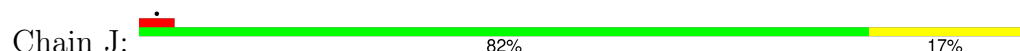
Chain D: 93% 7%

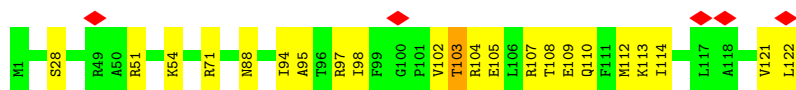


- Molecule 9: 50S ribosomal protein L4

Chain E: 90% 10%







- Molecule 15: 50S ribosomal protein L15

Chain K: 88% 10%



- Molecule 16: 50S ribosomal protein L16

Chain L: 93% 7%



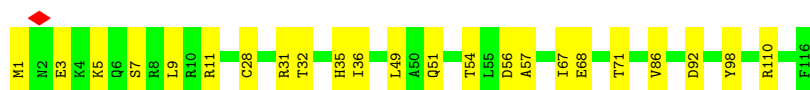
- Molecule 17: 50S ribosomal protein L17

Chain M: 92% 5%



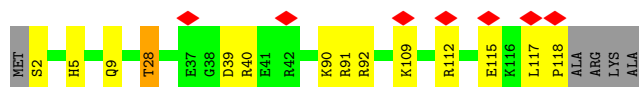
- Molecule 18: 50S ribosomal protein L18

Chain N: 80% 20%



- Molecule 19: 50S ribosomal protein L19

Chain O: 6% 84% 11%



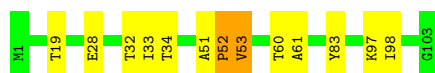
- Molecule 20: 50S ribosomal protein L20

Chain P: 94% 11%



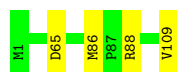
- Molecule 21: 50S ribosomal protein L21

Chain Q: 87% 11%



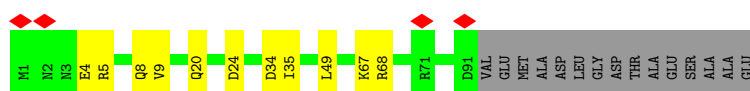
- Molecule 22: 50S ribosomal protein L22

Chain R: 96%



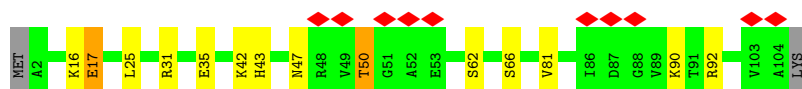
- Molecule 23: 50S ribosomal protein L23

Chain S: 75%



- Molecule 24: 50S ribosomal protein L24

Chain T: 10% 85% 11%



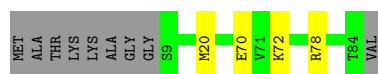
- Molecule 25: 50S ribosomal protein L25

Chain U: 86% 13%



- Molecule 26: 50S ribosomal protein L27

Chain V: 85% 5% 11%



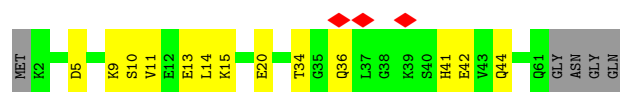
- Molecule 27: 50S ribosomal protein L28

Chain W: 88% 10%



- Molecule 28: 50S ribosomal protein L29

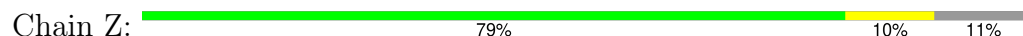
Chain X: 5% 72% 20% 8%



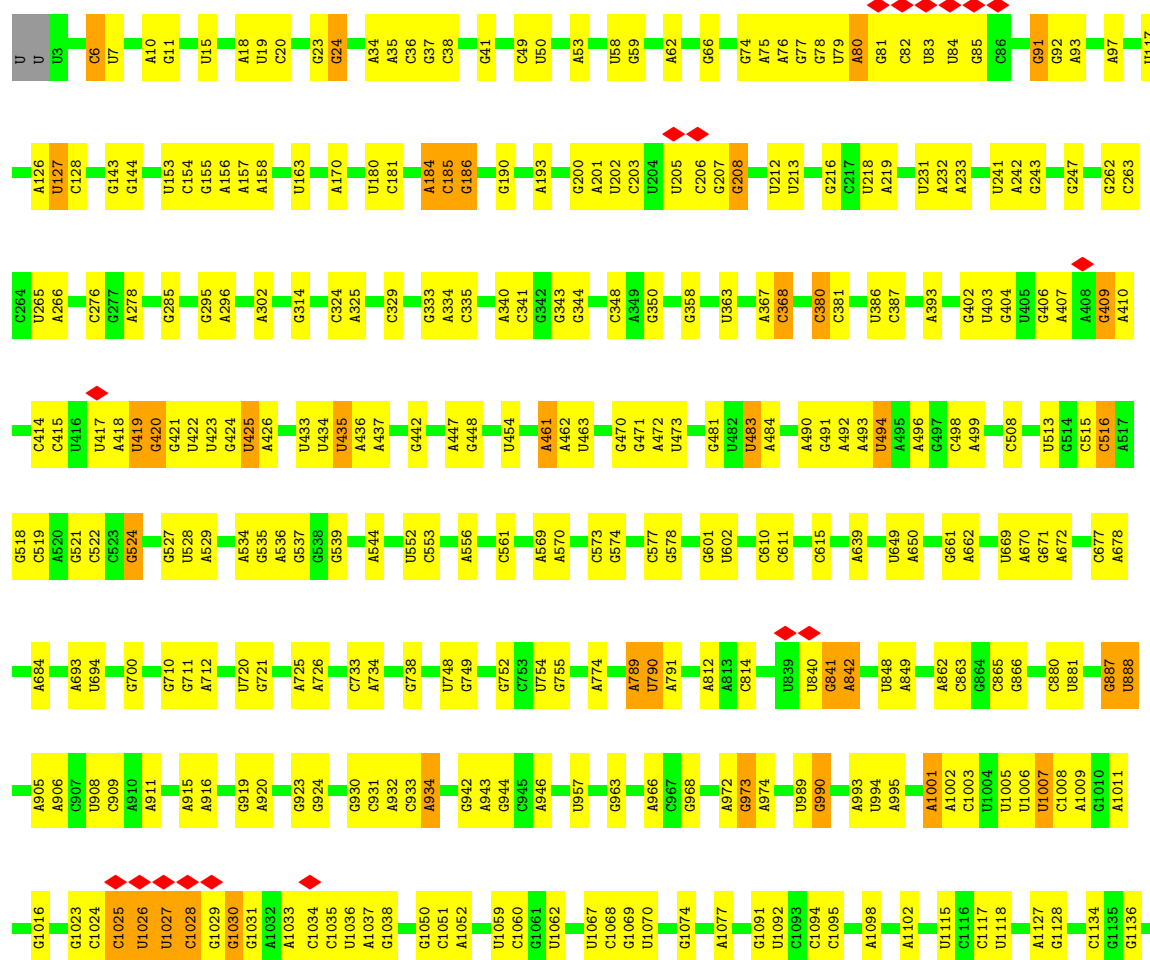
- Molecule 29: 50S ribosomal protein L30

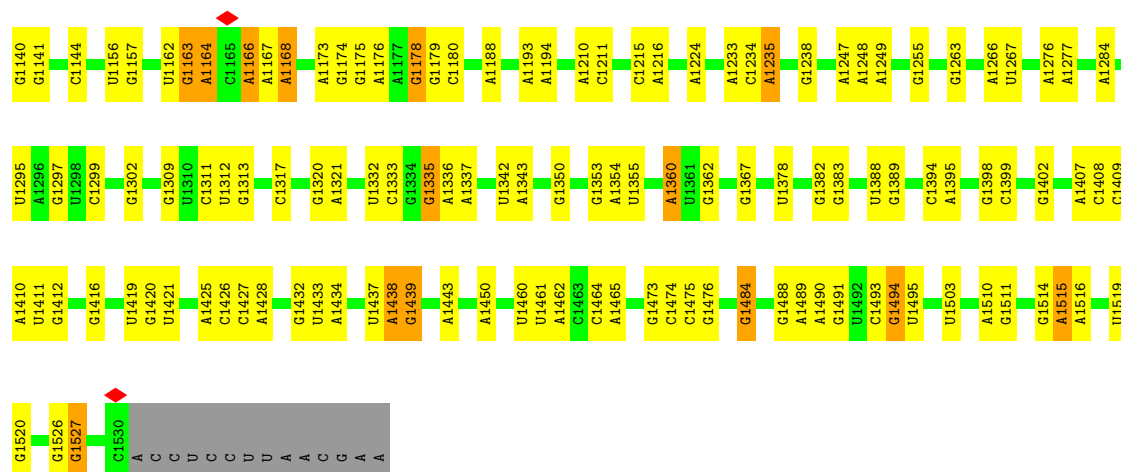


- Molecule 30: 50S ribosomal protein L32

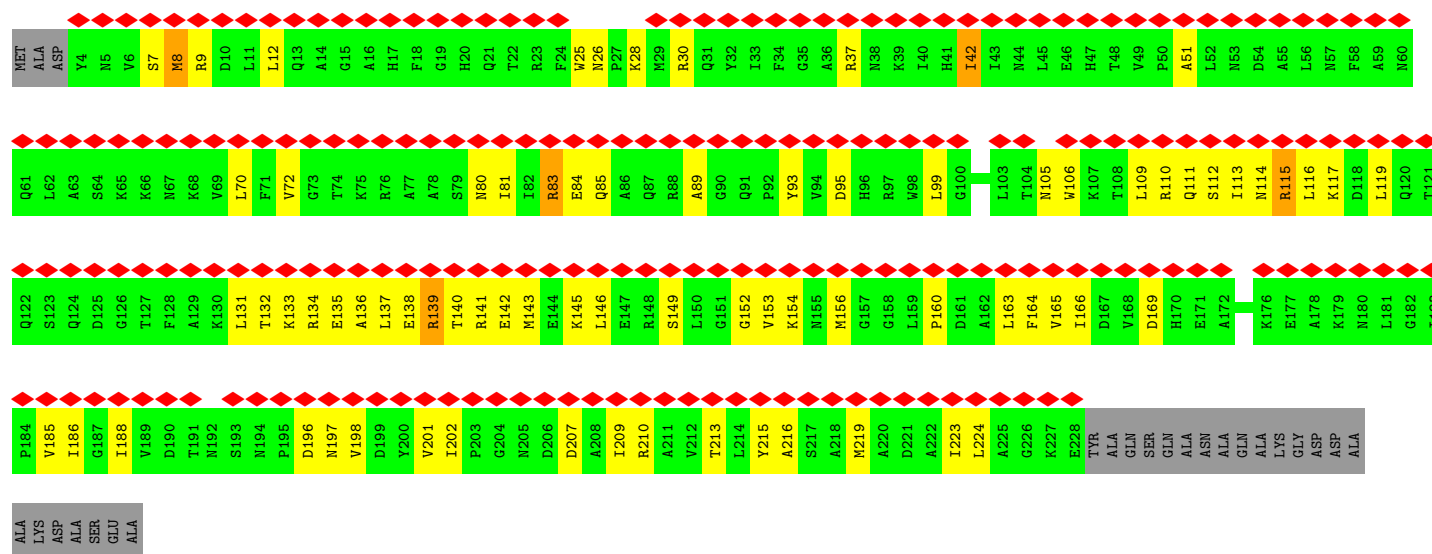
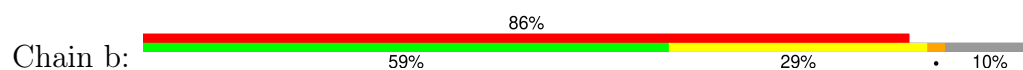


- Molecule 31: 16s Ribosomal RNA

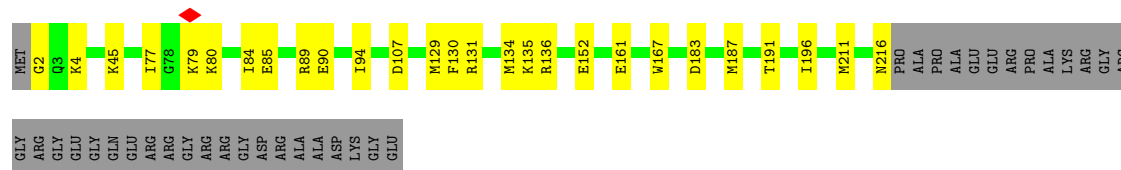




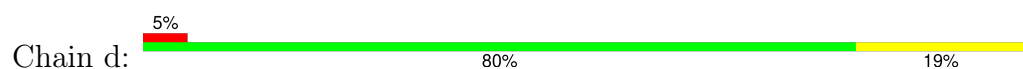
• Molecule 32: 30S ribosomal protein S2

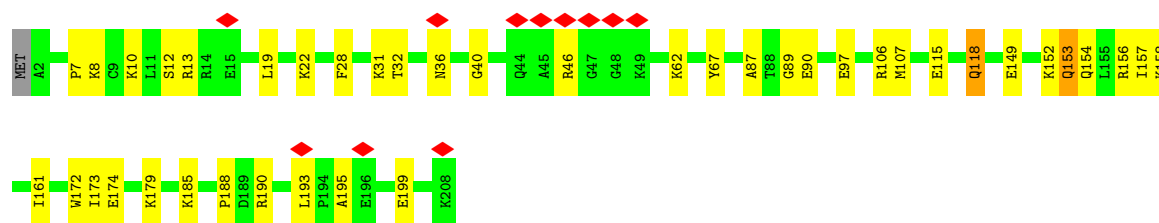


• Molecule 33: 30S ribosomal protein S3



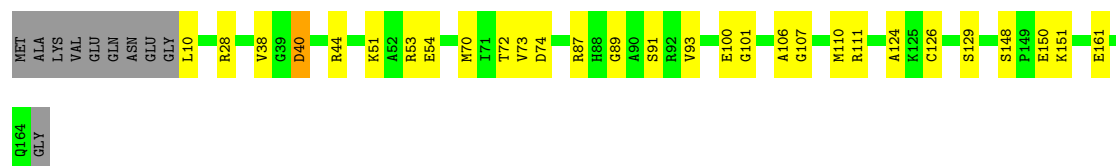
• Molecule 34: 30S ribosomal protein S4





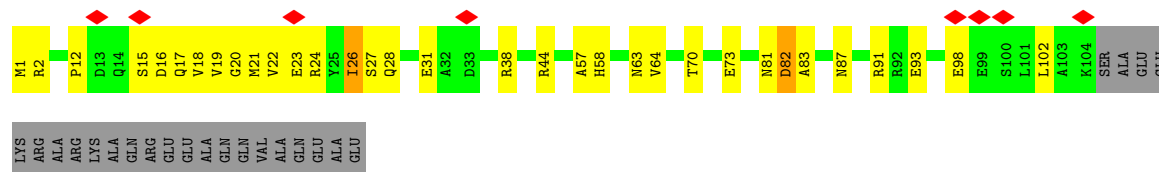
• Molecule 35: 30S ribosomal protein S5

Chain e: 76% 17% • 6%



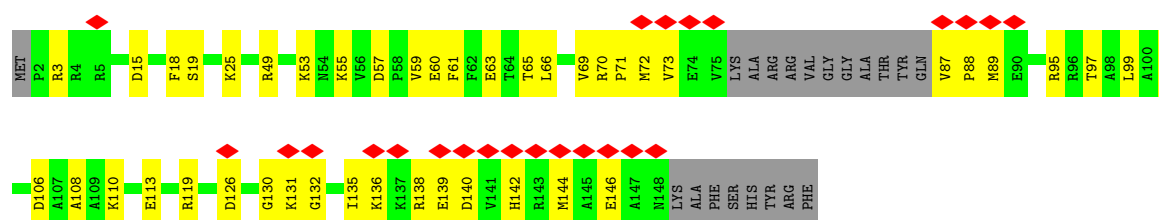
• Molecule 36: 30S ribosomal protein S6

Chain f: 6% 56% 24% • 18%



• Molecule 37: 30S ribosomal protein S7

Chain g: 15% 59% 28% 13%



• Molecule 38: 30S ribosomal protein S8

Chain h: 92% 8% •

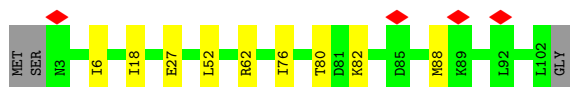
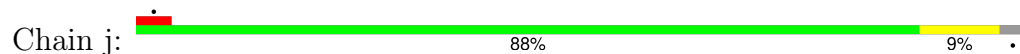


• Molecule 39: 30S ribosomal protein S9

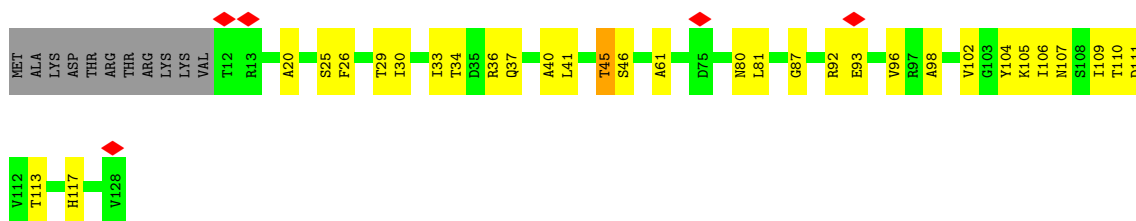
Chain i: 83% 16% •



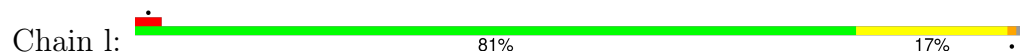
- Molecule 40: 30S ribosomal protein S10



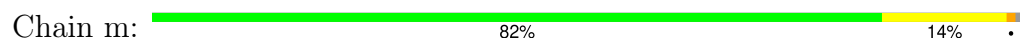
- Molecule 41: 30S ribosomal protein S11



- Molecule 42: 30S ribosomal protein S12



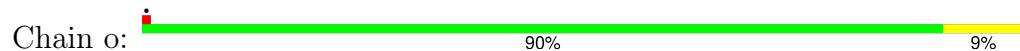
- Molecule 43: 30S ribosomal protein S13



- Molecule 44: 30S ribosomal protein S14

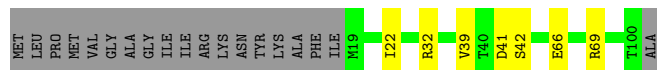


- Molecule 45: 30S ribosomal protein S15

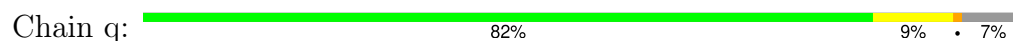




- Molecule 46: 30S ribosomal protein S16



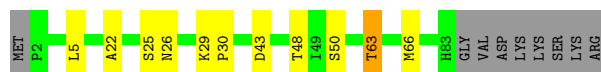
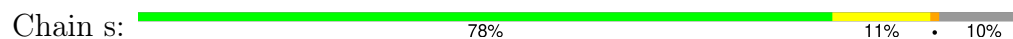
- Molecule 47: 30S ribosomal protein S17



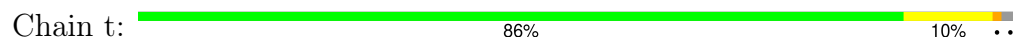
- Molecule 48: 30S ribosomal protein S18



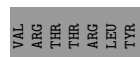
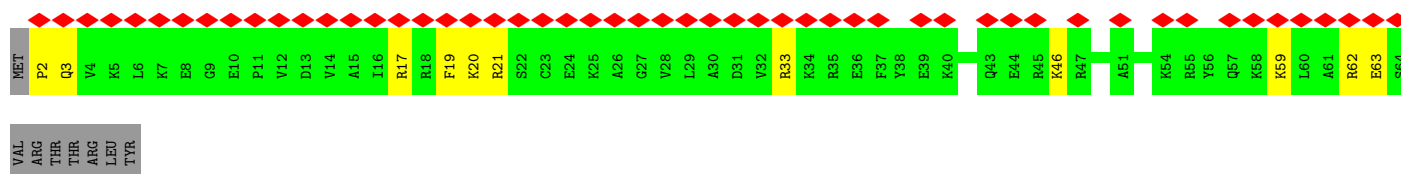
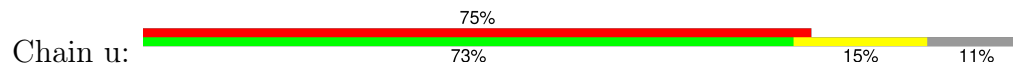
- Molecule 49: 30S ribosomal protein S19



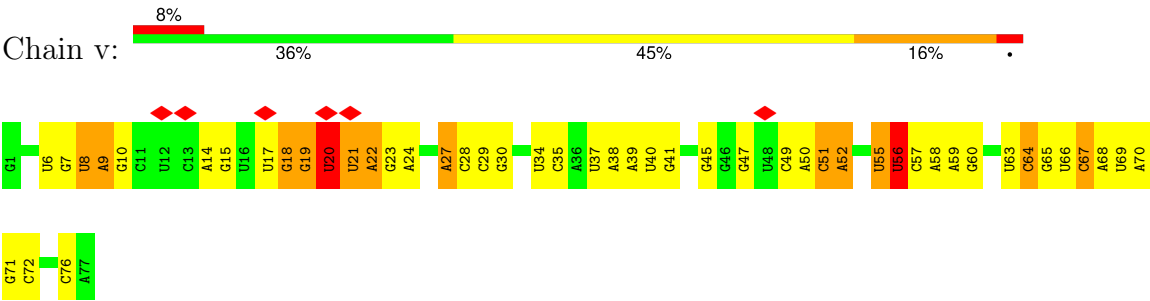
- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21



• Molecule 52: tRNA-met



• Molecule 53: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	109944	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)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.362	Depositor
Minimum map value	0.000	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.12	Depositor
Map size ($\text{\AA}$)	434.176, 434.176, 434.176	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.848, 0.848, 0.848	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.19	0/434	0.38	0/573
2	1	0.19	0/367	0.37	0/481
3	2	0.20	0/515	0.40	0/678
4	3	0.22	0/296	0.42	0/389
5	A	0.22	0/65034	0.32	0/101432
6	B	0.17	0/2739	0.30	0/4266
7	C	0.21	0/2152	0.46	0/2891
8	D	0.20	0/1590	0.37	0/2142
9	E	0.18	0/1537	0.36	0/2073
10	F	0.22	0/1390	0.63	5/1863 (0.3%)
11	G	0.17	0/1337	0.41	0/1807
12	H	0.15	0/461	0.43	0/616
13	I	0.21	0/1151	0.42	0/1551
14	J	0.21	0/956	0.49	0/1286
15	K	0.19	0/1079	0.39	0/1439
16	L	0.19	0/1104	0.39	0/1475
17	M	0.20	0/956	0.40	0/1282
18	N	0.18	0/881	0.46	0/1177
19	O	0.20	0/931	0.44	0/1249
20	P	0.21	0/947	0.37	0/1262
21	Q	0.19	0/818	0.37	0/1094
22	R	0.19	0/831	0.34	0/1113
23	S	0.16	0/716	0.32	0/957
24	T	0.15	0/770	0.33	0/1034
25	U	0.18	0/770	0.38	0/1036
26	V	0.21	0/585	0.36	0/783
27	W	0.20	0/642	0.39	0/856
28	X	0.14	0/487	0.31	0/646
29	Y	0.20	0/460	0.35	0/614
30	Z	0.19	0/453	0.45	0/604
31	a	0.19	0/36476	0.29	0/56895
32	b	0.21	0/1799	0.58	3/2429 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.18	0/1714	0.42	0/2304
34	d	0.16	0/1653	0.39	0/2213
35	e	0.17	0/1141	0.38	0/1537
36	f	0.17	0/882	0.46	0/1189
37	g	0.22	0/1087	0.59	0/1456
38	h	0.19	0/993	0.36	0/1331
39	i	0.19	0/1002	0.41	0/1339
40	j	0.20	0/811	0.42	0/1096
41	k	0.16	0/878	0.39	0/1189
42	l	0.19	0/958	0.48	0/1284
43	m	0.18	0/913	0.44	0/1226
44	n	0.19	0/803	0.37	0/1071
45	o	0.18	0/715	0.32	0/958
46	p	0.18	0/655	0.37	0/879
47	q	0.19	0/628	0.39	0/847
48	r	0.17	0/432	0.39	0/583
49	s	0.20	0/664	0.41	0/897
50	t	0.22	0/669	0.31	0/892
51	u	0.10	0/528	0.24	0/697
52	v	0.19	0/1739	0.31	0/2709
53	w	0.14	0/72	0.20	0/110
All	All	0.21	0/149601	0.34	8/223800 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	F	0	1
21	Q	0	1
All	All	0	2

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	b	115	ARG	CA-CB-CG	5.84	125.77	114.10
32	b	83	ARG	CG-CD-NE	-5.61	99.67	112.00
32	b	139	ARG	CB-CG-CD	5.53	124.02	111.30
10	F	115	ARG	CA-CB-CG	5.35	124.81	114.10
10	F	79	ILE	CA-C-N	5.32	130.60	121.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	F	79	ILE	C-N-CA	5.32	130.60	121.87
10	F	136	ILE	CA-C-N	5.25	131.42	121.97
10	F	136	ILE	C-N-CA	5.25	131.42	121.97

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	F	80	ARG	Peptide
21	Q	51	ALA	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	427	0	462	7	0
2	1	363	0	401	1	0
3	2	509	0	566	1	0
4	3	295	0	326	2	0
5	A	58332	0	29333	298	0
6	B	2450	0	1241	21	0
7	C	2111	0	2176	23	0
8	D	1572	0	1610	7	0
9	E	1516	0	1569	11	0
10	F	1370	0	1420	63	0
11	G	1318	0	1373	20	0
12	H	458	0	480	7	0
13	I	1125	0	1148	8	0
14	J	946	0	1007	24	0
15	K	1071	0	1141	9	0
16	L	1087	0	1162	7	0
17	M	942	0	987	2	0
18	N	873	0	917	15	0
19	O	919	0	973	12	0
20	P	934	0	997	4	0
21	Q	807	0	842	7	0
22	R	826	0	894	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	S	710	0	768	8	0
24	T	766	0	816	7	0
25	U	760	0	783	6	0
26	V	577	0	580	3	0
27	W	632	0	667	4	0
28	X	486	0	528	8	0
29	Y	455	0	476	5	0
30	Z	447	0	435	4	0
31	a	32782	0	16508	221	0
32	b	1769	0	1787	67	0
33	c	1690	0	1774	17	0
34	d	1631	0	1691	27	0
35	e	1129	0	1174	18	0
36	f	867	0	868	24	0
37	g	1073	0	1118	36	0
38	h	985	0	1047	4	0
39	i	991	0	1048	12	0
40	j	801	0	832	6	0
41	k	862	0	877	21	0
42	l	945	0	998	13	0
43	m	903	0	962	9	0
44	n	792	0	833	3	0
45	o	705	0	712	5	0
46	p	644	0	655	5	0
47	q	621	0	665	5	0
48	r	426	0	447	6	0
49	s	646	0	663	8	0
50	t	663	0	715	6	0
51	u	522	0	565	8	0
52	v	1636	0	835	32	0
53	w	65	0	33	4	0
54	3	1	0	0	0	0
All	All	138233	0	92885	1089	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 5.

All (1089) 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)
32:b:131:LEU:HD21	32:b:135:GLU:HG2	1.46	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:74:G:H1	31:a:93:A:H61	0.97	0.96
5:A:2093:U:H3	5:A:2188:G:H1	0.97	0.96
31:a:1007:U:H3	31:a:1016:G:H1	1.01	0.92
31:a:74:G:H1	31:a:93:A:N6	1.69	0.89
5:A:279:U:H3	5:A:366:G:H1	0.91	0.87
10:F:54:VAL:HG23	10:F:65:PRO:HG2	1.56	0.86
31:a:454:U:H3	31:a:470:G:H1	1.30	0.80
10:F:170:MET:HE3	10:F:175:PHE:HB3	1.64	0.79
10:F:80:ARG:HH12	10:F:83:TRP:HB2	1.46	0.79
10:F:80:ARG:HD3	10:F:80:ARG:N	1.97	0.79
19:O:39:ASP:OD1	19:O:40:ARG:NH2	2.12	0.77
14:J:51:ARG:HH22	14:J:94:ILE:HD12	1.50	0.77
5:A:1044:G:O2'	5:A:1108:A:N6	2.17	0.76
5:A:279:U:O2	5:A:366:G:N2	2.20	0.75
32:b:163:LEU:HB2	32:b:185:VAL:HG22	1.68	0.75
14:J:107:ARG:NH1	14:J:107:ARG:HA	2.02	0.75
5:A:1595:A:H5''	5:A:1596:A:H5'	1.68	0.75
14:J:107:ARG:HA	14:J:107:ARG:HH11	1.52	0.73
5:A:2300:G:H22	5:A:2308:U:H3	1.35	0.73
37:g:60:GLU:HA	37:g:63:GLU:HG3	1.71	0.73
31:a:409:G:N2	31:a:425:U:OP2	2.18	0.73
31:a:1163:G:O2'	31:a:1167:A:N6	2.22	0.72
5:A:52:G:H5''	5:A:53:G:H5'	1.72	0.71
52:v:18:G:H21	52:v:59:A:H5'	1.55	0.71
52:v:22:A:H61	52:v:47:G:H2'	1.55	0.71
31:a:1036:U:H2'	31:a:1037:A:H8	1.55	0.71
37:g:113:GLU:O	37:g:119:ARG:NH1	2.23	0.71
31:a:75:A:H61	31:a:92:G:H1	1.35	0.71
11:G:164:TYR:HB2	11:G:167:GLU:HB2	1.72	0.71
10:F:95:GLN:N	10:F:95:GLN:OE1	2.24	0.70
37:g:57:ASP:HB3	37:g:60:GLU:OE1	1.91	0.70
39:i:56:THR:OG1	39:i:57:GLU:OE2	2.09	0.70
31:a:841:G:H1'	31:a:842:A:C8	2.27	0.70
32:b:134:ARG:NH1	32:b:135:GLU:OE2	2.24	0.70
10:F:65:PRO:HB3	10:F:89:VAL:HG22	1.73	0.70
5:A:1865:G:N2	5:A:1868:A:OP2	2.17	0.69
5:A:2095:U:H3	5:A:2186:G:H1	1.37	0.69
10:F:5:LYS:HG2	10:F:6:ALA:H	1.57	0.69
5:A:1412:C:O2'	5:A:1585:G:O2'	2.11	0.69
10:F:12:LEU:HD12	10:F:172:ALA:HB1	1.74	0.69
45:o:76:GLU:OE2	45:o:76:GLU:N	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:k:34:THR:HG22	41:k:40:ALA:HA	1.72	0.69
10:F:7:ARG:HE	10:F:12:LEU:HD21	1.57	0.68
32:b:135:GLU:HB2	32:b:139:ARG:HH12	1.59	0.68
35:e:74:ASP:OD1	35:e:151:LYS:NZ	2.26	0.68
52:v:35:C:H42	53:w:3:G:H1	1.41	0.68
32:b:110:ARG:HD2	32:b:110:ARG:N	2.09	0.68
31:a:74:G:N2	31:a:93:A:N1	2.37	0.68
32:b:110:ARG:O	32:b:114:ASN:ND2	2.27	0.67
40:j:88:MET:HE3	40:j:88:MET:HA	1.75	0.67
10:F:4:LEU:C	10:F:5:LYS:HD3	2.18	0.67
29:Y:5:LYS:HB2	29:Y:57:GLU:HG2	1.75	0.67
5:A:2315:U:O2'	5:A:2317:G:N7	2.27	0.66
5:A:1903:G:H1	5:A:1919:U:H3	1.44	0.66
32:b:143:MET:HA	32:b:146:LEU:HD13	1.77	0.66
11:G:11:VAL:HG13	11:G:15:VAL:HG13	1.76	0.66
5:A:2804:A:O2'	5:A:2886:G:O6	2.12	0.66
37:g:95:ARG:O	37:g:99:LEU:HD12	1.96	0.66
5:A:2879:A:OP2	30:Z:49:ARG:NH2	2.27	0.66
48:r:27:ASP:OD1	48:r:27:ASP:N	2.21	0.66
5:A:1534:G:N2	5:A:1535:U:O4	2.28	0.66
46:p:22:ILE:HG12	46:p:39:VAL:HG22	1.77	0.66
5:A:2301:U:O2	10:F:133:LYS:NZ	2.29	0.66
7:C:183:LYS:HG2	7:C:268:ILE:HD11	1.76	0.66
37:g:70:ARG:O	37:g:138:ARG:NH1	2.29	0.66
37:g:70:ARG:NH2	37:g:97:THR:OG1	2.29	0.66
5:A:2324:A:H2'	5:A:2325:A:C8	2.32	0.65
36:f:2:ARG:HD3	36:f:91:ARG:HE	1.61	0.65
11:G:33:LEU:HD13	11:G:75:LEU:HD22	1.78	0.65
31:a:1527:G:O6	51:u:46:LYS:NZ	2.30	0.65
12:H:8:ARG:HB2	12:H:14:LYS:HD2	1.78	0.65
52:v:52:A:H61	52:v:64:C:H42	1.45	0.65
12:H:9:ILE:HG22	12:H:12:LEU:H	1.59	0.65
14:J:97:ARG:NH1	31:a:335:C:OP2	2.30	0.65
31:a:423:U:OP2	31:a:424:G:O2'	2.15	0.65
28:X:9:LYS:HG2	28:X:13:GLU:HB2	1.76	0.65
31:a:1394:C:OP2	35:e:28:ARG:NH2	2.30	0.65
9:E:110:GLU:OE1	9:E:113:ARG:NH1	2.31	0.64
10:F:156:ILE:HD12	10:F:156:ILE:O	1.98	0.64
14:J:95:ALA:O	14:J:113:LYS:NZ	2.26	0.64
18:N:56:ASP:OD1	18:N:57:ALA:N	2.31	0.64
37:g:88:PRO:C	37:g:89:MET:HE2	2.23	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:D:47:GLN:NE2	8:D:87:GLU:OE1	2.31	0.63
5:A:2287:U:H2'	5:A:2288:G:C8	2.34	0.63
36:f:28:GLN:NE2	36:f:73:GLU:OE1	2.32	0.63
15:K:89:GLY:O	15:K:120:ARG:NH2	2.32	0.63
31:a:1309:G:H5'	49:s:5:LEU:HD11	1.81	0.63
5:A:309:G:N1	5:A:312:A:OP2	2.31	0.63
31:a:1163:G:N2	31:a:1167:A:OP2	2.31	0.63
41:k:87:GLY:H	41:k:113:THR:HG22	1.62	0.63
52:v:19:G:N2	52:v:57:C:O2'	2.31	0.63
14:J:108:THR:HG22	14:J:110:GLN:H	1.63	0.62
36:f:38:ARG:NH1	36:f:98:GLU:O	2.30	0.62
1:O:49:LYS:HE2	1:O:49:LYS:H	1.64	0.62
35:e:44:ARG:NH1	35:e:72:THR:OG1	2.32	0.62
29:Y:5:LYS:NZ	29:Y:36:GLU:OE1	2.32	0.62
34:d:22:LYS:HD2	34:d:31:LYS:HE3	1.80	0.62
31:a:943:A:H2'	31:a:944:G:C8	2.34	0.62
36:f:12:PRO:HD3	36:f:57:ALA:HA	1.81	0.62
37:g:135:ILE:O	37:g:139:GLU:HG2	2.00	0.62
31:a:471:G:H2'	31:a:472:A:C8	2.34	0.62
45:o:53:ARG:O	45:o:57:ILE:HG12	1.99	0.62
8:D:42:GLU:N	8:D:42:GLU:OE1	2.33	0.61
11:G:84:GLU:OE1	11:G:84:GLU:N	2.32	0.61
31:a:358:G:H5''	42:l:58:THR:HG21	1.82	0.61
23:S:68:ARG:HG3	23:S:68:ARG:HH11	1.63	0.61
32:b:112:SER:HA	32:b:115:ARG:NE	2.15	0.61
33:c:152:GLU:HG3	33:c:167:TRP:HB3	1.82	0.61
14:J:71:ARG:HH22	14:J:104:ARG:HH21	1.49	0.61
5:A:1503:C:O2'	5:A:1505:A:N7	2.32	0.61
10:F:56:ASP:O	10:F:60:ILE:HG12	2.00	0.61
5:A:533:U:O2'	20:P:49:ASP:OD2	2.12	0.61
31:a:670:A:H2'	31:a:671:G:C8	2.36	0.61
5:A:2465:A:N6	5:A:2477:G:O2'	2.33	0.60
34:d:107:MET:HG2	34:d:173:ILE:HG21	1.83	0.60
46:p:32:ARG:HH11	46:p:32:ARG:HG2	1.66	0.60
49:s:22:ALA:O	49:s:25:SER:O	2.19	0.60
24:T:47:ASN:ND2	24:T:50:THR:OG1	2.34	0.60
5:A:1647:G:O2'	17:M:106:ASP:OD2	2.18	0.60
23:S:4:GLU:O	23:S:8:GLN:HG2	2.01	0.60
5:A:854:G:H2'	5:A:855:G:C8	2.36	0.60
6:B:55:A:O2'	10:F:27:GLU:OE2	2.13	0.60
19:O:39:ASP:H	19:O:40:ARG:NH2	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:89:GLY:HA3	34:d:199:GLU:HG3	1.84	0.60
34:d:97:GLU:OE1	34:d:106:ARG:NH1	2.34	0.60
5:A:294:U:H3	5:A:350:G:H1	1.50	0.60
5:A:1523:A:H2'	5:A:1524:A:C8	2.35	0.60
31:a:710:G:H2'	31:a:711:G:C8	2.37	0.60
31:a:1175:G:N2	31:a:1178:G:OP2	2.26	0.60
32:b:198:VAL:HB	32:b:201:VAL:HG22	1.84	0.60
36:f:38:ARG:NH2	36:f:63:ASN:OD1	2.29	0.60
31:a:733:C:H2'	31:a:734:A:H8	1.67	0.60
5:A:1416:G:H1'	5:A:1489:A:H61	1.67	0.59
34:d:149:GLU:HA	34:d:152:LYS:HG3	1.84	0.59
49:s:63:THR:HG23	49:s:66:MET:HE3	1.84	0.59
14:J:109:GLU:OE2	14:J:109:GLU:N	2.33	0.59
30:Z:52:GLN:OE1	30:Z:54:PHE:N	2.34	0.59
40:j:80:THR:HG22	40:j:82:LYS:H	1.66	0.59
31:a:143:G:H2'	31:a:144:G:C8	2.37	0.59
6:B:11:A:N1	6:B:67:G:O2'	2.34	0.59
10:F:128:TYR:HB3	10:F:156:ILE:HD11	1.83	0.59
31:a:1027:U:H3'	31:a:1028:C:H4'	1.85	0.59
34:d:118:GLN:HG2	34:d:156:ARG:HH22	1.68	0.59
5:A:2840:A:HO2'	19:O:2:SER:N	2.01	0.59
31:a:1068:C:H2'	31:a:1069:G:H8	1.68	0.59
5:A:1717:G:O2'	5:A:1735:A:N6	2.36	0.59
5:A:2543:A:H2'	5:A:2544:U:C6	2.38	0.58
31:a:265:U:H2'	31:a:266:A:C8	2.38	0.58
32:b:142:GLU:O	32:b:146:LEU:HD12	2.02	0.58
32:b:119:LEU:HD13	32:b:143:MET:HB3	1.85	0.58
47:q:18:MET:HG3	47:q:21:SER:HB2	1.86	0.58
33:c:130:PHE:O	33:c:134:MET:HG3	2.03	0.58
5:A:1605:G:H5''	5:A:1606:A:H5'	1.84	0.58
10:F:110:ARG:O	10:F:112:ARG:NH2	2.37	0.58
14:J:102:VAL:HG23	14:J:121:VAL:HG13	1.86	0.58
31:a:733:C:H2'	31:a:734:A:C8	2.38	0.58
5:A:1503:C:H4'	5:A:1505:A:C8	2.39	0.58
5:A:1523:A:H2'	5:A:1524:A:H8	1.68	0.58
11:G:98:VAL:HG12	11:G:125:THR:HG23	1.85	0.58
19:O:91:ARG:HD2	19:O:92:ARG:N	2.19	0.58
49:s:22:ALA:O	49:s:25:SER:C	2.46	0.58
9:E:170:ASP:OD1	9:E:171:ALA:N	2.36	0.58
39:i:57:GLU:OE2	39:i:57:GLU:N	2.36	0.58
5:A:499:G:N1	5:A:502:A:OP2	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:F:136:ILE:HG22	10:F:137:VAL:H	1.69	0.57
31:a:1036:U:H2'	31:a:1037:A:C8	2.39	0.57
37:g:132:GLY:O	37:g:135:ILE:N	2.36	0.57
10:F:110:ARG:HB2	10:F:137:VAL:HG12	1.86	0.57
10:F:122:PHE:CE1	10:F:128:TYR:HB2	2.39	0.57
23:S:20:GLN:NE2	23:S:24:ASP:OD2	2.37	0.57
31:a:207:G:O2'	31:a:208:G:O4'	2.20	0.57
31:a:711:G:H2'	31:a:712:A:C8	2.40	0.57
33:c:79:LYS:HG2	33:c:80:LYS:HG3	1.85	0.57
10:F:115:ARG:O	10:F:115:ARG:HD3	2.04	0.57
36:f:2:ARG:HD3	36:f:91:ARG:HH21	1.68	0.57
5:A:1718:A:N6	5:A:1734:G:O2'	2.36	0.57
14:J:105:GLU:N	14:J:105:GLU:OE2	2.38	0.57
32:b:141:ARG:O	32:b:145:LYS:HG2	2.05	0.57
37:g:106:ASP:O	37:g:110:LYS:NZ	2.37	0.57
5:A:1531:C:O2'	5:A:1533:U:O4	2.19	0.57
5:A:2060:C:H2'	5:A:2061:C:C6	2.40	0.57
16:L:76:GLU:HB2	16:L:91:GLU:HG3	1.87	0.57
37:g:15:ASP:OD1	37:g:19:SER:N	2.37	0.57
5:A:1359:G:OP1	27:W:3:LYS:NZ	2.38	0.57
10:F:74:ILE:HB	10:F:79:ILE:HD11	1.87	0.57
11:G:54:PRO:HB3	11:G:61:ALA:HB1	1.87	0.57
31:a:1438:A:O2'	31:a:1439:G:O5'	2.23	0.57
49:s:25:SER:OG	49:s:26:ASN:N	2.38	0.57
10:F:47:LYS:HA	10:F:47:LYS:HE2	1.85	0.56
37:g:136:LYS:H	37:g:136:LYS:HE2	1.69	0.56
32:b:135:GLU:HB2	32:b:139:ARG:NH1	2.20	0.56
37:g:59:VAL:HG23	37:g:60:GLU:OE2	2.05	0.56
5:A:71:G:H2'	5:A:72:C:C6	2.41	0.56
5:A:1530:A:H3'	5:A:1531:C:H4'	1.86	0.56
7:C:17:GLU:HB2	7:C:204:SER:HB3	1.88	0.56
11:G:84:GLU:HA	11:G:133:LEU:O	2.05	0.56
31:a:1353:G:H2'	31:a:1354:A:C8	2.39	0.56
32:b:209:ILE:HD12	32:b:210:ARG:N	2.21	0.56
39:i:55:ALA:HA	39:i:58:LYS:HD2	1.87	0.56
31:a:1024:C:H2'	31:a:1025:C:C6	2.41	0.56
52:v:15:G:OP2	52:v:15:G:N2	2.33	0.56
5:A:1306:G:OP2	5:A:1306:G:N2	2.26	0.56
11:G:127:THR:OG1	11:G:128:ALA:N	2.39	0.56
31:a:75:A:N6	31:a:92:G:H1	2.02	0.56
37:g:55:LYS:HE2	37:g:55:LYS:N	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:v:8:4SU:H6	52:v:14:A:N7	2.20	0.56
5:A:1634:G:H2'	5:A:1635:A:C8	2.40	0.56
31:a:930:G:N7	37:g:3:ARG:NH1	2.53	0.56
39:i:34:GLU:CD	39:i:34:GLU:H	2.14	0.56
42:l:74:LEU:HD11	42:l:104:CYS:SG	2.46	0.56
31:a:919:G:H2'	31:a:920:A:C8	2.41	0.56
31:a:1166:A:H4'	32:b:141:ARG:HH22	1.69	0.56
32:b:93:TYR:CZ	32:b:152:GLY:HA2	2.41	0.56
32:b:164:PHE:HA	32:b:186:ILE:O	2.06	0.55
14:J:109:GLU:HA	14:J:112:MET:HE2	1.88	0.55
36:f:21:MET:HE1	36:f:83:ALA:HB3	1.87	0.55
6:B:46:U:H2'	6:B:47:C:C6	2.41	0.55
31:a:1094:C:O2'	31:a:1166:A:N3	2.37	0.55
41:k:106:ILE:HD12	41:k:106:ILE:O	2.06	0.55
42:l:3:THR:HG22	42:l:5:ASN:H	1.72	0.55
5:A:1471:U:H2'	5:A:1472:A:H8	1.72	0.55
5:A:2096:G:H1	5:A:2185:U:H3	1.54	0.55
19:O:91:ARG:HD3	19:O:115:GLU:HG3	1.89	0.55
39:i:53:LEU:HD21	39:i:92:LEU:HD13	1.88	0.55
31:a:1030:G:H2'	31:a:1031:G:C8	2.41	0.55
39:i:22:GLY:HA3	39:i:60:ASP:OD1	2.07	0.55
5:A:1464:A:H2'	5:A:1465:A:C8	2.41	0.55
6:B:87:A:OP2	16:L:39:ARG:NE	2.39	0.55
10:F:135:GLN:HG2	10:F:149:ILE:HG13	1.89	0.55
32:b:111:GLN:HA	32:b:114:ASN:HD21	1.71	0.55
5:A:2373:A:H2'	5:A:2374:A:C8	2.42	0.54
18:N:32:THR:HG23	18:N:35:HIS:H	1.72	0.54
35:e:54:GLU:OE2	35:e:54:GLU:N	2.40	0.54
31:a:789:A:H4'	31:a:790:U:O5'	2.07	0.54
31:a:1411:U:H2'	31:a:1412:G:H8	1.73	0.54
32:b:135:GLU:HA	32:b:138:GLU:HB2	1.90	0.54
5:A:1749:G:N2	5:A:1752:G:OP2	2.37	0.54
8:D:39:LYS:NZ	8:D:82:GLU:OE2	2.38	0.54
32:b:99:LEU:HD11	32:b:149:SER:HB3	1.90	0.54
34:d:87:ALA:HB3	34:d:90:GLU:HB2	1.90	0.54
37:g:87:VAL:HG12	37:g:89:MET:HE3	1.88	0.54
5:A:591:U:H2'	5:A:592:U:C6	2.42	0.54
5:A:1792:U:H2'	5:A:1793:C:H6	1.73	0.54
7:C:266:MET:HE2	7:C:266:MET:HA	1.90	0.54
36:f:16:ASP:OD1	36:f:17:GLN:NE2	2.40	0.54
5:A:280:A:H2'	5:A:281:A:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1001:A:C5	31:a:1023:G:H1'	2.43	0.54
31:a:1050:G:H4'	31:a:1051:C:H3'	1.90	0.54
52:v:35:C:N4	53:w:3:G:H1	2.06	0.54
14:J:104:ARG:HH11	14:J:121:VAL:HG12	1.73	0.53
34:d:152:LYS:O	34:d:153:GLN:NE2	2.29	0.53
5:A:12:A:H2'	5:A:13:A:C8	2.44	0.53
5:A:1729:U:H2'	5:A:1730:U:H6	1.73	0.53
5:A:1792:U:H2'	5:A:1793:C:C6	2.43	0.53
10:F:123:ASP:OD2	10:F:127:ASN:ND2	2.37	0.53
31:a:295:G:H2'	31:a:296:A:C8	2.43	0.53
31:a:1402:G:O2'	31:a:1515:MA6:O2'	2.25	0.53
31:a:1320:G:H2'	31:a:1321:A:C8	2.43	0.53
1:O:6:ARG:HG3	1:O:50:ILE:HA	1.89	0.53
11:G:86:LYS:NZ	11:G:130:GLU:HG2	2.24	0.53
30:Z:52:GLN:OE1	30:Z:53:LEU:N	2.42	0.53
31:a:498:C:H2'	31:a:499:A:C8	2.44	0.53
31:a:498:C:H2'	31:a:499:A:H8	1.73	0.53
32:b:141:ARG:HG3	32:b:145:LYS:HE3	1.91	0.53
39:i:26:LEU:HD12	39:i:61:LEU:HB2	1.90	0.53
48:r:32:TYR:CD1	48:r:55:LEU:HD21	2.44	0.53
5:A:1477:U:H2'	5:A:1478:G:C8	2.44	0.53
9:E:110:GLU:HB3	15:K:3:LEU:HD22	1.90	0.53
31:a:1095:C:H1'	31:a:1164:A:H61	1.72	0.53
52:v:35:C:H42	53:w:3:G:H22	1.56	0.53
5:A:856:G:OP1	26:V:78:ARG:NH1	2.40	0.53
52:v:39:A:H2'	52:v:40:U:O4'	2.09	0.53
5:A:365:U:H4'	5:A:366:G:O5'	2.08	0.53
31:a:1030:G:H2'	31:a:1031:G:H8	1.74	0.53
31:a:1034:C:H2'	31:a:1035:C:C6	2.44	0.53
36:f:22:VAL:O	36:f:26:ILE:HD12	2.08	0.53
6:B:11:A:O2'	6:B:13:A:OP2	2.27	0.52
18:N:68:GLU:CD	18:N:68:GLU:H	2.16	0.52
31:a:231:U:H2'	31:a:232:A:H8	1.73	0.52
31:a:424:G:O3'	34:d:13:ARG:NH1	2.42	0.52
31:a:989:U:H4'	31:a:990:G:O5'	2.09	0.52
5:A:2843:U:H2'	5:A:2844:G:O4'	2.09	0.52
11:G:12:PRO:HD2	11:G:15:VAL:HG11	1.91	0.52
32:b:9:ARG:N	32:b:9:ARG:HD3	2.23	0.52
31:a:1388:U:H2'	31:a:1389:G:C8	2.45	0.52
32:b:8:MET:O	32:b:12:LEU:HD12	2.09	0.52
32:b:89:ALA:HA	32:b:224:LEU:HD21	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:36:ASN:HA	34:d:46:ARG:CZ	2.39	0.52
35:e:110:MET:HE2	35:e:126:CYS:SG	2.50	0.52
5:A:1587:U:H2'	5:A:1588:A:C8	2.45	0.52
5:A:2844:G:O2'	5:A:2864:A:N6	2.42	0.52
31:a:1070:U:O2'	32:b:105:ASN:OD1	2.18	0.52
5:A:2323:A:H2'	5:A:2324:A:C8	2.45	0.52
21:Q:28:GLU:CD	21:Q:28:GLU:H	2.17	0.52
31:a:79:U:H2'	31:a:80:A:C8	2.44	0.52
31:a:1008:C:H2'	31:a:1009:A:H8	1.75	0.52
39:i:40:GLU:HA	39:i:43:ARG:HE	1.75	0.52
15:K:82:SER:HB3	15:K:116:GLY:HA3	1.91	0.52
16:L:78:PRO:O	16:L:79:LEU:HB3	2.08	0.52
31:a:671:G:H2'	31:a:672:A:H8	1.74	0.52
31:a:725:A:H2'	31:a:726:A:C8	2.45	0.52
5:A:1506:U:H2'	5:A:1507:G:C8	2.45	0.52
32:b:135:GLU:HB2	32:b:139:ARG:HH22	1.74	0.52
32:b:156:MET:HE1	32:b:160:PRO:HD3	1.90	0.52
11:G:4:VAL:O	11:G:69:ARG:HD2	2.09	0.52
5:A:579:C:H2'	5:A:580:A:C8	2.45	0.52
14:J:88:ASN:HB3	14:J:94:ILE:HG21	1.91	0.52
47:q:49:ASP:OD2	47:q:76:LEU:HD23	2.10	0.52
5:A:1471:U:H2'	5:A:1472:A:C8	2.46	0.51
5:A:1479:U:H2'	5:A:1480:A:C8	2.46	0.51
5:A:2502:U:O2'	5:A:2503:C:OP1	2.27	0.51
10:F:162:THR:OG1	10:F:165:GLU:OE1	2.26	0.51
31:a:536:A:H2'	31:a:537:G:C8	2.45	0.51
31:a:1173:A:H2'	31:a:1174:G:C8	2.45	0.51
49:s:29:LYS:H	49:s:29:LYS:HD3	1.75	0.51
14:J:109:GLU:H	14:J:109:GLU:CD	2.17	0.51
29:Y:29:ARG:HH11	29:Y:29:ARG:HG2	1.73	0.51
31:a:19:U:H2'	31:a:20:C:C6	2.46	0.51
32:b:219:MET:O	32:b:223:ILE:HG12	2.09	0.51
52:v:20:H2U:H2'	52:v:20:H2U:O2	2.10	0.51
5:A:2313:C:H2'	5:A:2314:G:C8	2.46	0.51
32:b:112:SER:HA	32:b:115:ARG:CZ	2.40	0.51
5:A:2067:A:H2'	5:A:2068:C:C6	2.46	0.51
10:F:11:GLU:O	10:F:15:LYS:HG2	2.09	0.51
31:a:1409:C:H2'	31:a:1410:A:C8	2.46	0.51
5:A:308:U:H2'	5:A:309:G:O4'	2.10	0.51
5:A:2562:A:N1	14:J:28:SER:OG	2.43	0.51
6:B:16:A:H2'	6:B:17:A:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:b:70:LEU:HB3	32:b:163:LEU:HD22	1.92	0.51
47:q:24:VAL:HG11	47:q:62:ILE:HD13	1.93	0.51
5:A:740:G:H2'	5:A:741:U:C6	2.46	0.51
5:A:2269:A:H2'	5:A:2270:A:C8	2.46	0.51
7:C:107:PRO:HD2	7:C:110:LEU:HD22	1.93	0.51
10:F:38:MET:HG3	10:F:57:MET:HE3	1.93	0.51
33:c:131:ARG:HB2	33:c:131:ARG:NH1	2.26	0.51
48:r:26:ILE:O	48:r:30:LYS:HG3	2.11	0.51
14:J:71:ARG:HH22	14:J:104:ARG:NH2	2.07	0.51
31:a:973:G:OP2	31:a:1355:U:O2'	2.29	0.51
41:k:80:ASN:HB2	41:k:107:ASN:HD21	1.76	0.51
52:v:40:U:H2'	52:v:41:G:H8	1.74	0.51
10:F:8:TYR:HA	10:F:12:LEU:HD23	1.93	0.51
31:a:470:G:H2'	31:a:471:G:C8	2.46	0.51
31:a:1034:C:H2'	31:a:1035:C:H6	1.76	0.51
7:C:270:ASP:O	7:C:272:ARG:NH2	2.43	0.51
31:a:1007:U:O4	31:a:1016:G:O6	2.28	0.51
48:r:45:THR:OG1	48:r:47:THR:OG1	2.26	0.51
5:A:831:A:H2'	5:A:832:G:C8	2.46	0.51
7:C:271:ARG:NE	7:C:273:VAL:HG12	2.26	0.51
8:D:33:ASN:N	8:D:33:ASN:HD22	2.09	0.51
49:s:30:PRO:HA	49:s:48:THR:HG23	1.93	0.51
52:v:14:A:H3'	52:v:15:G:N2	2.26	0.51
5:A:1729:U:H2'	5:A:1730:U:C6	2.46	0.50
31:a:499:A:P	42:l:115:SER:HG	2.34	0.50
31:a:1025:C:H2'	31:a:1026:U:C6	2.46	0.50
34:d:7:PRO:HB2	34:d:10:LYS:HD2	1.93	0.50
5:A:2070:U:H2'	5:A:2071:U:C6	2.46	0.50
6:B:26:C:OP1	18:N:32:THR:HG21	2.11	0.50
34:d:174:GLU:OE2	34:d:185:LYS:HD3	2.11	0.50
38:h:3:MET:HE2	38:h:3:MET:HA	1.91	0.50
41:k:87:GLY:O	41:k:92:ARG:NH1	2.43	0.50
1:0:24:ARG:HG3	1:0:24:ARG:HH11	1.77	0.50
5:A:1193:U:H2'	5:A:1194:U:C6	2.47	0.50
28:X:11:VAL:O	28:X:15:LYS:HG3	2.11	0.50
31:a:1037:A:H2'	31:a:1038:G:H8	1.76	0.50
45:o:14:LYS:HD3	45:o:15:PHE:CE2	2.47	0.50
5:A:1795:G:OP1	7:C:258:ARG:NH1	2.42	0.50
31:a:265:U:H2'	31:a:266:A:H8	1.77	0.50
52:v:51:C:H2'	52:v:52:A:H8	1.76	0.50
32:b:110:ARG:HD2	32:b:110:ARG:H	1.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:m:3:ARG:NH1	43:m:8:ASN:OD1	2.44	0.50
5:A:1506:U:H2'	5:A:1507:G:H8	1.76	0.50
10:F:83:TRP:N	10:F:83:TRP:CD1	2.80	0.50
32:b:51:ALA:HB1	32:b:202:ILE:HG22	1.93	0.50
5:A:1587:U:H2'	5:A:1588:A:H8	1.77	0.50
10:F:80:ARG:NH1	10:F:83:TRP:HB2	2.23	0.50
32:b:166:ILE:O	32:b:188:ILE:HB	2.12	0.50
41:k:81:LEU:HD22	41:k:104:TYR:HB3	1.94	0.50
5:A:71:G:H2'	5:A:72:C:H6	1.74	0.50
5:A:2186:G:H2'	5:A:2187:A:C8	2.47	0.50
5:A:2853:G:N2	5:A:2856:A:OP2	2.37	0.50
6:B:60:U:H2'	6:B:61:C:C6	2.47	0.50
27:W:65:GLU:CD	27:W:65:GLU:H	2.20	0.50
32:b:85:GLN:HG2	32:b:216:ALA:C	2.36	0.50
5:A:1885:A:H2'	5:A:1886:A:C8	2.47	0.50
6:B:52:G:H21	10:F:26:MET:HE1	1.77	0.50
11:G:25:GLU:OE2	11:G:32:THR:HG23	2.11	0.50
31:a:472:A:H2'	31:a:473:U:C6	2.47	0.50
31:a:1410:A:H61	31:a:1484:G:H1	1.59	0.50
37:g:65:THR:O	37:g:69:VAL:HG23	2.12	0.50
47:q:76:LEU:HD12	47:q:77:VAL:N	2.26	0.50
28:X:10:SER:OG	28:X:11:VAL:N	2.44	0.49
34:d:157:ILE:O	34:d:161:ILE:HG23	2.12	0.49
5:A:715:C:H2'	5:A:716:A:O4'	2.12	0.49
5:A:2736:A:H2'	5:A:2737:A:C8	2.46	0.49
6:B:60:U:H2'	6:B:61:C:H6	1.77	0.49
20:P:86:ALA:HB2	20:P:116:ALA:HB2	1.93	0.49
32:b:80:ASN:ND2	32:b:84:GLU:OE2	2.41	0.49
39:i:34:GLU:HA	39:i:43:ARG:HH11	1.77	0.49
5:A:103:U:H2'	5:A:104:C:O4'	2.13	0.49
5:A:2082:U:H2'	5:A:2083:G:C8	2.47	0.49
41:k:109:ILE:HG12	51:u:19:PHE:CD1	2.47	0.49
52:v:55:5MU:H2'	52:v:56:PSU:C6	2.47	0.49
5:A:1577:A:H3'	5:A:1578:A:H8	1.78	0.49
5:A:1716:U:H2'	5:A:1717:G:O4'	2.13	0.49
23:S:67:LYS:HB2	23:S:67:LYS:NZ	2.26	0.49
41:k:30:ILE:HG12	41:k:45:THR:HG23	1.94	0.49
5:A:2463:C:H2'	5:A:2464:A:O4'	2.12	0.49
41:k:110:THR:HG22	51:u:3:GLN:HA	1.94	0.49
43:m:11:ASP:HA	43:m:45:ILE:HB	1.94	0.49
41:k:96:VAL:HG21	41:k:109:ILE:HD12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:p:32:ARG:HG2	46:p:32:ARG:NH1	2.27	0.49
31:a:212:U:H2'	31:a:213:U:C6	2.48	0.49
36:f:17:GLN:O	36:f:21:MET:HG3	2.13	0.49
40:j:6:ILE:HB	40:j:76:ILE:HB	1.95	0.49
52:v:20:H2U:H4'	52:v:21:U:H5'	1.93	0.49
5:A:10:U:H2'	5:A:11:C:C6	2.48	0.49
5:A:1477:U:H3	5:A:1502:U:H3	1.59	0.49
32:b:116:LEU:HD13	32:b:146:LEU:HB2	1.95	0.49
34:d:67:TYR:OH	34:d:97:GLU:OE2	2.19	0.49
36:f:21:MET:HG2	36:f:24:ARG:HH21	1.78	0.49
31:a:671:G:H21	41:k:117:HIS:HB2	1.78	0.48
33:c:90:GLU:O	33:c:94:ILE:HG12	2.13	0.48
35:e:40:ASP:OD1	35:e:44:ARG:HB2	2.13	0.48
37:g:113:GLU:HB3	37:g:119:ARG:HG3	1.95	0.48
5:A:291:G:H2'	5:A:292:U:C6	2.48	0.48
10:F:120:LYS:HD3	10:F:167:ARG:HH22	1.78	0.48
15:K:95:GLU:OE1	15:K:95:GLU:N	2.43	0.48
31:a:490:A:H2'	31:a:491:G:C8	2.48	0.48
36:f:21:MET:HA	36:f:24:ARG:HE	1.78	0.48
5:A:2533:U:H2'	5:A:2534:C:C6	2.48	0.48
5:A:2881:U:O2'	30:Z:31:GLN:OE1	2.18	0.48
13:I:60:GLU:CD	13:I:60:GLU:H	2.20	0.48
32:b:136:ALA:O	32:b:140:THR:HG23	2.13	0.48
37:g:72:MET:SD	37:g:72:MET:N	2.86	0.48
52:v:20:H2U:O2'	52:v:60:G:N7	2.36	0.48
10:F:136:ILE:O	10:F:137:VAL:HG22	2.13	0.48
12:H:44:THR:HG22	12:H:48:GLU:OE2	2.12	0.48
14:J:51:ARG:HH22	14:J:94:ILE:CD1	2.23	0.48
23:S:68:ARG:HG3	23:S:68:ARG:NH1	2.28	0.48
31:a:386:U:H2'	31:a:387:C:C6	2.48	0.48
36:f:81:ASN:OD1	36:f:82:ASP:N	2.46	0.48
5:A:34:G:N2	5:A:511:G:H1'	2.29	0.48
5:A:113:C:O2'	5:A:296:A:O2'	2.28	0.48
5:A:141:U:H2'	5:A:142:A:H8	1.79	0.48
5:A:2302:C:H3'	5:A:2303:G:H5''	1.95	0.48
13:I:77:HIS:ND1	13:I:78:THR:O	2.46	0.48
14:J:54:LYS:NZ	14:J:54:LYS:HB3	2.28	0.48
32:b:42:ILE:HD12	32:b:42:ILE:O	2.13	0.48
36:f:44:ARG:HG3	36:f:58:HIS:CD2	2.48	0.48
5:A:2247:OMG:HM23	5:A:2247:OMG:H1'	1.68	0.48
6:B:64:A:H61	6:B:104:U:H2'	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:G:124:GLU:OE1	11:G:134:LYS:NZ	2.38	0.48
24:T:25:LEU:HD21	24:T:35:GLU:HB2	1.96	0.48
25:U:14:ASP:OD2	25:U:14:ASP:N	2.44	0.48
31:a:1215:C:H2'	31:a:1216:A:C8	2.49	0.48
35:e:91:SER:OG	35:e:129:SER:O	2.26	0.48
5:A:90:G:OP1	24:T:90:LYS:NZ	2.27	0.48
5:A:292:U:H2'	5:A:293:U:C6	2.48	0.48
10:F:38:MET:HE2	10:F:152:MET:HG2	1.95	0.48
43:m:86:TYR:O	43:m:90:ARG:HG2	2.14	0.48
5:A:1520:A:H2'	5:A:1521:G:C8	2.49	0.48
5:A:2325:A:H2'	5:A:2326:G:C8	2.47	0.48
7:C:69:ARG:O	7:C:189:ARG:NH1	2.47	0.48
32:b:135:GLU:CG	32:b:139:ARG:HH22	2.27	0.48
34:d:172:TRP:CE2	34:d:188:PRO:HG3	2.49	0.48
5:A:726:G:H4'	7:C:13:ARG:HD3	1.95	0.48
5:A:985:A:N7	29:Y:14:HIS:NE2	2.49	0.48
5:A:1794:U:OP2	7:C:273:VAL:HB	2.13	0.48
10:F:51:ASP:HA	10:F:54:VAL:HG12	1.96	0.48
5:A:110:A:OP2	5:A:110:A:H8	1.97	0.48
5:A:1047:A:H2'	5:A:1048:G:C8	2.49	0.48
5:A:2548:OMU:H6	5:A:2548:OMU:O5'	2.13	0.48
15:K:112:ILE:HB	15:K:129:LEU:HD23	1.95	0.48
31:a:610:C:H2'	31:a:611:C:C6	2.49	0.48
31:a:1427:C:H2'	31:a:1428:A:C8	2.49	0.48
45:o:78:TYR:OH	45:o:89:ARG:OXT	2.24	0.48
5:A:161:A:H2'	5:A:162:A:C8	2.49	0.47
5:A:811:U:H2'	5:A:812:C:H6	1.79	0.47
5:A:1416:G:O2'	5:A:1489:A:N6	2.46	0.47
31:a:1433:U:H2'	31:a:1434:A:H8	1.79	0.47
32:b:25:TRP:HH2	32:b:30:ARG:HD3	1.79	0.47
5:A:578:U:H2'	5:A:579:C:C6	2.48	0.47
8:D:58:GLU:CD	8:D:58:GLU:H	2.22	0.47
31:a:232:A:H2'	31:a:233:A:C8	2.49	0.47
45:o:78:TYR:O	45:o:82:ILE:HG23	2.14	0.47
12:H:30:LEU:HD23	12:H:35:LYS:HB2	1.97	0.47
31:a:1074:G:N2	31:a:1077:A:OP2	2.40	0.47
32:b:83:ARG:HA	32:b:83:ARG:HE	1.79	0.47
34:d:179:LYS:H	34:d:179:LYS:HD3	1.79	0.47
41:k:46:SER:HB3	41:k:61:ALA:HB1	1.95	0.47
5:A:2464:A:O2'	5:A:2465:A:H5'	2.15	0.47
6:B:111:C:H2'	6:B:112:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:F:22:ILE:HD12	10:F:22:ILE:O	2.14	0.47
34:d:190:ARG:HH22	34:d:195:ALA:HA	1.79	0.47
37:g:25:LYS:HG3	37:g:101:MET:HE1	1.95	0.47
5:A:287:G:H2'	5:A:288:U:H6	1.80	0.47
9:E:14:SER:N	9:E:196:GLU:OE2	2.45	0.47
19:O:90:LYS:HE3	19:O:90:LYS:HB3	1.65	0.47
31:a:1077:A:OP1	35:e:51:LYS:HD2	2.14	0.47
48:r:65:LEU:O	48:r:66:SER:OG	2.30	0.47
5:A:709:G:H1	5:A:718:U:H3	1.63	0.47
5:A:1568:A:H2'	5:A:1569:A:C8	2.50	0.47
7:C:136:PRO:O	7:C:139:SER:OG	2.26	0.47
11:G:43:LEU:HD11	11:G:50:LEU:HB3	1.95	0.47
11:G:85:ARG:HA	11:G:85:ARG:HD2	1.75	0.47
41:k:98:ALA:O	41:k:102:VAL:HG23	2.15	0.47
52:v:9:A:H62	52:v:24:A:H62	1.62	0.47
18:N:31:ARG:HG3	18:N:36:ILE:HD12	1.96	0.47
31:a:37:G:H2'	31:a:38:C:C6	2.50	0.47
31:a:58:U:H2'	31:a:59:G:C8	2.49	0.47
31:a:1438:A:O2'	31:a:1439:G:C8	2.68	0.47
37:g:15:ASP:OD1	37:g:18:PHE:N	2.47	0.47
46:p:66:GLU:OE1	46:p:69:ARG:NH2	2.47	0.47
49:s:43:ASP:OD2	49:s:43:ASP:N	2.47	0.47
52:v:19:G:H5'	52:v:21:U:O4	2.15	0.47
4:3:15:LYS:HB2	4:3:15:LYS:HE2	1.56	0.47
5:A:1790:A:H2'	5:A:1791:C:C6	2.50	0.47
6:B:86:U:H4'	6:B:87:A:O5'	2.15	0.47
31:a:539:G:H5'	34:d:40:GLY:HA2	1.96	0.47
31:a:908:U:H2'	31:a:909:C:C6	2.49	0.47
31:a:1311:C:H2'	31:a:1312:U:C6	2.50	0.47
37:g:130:GLY:O	37:g:135:ILE:HG21	2.15	0.47
5:A:2324:A:H2'	5:A:2325:A:H8	1.79	0.47
7:C:181:MET:HG2	7:C:269:ARG:HE	1.80	0.47
13:I:115:GLY:HA2	13:I:118:MET:HE2	1.96	0.47
31:a:1001:A:C6	31:a:1023:G:H1'	2.50	0.47
32:b:37:ARG:HD2	32:b:37:ARG:O	2.15	0.47
32:b:117:LYS:HE2	32:b:154:LYS:HB2	1.96	0.47
5:A:42:G:H8	5:A:42:G:OP2	1.98	0.47
5:A:141:U:H2'	5:A:142:A:C8	2.50	0.47
5:A:709:G:H2'	5:A:710:G:H8	1.79	0.47
5:A:727:G:OP1	7:C:13:ARG:HG2	2.15	0.47
5:A:2798:U:H2'	5:A:2799:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:160:ALA:HA	7:C:177:ARG:NH1	2.30	0.47
31:a:78:G:H2'	31:a:79:U:C6	2.50	0.47
31:a:1069:G:OP1	35:e:53:ARG:NH1	2.31	0.47
36:f:21:MET:HA	36:f:24:ARG:NE	2.30	0.47
36:f:93:GLU:OE1	36:f:93:GLU:HA	2.15	0.47
5:A:992:C:N4	13:I:1:MET:HA	2.29	0.46
9:E:198:GLU:HA	9:E:198:GLU:OE1	2.14	0.46
31:a:242:A:C2	31:a:278:A:C5	3.03	0.46
35:e:107:GLY:O	35:e:111:ARG:HB2	2.15	0.46
41:k:36:ARG:O	41:k:37:GLN:HB2	2.15	0.46
5:A:719:A:H2'	5:A:720:A:C8	2.50	0.46
5:A:1924:A:H2'	5:A:1925:G:O4'	2.15	0.46
11:G:75:LEU:O	11:G:79:VAL:HG22	2.15	0.46
34:d:19:LEU:HD11	34:d:62:LYS:HG3	1.96	0.46
38:h:22:LYS:O	38:h:66:TYR:OH	2.25	0.46
5:A:1790:A:H2'	5:A:1791:C:H6	1.80	0.46
13:I:69:ALA:O	13:I:90:GLU:HG3	2.16	0.46
31:a:190:G:H4'	50:t:59:ASP:HB3	1.98	0.46
5:A:347:A:H1'	5:A:348:A:H2	1.81	0.46
10:F:32:THR:OG1	10:F:157:THR:O	2.24	0.46
23:S:5:ARG:O	23:S:9:VAL:HG23	2.14	0.46
24:T:16:LYS:HG3	24:T:17:GLU:HG2	1.96	0.46
31:a:661:G:H22	31:a:738:G:H1	1.62	0.46
31:a:1117:C:H2'	31:a:1118:U:H6	1.81	0.46
41:k:111:ASP:OD1	41:k:113:THR:HG23	2.16	0.46
47:q:48:HIS:HB3	47:q:75:THR:HG22	1.97	0.46
5:A:1025:A:N6	5:A:1122:G:H2'	2.30	0.46
5:A:2587:C:H2'	5:A:2588:G:C8	2.51	0.46
7:C:163:GLN:HE21	7:C:163:GLN:HB3	1.49	0.46
18:N:7:SER:O	18:N:11:ARG:HG3	2.16	0.46
18:N:36:ILE:HG22	18:N:54:THR:HG23	1.98	0.46
18:N:49:LEU:HD23	18:N:86:VAL:HG11	1.97	0.46
28:X:41:HIS:HA	28:X:44:GLN:OE1	2.15	0.46
34:d:28:PHE:O	34:d:32:THR:HG22	2.15	0.46
35:e:148:SER:OG	35:e:150:GLU:OE2	2.34	0.46
5:A:1185:G:H5'	15:K:34:GLY:HA2	1.97	0.46
16:L:59:LYS:HE2	16:L:59:LYS:HA	1.97	0.46
20:P:111:GLU:OE1	20:P:111:GLU:HA	2.16	0.46
31:a:18:A:H8	31:a:1077:A:O2'	1.98	0.46
37:g:61:PHE:O	37:g:65:THR:HG23	2.15	0.46
3:2:13:ARG:HD2	15:K:65:LYS:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:637:U:H2'	5:A:638:C:C6	2.51	0.46
7:C:167:ARG:HA	7:C:172:ALA:HA	1.97	0.46
5:A:418:U:H2'	5:A:419:C:C6	2.50	0.46
5:A:811:U:H2'	5:A:812:C:C6	2.51	0.46
5:A:1173:G:H4'	5:A:1174:U:OP1	2.16	0.46
5:A:2189:G:H2'	5:A:2190:U:H6	1.80	0.46
5:A:2189:G:H2'	5:A:2190:U:C6	2.51	0.46
31:a:865:C:H2'	31:a:866:G:O4'	2.16	0.46
32:b:7:SER:O	32:b:8:MET:HB2	2.15	0.46
5:A:142:A:H2'	5:A:143:C:H6	1.80	0.46
5:A:2490:G:H4'	16:L:80:GLU:HG3	1.97	0.46
10:F:34:ILE:CD1	10:F:156:ILE:HG22	2.46	0.46
10:F:96:MET:HG3	10:F:97:TYR:N	2.31	0.46
31:a:534:A:H2'	31:a:535:G:H8	1.80	0.46
31:a:905:A:H2'	31:a:906:A:H8	1.80	0.46
31:a:1163:G:N2	31:a:1166:A:H3'	2.31	0.46
43:m:77:ILE:HG22	43:m:81:MET:HE2	1.98	0.46
5:A:579:C:H2'	5:A:580:A:H8	1.79	0.46
5:A:1428:A:H2'	5:A:1429:A:C8	2.51	0.46
5:A:2553:G:H2'	5:A:2554:C:C6	2.51	0.46
23:S:34:ASP:OD2	23:S:35:ILE:N	2.49	0.46
31:a:470:G:H2'	31:a:471:G:H8	1.80	0.46
31:a:521:G:H2'	31:a:522:C:C6	2.51	0.46
31:a:1059:U:H2'	31:a:1060:C:C6	2.51	0.46
32:b:135:GLU:HB2	32:b:139:ARG:NH2	2.31	0.46
33:c:2:GLY:O	33:c:4:LYS:NZ	2.44	0.46
1:0:39:ILE:HD12	1:0:41:GLN:HB2	1.98	0.45
5:A:286:U:H2'	5:A:287:G:C8	2.52	0.45
5:A:1479:U:H2'	5:A:1480:A:H8	1.81	0.45
5:A:2308:U:O3'	10:F:68:THR:HG21	2.16	0.45
5:A:2798:U:H2'	5:A:2799:C:H6	1.80	0.45
12:H:2:ASP:HB3	12:H:39:ALA:HB3	1.97	0.45
26:V:70:GLU:HG3	26:V:72:LYS:HG3	1.99	0.45
27:W:34:HIS:NE2	27:W:56:MET:HE1	2.32	0.45
31:a:754:U:H2'	31:a:755:G:O4'	2.16	0.45
37:g:108:ALA:O	37:g:119:ARG:HD2	2.15	0.45
5:A:830:U:H2'	5:A:831:A:H8	1.81	0.45
5:A:2224:G:H2'	5:A:2225:U:C6	2.51	0.45
16:L:113:LEU:HD23	16:L:113:LEU:HA	1.83	0.45
5:A:284:U:H3	5:A:360:A:H62	1.64	0.45
5:A:592:U:H2'	5:A:593:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:50:A:H8	6:B:50:A:OP2	1.98	0.45
25:U:13:GLU:H	25:U:13:GLU:CD	2.24	0.45
31:a:23:G:H2'	31:a:24:G:C8	2.52	0.45
31:a:403:U:O2'	34:d:115:GLU:OE1	2.32	0.45
31:a:1263:G:N2	31:a:1266:A:OP2	2.36	0.45
5:A:357:C:H2'	5:A:358:A:H8	1.81	0.45
5:A:830:U:H2'	5:A:831:A:C8	2.50	0.45
9:E:124:ALA:H	9:E:136:LYS:NZ	2.13	0.45
31:a:930:G:OP2	37:g:3:ARG:HB2	2.16	0.45
1:O:33:LYS:HG2	1:O:44:ILE:HG12	1.99	0.45
5:A:846:U:H2'	5:A:847:A:C8	2.51	0.45
5:A:1128:G:OP1	5:A:1128:G:C8	2.69	0.45
13:I:75:TYR:CE1	13:I:86:GLU:HG3	2.51	0.45
31:a:536:A:H2'	31:a:537:G:H8	1.81	0.45
31:a:577:C:H2'	31:a:578:G:O4'	2.16	0.45
31:a:1464:C:H2'	31:a:1465:A:H8	1.81	0.45
36:f:87:ASN:OD1	36:f:87:ASN:N	2.48	0.45
42:l:35:THR:N	42:l:54:ARG:O	2.48	0.45
5:A:568:G:H2'	5:A:2026:6MZ:N7	2.32	0.45
5:A:2645:C:H2'	5:A:2646:U:H6	1.80	0.45
14:J:104:ARG:NH2	14:J:122:LEU:O	2.50	0.45
31:a:552:U:H2'	31:a:553:C:C6	2.52	0.45
31:a:1067:U:H3	31:a:1102:A:H61	1.63	0.45
37:g:130:GLY:HA2	37:g:135:ILE:HG13	1.99	0.45
38:h:114:ASP:OD2	38:h:118:ARG:NH2	2.50	0.45
52:v:35:C:N4	53:w:3:G:H22	2.14	0.45
5:A:84:U:H2'	5:A:85:C:C6	2.52	0.45
5:A:142:A:H2'	5:A:143:C:C6	2.52	0.45
5:A:709:G:N2	5:A:718:U:O2	2.42	0.45
5:A:1464:A:H2'	5:A:1465:A:H8	1.79	0.45
5:A:1918:G:H2'	5:A:1919:U:C6	2.51	0.45
5:A:2224:G:H2'	5:A:2225:U:H6	1.81	0.45
12:H:9:ILE:HG21	12:H:12:LEU:HD13	1.99	0.45
13:I:102:GLU:O	13:I:106:LYS:HB2	2.16	0.45
24:T:81:VAL:HG11	24:T:92:ARG:HD2	1.99	0.45
31:a:6:C:H42	31:a:610:C:H5''	1.82	0.45
48:r:35:GLU:CD	48:r:35:GLU:H	2.24	0.45
51:u:17:ARG:HB3	51:u:21:ARG:HH21	1.82	0.45
5:A:596:U:H2'	5:A:597:A:H8	1.82	0.45
5:A:2282:G:H4'	5:A:2283:A:O4'	2.16	0.45
9:E:21:GLU:OE1	9:E:22:PHE:N	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:F:140:GLU:HG2	10:F:141:ILE:O	2.17	0.45
14:J:104:ARG:O	14:J:107:ARG:HG2	2.17	0.45
31:a:200:G:C4	31:a:201:A:C8	3.05	0.45
31:a:454:U:O2	31:a:470:G:N2	2.38	0.45
31:a:1140:G:H2'	31:a:1141:G:H8	1.82	0.45
35:e:150:GLU:H	35:e:150:GLU:CD	2.24	0.45
5:A:1111:C:H2'	5:A:1112:G:C8	2.52	0.45
14:J:103:THR:HA	14:J:104:ARG:NH1	2.32	0.45
31:a:942:G:C2	31:a:943:A:C8	3.05	0.45
31:a:1162:U:H3	31:a:1168:A:H61	1.65	0.45
33:c:107:ASP:OD2	33:c:107:ASP:N	2.42	0.45
33:c:135:LYS:NZ	33:c:135:LYS:HB3	2.32	0.45
1:0:26:MET:HE1	1:0:30:MET:HG3	1.99	0.45
5:A:2239:U:H2'	5:A:2240:U:C6	2.52	0.45
5:A:2674:A:H2'	5:A:2675:A:C8	2.51	0.45
5:A:2805:A:H2'	5:A:2806:A:C8	2.52	0.45
6:B:28:C:H1'	6:B:55:A:H61	1.82	0.45
10:F:31:ILE:O	10:F:96:MET:HE1	2.16	0.45
18:N:67:ILE:O	18:N:71:THR:HG23	2.17	0.45
18:N:68:GLU:OE2	18:N:68:GLU:N	2.47	0.45
28:X:20:GLU:HA	28:X:20:GLU:OE1	2.16	0.45
31:a:202:U:H2'	31:a:203:C:C6	2.52	0.45
31:a:329:C:OP1	50:t:2:ALA:N	2.50	0.45
31:a:1008:C:H2'	31:a:1009:A:C8	2.52	0.45
32:b:37:ARG:HD2	32:b:37:ARG:C	2.41	0.45
36:f:70:THR:HA	36:f:73:GLU:HG2	1.98	0.45
50:t:28:VAL:HG23	50:t:61:MET:HG3	1.98	0.45
31:a:380:C:H2'	31:a:381:C:H6	1.82	0.44
31:a:649:U:O4	31:a:749:G:O2'	2.26	0.44
31:a:1433:U:H2'	31:a:1434:A:C8	2.52	0.44
37:g:140:ASP:O	37:g:144:MET:HG2	2.17	0.44
38:h:39:VAL:HG21	38:h:111:ILE:HG22	1.98	0.44
5:A:847:A:H2'	5:A:848:C:C6	2.53	0.44
5:A:2309:C:H2'	5:A:2310:A:H8	1.82	0.44
5:A:2587:C:H2'	5:A:2588:G:H8	1.82	0.44
5:A:2658:A:O5'	5:A:2658:A:H8	2.00	0.44
31:a:155:G:N2	31:a:158:A:OP2	2.49	0.44
32:b:215:TYR:O	32:b:219:MET:HG2	2.17	0.44
37:g:49:ARG:NH1	37:g:53:LYS:HD3	2.33	0.44
41:k:92:ARG:O	41:k:96:VAL:HG12	2.17	0.44
5:A:846:U:H2'	5:A:847:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:1403:U:H2'	5:A:1404:G:C8	2.52	0.44
18:N:1:MET:C	18:N:3:GLU:H	2.25	0.44
18:N:5:LYS:O	18:N:9:LEU:HD23	2.17	0.44
31:a:58:U:H2'	31:a:59:G:H8	1.82	0.44
31:a:993:A:H2'	31:a:994:U:C6	2.52	0.44
31:a:994:U:H2'	31:a:995:A:H8	1.81	0.44
32:b:81:ILE:HG21	32:b:213:THR:HA	1.98	0.44
36:f:20:GLY:O	36:f:23:GLU:HG3	2.17	0.44
37:g:71:PRO:HA	37:g:138:ARG:HH11	1.81	0.44
5:A:279:U:H2'	5:A:364:A:C6	2.53	0.44
5:A:1730:U:H2'	5:A:1731:C:H6	1.82	0.44
6:B:52:G:H21	10:F:26:MET:CE	2.30	0.44
25:U:5:VAL:HG22	25:U:66:GLU:HB2	2.00	0.44
25:U:77:LYS:HE2	25:U:77:LYS:HB3	1.76	0.44
52:v:71:G:H2'	52:v:72:C:C6	2.52	0.44
5:A:605:U:C5	5:A:618:G:C5	3.05	0.44
5:A:709:G:H2'	5:A:710:G:C8	2.53	0.44
5:A:2061:C:H2'	5:A:2062:C:H6	1.82	0.44
5:A:2303:G:H8	5:A:2303:G:OP1	2.00	0.44
5:A:2419:U:H4'	5:A:2420:C:O5'	2.17	0.44
7:C:165:LEU:HD12	7:C:181:MET:HE1	2.00	0.44
9:E:153:ASP:OD2	9:E:154:GLU:N	2.50	0.44
31:a:91:G:H2'	31:a:92:G:C8	2.53	0.44
31:a:671:G:H2'	31:a:672:A:C8	2.53	0.44
31:a:1026:U:O2	31:a:1028:C:O2'	2.26	0.44
31:a:1235:A:H2	31:a:1238:G:N3	2.15	0.44
31:a:1488:G:H2'	31:a:1489:A:C8	2.53	0.44
36:f:1:MET:HE3	36:f:1:MET:HB3	1.89	0.44
43:m:66:GLU:OE1	43:m:70:ARG:NH2	2.51	0.44
50:t:33:LYS:HE2	50:t:33:LYS:HB2	1.66	0.44
5:A:365:U:H5'	5:A:366:G:C8	2.53	0.44
5:A:643:U:H3'	5:A:644:A:H5'	2.00	0.44
5:A:1025:A:H2'	5:A:1026:A:C8	2.52	0.44
10:F:133:LYS:O	10:F:134:GLU:HB2	2.18	0.44
19:O:91:ARG:HD2	19:O:91:ARG:C	2.43	0.44
21:Q:34:THR:HG22	21:Q:60:THR:HG22	1.99	0.44
31:a:231:U:H2'	31:a:232:A:C8	2.51	0.44
31:a:493:A:H2'	31:a:494:U:H5	1.82	0.44
31:a:1409:C:H2'	31:a:1410:A:H8	1.83	0.44
32:b:111:GLN:O	32:b:115:ARG:HG3	2.17	0.44
33:c:45:LYS:HB3	33:c:45:LYS:HE3	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:k:26:PHE:HZ	51:u:33:ARG:HE	1.65	0.44
4:3:16:VAL:HG22	4:3:25:VAL:HG22	2.00	0.44
5:A:69:U:O4	5:A:70:A:N6	2.51	0.44
5:A:1166:A:H2'	5:A:1167:U:C6	2.53	0.44
5:A:2186:G:H2'	5:A:2187:A:H8	1.83	0.44
5:A:2469:U:H2'	5:A:2469:U:O2	2.16	0.44
6:B:16:A:H2'	6:B:17:A:C8	2.52	0.44
10:F:77:PHE:N	10:F:77:PHE:CD1	2.83	0.44
10:F:147:ASP:CG	10:F:148:ARG:H	2.25	0.44
12:H:30:LEU:HD22	12:H:36:ALA:HB2	2.00	0.44
25:U:67:ILE:HD12	25:U:76:VAL:HG21	2.00	0.44
31:a:1002:A:C5	31:a:1003:C:H1'	2.53	0.44
31:a:1005:U:H2'	31:a:1006:U:C6	2.53	0.44
37:g:55:LYS:HE2	37:g:55:LYS:H	1.81	0.44
37:g:72:MET:HG2	37:g:73:VAL:HG23	1.99	0.44
40:j:27:GLU:OE1	40:j:27:GLU:HA	2.18	0.44
5:A:161:A:H2'	5:A:162:A:H8	1.82	0.44
5:A:1680:G:H2'	5:A:1681:U:C6	2.52	0.44
10:F:51:ASP:HA	10:F:54:VAL:CG1	2.48	0.44
31:a:1011:A:C2	31:a:1216:A:H1'	2.52	0.44
32:b:119:LEU:HA	32:b:119:LEU:HD23	1.85	0.44
36:f:27:SER:O	36:f:31:GLU:HG3	2.18	0.44
44:n:56:SER:OG	44:n:58:VAL:HG22	2.18	0.44
10:F:8:TYR:OH	10:F:29:PRO:O	2.34	0.44
31:a:36:C:H2'	31:a:37:G:H8	1.83	0.44
31:a:406:G:OP2	34:d:31:LYS:NZ	2.32	0.44
52:v:51:C:H2'	52:v:52:A:C8	2.53	0.44
5:A:19:U:O2	5:A:2622:C:H4'	2.18	0.43
5:A:596:U:H2'	5:A:597:A:C8	2.53	0.43
5:A:741:U:O2'	5:A:1657:U:OP1	2.34	0.43
5:A:758:G:H2'	5:A:759:A:O4'	2.18	0.43
5:A:1535:U:H2'	5:A:1536:G:C8	2.53	0.43
5:A:2034:G:H2'	5:A:2035:U:O4'	2.18	0.43
7:C:179:GLY:O	7:C:269:ARG:NH2	2.51	0.43
24:T:31:ARG:HB3	24:T:62:SER:HB2	2.00	0.43
31:a:127:U:H2'	31:a:128:C:C6	2.53	0.43
31:a:1247:A:H2'	31:a:1248:A:C8	2.53	0.43
31:a:1313:G:H4'	44:n:58:VAL:HG11	1.98	0.43
40:j:6:ILE:N	40:j:6:ILE:HD12	2.34	0.43
41:k:80:ASN:HA	41:k:105:LYS:O	2.17	0.43
5:A:306:U:H2'	5:A:307:C:C6	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:1529:U:H3	5:A:1536:G:H1	1.66	0.43
5:A:1798:A:H2'	5:A:1799:A:C8	2.53	0.43
5:A:2060:C:H2'	5:A:2061:C:H6	1.83	0.43
9:E:1:MET:HE1	9:E:18:PHE:O	2.17	0.43
9:E:14:SER:H	9:E:196:GLU:CD	2.26	0.43
42:l:61:PHE:N	42:l:61:PHE:CD1	2.84	0.43
5:A:862:G:H2'	5:A:863:C:C6	2.54	0.43
5:A:1025:A:H61	5:A:1122:G:H2'	1.84	0.43
5:A:1261:G:O2'	5:A:2008:G:O6	2.32	0.43
5:A:1381:A:H2'	5:A:1382:U:C6	2.53	0.43
5:A:1521:G:H2'	5:A:1522:C:O4'	2.18	0.43
13:I:2:LYS:HE3	20:P:93:ARG:HH12	1.83	0.43
16:L:57:ARG:HD3	16:L:57:ARG:HA	1.68	0.43
26:V:20:MET:HE2	26:V:20:MET:HB2	1.87	0.43
31:a:78:G:H2'	31:a:79:U:H6	1.83	0.43
31:a:534:A:H2'	31:a:535:G:C8	2.53	0.43
33:c:211:MET:HE2	33:c:216:ASN:CG	2.43	0.43
5:A:606:A:H2'	5:A:607:A:C8	2.53	0.43
14:J:94:ILE:HD12	14:J:94:ILE:O	2.19	0.43
31:a:1248:A:H2'	31:a:1249:A:C8	2.53	0.43
32:b:110:ARG:HA	32:b:113:ILE:HB	2.00	0.43
35:e:38:VAL:HG23	35:e:70:MET:HE2	1.98	0.43
36:f:12:PRO:HA	36:f:15:SER:OG	2.19	0.43
39:i:69:GLY:O	39:i:73:GLN:HG3	2.17	0.43
46:p:41:ASP:OD2	46:p:42:SER:N	2.51	0.43
5:A:358:A:H2'	5:A:359:U:C6	2.53	0.43
5:A:944:A:H2'	5:A:945:C:C6	2.53	0.43
5:A:1182:G:H5'	21:Q:83:TYR:CE1	2.53	0.43
5:A:1579:G:H2'	5:A:1580:C:C6	2.52	0.43
5:A:2287:U:OP1	5:A:2376:U:O2'	2.35	0.43
10:F:69:LEU:HA	10:F:84:PRO:HA	2.00	0.43
14:J:97:ARG:O	14:J:98:ILE:HD13	2.19	0.43
15:K:102:VAL:HG23	15:K:103:VAL:HG23	2.01	0.43
18:N:32:THR:CG2	18:N:35:HIS:H	2.31	0.43
31:a:367:A:H2'	31:a:368:C:O4'	2.19	0.43
31:a:1117:C:H2'	31:a:1118:U:C6	2.53	0.43
31:a:1233:A:H2'	31:a:1234:C:C6	2.54	0.43
31:a:1425:A:H2'	31:a:1426:C:C6	2.53	0.43
31:a:1461:U:H2'	31:a:1462:A:H8	1.83	0.43
35:e:87:ARG:NH2	35:e:89:GLY:O	2.51	0.43
5:A:84:U:H2'	5:A:85:C:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:357:C:H2'	5:A:358:A:C8	2.53	0.43
5:A:844:A:H5''	5:A:845:A:C8	2.53	0.43
31:a:79:U:H2'	31:a:80:A:H8	1.83	0.43
31:a:333:G:H2'	31:a:334:A:C8	2.52	0.43
31:a:1432:G:H2'	31:a:1433:U:C6	2.53	0.43
33:c:191:THR:HG21	33:c:196:ILE:HD12	2.01	0.43
5:A:740:G:H2'	5:A:741:U:H6	1.83	0.43
6:B:46:U:H2'	6:B:47:C:H6	1.82	0.43
11:G:54:PRO:HB2	11:G:56:LYS:O	2.18	0.43
31:a:435:U:C2	31:a:436:A:C8	3.07	0.43
31:a:943:A:H2'	31:a:944:G:H8	1.78	0.43
31:a:1001:A:H2'	31:a:1002:A:O4'	2.19	0.43
5:A:719:A:H2'	5:A:720:A:H8	1.84	0.43
5:A:2428:A:H1'	52:v:76:C:O4'	2.19	0.43
5:A:2792:U:H1'	5:A:2793:U:C5	2.54	0.43
10:F:4:LEU:HB2	10:F:5:LYS:H	1.59	0.43
19:O:117:LEU:O	19:O:117:LEU:HD12	2.19	0.43
21:Q:32:THR:O	21:Q:33:ILE:HD13	2.19	0.43
31:a:519:C:H41	42:l:50:ARG:NH2	2.16	0.43
31:a:1068:C:H2'	31:a:1069:G:C8	2.50	0.43
31:a:1335:G:H2'	31:a:1336:A:C8	2.53	0.43
37:g:132:GLY:O	37:g:135:ILE:HB	2.18	0.43
5:A:1128:G:OP1	5:A:1128:G:H8	2.00	0.43
7:C:175:ARG:HB2	7:C:181:MET:SD	2.58	0.43
8:D:18:ASP:OD1	8:D:19:ALA:N	2.52	0.43
52:v:63:U:H2'	52:v:64:C:C6	2.54	0.43
52:v:67:C:H2'	52:v:68:A:C8	2.54	0.43
5:A:347:A:H1'	5:A:348:A:C2	2.54	0.43
18:N:28:CYS:HA	18:N:92:ASP:HB3	2.01	0.43
18:N:98:TYR:OH	18:N:110:ARG:NH2	2.51	0.43
29:Y:29:ARG:HG2	29:Y:29:ARG:NH1	2.34	0.43
31:a:185:C:H4'	31:a:186:G:O5'	2.19	0.43
31:a:1360:A:O2'	31:a:1362:G:N7	2.38	0.43
32:b:135:GLU:CB	32:b:139:ARG:HH22	2.31	0.43
5:A:113:C:HO2'	5:A:296:A:HO2'	1.59	0.42
5:A:1400:U:H2'	5:A:1401:U:C6	2.54	0.42
5:A:2242:G:H2'	5:A:2243:A:C8	2.54	0.42
5:A:2883:C:H2'	5:A:2884:U:C6	2.54	0.42
31:a:153:U:H2'	31:a:154:C:C6	2.54	0.42
31:a:436:A:C4	31:a:437:A:C8	3.06	0.42
32:b:132:THR:OG1	32:b:133:LYS:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:161:GLU:H	35:e:161:GLU:CD	2.26	0.42
42:l:3:THR:HG22	42:l:5:ASN:N	2.33	0.42
51:u:2:PRO:HB2	51:u:3:GLN:H	1.68	0.42
51:u:59:LYS:HG3	51:u:62:ARG:NH2	2.34	0.42
52:v:6:U:H2'	52:v:7:G:C8	2.54	0.42
5:A:1356:G:H2'	5:A:1357:C:C6	2.54	0.42
5:A:1403:U:H2'	5:A:1404:G:H8	1.84	0.42
27:W:13:VAL:HG22	27:W:29:PHE:HB2	2.00	0.42
28:X:5:ASP:OD1	28:X:5:ASP:N	2.52	0.42
31:a:1437:U:H2'	31:a:1438:A:N3	2.33	0.42
32:b:115:ARG:HH11	32:b:146:LEU:HD21	1.85	0.42
33:c:129:MET:HE2	33:c:129:MET:HB2	1.87	0.42
33:c:136:ARG:HG3	33:c:136:ARG:HH11	1.84	0.42
34:d:190:ARG:HA	34:d:190:ARG:HD2	1.81	0.42
37:g:66:LEU:HD21	37:g:97:THR:HG23	2.01	0.42
42:l:110:ARG:NH2	42:l:112:GLN:O	2.47	0.42
5:A:287:G:H2'	5:A:288:U:C6	2.54	0.42
5:A:1586:U:H2'	5:A:1587:U:C6	2.54	0.42
5:A:2309:C:H2'	5:A:2310:A:C8	2.54	0.42
10:F:106:ILE:HD11	10:F:139:PRO:HD3	2.01	0.42
10:F:143:PHE:O	10:F:146:ILE:HG12	2.20	0.42
14:J:114:ILE:H	14:J:114:ILE:HG13	1.71	0.42
37:g:140:ASP:O	37:g:144:MET:HE2	2.20	0.42
52:v:69:U:H2'	52:v:70:A:C8	2.54	0.42
5:A:198:A:H2'	5:A:199:G:N3	2.35	0.42
5:A:718:U:H2'	5:A:719:A:C8	2.54	0.42
5:A:2021:C:H2'	5:A:2022:U:C6	2.54	0.42
31:a:414:C:H2'	31:a:415:C:C6	2.54	0.42
31:a:669:U:H2'	31:a:670:A:H8	1.84	0.42
31:a:1464:C:H2'	31:a:1465:A:C8	2.54	0.42
32:b:25:TRP:CH2	32:b:30:ARG:HD3	2.53	0.42
32:b:72:VAL:HB	32:b:165:VAL:HG23	2.02	0.42
32:b:131:LEU:HD23	32:b:132:THR:O	2.19	0.42
36:f:15:SER:HA	36:f:18:VAL:HG13	2.01	0.42
36:f:98:GLU:CD	36:f:98:GLU:H	2.27	0.42
41:k:93:GLU:HB3	51:u:20:LYS:HE2	2.01	0.42
5:A:580:A:H2'	5:A:581:G:C8	2.55	0.42
5:A:782:G:H5'	5:A:783:G:OP1	2.20	0.42
6:B:13:A:O3'	6:B:14:G:H8	2.02	0.42
10:F:74:ILE:H	10:F:79:ILE:HD12	1.84	0.42
11:G:103:VAL:HG13	11:G:115:TYR:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:862:A:H2'	31:a:863:C:C6	2.55	0.42
39:i:128:ARG:NH2	52:v:34:U:OP2	2.52	0.42
5:A:655:U:H2'	5:A:656:U:C6	2.55	0.42
5:A:1151:C:H2'	5:A:1152:G:O4'	2.19	0.42
5:A:1310:C:H2'	5:A:1311:A:H8	1.85	0.42
5:A:2784:C:O2'	5:A:2805:A:N3	2.47	0.42
10:F:57:MET:SD	10:F:87:CYS:SG	3.18	0.42
31:a:693:A:H2'	31:a:694:U:H6	1.84	0.42
31:a:946:A:N7	43:m:105:ASN:ND2	2.68	0.42
1:0:24:ARG:HG3	1:0:24:ARG:NH1	2.34	0.42
5:A:1194:U:H2'	5:A:1195:C:H6	1.85	0.42
5:A:1687:A:H2'	5:A:1688:A:C8	2.54	0.42
23:S:4:GLU:CD	23:S:4:GLU:H	2.28	0.42
31:a:232:A:H2'	31:a:233:A:H8	1.83	0.42
31:a:1144:C:O2'	39:i:5:TYR:OH	2.30	0.42
43:m:16:VAL:HG13	43:m:34:LEU:HD12	2.01	0.42
5:A:1917:G:H2'	5:A:1918:G:O4'	2.20	0.42
5:A:2302:C:C3'	5:A:2303:G:H5''	2.50	0.42
6:B:64:A:N6	6:B:104:U:H2'	2.35	0.42
7:C:271:ARG:CZ	7:C:273:VAL:HG12	2.50	0.42
10:F:48:LYS:HA	10:F:51:ASP:OD1	2.20	0.42
11:G:42:GLU:HG3	11:G:53:ALA:O	2.20	0.42
31:a:1127:A:H2'	31:a:1128:G:H8	1.85	0.42
32:b:143:MET:HA	32:b:146:LEU:CD1	2.49	0.42
41:k:33:ILE:HG22	41:k:41:LEU:HB2	2.02	0.42
50:t:12:ARG:O	50:t:15:VAL:HG12	2.20	0.42
2:1:25:LYS:HB3	2:1:25:LYS:HE3	1.59	0.42
5:A:41:U:H4'	5:A:42:G:OP2	2.19	0.42
5:A:1193:U:H2'	5:A:1194:U:H6	1.84	0.42
10:F:70:ALA:HB2	10:F:85:ILE:CG1	2.49	0.42
10:F:103:LEU:HD12	10:F:107:ALA:HB2	2.01	0.42
31:a:218:U:H2'	31:a:219:A:H8	1.85	0.42
31:a:677:C:H2'	31:a:678:A:C8	2.54	0.42
34:d:158:LYS:O	34:d:161:ILE:HG12	2.19	0.42
5:A:1786:U:H2'	5:A:1787:A:C5	2.55	0.42
5:A:2063:G:H1	5:A:2439:U:H3	1.67	0.42
10:F:47:LYS:C	10:F:48:LYS:HE2	2.45	0.42
10:F:122:PHE:HB3	10:F:163:ASP:OD1	2.20	0.42
21:Q:52:PRO:HB2	21:Q:53:VAL:HG12	2.02	0.42
22:R:86:MET:HE3	22:R:88:ARG:HD3	2.02	0.42
31:a:409:G:H1'	31:a:424:G:N2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:433:U:O2'	31:a:434:U:H5'	2.20	0.42
31:a:887:G:H4'	31:a:888:U:O5'	2.20	0.42
31:a:1407:A:H2'	31:a:1408:C:C6	2.54	0.42
33:c:187:MET:HE3	33:c:187:MET:HB3	1.99	0.42
37:g:126:ASP:HB3	37:g:131:LYS:O	2.20	0.42
5:A:101:U:H2'	5:A:102:A:C8	2.55	0.41
5:A:843:G:N3	5:A:843:G:H5''	2.35	0.41
5:A:908:A:H2'	5:A:909:A:C8	2.55	0.41
5:A:1406:G:H2'	5:A:1407:U:C6	2.55	0.41
5:A:2586:A:H2'	5:A:2587:C:H6	1.84	0.41
10:F:23:LYS:H	10:F:23:LYS:HG2	1.68	0.41
19:O:109:LYS:HE3	19:O:112:ARG:NH2	2.34	0.41
31:a:1460:U:H2'	31:a:1461:U:H6	1.85	0.41
32:b:83:ARG:HA	32:b:83:ARG:NE	2.34	0.41
32:b:106:TRP:CZ3	32:b:110:ARG:NH2	2.88	0.41
34:d:154:GLN:HB3	34:d:157:ILE:HG12	2.02	0.41
52:v:66:U:H2'	52:v:67:C:H5''	2.02	0.41
5:A:157:U:H2'	5:A:158:U:C6	2.55	0.41
5:A:1533:U:H1'	5:A:1535:U:O2	2.20	0.41
19:O:117:LEU:HA	19:O:118:PRO:HD2	1.88	0.41
31:a:35:A:H2'	31:a:36:C:C6	2.55	0.41
31:a:1420:G:H2'	31:a:1421:U:C6	2.55	0.41
31:a:1438:A:O2'	31:a:1439:G:H8	2.02	0.41
31:a:1510:A:H2'	31:a:1511:G:C8	2.54	0.41
35:e:106:ALA:HB2	35:e:124:ALA:HB3	2.02	0.41
5:A:12:A:H2'	5:A:13:A:H8	1.85	0.41
5:A:997:A:H2'	5:A:998:A:C8	2.56	0.41
5:A:1047:A:C6	5:A:1048:G:C6	3.08	0.41
5:A:2314:G:H2'	5:A:2315:U:O4'	2.20	0.41
5:A:2533:U:H2'	5:A:2534:C:H6	1.85	0.41
10:F:120:LYS:HD3	10:F:167:ARG:NH2	2.35	0.41
21:Q:19:THR:HG22	21:Q:97:LYS:HG3	2.02	0.41
31:a:1164:A:H8	31:a:1164:A:OP1	2.03	0.41
31:a:1473:G:H2'	31:a:1474:C:C6	2.55	0.41
5:A:310:G:H2'	5:A:311:G:C8	2.55	0.41
5:A:1903:G:H2'	5:A:1904:C:C6	2.55	0.41
6:B:111:C:H2'	6:B:112:A:C8	2.56	0.41
7:C:269:ARG:HE	7:C:269:ARG:HB3	1.74	0.41
10:F:50:LEU:O	10:F:54:VAL:HG12	2.20	0.41
19:O:5:HIS:O	19:O:9:GLN:HG3	2.21	0.41
31:a:748:U:H2'	31:a:749:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:848:U:H2'	31:a:849:A:C8	2.55	0.41
31:a:1023:G:N3	31:a:1023:G:H2'	2.36	0.41
31:a:1382:G:H2'	31:a:1383:G:C8	2.55	0.41
31:a:1419:U:H2'	31:a:1420:G:C8	2.55	0.41
52:v:19:G:H3'	52:v:21:U:C4	2.55	0.41
5:A:100:A:H2'	5:A:101:U:C6	2.55	0.41
5:A:794:C:H2'	5:A:795:U:C6	2.55	0.41
5:A:2188:G:H2'	5:A:2189:G:H8	1.84	0.41
5:A:2420:C:OP2	5:A:2421:A:H2'	2.19	0.41
5:A:2892:C:H2'	5:A:2893:U:C6	2.56	0.41
21:Q:61:ALA:HB2	21:Q:98:ILE:HD13	2.02	0.41
25:U:34:ILE:HG12	25:U:95:PHE:HB2	2.03	0.41
31:a:156:A:H2'	31:a:157:A:O4'	2.20	0.41
31:a:905:A:H2'	31:a:906:A:C8	2.55	0.41
31:a:1493:C:H2'	31:a:1494:G:O4'	2.20	0.41
32:b:111:GLN:HA	32:b:114:ASN:ND2	2.35	0.41
32:b:134:ARG:CZ	32:b:134:ARG:HB3	2.49	0.41
32:b:207:ASP:OD1	32:b:207:ASP:N	2.53	0.41
33:c:77:ILE:HA	33:c:84:ILE:HG23	2.02	0.41
37:g:142:HIS:O	37:g:146:GLU:OE1	2.37	0.41
5:A:482:A:C8	24:T:43:HIS:HD2	2.38	0.41
5:A:1586:U:H2'	5:A:1587:U:H6	1.85	0.41
9:E:119:LEU:HD12	9:E:119:LEU:HA	1.88	0.41
31:a:421:G:H2'	31:a:422:U:C6	2.55	0.41
50:t:86:LEU:HD12	50:t:86:LEU:HA	1.83	0.41
5:A:1485:A:H2'	7:C:98:ASP:HB3	2.02	0.41
5:A:1687:A:H2'	5:A:1688:A:H8	1.86	0.41
5:A:2795:A:H2'	5:A:2797:G:OP2	2.20	0.41
28:X:14:LEU:HD23	28:X:14:LEU:HA	1.85	0.41
31:a:434:U:O2'	31:a:435:U:P	2.79	0.41
31:a:1475:C:H2'	31:a:1476:G:C8	2.56	0.41
43:m:59:GLU:OE1	43:m:59:GLU:HA	2.20	0.41
5:A:1311:A:H2'	5:A:1312:G:H8	1.85	0.41
5:A:1502:U:O2'	5:A:1505:A:H1'	2.21	0.41
5:A:2448:C:H2'	5:A:2449:A:C8	2.56	0.41
5:A:2645:C:H2'	5:A:2646:U:C6	2.54	0.41
5:A:2784:C:H2'	5:A:2785:C:C6	2.56	0.41
8:D:30:VAL:O	8:D:188:SER:OG	2.36	0.41
19:O:28:THR:CG2	19:O:91:ARG:HB3	2.51	0.41
31:a:403:U:H2'	31:a:404:G:C8	2.56	0.41
31:a:601:G:H2'	31:a:602:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:c:85:GLU:OE2	33:c:89:ARG:HG3	2.21	0.41
43:m:56:ILE:O	43:m:60:VAL:HG23	2.20	0.41
5:A:546:G:N3	5:A:546:G:H2'	2.35	0.41
5:A:844:A:H4'	5:A:845:A:O5'	2.19	0.41
5:A:1942:U:H2'	5:A:1943:C:C6	2.56	0.41
5:A:2341:A:N3	5:A:2377:A:H2'	2.35	0.41
15:K:131:LYS:HE3	15:K:131:LYS:HB2	1.71	0.41
28:X:34:THR:HG22	28:X:36:GLN:HG3	2.02	0.41
31:a:37:G:H2'	31:a:38:C:H6	1.85	0.41
31:a:880:C:O2'	31:a:881:U:H5'	2.21	0.41
31:a:915:A:H2'	31:a:916:A:C8	2.56	0.41
31:a:933:C:C2	31:a:934:A:C8	3.08	0.41
32:b:137:LEU:HA	32:b:140:THR:OG1	2.21	0.41
33:c:183:ASP:OD2	33:c:183:ASP:C	2.64	0.41
35:e:93:VAL:HG12	35:e:126:CYS:SG	2.61	0.41
40:j:52:LEU:HD23	40:j:62:ARG:HG2	2.02	0.41
52:v:29:C:H2'	52:v:30:G:C8	2.54	0.41
5:A:293:U:H2'	5:A:294:U:C6	2.56	0.41
5:A:630:A:H2'	5:A:631:A:C8	2.56	0.41
5:A:701:U:H2'	5:A:702:G:O4'	2.20	0.41
31:a:483:U:H2'	31:a:484:A:H8	1.86	0.41
5:A:177:G:H2'	5:A:178:U:C6	2.55	0.40
5:A:478:A:H4'	5:A:479:A:OP1	2.21	0.40
22:R:65:ASP:OD1	22:R:65:ASP:N	2.51	0.40
31:a:35:A:H2'	31:a:36:C:H6	1.85	0.40
34:d:12:SER:HA	34:d:19:LEU:HD23	2.02	0.40
41:k:20:ALA:HB2	41:k:81:LEU:HD12	2.02	0.40
5:A:46:G:H2'	5:A:47:U:C6	2.56	0.40
5:A:1579:G:C6	5:A:1580:C:N4	2.89	0.40
5:A:1904:C:H2'	5:A:1905:C:C6	2.57	0.40
5:A:2379:G:HO2'	5:A:2380:U:P	2.42	0.40
7:C:5:LYS:HZ1	7:C:16:VAL:H	1.70	0.40
10:F:128:TYR:HB3	10:F:156:ILE:CD1	2.50	0.40
31:a:180:U:C2	31:a:181:C:C5	3.09	0.40
31:a:677:C:H2'	31:a:678:A:H8	1.85	0.40
35:e:100:GLU:OE2	35:e:101:GLY:N	2.54	0.40
52:v:27:A:H61	52:v:45:G:H1	1.69	0.40
5:A:1549:U:H2'	5:A:1550:G:O4'	2.21	0.40
11:G:121:VAL:HG13	11:G:135:SER:HB2	2.03	0.40
17:M:114:GLU:HG2	17:M:115:LEU:O	2.21	0.40
31:a:184:A:H3'	31:a:185:C:O2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:b:196:ASP:OD1	32:b:197:ASN:N	2.54	0.40
42:l:89:ASP:OD1	42:l:89:ASP:C	2.64	0.40
42:l:123:LYS:HD2	42:l:123:LYS:HA	1.69	0.40
5:A:568:G:H2'	5:A:2026:6MZ:C8	2.51	0.40
5:A:1902:G:H2'	5:A:1903:G:H8	1.87	0.40
31:a:200:G:C8	31:a:461:A:N1	2.89	0.40
31:a:419:U:O2'	31:a:420:G:H8	2.04	0.40
31:a:1515:MA6:H8	31:a:1515:MA6:O5'	2.22	0.40
31:a:1519:U:H2'	31:a:1520:G:H8	1.86	0.40
42:l:54:ARG:HE	42:l:54:ARG:HB3	1.75	0.40
44:n:73:TYR:CE2	44:n:75:ARG:HA	2.57	0.40
5:A:119:U:H2'	5:A:120:G:O4'	2.21	0.40
5:A:410:G:OP2	5:A:2402:U:O2'	2.38	0.40
5:A:1348:A:H2'	5:A:1349:A:C8	2.56	0.40
5:A:1732:C:H2'	5:A:1733:U:C6	2.57	0.40
5:A:1876:U:H2'	5:A:1877:C:C6	2.57	0.40
5:A:2263:A:H5''	5:A:2264:A:H5'	2.02	0.40
31:a:516:C:OP2	42:l:47:SER:OG	2.37	0.40
31:a:1115:U:H1'	31:a:1176:A:C5	2.57	0.40
32:b:26:ASN:OD1	32:b:28:LYS:HG3	2.22	0.40
32:b:111:GLN:NE2	32:b:115:ARG:HE	2.19	0.40
34:d:8:LYS:HE2	34:d:8:LYS:HB2	1.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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%)	49 (100%)	0	0	100	100
2	1	42/44 (96%)	42 (100%)	0	0	100	100
3	2	61/64 (95%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	3	36/38 (95%)	36 (100%)	0	0	100	100
7	C	270/274 (98%)	262 (97%)	7 (3%)	1 (0%)	30	40
8	D	209/212 (99%)	201 (96%)	8 (4%)	0	100	100
9	E	198/200 (99%)	198 (100%)	0	0	100	100
10	F	172/178 (97%)	159 (92%)	11 (6%)	2 (1%)	10	14
11	G	172/177 (97%)	164 (95%)	7 (4%)	1 (1%)	21	30
12	H	58/148 (39%)	55 (95%)	3 (5%)	0	100	100
13	I	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
14	J	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
15	K	142/146 (97%)	139 (98%)	3 (2%)	0	100	100
16	L	135/137 (98%)	132 (98%)	2 (2%)	1 (1%)	18	26
17	M	117/125 (94%)	115 (98%)	2 (2%)	0	100	100
18	N	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
19	O	115/122 (94%)	113 (98%)	2 (2%)	0	100	100
20	P	115/119 (97%)	115 (100%)	0	0	100	100
21	Q	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	17
22	R	107/109 (98%)	106 (99%)	1 (1%)	0	100	100
23	S	89/106 (84%)	88 (99%)	1 (1%)	0	100	100
24	T	101/105 (96%)	98 (97%)	3 (3%)	0	100	100
25	U	95/98 (97%)	94 (99%)	1 (1%)	0	100	100
26	V	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
27	W	75/78 (96%)	75 (100%)	0	0	100	100
28	X	58/65 (89%)	58 (100%)	0	0	100	100
29	Y	55/58 (95%)	53 (96%)	2 (4%)	0	100	100
30	Z	52/61 (85%)	50 (96%)	2 (4%)	0	100	100
32	b	223/250 (89%)	209 (94%)	13 (6%)	1 (0%)	30	40
33	c	213/250 (85%)	206 (97%)	7 (3%)	0	100	100
34	d	205/208 (99%)	200 (98%)	5 (2%)	0	100	100
35	e	153/165 (93%)	152 (99%)	1 (1%)	0	100	100
36	f	102/127 (80%)	97 (95%)	5 (5%)	0	100	100
37	g	132/156 (85%)	127 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	h	128/131 (98%)	123 (96%)	5 (4%)	0	100	100
39	i	124/128 (97%)	121 (98%)	3 (2%)	0	100	100
40	j	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
41	k	115/128 (90%)	111 (96%)	4 (4%)	0	100	100
42	l	120/124 (97%)	114 (95%)	6 (5%)	0	100	100
43	m	113/118 (96%)	109 (96%)	4 (4%)	0	100	100
44	n	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
45	o	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
46	p	80/101 (79%)	80 (100%)	0	0	100	100
47	q	77/85 (91%)	77 (100%)	0	0	100	100
48	r	50/75 (67%)	50 (100%)	0	0	100	100
49	s	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
50	t	84/88 (96%)	84 (100%)	0	0	100	100
51	u	61/71 (86%)	59 (97%)	2 (3%)	0	100	100
All	All	5414/5872 (92%)	5264 (97%)	143 (3%)	7 (0%)	49	62

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	F	137	VAL
32	b	8	MET
10	F	5	LYS
11	G	13	ASN
16	L	79	LEU
7	C	3	ILE
21	Q	52	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%)	45 (96%)	2 (4%)	26	41
2	1	36/36 (100%)	35 (97%)	1 (3%)	38	58
3	2	52/53 (98%)	51 (98%)	1 (2%)	50	69
4	3	33/33 (100%)	31 (94%)	2 (6%)	17	27
7	C	218/220 (99%)	217 (100%)	1 (0%)	81	90
8	D	166/167 (99%)	163 (98%)	3 (2%)	51	71
9	E	155/155 (100%)	150 (97%)	5 (3%)	34	53
10	F	144/147 (98%)	136 (94%)	8 (6%)	19	30
11	G	139/142 (98%)	132 (95%)	7 (5%)	22	35
12	H	45/112 (40%)	44 (98%)	1 (2%)	45	65
13	I	118/118 (100%)	117 (99%)	1 (1%)	73	85
14	J	103/103 (100%)	102 (99%)	1 (1%)	68	82
15	K	106/108 (98%)	104 (98%)	2 (2%)	50	69
16	L	113/113 (100%)	112 (99%)	1 (1%)	70	84
17	M	96/101 (95%)	95 (99%)	1 (1%)	68	82
18	N	85/85 (100%)	84 (99%)	1 (1%)	63	79
19	O	99/102 (97%)	98 (99%)	1 (1%)	68	82
20	P	85/86 (99%)	85 (100%)	0	100	100
21	Q	84/84 (100%)	83 (99%)	1 (1%)	63	79
22	R	88/88 (100%)	87 (99%)	1 (1%)	65	81
23	S	77/87 (88%)	76 (99%)	1 (1%)	61	78
24	T	83/85 (98%)	79 (95%)	4 (5%)	23	37
25	U	79/80 (99%)	75 (95%)	4 (5%)	21	34
26	V	59/64 (92%)	59 (100%)	0	100	100
27	W	69/70 (99%)	67 (97%)	2 (3%)	37	57
28	X	53/56 (95%)	52 (98%)	1 (2%)	50	69
29	Y	53/54 (98%)	52 (98%)	1 (2%)	50	69
30	Z	46/50 (92%)	45 (98%)	1 (2%)	45	65
32	b	185/200 (92%)	180 (97%)	5 (3%)	39	59
33	c	175/198 (88%)	174 (99%)	1 (1%)	78	88
34	d	170/171 (99%)	167 (98%)	3 (2%)	51	71
35	e	113/120 (94%)	110 (97%)	3 (3%)	39	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	f	94/111 (85%)	89 (95%)	5 (5%)	20	33
37	g	113/128 (88%)	113 (100%)	0	100	100
38	h	108/109 (99%)	105 (97%)	3 (3%)	38	58
39	i	99/100 (99%)	96 (97%)	3 (3%)	36	56
40	j	89/91 (98%)	88 (99%)	1 (1%)	65	81
41	k	88/98 (90%)	85 (97%)	3 (3%)	32	51
42	l	104/106 (98%)	96 (92%)	8 (8%)	12	18
43	m	95/98 (97%)	92 (97%)	3 (3%)	34	53
44	n	81/82 (99%)	80 (99%)	1 (1%)	63	79
45	o	71/72 (99%)	71 (100%)	0	100	100
46	p	63/77 (82%)	63 (100%)	0	100	100
47	q	71/76 (93%)	70 (99%)	1 (1%)	59	77
48	r	46/66 (70%)	45 (98%)	1 (2%)	45	65
49	s	70/78 (90%)	68 (97%)	2 (3%)	37	57
50	t	65/67 (97%)	62 (95%)	3 (5%)	24	38
51	u	54/62 (87%)	53 (98%)	1 (2%)	50	69
All	All	4485/4756 (94%)	4383 (98%)	102 (2%)	44	64

All (102) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	5	ILE
1	0	44	ILE
2	1	44	VAL
3	2	64	ILE
4	3	8	LYS
4	3	26	ILE
7	C	163	GLN
8	D	59	SER
8	D	141	VAL
8	D	192	VAL
9	E	5	THR
9	E	119	LEU
9	E	120	VAL
9	E	139	ASP
9	E	199	LEU

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Mol	Chain	Res	Type
10	F	16	LEU
10	F	22	ILE
10	F	31	ILE
10	F	36	LEU
10	F	54	VAL
10	F	90	THR
10	F	101	ASP
10	F	177	PHE
11	G	16	THR
11	G	18	THR
11	G	24	VAL
11	G	29	SER
11	G	76	VAL
11	G	98	VAL
11	G	121	VAL
12	H	4	ILE
13	I	78	THR
14	J	103	THR
15	K	29	VAL
15	K	144	VAL
16	L	135	THR
17	M	14	SER
18	N	51	GLN
19	O	28	THR
21	Q	53	VAL
22	R	109	VAL
23	S	49	LEU
24	T	17	GLU
24	T	42	LYS
24	T	50	THR
24	T	66	SER
25	U	45	THR
25	U	59	VAL
25	U	62	GLU
25	U	69	VAL
27	W	24	LYS
27	W	42	SER
28	X	42	GLU
29	Y	57	GLU
30	Z	33	THR
32	b	42	ILE
32	b	95	ASP

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Mol	Chain	Res	Type
32	b	109	LEU
32	b	153	VAL
32	b	169	ASP
33	c	161	GLU
34	d	118	GLN
34	d	153	GLN
34	d	193	LEU
35	e	10	LEU
35	e	40	ASP
35	e	73	VAL
36	f	19	VAL
36	f	26	ILE
36	f	64	VAL
36	f	82	ASP
36	f	102	LEU
38	h	29	SER
38	h	30	SER
38	h	108	SER
39	i	27	VAL
39	i	70	ILE
39	i	95	VAL
40	j	18	ILE
41	k	25	SER
41	k	29	THR
41	k	45	THR
42	l	10	LYS
42	l	13	THR
42	l	14	THR
42	l	15	LEU
42	l	35	THR
42	l	39	THR
42	l	62	GLU
42	l	65	SER
43	m	16	VAL
43	m	32	ASN
43	m	75	MET
44	n	100	SER
47	q	75	THR
48	r	27	ASP
49	s	50	SER
49	s	63	THR
50	t	30	THR

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Mol	Chain	Res	Type
50	t	48	THR
50	t	86	LEU
51	u	63	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
7	C	53	HIS
7	C	134	ASN
8	D	65	GLN
8	D	133	GLN
8	D	143	HIS
9	E	28	HIS
13	I	47	HIS
13	I	58	ASN
13	I	63	GLN
15	K	101	ASN
19	O	55	ASN
20	P	72	ASN
24	T	47	ASN
24	T	64	HIS
29	Y	8	GLN
32	b	5	ASN
32	b	114	ASN
33	c	139	GLN
34	d	44	GLN
34	d	50	GLN
34	d	118	GLN
36	f	58	HIS
39	i	48	GLN
40	j	64	GLN
41	k	118	ASN
42	l	111	ASN
44	n	54	ASN
50	t	3	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	a	1527/1544 (98%)	195 (12%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	A	2714/2918 (93%)	369 (13%)	20 (0%)
52	v	76/77 (98%)	23 (30%)	0
53	w	2/3 (66%)	0	0
6	B	114/115 (99%)	15 (13%)	2 (1%)
All	All	4433/4657 (95%)	602 (13%)	22 (0%)

All (602) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	41	U
5	A	42	G
5	A	50	G
5	A	53	G
5	A	58	G
5	A	67	G
5	A	78	A
5	A	81	A
5	A	82	G
5	A	92	G
5	A	102	A
5	A	109	G
5	A	110	A
5	A	117	G
5	A	125	A
5	A	126	A
5	A	127	U
5	A	138	A
5	A	147	A
5	A	149	G
5	A	170	A
5	A	188	A
5	A	193	G
5	A	203	A
5	A	206	A
5	A	222	G
5	A	223	A
5	A	228	A
5	A	229	A
5	A	235	U
5	A	236	U
5	A	240	A
5	A	246	U

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Mol	Chain	Res	Type
5	A	255	G
5	A	257	G
5	A	262	A
5	A	278	U
5	A	279	U
5	A	297	G
5	A	313	A
5	A	326	A
5	A	331	G
5	A	332	A
5	A	336	U
5	A	347	A
5	A	348	A
5	A	349	A
5	A	360	A
5	A	365	U
5	A	366	G
5	A	369	G
5	A	370	A
5	A	371	G
5	A	385	G
5	A	395	G
5	A	403	A
5	A	410	G
5	A	416	C
5	A	423	G
5	A	435	C
5	A	455	C
5	A	479	A
5	A	480	G
5	A	493	G
5	A	504	A
5	A	508	C
5	A	529	G
5	A	531	A
5	A	532	G
5	A	544	U
5	A	545	C
5	A	546	G
5	A	548	G
5	A	554	A
5	A	561	A

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Mol	Chain	Res	Type
5	A	571	U
5	A	573	A
5	A	601	A
5	A	611	U
5	A	612	A
5	A	613	U
5	A	625	A
5	A	626	G
5	A	633	C
5	A	635	A
5	A	643	U
5	A	644	A
5	A	649	G
5	A	651	U
5	A	684	U
5	A	714	A
5	A	728	A
5	A	745	U
5	A	762	A
5	A	773	G
5	A	774	G
5	A	780	A
5	A	782	G
5	A	783	G
5	A	803	G
5	A	810	C
5	A	817	A
5	A	825	U
5	A	826	U
5	A	843	G
5	A	844	A
5	A	845	A
5	A	846	U
5	A	857	G
5	A	864	A
5	A	900	C
5	A	905	G
5	A	908	A
5	A	913	C
5	A	929	C
5	A	930	U
5	A	938	A

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Mol	Chain	Res	Type
5	A	942	A
5	A	943	G
5	A	958	C
5	A	971	G
5	A	980	A
5	A	993	A
5	A	1009	U
5	A	1010	C
5	A	1014	G
5	A	1023	G
5	A	1030	U
5	A	1033	G
5	A	1043	A
5	A	1044	G
5	A	1103	A
5	A	1105	U
5	A	1106	C
5	A	1107	G
5	A	1108	A
5	A	1109	G
5	A	1115	C
5	A	1125	G
5	A	1128	G
5	A	1129	U
5	A	1130	A
5	A	1131	A
5	A	1132	C
5	A	1133	G
5	A	1140	A
5	A	1169	C
5	A	1170	U
5	A	1171	U
5	A	1173	G
5	A	1174	U
5	A	1242	A
5	A	1245	G
5	A	1248	A
5	A	1251	G
5	A	1266	G
5	A	1267	A
5	A	1296	A
5	A	1316	A

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Mol	Chain	Res	Type
5	A	1324	U
5	A	1347	U
5	A	1360	A
5	A	1363	G
5	A	1373	A
5	A	1374	U
5	A	1378	A
5	A	1390	A
5	A	1391	U
5	A	1411	G
5	A	1414	A
5	A	1422	A
5	A	1423	C
5	A	1428	A
5	A	1432	C
5	A	1447	G
5	A	1448	U
5	A	1462	G
5	A	1477	U
5	A	1485	A
5	A	1488	C
5	A	1489	A
5	A	1504	U
5	A	1505	A
5	A	1509	U
5	A	1518	A
5	A	1519	U
5	A	1522	C
5	A	1523	A
5	A	1527	U
5	A	1528	G
5	A	1529	U
5	A	1530	A
5	A	1531	C
5	A	1532	U
5	A	1533	U
5	A	1534	G
5	A	1535	U
5	A	1536	G
5	A	1538	A
5	A	1539	G
5	A	1540	C

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Mol	Chain	Res	Type
5	A	1547	G
5	A	1548	U
5	A	1557	U
5	A	1558	G
5	A	1564	A
5	A	1565	G
5	A	1567	A
5	A	1576	U
5	A	1580	C
5	A	1581	U
5	A	1582	U
5	A	1583	C
5	A	1586	U
5	A	1606	A
5	A	1607	A
5	A	1616	A
5	A	1632	U
5	A	1642	C
5	A	1645	U
5	A	1646	U
5	A	1647	G
5	A	1672	G
5	A	1675	A
5	A	1723	A
5	A	1725	U
5	A	1726	C
5	A	1727	G
5	A	1731	C
5	A	1760	G
5	A	1769	A
5	A	1776	A
5	A	1796	C
5	A	1797	A
5	A	1807	G
5	A	1812	C
5	A	1825	A
5	A	1844	A
5	A	1845	G
5	A	1854	A
5	A	1865	G
5	A	1869	G
5	A	1872	A

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Mol	Chain	Res	Type
5	A	1902	G
5	A	1918	G
5	A	1923	A
5	A	1925	G
5	A	1926	G
5	A	1932	A
5	A	1934	A
5	A	1936	U
5	A	1951	U
5	A	1959	U
5	A	1960	G
5	A	1963	C
5	A	1966	A
5	A	1967	U
5	A	1968	G
5	A	1987	U
5	A	1989	U
5	A	2017	A
5	A	2018	U
5	A	2019	C
5	A	2027	A
5	A	2029	A
5	A	2039	C
5	A	2051	C
5	A	2052	G
5	A	2056	A
5	A	2057	G
5	A	2058	A
5	A	2065	7MG
5	A	2092	C
5	A	2093	U
5	A	2194	A
5	A	2200	G
5	A	2207	G
5	A	2216	C
5	A	2219	G
5	A	2221	A
5	A	2234	G
5	A	2279	U
5	A	2283	A
5	A	2284	A
5	A	2299	G

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Mol	Chain	Res	Type
5	A	2301	U
5	A	2303	G
5	A	2304	G
5	A	2305	A
5	A	2307	A
5	A	2314	G
5	A	2316	A
5	A	2317	G
5	A	2318	A
5	A	2321	A
5	A	2323	A
5	A	2341	A
5	A	2343	C
5	A	2346	C
5	A	2378	G
5	A	2379	G
5	A	2380	U
5	A	2381	C
5	A	2399	C
5	A	2402	U
5	A	2420	C
5	A	2421	A
5	A	2425	G
5	A	2426	A
5	A	2430	A
5	A	2431	A
5	A	2437	U
5	A	2444	A
5	A	2465	A
5	A	2466	G
5	A	2469	U
5	A	2471	C
5	A	2472	A
5	A	2474	A
5	A	2487	U
5	A	2498	G
5	A	2499	2MA
5	A	2503	C
5	A	2514	A
5	A	2516	C
5	A	2525	G
5	A	2543	A

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Mol	Chain	Res	Type
5	A	2550	U
5	A	2562	A
5	A	2563	G
5	A	2578	G
5	A	2598	A
5	A	2599	G
5	A	2605	U
5	A	2609	U
5	A	2625	U
5	A	2657	G
5	A	2661	A
5	A	2685	U
5	A	2686	A
5	A	2687	C
5	A	2710	G
5	A	2722	U
5	A	2729	A
5	A	2744	A
5	A	2754	A
5	A	2761	A
5	A	2774	A
5	A	2776	A
5	A	2786	U
5	A	2787	A
5	A	2793	U
5	A	2796	U
5	A	2797	G
5	A	2799	C
5	A	2816	G
5	A	2817	A
5	A	2830	G
5	A	2831	A
5	A	2845	G
5	A	2851	U
5	A	2852	A
5	A	2857	U
5	A	2863	A
5	A	2869	A
5	A	2876	C
5	A	2881	U
5	A	2882	G
5	A	2898	U

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Mol	Chain	Res	Type
6	B	2	C
6	B	13	A
6	B	14	G
6	B	40	C
6	B	44	A
6	B	49	G
6	B	50	A
6	B	59	C
6	B	64	A
6	B	65	G
6	B	66	C
6	B	71	A
6	B	87	A
6	B	105	C
6	B	106	A
31	a	6	C
31	a	7	U
31	a	10	A
31	a	11	G
31	a	15	U
31	a	24	G
31	a	34	A
31	a	41	G
31	a	49	C
31	a	50	U
31	a	53	A
31	a	62	A
31	a	66	G
31	a	76	A
31	a	77	G
31	a	80	A
31	a	81	G
31	a	82	C
31	a	83	U
31	a	84	U
31	a	85	G
31	a	91	G
31	a	97	A
31	a	117	U
31	a	126	A
31	a	127	U
31	a	163	U

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Mol	Chain	Res	Type
31	a	170	A
31	a	184	A
31	a	185	C
31	a	186	G
31	a	193	A
31	a	205	U
31	a	206	C
31	a	208	G
31	a	216	G
31	a	241	U
31	a	243	G
31	a	247	G
31	a	262	G
31	a	263	C
31	a	276	C
31	a	285	G
31	a	302	A
31	a	314	G
31	a	324	C
31	a	325	A
31	a	340	A
31	a	341	C
31	a	343	G
31	a	344	G
31	a	348	C
31	a	350	G
31	a	363	U
31	a	368	C
31	a	380	C
31	a	393	A
31	a	402	G
31	a	407	A
31	a	409	G
31	a	410	A
31	a	417	U
31	a	418	A
31	a	419	U
31	a	420	G
31	a	425	U
31	a	426	A
31	a	435	U
31	a	442	G

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Mol	Chain	Res	Type
31	a	447	A
31	a	448	G
31	a	461	A
31	a	462	A
31	a	463	U
31	a	481	G
31	a	483	U
31	a	492	A
31	a	494	U
31	a	496	A
31	a	508	C
31	a	515	C
31	a	516	C
31	a	518	G
31	a	524	7MG
31	a	527	G
31	a	528	U
31	a	529	A
31	a	544	A
31	a	556	A
31	a	561	C
31	a	569	A
31	a	570	A
31	a	573	C
31	a	574	G
31	a	615	C
31	a	639	A
31	a	650	A
31	a	662	A
31	a	684	A
31	a	700	G
31	a	720	U
31	a	721	G
31	a	752	G
31	a	774	A
31	a	789	A
31	a	790	U
31	a	791	A
31	a	812	A
31	a	814	C
31	a	840	U
31	a	841	G

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Mol	Chain	Res	Type
31	a	842	A
31	a	887	G
31	a	888	U
31	a	911	A
31	a	923	G
31	a	924	G
31	a	931	C
31	a	932	A
31	a	934	A
31	a	957	U
31	a	963	2MG
31	a	966	A
31	a	968	G
31	a	972	A
31	a	973	G
31	a	974	A
31	a	990	G
31	a	1001	A
31	a	1007	U
31	a	1025	C
31	a	1026	U
31	a	1027	U
31	a	1028	C
31	a	1029	G
31	a	1030	G
31	a	1033	A
31	a	1052	A
31	a	1062	U
31	a	1091	G
31	a	1092	U
31	a	1098	A
31	a	1134	C
31	a	1136	G
31	a	1156	U
31	a	1157	G
31	a	1163	G
31	a	1164	A
31	a	1166	A
31	a	1168	A
31	a	1178	G
31	a	1179	G
31	a	1180	C

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Mol	Chain	Res	Type
31	a	1188	A
31	a	1193	A
31	a	1194	A
31	a	1210	A
31	a	1211	C
31	a	1224	A
31	a	1235	A
31	a	1255	G
31	a	1267	U
31	a	1276	A
31	a	1277	A
31	a	1284	A
31	a	1295	U
31	a	1297	G
31	a	1299	C
31	a	1302	G
31	a	1317	C
31	a	1332	U
31	a	1333	C
31	a	1335	G
31	a	1337	A
31	a	1342	U
31	a	1343	A
31	a	1350	G
31	a	1360	A
31	a	1367	G
31	a	1378	U
31	a	1395	A
31	a	1398	G
31	a	1416	G
31	a	1438	A
31	a	1439	G
31	a	1443	A
31	a	1450	A
31	a	1484	G
31	a	1490	A
31	a	1491	G
31	a	1494	G
31	a	1503	U
31	a	1514	G
31	a	1526	G
31	a	1527	G

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Mol	Chain	Res	Type
52	v	9	A
52	v	10	G
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	27	A
52	v	28	C
52	v	37	U
52	v	38	A
52	v	49	C
52	v	50	A
52	v	51	C
52	v	52	A
52	v	55	5MU
52	v	56	PSU
52	v	58	A
52	v	64	C
52	v	65	G
52	v	67	C

All (22) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	91	A
5	A	109	G
5	A	256	C
5	A	365	U
5	A	368	C
5	A	424	G
5	A	478	A
5	A	507	U
5	A	625	A
5	A	782	G
5	A	844	A
5	A	1173	G
5	A	1179	G
5	A	1187	G
5	A	1564	A

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Mol	Chain	Res	Type
5	A	2379	G
5	A	2419	U
5	A	2443	G
5	A	2502	U
5	A	2786	U
6	B	13	A
6	B	86	U

5.4 Non-standard residues in protein, DNA, RNA chains

25 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	OMU	A	2548	5	19,22,23	2.95	8 (42%)	25,31,34	1.85	5 (20%)
5	PSU	A	2500	5	18,21,22	1.08	1 (5%)	21,30,33	1.90	4 (19%)
31	2MG	a	963	31	23,26,27	0.50	0	33,38,41	0.50	0
31	MA6	a	1515	31	23,26,27	1.41	4 (17%)	33,38,41	3.21	11 (33%)
5	2MA	A	2499	5	22,25,26	3.91	9 (40%)	32,37,40	2.67	10 (31%)
52	4SU	v	8	52	18,21,22	4.45	8 (44%)	25,30,33	2.28	5 (20%)
5	PSU	A	2453	5	18,21,22	1.08	1 (5%)	21,30,33	1.97	5 (23%)
5	2MG	A	2441	5	23,26,27	0.55	0	33,38,41	0.48	0
31	7MG	a	524	31	23,26,27	1.09	1 (4%)	27,39,42	0.89	2 (7%)
52	PSU	v	56	52	18,21,22	1.06	1 (5%)	21,30,33	1.90	5 (23%)
5	OMG	A	2247	5	23,26,27	0.52	0	32,38,41	0.47	0
5	7MG	A	2065	5	23,26,27	1.00	1 (4%)	27,39,42	0.92	2 (7%)
31	MA6	a	1516	31	23,26,27	1.43	4 (17%)	33,38,41	3.31	12 (36%)
31	UR3	a	1495	31	19,22,23	2.87	7 (36%)	26,32,35	1.61	3 (11%)
5	PSU	A	2576	5	18,21,22	1.11	2 (11%)	21,30,33	2.02	5 (23%)
31	PSU	a	513	31	18,21,22	1.10	1 (5%)	21,30,33	1.96	5 (23%)
5	6MZ	A	2026	5	22,25,26	2.49	4 (18%)	29,36,39	3.36	10 (34%)
52	5MU	v	55	52	19,22,23	0.41	0	27,32,35	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
31	4OC	a	1399	31	20,23,24	3.12	8 (40%)	25,32,35	0.90	1 (4%)
31	2MG	a	1204	31	23,26,27	0.49	0	33,38,41	0.52	0
31	5MC	a	964	31	19,22,23	0.60	0	26,32,35	0.58	0
5	PSU	A	2601	5	18,21,22	1.06	1 (5%)	21,30,33	1.97	5 (23%)
5	5MU	A	1935	5	19,22,23	0.50	0	27,32,35	0.48	0
5	PSU	A	952	5	18,21,22	1.05	1 (5%)	21,30,33	1.97	4 (19%)
52	H2U	v	20	52	18,21,22	0.50	0	19,30,33	1.46	3 (15%)

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	OMU	A	2548	5	-	0/9/27/28	0/2/2/2
5	PSU	A	2500	5	-	1/7/25/26	0/2/2/2
31	2MG	a	963	31	-	0/9/27/28	0/3/3/3
31	MA6	a	1515	31	-	0/11/29/30	0/3/3/3
5	2MA	A	2499	5	-	2/7/25/26	0/3/3/3
52	4SU	v	8	52	-	3/7/25/26	0/2/2/2
5	PSU	A	2453	5	-	0/7/25/26	0/2/2/2
5	2MG	A	2441	5	-	2/9/27/28	0/3/3/3
31	7MG	a	524	31	-	2/7/37/38	0/3/3/3
52	PSU	v	56	52	-	1/7/25/26	0/2/2/2
5	OMG	A	2247	5	-	1/9/27/28	0/3/3/3
5	7MG	A	2065	5	-	0/7/37/38	0/3/3/3
31	MA6	a	1516	31	-	0/11/29/30	0/3/3/3
31	UR3	a	1495	31	-	0/7/25/26	0/2/2/2
5	PSU	A	2576	5	-	0/7/25/26	0/2/2/2
31	PSU	a	513	31	-	0/7/25/26	0/2/2/2
5	6MZ	A	2026	5	-	2/9/27/28	0/3/3/3
52	5MU	v	55	52	-	7/7/25/26	0/2/2/2
31	4OC	a	1399	31	-	1/9/29/30	0/2/2/2
31	2MG	a	1204	31	-	0/9/27/28	0/3/3/3
31	5MC	a	964	31	-	0/7/25/26	0/2/2/2
5	PSU	A	2601	5	-	0/7/25/26	0/2/2/2
5	5MU	A	1935	5	-	0/7/25/26	0/2/2/2
5	PSU	A	952	5	-	0/7/25/26	0/2/2/2
52	H2U	v	20	52	-	3/7/38/39	0/2/2/2

All (62) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	2499	2MA	C4-N3	11.90	1.49	1.34
5	A	2026	6MZ	C6-N6	9.73	1.45	1.34
52	v	8	4SU	C2-N1	9.72	1.53	1.38
52	v	8	4SU	C4-N3	8.87	1.46	1.37
52	v	8	4SU	C5-C4	7.25	1.51	1.42
52	v	8	4SU	C2-N3	7.20	1.50	1.38
5	A	2499	2MA	C2-N3	7.11	1.46	1.34
31	a	1495	UR3	C2-N1	7.01	1.48	1.38
31	a	1399	4OC	C4-N3	6.94	1.44	1.32
5	A	2499	2MA	C6-N1	6.75	1.44	1.35
5	A	2548	OMU	C2-N1	6.75	1.49	1.38
31	a	1495	UR3	C6-C5	6.70	1.50	1.35
5	A	2548	OMU	C2-N3	6.51	1.49	1.38
52	v	8	4SU	C6-C5	6.39	1.49	1.35
31	a	1399	4OC	C6-C5	6.19	1.49	1.35
31	a	1399	4OC	C2-N3	6.13	1.48	1.36
5	A	2499	2MA	C2-N1	5.98	1.44	1.34
31	a	1495	UR3	C2-N3	5.52	1.49	1.39
5	A	2548	OMU	C6-C5	5.48	1.47	1.35
52	v	8	4SU	C4-S4	-4.88	1.60	1.68
31	a	1399	4OC	C4-N4	4.67	1.45	1.36
5	A	2499	2MA	C5-C6	4.56	1.53	1.41
31	a	524	7MG	C5-N7	4.52	1.41	1.35
31	a	1399	4OC	C2-N1	4.20	1.48	1.40
5	A	2065	7MG	C5-N7	4.01	1.40	1.35
5	A	2548	OMU	C4-N3	4.01	1.45	1.38
31	a	1515	MA6	C6-N6	3.83	1.47	1.36
31	a	1516	MA6	C6-N6	3.77	1.47	1.36
5	A	2499	2MA	C6-N6	-3.65	1.24	1.34
31	a	1399	4OC	C5-C4	3.51	1.48	1.41
31	a	513	PSU	C6-C5	3.48	1.39	1.35
52	v	56	PSU	C6-C5	3.45	1.39	1.35
5	A	2500	PSU	C6-C5	3.44	1.39	1.35
5	A	2026	6MZ	C5-N7	-3.35	1.33	1.39
5	A	2576	PSU	C6-C5	3.33	1.39	1.35
5	A	2453	PSU	C6-C5	3.32	1.39	1.35
31	a	1495	UR3	C6-N1	3.31	1.46	1.38
31	a	1516	MA6	C5-C4	-3.20	1.33	1.39
5	A	2601	PSU	C6-C5	3.18	1.38	1.35
5	A	2548	OMU	O4-C4	-3.17	1.18	1.24
5	A	952	PSU	C6-C5	3.15	1.38	1.35
5	A	2026	6MZ	C5-C4	-3.14	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	a	1399	4OC	C6-N1	3.11	1.45	1.38
31	a	1515	MA6	C5-C4	-3.07	1.33	1.39
31	a	1399	4OC	O2-C2	-2.81	1.18	1.23
5	A	2026	6MZ	C8-N9	-2.77	1.32	1.37
5	A	2548	OMU	O2-C2	-2.75	1.18	1.23
5	A	2548	OMU	C6-N1	2.71	1.44	1.38
5	A	2499	2MA	C4-N9	-2.68	1.32	1.37
52	v	8	4SU	O2-C2	-2.68	1.18	1.23
5	A	2499	2MA	C5-N7	-2.60	1.34	1.39
52	v	8	4SU	C6-N1	2.58	1.44	1.38
31	a	1516	MA6	C5-N7	-2.51	1.34	1.39
31	a	1515	MA6	C5-N7	-2.49	1.34	1.39
31	a	1495	UR3	C4-N3	2.42	1.45	1.40
31	a	1516	MA6	C8-N9	-2.32	1.33	1.37
5	A	2548	OMU	C5-C4	2.28	1.48	1.43
31	a	1515	MA6	C8-N9	-2.23	1.33	1.37
31	a	1495	UR3	C5-C4	2.20	1.49	1.43
5	A	2499	2MA	C8-N7	2.08	1.35	1.31
5	A	2576	PSU	O4'-C1'	-2.07	1.41	1.43
31	a	1495	UR3	O2-C2	-2.00	1.18	1.22

All (97) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	1516	MA6	N1-C6-N6	-12.14	102.07	116.86
31	a	1515	MA6	N1-C6-N6	-11.67	102.63	116.86
5	A	2026	6MZ	C4-N9-C1'	-9.17	105.19	126.63
5	A	2026	6MZ	C1'-N9-C8	9.00	147.06	127.09
31	a	1516	MA6	C5-C6-N6	8.00	138.00	125.33
31	a	1515	MA6	C5-C6-N6	7.75	137.60	125.33
52	v	8	4SU	C4-N3-C2	-7.59	120.04	127.31
5	A	2499	2MA	C1'-N9-C8	-6.93	111.71	127.09
5	A	2499	2MA	N9-C8-N7	-6.11	105.26	113.94
5	A	2026	6MZ	C5-C4-N3	-5.97	118.50	126.72
31	a	1516	MA6	N1-C2-N3	-5.77	119.86	128.58
5	A	2548	OMU	C4-N3-C2	-5.76	119.46	126.61
31	a	1515	MA6	N1-C2-N3	-5.67	120.00	128.58
31	a	1495	UR3	C4-N3-C2	-5.55	120.11	124.58
5	A	2499	2MA	C4-N9-C8	5.46	111.47	105.74
52	v	8	4SU	C5-C4-N3	5.36	119.74	114.75
5	A	2026	6MZ	N1-C2-N3	-5.25	120.64	128.58
5	A	2499	2MA	C5-C4-N3	-5.23	121.67	127.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	2576	PSU	N1-C2-N3	5.09	120.53	115.17
5	A	2453	PSU	C4-N3-C2	-5.04	119.43	126.37
5	A	2601	PSU	C4-N3-C2	-5.04	119.43	126.37
5	A	952	PSU	N1-C2-N3	4.99	120.43	115.17
5	A	952	PSU	C4-N3-C2	-4.98	119.51	126.37
5	A	2453	PSU	N1-C2-N3	4.98	120.42	115.17
5	A	2026	6MZ	C4-C5-C6	4.93	120.88	116.78
5	A	2601	PSU	N1-C2-N3	4.89	120.33	115.17
5	A	2576	PSU	C4-N3-C2	-4.89	119.64	126.37
31	a	513	PSU	N1-C2-N3	4.88	120.32	115.17
5	A	2500	PSU	N1-C2-N3	4.86	120.29	115.17
5	A	2500	PSU	C4-N3-C2	-4.77	119.80	126.37
31	a	513	PSU	C4-N3-C2	-4.73	119.86	126.37
52	v	56	PSU	C4-N3-C2	-4.71	119.89	126.37
31	a	1516	MA6	C5-C4-N3	-4.71	120.24	126.72
31	a	1515	MA6	C5-C4-N3	-4.70	120.24	126.72
52	v	56	PSU	N1-C2-N3	4.70	120.13	115.17
31	a	1516	MA6	N9-C8-N7	-4.49	107.56	113.94
5	A	2499	2MA	C4-N9-C1'	4.35	136.81	126.63
31	a	1515	MA6	N9-C8-N7	-4.27	107.87	113.94
5	A	2026	6MZ	N3-C4-N9	4.05	134.06	127.17
5	A	2548	OMU	N3-C2-N1	3.97	120.06	114.89
5	A	2499	2MA	N3-C4-N9	3.96	132.01	126.99
31	a	1515	MA6	C4-C5-C6	3.88	119.93	115.91
52	v	20	H2U	C5-C4-N3	-3.84	112.60	116.69
5	A	2026	6MZ	N9-C8-N7	-3.84	108.49	113.94
52	v	8	4SU	C5-C4-S4	-3.82	119.95	124.31
31	a	1516	MA6	C4-C5-C6	3.80	119.83	115.91
31	a	1495	UR3	C5-C4-N3	3.79	120.04	115.04
5	A	2548	OMU	C5-C4-N3	3.76	120.07	114.80
52	v	8	4SU	N3-C2-N1	3.65	119.64	114.89
5	A	2026	6MZ	C2-N3-C4	3.54	120.47	111.83
52	v	20	H2U	O2-C2-N1	3.50	127.32	123.10
5	A	2499	2MA	N3-C2-N1	-3.45	119.69	125.77
31	a	1515	MA6	C2-N1-C6	3.43	120.22	111.83
31	a	1516	MA6	C2-N1-C6	3.41	120.17	111.83
5	A	2499	2MA	C5-N7-C8	3.37	108.75	103.45
31	a	1516	MA6	C2-N3-C4	3.33	119.97	111.83
31	a	1515	MA6	C2-N3-C4	3.28	119.84	111.83
52	v	56	PSU	O2-C2-N1	-3.18	119.50	122.79
31	a	513	PSU	O2-C2-N1	-2.98	119.72	122.79
5	A	952	PSU	O2-C2-N1	-2.95	119.75	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	1516	MA6	C5-N7-C8	2.93	108.06	103.45
31	a	1515	MA6	N3-C4-N9	2.93	132.14	127.17
5	A	2548	OMU	O4-C4-C5	-2.91	120.14	125.16
5	A	2026	6MZ	C5-N7-C8	2.90	108.02	103.45
31	a	1516	MA6	N3-C4-N9	2.88	132.06	127.17
5	A	2500	PSU	O2-C2-N1	-2.80	119.90	122.79
31	a	1515	MA6	C5-N7-C8	2.80	107.85	103.45
5	A	2576	PSU	O2-C2-N1	-2.73	119.97	122.79
31	a	1516	MA6	C4-N9-C8	2.68	108.56	105.74
5	A	2453	PSU	O2-C2-N1	-2.66	120.04	122.79
31	a	513	PSU	C6-N1-C2	-2.64	120.25	122.69
5	A	2576	PSU	C6-N1-C2	-2.63	120.25	122.69
5	A	2576	PSU	O4'-C1'-C2'	2.54	108.66	105.15
52	v	56	PSU	C6-N1-C2	-2.53	120.34	122.69
5	A	2500	PSU	C6-N1-C2	-2.52	120.35	122.69
31	a	1515	MA6	C4-N9-C8	2.49	108.36	105.74
5	A	2499	2MA	CM2-C2-N1	2.49	120.85	117.13
5	A	2548	OMU	O2-C2-N1	-2.47	119.58	122.80
52	v	8	4SU	C1'-N1-C2	2.46	122.02	117.59
5	A	2601	PSU	O2-C2-N1	-2.44	120.27	122.79
5	A	2065	7MG	C4-C5-N7	2.42	108.24	105.38
5	A	952	PSU	C6-N1-C2	-2.42	120.44	122.69
52	v	56	PSU	C6-C5-C4	2.40	119.80	118.17
31	a	524	7MG	C4-C5-N7	2.38	108.19	105.38
31	a	513	PSU	O4'-C1'-C2'	2.37	108.44	105.15
5	A	2026	6MZ	C5-C6-N1	2.37	120.69	118.15
31	a	524	7MG	C5-C4-N9	2.32	109.30	106.33
31	a	1399	4OC	C6-C5-C4	2.31	119.79	117.00
5	A	2065	7MG	C5-C4-N9	2.28	109.26	106.33
5	A	2453	PSU	C6-N1-C2	-2.27	120.58	122.69
52	v	20	H2U	O2-C2-N3	-2.27	117.30	121.49
5	A	2601	PSU	C6-N1-C2	-2.21	120.64	122.69
31	a	1495	UR3	C6-N1-C2	-2.18	120.02	121.80
31	a	1516	MA6	C4-C5-N7	-2.15	108.12	110.58
5	A	2499	2MA	C4-C5-N7	-2.09	108.19	110.58
5	A	2601	PSU	C6-C5-C4	2.06	119.56	118.17
5	A	2453	PSU	O4'-C1'-C2'	2.02	107.95	105.15

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
52	v	8	4SU	O4'-C1'-N1-C2
52	v	20	H2U	C2'-C1'-N1-C2
52	v	55	5MU	O4'-C4'-C5'-O5'
5	A	2247	OMG	C1'-C2'-O2'-CM2
5	A	2499	2MA	O4'-C4'-C5'-O5'
52	v	55	5MU	C3'-C4'-C5'-O5'
52	v	8	4SU	O4'-C1'-N1-C6
31	a	524	7MG	C3'-C4'-C5'-O5'
5	A	2499	2MA	C3'-C4'-C5'-O5'
52	v	20	H2U	C2'-C1'-N1-C6
52	v	55	5MU	C2'-C1'-N1-C6
5	A	2026	6MZ	O4'-C4'-C5'-O5'
5	A	2026	6MZ	C3'-C4'-C5'-O5'
5	A	2441	2MG	C3'-C4'-C5'-O5'
31	a	524	7MG	O4'-C4'-C5'-O5'
5	A	2441	2MG	O4'-C4'-C5'-O5'
52	v	55	5MU	O4'-C1'-N1-C6
52	v	55	5MU	C2'-C1'-N1-C2
31	a	1399	4OC	O4'-C4'-C5'-O5'
52	v	55	5MU	O4'-C1'-N1-C2
52	v	55	5MU	C4'-C5'-O5'-P
52	v	56	PSU	C4'-C5'-O5'-P
5	A	2500	PSU	O4'-C4'-C5'-O5'
52	v	8	4SU	O4'-C4'-C5'-O5'
52	v	20	H2U	O4'-C1'-N1-C2

There are no ring outliers.

8 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2548	OMU	1	0
31	a	1515	MA6	2	0
52	v	8	4SU	1	0
52	v	56	PSU	1	0
5	A	2247	OMG	1	0
5	A	2026	6MZ	2	0
52	v	55	5MU	1	0
52	v	20	H2U	3	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

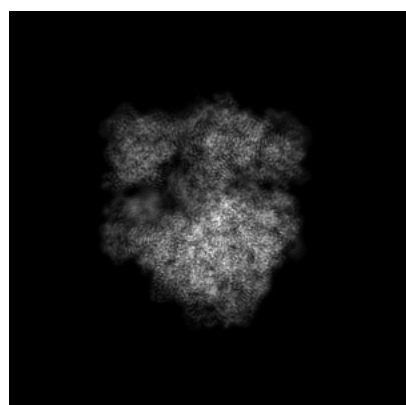
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26818. These allow visual inspection of the internal detail of the map and identification of artifacts.

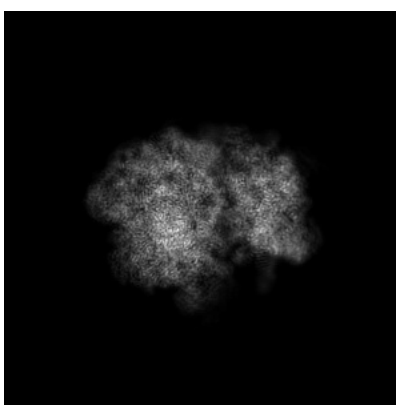
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

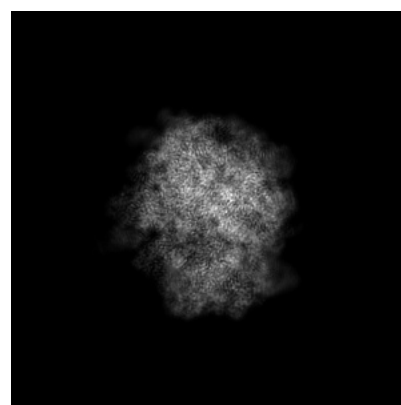
6.1.1 Primary map



X



Y

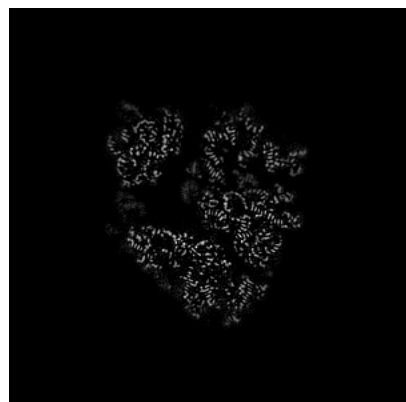


Z

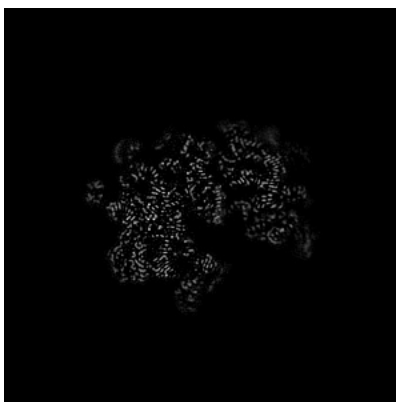
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

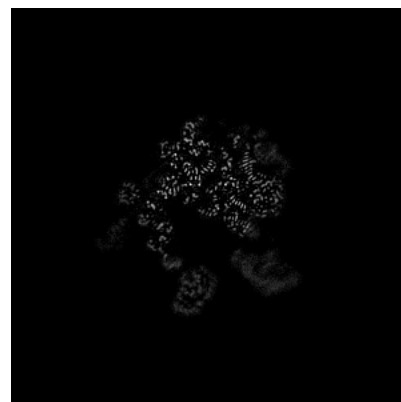
6.2.1 Primary map



X Index: 256



Y Index: 256

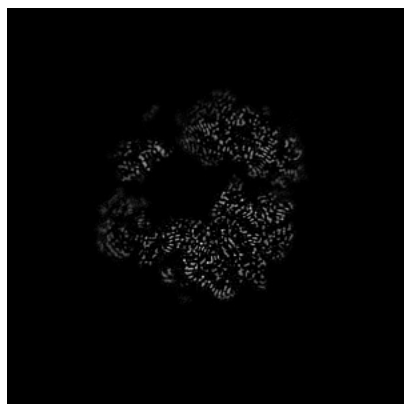


Z Index: 256

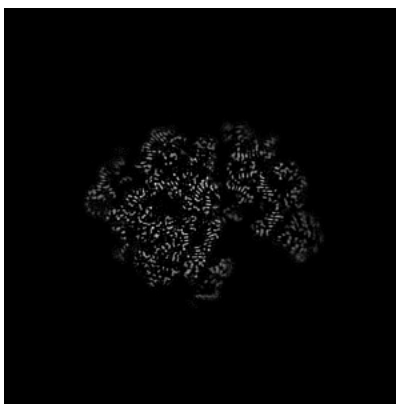
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

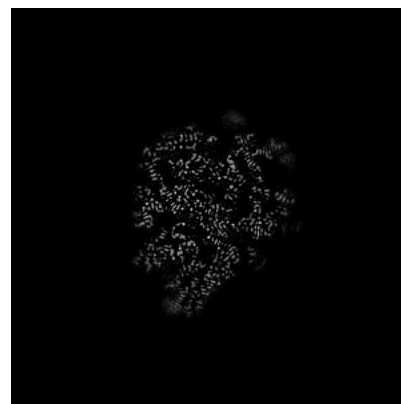
6.3.1 Primary map



X Index: 228



Y Index: 276

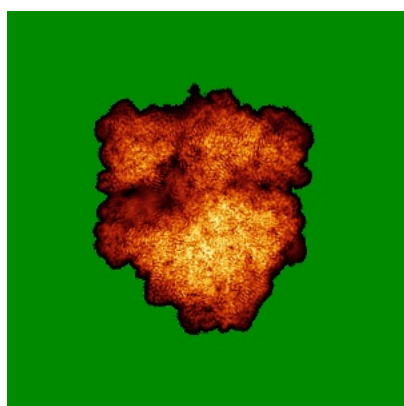


Z Index: 208

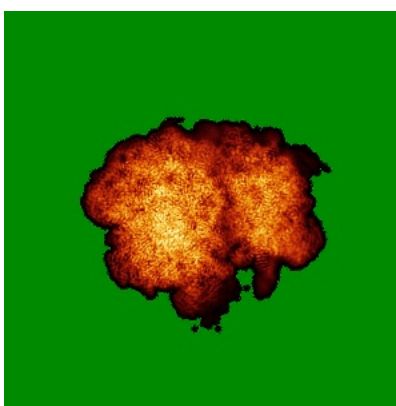
The images above show the largest variance slices of the map in three orthogonal directions.

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

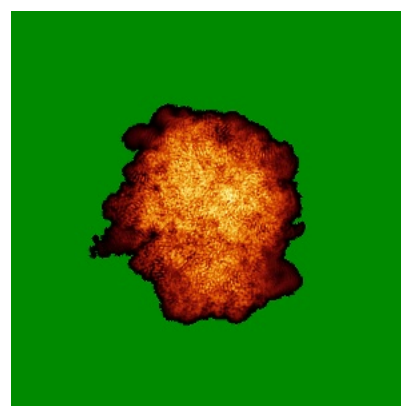
6.4.1 Primary map



X



Y



Z

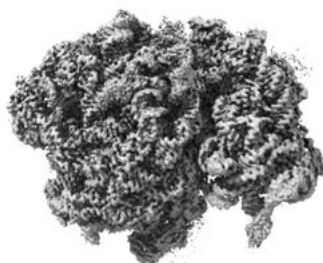
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

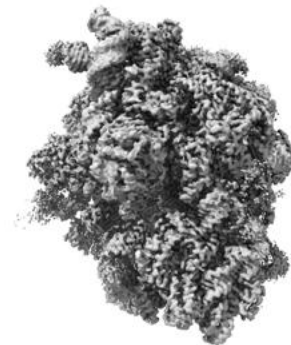
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

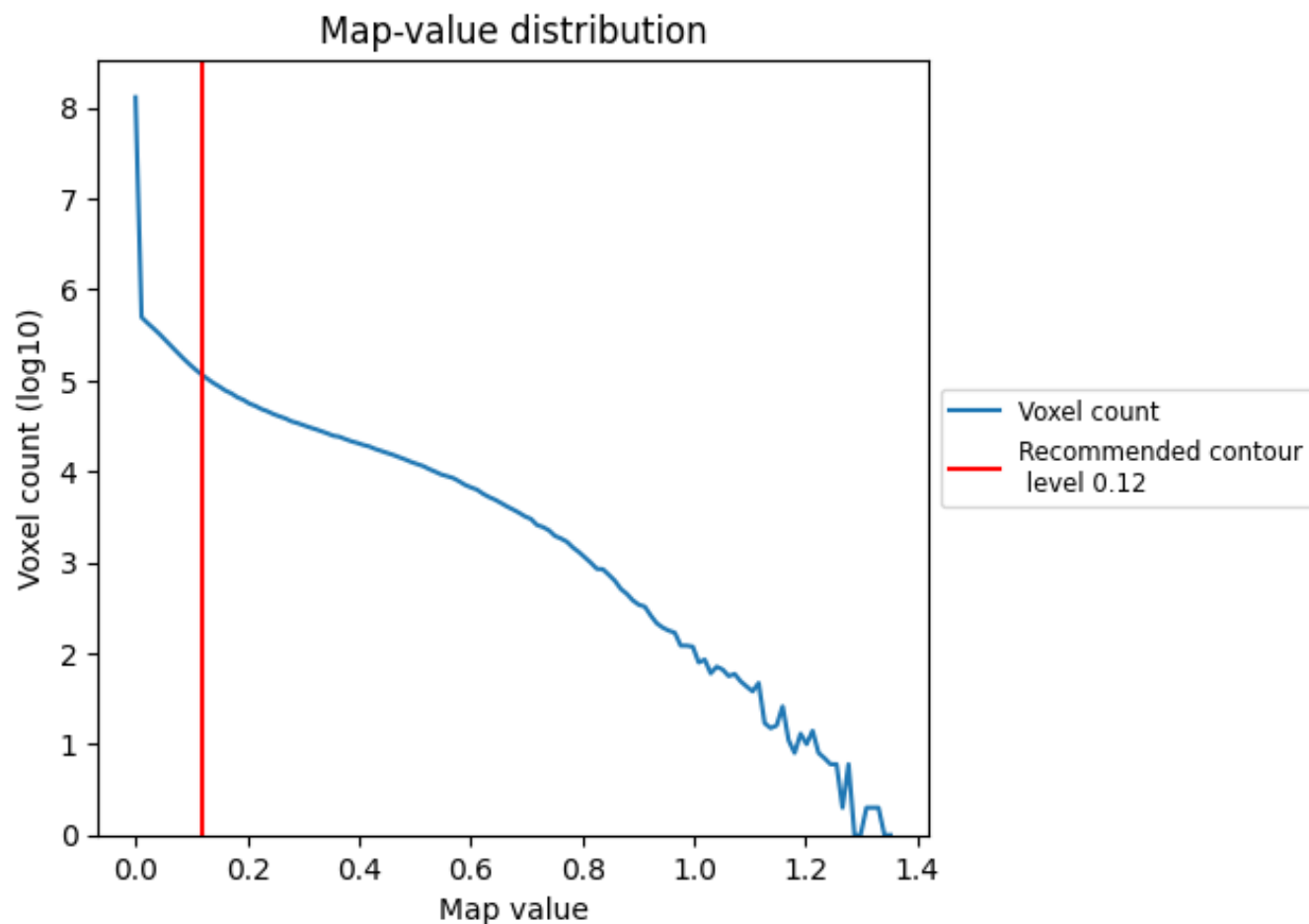
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

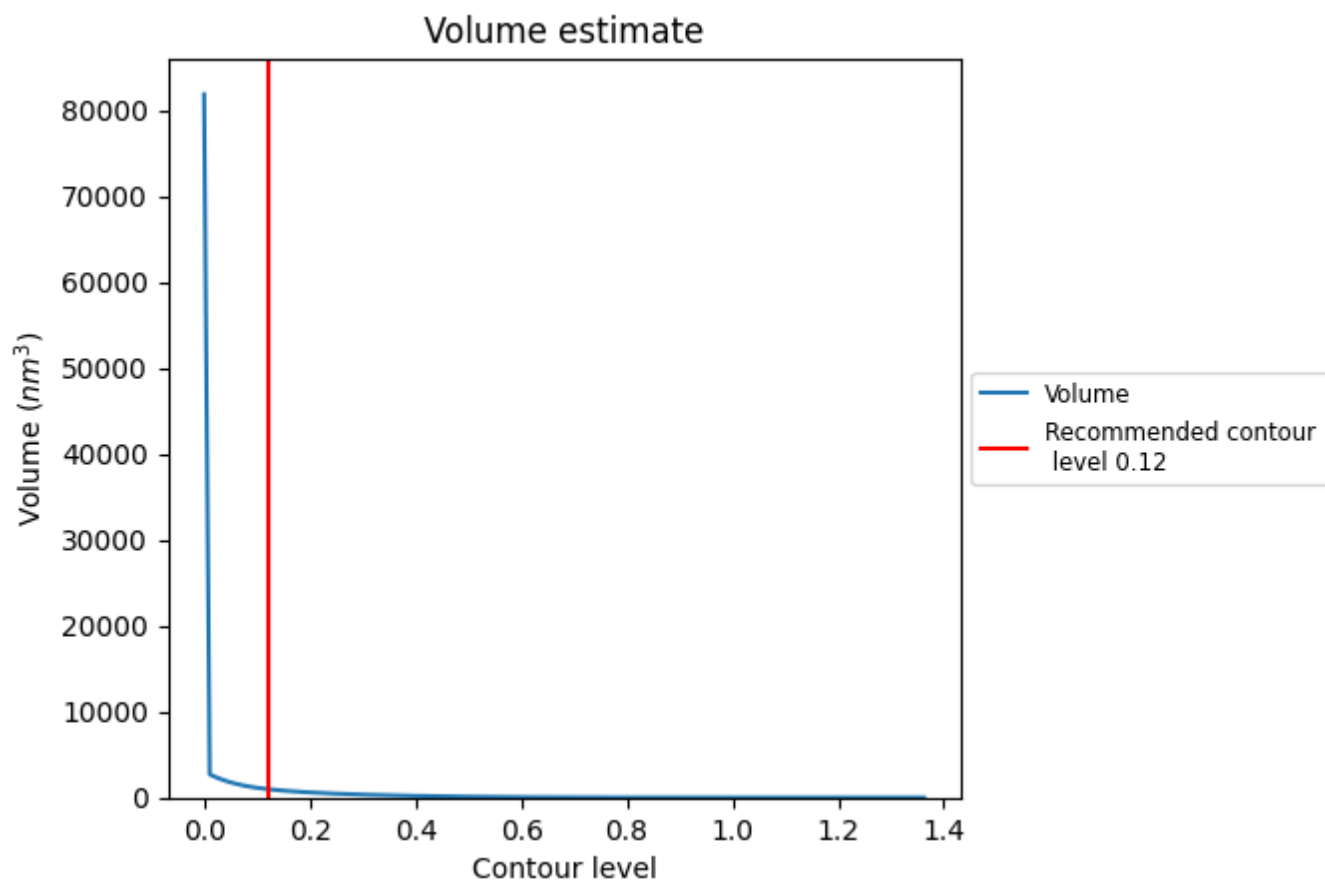
This section contains the results of statistical analysis of the map.

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.

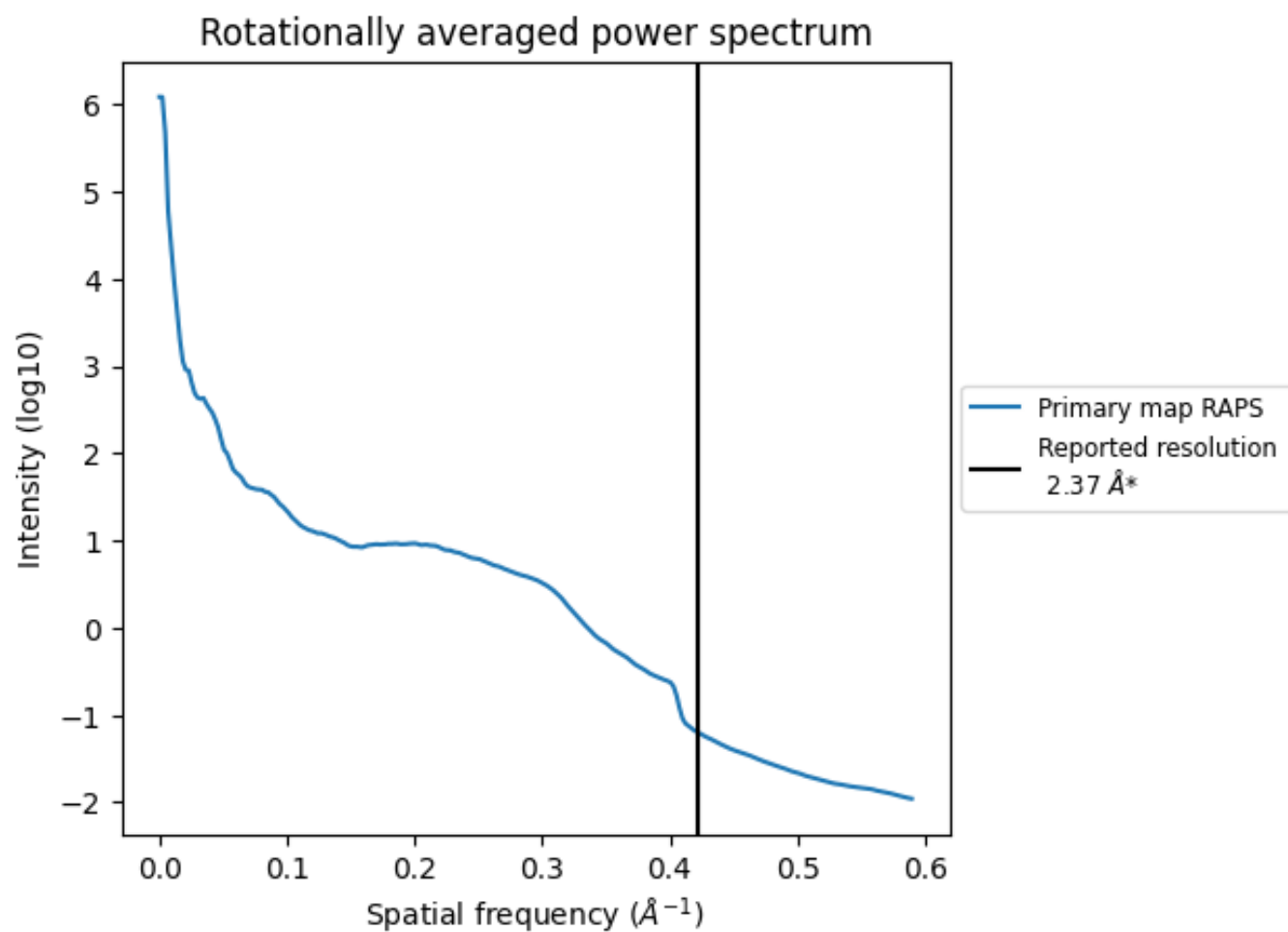
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 982 nm³; this corresponds to an approximate mass of 887 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 0.422 Å⁻¹

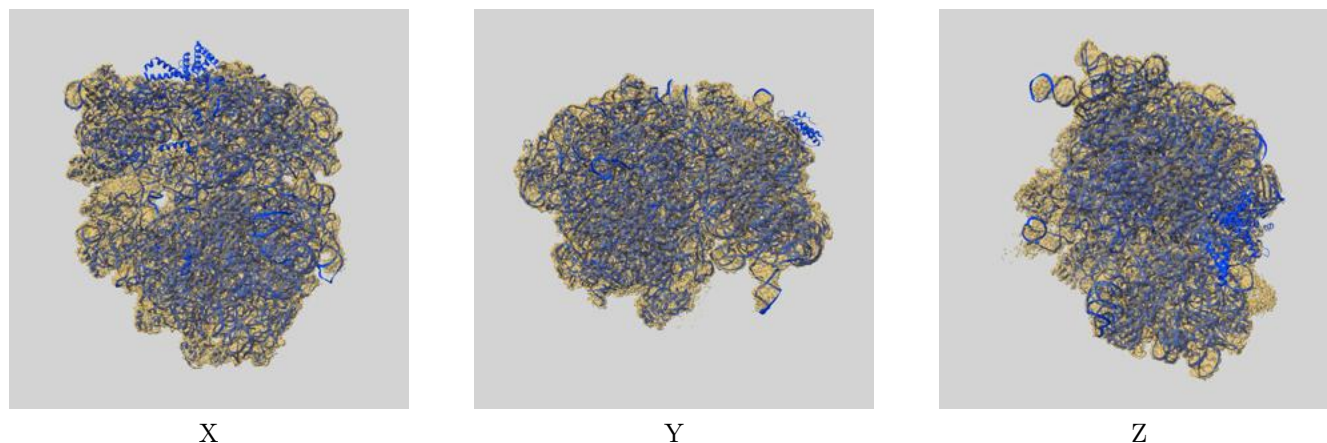
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

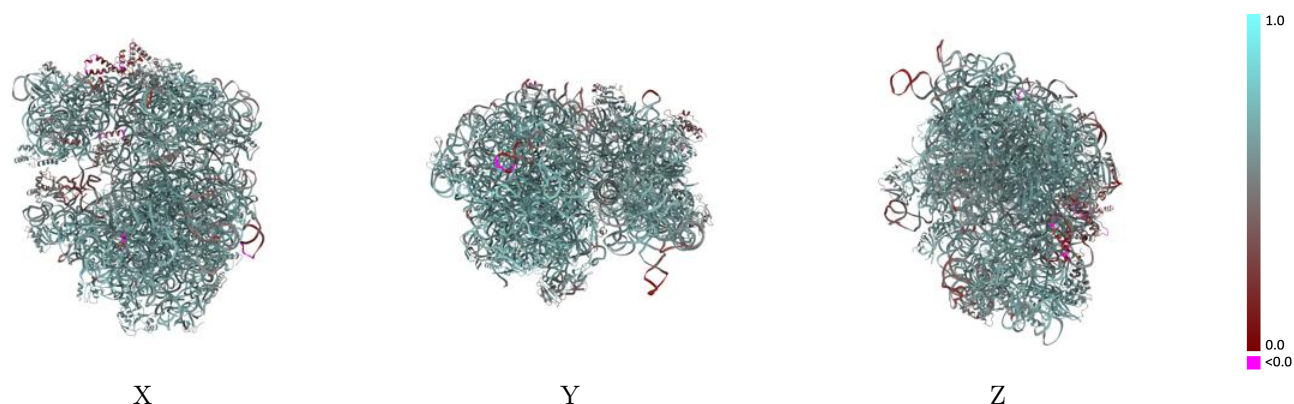
This section contains information regarding the fit between EMDB map EMD-26818 and PDB model 7UVW. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



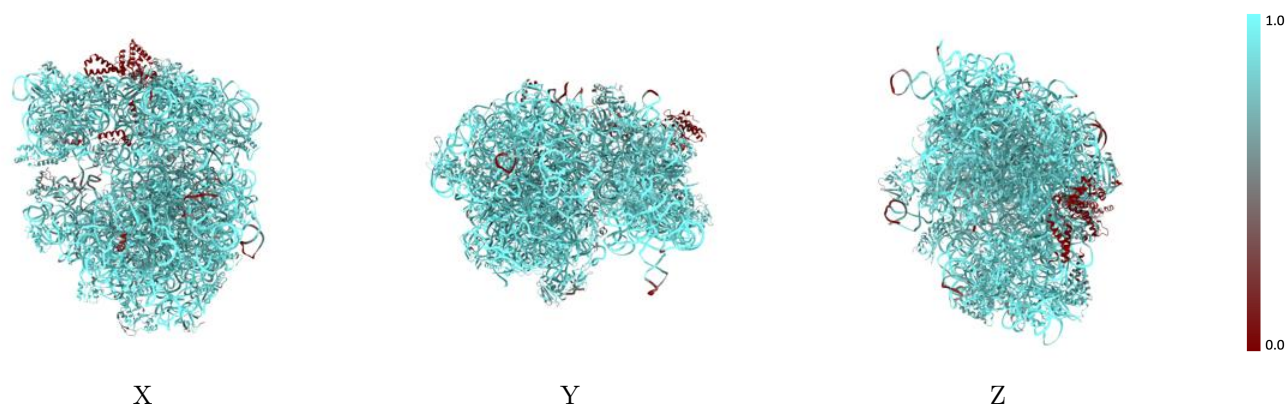
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



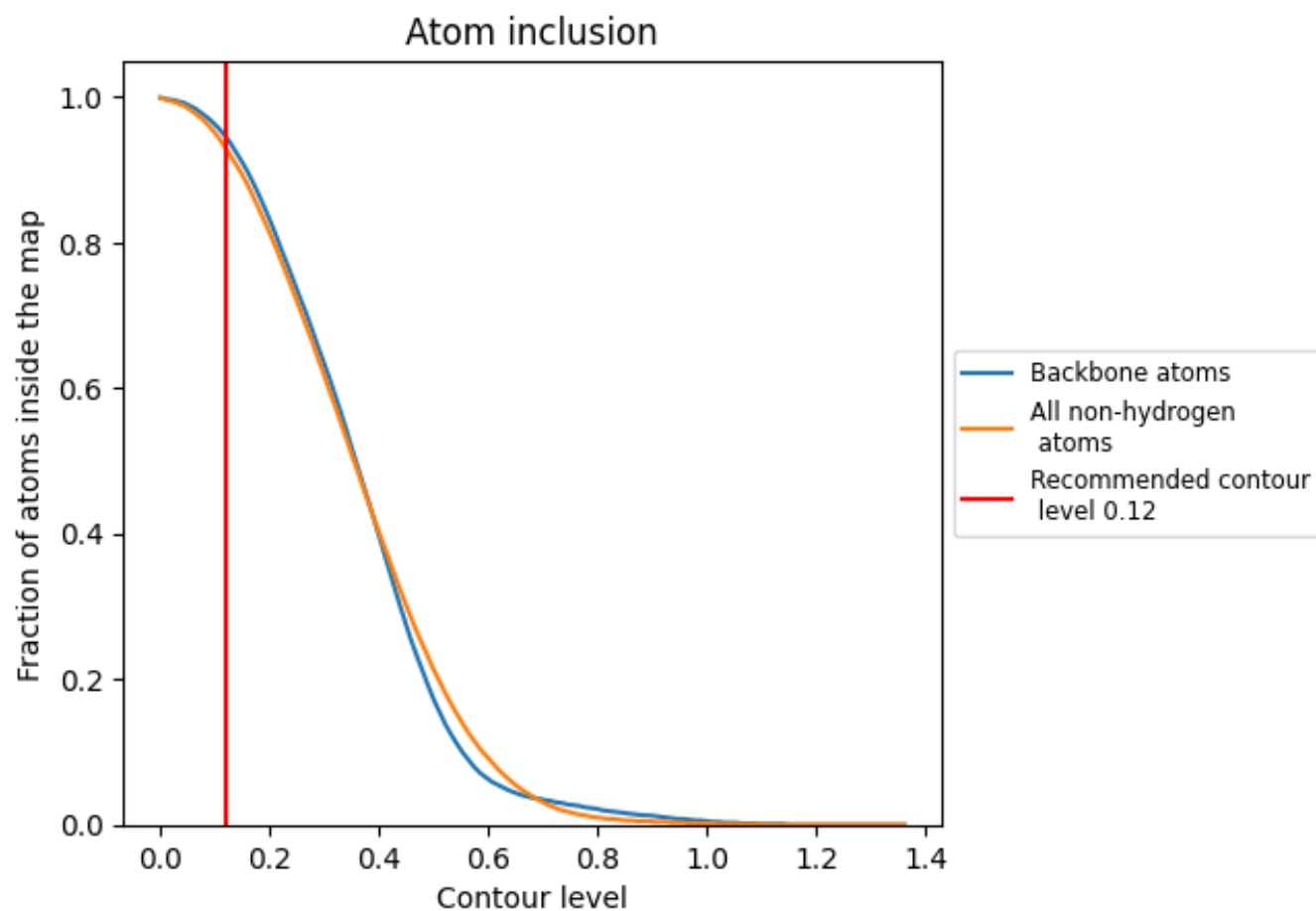
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9290	 0.6170
0	 0.9180	 0.6600
1	 0.9650	 0.6970
2	 0.9920	 0.7050
3	 0.9550	 0.6580
A	 0.9710	 0.6430
B	 0.9840	 0.5890
C	 0.9420	 0.6660
D	 0.9570	 0.6770
E	 0.9090	 0.6500
F	 0.6660	 0.4320
G	 0.8390	 0.5580
H	 0.4230	 0.4090
I	 0.9590	 0.6750
J	 0.8600	 0.6230
K	 0.9640	 0.6730
L	 0.9440	 0.6630
M	 0.9810	 0.6900
N	 0.9360	 0.5950
O	 0.8870	 0.6340
P	 0.9880	 0.6910
Q	 0.9620	 0.6660
R	 0.9530	 0.6750
S	 0.8800	 0.6230
T	 0.8310	 0.5960
U	 0.9290	 0.6310
V	 0.9770	 0.6900
W	 0.9450	 0.6690
X	 0.8170	 0.5540
Y	 0.9570	 0.6740
Z	 0.9460	 0.6700
a	 0.9660	 0.6020
b	 0.0830	 0.3320
c	 0.8990	 0.6040
d	 0.7790	 0.5230



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Chain	Atom inclusion	Q-score
e	 0.9240	 0.6150
f	 0.7280	 0.5100
g	 0.6780	 0.5050
h	 0.9380	 0.6280
i	 0.9370	 0.6290
j	 0.8600	 0.5900
k	 0.7100	 0.4990
l	 0.8380	 0.6070
m	 0.9270	 0.6160
n	 0.9330	 0.6320
o	 0.9310	 0.6200
p	 0.9530	 0.6390
q	 0.8880	 0.6000
r	 0.8690	 0.5880
s	 0.9430	 0.6230
t	 0.9500	 0.6170
u	 0.1710	 0.3520
v	 0.7730	 0.4380
w	 0.8770	 0.5180