



Full wwPDB EM Validation Report ⓘ

Jun 24, 2026 – 01:18 AM EDT

PDB ID : 7M4Z / pdb_00007m4z
EMDB ID : EMD-23671
Title : A. baumannii Ribosome-Eravacycline complex: hpf-bound 70S
Authors : Morgan, C.E.; Yu, E.W.
Deposited on : 2021-03-22
Resolution : 2.92 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:

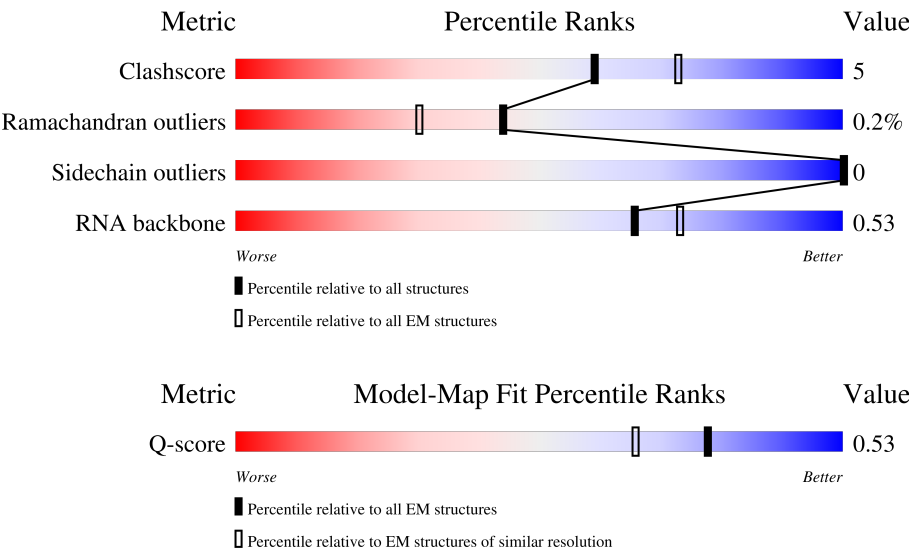
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.92 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	13007 (2.42 - 3.42)

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	6% 78% 18% .
2	1	44	98% .
3	2	64	92% 6% .

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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	116	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 138172 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	49	Total	C	N	O	S	0	0
			409	263	74	70	2		

- 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	2730	Total	C	N	O	P	0	0
			58566	26143	10721	18972	2730		

- 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	210	Total	C	N	O	S	0	0
			1566	969	296	298	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	141	Total	C	N	O	S	0	0
			1117	713	199	202	3		

- 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	114	Total	C	N	O	S	0	0
			857	528	173	155	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	116	Total	C	N	O	S	0	0
			913	575	176	162			

- 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	77	Total	C	N	O	S	0	0
			585	363	112	108	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	58	Total	C	N	O	S	0	0
			463	286	88	85	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	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	151	Total	C	N	O	S	0	0
			1188	743	225	213	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		

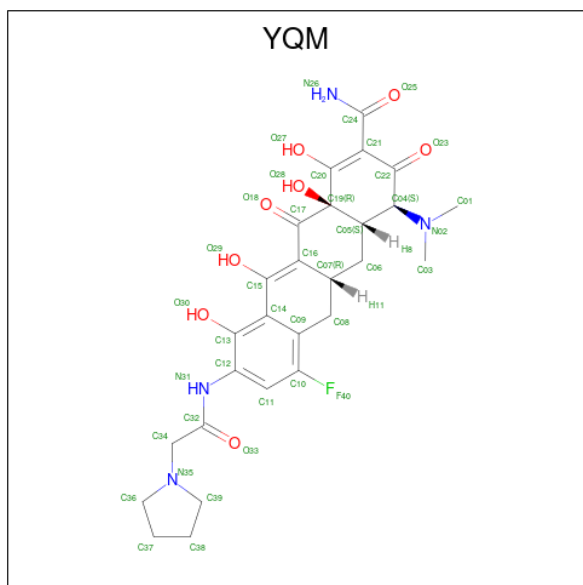
- Molecule 52 is a protein called Ribosomal subunit interface protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	102	Total	C	N	O	S	0	0
			824	508	157	156	3		

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
53	3	1	Total	Zn	0
			1	1	

- Molecule 54 is Eravacycline (CCD ID: YQM) (formula: C₂₇H₃₁FN₄O₈) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
54	A	1	Total	C	F	N	O	0
			40	27	1	4	8	
54	A	1	Total	C	F	N	O	0
			40	27	1	4	8	

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	A	135	Total	Mg	0
			135	135	
55	B	1	Total	Mg	0
			1	1	
55	C	1	Total	Mg	0
			1	1	
55	K	1	Total	Mg	0
			1	1	
55	a	48	Total	Mg	0
			48	48	
55	t	1	Total	Mg	0
			1	1	

- Molecule 56 is water.

Mol	Chain	Residues	Atoms		AltConf
56	1	1	Total	O	0
			1	1	

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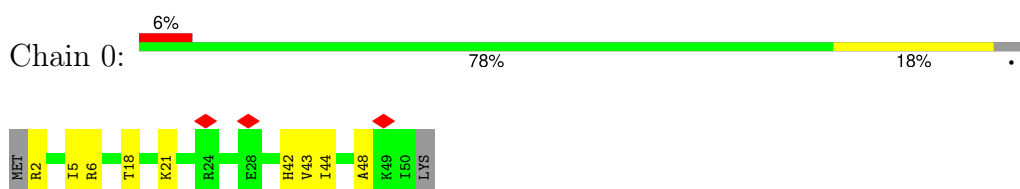
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Mol	Chain	Residues	Atoms		AltConf
56	2	1	Total 1	O 1	0
56	A	179	Total 179	O 179	0
56	D	2	Total 2	O 2	0
56	K	1	Total 1	O 1	0
56	Z	2	Total 2	O 2	0
56	a	38	Total 38	O 38	0
56	d	1	Total 1	O 1	0
56	i	1	Total 1	O 1	0
56	q	1	Total 1	O 1	0
56	t	2	Total 2	O 2	0

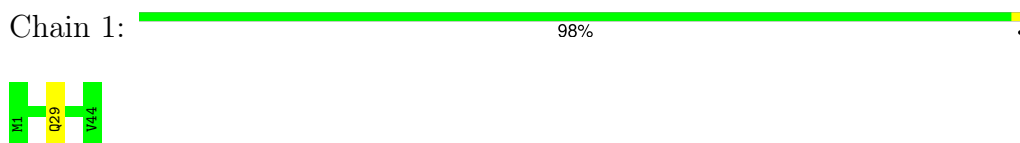
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

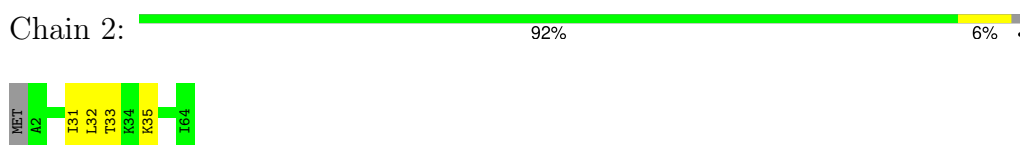
- Molecule 1: 50S ribosomal protein L33



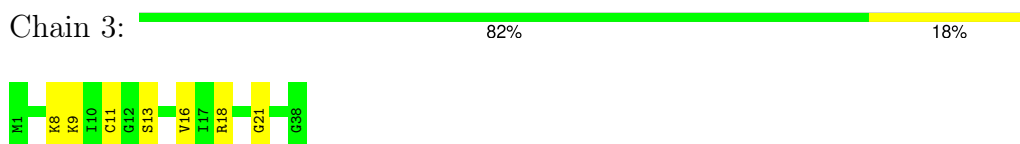
- Molecule 2: 50S ribosomal protein L34



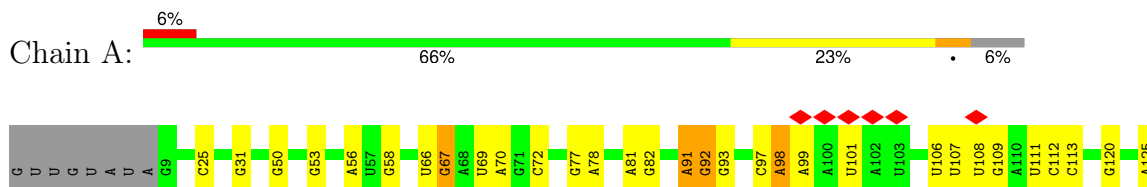
- Molecule 3: 50S ribosomal protein L35

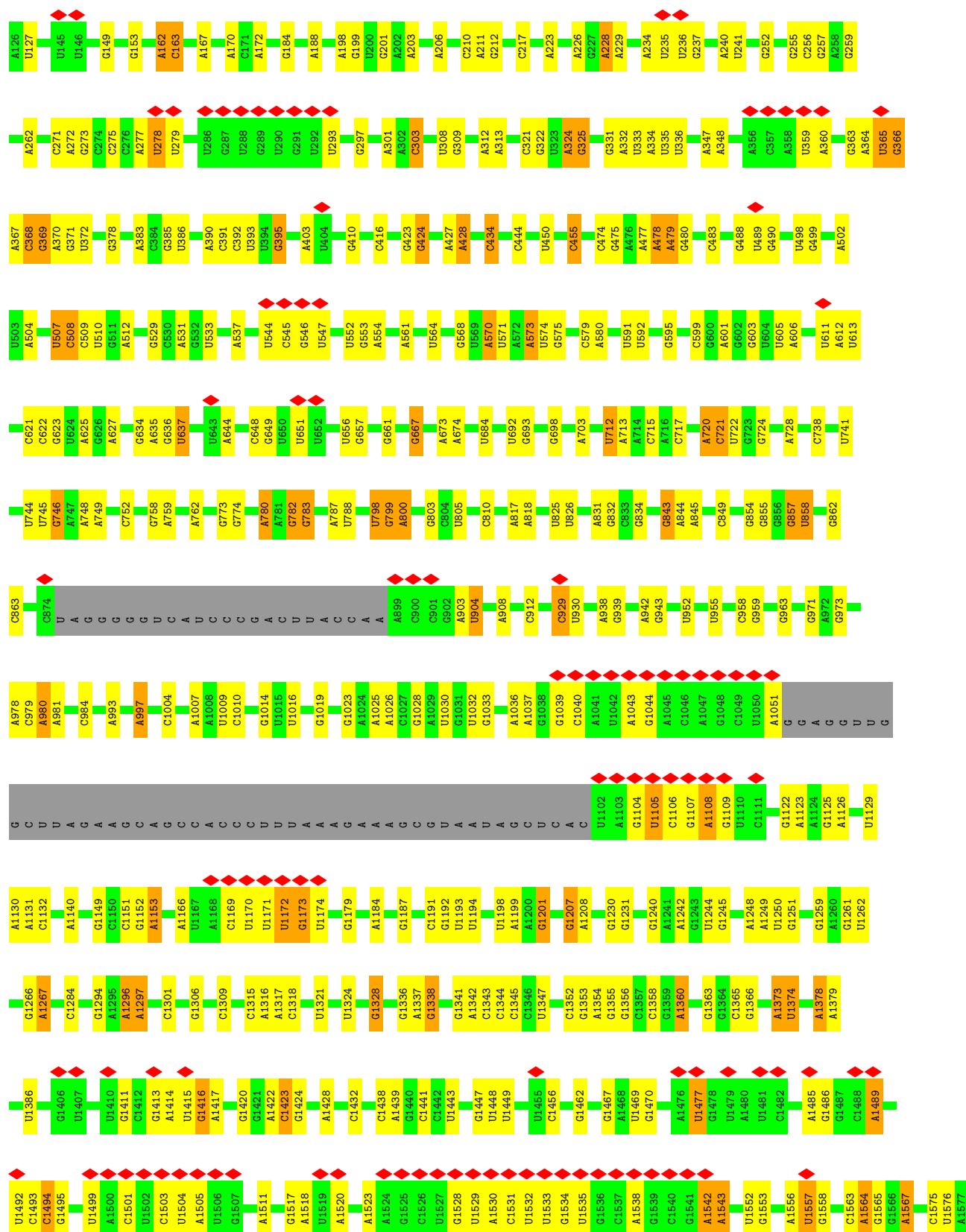


- Molecule 4: 50S ribosomal protein L36

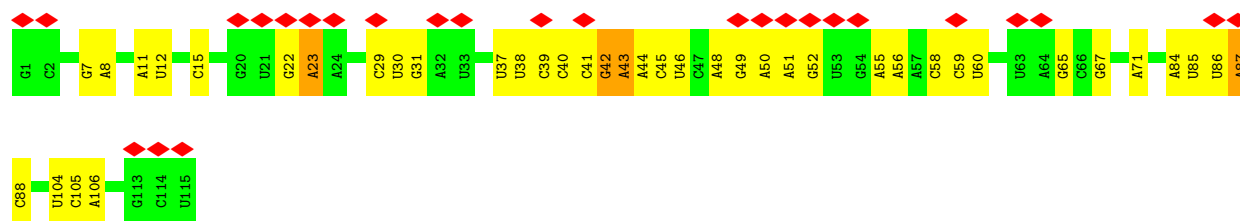


- Molecule 5: 23s ribosomal RNA



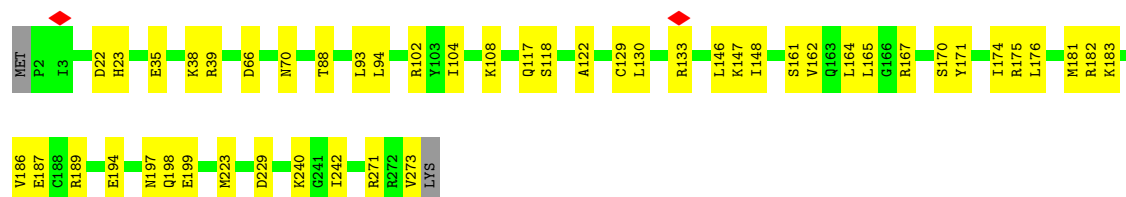






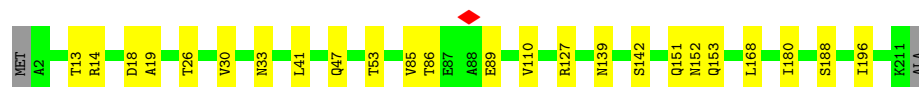
- Molecule 7: 50S ribosomal protein L2

Chain C: 82% 18%



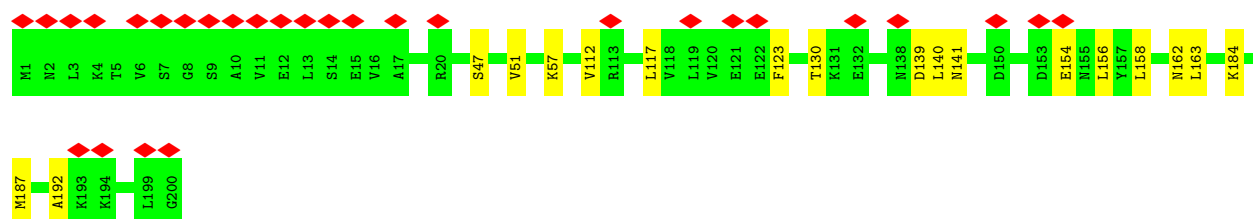
- Molecule 8: 50S ribosomal protein L3

Chain D: 88% 11%



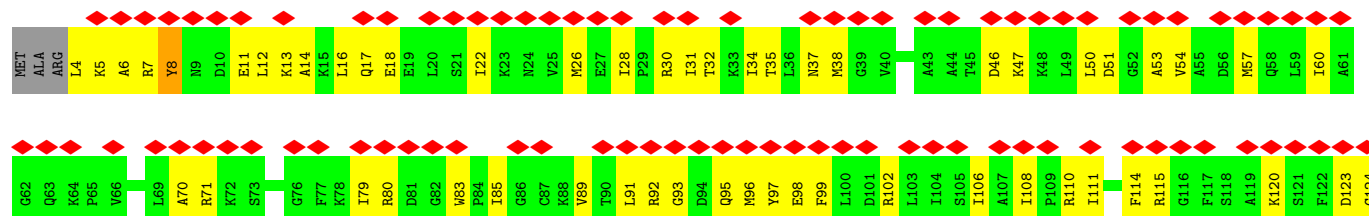
- Molecule 9: 50S ribosomal protein L4

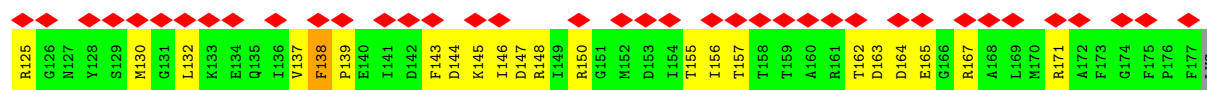
Chain E: 14% 91% 9%



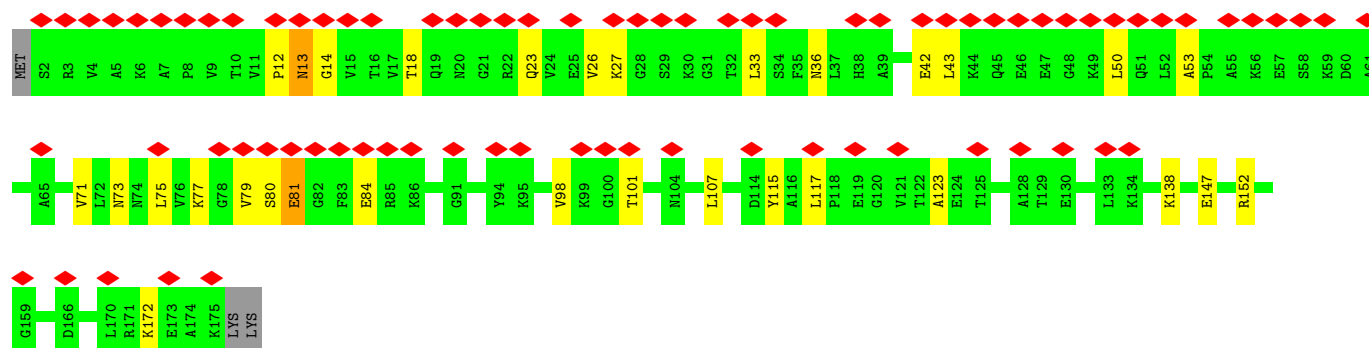
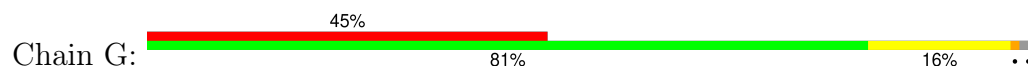
- Molecule 10: 50S ribosomal protein L5

Chain F: 71% 54% 42%

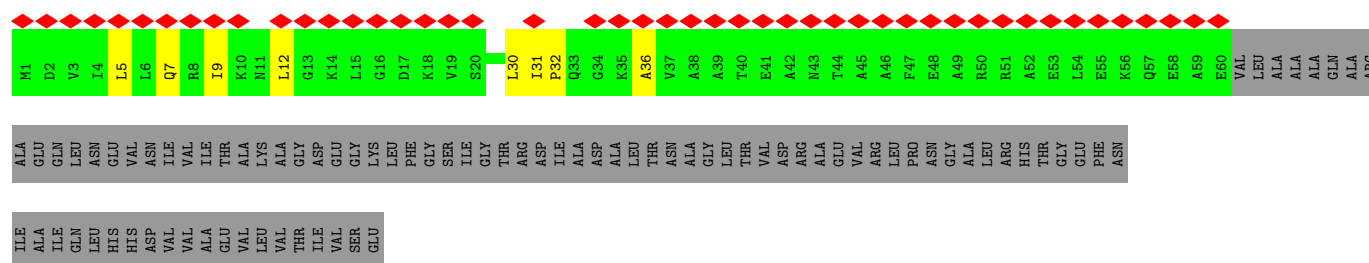
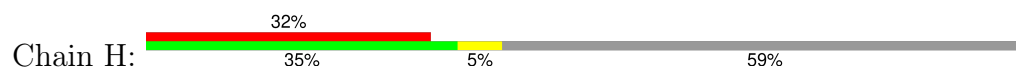




• Molecule 11: 50S ribosomal protein L6



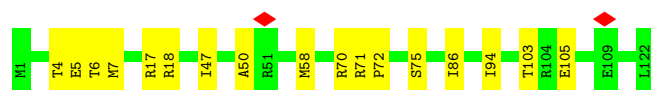
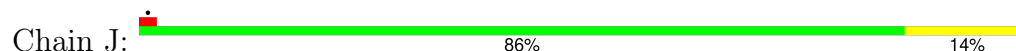
• Molecule 12: 50S ribosomal protein L9



• Molecule 13: 50S ribosomal protein L13



• Molecule 14: 50S ribosomal protein L14

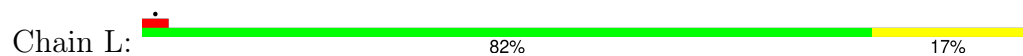


• Molecule 15: 50S ribosomal protein L15

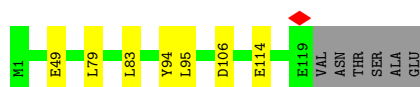




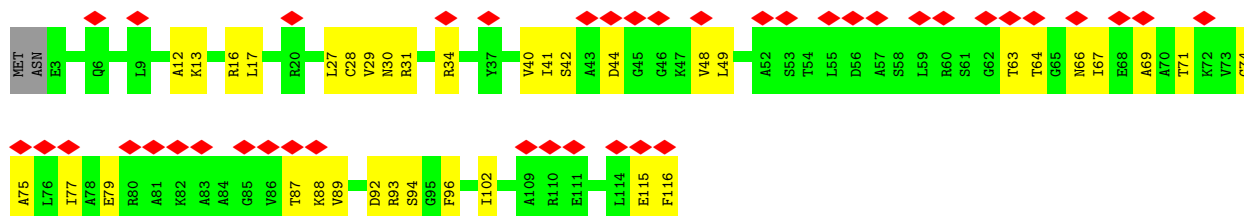
- Molecule 16: 50S ribosomal protein L16



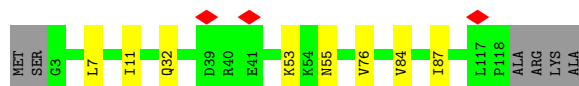
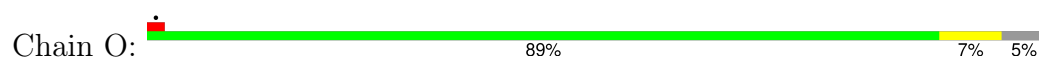
- Molecule 17: 50S ribosomal protein L17



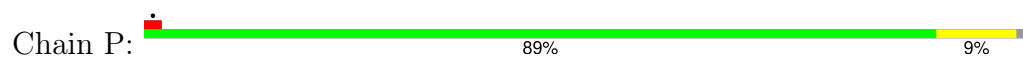
- Molecule 18: 50S ribosomal protein L18



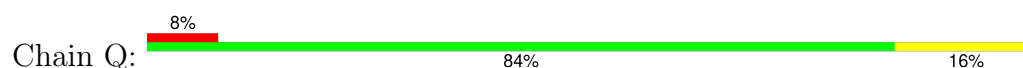
- Molecule 19: 50S ribosomal protein L19

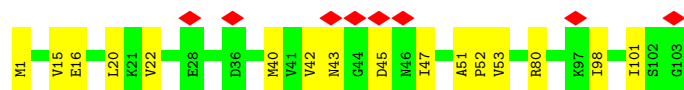


- Molecule 20: 50S ribosomal protein L20



- Molecule 21: 50S ribosomal protein L21

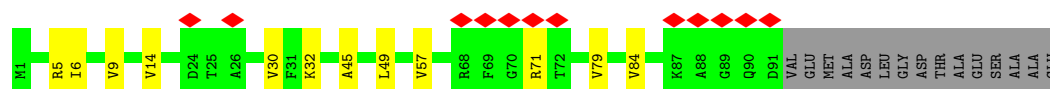




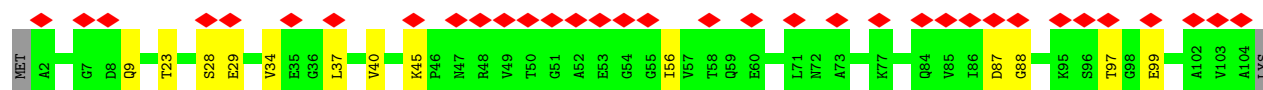
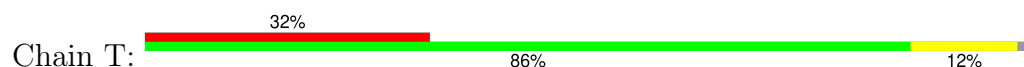
- Molecule 22: 50S ribosomal protein L22



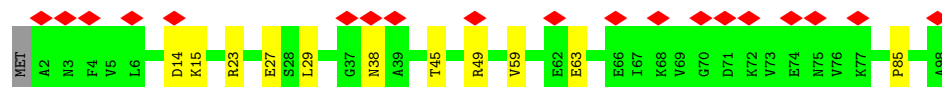
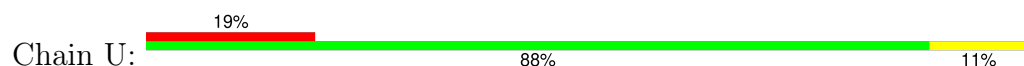
- Molecule 23: 50S ribosomal protein L23



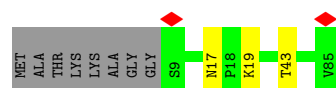
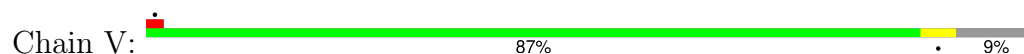
- Molecule 24: 50S ribosomal protein L24



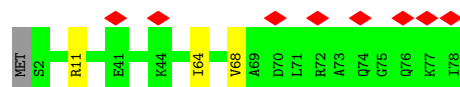
- Molecule 25: 50S ribosomal protein L25



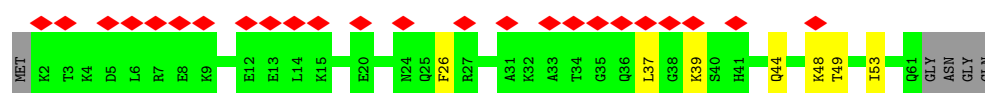
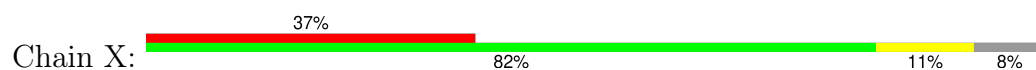
- Molecule 26: 50S ribosomal protein L27



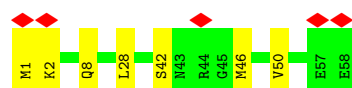
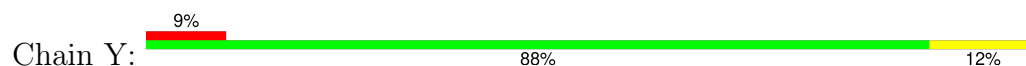
- Molecule 27: 50S ribosomal protein L28



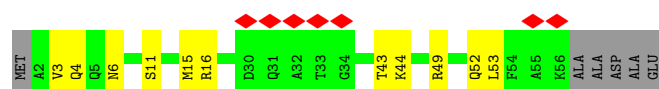
- Molecule 28: 50S ribosomal protein L29



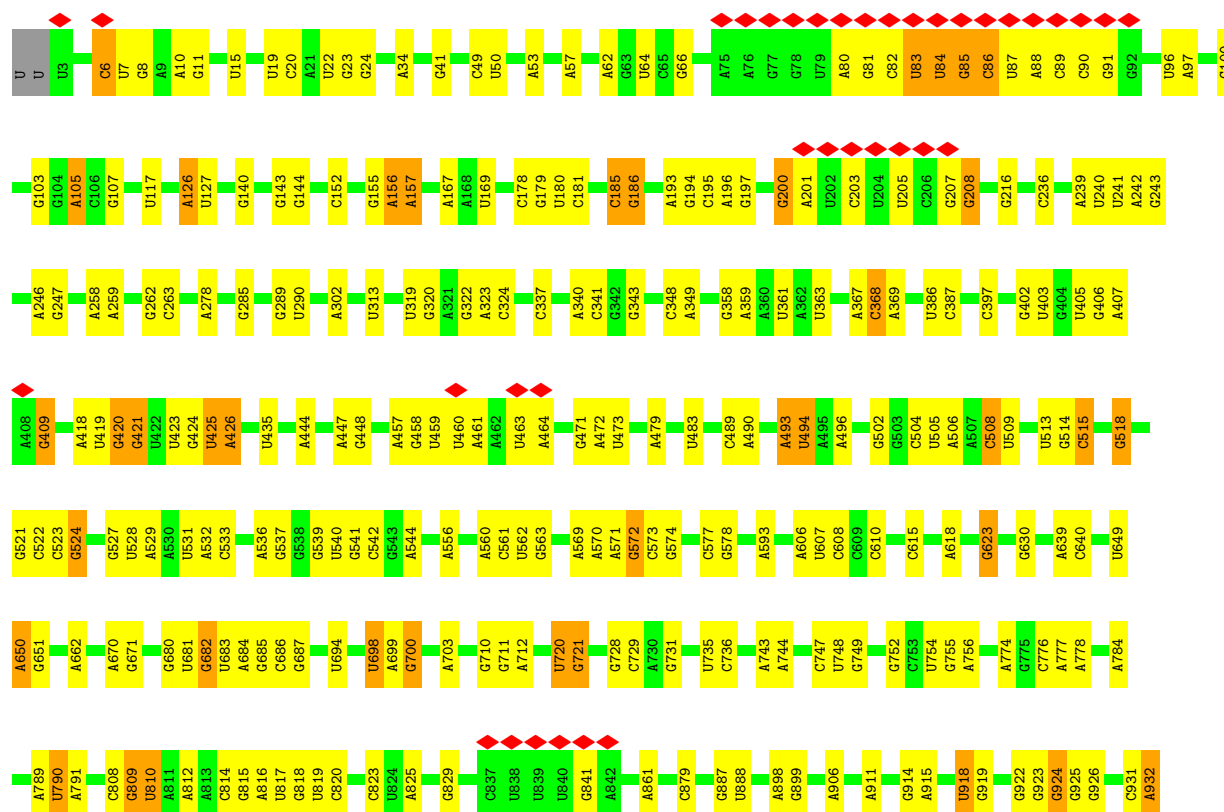
- Molecule 29: 50S ribosomal protein L30

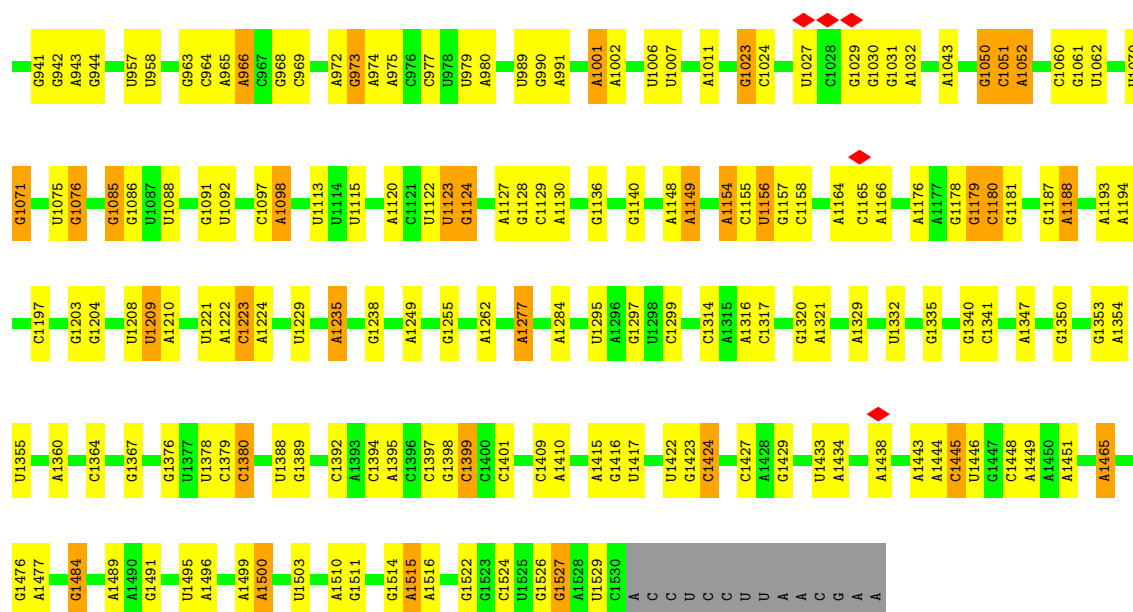


- Molecule 30: 50S ribosomal protein L32



- Molecule 31: 16s Ribosomal RNA

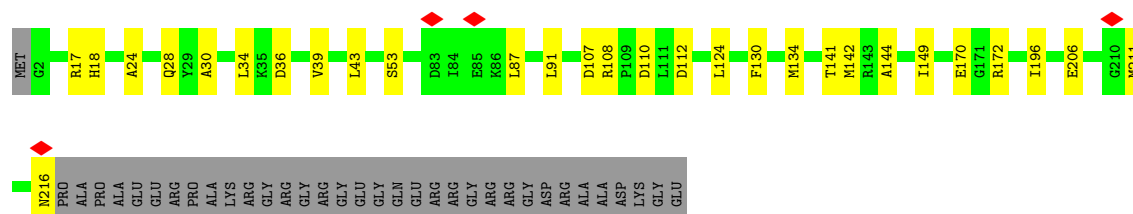




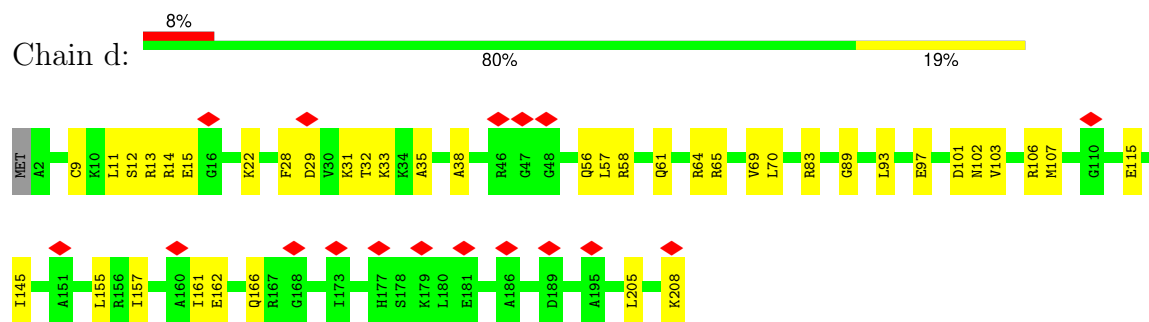
• Molecule 32: 30S ribosomal protein S2



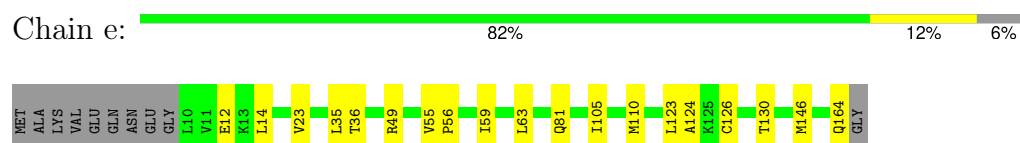
• Molecule 33: 30S ribosomal protein S3



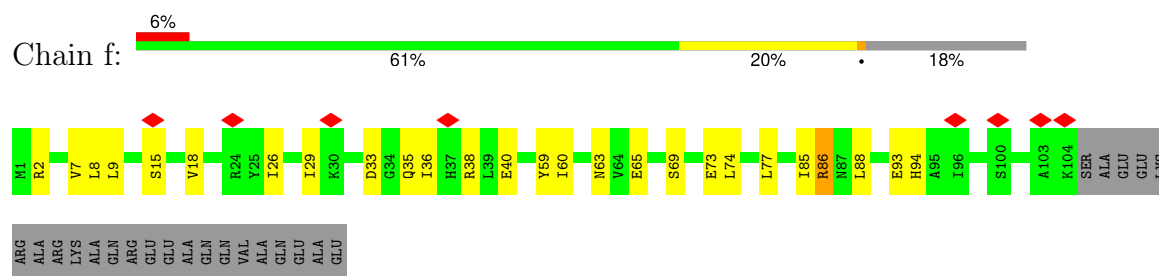
- Molecule 34: 30S ribosomal protein S4



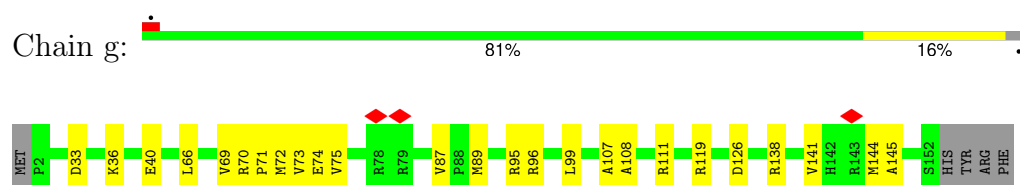
- Molecule 35: 30S ribosomal protein S5



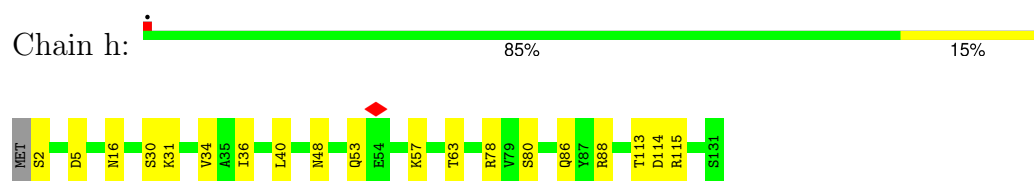
- Molecule 36: 30S ribosomal protein S6



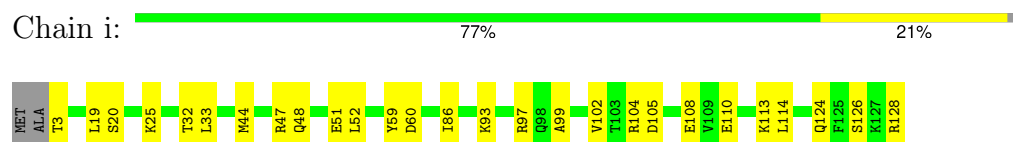
- Molecule 37: 30S ribosomal protein S7



- Molecule 38: 30S ribosomal protein S8



- Molecule 39: 30S ribosomal protein S9



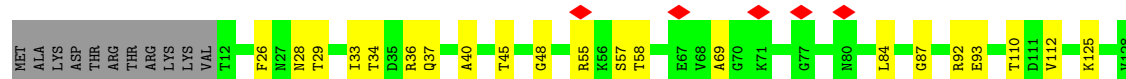
- Molecule 40: 30S ribosomal protein S10

Chain j:  75% 22%



- Molecule 41: 30S ribosomal protein S11

Chain k:  75% 16% 9%



- Molecule 42: 30S ribosomal protein S12

Chain l:  90% 9%



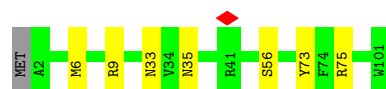
- Molecule 43: 30S ribosomal protein S13

Chain m:  88% 9%



- Molecule 44: 30S ribosomal protein S14

Chain n:  92% 7%



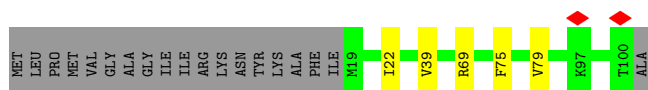
- Molecule 45: 30S ribosomal protein S15

Chain o:  78% 21%

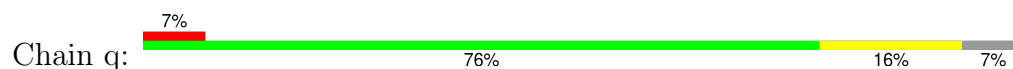


- Molecule 46: 30S ribosomal protein S16

Chain p:  76% 5% 19%



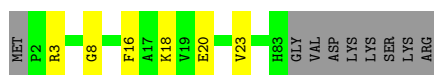
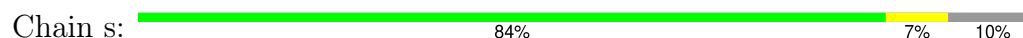
- Molecule 47: 30S ribosomal protein S17



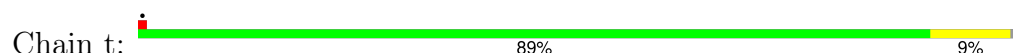
- Molecule 48: 30S ribosomal protein S18



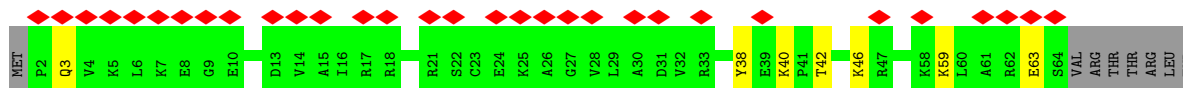
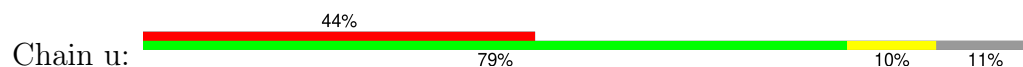
- Molecule 49: 30S ribosomal protein S19



- Molecule 50: 30S ribosomal protein S20

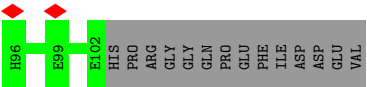


- Molecule 51: 30S ribosomal protein S21



- Molecule 52: Ribosomal subunit interface protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11390	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 ($e^-/\text{\AA}^2$)	46	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.646	Depositor
Minimum map value	-0.413	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.054	Depositor
Recommended contour level	0.1	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: 2MG, 6MZ, OMU, OMG, 3TD, 4OC, 7MG, 2MA, ZN, 5MC, YQM, MA6, UR3, MG, PSU, 5MU

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	0.10	0/416	0.32	0/552
2	1	0.13	0/367	0.28	0/481
3	2	0.10	0/515	0.32	0/678
4	3	0.16	0/296	0.27	0/389
5	A	0.09	0/65229	0.26	0/101736
6	B	0.08	0/2739	0.26	0/4266
7	C	0.12	0/2152	0.32	0/2891
8	D	0.12	0/1584	0.31	0/2135
9	E	0.11	0/1537	0.27	0/2073
10	F	0.22	0/1390	0.59	0/1863
11	G	0.13	0/1337	0.35	0/1807
12	H	0.13	0/461	0.32	0/616
13	I	0.12	0/1143	0.28	0/1541
14	J	0.12	0/956	0.30	0/1286
15	K	0.10	0/1079	0.29	0/1439
16	L	0.17	0/1104	0.37	0/1475
17	M	0.12	0/956	0.30	0/1282
18	N	0.14	0/865	0.33	0/1156
19	O	0.12	0/925	0.30	0/1241
20	P	0.12	0/947	0.29	0/1262
21	Q	0.13	0/818	0.33	0/1094
22	R	0.12	0/831	0.30	0/1113
23	S	0.13	0/716	0.26	0/957
24	T	0.11	0/770	0.31	0/1034
25	U	0.10	0/770	0.30	0/1036
26	V	0.11	0/593	0.29	0/793
27	W	0.11	0/642	0.28	0/856
28	X	0.10	0/487	0.24	0/646
29	Y	0.13	0/468	0.28	0/624
30	Z	0.11	0/462	0.27	0/615
31	a	0.12	0/36476	0.26	0/56895
32	b	0.19	0/1799	0.45	0/2429

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.15	0/1714	0.33	0/2304
34	d	0.13	0/1653	0.33	0/2213
35	e	0.14	0/1141	0.33	0/1537
36	f	0.16	0/882	0.39	0/1189
37	g	0.16	0/1205	0.35	0/1614
38	h	0.12	0/993	0.30	0/1331
39	i	0.13	0/1002	0.32	0/1339
40	j	0.14	0/811	0.37	0/1096
41	k	0.13	0/878	0.31	0/1189
42	l	0.25	1/958 (0.1%)	0.52	2/1284 (0.2%)
43	m	0.13	0/913	0.34	0/1226
44	n	0.14	0/803	0.32	0/1071
45	o	0.12	0/715	0.26	0/958
46	p	0.11	0/655	0.29	0/879
47	q	0.13	0/628	0.35	0/847
48	r	0.12	0/432	0.33	0/583
49	s	0.15	0/664	0.29	0/897
50	t	0.16	0/669	0.34	0/892
51	u	0.11	0/528	0.28	0/697
52	v	0.19	0/839	0.41	0/1123
All	All	0.11	1/148913 (0.0%)	0.28	2/222530 (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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	l	122	PRO	CG-CD	-5.87	1.30	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	l	122	PRO	N-CD-CG	-8.69	90.17	103.20
42	l	122	PRO	CA-N-CD	-8.09	100.67	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	F	138	PHE	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	409	0	437	6	0
2	1	363	0	401	1	0
3	2	509	0	566	3	0
4	3	295	0	326	5	0
5	A	58566	0	29451	287	0
6	B	2450	0	1241	20	0
7	C	2111	0	2176	35	0
8	D	1566	0	1605	14	0
9	E	1516	0	1569	13	0
10	F	1370	0	1420	73	0
11	G	1318	0	1373	23	0
12	H	458	0	480	7	0
13	I	1117	0	1136	8	0
14	J	946	0	1007	11	0
15	K	1071	0	1140	6	0
16	L	1087	0	1162	19	0
17	M	942	0	987	5	0
18	N	857	0	899	23	0
19	O	913	0	968	6	0
20	P	934	0	997	9	0
21	Q	807	0	842	17	0
22	R	826	0	894	7	0
23	S	710	0	768	7	0
24	T	766	0	816	9	0
25	U	760	0	783	7	0
26	V	585	0	589	3	0
27	W	632	0	667	2	0
28	X	486	0	528	4	0
29	Y	463	0	488	4	0
30	Z	456	0	448	8	0
31	a	32782	0	16508	199	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	b	1769	0	1787	66	0
33	c	1690	0	1774	16	0
34	d	1631	0	1691	32	0
35	e	1129	0	1174	16	0
36	f	867	0	868	20	0
37	g	1188	0	1239	18	0
38	h	985	0	1047	12	0
39	i	991	0	1048	19	0
40	j	801	0	832	17	0
41	k	862	0	877	17	0
42	l	945	0	998	7	0
43	m	903	0	962	6	0
44	n	792	0	833	4	0
45	o	705	0	712	13	0
46	p	644	0	655	3	0
47	q	621	0	665	10	0
48	r	426	0	447	6	0
49	s	646	0	663	4	0
50	t	663	0	715	5	0
51	u	522	0	565	6	0
52	v	824	0	810	31	0
53	3	1	0	0	0	0
54	A	80	0	0	2	0
55	A	135	0	0	0	0
55	B	1	0	0	0	0
55	C	1	0	0	0	0
55	K	1	0	0	0	0
55	a	48	0	0	0	0
55	t	1	0	0	0	0
56	1	1	0	0	0	0
56	2	1	0	0	0	0
56	A	179	0	0	6	0
56	D	2	0	0	0	0
56	K	1	0	0	0	0
56	Z	2	0	0	0	0
56	a	38	0	0	2	0
56	d	1	0	0	0	0
56	i	1	0	0	0	0
56	q	1	0	0	0	0
56	t	2	0	0	0	0
All	All	138172	0	93034	1061	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 (1061) 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)
10:F:17:GLN:NE2	10:F:22:ILE:O	2.00	0.94
31:a:85:G:O2'	31:a:86:C:OP2	1.87	0.93
5:A:1865:G:N2	5:A:1868:A:OP2	2.02	0.93
38:h:86:GLN:OE1	38:h:88:ARG:NH1	2.01	0.92
41:k:87:GLY:O	41:k:92:ARG:NH1	2.03	0.92
33:c:53:SER:OG	33:c:112:ASP:OD2	1.88	0.91
5:A:799:G:O2'	5:A:800:A:OP1	1.90	0.89
10:F:30:ARG:NH1	10:F:31:ILE:O	2.05	0.89
5:A:363:G:OP2	5:A:364:A:O2'	1.91	0.89
5:A:2401:G:O2'	5:A:2408:A:N6	2.04	0.89
5:A:1563:C:O2	5:A:1564:A:O2'	1.89	0.89
31:a:541:G:OP1	34:d:58:ARG:NH2	2.07	0.88
32:b:106:TRP:O	32:b:110:ARG:NH1	2.06	0.88
10:F:4:LEU:N	10:F:7:ARG:O	2.07	0.88
31:a:1098:A:OP2	32:b:97:ARG:NH2	2.06	0.88
5:A:184:G:N2	5:A:184:G:OP2	2.08	0.87
31:a:687:G:N2	31:a:694:U:O4	2.08	0.87
31:a:682:G:O2'	31:a:683:U:O4'	1.93	0.86
35:e:164:GLN:OE1	38:h:115:ARG:NH2	2.08	0.86
31:a:640:C:OP1	38:h:31:LYS:NZ	2.07	0.86
52:v:5:ILE:HG22	52:v:41:VAL:HG22	1.57	0.86
5:A:1843:A:O2'	5:A:1844:A:N7	2.07	0.85
7:C:133:ARG:O	7:C:167:ARG:NH2	2.10	0.84
5:A:2379:G:O2'	5:A:2380:U:O5'	1.95	0.84
5:A:1198:U:OP2	5:A:1199:A:O2'	1.94	0.84
45:o:29:VAL:HG11	45:o:81:LEU:HD21	1.57	0.84
41:k:125:LYS:NZ	51:u:38:TYR:O	2.10	0.84
5:A:2058:A:OP1	56:A:3401:HOH:O	1.94	0.83
5:A:1824:G:OP2	56:A:3402:HOH:O	1.96	0.83
5:A:97:C:OP2	5:A:98:A:O2'	1.95	0.83
6:B:37:U:O2	6:B:44:A:N6	2.12	0.82
31:a:789:A:O2'	31:a:790:U:OP2	1.97	0.82
31:a:1527:G:N7	51:u:46:LYS:NZ	2.28	0.82
5:A:1306:G:N2	5:A:1306:G:OP2	2.11	0.82
14:J:7:MET:SD	14:J:18:ARG:NH2	2.53	0.82
39:i:104:ARG:NH1	39:i:105:ASP:O	2.13	0.82
31:a:1522:G:OP2	51:u:40:LYS:NZ	2.12	0.81
31:a:403:U:O2'	34:d:115:GLU:OE1	1.99	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:b:29:MET:O	32:b:31:GLN:N	2.14	0.80
5:A:199:G:O6	5:A:210:C:O2'	1.99	0.80
5:A:1517:G:OP2	5:A:1518:A:O2'	1.98	0.80
31:a:207:G:O2'	31:a:208:G:O4'	2.00	0.79
31:a:966:A:N1	52:v:6:ARG:NH1	2.30	0.79
12:H:5:LEU:HD13	12:H:9:ILE:HD13	1.66	0.78
5:A:1007:A:OP2	56:A:3403:HOH:O	2.00	0.78
5:A:2518:U:O2'	5:A:2643:U:OP1	2.00	0.78
5:A:364:A:OP2	5:A:424:G:O2'	2.01	0.78
31:a:964:5MC:OP2	31:a:965:A:O2'	2.01	0.77
14:J:103:THR:OG1	14:J:105:GLU:OE1	2.01	0.77
5:A:2861:U:OP2	5:A:2862:G:O2'	2.00	0.77
7:C:165:LEU:HD11	7:C:175:ARG:HG3	1.64	0.77
16:L:6:ARG:NH1	16:L:7:THR:O	2.18	0.77
45:o:29:VAL:HG23	45:o:63:ARG:HG3	1.66	0.77
11:G:115:TYR:OH	11:G:147:GLU:OE1	2.02	0.76
5:A:2309:C:O4'	10:F:37:ASN:ND2	2.18	0.76
31:a:686:C:OP1	41:k:45:THR:OG1	2.01	0.76
31:a:425:U:O3'	34:d:22:LYS:NZ	2.18	0.76
5:A:1794:U:OP2	7:C:271:ARG:NH2	2.19	0.76
31:a:649:U:O4	31:a:749:G:O2'	2.02	0.76
31:a:1122:U:O2	31:a:1123:U:O2'	2.04	0.75
52:v:5:ILE:HD11	52:v:18:ILE:HA	1.68	0.75
31:a:969:C:OP2	40:j:59:LYS:NZ	2.19	0.75
5:A:1810:G:OP2	5:A:1811:A:O2'	2.01	0.75
18:N:42:SER:OG	18:N:44:ASP:OD1	2.05	0.75
52:v:60:ILE:CG2	52:v:90:LEU:HD11	2.16	0.75
5:A:1016:U:OP1	5:A:1032:U:O2'	2.04	0.74
5:A:2853:G:N2	5:A:2856:A:OP2	2.20	0.74
40:j:85:ASP:OD1	40:j:86:ALA:N	2.21	0.74
16:L:136:VAL:HG12	16:L:137:MET:SD	2.28	0.74
34:d:9:CYS:SG	34:d:22:LYS:NZ	2.57	0.74
31:a:941:G:N1	31:a:1335:G:OP2	2.21	0.74
31:a:735:U:OP1	36:f:2:ARG:NH2	2.20	0.74
31:a:977:C:O2	56:a:1701:HOH:O	2.06	0.74
34:d:56:GLN:OE1	34:d:208:LYS:NZ	2.20	0.74
32:b:67:ASN:ND2	32:b:161:ASP:OD2	2.19	0.74
10:F:79:ILE:HG22	10:F:83:TRP:CE3	2.23	0.73
37:g:111:ARG:NH1	37:g:126:ASP:OD2	2.20	0.73
5:A:1542:A:O2'	5:A:1543:A:O5'	2.06	0.73
5:A:1749:G:N2	5:A:1752:G:OP2	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:504:C:OP2	31:a:505:U:O2'	2.03	0.73
52:v:60:ILE:HG21	52:v:90:LEU:HD11	1.68	0.73
19:O:53:LYS:NZ	19:O:55:ASN:OD1	2.21	0.73
31:a:683:U:O4	31:a:700:G:O2'	2.07	0.72
5:A:1938:C:OP2	5:A:1939:U:O2'	2.05	0.72
5:A:1709:U:O2'	5:A:1710:U:OP1	2.07	0.72
5:A:2274:A:OP1	16:L:10:ARG:NH2	2.23	0.72
40:j:36:VAL:HG12	40:j:76:ILE:HG22	1.70	0.72
5:A:1542:A:O2'	5:A:1543:A:O4'	2.07	0.71
31:a:105:A:O2'	31:a:322:G:N2	2.23	0.71
36:f:35:GLN:NE2	36:f:65:GLU:OE1	2.23	0.71
4:3:9:LYS:HE3	4:3:16:VAL:HG23	1.72	0.71
5:A:1962:A:N3	5:A:2588:G:O2'	2.21	0.71
6:B:43:A:O4'	10:F:92:ARG:NH1	2.23	0.71
5:A:1025:A:N3	5:A:2482:C:O2'	2.24	0.71
13:I:19:ASP:OD2	13:I:58:ASN:ND2	2.23	0.71
31:a:623:G:O3'	46:p:69:ARG:NH2	2.24	0.71
10:F:147:ASP:OD2	10:F:148:ARG:NH1	2.23	0.71
10:F:138:PHE:CD2	10:F:139:PRO:HD3	2.26	0.70
41:k:45:THR:HG23	41:k:48:GLY:H	1.55	0.70
5:A:749:A:OP1	56:A:3405:HOH:O	2.08	0.70
9:E:47:SER:O	9:E:51:VAL:HG23	1.90	0.70
5:A:2298:U:O2'	10:F:123:ASP:O	2.10	0.70
32:b:135:GLU:OE2	32:b:139:ARG:NH1	2.24	0.70
8:D:30:VAL:O	8:D:188:SER:OG	2.10	0.70
18:N:28:CYS:SG	18:N:94:SER:OG	2.48	0.70
5:A:2373:A:O2'	18:N:116:PHE:OXT	2.05	0.70
32:b:142:GLU:O	32:b:146:LEU:HD23	1.92	0.70
30:Z:52:GLN:NE2	30:Z:53:LEU:O	2.25	0.69
31:a:1221:U:OP1	56:a:1702:HOH:O	2.10	0.69
5:A:537:A:N6	5:A:553:G:O2'	2.24	0.69
5:A:2026:6MZ:O2'	5:A:2027:A:OP2	2.06	0.69
18:N:63:THR:O	18:N:64:THR:OG1	2.10	0.69
10:F:12:LEU:O	10:F:16:LEU:HD23	1.91	0.69
10:F:123:ASP:O	10:F:125:ARG:NH1	2.26	0.69
5:A:277:A:N6	5:A:367:A:OP2	2.26	0.69
5:A:322:G:O2'	5:A:324:A:OP2	2.09	0.69
39:i:128:ARG:O	52:v:63:ARG:NH1	2.26	0.69
44:n:6:MET:SD	44:n:9:ARG:NH2	2.66	0.69
10:F:91:LEU:HD12	10:F:95:GLN:HG3	1.75	0.68
40:j:7:ARG:HD2	40:j:73:LEU:HD11	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:v:59:MET:CE	52:v:71:ALA:HB1	2.23	0.68
13:I:89:PHE:O	13:I:93:VAL:HG13	1.93	0.68
5:A:673:A:OP1	9:E:57:LYS:NZ	2.26	0.68
5:A:226:A:N3	5:A:241:U:O2'	2.21	0.68
6:B:12:U:O3'	6:B:104:U:O2'	2.09	0.68
7:C:198:GLN:NE2	7:C:199:GLU:OE1	2.27	0.68
32:b:11:LEU:HD23	32:b:45:LEU:HD12	1.75	0.68
41:k:84:LEU:HD12	41:k:112:VAL:CG2	2.24	0.68
5:A:2013:C:OP1	56:A:3406:HOH:O	2.12	0.67
24:T:34:VAL:HG11	24:T:37:LEU:HD12	1.75	0.67
31:a:518:G:HO2'	31:a:533:C:HO2'	1.34	0.67
5:A:978:A:OP2	5:A:979:C:N4	2.27	0.67
24:T:28:SER:OG	24:T:29:GLU:OE1	2.04	0.67
31:a:84:U:O4'	31:a:85:G:N2	2.28	0.67
19:O:7:LEU:O	19:O:11:ILE:HD12	1.95	0.66
21:Q:51:ALA:HB3	21:Q:52:PRO:HD3	1.78	0.66
14:J:75:SER:OG	19:O:76:VAL:O	2.09	0.66
5:A:1004:C:OP1	13:I:37:ARG:NH1	2.28	0.66
32:b:22:THR:HG23	32:b:39:LYS:O	1.96	0.66
22:R:29:VAL:O	22:R:33:LEU:HD23	1.96	0.66
52:v:59:MET:HE3	52:v:71:ALA:HB1	1.79	0.65
5:A:1775:U:OP2	5:A:1780:A:N6	2.26	0.65
5:A:2687:C:HO2'	5:A:2867:U:HO2'	1.42	0.65
6:B:55:A:C8	10:F:26:MET:HE1	2.32	0.65
7:C:133:ARG:NH2	7:C:187:GLU:OE2	2.30	0.65
41:k:26:PHE:O	41:k:57:SER:OG	2.11	0.65
11:G:23:GLN:NE2	11:G:36:ASN:OD1	2.27	0.65
10:F:137:VAL:HG23	10:F:137:VAL:O	1.97	0.64
24:T:9:GLN:OE1	24:T:23:THR:OG1	2.15	0.64
5:A:2742:U:O3'	11:G:138:LYS:NZ	2.30	0.64
5:A:1441:C:O2'	5:A:1543:A:O2'	2.04	0.64
32:b:199:ASP:OD1	32:b:200:TYR:N	2.31	0.64
24:T:97:THR:OG1	24:T:99:GLU:OE1	2.12	0.64
16:L:53:THR:HA	16:L:56:ARG:HE	1.62	0.64
1:O:43:VAL:HG22	1:O:44:ILE:H	1.63	0.63
11:G:43:LEU:HD11	11:G:50:LEU:HD21	1.80	0.63
31:a:423:U:OP2	31:a:424:G:O2'	2.12	0.63
31:a:1097:C:O5'	32:b:97:ARG:NH1	2.31	0.63
31:a:1122:U:H2'	31:a:1123:U:H2'	1.80	0.63
5:A:2568:A:O2'	5:A:2571:C:OP1	2.10	0.63
31:a:820:C:HO2'	38:h:2:SER:N	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:l:62:GLU:N	42:l:62:GLU:OE1	2.31	0.63
32:b:118:ASP:OD1	32:b:122:GLN:NE2	2.32	0.63
7:C:165:LEU:HD21	7:C:175:ARG:HE	1.64	0.63
31:a:406:G:OP2	34:d:31:LYS:NZ	2.28	0.63
32:b:196:ASP:OD1	32:b:197:ASN:N	2.32	0.62
36:f:38:ARG:NE	36:f:63:ASN:OD1	2.32	0.62
52:v:5:ILE:CG2	52:v:41:VAL:HG22	2.28	0.62
5:A:2784:C:O2'	5:A:2805:A:N3	2.33	0.62
5:A:570:A:OP2	21:Q:80:ARG:NH1	2.30	0.62
40:j:36:VAL:CG1	40:j:76:ILE:HG22	2.28	0.62
8:D:13:THR:HG22	8:D:14:ARG:H	1.65	0.62
32:b:123:SER:CB	32:b:143:MET:HE1	2.30	0.61
36:f:9:LEU:HD11	36:f:59:TYR:CE2	2.35	0.61
5:A:483:C:OP2	24:T:45:LYS:NZ	2.29	0.61
31:a:560:A:O2'	31:a:563:G:O2'	2.17	0.61
39:i:86:ILE:HD11	39:i:102:VAL:HG22	1.83	0.61
12:H:5:LEU:HD11	12:H:12:LEU:HB3	1.82	0.61
32:b:99:LEU:HD12	32:b:150:LEU:HD21	1.82	0.61
5:A:1328:G:OP2	56:A:3409:HOH:O	2.16	0.61
31:a:87:U:O4	31:a:88:A:N6	2.33	0.61
48:r:37:GLY:O	48:r:63:ARG:NH2	2.32	0.61
31:a:682:G:HO2'	31:a:683:U:C1'	2.14	0.61
36:f:93:GLU:O	36:f:94:HIS:ND1	2.33	0.60
31:a:1011:A:OP2	49:s:18:LYS:NZ	2.31	0.60
32:b:51:ALA:CB	32:b:202:ILE:HG22	2.31	0.60
51:u:59:LYS:O	51:u:63:GLU:OE1	2.19	0.60
11:G:13:ASN:OD1	11:G:14:GLY:N	2.31	0.60
50:t:45:ALA:O	50:t:49:GLU:OE1	2.20	0.60
40:j:52:LEU:HD23	40:j:62:ARG:HG2	1.84	0.60
5:A:1044:G:H2'	5:A:1108:A:H61	1.67	0.60
38:h:5:ASP:OD1	38:h:78:ARG:NH1	2.34	0.60
39:i:52:LEU:HD11	39:i:99:ALA:HB2	1.84	0.60
52:v:13:ASN:OD1	52:v:14:SER:N	2.35	0.59
5:A:2591:G:N2	5:A:2594:A:OP2	2.27	0.59
35:e:14:LEU:HD12	35:e:36:THR:HG22	1.84	0.59
10:F:114:PHE:O	10:F:115:ARG:HD3	2.01	0.59
23:S:49:LEU:HD13	28:X:26:PHE:CE2	2.37	0.59
5:A:2200:G:OP2	7:C:147:LYS:NZ	2.33	0.59
31:a:178:C:OP2	31:a:179:G:N2	2.36	0.59
5:A:1423:C:O2'	5:A:1567:A:OP2	2.16	0.59
5:A:1717:G:O2'	5:A:1735:A:N6	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:110:MET:HE2	35:e:126:CYS:SG	2.42	0.59
5:A:72:C:O2'	5:A:455:C:N3	2.36	0.59
6:B:55:A:N9	10:F:26:MET:HE1	2.18	0.59
31:a:649:U:O2'	31:a:650:A:OP2	2.18	0.59
5:A:1937:C:N4	5:A:1961:C:O4'	2.36	0.59
11:G:18:THR:HG22	11:G:27:LYS:NZ	2.17	0.59
36:f:69:SER:O	36:f:73:GLU:OE1	2.21	0.59
5:A:1037:A:OP1	25:U:49:ARG:NH2	2.36	0.59
31:a:126:A:O4'	47:q:66:ARG:NH2	2.36	0.59
32:b:120:GLN:OE1	32:b:143:MET:HE2	2.02	0.58
5:A:1719:U:O4	5:A:1734:G:N2	2.36	0.58
10:F:130:MET:HE1	10:F:132:LEU:HD21	1.84	0.58
31:a:572:G:O2'	31:a:818:G:OP2	2.19	0.58
31:a:610:C:OP1	34:d:83:ARG:NH1	2.33	0.58
31:a:1203:G:C2'	31:a:1204:2MG:H5'	2.33	0.58
23:S:5:ARG:O	23:S:9:VAL:HG23	2.03	0.58
31:a:1208:U:O2'	31:a:1209:U:OP1	2.16	0.58
35:e:55:VAL:HG23	35:e:56:PRO:HD3	1.85	0.58
52:v:41:VAL:HG12	52:v:60:ILE:HG23	1.85	0.58
5:A:698:G:O2'	5:A:1630:A:N3	2.28	0.58
10:F:147:ASP:OD1	10:F:148:ARG:N	2.33	0.58
11:G:75:LEU:O	11:G:79:VAL:HG23	2.04	0.58
52:v:35:ARG:O	52:v:65:SER:N	2.36	0.58
10:F:14:ALA:O	10:F:18:GLU:OE1	2.21	0.58
35:e:105:ILE:HD12	35:e:123:LEU:CD2	2.34	0.58
32:b:83:ARG:NE	32:b:95:ASP:OD2	2.29	0.58
32:b:190:ASP:OD1	32:b:191:THR:N	2.37	0.58
20:P:97:ASP:OD1	20:P:101:HIS:ND1	2.33	0.57
31:a:1429:G:O2'	31:a:1465:A:N6	2.37	0.57
32:b:98:TRP:NE1	32:b:177:GLU:OE1	2.36	0.57
32:b:188:ILE:CD1	32:b:202:ILE:HD11	2.34	0.57
34:d:157:ILE:O	34:d:161:ILE:HG23	2.04	0.57
36:f:15:SER:O	36:f:18:VAL:HG22	2.04	0.57
6:B:50:A:N7	18:N:34:ARG:NH1	2.52	0.57
32:b:150:LEU:HD12	32:b:153:VAL:HG21	1.85	0.57
34:d:13:ARG:NH2	34:d:38:ALA:O	2.38	0.57
16:L:79:LEU:HG	16:L:80:GLU:OE1	2.04	0.57
31:a:100:G:OP1	50:t:16:LYS:NZ	2.28	0.57
31:a:126:A:N3	31:a:259:A:O2'	2.33	0.57
31:a:1120:A:O2'	40:j:39:PRO:O	2.17	0.57
37:g:73:VAL:HG23	37:g:145:ALA:CB	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:955:U:OP2	16:L:14:LYS:NZ	2.38	0.57
5:A:1106:C:H2'	5:A:1107:G:C4	2.39	0.57
7:C:129:CYS:C	7:C:130:LEU:HD12	2.30	0.57
31:a:1410:A:H2	31:a:1484:G:H22	1.53	0.57
3:2:33:THR:OG1	5:A:2416:C:OP1	2.15	0.57
49:s:16:PHE:O	49:s:20:GLU:HG2	2.04	0.56
5:A:627:A:N3	5:A:637:U:O2'	2.38	0.56
32:b:106:TRP:CD1	32:b:110:ARG:HH22	2.23	0.56
5:A:198:A:H3'	5:A:199:G:H21	1.69	0.56
50:t:78:ARG:O	50:t:82:GLN:OE1	2.22	0.56
5:A:857:G:O2'	5:A:858:U:P	2.64	0.56
31:a:571:A:HO2'	31:a:879:C:HO2'	1.50	0.56
5:A:1338:G:O2'	5:A:1379:A:N1	2.33	0.56
31:a:924:G:O2'	31:a:1500:A:N7	2.31	0.56
41:k:84:LEU:HD12	41:k:112:VAL:HG21	1.87	0.56
5:A:1373:A:O2'	5:A:1374:U:OP2	2.19	0.56
5:A:1924:A:H2'	5:A:1925:G:O4'	2.06	0.56
18:N:34:ARG:O	18:N:64:THR:OG1	2.24	0.56
5:A:1259:G:OP1	30:Z:16:ARG:NH2	2.38	0.56
21:Q:98:ILE:HG23	21:Q:98:ILE:O	2.06	0.56
52:v:54:LYS:O	52:v:76:ALA:O	2.23	0.56
5:A:25:C:O2'	5:A:552:U:OP1	2.22	0.56
5:A:2379:G:HO2'	5:A:2380:U:P	2.28	0.56
42:l:99:ARG:NE	42:l:104:CYS:SG	2.79	0.56
5:A:2581:U:O2'	5:A:2582:U:O5'	2.24	0.55
38:h:78:ARG:NE	38:h:80:SER:O	2.40	0.55
8:D:110:VAL:HG21	8:D:180:ILE:HD11	1.89	0.55
10:F:92:ARG:HA	10:F:96:MET:HE2	1.88	0.55
31:a:542:C:OP2	34:d:64:ARG:NH2	2.39	0.55
34:d:101:ASP:OD1	34:d:102:ASN:N	2.40	0.55
31:a:670:A:H2'	31:a:671:G:C8	2.42	0.55
3:2:31:ILE:O	3:2:35:LYS:NZ	2.33	0.55
49:s:3:ARG:NE	49:s:8:GLY:O	2.40	0.55
25:U:14:ASP:OD1	25:U:15:LYS:N	2.40	0.55
31:a:1229:U:OP1	39:i:126:SER:OG	2.14	0.55
5:A:1106:C:O2'	5:A:1107:G:O4'	2.19	0.54
40:j:91:ASP:OD1	40:j:92:LEU:N	2.38	0.54
32:b:50:PRO:O	32:b:53:ASN:OD1	2.25	0.54
32:b:51:ALA:HB1	32:b:202:ILE:HG22	1.89	0.54
33:c:211:MET:HE3	33:c:216:ASN:HB2	1.89	0.54
5:A:2577:G:OP2	5:A:2577:G:N2	2.32	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:420:G:O2'	31:a:421:G:OP2	2.23	0.54
31:a:808:C:O2'	31:a:898:A:N1	2.41	0.54
32:b:88:ARG:NH1	32:b:220:ALA:HB1	2.23	0.54
45:o:29:VAL:HG23	45:o:63:ARG:CG	2.36	0.54
5:A:1794:U:O2'	5:A:1798:A:N3	2.39	0.54
30:Z:4:GLN:NE2	30:Z:6:ASN:O	2.40	0.54
37:g:87:VAL:HG23	37:g:87:VAL:O	2.07	0.54
52:v:36:ILE:HD12	52:v:39:PHE:CZ	2.42	0.54
41:k:84:LEU:HD13	41:k:110:THR:OG1	2.08	0.54
5:A:2379:G:O2'	5:A:2380:U:P	2.65	0.54
13:I:89:PHE:CZ	13:I:93:VAL:HG11	2.42	0.54
45:o:78:TYR:OH	45:o:89:ARG:OXT	2.17	0.54
5:A:1718:A:N6	5:A:1734:G:O2'	2.40	0.54
5:A:1865:G:O2'	5:A:1868:A:N6	2.41	0.54
34:d:162:GLU:O	34:d:166:GLN:OE1	2.25	0.54
5:A:2287:U:O2'	5:A:2370:C:O2	2.25	0.54
32:b:33:ILE:HD11	32:b:41:HIS:CG	2.43	0.54
5:A:1378:A:O2'	5:A:1379:A:O4'	2.19	0.54
7:C:146:LEU:HD21	7:C:182:ARG:HH12	1.73	0.54
5:A:2879:A:OP2	30:Z:49:ARG:NH1	2.40	0.54
8:D:139:ASN:ND2	8:D:142:SER:O	2.41	0.54
31:a:942:G:C2	31:a:943:A:C8	2.96	0.54
33:c:110:ASP:OD2	33:c:144:ALA:HB2	2.08	0.54
5:A:228:A:O4'	5:A:240:A:O2'	2.21	0.53
10:F:32:THR:O	10:F:96:MET:HE1	2.08	0.53
34:d:28:PHE:O	34:d:32:THR:HG22	2.07	0.53
31:a:1176:A:OP2	39:i:97:ARG:NH2	2.41	0.53
1:O:2:ARG:NH1	5:A:2281:C:OP2	2.37	0.53
17:M:106:ASP:N	17:M:106:ASP:OD2	2.42	0.53
38:h:30:SER:O	38:h:34:VAL:HG23	2.08	0.53
11:G:101:THR:O	11:G:101:THR:HG22	2.09	0.53
32:b:49:VAL:HG23	32:b:50:PRO:HD3	1.91	0.53
37:g:73:VAL:HG23	37:g:145:ALA:HB3	1.90	0.53
8:D:41:LEU:N	8:D:47:GLN:OE1	2.41	0.53
32:b:22:THR:O	32:b:25:TRP:N	2.40	0.53
5:A:782:G:H5'	5:A:783:G:OP1	2.09	0.53
5:A:1413:G:H1'	5:A:1578:A:H61	1.73	0.53
5:A:1469:U:H2'	5:A:1470:G:O4'	2.09	0.53
7:C:171:TYR:HB3	7:C:183:LYS:HE3	1.91	0.53
19:O:84:VAL:CG1	19:O:87:ILE:HD11	2.39	0.53
31:a:963:2MG:C5	52:v:59:MET:HE1	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1314:C:OP1	44:n:56:SER:OG	2.21	0.53
31:a:127:U:O2'	31:a:258:A:N3	2.36	0.53
36:f:29:ILE:HD11	36:f:74:LEU:HD11	1.91	0.52
5:A:929:C:H41	5:A:1166:A:H4'	1.72	0.52
7:C:170:SER:O	7:C:186:VAL:HG13	2.10	0.52
43:m:39:ILE:HD11	43:m:52:GLN:HB3	1.91	0.52
13:I:125:TYR:HH	13:I:132:HIS:HE2	1.58	0.52
19:O:84:VAL:HG11	19:O:87:ILE:HD11	1.91	0.52
32:b:171:GLU:O	32:b:175:ILE:HD12	2.09	0.52
4:3:11:CYS:SG	4:3:13:SER:OG	2.68	0.52
5:A:1230:G:O2'	5:A:1231:G:O4'	2.21	0.52
7:C:108:LYS:N	7:C:194:GLU:O	2.27	0.52
22:R:55:ILE:O	22:R:59:GLU:OE1	2.27	0.52
31:a:358:G:N1	31:a:361:U:OP2	2.38	0.52
5:A:720:A:O2'	5:A:721:C:OP1	2.27	0.52
10:F:164:ASP:OD1	10:F:165:GLU:N	2.43	0.52
10:F:53:ALA:HB2	10:F:150:ARG:HE	1.74	0.52
20:P:98:ILE:HD13	21:Q:40:MET:HE1	1.90	0.52
31:a:1070:U:O2'	32:b:105:ASN:ND2	2.42	0.52
36:f:93:GLU:O	36:f:94:HIS:CG	2.62	0.52
47:q:81:GLU:O	47:q:82:ALA:HB3	2.09	0.52
31:a:320:G:N1	31:a:323:A:OP2	2.40	0.52
31:a:489:C:H2'	31:a:490:A:C8	2.45	0.52
26:V:43:THR:HG23	26:V:43:THR:O	2.10	0.52
31:a:861:A:O2'	31:a:1075:U:O4	2.28	0.52
31:a:1222:A:H2'	31:a:1223:C:C5	2.45	0.52
18:N:87:THR:OG1	18:N:115:GLU:OE2	2.26	0.52
19:O:32:GLN:HA	19:O:32:GLN:OE1	2.10	0.52
31:a:681:U:C2'	31:a:682:G:O5'	2.58	0.52
31:a:1176:A:OP2	39:i:93:LYS:NZ	2.41	0.52
5:A:308:U:H2'	5:A:309:G:O4'	2.10	0.51
5:A:2548:OMU:OP2	5:A:2548:OMU:H6	2.10	0.51
52:v:54:LYS:O	52:v:77:GLY:HA2	2.10	0.51
5:A:455:C:O2'	23:S:71:ARG:NH2	2.43	0.51
5:A:2843:U:H2'	5:A:2844:G:O4'	2.10	0.51
36:f:73:GLU:O	36:f:77:LEU:HD13	2.10	0.51
42:l:79:VAL:N	42:l:103:ASP:OD2	2.43	0.51
11:G:80:SER:O	11:G:81:GLU:HB2	2.10	0.51
22:R:80:MET:O	22:R:100:THR:OG1	2.24	0.51
45:o:70:LEU:HD11	45:o:77:ARG:HG3	1.92	0.51
5:A:1812:C:N4	7:C:35:GLU:OE2	2.31	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:C:162:VAL:HG12	7:C:176:LEU:HD23	1.91	0.51
8:D:18:ASP:OD1	8:D:19:ALA:N	2.44	0.51
52:v:29:PHE:CE1	52:v:94:LEU:HD12	2.45	0.51
20:P:74:LEU:HD11	20:P:114:LYS:HE2	1.93	0.51
35:e:81:GLN:H	35:e:146:MET:CE	2.24	0.51
5:A:1695:G:OP2	5:A:1696:A:O2'	2.21	0.51
41:k:112:VAL:HG12	41:k:112:VAL:O	2.11	0.51
37:g:74:GLU:HG3	37:g:141:VAL:HG21	1.93	0.51
5:A:798:U:H4'	5:A:799:G:OP1	2.10	0.51
10:F:6:ALA:O	10:F:8:TYR:N	2.39	0.51
10:F:53:ALA:HB1	10:F:57:MET:HE1	1.92	0.51
36:f:85:ILE:O	36:f:85:ILE:HG13	2.11	0.51
1:0:18:THR:HG21	5:A:2415:U:H4'	1.93	0.50
33:c:43:LEU:HD21	33:c:91:LEU:HD21	1.94	0.50
10:F:38:MET:HE2	10:F:53:ALA:HB1	1.93	0.50
10:F:57:MET:HA	10:F:60:ILE:HG12	1.92	0.50
31:a:1235:A:OP1	31:a:1332:U:O2'	2.21	0.50
32:b:143:MET:O	32:b:144:GLU:C	2.55	0.50
43:m:50:ASP:OD1	43:m:51:ALA:N	2.44	0.50
34:d:11:LEU:O	34:d:15:GLU:OE1	2.29	0.50
46:p:22:ILE:HG12	46:p:39:VAL:HG22	1.93	0.50
31:a:809:G:H1'	31:a:810:U:OP2	2.12	0.50
37:g:71:PRO:O	37:g:72:MET:HE2	2.11	0.50
5:A:1580:C:O2'	5:A:1583:C:O2	2.28	0.50
5:A:1861:U:HO2'	5:A:1862:A:H8	1.58	0.50
5:A:2526:A:N7	11:G:172:LYS:NZ	2.59	0.50
11:G:117:LEU:HD11	11:G:123:ALA:HB3	1.94	0.50
21:Q:42:VAL:HG13	21:Q:47:ILE:HG12	1.94	0.50
31:a:1353:G:H2'	31:a:1354:A:C8	2.46	0.50
31:a:562:U:OP2	31:a:563:G:O2'	2.28	0.50
52:v:11:ILE:O	52:v:12:HIS:HB3	2.11	0.50
10:F:31:ILE:O	10:F:31:ILE:HG23	2.12	0.50
5:A:575:G:O2'	5:A:1249:A:OP1	2.30	0.50
5:A:1315:C:H2'	5:A:1324:U:OP1	2.12	0.50
16:L:78:PRO:HD2	16:L:81:VAL:HG21	1.94	0.50
31:a:242:A:C2	31:a:278:A:C5	2.99	0.50
10:F:34:ILE:HD12	10:F:156:ILE:HG22	1.94	0.49
5:A:67:G:O2'	5:A:69:U:OP2	2.17	0.49
5:A:2524:U:O2'	5:A:2526:A:OP1	2.20	0.49
10:F:138:PHE:CD2	10:F:139:PRO:CD	2.95	0.49
18:N:74:GLY:O	18:N:77:ILE:HG22	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:721:G:OP1	31:a:829:G:N2	2.45	0.49
40:j:57:VAL:HG23	40:j:57:VAL:O	2.13	0.49
5:A:474:C:O2	5:A:478:A:N6	2.42	0.49
17:M:94:TYR:C	17:M:95:LEU:HD12	2.38	0.49
31:a:493:A:O2'	31:a:494:U:C6	2.64	0.49
32:b:202:ILE:HG13	32:b:202:ILE:O	2.12	0.49
35:e:36:THR:HG21	35:e:63:LEU:HD22	1.94	0.49
7:C:94:LEU:HD23	7:C:104:ILE:HG12	1.95	0.49
12:H:5:LEU:HD23	12:H:36:ALA:HB2	1.94	0.49
31:a:607:U:N3	31:a:608:C:C5	2.81	0.49
32:b:7:SER:O	32:b:8:MET:CB	2.59	0.49
32:b:118:ASP:O	32:b:122:GLN:OE1	2.31	0.49
5:A:1715:G:C2	5:A:1738:U:O2	2.66	0.49
11:G:73:ASN:OD1	11:G:77:LYS:NZ	2.44	0.49
5:A:674:A:HO2'	5:A:2438:C:HO2'	1.59	0.49
18:N:75:ALA:O	18:N:79:GLU:OE1	2.31	0.49
31:a:754:U:H2'	31:a:755:G:O4'	2.12	0.49
5:A:939:G:O2'	5:A:1184:A:N3	2.44	0.49
31:a:1001:A:H2'	31:a:1002:A:O4'	2.13	0.49
47:q:6:VAL:HG23	47:q:6:VAL:O	2.13	0.49
5:A:2256:C:HO2'	5:A:2384:A:HO2'	1.57	0.49
5:A:2311:C:O2	10:F:125:ARG:NH2	2.44	0.49
40:j:85:ASP:OD1	40:j:85:ASP:C	2.55	0.49
5:A:844:A:H61	5:A:929:C:H1'	1.78	0.49
10:F:79:ILE:HG22	10:F:83:TRP:HE3	1.72	0.49
23:S:57:VAL:HG22	23:S:84:VAL:HG12	1.94	0.49
28:X:37:LEU:HD21	28:X:39:LYS:O	2.13	0.49
5:A:391:C:C2	5:A:392:C:C5	3.01	0.48
17:M:79:LEU:HD12	17:M:83:LEU:HD12	1.95	0.48
18:N:67:ILE:O	18:N:71:THR:HG23	2.13	0.48
32:b:7:SER:O	32:b:8:MET:HB2	2.13	0.48
34:d:107:MET:HE1	34:d:145:ILE:HB	1.94	0.48
41:k:45:THR:HG23	41:k:48:GLY:N	2.26	0.48
5:A:2818:G:O2'	5:A:2820:C:OP2	2.27	0.48
23:S:14:VAL:HG21	23:S:30:VAL:HG12	1.94	0.48
31:a:290:U:OP1	31:a:607:U:O2'	2.31	0.48
33:c:110:ASP:CG	33:c:144:ALA:HB2	2.38	0.48
39:i:3:THR:N	39:i:20:SER:HG	2.09	0.48
5:A:568:G:O4'	5:A:980:A:N6	2.47	0.48
8:D:13:THR:HG22	8:D:14:ARG:N	2.29	0.48
14:J:94:ILE:HG13	14:J:94:ILE:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:g:36:LYS:O	37:g:40:GLU:HG3	2.14	0.48
10:F:162:THR:OG1	10:F:163:ASP:N	2.45	0.48
31:a:1156:U:O4'	31:a:1179:G:N2	2.46	0.48
32:b:22:THR:O	32:b:24:PHE:N	2.46	0.48
52:v:41:VAL:HG12	52:v:60:ILE:HG12	1.95	0.48
5:A:799:G:HO2'	5:A:800:A:P	2.26	0.48
18:N:40:VAL:O	18:N:49:LEU:N	2.46	0.48
18:N:66:ASN:OD1	18:N:69:ALA:N	2.36	0.48
21:Q:51:ALA:HB3	21:Q:52:PRO:CD	2.44	0.48
31:a:85:G:HO2'	31:a:86:C:P	2.24	0.48
31:a:369:A:O2'	31:a:447:A:N7	2.46	0.48
31:a:577:C:H2'	31:a:578:G:O4'	2.13	0.48
31:a:1423:G:H2'	31:a:1424:C:O4'	2.14	0.48
41:k:36:ARG:O	41:k:37:GLN:HB2	2.13	0.48
5:A:752:C:O2'	5:A:1267:A:N1	2.41	0.48
9:E:130:THR:HG23	9:E:163:LEU:HD11	1.96	0.48
32:b:158:GLY:O	32:b:159:LEU:C	2.57	0.48
42:l:87:VAL:HG12	42:l:89:ASP:OD1	2.13	0.48
47:q:71:THR:O	47:q:71:THR:HG22	2.14	0.48
5:A:91:A:H1'	5:A:92:G:OP2	2.14	0.48
5:A:849:C:O2'	29:Y:42:SER:O	2.32	0.48
5:A:2480:G:O2'	16:L:124:LYS:O	2.29	0.48
54:A:3202:YQM:O27	54:A:3202:YQM:O18	2.30	0.48
6:B:55:A:C4	6:B:56:A:C8	3.02	0.48
31:a:6:C:O2'	31:a:8:G:OP1	2.32	0.48
48:r:33:ILE:HD11	48:r:59:ILE:HD13	1.94	0.48
5:A:162:A:O2'	5:A:163:C:OP1	2.24	0.48
16:L:49:ALA:O	16:L:53:THR:HG22	2.12	0.48
26:V:17:ASN:O	26:V:19:LYS:NZ	2.47	0.48
32:b:17:HIS:O	32:b:42:ILE:HD12	2.13	0.48
49:s:20:GLU:HA	49:s:23:VAL:HG12	1.95	0.48
5:A:498:U:H2'	5:A:499:G:O4'	2.14	0.47
5:A:1672:G:O2'	5:A:1674:A:N6	2.43	0.47
21:Q:20:LEU:CD1	21:Q:22:VAL:HG13	2.44	0.47
22:R:1:MET:HE2	22:R:1:MET:HA	1.96	0.47
28:X:49:THR:O	28:X:53:ILE:HG13	2.14	0.47
31:a:169:U:H6	31:a:194:G:HO2'	1.60	0.47
31:a:1347:A:O2'	37:g:33:ASP:OD1	2.22	0.47
43:m:72:GLU:OE2	43:m:76:ASN:ND2	2.42	0.47
10:F:120:LYS:O	10:F:120:LYS:HG3	2.14	0.47
31:a:1001:A:C6	31:a:1023:G:H1'	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:572:G:H2'	31:a:818:G:OP2	2.15	0.47
31:a:943:A:H2'	31:a:944:G:C8	2.49	0.47
31:a:1397:C:O3'	52:v:89:LYS:NZ	2.47	0.47
13:I:60:GLU:OE1	13:I:60:GLU:N	2.38	0.47
31:a:906:A:N3	31:a:1410:A:O2'	2.44	0.47
32:b:106:TRP:CG	32:b:110:ARG:HH22	2.33	0.47
32:b:110:ARG:HA	32:b:113:ILE:HB	1.94	0.47
34:d:32:THR:HG23	34:d:33:LYS:N	2.29	0.47
5:A:1344:C:C2	5:A:1345:C:C5	3.02	0.47
5:A:1835:G:C2	5:A:1836:G:C8	3.02	0.47
7:C:148:ILE:H	7:C:148:ILE:HD12	1.80	0.47
5:A:1854:A:N6	5:A:1880:G:O2'	2.48	0.47
5:A:2316:A:N6	5:A:2329:A:H61	2.13	0.47
10:F:11:GLU:HG3	10:F:12:LEU:HD12	1.96	0.47
11:G:26:VAL:HG23	11:G:79:VAL:HG21	1.97	0.47
24:T:87:ASP:OD2	24:T:88:GLY:N	2.47	0.47
25:U:59:VAL:HG23	25:U:63:GLU:OE1	2.14	0.47
31:a:1050:G:H4'	31:a:1051:C:H3'	1.97	0.47
32:b:53:ASN:OD1	32:b:54:ASP:N	2.47	0.47
43:m:108:THR:HG22	43:m:108:THR:O	2.15	0.47
5:A:252:G:O2'	5:A:383:A:N1	2.41	0.47
5:A:477:A:N6	5:A:499:G:O2'	2.46	0.47
5:A:1477:U:C2	5:A:1503:C:C2	3.03	0.47
32:b:149:SER:C	32:b:150:LEU:HD22	2.40	0.47
31:a:1320:G:H2'	31:a:1321:A:C8	2.50	0.47
37:g:69:VAL:HG12	37:g:69:VAL:O	2.15	0.47
50:t:47:ALA:HB1	50:t:83:VAL:HG22	1.96	0.47
5:A:799:G:C2'	5:A:800:A:OP1	2.62	0.46
5:A:2683:U:H2'	5:A:2684:G:O4'	2.15	0.46
16:L:83:MET:HA	16:L:83:MET:HE2	1.97	0.46
31:a:472:A:H2'	31:a:473:U:O4'	2.15	0.46
5:A:552:U:H2'	5:A:553:G:O4'	2.15	0.46
31:a:1051:C:H1'	31:a:1052:A:OP2	2.15	0.46
40:j:15:HIS:HA	40:j:18:ILE:HG22	1.98	0.46
10:F:91:LEU:HD12	10:F:95:GLN:CG	2.45	0.46
31:a:200:G:O2'	31:a:201:A:O5'	2.32	0.46
5:A:303:C:H5''	5:A:336:U:H2'	1.97	0.46
5:A:1044:G:C2'	5:A:1108:A:H61	2.27	0.46
5:A:1358:C:O2'	5:A:1805:A:N3	2.43	0.46
7:C:170:SER:C	7:C:186:VAL:HG13	2.40	0.46
20:P:91:ASP:C	20:P:91:ASP:OD1	2.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1203:G:O2'	31:a:1204:2MG:H5'	2.16	0.46
33:c:24:ALA:HB1	33:c:28:GLN:HG3	1.98	0.46
36:f:40:GLU:O	36:f:60:ILE:HD12	2.15	0.46
40:j:83:THR:O	40:j:87:LEU:HD13	2.16	0.46
5:A:2371:G:N1	5:A:2374:A:OP2	2.44	0.46
16:L:44:ALA:HA	16:L:47:ILE:HD12	1.96	0.46
31:a:776:C:H2'	31:a:777:A:O4'	2.15	0.46
33:c:107:ASP:OD2	33:c:108:ARG:NE	2.47	0.46
5:A:1294:G:HO2'	5:A:1296:A:N6	2.14	0.46
5:A:1494:C:C2	5:A:1495:G:C8	3.04	0.46
31:a:1203:G:H2'	31:a:1204:2MG:H5'	1.98	0.46
31:a:1524:C:OP2	51:u:42:THR:HG22	2.16	0.46
34:d:103:VAL:HG12	34:d:107:MET:HE3	1.98	0.46
39:i:3:THR:N	39:i:20:SER:OG	2.49	0.46
5:A:31:G:O2'	22:R:78:GLU:O	2.34	0.46
5:A:1122:G:OP2	5:A:1123:A:O2'	2.18	0.46
5:A:1240:G:OP1	15:K:15:LYS:NZ	2.31	0.46
6:B:38:U:O2'	6:B:41:C:OP2	2.19	0.46
10:F:5:LYS:HD2	10:F:97:TYR:HB3	1.98	0.46
18:N:12:ALA:HB3	18:N:16:ARG:HH12	1.81	0.46
31:a:508:C:O2'	31:a:509:U:OP2	2.25	0.46
45:o:25:PRO:O	45:o:29:VAL:HG12	2.16	0.46
5:A:1199:A:O4'	5:A:1201:G:C8	2.69	0.46
31:a:83:U:O2'	31:a:84:U:O2	2.27	0.46
9:E:154:GLU:O	9:E:158:LEU:HD23	2.15	0.46
31:a:155:G:H2'	31:a:156:A:H3'	1.98	0.46
31:a:155:G:O2'	31:a:157:A:N7	2.47	0.46
31:a:539:G:O3'	34:d:14:ARG:NH2	2.49	0.46
31:a:682:G:N2	31:a:703:A:N6	2.63	0.46
32:b:81:ILE:HD11	32:b:209:ILE:HG23	1.98	0.46
42:l:35:THR:HB	42:l:54:ARG:HE	1.80	0.46
7:C:199:GLU:N	7:C:199:GLU:OE2	2.48	0.46
10:F:164:ASP:OD1	10:F:165:GLU:OE1	2.33	0.46
16:L:27:VAL:HG13	16:L:105:GLU:OE1	2.15	0.46
32:b:16:ALA:O	32:b:43:ILE:HD11	2.16	0.46
33:c:30:ALA:O	33:c:34:LEU:HD23	2.15	0.46
5:A:234:A:C2	5:A:2403:A:H1'	2.51	0.45
5:A:843:G:O2'	5:A:845:A:N7	2.49	0.45
5:A:1207:G:O2'	5:A:1208:A:OP2	2.33	0.45
9:E:139:ASP:OD1	9:E:140:LEU:N	2.49	0.45
11:G:33:LEU:HD23	11:G:75:LEU:HG	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:R:33:LEU:HD11	22:R:52:GLU:OE2	2.16	0.45
25:U:23:ARG:O	25:U:27:GLU:OE1	2.34	0.45
31:a:457:A:C2	31:a:458:G:C8	3.04	0.45
32:b:83:ARG:O	32:b:87:GLN:HG2	2.16	0.45
5:A:973:G:O2'	5:A:1153:A:O2'	2.27	0.45
5:A:1360:A:O2'	27:W:11:ARG:NH2	2.49	0.45
5:A:2699:C:C2	5:A:2700:C:C5	3.04	0.45
8:D:152:ASN:O	8:D:153:GLN:C	2.59	0.45
32:b:8:MET:O	32:b:12:LEU:HD23	2.16	0.45
5:A:1026:A:O3'	16:L:128:LYS:NZ	2.50	0.45
10:F:34:ILE:CD1	10:F:156:ILE:HG22	2.46	0.45
10:F:143:PHE:HA	10:F:146:ILE:HD11	1.98	0.45
10:F:144:ASP:OD1	10:F:145:LYS:N	2.49	0.45
31:a:1515:MA6:O5'	31:a:1515:MA6:H8	2.16	0.45
32:b:209:ILE:HD12	32:b:209:ILE:H	1.81	0.45
43:m:9:ILE:HG21	43:m:22:ILE:HD11	1.99	0.45
47:q:66:ARG:O	47:q:68:ILE:HD12	2.17	0.45
5:A:1191:C:C2	5:A:1192:G:C8	3.04	0.45
12:H:31:ILE:HB	12:H:32:PRO:HD3	1.99	0.45
14:J:58:MET:HE2	14:J:86:ILE:CG2	2.46	0.45
16:L:78:PRO:O	16:L:79:LEU:HB2	2.16	0.45
17:M:114:GLU:OE1	30:Z:53:LEU:HD11	2.17	0.45
31:a:922:G:H1'	31:a:1499:A:C4	2.52	0.45
31:a:975:A:C2	31:a:1316:A:C4	3.04	0.45
5:A:77:G:O2'	5:A:120:G:O2'	2.30	0.45
7:C:117:GLN:OE1	7:C:122:ALA:HB2	2.16	0.45
7:C:161:SER:OG	7:C:194:GLU:HG2	2.16	0.45
10:F:167:ARG:O	10:F:171:ARG:NH1	2.50	0.45
10:F:167:ARG:HG3	10:F:171:ARG:HH12	1.82	0.45
20:P:86:ALA:O	20:P:87:GLN:HB2	2.17	0.45
31:a:810:U:OP2	31:a:810:U:H6	1.99	0.45
31:a:1122:U:O2	31:a:1122:U:H2'	2.15	0.45
52:v:79:ILE:H	52:v:79:ILE:HD12	1.82	0.45
5:A:533:U:O2'	20:P:49:ASP:OD2	2.35	0.45
5:A:573:A:C2	5:A:574:U:C5	3.04	0.45
37:g:72:MET:HE1	37:g:96:ARG:NH2	2.32	0.45
38:h:53:GLN:OE1	38:h:57:LYS:N	2.49	0.45
47:q:18:MET:HE3	47:q:21:SER:OG	2.15	0.45
1:O:42:HIS:ND1	5:A:2367:G:O2'	2.41	0.45
8:D:127:ARG:HG3	8:D:168:LEU:HD13	1.99	0.45
10:F:92:ARG:HA	10:F:96:MET:CE	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:G:43:LEU:HD11	11:G:50:LEU:CD2	2.47	0.45
20:P:98:ILE:CD1	21:Q:40:MET:HE1	2.46	0.45
21:Q:43:ASN:O	21:Q:45:ASP:N	2.47	0.45
36:f:85:ILE:O	36:f:86:ARG:CB	2.64	0.45
41:k:34:THR:HG22	41:k:40:ALA:HA	1.99	0.45
5:A:805:U:OP2	15:K:43:ARG:NH2	2.45	0.45
5:A:818:A:H4'	5:A:834:G:H22	1.82	0.45
8:D:33:ASN:ND2	8:D:53:THR:OG1	2.49	0.45
10:F:98:GLU:HB3	10:F:102:ARG:HH21	1.81	0.45
24:T:56:ILE:O	24:T:56:ILE:HG13	2.17	0.45
31:a:1113:U:O2'	39:i:108:GLU:OE1	2.27	0.45
35:e:105:ILE:HD12	35:e:123:LEU:HD21	1.99	0.45
39:i:32:THR:HG22	39:i:33:LEU:N	2.32	0.45
39:i:110:GLU:OE2	39:i:113:LYS:NZ	2.33	0.45
7:C:66:ASP:OD2	7:C:102:ARG:NH1	2.49	0.45
31:a:83:U:OP2	31:a:84:U:N3	2.40	0.45
33:c:172:ARG:NH2	33:c:206:GLU:OE2	2.48	0.45
38:h:113:THR:HG22	38:h:114:ASP:N	2.32	0.45
5:A:365:U:H1'	5:A:366:G:OP2	2.17	0.45
5:A:1556:A:H4'	5:A:1557:U:H3'	1.98	0.45
9:E:139:ASP:OD1	9:E:139:ASP:C	2.60	0.45
10:F:123:ASP:OD1	10:F:124:GLY:N	2.50	0.45
21:Q:51:ALA:CB	21:Q:52:PRO:HD3	2.46	0.45
31:a:85:G:C2'	31:a:86:C:OP2	2.65	0.45
31:a:682:G:H2'	31:a:683:U:C6	2.52	0.45
32:b:106:TRP:O	32:b:110:ARG:CZ	2.64	0.45
34:d:32:THR:HG21	34:d:35:ALA:HB2	1.99	0.45
5:A:673:A:N3	5:A:2439:U:O2'	2.49	0.44
6:B:59:C:C2	6:B:60:U:C5	3.05	0.44
10:F:4:LEU:N	10:F:7:ARG:HB2	2.32	0.44
29:Y:46:MET:O	29:Y:50:VAL:HG22	2.17	0.44
30:Z:11:SER:O	30:Z:15:MET:HG3	2.17	0.44
32:b:173:ILE:HD12	32:b:173:ILE:H	1.82	0.44
44:n:33:ASN:ND2	44:n:35:ASN:OD1	2.50	0.44
52:v:60:ILE:CB	52:v:90:LEU:HD11	2.48	0.44
31:a:143:G:H2'	31:a:144:G:C8	2.52	0.44
31:a:680:G:C6	31:a:681:U:C4	3.06	0.44
31:a:1023:G:C2	31:a:1024:C:C6	3.05	0.44
31:a:1448:C:O2	31:a:1448:C:O4'	2.35	0.44
36:f:88:LEU:CD2	48:r:65:LEU:HD11	2.48	0.44
47:q:31:GLN:OE1	47:q:37:LYS:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:605:U:O2	5:A:606:A:C8	2.70	0.44
5:A:2289:C:C2	5:A:2290:G:C8	3.06	0.44
31:a:1070:U:H2'	31:a:1071:G:O4'	2.17	0.44
5:A:984:C:O2'	5:A:997:A:N3	2.44	0.44
9:E:187:MET:HE3	9:E:192:ALA:HB2	1.99	0.44
10:F:108:ILE:O	10:F:111:ILE:HG22	2.17	0.44
11:G:107:LEU:HD11	11:G:152:ARG:HB3	1.99	0.44
15:K:87:VAL:O	15:K:120:ARG:NH2	2.49	0.44
18:N:41:ILE:HG12	18:N:48:VAL:HG22	1.99	0.44
31:a:405:U:H2'	31:a:406:G:O4'	2.18	0.44
31:a:720:U:C4'	31:a:721:G:OP2	2.65	0.44
31:a:963:2MG:O2'	31:a:964:5MC:H5'	2.18	0.44
31:a:1123:U:O3'	31:a:1124:G:H8	2.00	0.44
33:c:142:MET:HE2	33:c:170:GLU:OE1	2.17	0.44
36:f:88:LEU:HD22	48:r:65:LEU:HD11	1.99	0.44
5:A:634:G:N7	15:K:111:ARG:NH2	2.58	0.44
5:A:1172:U:OP2	5:A:1173:G:N2	2.46	0.44
31:a:922:G:C6	31:a:924:G:N7	2.86	0.44
35:e:110:MET:SD	35:e:124:ALA:HB1	2.58	0.44
37:g:95:ARG:O	37:g:99:LEU:HG	2.17	0.44
5:A:1793:C:OP1	7:C:273:VAL:HG22	2.18	0.44
5:A:1933:A:O2'	5:A:1934:A:O5'	2.25	0.44
5:A:2302:C:H3'	5:A:2303:G:H5''	1.98	0.44
7:C:117:GLN:OE1	7:C:118:SER:N	2.51	0.44
9:E:162:ASN:O	9:E:162:ASN:OD1	2.35	0.44
25:U:38:ASN:C	25:U:38:ASN:OD1	2.60	0.44
30:Z:3:VAL:HG22	30:Z:4:GLN:N	2.33	0.44
31:a:185:C:H1'	31:a:186:G:OP2	2.18	0.44
31:a:1433:U:C2	31:a:1434:A:C8	3.06	0.44
35:e:59:ILE:O	35:e:63:LEU:HD23	2.18	0.44
3:2:32:LEU:HD13	5:A:2415:U:OP2	2.17	0.44
5:A:92:G:H2'	5:A:93:G:O4'	2.18	0.44
54:A:3201:YQM:O30	54:A:3201:YQM:O33	2.35	0.44
7:C:146:LEU:HD21	7:C:182:ARG:NH1	2.32	0.44
7:C:175:ARG:HG2	7:C:181:MET:HG2	2.00	0.44
9:E:141:ASN:O	9:E:184:LYS:NZ	2.46	0.44
10:F:80:ARG:HD3	10:F:83:TRP:CD1	2.53	0.44
16:L:128:LYS:HE2	16:L:128:LYS:HA	2.00	0.44
31:a:698:U:O2	31:a:700:G:N1	2.51	0.44
39:i:44:MET:O	39:i:48:GLN:HG3	2.18	0.44
5:A:1044:G:O2'	5:A:1108:A:N6	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:N:30:ASN:OD1	18:N:31:ARG:N	2.51	0.44
39:i:47:ARG:O	39:i:51:GLU:OE1	2.36	0.44
5:A:507:U:C4'	5:A:508:C:OP2	2.66	0.44
24:T:34:VAL:CG1	24:T:37:LEU:HD12	2.46	0.44
5:A:1125:G:O4'	5:A:2512:U:O2'	2.36	0.43
10:F:93:GLY:O	10:F:96:MET:HG2	2.18	0.43
12:H:7:GLN:O	12:H:9:ILE:HD12	2.17	0.43
31:a:180:U:C2	31:a:181:C:C5	3.06	0.43
31:a:185:C:H4'	31:a:186:G:O5'	2.18	0.43
35:e:35:LEU:HD13	35:e:49:ARG:HG2	2.00	0.43
5:A:271:C:O2	5:A:271:C:O4'	2.36	0.43
5:A:301:A:N3	5:A:321:C:O2'	2.43	0.43
5:A:2830:G:H2'	5:A:2875:A:H61	1.82	0.43
6:B:7:G:C2	6:B:8:A:C8	3.07	0.43
21:Q:15:VAL:HG12	21:Q:16:GLU:N	2.32	0.43
32:b:163:LEU:HD22	32:b:185:VAL:HG23	1.99	0.43
35:e:12:GLU:HB2	35:e:63:LEU:HD11	1.99	0.43
4:3:9:LYS:CE	4:3:16:VAL:HG23	2.44	0.43
5:A:112:C:C2	5:A:113:C:C5	3.07	0.43
5:A:1341:G:H2'	5:A:1342:A:O4'	2.18	0.43
9:E:123:PHE:CD2	9:E:156:LEU:HD11	2.54	0.43
30:Z:43:THR:HG22	30:Z:44:LYS:N	2.33	0.43
31:a:458:G:C5	31:a:459:U:C4	3.06	0.43
31:a:736:C:O2'	45:o:42:HIS:ND1	2.44	0.43
31:a:743:A:H2'	31:a:744:A:C8	2.53	0.43
31:a:1123:U:O2	31:a:1277:A:H2'	2.18	0.43
39:i:124:GLN:NE2	39:i:126:SER:OG	2.51	0.43
41:k:93:GLU:OE1	41:k:93:GLU:N	2.49	0.43
1:0:5:ILE:HD13	1:0:21:LYS:HD2	1.99	0.43
5:A:199:G:N2	5:A:199:G:OP2	2.52	0.43
5:A:499:G:N1	5:A:502:A:OP2	2.44	0.43
5:A:621:C:C2	5:A:622:C:C5	3.06	0.43
5:A:715:C:O2	5:A:715:C:O4'	2.34	0.43
5:A:2360:C:H2'	5:A:2361:G:O4'	2.18	0.43
5:A:2679:C:O2	14:J:70:ARG:NH2	2.50	0.43
6:B:55:A:C1'	10:F:26:MET:HE1	2.48	0.43
33:c:87:LEU:O	33:c:91:LEU:HG	2.18	0.43
39:i:25:LYS:N	39:i:60:ASP:OD1	2.49	0.43
40:j:6:ILE:HB	40:j:76:ILE:CG1	2.48	0.43
5:A:321:C:H2'	5:A:322:G:O4'	2.18	0.43
5:A:1261:G:O2'	5:A:1262:U:OP2	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:2256:C:O2'	5:A:2384:A:O2'	2.29	0.43
5:A:2324:A:H2'	5:A:2325:A:C8	2.53	0.43
5:A:2470:U:O2	5:A:2470:U:H2'	2.18	0.43
10:F:32:THR:N	10:F:157:THR:O	2.52	0.43
21:Q:1:MET:SD	21:Q:43:ASN:HB2	2.59	0.43
31:a:748:U:H2'	31:a:749:G:O4'	2.18	0.43
32:b:143:MET:O	32:b:147:GLU:OE1	2.37	0.43
39:i:19:LEU:HD11	39:i:59:TYR:HB3	1.99	0.43
5:A:1879:U:H2'	5:A:1880:G:O4'	2.19	0.43
5:A:1971:A:H2'	5:A:1972:U:O4'	2.18	0.43
5:A:2327:G:O2'	26:V:43:THR:HG22	2.18	0.43
10:F:13:LYS:HG3	10:F:28:ILE:HD13	2.01	0.43
31:a:515:C:O2	31:a:515:C:O4'	2.37	0.43
31:a:1510:A:H2'	31:a:1511:G:H8	1.83	0.43
34:d:57:LEU:O	34:d:61:GLN:HG2	2.18	0.43
37:g:107:ALA:O	37:g:111:ARG:HG3	2.18	0.43
5:A:309:G:N1	5:A:312:A:OP2	2.46	0.43
5:A:667:G:N3	5:A:667:G:H2'	2.32	0.43
5:A:1343:C:C5	5:A:1344:C:C5	3.07	0.43
11:G:71:VAL:O	11:G:75:LEU:HD13	2.19	0.43
17:M:49:GLU:CG	17:M:95:LEU:HD13	2.47	0.43
31:a:523:C:OP2	42:l:88:LYS:NZ	2.42	0.43
31:a:1085:G:H21	31:a:1164:A:H61	1.66	0.43
33:c:124:LEU:HD21	33:c:196:ILE:HG21	2.01	0.43
41:k:28:ASN:OD1	41:k:29:THR:N	2.50	0.43
47:q:29:ARG:NH2	47:q:38:SER:OG	2.52	0.43
5:A:509:C:N3	5:A:510:U:C5	2.87	0.43
5:A:1193:U:C2	5:A:1194:U:C5	3.06	0.43
5:A:1438:C:C2	5:A:1439:A:C8	3.07	0.43
5:A:2420:C:O2	5:A:2425:G:O2'	2.34	0.43
7:C:88:THR:O	7:C:197:ASN:ND2	2.47	0.43
7:C:165:LEU:HD21	7:C:175:ARG:NE	2.32	0.43
10:F:89:VAL:HG12	10:F:91:LEU:HD22	2.00	0.43
10:F:93:GLY:H	10:F:96:MET:HE3	1.84	0.43
10:F:99:PHE:O	10:F:102:ARG:HG2	2.18	0.43
14:J:47:ILE:HG13	14:J:50:ALA:HB2	1.99	0.43
23:S:32:LYS:CE	23:S:79:VAL:HG21	2.48	0.43
31:a:103:G:N7	50:t:10:ARG:NH2	2.61	0.43
31:a:754:U:OP1	31:a:819:U:O2'	2.34	0.43
32:b:123:SER:HB3	32:b:143:MET:HE1	2.01	0.43
44:n:73:TYR:CE1	44:n:75:ARG:HA	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:o:3:LEU:HD11	45:o:34:ALA:HB1	2.00	0.43
5:A:862:G:H2'	5:A:863:C:C6	2.54	0.43
10:F:108:ILE:HD12	10:F:108:ILE:H	1.83	0.43
16:L:48:GLU:OE1	16:L:51:ARG:NH2	2.52	0.43
36:f:7:VAL:HG11	48:r:65:LEU:CD2	2.48	0.43
40:j:82:LYS:O	40:j:85:ASP:OD1	2.36	0.43
5:A:758:G:H2'	5:A:759:A:O4'	2.18	0.43
6:B:30:U:C2	6:B:49:G:N2	2.87	0.43
21:Q:1:MET:HE3	21:Q:101:ILE:HG13	2.00	0.43
31:a:239:A:H4'	31:a:240:U:H3'	2.01	0.43
31:a:963:2MG:C4	52:v:59:MET:HE1	2.54	0.43
32:b:36:ALA:HB2	32:b:41:HIS:ND1	2.34	0.43
36:f:8:LEU:HB2	36:f:60:ILE:CG2	2.49	0.43
36:f:26:ILE:HG23	36:f:36:ILE:HG13	2.00	0.43
5:A:1852:U:H2'	5:A:1853:G:C1'	2.48	0.42
5:A:2026:6MZ:O2'	5:A:2027:A:P	2.76	0.42
5:A:2794:U:O2	5:A:2795:A:N6	2.52	0.42
9:E:112:VAL:HG22	9:E:117:LEU:HD23	2.01	0.42
35:e:130:THR:O	35:e:130:THR:HG22	2.19	0.42
5:A:963:G:C1'	5:A:2263:A:H62	2.31	0.42
5:A:1317:A:C5	5:A:1318:C:C5	3.07	0.42
10:F:46:ASP:O	10:F:47:LYS:HB2	2.19	0.42
11:G:26:VAL:CG2	11:G:79:VAL:HG21	2.49	0.42
18:N:27:LEU:HB2	18:N:89:VAL:HG21	2.00	0.42
31:a:471:G:H2'	31:a:472:A:C8	2.54	0.42
31:a:711:G:H2'	31:a:712:A:C8	2.54	0.42
31:a:1364:C:H5''	39:i:114:LEU:HD12	2.01	0.42
32:b:72:VAL:O	32:b:72:VAL:HG13	2.18	0.42
32:b:188:ILE:HD13	32:b:202:ILE:HD11	1.99	0.42
32:b:189:VAL:O	32:b:189:VAL:HG23	2.19	0.42
34:d:69:VAL:HG12	34:d:70:LEU:N	2.33	0.42
34:d:205:LEU:C	34:d:205:LEU:HD23	2.45	0.42
36:f:9:LEU:O	36:f:85:ILE:N	2.50	0.42
4:3:18:ARG:HE	4:3:21:GLY:HA2	1.84	0.42
5:A:111:U:C5	5:A:112:C:C5	3.07	0.42
5:A:599:C:O2'	5:A:603:G:OP1	2.35	0.42
31:a:536:A:H2'	31:a:537:G:C8	2.54	0.42
31:a:1127:A:C2	31:a:1128:G:C8	3.07	0.42
33:c:17:ARG:NH1	33:c:18:HIS:HB2	2.34	0.42
52:v:25:LEU:HD21	52:v:39:PHE:CD2	2.54	0.42
5:A:368:C:O2	5:A:368:C:O4'	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:F:144:ASP:O	10:F:145:LYS:HB2	2.19	0.42
13:I:73:LYS:HD2	13:I:86:GLU:OE2	2.20	0.42
14:J:17:ARG:NH1	14:J:47:ILE:HG22	2.35	0.42
18:N:29:VAL:HG21	18:N:102:ILE:HG23	2.02	0.42
5:A:981:A:N3	5:A:981:A:H2'	2.34	0.42
5:A:2456:U:C2	5:A:2457:A:C8	3.08	0.42
12:H:30:LEU:HB3	12:H:36:ALA:HB3	2.01	0.42
29:Y:8:GLN:HB2	29:Y:28:LEU:HD23	2.02	0.42
31:a:932:A:O2'	31:a:1380:C:O2	2.34	0.42
31:a:973:G:OP2	31:a:1355:U:O2'	2.38	0.42
32:b:96:HIS:ND1	32:b:148:ARG:CZ	2.83	0.42
37:g:108:ALA:O	37:g:119:ARG:HD2	2.20	0.42
40:j:21:SER:O	40:j:25:ILE:HG12	2.19	0.42
43:m:66:GLU:O	43:m:70:ARG:HG3	2.19	0.42
5:A:579:C:H2'	5:A:580:A:H8	1.82	0.42
6:B:84:A:C2	6:B:88:C:N3	2.88	0.42
31:a:319:U:H2'	31:a:320:G:O4'	2.20	0.42
31:a:823:C:O2	38:h:16:ASN:ND2	2.53	0.42
32:b:29:MET:O	32:b:30:ARG:C	2.62	0.42
37:g:71:PRO:HB2	37:g:74:GLU:OE2	2.19	0.42
5:A:1126:A:O2'	5:A:2511:C:O2'	2.34	0.42
5:A:1355:G:N7	5:A:1356:G:C8	2.87	0.42
5:A:1365:C:H2'	5:A:1366:G:O4'	2.19	0.42
5:A:1953:C:C2	5:A:1954:C:C5	3.08	0.42
5:A:2287:U:H2'	5:A:2288:G:C8	2.54	0.42
7:C:22:ASP:OD1	7:C:23:HIS:N	2.52	0.42
18:N:28:CYS:HA	18:N:92:ASP:HB3	2.01	0.42
18:N:93:ARG:NE	18:N:96:PHE:O	2.53	0.42
27:W:64:ILE:O	27:W:68:VAL:HG23	2.19	0.42
31:a:924:G:H2'	31:a:925:G:O4'	2.20	0.42
31:a:979:U:H4'	31:a:980:A:O4'	2.19	0.42
32:b:51:ALA:HB3	32:b:202:ILE:HG22	2.01	0.42
32:b:131:LEU:CB	32:b:135:GLU:OE1	2.68	0.42
5:A:746:G:O2'	5:A:748:A:OP2	2.24	0.42
5:A:831:A:H2'	5:A:832:G:C8	2.55	0.42
5:A:2307:A:O2'	10:F:85:ILE:HD12	2.20	0.42
5:A:2317:G:H3'	5:A:2317:G:N3	2.34	0.42
21:Q:42:VAL:HG22	21:Q:47:ILE:HG23	2.02	0.42
31:a:367:A:H2'	31:a:368:C:O4'	2.19	0.42
31:a:710:G:H2'	31:a:711:G:C8	2.55	0.42
33:c:36:ASP:O	33:c:39:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:o:26:GLU:HG3	45:o:81:LEU:HD22	2.02	0.42
1:0:6:ARG:O	1:0:48:ALA:N	2.52	0.42
5:A:1910:C:O2	5:A:1910:C:H2'	2.19	0.42
5:A:2282:G:H4'	5:A:2283:A:O4'	2.19	0.42
6:B:42:G:H1'	6:B:45:C:N4	2.34	0.42
15:K:112:ILE:HB	15:K:129:LEU:HD23	2.01	0.42
31:a:809:G:C1'	31:a:810:U:OP2	2.68	0.42
32:b:49:VAL:CG2	32:b:50:PRO:HD3	2.50	0.42
2:1:29:GLN:NE2	5:A:217:C:OP1	2.53	0.42
5:A:324:A:H1'	5:A:325:G:OP1	2.20	0.42
5:A:475:G:N1	5:A:478:A:OP2	2.52	0.42
5:A:1952:U:O2	5:A:1952:U:H2'	2.20	0.42
6:B:23:A:N3	6:B:23:A:H2'	2.35	0.42
12:H:5:LEU:HD13	12:H:9:ILE:CD1	2.42	0.42
29:Y:1:MET:O	29:Y:2:LYS:HB3	2.19	0.42
31:a:681:U:H2'	31:a:682:G:O5'	2.18	0.42
31:a:1097:C:P	32:b:97:ARG:NH1	2.93	0.42
31:a:1510:A:H2'	31:a:1511:G:C8	2.54	0.42
5:A:479:A:O4'	24:T:40:VAL:HG21	2.20	0.41
5:A:1954:C:C2	5:A:1955:G:C8	3.07	0.41
6:B:41:C:O2'	10:F:92:ARG:HD2	2.20	0.41
8:D:85:VAL:CG1	8:D:89:GLU:HB2	2.49	0.41
16:L:79:LEU:O	16:L:81:VAL:HG23	2.20	0.41
34:d:9:CYS:HA	34:d:12:SER:OG	2.19	0.41
34:d:97:GLU:OE1	34:d:106:ARG:NH2	2.52	0.41
35:e:55:VAL:CG2	35:e:56:PRO:HD3	2.49	0.41
38:h:36:ILE:O	38:h:40:LEU:HD13	2.20	0.41
5:A:392:C:C2	5:A:393:U:C5	3.08	0.41
5:A:591:U:H2'	5:A:592:U:C6	2.55	0.41
5:A:2323:A:H2'	5:A:2324:A:C8	2.55	0.41
5:A:2700:C:H2'	5:A:2701:A:O4'	2.21	0.41
14:J:4:THR:O	14:J:5:GLU:HB2	2.20	0.41
15:K:87:VAL:HG13	15:K:96:THR:HG22	2.03	0.41
31:a:19:U:H2'	31:a:20:C:C6	2.55	0.41
31:a:179:G:C5	31:a:180:U:C6	3.08	0.41
32:b:21:GLN:OE1	32:b:23:ARG:HG2	2.20	0.41
34:d:29:ASP:O	34:d:33:LYS:N	2.52	0.41
52:v:29:PHE:HE1	52:v:94:LEU:HD12	1.84	0.41
5:A:325:G:H2'	9:E:162:ASN:OD1	2.20	0.41
5:A:2685:U:H4'	5:A:2686:A:OP2	2.19	0.41
10:F:35:THR:CG2	10:F:155:THR:HB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:22:U:H2'	31:a:23:G:O4'	2.19	0.41
31:a:1031:G:C2	31:a:1032:A:C8	3.08	0.41
40:j:27:GLU:O	40:j:31:ARG:HG2	2.20	0.41
41:k:110:THR:HG22	51:u:3:GLN:HA	2.00	0.41
47:q:23:VAL:HG13	47:q:23:VAL:O	2.20	0.41
52:v:28:GLU:HG2	52:v:87:ILE:CG2	2.51	0.41
5:A:368:C:C4'	5:A:369:G:OP2	2.67	0.41
5:A:2300:G:H22	5:A:2308:U:H3	1.68	0.41
5:A:2372:A:H2'	5:A:2373:A:O4'	2.20	0.41
6:B:31:G:C6	6:B:48:A:N1	2.88	0.41
6:B:46:U:OP2	18:N:31:ARG:NH2	2.53	0.41
7:C:38:LYS:HD2	7:C:39:ARG:O	2.21	0.41
10:F:37:ASN:OD1	10:F:38:MET:N	2.53	0.41
10:F:106:ILE:HG13	10:F:110:ARG:HH21	1.85	0.41
25:U:29:LEU:HB3	25:U:45:THR:CG2	2.51	0.41
31:a:1154:A:C2	31:a:1178:G:C4	3.08	0.41
31:a:1409:C:H2'	31:a:1410:A:C8	2.54	0.41
5:A:903:A:H3'	5:A:904:U:H5''	2.02	0.41
5:A:1416:G:H1'	5:A:1489:A:H61	1.85	0.41
5:A:1822:G:H5''	7:C:223:MET:HE2	2.02	0.41
5:A:2294:A:H5''	10:F:71:ARG:NH2	2.35	0.41
10:F:50:LEU:HD12	10:F:51:ASP:N	2.36	0.41
10:F:51:ASP:O	10:F:54:VAL:HG12	2.19	0.41
20:P:15:LYS:HE2	20:P:15:LYS:HB3	1.94	0.41
21:Q:52:PRO:C	21:Q:53:VAL:HG23	2.46	0.41
31:a:493:A:N3	31:a:493:A:H2'	2.35	0.41
45:o:36:ILE:O	45:o:40:GLN:HG2	2.21	0.41
5:A:427:A:C2'	5:A:428:A:O5'	2.68	0.41
5:A:1151:C:H2'	5:A:1152:G:O4'	2.19	0.41
5:A:1192:G:C2	5:A:1193:U:C5	3.09	0.41
5:A:2262:A:H4'	5:A:2263:A:N3	2.36	0.41
5:A:2490:G:C2	5:A:2491:G:C8	3.09	0.41
7:C:164:LEU:HA	7:C:174:ILE:HD13	2.02	0.41
10:F:70:ALA:HB2	10:F:85:ILE:HD13	2.02	0.41
18:N:87:THR:HG23	18:N:88:LYS:N	2.36	0.41
22:R:51:LEU:O	22:R:55:ILE:HG12	2.21	0.41
31:a:358:G:N2	31:a:361:U:OP2	2.52	0.41
31:a:409:G:N7	34:d:33:LYS:NZ	2.62	0.41
31:a:1075:U:C2'	31:a:1076:G:O5'	2.68	0.41
32:b:79:SER:O	32:b:83:ARG:HG3	2.20	0.41
48:r:40:VAL:HG12	48:r:45:THR:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:434:C:O2	5:A:434:C:O4'	2.36	0.41
5:A:444:C:OP1	20:P:2:ALA:N	2.54	0.41
5:A:509:C:O2	5:A:509:C:H2'	2.20	0.41
5:A:780:A:C2	7:C:229:ASP:OD1	2.73	0.41
5:A:1493:C:O4'	5:A:1575:C:H4'	2.20	0.41
6:B:87:A:H2'	6:B:87:A:N3	2.35	0.41
7:C:93:LEU:C	7:C:94:LEU:HD22	2.45	0.41
8:D:26:THR:HG21	8:D:196:ILE:HG12	2.03	0.41
9:E:123:PHE:CE2	9:E:156:LEU:HD11	2.56	0.41
16:L:52:ARG:NH1	16:L:56:ARG:NH2	2.68	0.41
18:N:13:LYS:O	18:N:17:LEU:HD13	2.20	0.41
23:S:6:ILE:HG23	23:S:45:ALA:HA	2.02	0.41
31:a:747:C:C2	31:a:748:U:C5	3.09	0.41
31:a:1124:G:H5'	31:a:1277:A:O2'	2.20	0.41
34:d:33:LYS:HG2	34:d:33:LYS:O	2.20	0.41
37:g:138:ARG:O	37:g:141:VAL:HG12	2.20	0.41
52:v:3:ILE:HD13	52:v:39:PHE:HB2	2.02	0.41
5:A:211:A:O3'	5:A:212:G:H4'	2.21	0.41
5:A:622:C:C2	5:A:623:G:C8	3.09	0.41
5:A:741:U:O2'	5:A:1657:U:OP1	2.38	0.41
5:A:1664:G:H4'	14:J:6:THR:HG23	2.03	0.41
5:A:1828:C:H2'	5:A:1829:C:O4'	2.21	0.41
11:G:84:GLU:OE1	11:G:84:GLU:N	2.53	0.41
31:a:572:G:C2'	31:a:818:G:OP2	2.68	0.41
31:a:1444:A:C3'	31:a:1445:C:H5'	2.51	0.41
32:b:106:TRP:CZ2	32:b:159:LEU:HD22	2.55	0.41
42:l:79:VAL:HG12	42:l:103:ASP:OD2	2.21	0.41
5:A:712:U:H5'	5:A:713:A:OP2	2.21	0.41
5:A:1296:A:C4'	5:A:1297:A:OP1	2.68	0.41
5:A:1470:G:H1'	5:A:1728:C:H41	1.86	0.41
5:A:1787:A:N6	5:A:1824:G:O2'	2.52	0.41
5:A:1835:G:H1'	5:A:1923:A:C8	2.56	0.41
5:A:2294:A:OP1	10:F:71:ARG:NE	2.53	0.41
5:A:2316:A:H61	5:A:2329:A:H61	1.69	0.41
5:A:2534:C:C2	5:A:2535:C:C5	3.09	0.41
10:F:114:PHE:C	10:F:115:ARG:HD3	2.46	0.41
11:G:42:GLU:OE2	11:G:53:ALA:HB3	2.21	0.41
31:a:1115:U:H1'	31:a:1176:A:C5	2.56	0.41
31:a:1128:G:C6	31:a:1129:C:C5	3.08	0.41
31:a:1187:G:C4'	31:a:1188:A:OP2	2.68	0.41
38:h:48:ASN:N	38:h:63:THR:OG1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:k:55:ARG:HA	41:k:58:THR:HG23	2.02	0.41
45:o:4:THR:C	45:o:8:ARG:HE	2.28	0.41
45:o:12:ILE:HG22	45:o:27:VAL:HG13	2.03	0.41
46:p:75:PHE:O	46:p:79:VAL:HG23	2.20	0.41
52:v:3:ILE:HG22	52:v:5:ILE:HG23	2.02	0.41
52:v:83:ILE:O	52:v:87:ILE:HG13	2.20	0.41
5:A:1715:G:N1	5:A:1738:U:C2	2.89	0.41
5:A:1827:G:C6	5:A:1971:A:C2	3.09	0.41
5:A:1837:U:C2	5:A:1838:G:C8	3.09	0.41
5:A:2059:C:O2	5:A:2059:C:H2'	2.20	0.41
10:F:79:ILE:HA	10:F:83:TRP:CD2	2.55	0.41
10:F:80:ARG:HH11	10:F:83:TRP:CD1	2.38	0.41
11:G:98:VAL:O	11:G:98:VAL:HG13	2.21	0.41
31:a:105:A:H2'	31:a:105:A:N3	2.36	0.41
31:a:397:C:O2'	31:a:618:A:N3	2.48	0.41
31:a:425:U:H1'	31:a:426:A:OP2	2.20	0.41
31:a:506:A:N3	31:a:540:U:O2'	2.48	0.41
31:a:1157:G:C2	31:a:1158:C:C6	3.09	0.41
31:a:1179:G:C4'	31:a:1180:C:OP2	2.69	0.41
34:d:89:GLY:O	34:d:93:LEU:HD23	2.21	0.41
36:f:85:ILE:O	36:f:86:ARG:HB3	2.20	0.41
47:q:16:ASP:OD1	47:q:16:ASP:N	2.55	0.41
5:A:91:A:H4'	5:A:92:G:O5'	2.21	0.40
5:A:1352:C:H2'	5:A:1353:G:O4'	2.21	0.40
7:C:240:LYS:O	7:C:242:ILE:HG22	2.21	0.40
11:G:12:PRO:O	11:G:13:ASN:HB3	2.21	0.40
18:N:12:ALA:HB3	18:N:16:ARG:NH1	2.35	0.40
31:a:337:C:O2	31:a:337:C:H2'	2.22	0.40
31:a:1052:A:OP2	52:v:50:LYS:NZ	2.54	0.40
31:a:1060:C:OP2	31:a:1061:G:O2'	2.24	0.40
31:a:1388:U:H2'	31:a:1389:G:C8	2.56	0.40
33:c:141:THR:HG21	33:c:149:ILE:HD12	2.03	0.40
35:e:55:VAL:N	35:e:56:PRO:HD2	2.36	0.40
37:g:75:VAL:HG22	37:g:144:MET:HE1	2.02	0.40
5:A:1105:U:H5'	5:A:1107:G:O6	2.21	0.40
5:A:1733:U:O3'	5:A:1734:G:O4'	2.39	0.40
5:A:2048:A:H4'	8:D:151:GLN:O	2.22	0.40
5:A:2061:C:C2	5:A:2062:C:C5	3.10	0.40
10:F:110:ARG:HH11	10:F:110:ARG:HB2	1.85	0.40
14:J:71:ARG:HB3	14:J:72:PRO:HD2	2.03	0.40
31:a:195:C:C2	31:a:196:A:C8	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:386:U:H2'	31:a:387:C:C6	2.56	0.40
31:a:606:A:C5	31:a:607:U:C6	3.09	0.40
31:a:1148:A:O2'	31:a:1149:A:O5'	2.38	0.40
31:a:1340:G:H2'	31:a:1341:C:O4'	2.21	0.40
34:d:32:THR:O	34:d:33:LYS:HB3	2.22	0.40
41:k:33:ILE:CD1	41:k:69:ALA:HB1	2.50	0.40
4:3:8:LYS:HE3	5:A:1028:G:H5''	2.02	0.40
5:A:721:C:C2	5:A:722:U:C6	3.10	0.40
7:C:70:ASN:OD1	7:C:189:ARG:NH2	2.54	0.40
8:D:85:VAL:HG12	8:D:86:THR:N	2.36	0.40
21:Q:15:VAL:O	21:Q:98:ILE:HG21	2.21	0.40
21:Q:52:PRO:O	21:Q:53:VAL:HG23	2.20	0.40
31:a:789:A:C2'	31:a:790:U:OP2	2.68	0.40
31:a:914:G:H2'	31:a:915:A:C8	2.56	0.40
32:b:29:MET:HE1	32:b:190:ASP:O	2.21	0.40
33:c:130:PHE:O	33:c:134:MET:HG3	2.21	0.40
34:d:97:GLU:OE2	34:d:106:ARG:NE	2.54	0.40
39:i:32:THR:HG22	39:i:33:LEU:H	1.86	0.40
52:v:61:GLU:OE2	52:v:69:PRO:HB3	2.22	0.40
5:A:278:U:O2	5:A:278:U:H3'	2.21	0.40
5:A:378:G:N1	5:A:395:G:C6	2.90	0.40
5:A:390:A:C5	5:A:391:C:C5	3.10	0.40
5:A:744:U:O4'	5:A:746:G:N2	2.54	0.40
5:A:963:G:H1'	5:A:2263:A:H62	1.86	0.40
6:B:58:C:C4	6:B:59:C:C5	3.10	0.40
13:I:70:LEU:C	13:I:70:LEU:HD23	2.46	0.40
28:X:44:GLN:NE2	28:X:48:LYS:HE2	2.36	0.40
31:a:1051:C:O2'	31:a:1052:A:OP2	2.39	0.40
34:d:61:GLN:O	34:d:65:ARG:HD3	2.22	0.40
34:d:155:LEU:N	34:d:155:LEU:HD12	2.36	0.40
37:g:66:LEU:O	37:g:70:ARG:HG3	2.22	0.40
40:j:36:VAL:HG12	40:j:76:ILE:CG2	2.46	0.40
5:A:1517:G:P	5:A:1518:A:HO2'	2.31	0.40
5:A:2287:U:OP1	5:A:2376:U:O2'	2.36	0.40
11:G:43:LEU:CD1	11:G:50:LEU:HD21	2.51	0.40
16:L:35:LYS:NZ	25:U:85:PRO:O	2.52	0.40
31:a:918:U:O2'	35:e:23:VAL:O	2.30	0.40
37:g:74:GLU:O	37:g:89:MET:N	2.48	0.40
45:o:29:VAL:HG21	45:o:67:LEU:HD21	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	47/51 (92%)	46 (98%)	1 (2%)	0	100	100
2	1	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
3	2	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
4	3	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
7	C	270/274 (98%)	262 (97%)	8 (3%)	0	100	100
8	D	208/212 (98%)	199 (96%)	9 (4%)	0	100	100
9	E	198/200 (99%)	197 (100%)	1 (0%)	0	100	100
10	F	172/178 (97%)	155 (90%)	16 (9%)	1 (1%)	21	50
11	G	172/177 (97%)	166 (96%)	4 (2%)	2 (1%)	10	32
12	H	58/148 (39%)	57 (98%)	1 (2%)	0	100	100
13	I	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
14	J	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
15	K	142/146 (97%)	138 (97%)	4 (3%)	0	100	100
16	L	135/137 (98%)	131 (97%)	3 (2%)	1 (1%)	18	46
17	M	117/125 (94%)	117 (100%)	0	0	100	100
18	N	112/116 (97%)	112 (100%)	0	0	100	100
19	O	114/122 (93%)	112 (98%)	2 (2%)	0	100	100
20	P	115/119 (97%)	114 (99%)	1 (1%)	0	100	100
21	Q	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
22	R	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
23	S	89/106 (84%)	87 (98%)	2 (2%)	0	100	100
24	T	101/105 (96%)	97 (96%)	4 (4%)	0	100	100
25	U	95/98 (97%)	93 (98%)	2 (2%)	0	100	100
26	V	75/85 (88%)	75 (100%)	0	0	100	100
27	W	75/78 (96%)	74 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	X	58/65 (89%)	57 (98%)	1 (2%)	0	100	100
29	Y	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
30	Z	53/61 (87%)	51 (96%)	2 (4%)	0	100	100
32	b	223/250 (89%)	206 (92%)	15 (7%)	2 (1%)	14	40
33	c	213/250 (85%)	205 (96%)	8 (4%)	0	100	100
34	d	205/208 (99%)	199 (97%)	6 (3%)	0	100	100
35	e	153/165 (93%)	151 (99%)	2 (1%)	0	100	100
36	f	102/127 (80%)	97 (95%)	3 (3%)	2 (2%)	6	21
37	g	149/156 (96%)	145 (97%)	4 (3%)	0	100	100
38	h	128/131 (98%)	123 (96%)	5 (4%)	0	100	100
39	i	124/128 (97%)	119 (96%)	5 (4%)	0	100	100
40	j	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
41	k	115/128 (90%)	112 (97%)	3 (3%)	0	100	100
42	l	120/124 (97%)	110 (92%)	10 (8%)	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%)	85 (99%)	1 (1%)	0	100	100
46	p	80/101 (79%)	79 (99%)	1 (1%)	0	100	100
47	q	77/85 (91%)	75 (97%)	2 (3%)	0	100	100
48	r	50/75 (67%)	50 (100%)	0	0	100	100
49	s	80/91 (88%)	78 (98%)	2 (2%)	0	100	100
50	t	84/88 (96%)	84 (100%)	0	0	100	100
51	u	61/71 (86%)	61 (100%)	0	0	100	100
52	v	100/116 (86%)	91 (91%)	8 (8%)	1 (1%)	12	37
All	All	5527/5988 (92%)	5353 (97%)	165 (3%)	9 (0%)	44	71

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	G	81	GLU
32	b	30	ARG
36	f	33	ASP
10	F	8	TYR
11	G	13	ASN

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Mol	Chain	Res	Type
32	b	8	MET
36	f	86	ARG
52	v	12	HIS
16	L	78	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	45/47 (96%)	45 (100%)	0	100	100
2	1	36/36 (100%)	36 (100%)	0	100	100
3	2	52/53 (98%)	52 (100%)	0	100	100
4	3	33/33 (100%)	33 (100%)	0	100	100
7	C	218/220 (99%)	218 (100%)	0	100	100
8	D	166/167 (99%)	166 (100%)	0	100	100
9	E	155/155 (100%)	155 (100%)	0	100	100
10	F	144/147 (98%)	144 (100%)	0	100	100
11	G	139/142 (98%)	139 (100%)	0	100	100
12	H	45/112 (40%)	45 (100%)	0	100	100
13	I	117/118 (99%)	117 (100%)	0	100	100
14	J	103/103 (100%)	103 (100%)	0	100	100
15	K	106/108 (98%)	106 (100%)	0	100	100
16	L	113/113 (100%)	113 (100%)	0	100	100
17	M	96/101 (95%)	96 (100%)	0	100	100
18	N	83/85 (98%)	83 (100%)	0	100	100
19	O	98/102 (96%)	98 (100%)	0	100	100
20	P	85/86 (99%)	85 (100%)	0	100	100
21	Q	84/84 (100%)	84 (100%)	0	100	100
22	R	88/88 (100%)	88 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	S	77/87 (88%)	77 (100%)	0	100	100
24	T	83/85 (98%)	83 (100%)	0	100	100
25	U	79/80 (99%)	79 (100%)	0	100	100
26	V	60/64 (94%)	60 (100%)	0	100	100
27	W	69/70 (99%)	69 (100%)	0	100	100
28	X	53/56 (95%)	53 (100%)	0	100	100
29	Y	54/54 (100%)	54 (100%)	0	100	100
30	Z	47/50 (94%)	47 (100%)	0	100	100
32	b	185/200 (92%)	185 (100%)	0	100	100
33	c	175/198 (88%)	175 (100%)	0	100	100
34	d	170/171 (99%)	170 (100%)	0	100	100
35	e	113/120 (94%)	113 (100%)	0	100	100
36	f	94/111 (85%)	94 (100%)	0	100	100
37	g	123/128 (96%)	123 (100%)	0	100	100
38	h	108/109 (99%)	108 (100%)	0	100	100
39	i	99/100 (99%)	99 (100%)	0	100	100
40	j	89/91 (98%)	89 (100%)	0	100	100
41	k	88/98 (90%)	88 (100%)	0	100	100
42	l	104/106 (98%)	104 (100%)	0	100	100
43	m	95/98 (97%)	95 (100%)	0	100	100
44	n	81/82 (99%)	81 (100%)	0	100	100
45	o	71/72 (99%)	71 (100%)	0	100	100
46	p	63/77 (82%)	63 (100%)	0	100	100
47	q	71/76 (93%)	71 (100%)	0	100	100
48	r	46/66 (70%)	46 (100%)	0	100	100
49	s	70/78 (90%)	70 (100%)	0	100	100
50	t	65/67 (97%)	65 (100%)	0	100	100
51	u	54/62 (87%)	54 (100%)	0	100	100
52	v	90/102 (88%)	90 (100%)	0	100	100
All	All	4582/4858 (94%)	4582 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
4	3	4	GLN
4	3	35	GLN
7	C	143	ASN
8	D	133	GLN
8	D	153	GLN
9	E	96	ASN
13	I	63	GLN
13	I	95	HIS
14	J	110	GLN
17	M	31	HIS
18	N	39	GLN
19	O	15	GLN
25	U	88	ASN
26	V	29	GLN
26	V	46	HIS
28	X	25	GLN
30	Z	19	HIS
30	Z	37	HIS
30	Z	52	GLN
32	b	205	ASN
34	d	50	GLN
34	d	148	HIS
35	e	88	HIS
35	e	131	ASN
36	f	55	HIS
36	f	58	HIS
38	h	16	ASN
39	i	124	GLN
40	j	23	GLN
46	p	44	ASN
49	s	69	HIS
52	v	10	ASN
52	v	32	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	a	1527/1544 (98%)	255 (16%)	0
5	A	2726/2918 (93%)	480 (17%)	32 (1%)
6	B	114/115 (99%)	19 (16%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4367/4577 (95%)	754 (17%)	33 (0%)

All (754) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	50	G
5	A	53	G
5	A	56	A
5	A	58	G
5	A	66	U
5	A	67	G
5	A	70	A
5	A	78	A
5	A	81	A
5	A	82	G
5	A	91	A
5	A	92	G
5	A	98	A
5	A	99	A
5	A	101	U
5	A	106	U
5	A	107	U
5	A	108	U
5	A	109	G
5	A	125	A
5	A	127	U
5	A	149	G
5	A	153	G
5	A	163	C
5	A	167	A
5	A	170	A
5	A	172	A
5	A	188	A
5	A	201	G
5	A	203	A
5	A	206	A
5	A	223	A
5	A	228	A
5	A	229	A
5	A	235	U
5	A	236	U
5	A	237	G

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Mol	Chain	Res	Type
5	A	255	G
5	A	257	G
5	A	259	G
5	A	262	A
5	A	272	A
5	A	273	G
5	A	275	C
5	A	278	U
5	A	279	U
5	A	293	U
5	A	297	G
5	A	303	C
5	A	313	A
5	A	324	A
5	A	325	G
5	A	331	G
5	A	332	A
5	A	333	U
5	A	335	U
5	A	347	A
5	A	348	A
5	A	359	U
5	A	360	A
5	A	365	U
5	A	366	G
5	A	368	C
5	A	369	G
5	A	370	A
5	A	371	G
5	A	372	U
5	A	385	G
5	A	386	U
5	A	395	G
5	A	403	A
5	A	410	G
5	A	416	C
5	A	423	G
5	A	428	A
5	A	434	C
5	A	450	U
5	A	455	C
5	A	479	A

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Mol	Chain	Res	Type
5	A	480	G
5	A	488	G
5	A	489	U
5	A	490	G
5	A	504	A
5	A	507	U
5	A	508	C
5	A	512	A
5	A	529	G
5	A	531	A
5	A	544	U
5	A	545	C
5	A	546	G
5	A	547	U
5	A	554	A
5	A	561	A
5	A	564	U
5	A	570	A
5	A	571	U
5	A	573	A
5	A	595	G
5	A	601	A
5	A	611	U
5	A	612	A
5	A	613	U
5	A	625	A
5	A	635	A
5	A	636	G
5	A	637	U
5	A	644	A
5	A	648	C
5	A	649	G
5	A	651	U
5	A	656	U
5	A	657	G
5	A	661	G
5	A	667	G
5	A	684	U
5	A	692	U
5	A	693	G
5	A	703	A
5	A	712	U

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Mol	Chain	Res	Type
5	A	717	C
5	A	721	C
5	A	724	G
5	A	728	A
5	A	738	C
5	A	745	U
5	A	746	G
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	787	A
5	A	788	U
5	A	799	G
5	A	800	A
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	854	G
5	A	855	G
5	A	857	G
5	A	858	U
5	A	904	U
5	A	908	A
5	A	912	C
5	A	929	C
5	A	930	U
5	A	938	A
5	A	942	A
5	A	943	G
5	A	958	C
5	A	959	G
5	A	971	G
5	A	980	A
5	A	993	A
5	A	997	A
5	A	1009	U

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Mol	Chain	Res	Type
5	A	1010	C
5	A	1014	G
5	A	1019	G
5	A	1023	G
5	A	1030	U
5	A	1033	G
5	A	1036	A
5	A	1039	G
5	A	1040	C
5	A	1043	A
5	A	1051	A
5	A	1104	G
5	A	1105	U
5	A	1108	A
5	A	1109	G
5	A	1129	U
5	A	1130	A
5	A	1131	A
5	A	1132	C
5	A	1140	A
5	A	1149	G
5	A	1153	A
5	A	1169	C
5	A	1170	U
5	A	1171	U
5	A	1173	G
5	A	1174	U
5	A	1201	G
5	A	1207	G
5	A	1242	A
5	A	1244	U
5	A	1245	G
5	A	1248	A
5	A	1250	U
5	A	1251	G
5	A	1266	G
5	A	1267	A
5	A	1284	C
5	A	1296	A
5	A	1297	A
5	A	1301	C
5	A	1309	C

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Mol	Chain	Res	Type
5	A	1316	A
5	A	1321	U
5	A	1328	G
5	A	1336	G
5	A	1337	A
5	A	1338	G
5	A	1347	U
5	A	1354	A
5	A	1360	A
5	A	1363	G
5	A	1373	A
5	A	1374	U
5	A	1378	A
5	A	1386	U
5	A	1411	G
5	A	1414	A
5	A	1415	U
5	A	1416	G
5	A	1417	A
5	A	1420	G
5	A	1422	A
5	A	1423	C
5	A	1424	G
5	A	1428	A
5	A	1432	C
5	A	1443	U
5	A	1447	G
5	A	1448	U
5	A	1449	U
5	A	1456	C
5	A	1462	G
5	A	1467	G
5	A	1477	U
5	A	1485	A
5	A	1486	G
5	A	1489	A
5	A	1492	U
5	A	1494	C
5	A	1499	U
5	A	1501	C
5	A	1504	U
5	A	1505	A

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Mol	Chain	Res	Type
5	A	1511	A
5	A	1520	A
5	A	1523	A
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	1538	A
5	A	1542	A
5	A	1543	A
5	A	1552	U
5	A	1553	G
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	1579	G
5	A	1581	U
5	A	1582	U
5	A	1583	C
5	A	1605	G
5	A	1606	A
5	A	1608	A
5	A	1609	C
5	A	1616	A
5	A	1632	U
5	A	1644	C
5	A	1645	U
5	A	1646	U
5	A	1662	A
5	A	1672	G
5	A	1691	U
5	A	1697	G
5	A	1705	G
5	A	1710	U
5	A	1711	G

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Mol	Chain	Res	Type
5	A	1726	C
5	A	1728	C
5	A	1729	U
5	A	1733	U
5	A	1734	G
5	A	1760	G
5	A	1769	A
5	A	1776	A
5	A	1783	A
5	A	1787	A
5	A	1796	C
5	A	1797	A
5	A	1805	A
5	A	1812	C
5	A	1817	A
5	A	1825	A
5	A	1829	C
5	A	1844	A
5	A	1861	U
5	A	1862	A
5	A	1869	G
5	A	1871	G
5	A	1872	A
5	A	1885	A
5	A	1895	A
5	A	1902	G
5	A	1908	A
5	A	1909	A
5	A	1910	C
5	A	1911	3TD
5	A	1918	G
5	A	1925	G
5	A	1926	G
5	A	1927	U
5	A	1934	A
5	A	1936	U
5	A	1950	G
5	A	1951	U
5	A	1952	U
5	A	1959	U
5	A	1963	C
5	A	1966	A

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Mol	Chain	Res	Type
5	A	1967	U
5	A	1968	G
5	A	1978	U
5	A	1987	U
5	A	1989	U
5	A	2010	A
5	A	2017	A
5	A	2018	U
5	A	2019	C
5	A	2026	6MZ
5	A	2027	A
5	A	2029	A
5	A	2030	U
5	A	2039	C
5	A	2048	A
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	2089	G
5	A	2194	A
5	A	2195	A
5	A	2200	G
5	A	2204	C
5	A	2207	G
5	A	2210	C
5	A	2216	C
5	A	2221	A
5	A	2222	C
5	A	2234	G
5	A	2235	G
5	A	2261	U
5	A	2274	A
5	A	2279	U
5	A	2282	G
5	A	2283	A
5	A	2299	G
5	A	2301	U
5	A	2303	G
5	A	2304	G

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Mol	Chain	Res	Type
5	A	2305	A
5	A	2308	U
5	A	2316	A
5	A	2317	G
5	A	2321	A
5	A	2323	A
5	A	2341	A
5	A	2343	C
5	A	2346	C
5	A	2350	A
5	A	2355	C
5	A	2371	G
5	A	2378	G
5	A	2379	G
5	A	2380	U
5	A	2381	C
5	A	2398	U
5	A	2402	U
5	A	2417	G
5	A	2420	C
5	A	2422	A
5	A	2425	G
5	A	2426	A
5	A	2427	U
5	A	2430	A
5	A	2431	A
5	A	2437	U
5	A	2442	G
5	A	2443	G
5	A	2444	A
5	A	2446	A
5	A	2455	A
5	A	2465	A
5	A	2466	G
5	A	2469	U
5	A	2470	U
5	A	2472	A
5	A	2475	U
5	A	2476	C
5	A	2489	U
5	A	2493	A
5	A	2494	C

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Mol	Chain	Res	Type
5	A	2498	G
5	A	2499	2MA
5	A	2502	U
5	A	2503	C
5	A	2514	A
5	A	2516	C
5	A	2525	G
5	A	2528	G
5	A	2543	A
5	A	2548	OMU
5	A	2550	U
5	A	2562	A
5	A	2563	G
5	A	2568	A
5	A	2569	C
5	A	2578	G
5	A	2581	U
5	A	2582	U
5	A	2598	A
5	A	2605	U
5	A	2609	U
5	A	2611	U
5	A	2625	U
5	A	2626	G
5	A	2636	G
5	A	2642	C
5	A	2661	A
5	A	2685	U
5	A	2686	A
5	A	2687	C
5	A	2709	C
5	A	2710	G
5	A	2722	U
5	A	2725	U
5	A	2728	G
5	A	2729	A
5	A	2732	G
5	A	2735	U
5	A	2740	G
5	A	2744	A
5	A	2754	A
5	A	2761	A

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Mol	Chain	Res	Type
5	A	2762	G
5	A	2774	A
5	A	2775	U
5	A	2777	A
5	A	2793	U
5	A	2796	U
5	A	2797	G
5	A	2800	C
5	A	2805	A
5	A	2816	G
5	A	2817	A
5	A	2829	U
5	A	2830	G
5	A	2831	A
5	A	2845	G
5	A	2846	A
5	A	2851	U
5	A	2852	A
5	A	2863	A
5	A	2868	G
5	A	2873	A
5	A	2879	A
5	A	2880	U
6	B	11	A
6	B	15	C
6	B	22	G
6	B	23	A
6	B	29	C
6	B	39	C
6	B	40	C
6	B	42	G
6	B	43	A
6	B	51	A
6	B	52	G
6	B	65	G
6	B	67	G
6	B	71	A
6	B	85	U
6	B	86	U
6	B	87	A
6	B	105	C
6	B	106	A

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Mol	Chain	Res	Type
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	57	A
31	a	62	A
31	a	64	U
31	a	66	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	86	C
31	a	89	C
31	a	90	C
31	a	91	G
31	a	96	U
31	a	97	A
31	a	105	A
31	a	107	G
31	a	117	U
31	a	126	A
31	a	140	G
31	a	152	C
31	a	156	A
31	a	157	A
31	a	167	A
31	a	185	C
31	a	186	G
31	a	193	A
31	a	197	G
31	a	200	G
31	a	203	C

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Mol	Chain	Res	Type
31	a	205	U
31	a	208	G
31	a	216	G
31	a	236	C
31	a	241	U
31	a	243	G
31	a	246	A
31	a	247	G
31	a	262	G
31	a	263	C
31	a	285	G
31	a	289	G
31	a	302	A
31	a	313	U
31	a	324	C
31	a	340	A
31	a	341	C
31	a	343	G
31	a	348	C
31	a	349	A
31	a	359	A
31	a	363	U
31	a	368	C
31	a	402	G
31	a	407	A
31	a	409	G
31	a	418	A
31	a	419	U
31	a	420	G
31	a	421	G
31	a	425	U
31	a	426	A
31	a	435	U
31	a	444	A
31	a	448	G
31	a	460	U
31	a	461	A
31	a	463	U
31	a	464	A
31	a	479	A
31	a	483	U
31	a	493	A

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Mol	Chain	Res	Type
31	a	494	U
31	a	496	A
31	a	502	G
31	a	508	C
31	a	514	G
31	a	515	C
31	a	518	G
31	a	521	G
31	a	522	C
31	a	524	7MG
31	a	527	G
31	a	528	U
31	a	529	A
31	a	531	U
31	a	532	A
31	a	544	A
31	a	556	A
31	a	561	C
31	a	569	A
31	a	570	A
31	a	572	G
31	a	573	C
31	a	574	G
31	a	593	A
31	a	615	C
31	a	623	G
31	a	630	G
31	a	639	A
31	a	650	A
31	a	651	G
31	a	662	A
31	a	682	G
31	a	684	A
31	a	685	G
31	a	698	U
31	a	699	A
31	a	700	G
31	a	720	U
31	a	721	G
31	a	728	G
31	a	729	C
31	a	731	G

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Mol	Chain	Res	Type
31	a	752	G
31	a	756	A
31	a	774	A
31	a	778	A
31	a	784	A
31	a	790	U
31	a	791	A
31	a	809	G
31	a	810	U
31	a	812	A
31	a	814	C
31	a	815	G
31	a	816	A
31	a	817	U
31	a	825	A
31	a	841	G
31	a	887	G
31	a	888	U
31	a	899	G
31	a	911	A
31	a	918	U
31	a	919	G
31	a	923	G
31	a	924	G
31	a	926	G
31	a	931	C
31	a	932	A
31	a	957	U
31	a	958	U
31	a	966	A
31	a	968	G
31	a	972	A
31	a	973	G
31	a	974	A
31	a	989	U
31	a	990	G
31	a	991	A
31	a	1001	A
31	a	1006	U
31	a	1007	U
31	a	1023	G
31	a	1027	U

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Mol	Chain	Res	Type
31	a	1029	G
31	a	1030	G
31	a	1043	A
31	a	1050	G
31	a	1051	C
31	a	1052	A
31	a	1062	U
31	a	1071	G
31	a	1076	G
31	a	1085	G
31	a	1086	G
31	a	1088	U
31	a	1091	G
31	a	1092	U
31	a	1098	A
31	a	1123	U
31	a	1124	G
31	a	1130	A
31	a	1136	G
31	a	1140	G
31	a	1149	A
31	a	1154	A
31	a	1155	C
31	a	1156	U
31	a	1165	C
31	a	1166	A
31	a	1179	G
31	a	1180	C
31	a	1181	G
31	a	1188	A
31	a	1193	A
31	a	1194	A
31	a	1197	C
31	a	1209	U
31	a	1210	A
31	a	1223	C
31	a	1224	A
31	a	1235	A
31	a	1238	G
31	a	1249	A
31	a	1255	G
31	a	1262	A

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Mol	Chain	Res	Type
31	a	1277	A
31	a	1284	A
31	a	1295	U
31	a	1297	G
31	a	1299	C
31	a	1317	C
31	a	1329	A
31	a	1350	G
31	a	1360	A
31	a	1367	G
31	a	1376	G
31	a	1378	U
31	a	1379	C
31	a	1380	C
31	a	1392	C
31	a	1394	C
31	a	1395	A
31	a	1398	G
31	a	1399	4OC
31	a	1401	C
31	a	1415	A
31	a	1416	G
31	a	1417	U
31	a	1422	U
31	a	1424	C
31	a	1427	C
31	a	1438	A
31	a	1443	A
31	a	1445	C
31	a	1446	U
31	a	1449	A
31	a	1451	A
31	a	1465	A
31	a	1476	G
31	a	1477	A
31	a	1484	G
31	a	1489	A
31	a	1491	G
31	a	1496	A
31	a	1500	A
31	a	1503	U
31	a	1514	G

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Mol	Chain	Res	Type
31	a	1526	G
31	a	1527	G
31	a	1529	U

All (33) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	91	A
5	A	162	A
5	A	256	C
5	A	272	A
5	A	324	A
5	A	334	A
5	A	365	U
5	A	368	C
5	A	370	A
5	A	371	G
5	A	424	G
5	A	478	A
5	A	488	G
5	A	507	U
5	A	720	A
5	A	782	G
5	A	798	U
5	A	799	G
5	A	857	G
5	A	1172	U
5	A	1179	G
5	A	1187	G
5	A	1296	A
5	A	1337	A
5	A	1542	A
5	A	1557	U
5	A	1564	A
5	A	1709	U
5	A	2029	A
5	A	2419	U
5	A	2568	A
5	A	2581	U
6	B	86	U

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

24 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
31	2MG	a	963	31	23,26,27	0.44	0	33,38,41	0.48	0
31	2MG	a	1204	31	23,26,27	0.48	0	33,38,41	0.51	0
5	6MZ	A	2026	5	22,25,26	2.45	4 (18%)	29,36,39	3.38	12 (41%)
31	UR3	a	1495	31	19,22,23	2.97	6 (31%)	26,32,35	1.62	4 (15%)
5	2MG	A	2441	5	23,26,27	0.43	0	33,38,41	0.52	0
5	PSU	A	1913	5	18,21,22	1.15	1 (5%)	21,30,33	1.90	5 (23%)
5	3TD	A	1911	5	19,22,23	4.46	6 (31%)	23,32,35	1.78	3 (13%)
5	PSU	A	2453	5	18,21,22	1.12	1 (5%)	21,30,33	1.95	6 (28%)
31	5MC	a	964	31	19,22,23	0.52	0	26,32,35	0.60	0
5	OMU	A	2548	5	19,22,23	3.12	8 (42%)	25,31,34	1.82	4 (16%)
31	MA6	a	1516	31	23,26,27	1.37	4 (17%)	33,38,41	3.30	13 (39%)
5	PSU	A	952	5	18,21,22	1.13	1 (5%)	21,30,33	1.90	5 (23%)
5	2MA	A	2499	5	22,25,26	4.01	9 (40%)	32,37,40	2.79	10 (31%)
5	PSU	A	2500	5	18,21,22	1.11	1 (5%)	21,30,33	1.96	5 (23%)
5	OMG	A	2247	5	23,26,27	0.45	0	32,38,41	0.47	0
31	MA6	a	1515	31	23,26,27	1.38	4 (17%)	33,38,41	3.21	12 (36%)
5	PSU	A	2576	5	18,21,22	1.13	1 (5%)	21,30,33	1.98	5 (23%)
31	4OC	a	1399	31	20,23,24	3.20	8 (40%)	25,32,35	0.88	1 (4%)
31	7MG	a	524	31	23,26,27	1.08	1 (4%)	27,39,42	0.86	2 (7%)
5	PSU	A	2601	5	18,21,22	1.12	1 (5%)	21,30,33	1.92	4 (19%)
5	7MG	A	2065	5	23,26,27	1.10	1 (4%)	27,39,42	0.91	2 (7%)
5	PSU	A	1907	5	18,21,22	1.14	1 (5%)	21,30,33	1.96	5 (23%)
31	PSU	a	513	31	18,21,22	1.12	1 (5%)	21,30,33	1.95	6 (28%)
5	5MU	A	1935	5	19,22,23	0.38	0	27,32,35	0.48	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	2MG	a	963	31	-	1/9/27/28	0/3/3/3
31	2MG	a	1204	31	-	2/9/27/28	0/3/3/3
5	6MZ	A	2026	5	-	0/9/27/28	0/3/3/3
31	UR3	a	1495	31	-	0/7/25/26	0/2/2/2
5	2MG	A	2441	5	-	0/9/27/28	0/3/3/3
5	PSU	A	1913	5	-	1/7/25/26	0/2/2/2
5	3TD	A	1911	5	-	3/7/25/26	0/2/2/2
5	PSU	A	2453	5	-	0/7/25/26	0/2/2/2
31	5MC	a	964	31	-	0/7/25/26	0/2/2/2
5	OMU	A	2548	5	-	4/9/27/28	0/2/2/2
31	MA6	a	1516	31	-	0/11/29/30	0/3/3/3
5	PSU	A	952	5	-	0/7/25/26	0/2/2/2
5	2MA	A	2499	5	-	0/7/25/26	0/3/3/3
5	PSU	A	2500	5	-	0/7/25/26	0/2/2/2
5	OMG	A	2247	5	-	1/9/27/28	0/3/3/3
31	MA6	a	1515	31	-	0/11/29/30	0/3/3/3
5	PSU	A	2576	5	-	0/7/25/26	0/2/2/2
31	4OC	a	1399	31	-	2/9/29/30	0/2/2/2
31	7MG	a	524	31	-	2/7/37/38	0/3/3/3
5	PSU	A	2601	5	-	0/7/25/26	0/2/2/2
5	7MG	A	2065	5	-	2/7/37/38	0/3/3/3
5	PSU	A	1907	5	-	2/7/25/26	0/2/2/2
31	PSU	a	513	31	-	2/7/25/26	0/2/2/2
5	5MU	A	1935	5	-	0/7/25/26	0/2/2/2

All (59) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1911	3TD	C6-C5	13.44	1.50	1.35
5	A	2499	2MA	C4-N3	12.33	1.50	1.34
5	A	1911	3TD	C2-N1	10.77	1.50	1.37
5	A	2026	6MZ	C6-N6	10.13	1.45	1.34
5	A	2499	2MA	C2-N3	7.53	1.47	1.34
5	A	2548	OMU	C2-N1	7.44	1.50	1.38
31	a	1495	UR3	C2-N1	7.42	1.48	1.38
5	A	2499	2MA	C6-N1	7.12	1.44	1.35
31	a	1399	4OC	C4-N3	7.10	1.44	1.32
5	A	2548	OMU	C2-N3	6.98	1.50	1.38
31	a	1495	UR3	C6-C5	6.80	1.50	1.35
31	a	1399	4OC	C6-C5	6.30	1.49	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	a	1399	4OC	C2-N3	6.29	1.48	1.36
5	A	2499	2MA	C2-N1	6.12	1.44	1.34
31	a	1495	UR3	C2-N3	5.79	1.50	1.39
5	A	1911	3TD	C6-N1	5.75	1.45	1.36
5	A	2548	OMU	C6-C5	5.69	1.48	1.35
5	A	1911	3TD	C2-N3	4.96	1.49	1.38
31	a	1399	4OC	C4-N4	4.87	1.46	1.36
5	A	2499	2MA	C5-C6	4.68	1.54	1.41
5	A	2065	7MG	C5-N7	4.54	1.41	1.35
31	a	524	7MG	C5-N7	4.38	1.41	1.35
5	A	2548	OMU	C4-N3	4.37	1.46	1.38
31	a	1399	4OC	C2-N1	4.29	1.49	1.40
31	a	1515	MA6	C6-N6	3.99	1.47	1.36
31	a	1516	MA6	C6-N6	3.94	1.47	1.36
5	A	1913	PSU	C6-C5	3.84	1.39	1.35
5	A	952	PSU	C6-C5	3.77	1.39	1.35
5	A	1907	PSU	C6-C5	3.73	1.39	1.35
5	A	2601	PSU	C6-C5	3.72	1.39	1.35
5	A	2453	PSU	C6-C5	3.69	1.39	1.35
31	a	1399	4OC	C5-C4	3.67	1.49	1.41
31	a	513	PSU	C6-C5	3.64	1.39	1.35
5	A	2576	PSU	C6-C5	3.63	1.39	1.35
5	A	2500	PSU	C6-C5	3.62	1.39	1.35
31	a	1495	UR3	C6-N1	3.41	1.46	1.38
5	A	2499	2MA	C6-N6	-3.32	1.25	1.34
31	a	1399	4OC	C6-N1	3.31	1.46	1.38
5	A	1911	3TD	C4-N3	3.11	1.46	1.40
5	A	2548	OMU	O4-C4	-2.95	1.18	1.24
5	A	2026	6MZ	C5-N7	-2.88	1.33	1.39
5	A	2548	OMU	C6-N1	2.83	1.44	1.38
31	a	1516	MA6	C5-C4	-2.80	1.34	1.39
31	a	1515	MA6	C5-C4	-2.78	1.34	1.39
31	a	1495	UR3	C4-N3	2.73	1.46	1.40
5	A	2026	6MZ	C5-C4	-2.72	1.34	1.39
31	a	1399	4OC	O2-C2	-2.63	1.18	1.23
5	A	2499	2MA	C5-N7	-2.54	1.34	1.39
5	A	2548	OMU	O2-C2	-2.41	1.18	1.23
5	A	2548	OMU	C5-C4	2.39	1.48	1.43
31	a	1515	MA6	C5-N7	-2.39	1.34	1.39
31	a	1495	UR3	C5-C4	2.31	1.49	1.43
31	a	1516	MA6	C5-N7	-2.29	1.34	1.39
5	A	1911	3TD	O2-C2	-2.24	1.19	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	2026	6MZ	C8-N9	-2.13	1.33	1.37
31	a	1515	MA6	C8-N9	-2.10	1.34	1.37
5	A	2499	2MA	C8-N7	2.09	1.35	1.31
5	A	2499	2MA	C4-N9	-2.08	1.33	1.37
31	a	1516	MA6	C8-N9	-2.06	1.34	1.37

All (104) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	1516	MA6	N1-C6-N6	-12.03	102.19	116.86
31	a	1515	MA6	N1-C6-N6	-11.52	102.82	116.86
5	A	2026	6MZ	C1'-N9-C8	8.94	146.94	127.09
5	A	2026	6MZ	C4-N9-C1'	-8.91	105.80	126.63
31	a	1516	MA6	C5-C6-N6	8.07	138.10	125.33
31	a	1515	MA6	C5-C6-N6	7.74	137.58	125.33
5	A	2499	2MA	C1'-N9-C8	-7.71	109.97	127.09
5	A	2026	6MZ	C5-C4-N3	-6.33	118.00	126.72
5	A	2499	2MA	C5-C4-N3	-5.84	121.02	127.18
5	A	2026	6MZ	N1-C2-N3	-5.74	119.90	128.58
31	a	1516	MA6	N1-C2-N3	-5.70	119.96	128.58
5	A	2499	2MA	N9-C8-N7	-5.62	105.96	113.94
5	A	1911	3TD	N1-C2-N3	5.58	120.19	116.13
5	A	2548	OMU	C4-N3-C2	-5.54	119.73	126.61
31	a	1495	UR3	C4-N3-C2	-5.51	120.14	124.58
31	a	1515	MA6	N1-C2-N3	-5.49	120.27	128.58
5	A	2499	2MA	C4-N9-C1'	5.37	139.19	126.63
31	a	1515	MA6	C5-C4-N3	-4.97	119.87	126.72
5	A	2500	PSU	C4-N3-C2	-4.91	119.61	126.37
31	a	513	PSU	N1-C2-N3	4.88	120.31	115.17
5	A	1907	PSU	N1-C2-N3	4.87	120.30	115.17
5	A	2601	PSU	C4-N3-C2	-4.86	119.67	126.37
5	A	2576	PSU	C4-N3-C2	-4.86	119.67	126.37
5	A	2499	2MA	C4-N9-C8	4.86	110.84	105.74
5	A	2500	PSU	N1-C2-N3	4.84	120.27	115.17
5	A	2601	PSU	N1-C2-N3	4.83	120.26	115.17
31	a	513	PSU	C4-N3-C2	-4.83	119.72	126.37
31	a	1516	MA6	C5-C4-N3	-4.82	120.07	126.72
5	A	2576	PSU	N1-C2-N3	4.82	120.25	115.17
5	A	1907	PSU	C4-N3-C2	-4.82	119.73	126.37
5	A	2453	PSU	N1-C2-N3	4.80	120.23	115.17
5	A	952	PSU	N1-C2-N3	4.79	120.22	115.17
5	A	952	PSU	C4-N3-C2	-4.77	119.79	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	2453	PSU	C4-N3-C2	-4.76	119.81	126.37
5	A	1913	PSU	C4-N3-C2	-4.76	119.82	126.37
5	A	1913	PSU	N1-C2-N3	4.70	120.12	115.17
5	A	2499	2MA	N3-C4-N9	4.53	132.74	126.99
5	A	1911	3TD	C4-N3-C2	-4.30	120.06	124.61
31	a	1516	MA6	N9-C8-N7	-4.26	107.89	113.94
31	a	1515	MA6	C4-C5-C6	4.24	120.30	115.91
5	A	2026	6MZ	N3-C4-N9	4.23	134.37	127.17
5	A	2026	6MZ	C4-C5-C6	4.13	120.22	116.78
31	a	1515	MA6	N9-C8-N7	-4.13	108.08	113.94
5	A	2026	6MZ	C2-N3-C4	4.02	121.65	111.83
5	A	2548	OMU	N3-C2-N1	3.81	119.85	114.89
31	a	1516	MA6	C4-C5-C6	3.77	119.81	115.91
5	A	2026	6MZ	N9-C8-N7	-3.64	108.77	113.94
31	a	1495	UR3	C5-C4-N3	3.59	119.77	115.04
5	A	2548	OMU	C5-C4-N3	3.57	119.80	114.80
31	a	1516	MA6	C2-N1-C6	3.49	120.35	111.83
31	a	1515	MA6	C2-N1-C6	3.40	120.14	111.83
31	a	1516	MA6	C2-N3-C4	3.39	120.10	111.83
5	A	2499	2MA	C5-N7-C8	3.36	108.73	103.45
31	a	1515	MA6	C2-N3-C4	3.27	119.82	111.83
5	A	2499	2MA	N3-C2-N1	-3.26	120.02	125.77
31	a	1515	MA6	N3-C4-N9	3.08	132.40	127.17
5	A	2576	PSU	O2-C2-N1	-2.95	119.75	122.79
5	A	2548	OMU	O4-C4-C5	-2.95	120.08	125.16
31	a	1516	MA6	C5-N7-C8	2.93	108.05	103.45
5	A	2026	6MZ	C5-N7-C8	2.93	108.05	103.45
31	a	1515	MA6	C5-N7-C8	2.90	108.01	103.45
5	A	1907	PSU	O2-C2-N1	-2.84	119.86	122.79
5	A	2453	PSU	O2-C2-N1	-2.81	119.89	122.79
5	A	2601	PSU	O2-C2-N1	-2.78	119.92	122.79
5	A	1913	PSU	O2-C2-N1	-2.76	119.94	122.79
31	a	1516	MA6	N3-C4-N9	2.75	131.85	127.17
5	A	2500	PSU	O2-C2-N1	-2.74	119.96	122.79
31	a	513	PSU	O2-C2-N1	-2.72	119.99	122.79
5	A	2026	6MZ	C5-C6-N1	2.64	120.98	118.15
5	A	2500	PSU	C6-C5-C4	2.55	119.90	118.17
5	A	952	PSU	O2-C2-N1	-2.54	120.17	122.79
5	A	2576	PSU	O4'-C1'-C2'	2.49	108.60	105.15
5	A	1907	PSU	C6-N1-C2	-2.49	120.38	122.69
31	a	524	7MG	C4-C5-N7	2.48	108.31	105.38
5	A	2453	PSU	C6-N1-C2	-2.46	120.41	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1907	PSU	C6-C5-C4	2.46	119.83	118.17
5	A	952	PSU	C6-N1-C2	-2.43	120.44	122.69
31	a	1399	4OC	C6-C5-C4	2.43	119.92	117.00
5	A	2576	PSU	C6-N1-C2	-2.41	120.45	122.69
5	A	1913	PSU	C6-N1-C2	-2.41	120.45	122.69
31	a	513	PSU	C6-N1-C2	-2.40	120.46	122.69
5	A	2601	PSU	C6-N1-C2	-2.40	120.46	122.69
31	a	1516	MA6	C4-C5-N7	-2.39	107.85	110.58
31	a	1495	UR3	C1'-N1-C2	2.39	120.94	117.04
5	A	2026	6MZ	C9-N6-C6	-2.38	120.64	122.85
5	A	2065	7MG	C5-C4-N9	2.37	109.37	106.33
31	a	1495	UR3	C6-N1-C2	-2.36	119.87	121.80
5	A	2065	7MG	C4-C5-N7	2.32	108.12	105.38
5	A	2499	2MA	N6-C6-N1	2.30	120.14	117.03
31	a	513	PSU	O4'-C1'-C2'	2.30	108.33	105.15
5	A	2453	PSU	C6-C5-C4	2.29	119.72	118.17
31	a	1516	MA6	C4-N9-C8	2.28	108.14	105.74
5	A	2500	PSU	C6-N1-C2	-2.26	120.60	122.69
31	a	524	7MG	C5-C4-N9	2.22	109.18	106.33
31	a	1515	MA6	C4-N9-C8	2.22	108.07	105.74
5	A	2453	PSU	O4'-C1'-C2'	2.20	108.20	105.15
31	a	1515	MA6	C4-C5-N7	-2.16	108.11	110.58
5	A	1913	PSU	O4'-C1'-C2'	2.15	108.12	105.15
5	A	1911	3TD	C1'-C5-C4	2.12	120.83	117.61
5	A	952	PSU	C6-C5-C4	2.09	119.59	118.17
31	a	513	PSU	C6-C5-C4	2.09	119.58	118.17
31	a	1516	MA6	C5-C4-N9	2.08	108.08	105.81
5	A	2499	2MA	C4-C5-N7	-2.06	108.23	110.58
5	A	2026	6MZ	C4-C5-N7	-2.01	108.28	110.58

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1911	3TD	C3'-C4'-C5'-O5'
5	A	1911	3TD	O4'-C4'-C5'-O5'
5	A	2247	OMG	C1'-C2'-O2'-CM2
31	a	513	PSU	C3'-C4'-C5'-O5'
31	a	524	7MG	C3'-C4'-C5'-O5'
31	a	1399	4OC	O4'-C4'-C5'-O5'
31	a	1399	4OC	C3'-C4'-C5'-O5'
31	a	513	PSU	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
31	a	524	7MG	O4'-C4'-C5'-O5'
31	a	1204	2MG	O4'-C4'-C5'-O5'
31	a	1204	2MG	C3'-C4'-C5'-O5'
5	A	2548	OMU	C3'-C4'-C5'-O5'
5	A	1907	PSU	C3'-C4'-C5'-O5'
5	A	2548	OMU	C3'-C2'-O2'-CM2
5	A	2065	7MG	C4'-C5'-O5'-P
5	A	2548	OMU	C4'-C5'-O5'-P
5	A	1911	3TD	C4'-C5'-O5'-P
5	A	2548	OMU	O4'-C4'-C5'-O5'
31	a	963	2MG	O4'-C4'-C5'-O5'
5	A	1907	PSU	O4'-C4'-C5'-O5'
5	A	1913	PSU	C3'-C4'-C5'-O5'
5	A	2065	7MG	O4'-C4'-C5'-O5'

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	a	963	2MG	3	0
31	a	1204	2MG	3	0
5	A	2026	6MZ	2	0
31	a	964	5MC	2	0
5	A	2548	OMU	1	0
31	a	1515	MA6	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 190 ligands modelled in this entry, 188 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	YQM	A	3201	55	43,44,44	3.70	21 (48%)	53,69,69	2.91	23 (43%)
54	YQM	A	3202	55	43,44,44	3.88	21 (48%)	53,69,69	2.81	20 (37%)

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
54	YQM	A	3201	55	-	6/16/81/81	0/5/5/5
54	YQM	A	3202	55	-	2/16/81/81	0/5/5/5

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	A	3202	YQM	C19-C20	14.84	1.65	1.52
54	A	3201	YQM	C19-C20	13.27	1.63	1.52
54	A	3202	YQM	C19-C17	8.92	1.66	1.55
54	A	3201	YQM	C19-C17	8.85	1.66	1.55
54	A	3202	YQM	C05-C04	8.50	1.62	1.54
54	A	3201	YQM	C05-C04	8.25	1.62	1.54
54	A	3202	YQM	C19-C05	6.27	1.58	1.53
54	A	3202	YQM	C21-C24	5.81	1.59	1.47
54	A	3201	YQM	C21-C24	5.57	1.59	1.47
54	A	3202	YQM	C09-C10	4.65	1.45	1.38
54	A	3202	YQM	C32-N31	4.55	1.45	1.35
54	A	3201	YQM	C32-N31	4.53	1.45	1.35
54	A	3201	YQM	C09-C10	4.41	1.45	1.38
54	A	3201	YQM	C19-C05	4.28	1.57	1.53
54	A	3201	YQM	C14-C15	4.19	1.57	1.45
54	A	3202	YQM	C08-C09	4.05	1.57	1.51
54	A	3201	YQM	C12-N31	3.99	1.49	1.41
54	A	3202	YQM	C14-C15	3.96	1.57	1.45
54	A	3202	YQM	C14-C13	3.89	1.49	1.41
54	A	3201	YQM	C17-C16	3.87	1.53	1.46
54	A	3201	YQM	C14-C13	3.86	1.48	1.41
54	A	3202	YQM	C12-N31	3.83	1.49	1.41
54	A	3202	YQM	C17-C16	3.79	1.53	1.46
54	A	3201	YQM	C15-C16	3.59	1.42	1.36
54	A	3201	YQM	C34-C32	3.27	1.58	1.52
54	A	3202	YQM	C24-N26	3.25	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	A	3201	YQM	C24-N26	3.23	1.42	1.33
54	A	3201	YQM	C21-C22	3.21	1.54	1.44
54	A	3201	YQM	C04-N02	3.03	1.53	1.47
54	A	3201	YQM	C36-N35	3.02	1.53	1.47
54	A	3202	YQM	C34-C32	2.98	1.57	1.52
54	A	3201	YQM	C12-C13	2.97	1.44	1.40
54	A	3202	YQM	C15-C16	2.92	1.41	1.36
54	A	3202	YQM	C12-C13	2.89	1.44	1.40
54	A	3202	YQM	C08-C07	2.65	1.59	1.52
54	A	3202	YQM	C21-C22	2.63	1.52	1.44
54	A	3202	YQM	C11-C10	2.51	1.42	1.37
54	A	3201	YQM	C08-C09	2.50	1.55	1.51
54	A	3201	YQM	C11-C10	2.45	1.41	1.37
54	A	3202	YQM	C04-N02	2.42	1.52	1.47
54	A	3201	YQM	C08-C07	2.41	1.58	1.52
54	A	3202	YQM	C36-N35	2.10	1.51	1.47

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	A	3201	YQM	C34-N35-C39	-8.40	102.46	113.34
54	A	3201	YQM	C34-C32-N31	7.34	127.81	114.23
54	A	3202	YQM	C34-C32-N31	7.10	127.36	114.23
54	A	3202	YQM	C34-N35-C39	-7.03	104.24	113.34
54	A	3201	YQM	C11-C12-C13	-5.90	114.81	120.53
54	A	3202	YQM	O27-C20-C21	5.87	127.86	121.90
54	A	3202	YQM	C11-C12-C13	-5.76	114.96	120.53
54	A	3201	YQM	O27-C20-C21	5.12	127.09	121.90
54	A	3201	YQM	C39-N35-C36	5.05	110.00	104.04
54	A	3201	YQM	O18-C17-C16	4.97	128.58	121.47
54	A	3202	YQM	O18-C17-C16	4.91	128.50	121.47
54	A	3201	YQM	O33-C32-C34	-4.71	112.77	121.02
54	A	3202	YQM	O33-C32-C34	-4.70	112.80	121.02
54	A	3202	YQM	O18-C17-C19	-4.49	110.57	119.11
54	A	3201	YQM	O18-C17-C19	-4.48	110.59	119.11
54	A	3202	YQM	C19-C05-C04	4.42	117.68	111.64
54	A	3202	YQM	C07-C16-C15	-4.31	115.16	121.44
54	A	3201	YQM	C21-C24-N26	4.17	127.16	118.64
54	A	3202	YQM	C21-C24-N26	4.15	127.10	118.64
54	A	3201	YQM	C24-C21-C22	-3.97	116.14	120.87
54	A	3202	YQM	C07-C06-C05	3.73	116.74	110.38
54	A	3201	YQM	O25-C24-N26	-3.65	114.70	122.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	A	3201	YQM	C19-C05-C04	3.62	116.59	111.64
54	A	3202	YQM	O25-C24-N26	-3.62	114.78	122.89
54	A	3201	YQM	C07-C06-C05	3.61	116.53	110.38
54	A	3201	YQM	O27-C20-C19	-3.24	108.68	113.37
54	A	3202	YQM	C14-C13-C12	3.22	124.55	118.98
54	A	3202	YQM	C24-C21-C22	-3.19	117.06	120.87
54	A	3201	YQM	C14-C13-C12	3.15	124.43	118.98
54	A	3201	YQM	C07-C16-C15	-3.11	116.91	121.44
54	A	3201	YQM	C17-C19-C20	3.07	113.48	109.88
54	A	3202	YQM	C06-C05-C04	-3.06	109.31	113.73
54	A	3202	YQM	O27-C20-C19	-2.80	109.31	113.37
54	A	3201	YQM	C06-C05-C04	-2.77	109.72	113.73
54	A	3201	YQM	C19-C20-C21	-2.48	119.33	122.89
54	A	3202	YQM	O28-C19-C20	-2.37	106.35	110.14
54	A	3201	YQM	O33-C32-N31	-2.36	119.41	123.64
54	A	3201	YQM	O28-C19-C20	-2.32	106.44	110.14
54	A	3201	YQM	C34-N35-C36	-2.22	110.46	113.34
54	A	3202	YQM	C37-C36-N35	-2.20	101.31	103.90
54	A	3202	YQM	O33-C32-N31	-2.12	119.84	123.64
54	A	3202	YQM	C39-N35-C36	2.11	106.53	104.04
54	A	3201	YQM	O29-C15-C14	-2.05	113.93	118.45

There are no chirality outliers.

All (8) torsion outliers are listed below:

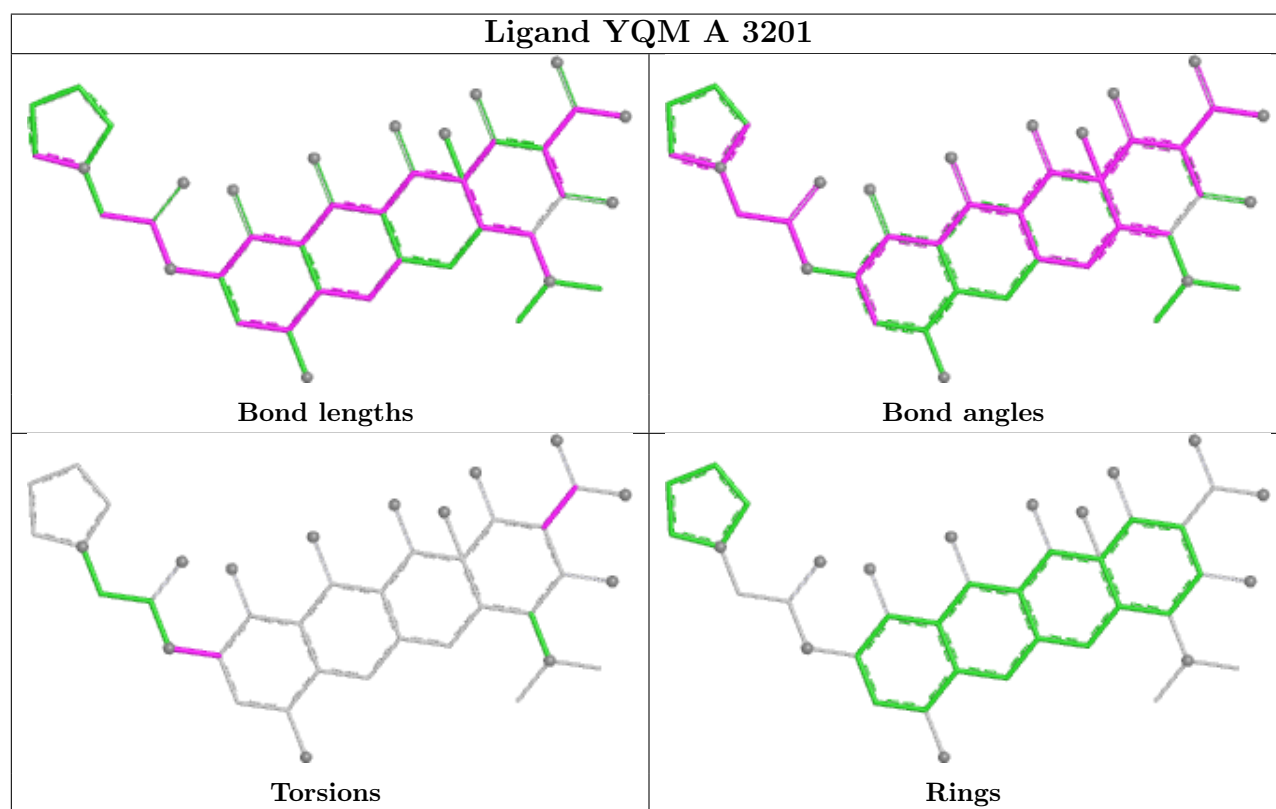
Mol	Chain	Res	Type	Atoms
54	A	3201	YQM	C22-C21-C24-N26
54	A	3201	YQM	C22-C21-C24-O25
54	A	3202	YQM	C20-C21-C24-N26
54	A	3202	YQM	C20-C21-C24-O25
54	A	3201	YQM	C11-C12-N31-C32
54	A	3201	YQM	C13-C12-N31-C32
54	A	3201	YQM	C20-C21-C24-N26
54	A	3201	YQM	C20-C21-C24-O25

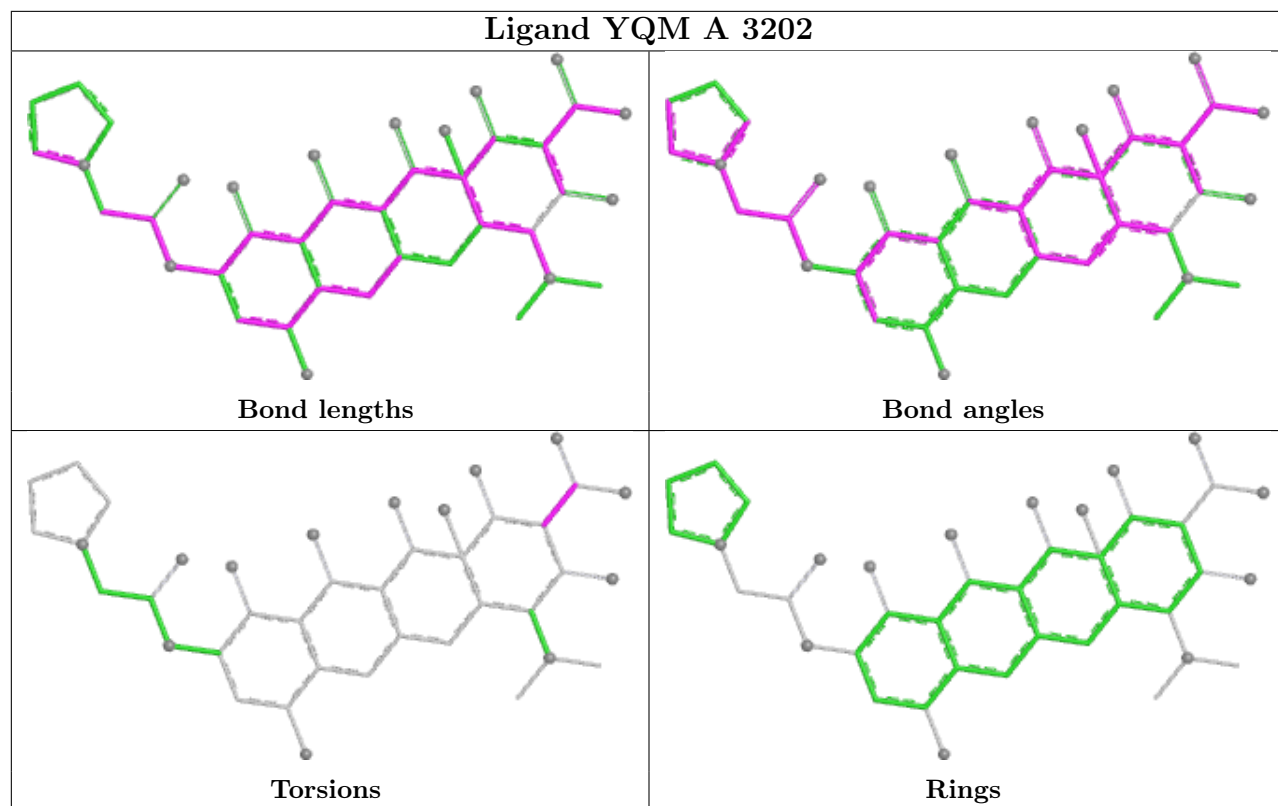
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	A	3201	YQM	1	0
54	A	3202	YQM	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

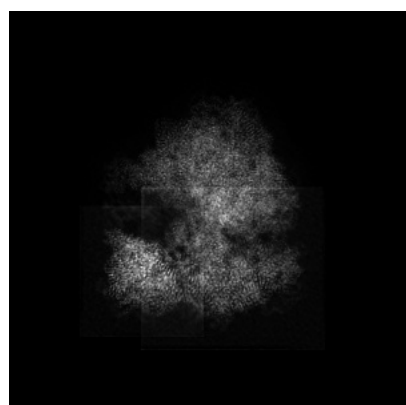
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23671. These allow visual inspection of the internal detail of the map and identification of artifacts.

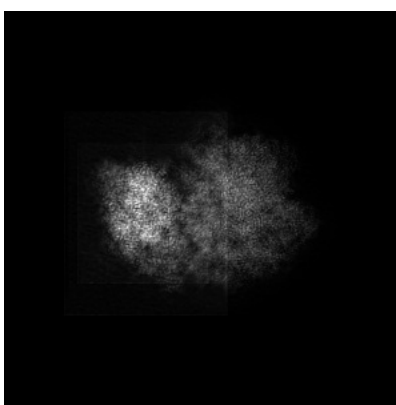
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

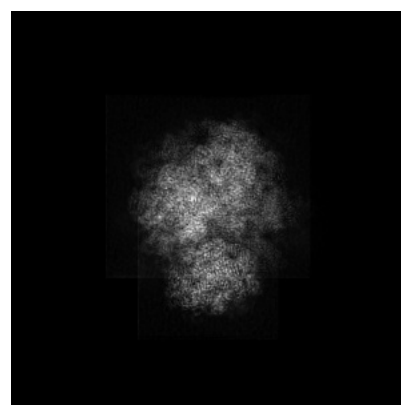
6.1.1 Primary map



X



Y



Z

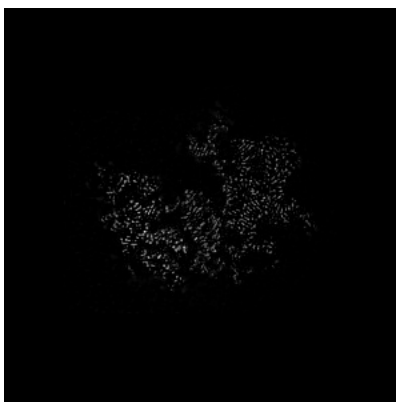
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

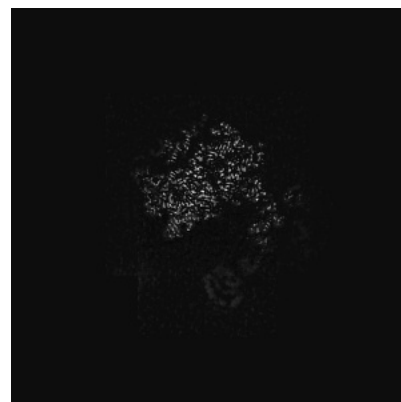
6.2.1 Primary map



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](#)

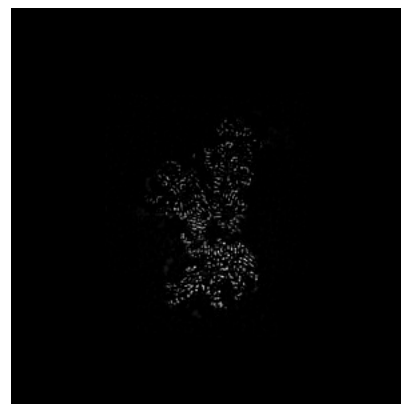
6.3.1 Primary map



X Index: 236



Y Index: 270

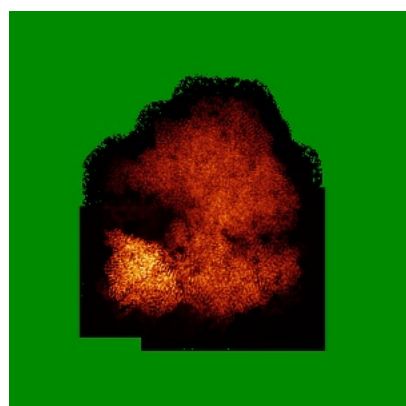


Z Index: 169

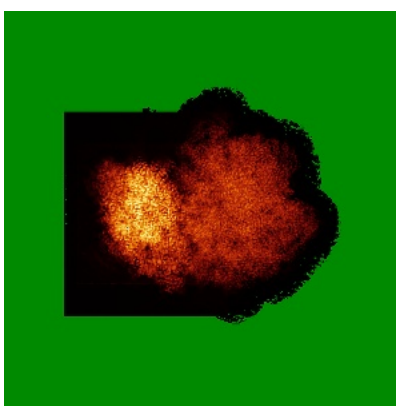
The images above show the largest variance slices of the map in three orthogonal directions.

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

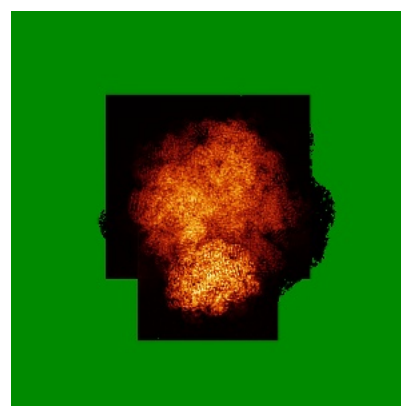
6.4.1 Primary map



X



Y

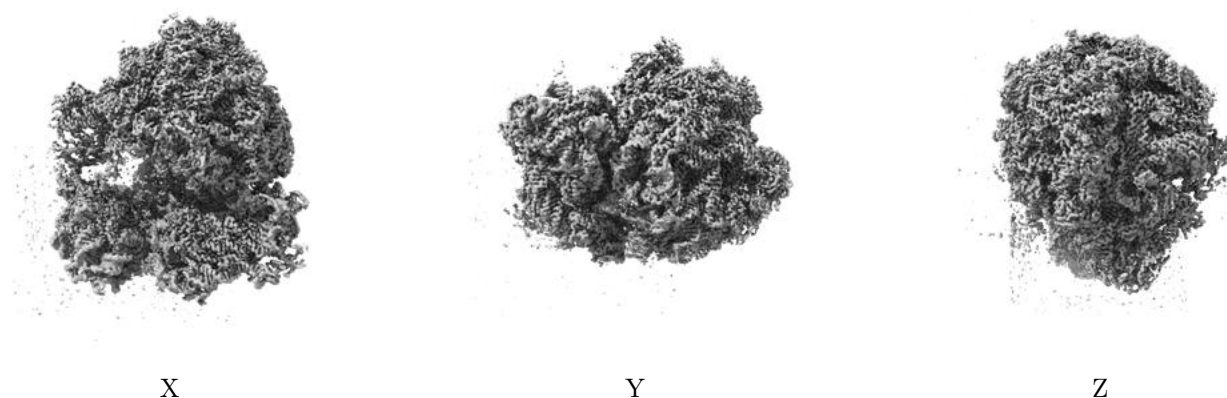


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

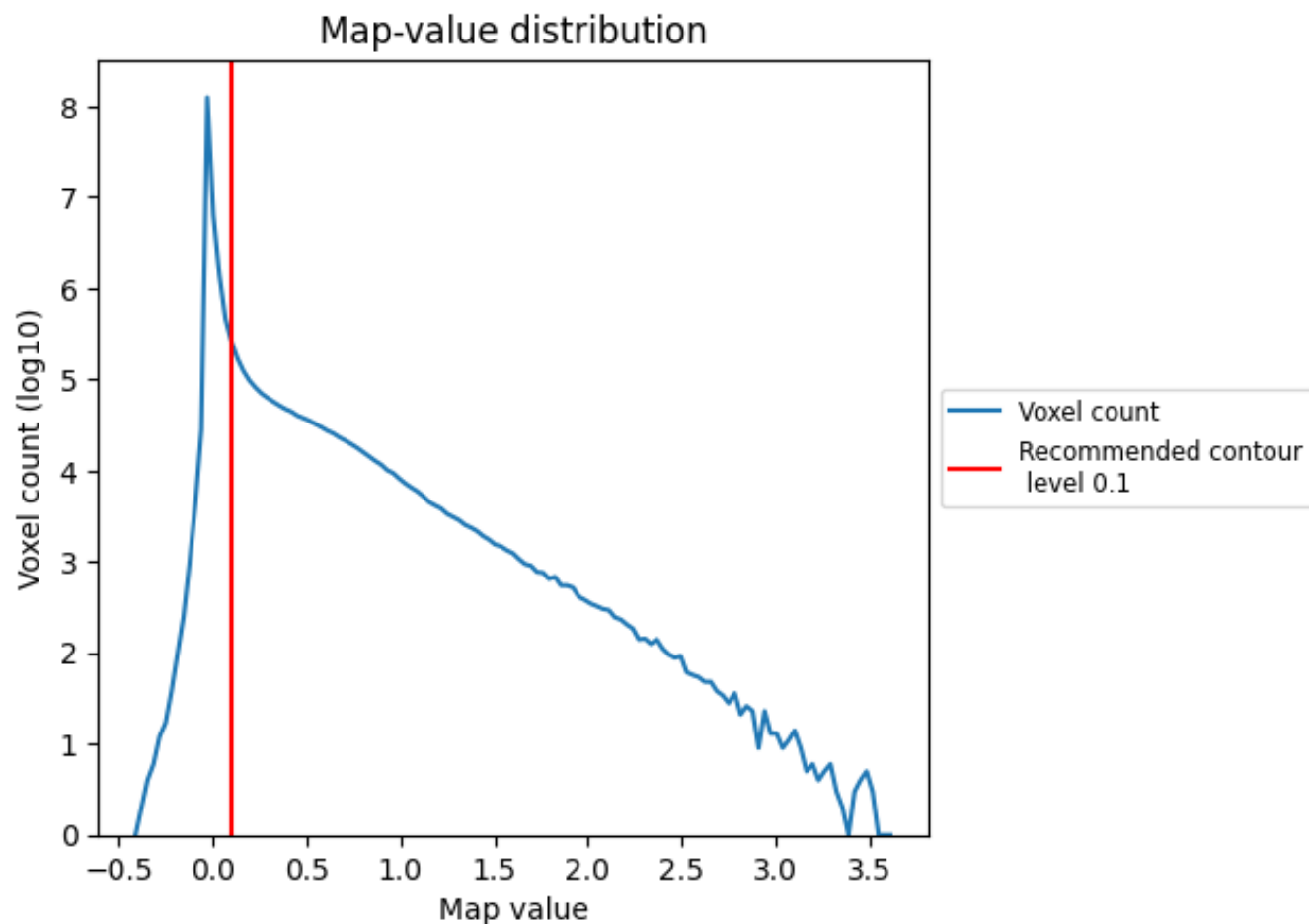
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

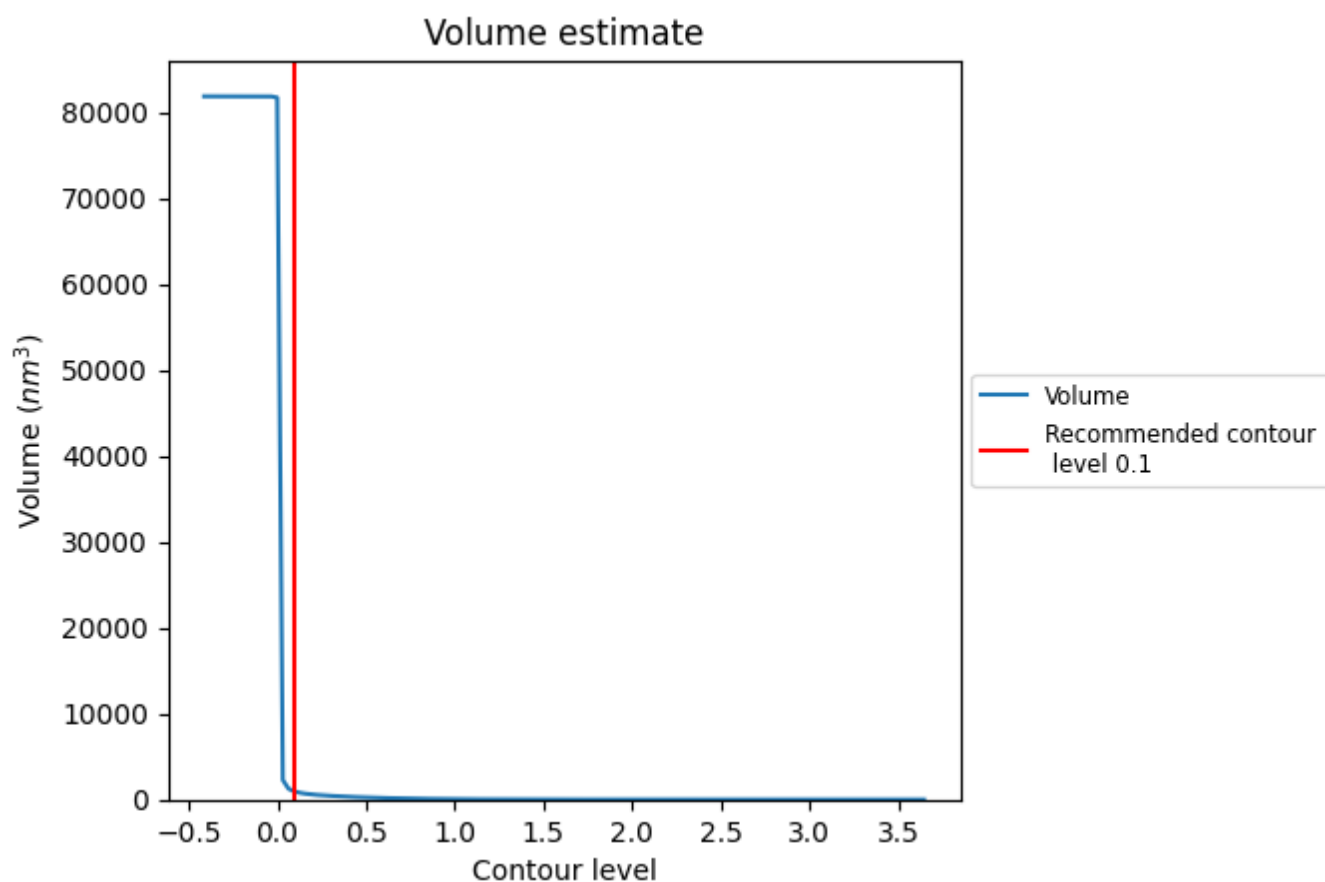
This section contains the results of statistical analysis of the map.

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.

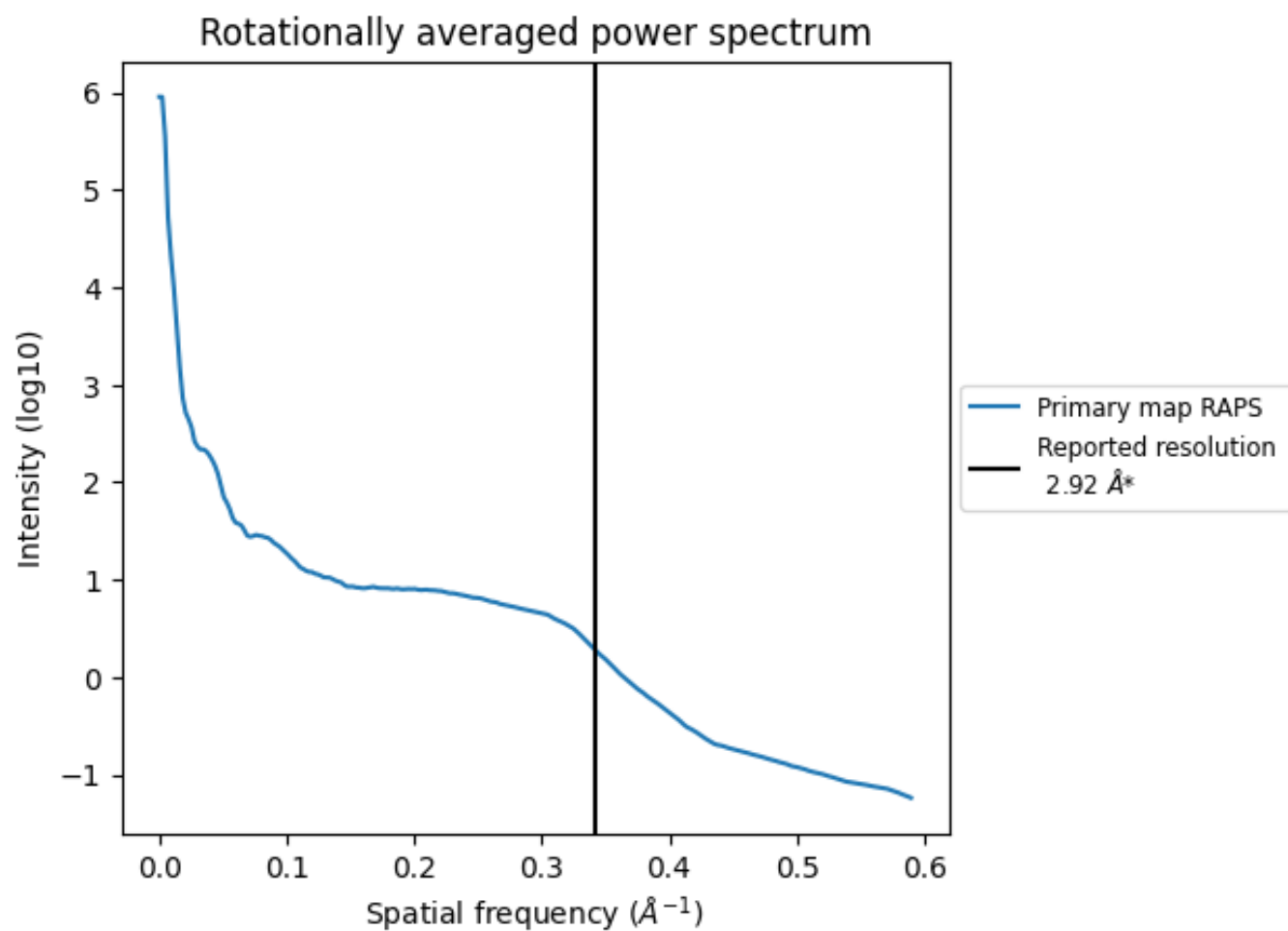
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 928 nm³; this corresponds to an approximate mass of 839 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 0.342 Å⁻¹

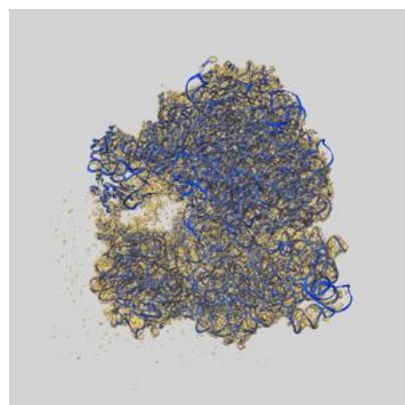
8 Fourier-Shell correlation ⓘ

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

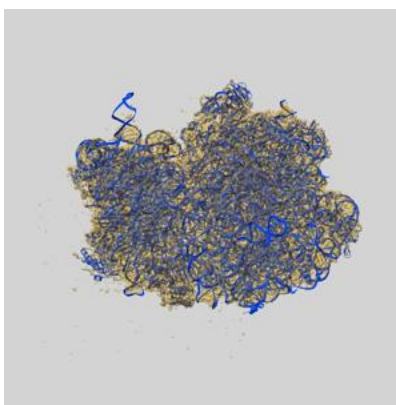
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23671 and PDB model 7M4Z. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

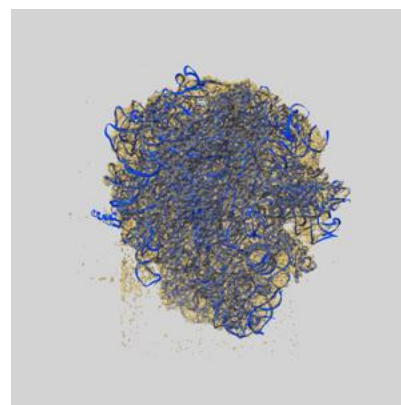
9.1 Map-model overlay [i](#)



X



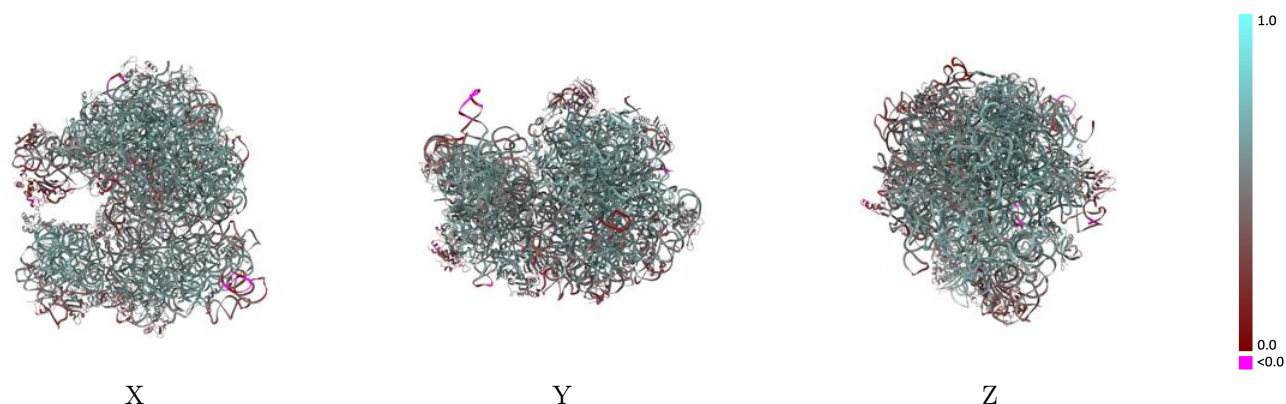
Y



Z

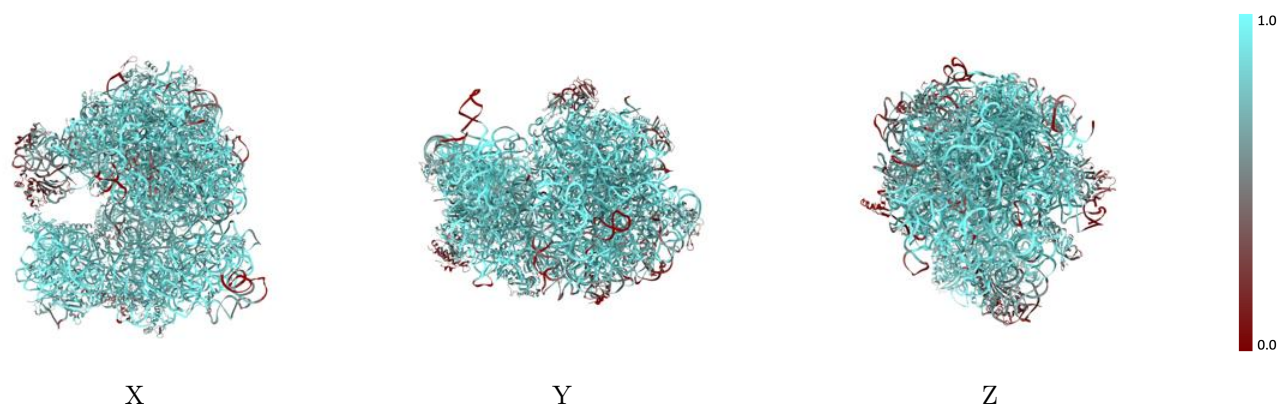
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



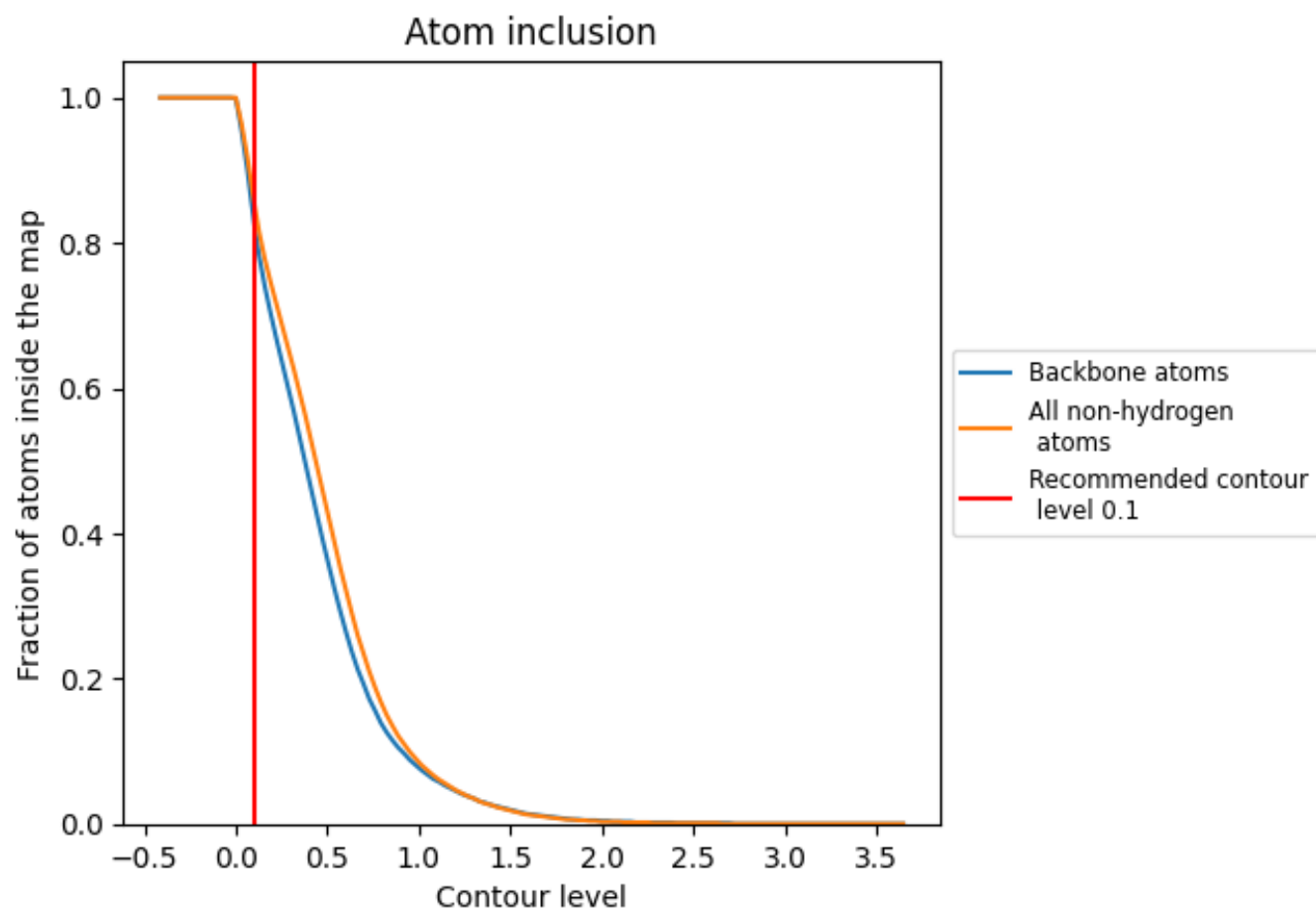
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 85% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8540	 0.5300
0	 0.7890	 0.5250
1	 0.9620	 0.6530
2	 0.9590	 0.6390
3	 0.9060	 0.5370
A	 0.8850	 0.5510
B	 0.6360	 0.4470
C	 0.9310	 0.5400
D	 0.9120	 0.5810
E	 0.7650	 0.5310
F	 0.2880	 0.1900
G	 0.4590	 0.3690
H	 0.1800	 0.2810
I	 0.9010	 0.5890
J	 0.8860	 0.5470
K	 0.8790	 0.5890
L	 0.8560	 0.5320
M	 0.9470	 0.6240
N	 0.5380	 0.3890
O	 0.8720	 0.5580
P	 0.9210	 0.6150
Q	 0.7870	 0.5300
R	 0.8900	 0.5940
S	 0.6960	 0.4800
T	 0.5090	 0.4120
U	 0.6690	 0.4820
V	 0.8950	 0.5990
W	 0.8210	 0.5570
X	 0.4620	 0.3620
Y	 0.7970	 0.5430
Z	 0.8020	 0.5600
a	 0.9220	 0.5430
b	 0.2580	 0.2570
c	 0.8760	 0.5060
d	 0.7240	 0.4390



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Chain	Atom inclusion	Q-score
e	 0.8920	 0.5350
f	 0.7200	 0.4110
g	 0.8240	 0.4430
h	 0.9020	 0.5660
i	 0.9110	 0.5560
j	 0.8560	 0.5110
k	 0.8160	 0.4500
l	 0.8750	 0.5280
m	 0.9190	 0.5350
n	 0.9330	 0.5730
o	 0.9240	 0.5590
p	 0.8730	 0.5550
q	 0.7810	 0.4760
r	 0.8860	 0.5200
s	 0.9520	 0.5840
t	 0.9040	 0.5300
u	 0.4520	 0.3340
v	 0.8360	 0.4370