



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 08:16 PM UTC

PDB ID : 7S0S / pdb_00007s0s
EMDB ID : EMD-24792
Title : M. tuberculosis ribosomal RNA methyltransferase TlyA bound to M. smegmatis 50S ribosomal subunit
Authors : Laughlin, Z.T.; Dunham, C.M.; Conn, G.L.
Deposited on : 2021-08-31
Resolution : 3.05 Å (reported)
Based on initial models : 3HP7, 5O60, 5KYG

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

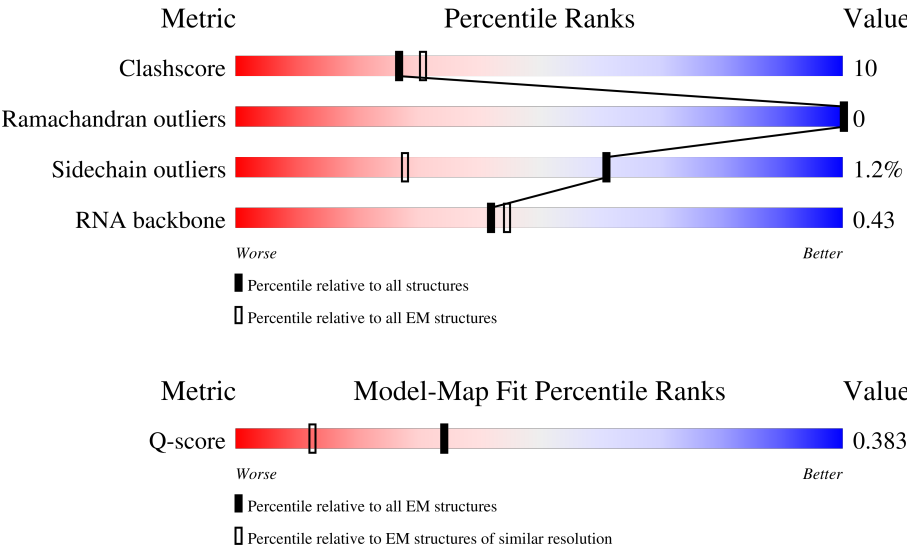
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.05 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	13971 (2.55 - 3.55)

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	3	23	96%
2	B	284	84%
3	C	3120	12%

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Mol	Chain	Length	Quality of chain
4	D	275	
5	E	214	
6	F	210	
7	G	182	
8	H	176	
9	I	151	
10	J	126	
11	K	133	
12	L	146	
13	M	122	
14	N	145	
15	O	136	
16	P	118	
17	Q	126	
18	R	113	
19	S	124	
20	T	100	
21	U	114	
22	V	97	
23	W	105	
24	X	192	
25	Y	79	
26	Z	63	
27	a	64	
28	b	59	

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Mol	Chain	Length	Quality of chain
29	c	54	 89%11%
30	d	49	 76%24%
31	e	46	 89%11%
32	f	63	 83%17%
33	g	37	 16%70%30%
34	h	48	 85%56%44%
35	i	118	 8%53%40%7%

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 100057 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 ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 2 is a protein called 16S/23S rRNA (Cytidine-2'-O)-methyltransferase TlyA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	265	Total	C	N	O	S	0	0
			1954	1221	372	359	2		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	MET	-	initiating methionine	UNP A0A045KH60
B	-14	HIS	-	expression tag	UNP A0A045KH60
B	-13	HIS	-	expression tag	UNP A0A045KH60
B	-12	HIS	-	expression tag	UNP A0A045KH60
B	-11	HIS	-	expression tag	UNP A0A045KH60
B	-10	HIS	-	expression tag	UNP A0A045KH60
B	-9	HIS	-	expression tag	UNP A0A045KH60
B	-8	ALA	-	expression tag	UNP A0A045KH60
B	-7	SER	-	expression tag	UNP A0A045KH60
B	-6	GLY	-	expression tag	UNP A0A045KH60
B	-5	LEU	-	expression tag	UNP A0A045KH60
B	-4	VAL	-	expression tag	UNP A0A045KH60
B	-3	PRO	-	expression tag	UNP A0A045KH60
B	-2	ARG	-	expression tag	UNP A0A045KH60
B	-1	GLY	-	expression tag	UNP A0A045KH60
B	0	SER	-	expression tag	UNP A0A045KH60

- Molecule 3 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	3119	Total	C	N	O	P	0	0
			67010	29871	12320	21700	3119		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 21 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	V	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 24 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	X	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Y	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	b	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	63	Total	C	N	O		0	0
			502	302	115	85			

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 34 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 35 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	C	380	Total	Mg	0
			380	380	
36	D	5	Total	Mg	0
			5	5	
36	E	2	Total	Mg	0
			2	2	
36	N	1	Total	Mg	0
			1	1	
36	O	4	Total	Mg	0
			4	4	
36	U	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
36	i	9	Total 9	Mg 9	0

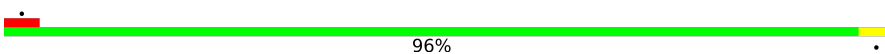
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	Z	1	Total 1	Zn 1	0
37	d	1	Total 1	Zn 1	0
37	g	1	Total 1	Zn 1	0
37	h	1	Total 1	Zn 1	0

3 Residue-property plots

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.

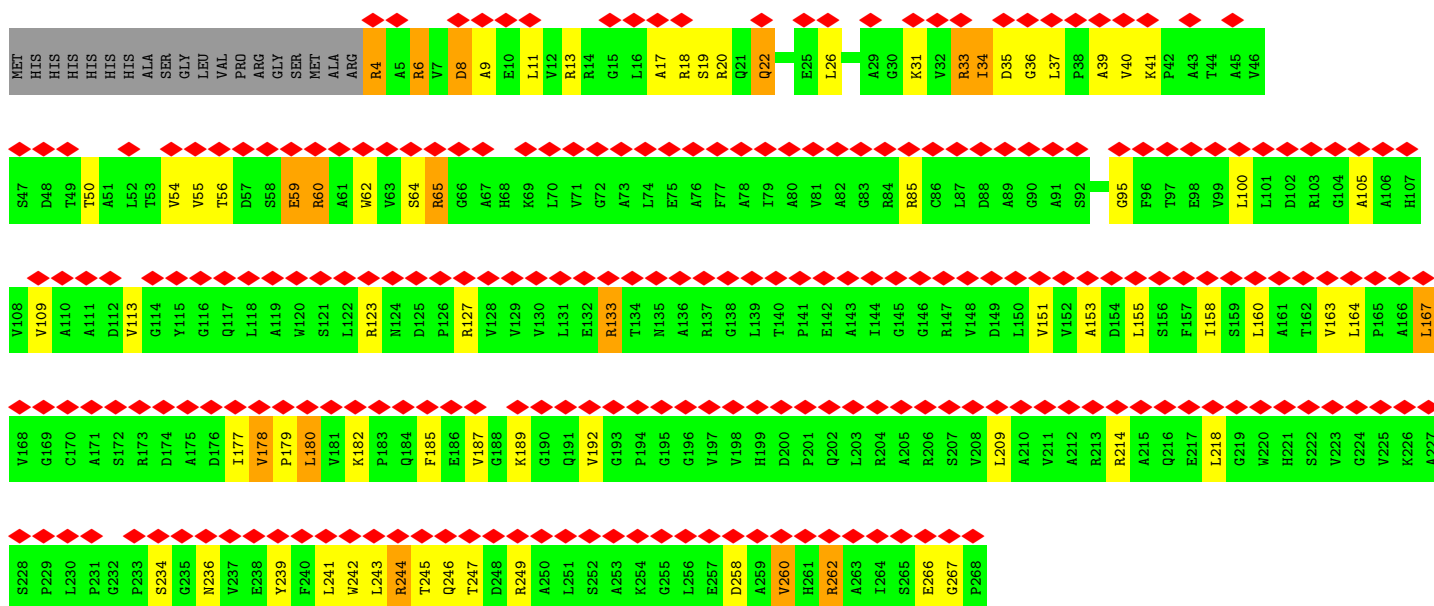
- Molecule 1: ribosomal protein bL37

Chain 3: 



- Molecule 2: 16S/23S rRNA (Cytidine-2'-O)-methyltransferase TlyA

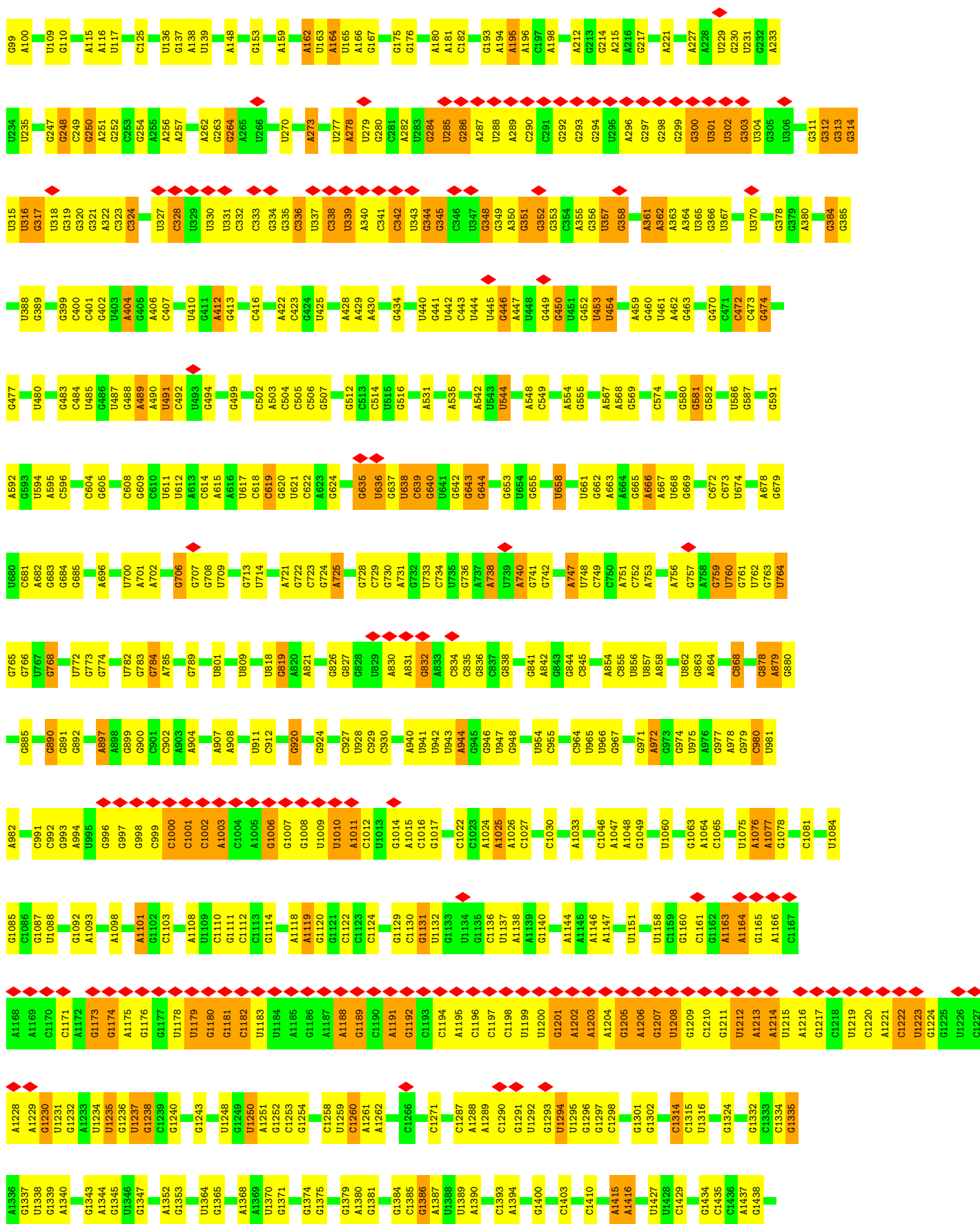
Chain B: 

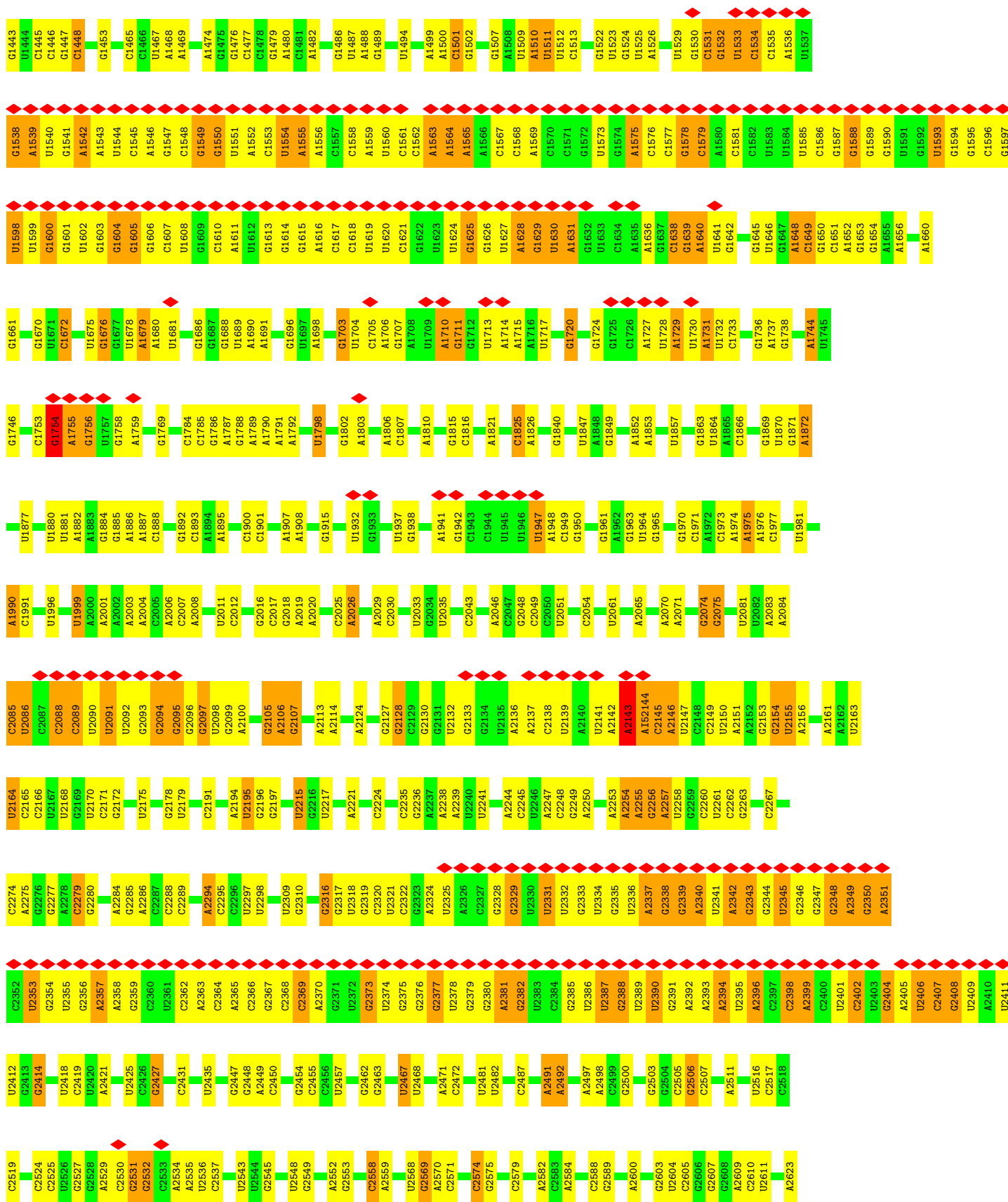


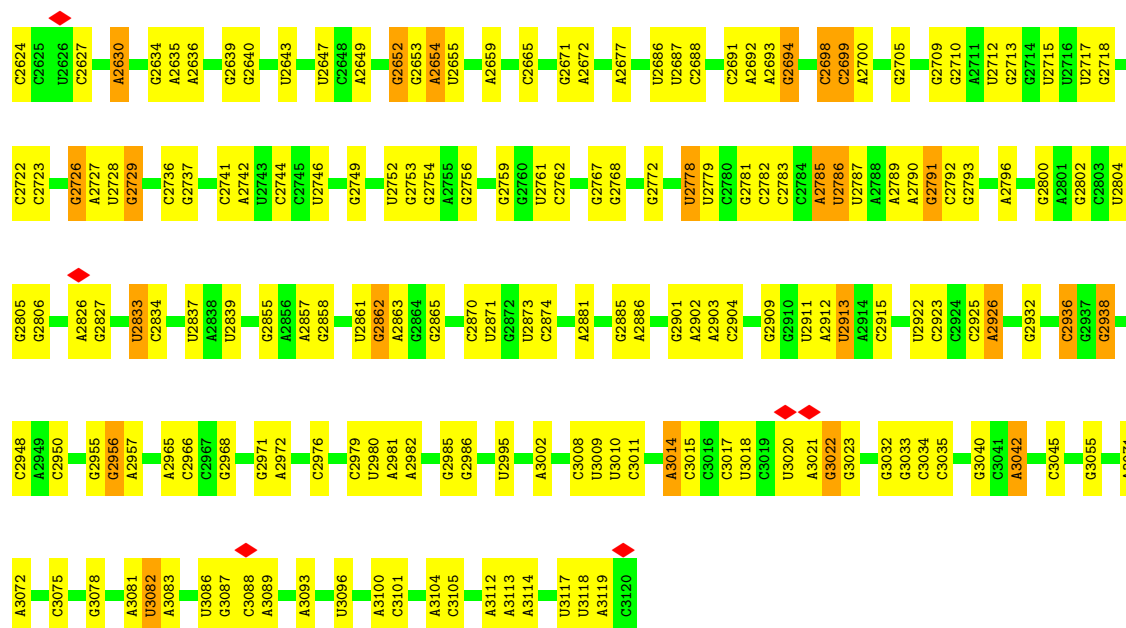
- Molecule 3: 23S rRNA

Chain C: 

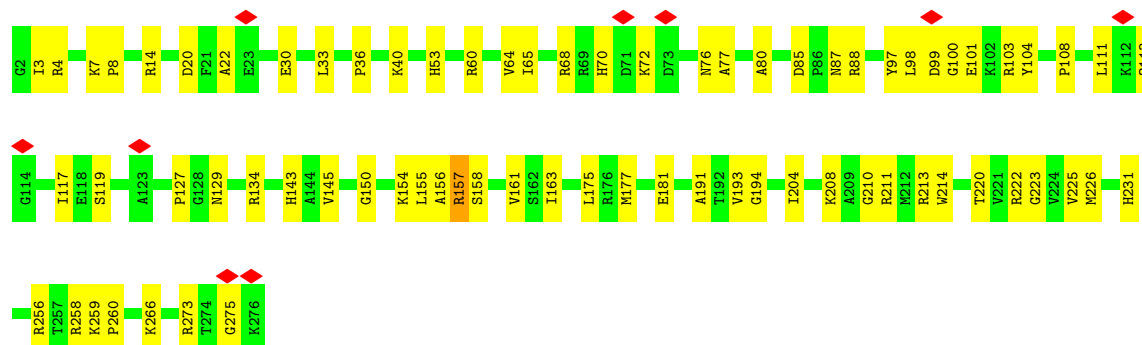




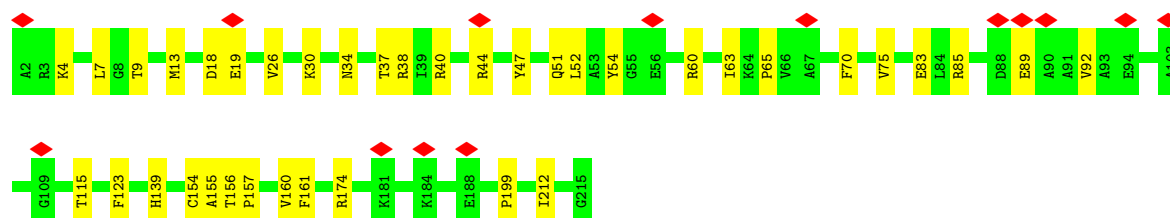
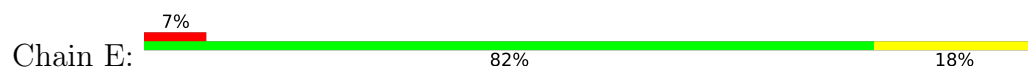




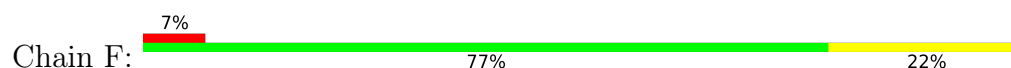
• Molecule 4: 50S ribosomal protein L2

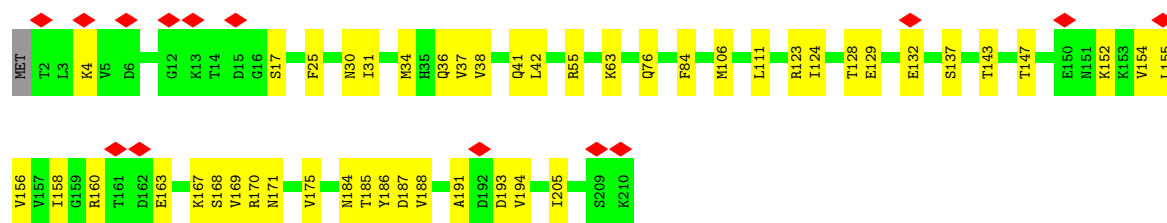


• Molecule 5: 50S ribosomal protein L3

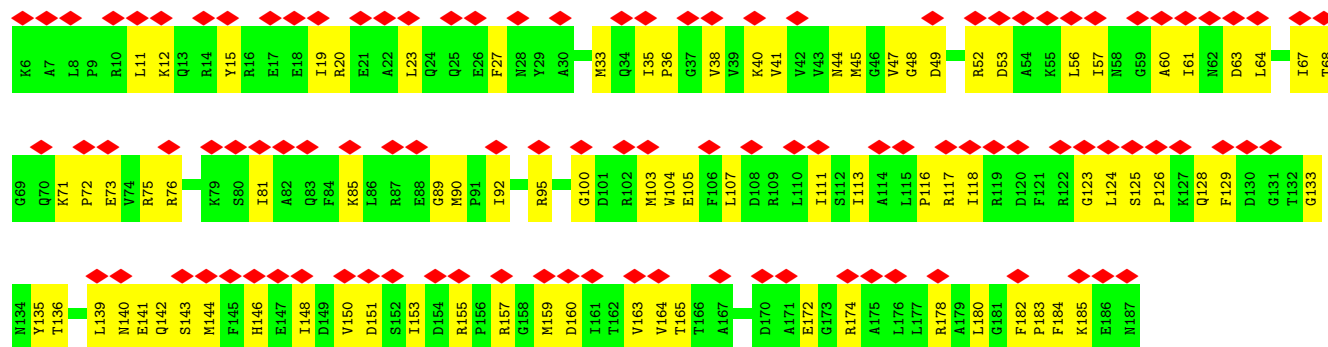


• Molecule 6: 50S ribosomal protein L4

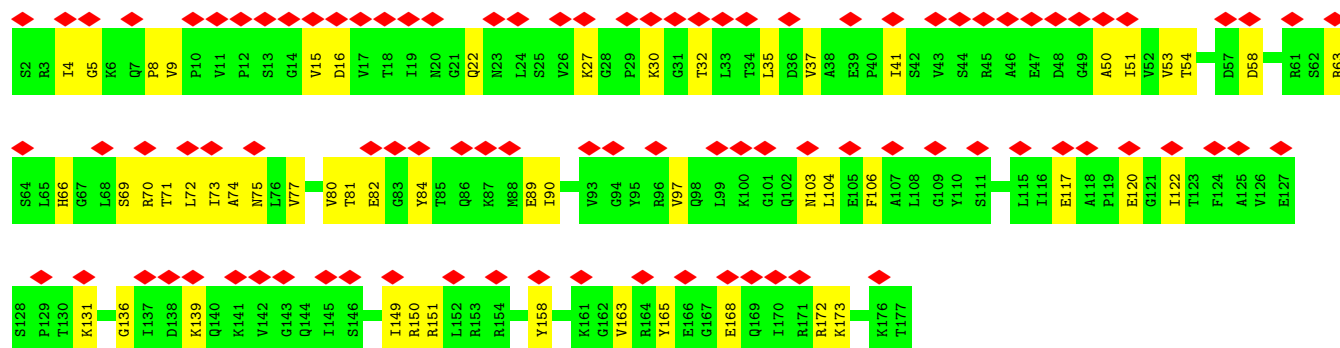




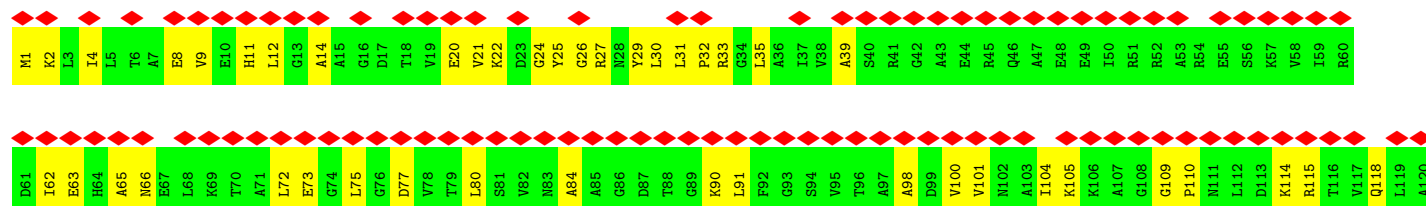
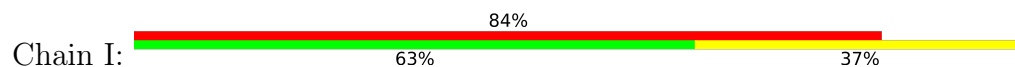
• Molecule 7: 50S ribosomal protein L5



• Molecule 8: 50S ribosomal protein L6



• Molecule 9: 50S ribosomal protein L9

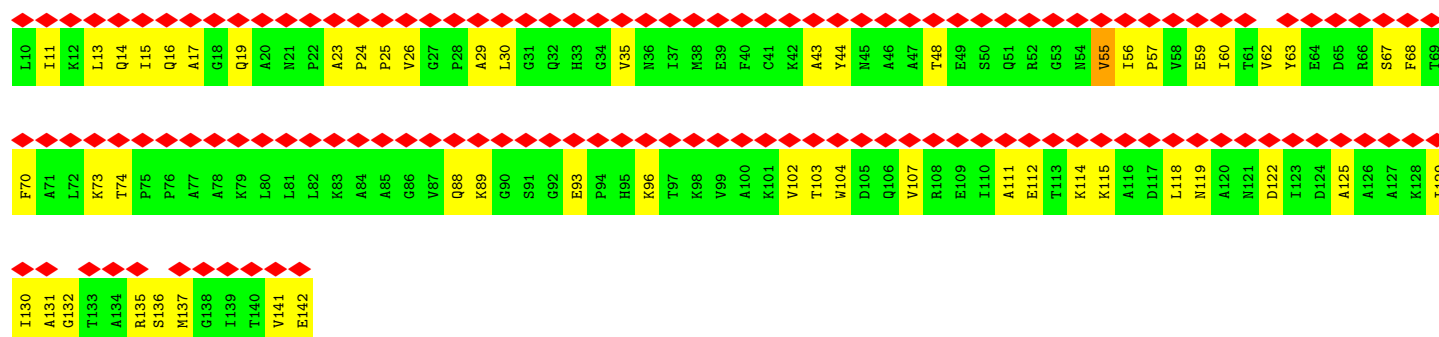




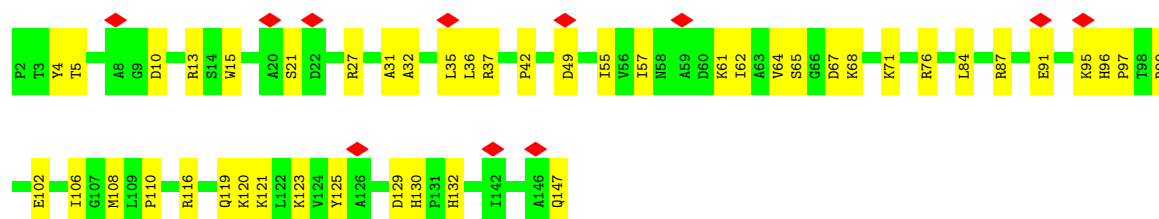
• Molecule 10: 50S ribosomal protein L10



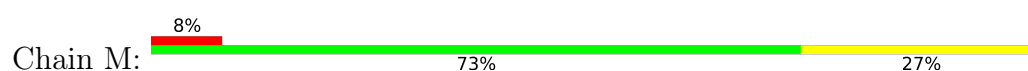
• Molecule 11: 50S ribosomal protein L11

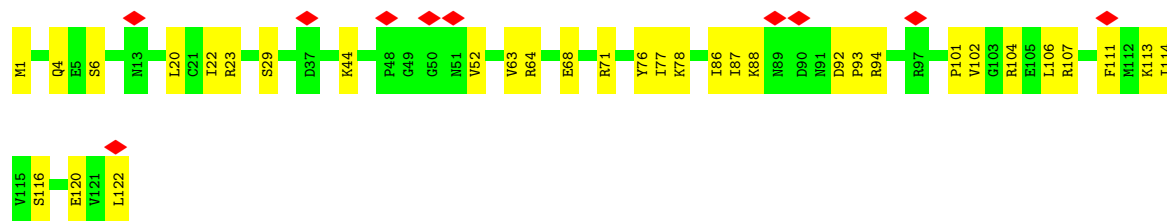


• Molecule 12: 50S ribosomal protein L13

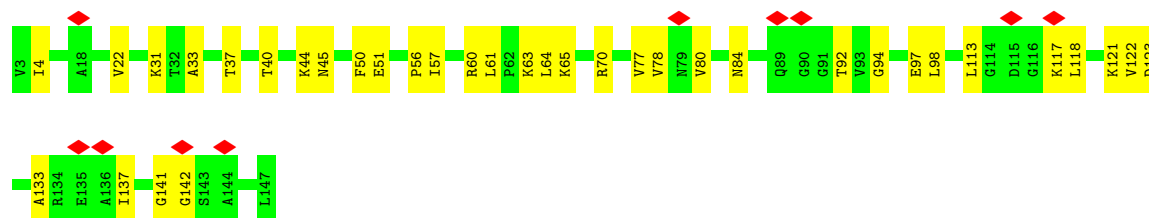
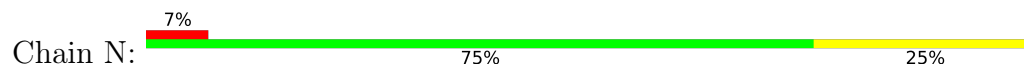


• Molecule 13: 50S ribosomal protein L14

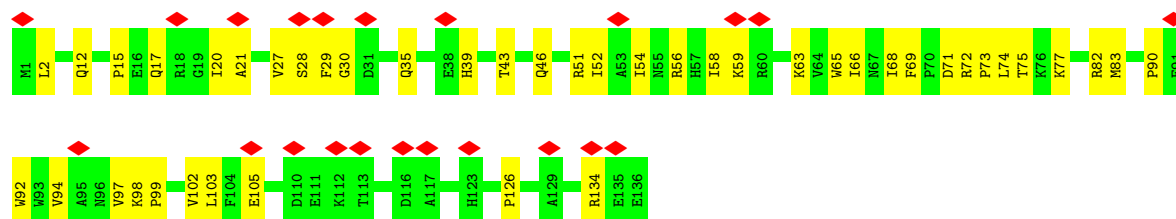




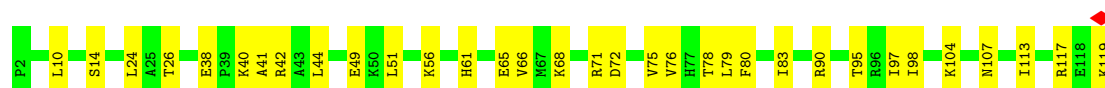
- Molecule 14: 50S ribosomal protein L15



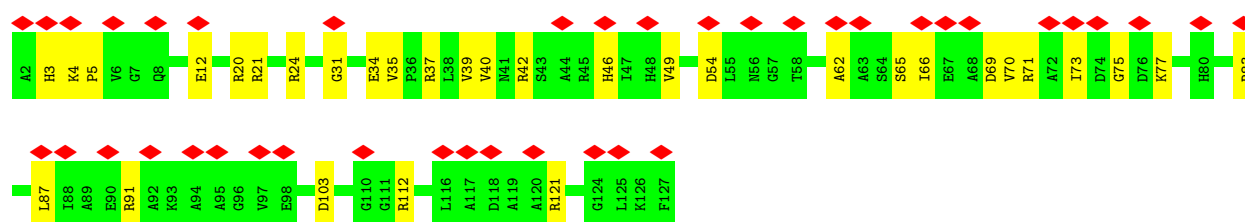
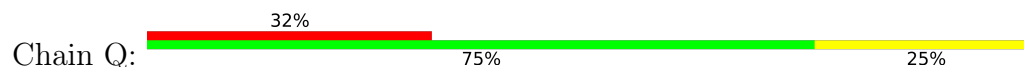
- Molecule 15: 50S ribosomal protein L16



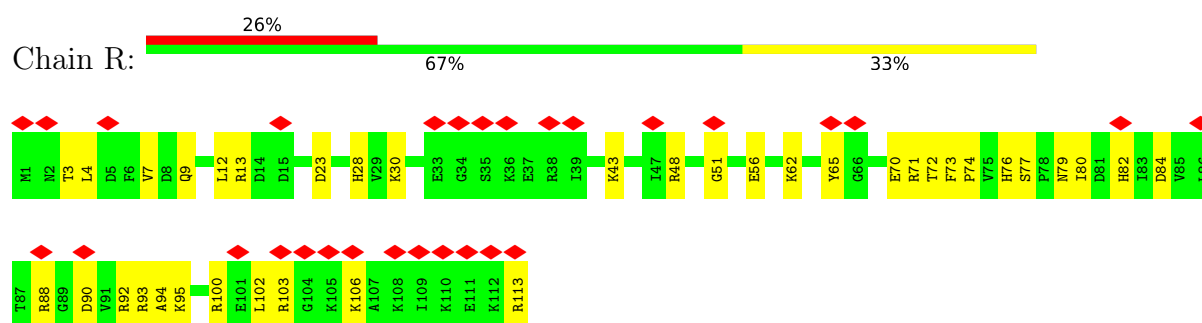
- Molecule 16: 50S ribosomal protein L17



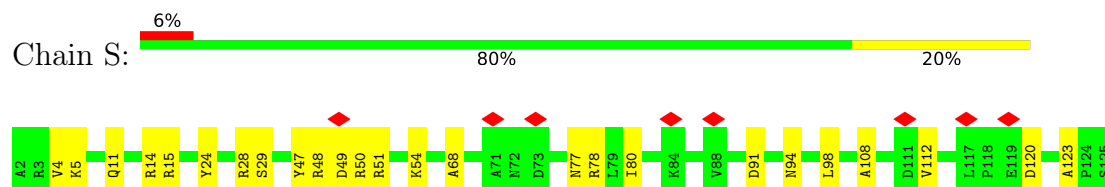
- Molecule 17: 50S ribosomal protein L18



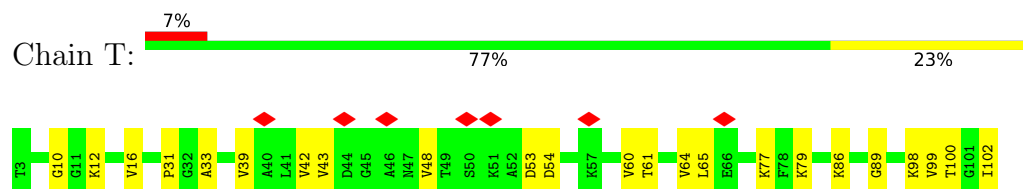
- Molecule 18: 50S ribosomal protein L19



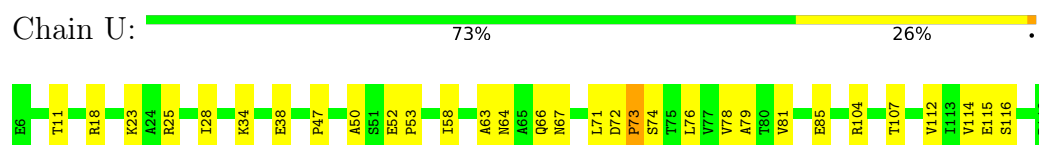
- Molecule 19: 50S ribosomal protein L20



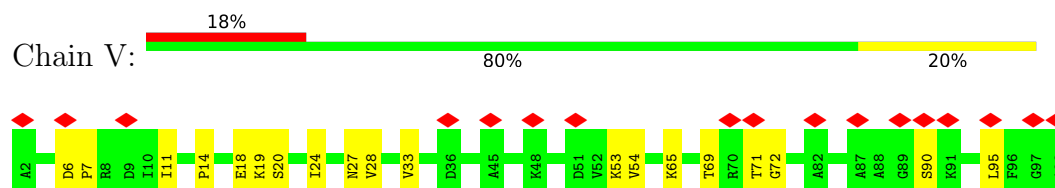
- Molecule 20: 50S ribosomal protein L21



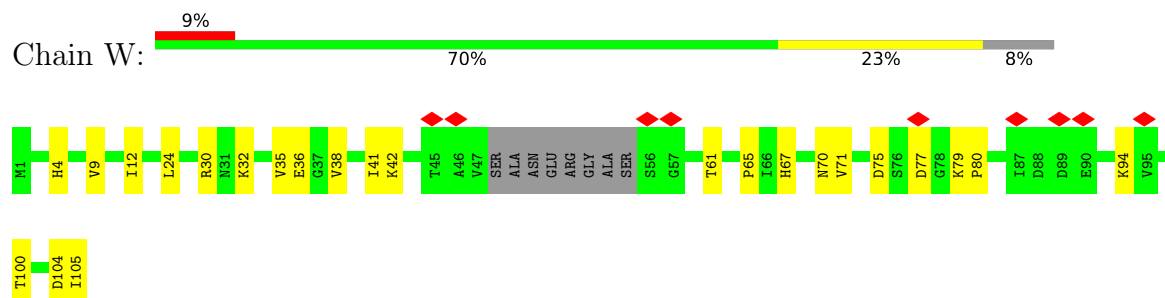
- Molecule 21: 50S ribosomal protein L22



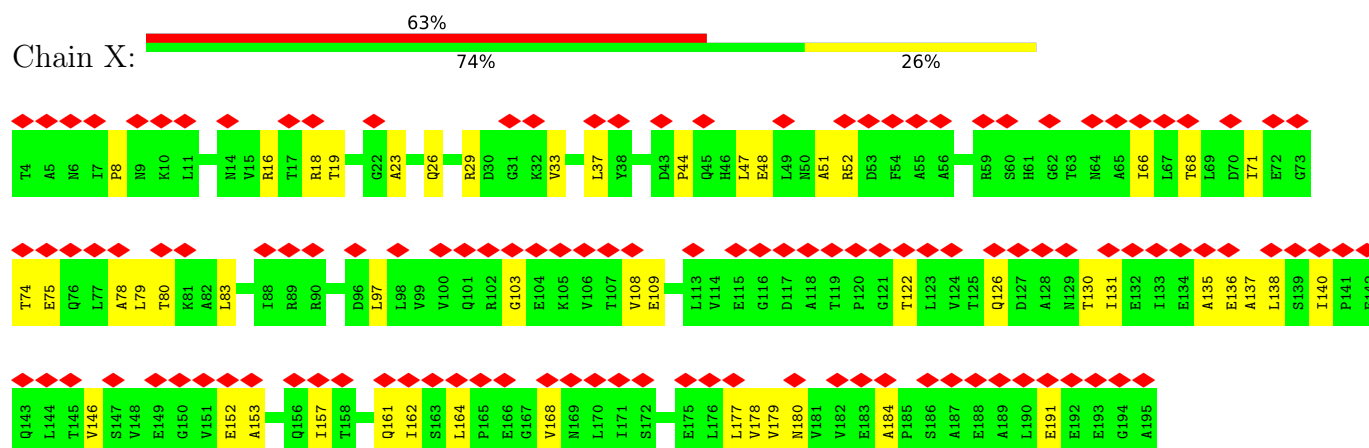
- Molecule 22: 50S ribosomal protein L23



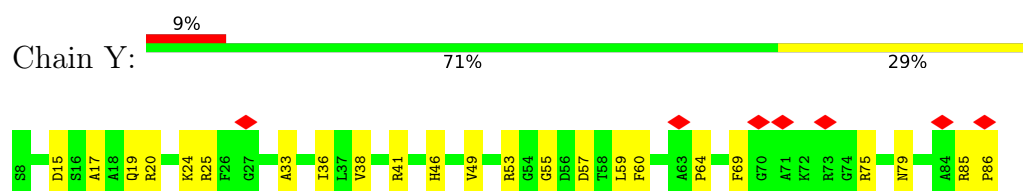
- Molecule 23: 50S ribosomal protein L24



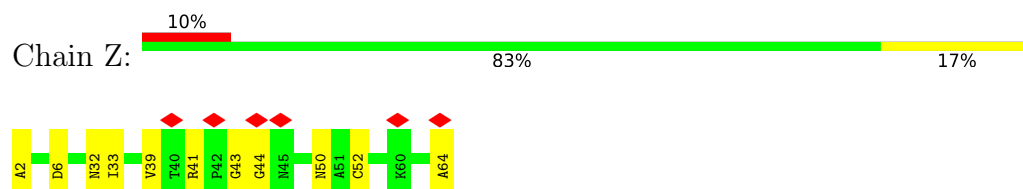
- Molecule 24: 50S ribosomal protein L25



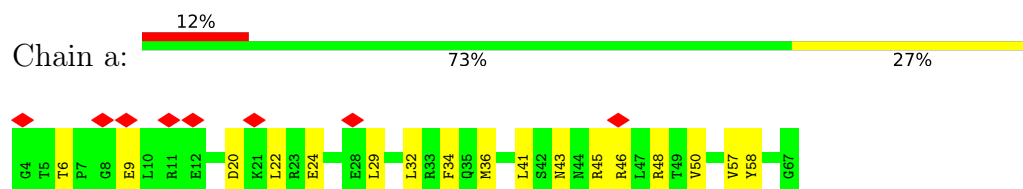
- Molecule 25: 50S ribosomal protein L27



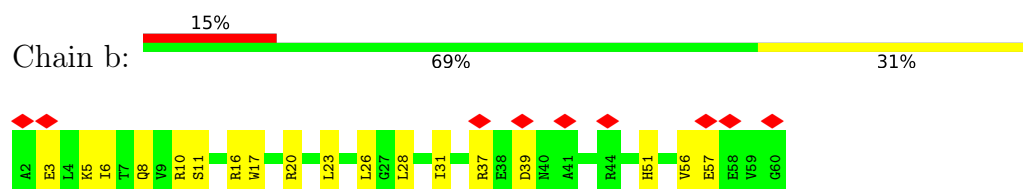
- Molecule 26: 50S ribosomal protein L28



- Molecule 27: 50S ribosomal protein L29



- Molecule 28: 50S ribosomal protein L30

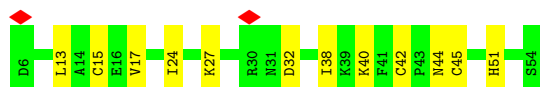
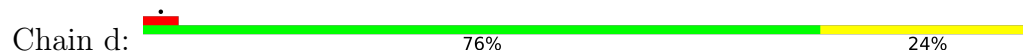


- Molecule 29: 50S ribosomal protein L32

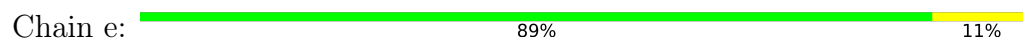




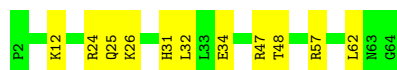
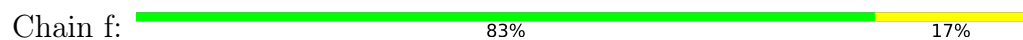
- Molecule 30: 50S ribosomal protein L33



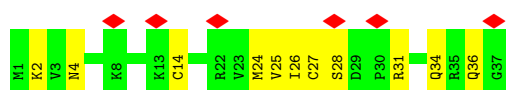
- Molecule 31: 50S ribosomal protein L34



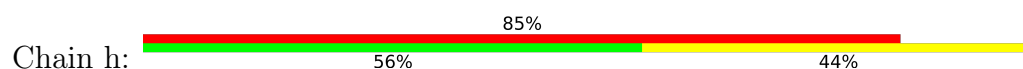
- Molecule 32: 50S ribosomal protein L35



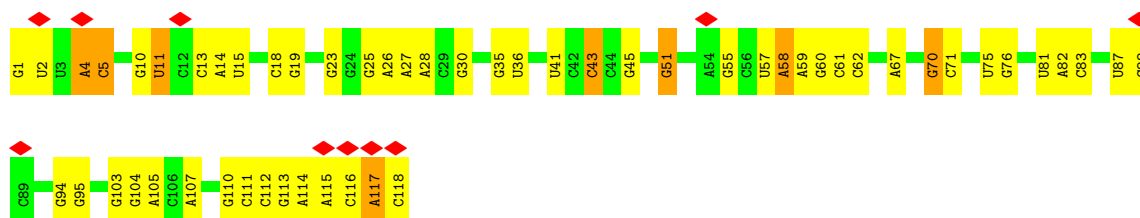
- Molecule 33: 50S ribosomal protein L36



- Molecule 34: 50S ribosomal protein L31



- Molecule 35: 5S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	129011	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.79	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.163	Depositor
Minimum map value	-0.097	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0179	Depositor
Map size ($\text{\AA}$)	299.32, 299.32, 299.32	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.069, 1.069, 1.069	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, AI5, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	3	0.38	0/191	0.54	0/247
2	B	0.73	0/1986	0.96	2/2702 (0.1%)
3	C	0.39	0/74978	0.41	3/116989 (0.0%)
4	D	0.40	0/2153	0.50	0/2895
5	E	0.40	0/1609	0.56	0/2165
6	F	0.39	0/1592	0.47	0/2153
7	G	0.25	0/1467	0.48	0/1973
8	H	0.25	0/1369	0.47	0/1848
9	I	0.22	0/1027	0.49	0/1398
10	J	0.20	0/925	0.48	1/1246 (0.1%)
11	K	0.21	0/1006	0.53	2/1364 (0.1%)
12	L	0.39	0/1157	0.49	0/1567
13	M	0.35	0/946	0.48	0/1268
14	N	0.37	0/1091	0.53	0/1457
15	O	0.36	0/1118	0.52	0/1506
16	P	0.38	0/945	0.47	0/1267
17	Q	0.25	0/966	0.37	0/1298
18	R	0.34	0/921	0.48	0/1236
19	S	0.40	0/1000	0.46	0/1341
20	T	0.37	0/764	0.43	0/1030
21	U	0.39	0/887	0.51	1/1204 (0.1%)
22	V	0.37	0/766	0.43	0/1030
23	W	0.35	0/738	0.48	0/987
24	X	0.27	0/1443	0.49	0/1970
25	Y	0.40	0/595	0.45	0/798
26	Z	0.41	0/478	0.47	0/641
27	a	0.35	0/534	0.56	0/713
28	b	0.39	0/477	0.52	0/640
29	c	0.40	0/427	0.57	0/572
30	d	0.32	0/413	0.42	0/553
31	e	0.40	0/380	0.53	0/500
32	f	0.39	0/507	0.43	0/672

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.36	0/303	0.53	0/401
34	h	0.18	0/372	0.36	0/503
35	i	0.29	0/2821	0.36	0/4396
All	All	0.39	0/108352	0.44	9/162530 (0.0%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2154	G	C2'-C3'-O3'	11.91	127.36	109.50
3	C	2143	A	C2'-C3'-O3'	7.57	120.86	109.50
21	U	73	PRO	CA-N-CD	-6.17	103.37	112.00
11	K	55	VAL	CA-C-N	-6.00	118.11	123.33
11	K	55	VAL	C-N-CA	-6.00	118.11	123.33
2	B	178	VAL	CA-C-O	-5.55	117.11	120.88
2	B	113	VAL	N-CA-C	-5.43	106.12	111.77
3	C	1754	G	C4'-C3'-O3'	-5.21	105.18	113.00
10	J	66	ILE	N-CA-C	-5.02	107.44	111.91

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3	189	0	205	1	0
2	B	1954	0	2002	55	0
3	C	67010	0	33685	902	0
4	D	2110	0	2165	59	0
5	E	1587	0	1630	32	0
6	F	1569	0	1607	34	0
7	G	1445	0	1476	66	0
8	H	1348	0	1399	38	0
9	I	1018	0	988	47	0
10	J	918	0	959	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	K	990	0	1021	46	0
12	L	1130	0	1167	39	0
13	M	938	0	1000	26	0
14	N	1078	0	1151	30	0
15	O	1092	0	1128	30	0
16	P	928	0	972	27	0
17	Q	956	0	991	24	0
18	R	907	0	938	24	0
19	S	988	0	1038	20	0
20	T	754	0	802	16	0
21	U	873	0	909	24	0
22	V	756	0	802	15	0
23	W	732	0	782	20	0
24	X	1428	0	1443	38	0
25	Y	586	0	601	22	0
26	Z	470	0	480	9	0
27	a	531	0	541	24	0
28	b	474	0	500	12	0
29	c	423	0	463	8	0
30	d	405	0	407	8	0
31	e	377	0	411	5	0
32	f	502	0	541	11	0
33	g	299	0	321	7	0
34	h	364	0	350	22	0
35	i	2522	0	1285	36	0
36	C	380	0	0	0	0
36	D	5	0	0	0	0
36	E	2	0	0	0	0
36	N	1	0	0	0	0
36	O	4	0	0	0	0
36	U	1	0	0	0	0
36	i	9	0	0	0	0
37	Z	1	0	0	0	0
37	d	1	0	0	0	0
37	g	1	0	0	0	0
37	h	1	0	0	0	0
All	All	100057	0	66160	1610	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 10.

All (1610) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:65:ARG:NH1	3:C:2146:A:H5''	1.52	1.23
2:B:65:ARG:HH12	3:C:2146:A:C5'	1.66	1.06
3:C:273:A:H62	3:C:313:G:N2	1.60	0.99
2:B:65:ARG:HH12	3:C:2146:A:H5''	0.82	0.97
3:C:353:G:H1	3:C:442:U:H3	1.06	0.96
27:a:43:ASN:HD22	27:a:46:ARG:HD2	1.32	0.95
14:N:84:ASN:HD21	14:N:118:LEU:HA	1.33	0.94
3:C:341:C:C4	3:C:342:C:N4	2.39	0.91
3:C:2086:U:H3	3:C:2096:G:H1	1.18	0.90
3:C:2321:U:H3	3:C:2414:G:H1	1.20	0.89
3:C:2329:G:H1	3:C:2406:U:H3	0.90	0.88
27:a:43:ASN:ND2	27:a:46:ARG:HG3	1.89	0.88
5:E:63:ILE:HG22	5:E:65:PRO:HD2	1.55	0.87
2:B:33:ARG:HG3	2:B:39:ALA:HA	1.54	0.87
3:C:1636:A:H62	3:C:1802:G:H21	1.23	0.86
7:G:44:ASN:O	7:G:160:ASP:HB2	1.77	0.84
3:C:1118:A:H4'	28:b:10:ARG:HH22	1.41	0.84
5:E:34:ASN:HD21	5:E:54:TYR:HB2	1.43	0.83
18:R:74:PRO:HG2	18:R:77:SER:HB2	1.62	0.82
7:G:64:LEU:HD22	7:G:72:PRO:HG3	1.62	0.82
3:C:137:G:H21	3:C:1524:G:H1'	1.44	0.81
10:J:10:VAL:HG13	10:J:60:ALA:HB2	1.61	0.81
3:C:341:C:N4	3:C:342:C:N4	2.30	0.80
34:h:16:CYS:SG	34:h:22:PHE:HE2	2.04	0.80
3:C:2331:U:H1'	3:C:2404:G:H22	1.47	0.79
3:C:2532:G:H1	3:C:2535:A:H62	1.29	0.79
7:G:20:ARG:HH21	7:G:35:ILE:HB	1.47	0.79
9:I:26:GLY:HA2	9:I:31:LEU:HD13	1.65	0.79
34:h:16:CYS:SG	34:h:22:PHE:CE2	2.75	0.79
3:C:262:A:H62	3:C:263:G:H21	1.29	0.78
3:C:273:A:H62	3:C:313:G:H21	1.29	0.77
5:E:34:ASN:ND2	5:E:54:TYR:HB2	1.99	0.77
3:C:964:C:H4'	28:b:17:TRP:HH2	1.48	0.77
9:I:118:GLN:HG3	9:I:133:THR:HG23	1.66	0.77
6:F:169:VAL:HG22	6:F:175:VAL:HG11	1.66	0.76
3:C:1550:G:H1	3:C:1620:U:H3	0.80	0.76
5:E:7:LEU:HD13	5:E:52:LEU:HD11	1.67	0.76
27:a:43:ASN:ND2	27:a:46:ARG:CG	2.48	0.76
3:C:81:A:OP1	23:W:4:HIS:CE1	2.39	0.76
4:D:273:ARG:HH11	4:D:275:GLY:H	1.33	0.76
17:Q:12:GLU:HG3	35:i:60:G:H4'	1.68	0.75
3:C:724:G:OP1	32:f:47:ARG:NH2	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:470:G:H22	3:C:480:U:H3	1.31	0.75
7:G:41:VAL:HG13	7:G:103:MET:HE1	1.68	0.75
3:C:920:G:OP2	14:N:44:LYS:NZ	2.20	0.74
3:C:262:A:N6	3:C:263:G:H21	1.84	0.74
3:C:1181:G:H2'	3:C:1182:C:H5''	1.67	0.74
3:C:993:G:N2	3:C:1015:A:OP2	2.20	0.74
23:W:79:LYS:HD3	23:W:80:PRO:HD2	1.70	0.74
14:N:63:LYS:HE3	32:f:12:LYS:HD3	1.70	0.74
34:h:16:CYS:SG	34:h:20:HIS:HB3	2.27	0.73
3:C:297:G:H2'	3:C:298:G:C8	2.22	0.73
34:h:46:THR:OG1	34:h:48:LYS:NZ	2.20	0.73
3:C:293:G:H2'	3:C:294:G:C8	2.24	0.73
3:C:273:A:N6	3:C:313:G:H21	1.87	0.73
12:L:99:ARG:HA	12:L:102:GLU:HG2	1.70	0.73
3:C:1174:G:H4'	3:C:1204:A:H8	1.53	0.73
16:P:98:ILE:HD11	29:c:51:LEU:HD22	1.71	0.73
11:K:59:GLU:HB2	11:K:73:LYS:HB2	1.70	0.72
24:X:80:THR:HG21	24:X:83:LEU:HD11	1.71	0.72
3:C:747:A:N6	3:C:768:G:O2'	2.21	0.72
3:C:1175:A:H1'	10:J:33:VAL:HG11	1.71	0.72
27:a:43:ASN:HD22	27:a:46:ARG:CD	2.02	0.72
7:G:142:GLN:HG3	7:G:157:ARG:HH21	1.54	0.72
3:C:1629:G:O2'	3:C:1631:A:N6	2.23	0.72
24:X:16:ARG:HG2	24:X:48:GLU:HG3	1.72	0.72
3:C:1174:G:H4'	3:C:1204:A:C8	2.25	0.72
3:C:1223:U:H2'	3:C:1224:G:H8	1.54	0.72
7:G:73:GLU:OE1	7:G:75:ARG:NH1	2.23	0.71
9:I:29:TYR:HD1	9:I:30:LEU:HD12	1.54	0.71
3:C:273:A:N6	3:C:313:G:N2	2.38	0.71
3:C:1002:C:H2'	3:C:1003:A:H5''	1.71	0.71
3:C:1575:A:H61	3:C:1596:C:H42	1.38	0.71
3:C:2531:G:H1	7:G:48:GLY:HA3	1.53	0.71
20:T:77:LYS:HD2	20:T:86:LYS:HD2	1.73	0.71
13:M:76:TYR:HB2	18:R:72:THR:HB	1.73	0.71
3:C:1160:G:N2	3:C:1231:U:O2	2.24	0.70
10:J:38:GLU:HA	10:J:41:ARG:HD2	1.74	0.70
3:C:1077:A:H61	15:O:83:MET:HE3	1.56	0.70
3:C:821:A:H5'	4:D:7:LYS:HD2	1.73	0.70
11:K:17:ALA:H	11:K:55:VAL:HG12	1.56	0.70
7:G:103:MET:HE3	7:G:107:LEU:HD11	1.72	0.70
3:C:2362:C:H2'	3:C:2363:A:C8	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:30:GLY:O	15:O:134:ARG:NH1	2.24	0.69
3:C:384:G:H2'	3:C:385:G:H8	1.57	0.69
3:C:2088:C:H2'	3:C:2089:C:C6	2.27	0.69
17:Q:34:GLU:HG2	17:Q:35:VAL:HG23	1.74	0.69
3:C:2075:G:O2'	3:C:2107:G:N2	2.21	0.69
27:a:22:LEU:HB2	27:a:57:VAL:HG11	1.74	0.69
7:G:48:GLY:HA2	7:G:92:ILE:HG23	1.75	0.69
8:H:15:VAL:HG21	8:H:81:THR:HG22	1.72	0.69
3:C:284:G:O2'	3:C:285:U:OP1	2.10	0.69
3:C:1381:G:OP2	29:c:16:ARG:NH1	2.25	0.69
30:d:38:ILE:HD12	30:d:40:LYS:HD3	1.75	0.69
3:C:1400:G:N2	3:C:1443:G:H5''	2.07	0.69
7:G:100:GLY:O	7:G:103:MET:HB3	1.93	0.69
30:d:24:ILE:HG12	32:f:34:GLU:HG3	1.74	0.69
3:C:1211:G:H21	3:C:1216:A:H62	1.39	0.68
24:X:80:THR:CG2	24:X:83:LEU:HD11	2.23	0.68
3:C:333:C:H2'	3:C:334:G:H8	1.59	0.68
10:J:38:GLU:OE1	10:J:41:ARG:NH1	2.25	0.68
16:P:38:GLU:OE2	16:P:42:ARG:NE	2.27	0.68
3:C:449:G:O5'	3:C:449:G:H8	1.76	0.68
24:X:26:GLN:OE1	24:X:29:ARG:NH1	2.26	0.68
10:J:21:THR:HG22	10:J:86:ALA:HB2	1.76	0.68
3:C:1720:G:H21	4:D:100:GLY:HA3	1.59	0.67
8:H:69:SER:O	8:H:73:ILE:HG12	1.94	0.67
35:i:114:A:H2'	35:i:115:A:C8	2.29	0.67
3:C:1542:A:H61	3:C:1628:A:H1'	1.58	0.67
14:N:78:VAL:HG21	14:N:98:LEU:HD21	1.75	0.67
3:C:285:U:H1'	3:C:287:A:H5'	1.76	0.67
21:U:71:LEU:HD11	21:U:76:LEU:HD21	1.77	0.67
2:B:34:ILE:CD1	3:C:1588:G:N2	2.58	0.67
3:C:1755:A:O2'	3:C:1758:G:N1	2.23	0.67
7:G:117:ARG:NH1	7:G:143:SER:O	2.28	0.67
3:C:844:G:H4'	3:C:878:G:H5'	1.77	0.67
3:C:2342:A:N6	3:C:2392:A:OP2	2.26	0.67
24:X:8:PRO:HB2	24:X:68:THR:HG23	1.77	0.67
3:C:1825:C:N4	3:C:1840:G:OP2	2.27	0.67
11:K:73:LYS:HG2	11:K:74:THR:HG23	1.75	0.67
2:B:262:ARG:HG3	2:B:262:ARG:HH11	1.58	0.66
7:G:141:GLU:HB3	7:G:144:MET:HE1	1.76	0.66
24:X:146:VAL:HG12	24:X:162:ILE:HD12	1.77	0.66
3:C:1201:G:N2	3:C:1204:A:OP2	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1610:C:H2'	3:C:1611:A:C8	2.31	0.66
3:C:535:A:OP1	19:S:5:LYS:NZ	2.24	0.66
3:C:1198:C:O4'	11:K:135:ARG:NH2	2.27	0.66
3:C:1555:A:H3'	3:C:1556:A:H8	1.60	0.66
22:V:20:SER:O	22:V:24:ILE:HG12	1.96	0.66
3:C:163:U:O2	9:I:115:ARG:NH1	2.29	0.66
5:E:40:ARG:HD2	5:E:47:TYR:OH	1.96	0.66
17:Q:73:ILE:HG22	17:Q:75:GLY:H	1.60	0.66
24:X:108:VAL:HG21	24:X:140:ILE:HD11	1.78	0.66
3:C:81:A:OP1	23:W:4:HIS:NE2	2.29	0.66
14:N:60:ARG:HG3	14:N:61:LEU:HD12	1.77	0.66
3:C:747:A:H2	3:C:768:G:H21	1.43	0.66
14:N:94:GLY:H	14:N:97:GLU:CD	2.04	0.66
3:C:87:C:H3'	3:C:88:A:H2'	1.78	0.65
7:G:118:ILE:HD13	7:G:144:MET:HG2	1.78	0.65
25:Y:53:ARG:NH2	25:Y:57:ASP:OD1	2.28	0.65
3:C:2337:A:C5	3:C:2390:U:H4'	2.31	0.65
2:B:65:ARG:NH1	3:C:2146:A:C5'	2.37	0.65
3:C:1561:C:H42	3:C:1610:C:H42	1.43	0.65
7:G:63:ASP:OD1	7:G:64:LEU:N	2.30	0.65
20:T:53:ASP:OD1	20:T:54:ASP:N	2.30	0.65
3:C:2095:G:HO2'	3:C:2096:G:H8	1.45	0.65
8:H:9:VAL:HG22	8:H:51:ILE:HB	1.77	0.65
12:L:32:ALA:O	12:L:36:LEU:HB2	1.97	0.65
10:J:82:VAL:HG12	10:J:84:GLY:H	1.62	0.65
11:K:30:LEU:HB2	11:K:35:VAL:HB	1.78	0.65
3:C:2381:A:H1'	3:C:2382:G:H21	1.62	0.65
3:C:678:A:N1	3:C:924:G:O2'	2.27	0.65
3:C:2398:C:H2'	3:C:2399:A:C8	2.32	0.65
8:H:77:VAL:O	8:H:81:THR:HG23	1.95	0.65
11:K:48:THR:HA	11:K:56:ILE:HG13	1.78	0.65
3:C:1410:C:H5''	16:P:71:ARG:HH21	1.62	0.65
16:P:90:ARG:HH21	16:P:119:LYS:HB3	1.61	0.65
3:C:1602:U:H2'	3:C:1603:G:C8	2.31	0.65
3:C:2552:A:H2'	3:C:2553:G:C8	2.31	0.65
7:G:33:MET:HE1	35:i:55:G:H21	1.61	0.64
9:I:62:ILE:O	9:I:66:ASN:N	2.30	0.64
16:P:24:LEU:HB3	16:P:44:LEU:HD22	1.80	0.64
3:C:2527:G:H21	7:G:136:THR:HG21	1.61	0.64
7:G:117:ARG:HD3	7:G:144:MET:HA	1.78	0.64
20:T:10:GLY:O	20:T:12:LYS:NZ	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1081:C:O2'	3:C:2497:A:N3	2.30	0.64
3:C:1629:G:H4'	3:C:1630:U:H5	1.62	0.64
4:D:108:PRO:HD2	4:D:111:LEU:HD22	1.80	0.64
5:E:60:ARG:HH11	5:E:60:ARG:HG2	1.63	0.64
7:G:41:VAL:HG11	7:G:107:LEU:HD21	1.80	0.64
14:N:84:ASN:ND2	14:N:118:LEU:HA	2.10	0.64
15:O:68:ILE:HD13	15:O:103:LEU:HD22	1.79	0.63
31:e:27:THR:O	31:e:31:ARG:NH1	2.32	0.63
4:D:80:ALA:O	4:D:113:GLN:NE2	2.31	0.63
16:P:66:VAL:HG11	16:P:80:PHE:HE1	1.61	0.63
3:C:1289:A:H2'	3:C:1290:C:C6	2.34	0.63
3:C:1529:U:H3'	3:C:1530:G:H8	1.63	0.63
3:C:2061:U:H5''	4:D:256:ARG:HG2	1.81	0.63
7:G:172:GLU:OE2	17:Q:3:HIS:NE2	2.32	0.63
9:I:90:LYS:NZ	9:I:91:LEU:O	2.32	0.63
18:R:82:HIS:NE2	18:R:84:ASP:OD1	2.31	0.63
3:C:2:A:H2'	3:C:3:A:C8	2.34	0.63
3:C:2726:G:H5''	3:C:2727:A:H5''	1.79	0.63
3:C:2350:G:O2'	3:C:2351:A:OP1	2.15	0.62
3:C:1479:G:OP1	26:Z:2:ALA:N	2.32	0.62
10:J:5:ASP:HA	10:J:8:THR:HG22	1.81	0.62
15:O:74:LEU:HD12	15:O:92:TRP:HE1	1.65	0.62
3:C:1550:G:N2	3:C:1551:U:O2'	2.32	0.62
3:C:2294:A:H2'	3:C:2295:C:C6	2.35	0.62
23:W:9:VAL:HB	23:W:71:VAL:HG22	1.81	0.62
9:I:25:TYR:CG	9:I:30:LEU:HD13	2.34	0.62
22:V:18:GLU:HG2	22:V:19:LYS:N	2.15	0.62
3:C:459:A:H61	3:C:489:A:H3'	1.63	0.62
3:C:1415:A:H4'	3:C:1416:A:H5''	1.81	0.62
3:C:1616:A:O5'	3:C:1616:A:H8	1.81	0.62
3:C:2340:A:H62	3:C:2394:A:H61	1.46	0.62
3:C:2491:A:H5''	3:C:2492:A:H5''	1.81	0.62
3:C:2902:A:H2'	3:C:2903:A:C8	2.34	0.62
7:G:71:LYS:NZ	35:i:43:C:OP1	2.33	0.62
20:T:31:PRO:HA	20:T:64:VAL:HG13	1.81	0.61
27:a:22:LEU:HD21	27:a:58:TYR:CE1	2.35	0.61
27:a:43:ASN:ND2	27:a:46:ARG:CD	2.63	0.61
9:I:124:ILE:O	9:I:125:LYS:HG2	2.00	0.61
3:C:491:U:H4'	3:C:492:C:H5'	1.82	0.61
3:C:1206:A:H4'	3:C:1207:G:H5''	1.80	0.61
24:X:103:GLY:N	24:X:136:GLU:OE2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:706:G:O2'	6:F:160:ARG:NH2	2.31	0.61
3:C:1476:G:H2'	3:C:1477:C:C6	2.36	0.61
3:C:1636:A:H62	3:C:1802:G:N2	1.97	0.61
9:I:62:ILE:H	9:I:65:ALA:HB3	1.65	0.61
17:Q:31:GLY:N	17:Q:54:ASP:OD2	2.33	0.61
3:C:1410:C:H5''	16:P:71:ARG:NH2	2.15	0.61
20:T:16:VAL:HG13	20:T:99:VAL:HG21	1.82	0.61
3:C:608:C:H2'	3:C:609:G:H8	1.64	0.61
20:T:65:LEU:HD11	20:T:98:LYS:HB2	1.83	0.61
28:b:23:LEU:HD22	28:b:28:LEU:HD11	1.83	0.61
3:C:2321:U:O2	3:C:2414:G:N2	2.26	0.61
34:h:1:MET:N	35:i:41:U:O4	2.34	0.61
3:C:1118:A:H2'	3:C:1119:A:C8	2.36	0.61
10:J:20:SER:HA	10:J:83:LYS:HA	1.83	0.61
12:L:15:TRP:HE3	12:L:55:ILE:HD11	1.66	0.61
33:g:25:VAL:HG12	33:g:34:GLN:HB3	1.83	0.61
3:C:1337:G:N2	3:C:1340:A:OP2	2.25	0.60
24:X:164:LEU:HG	24:X:168:VAL:HG23	1.81	0.60
34:h:14:VAL:HG22	34:h:33:ILE:HB	1.81	0.60
3:C:159:A:N3	3:C:2431:C:O2'	2.34	0.60
9:I:21:VAL:HG21	9:I:25:TYR:CD2	2.36	0.60
16:P:66:VAL:HG11	16:P:80:PHE:CE1	2.37	0.60
3:C:635:G:O2'	3:C:636:U:O4'	2.18	0.60
12:L:102:GLU:O	12:L:106:ILE:HG12	2.02	0.60
3:C:248:G:H5'	3:C:250:G:N7	2.16	0.60
3:C:1211:G:H2'	3:C:1212:U:C6	2.36	0.60
4:D:68:ARG:NH1	4:D:150:GLY:O	2.33	0.60
3:C:2610:C:O2'	25:Y:41:ARG:NH1	2.35	0.60
3:C:26:U:H2'	3:C:27:G:C8	2.37	0.60
3:C:1111:G:OP1	19:S:50:ARG:NH1	2.33	0.60
18:R:51:GLY:HA2	18:R:56:GLU:OE1	2.01	0.60
27:a:43:ASN:ND2	27:a:46:ARG:HD2	2.11	0.60
28:b:8:GLN:HB2	28:b:28:LEU:HD13	1.83	0.60
3:C:296:A:N1	3:C:340:A:N6	2.49	0.60
3:C:2317:G:H4'	9:I:25:TYR:OH	2.01	0.60
3:C:2338:G:O2'	3:C:2388:G:N2	2.33	0.60
3:C:2467:U:H2'	3:C:2468:U:C6	2.37	0.60
8:H:58:ASP:O	8:H:63:ARG:NH1	2.35	0.60
3:C:789:G:OP1	6:F:55:ARG:NH2	2.33	0.60
3:C:1212:U:H1'	3:C:1216:A:C6	2.37	0.60
3:C:1564:A:N6	3:C:1608:U:O2'	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1706:A:H2'	3:C:1707:G:H8	1.67	0.60
32:f:31:HIS:ND1	32:f:32:LEU:HD13	2.16	0.60
3:C:2558:C:H42	25:Y:75:ARG:HD2	1.67	0.59
4:D:223:GLY:HA2	4:D:226:MET:HG2	1.82	0.59
11:K:132:GLY:HA2	11:K:135:ARG:HG2	1.84	0.59
14:N:133:ALA:O	14:N:137:ILE:HG12	2.02	0.59
3:C:2249:G:H2'	3:C:2250:A:C8	2.38	0.59
18:R:9:GLN:HA	18:R:12:LEU:HD12	1.84	0.59
3:C:338:C:H2'	3:C:338:C:O2	2.01	0.59
3:C:1510:A:O2'	3:C:1511:U:O5'	2.20	0.59
3:C:2367:G:N2	3:C:2369:C:O2'	2.36	0.59
34:h:17:GLY:N	34:h:35:VAL:O	2.35	0.59
3:C:1364:U:H4'	19:S:4:VAL:HG21	1.85	0.59
7:G:141:GLU:HG2	7:G:143:SER:H	1.68	0.59
8:H:27:LYS:HG2	8:H:32:THR:HG22	1.85	0.59
34:h:11:ASP:HA	34:h:25:ARG:HG2	1.84	0.59
3:C:1211:G:N2	3:C:1217:G:O6	2.35	0.59
3:C:1214:A:C8	3:C:1214:A:O5'	2.56	0.59
3:C:1290:C:H2'	3:C:1291:G:O4'	2.01	0.59
4:D:163:ILE:HG21	4:D:175:LEU:HD13	1.84	0.59
14:N:84:ASN:ND2	14:N:117:LYS:O	2.35	0.59
15:O:17:GLN:HG2	15:O:39:HIS:HB3	1.84	0.59
17:Q:62:ALA:O	17:Q:91:ARG:NH1	2.33	0.59
3:C:615:A:H5''	12:L:116:ARG:HH12	1.66	0.59
3:C:858:A:O2'	3:C:1877:U:OP1	2.21	0.59
3:C:1343:G:H2'	3:C:1345:G:N7	2.18	0.59
3:C:1549:G:O2'	3:C:1550:G:O5'	2.19	0.59
3:C:2347:G:N7	3:C:2348:G:N2	2.50	0.59
11:K:114:LYS:HG2	11:K:130:ILE:HD11	1.85	0.58
3:C:2398:C:O2'	3:C:2399:A:OP1	2.21	0.58
26:Z:2:ALA:C	26:Z:33:ILE:HD11	2.28	0.58
3:C:3117:U:H2'	3:C:3118:U:C6	2.39	0.58
24:X:80:THR:CG2	24:X:83:LEU:CD1	2.82	0.58
3:C:929:C:H1'	3:C:1339:G:H21	1.68	0.58
3:C:2385:G:H5''	3:C:2394:A:C8	2.38	0.58
7:G:45:MET:HG3	7:G:64:LEU:HD12	1.83	0.58
11:K:24:PRO:HG2	11:K:25:PRO:HD3	1.84	0.58
3:C:1181:G:H4'	11:K:137:MET:HE1	1.85	0.58
3:C:2016:G:OP1	4:D:258:ARG:NH1	2.36	0.58
6:F:155:LEU:HD21	6:F:187:ASP:HB3	1.85	0.58
17:Q:65:SER:HA	17:Q:70:VAL:HG11	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:34:ILE:HD11	3:C:1588:G:H21	1.67	0.58
3:C:857:U:H2'	3:C:858:A:C8	2.38	0.58
3:C:1010:U:O2'	3:C:1011:A:OP1	2.18	0.58
3:C:2394:A:O2'	3:C:2396:A:OP1	2.20	0.58
3:C:332:C:H2'	3:C:333:C:C6	2.38	0.58
3:C:666:A:N6	3:C:2258:U:OP1	2.36	0.58
3:C:2385:G:H5''	3:C:2394:A:H8	1.67	0.58
27:a:22:LEU:HD21	27:a:58:TYR:HE1	1.68	0.58
35:i:81:U:H2'	35:i:82:A:C8	2.39	0.58
3:C:544:U:H1'	22:V:71:THR:HG23	1.85	0.58
3:C:879:A:OP1	4:D:208:LYS:NZ	2.37	0.58
3:C:991:C:H2'	3:C:992:C:C6	2.38	0.58
3:C:1314:C:H1'	19:S:4:VAL:HG12	1.85	0.58
17:Q:37:ARG:NH2	17:Q:54:ASP:OD1	2.36	0.58
2:B:60:ARG:NE	2:B:60:ARG:HA	2.19	0.58
3:C:333:C:H2'	3:C:334:G:C8	2.39	0.57
3:C:3009:U:H2'	3:C:3010:U:C6	2.39	0.57
3:C:2019:A:H2'	3:C:2020:A:C8	2.39	0.57
5:E:9:THR:HG22	5:E:30:LYS:HB3	1.85	0.57
7:G:15:TYR:HA	7:G:19:ILE:HD12	1.86	0.57
3:C:879:A:H5''	4:D:210:GLY:HA3	1.86	0.57
3:C:1755:A:HO2'	3:C:1758:G:H1	1.38	0.57
3:C:835:C:H2'	3:C:836:G:C8	2.40	0.57
3:C:885:G:OP2	31:e:14:ARG:NH2	2.37	0.57
3:C:3032:G:H5''	5:E:63:ILE:HG23	1.85	0.57
9:I:80:LEU:HD13	9:I:146:LEU:HD21	1.85	0.57
3:C:138:A:H2'	3:C:139:U:O2	2.04	0.57
3:C:2089:C:H2'	3:C:2090:U:C6	2.40	0.57
8:H:9:VAL:HG12	8:H:70:ARG:NH1	2.19	0.57
9:I:149:VAL:O	9:I:151:GLN:NE2	2.38	0.57
23:W:24:LEU:HD11	23:W:36:GLU:HB3	1.86	0.57
3:C:701:A:H2'	3:C:702:A:C8	2.40	0.57
3:C:2035:U:H2'	4:D:157:ARG:HD2	1.85	0.57
9:I:1:MET:SD	9:I:26:GLY:HA3	2.43	0.57
13:M:68:GLU:HG3	13:M:78:LYS:HD2	1.86	0.57
26:Z:33:ILE:HA	26:Z:52:CYS:HA	1.85	0.57
3:C:920:G:N2	3:C:944:A:OP1	2.38	0.57
10:J:57:VAL:HA	10:J:60:ALA:HB3	1.86	0.57
16:P:107:ASN:HD21	21:U:47:PRO:HB2	1.69	0.57
3:C:286:G:O2'	3:C:300:G:O6	2.22	0.57
3:C:2288:C:H2'	3:C:2289:C:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1560:U:H2'	3:C:1561:C:C6	2.40	0.57
7:G:56:LEU:HD11	7:G:155:ARG:HD3	1.87	0.57
24:X:19:THR:HG21	35:i:76:G:H5''	1.85	0.57
2:B:65:ARG:CZ	3:C:2146:A:OP1	2.53	0.56
3:C:621:U:H2'	3:C:622:C:C6	2.40	0.56
3:C:672:C:H2'	3:C:673:C:C6	2.40	0.56
3:C:2537:C:O4'	7:G:44:ASN:ND2	2.38	0.56
7:G:128:GLN:HB3	7:G:135:TYR:CE1	2.40	0.56
9:I:98:ALA:HA	9:I:101:VAL:HG12	1.86	0.56
11:K:57:PRO:HG2	11:K:74:THR:O	2.06	0.56
3:C:964:C:H2'	3:C:965:U:C6	2.40	0.56
3:C:1146:A:H2'	3:C:1147:A:C8	2.40	0.56
3:C:1453:G:N7	22:V:65:LYS:NZ	2.51	0.56
2:B:234:SER:HB2	3:C:2144:AI5:C14	2.35	0.56
3:C:277:U:H2'	3:C:278:A:C8	2.41	0.56
3:C:1235:U:H2'	3:C:1236:G:C8	2.41	0.56
3:C:1577:C:H2'	3:C:1578:G:C8	2.40	0.56
4:D:226:MET:HG3	4:D:231:HIS:HB2	1.87	0.56
7:G:41:VAL:HG13	7:G:103:MET:CE	2.35	0.56
24:X:136:GLU:OE1	24:X:138:LEU:HG	2.04	0.56
3:C:1543:A:N1	3:C:1628:A:O2'	2.39	0.56
3:C:1947:U:O2'	3:C:1948:A:O4'	2.24	0.56
3:C:3078:G:N2	3:C:3081:A:OP2	2.34	0.56
21:U:81:VAL:HG23	21:U:112:VAL:HG12	1.86	0.56
31:e:27:THR:HG23	31:e:30:GLY:H	1.69	0.56
3:C:1223:U:H2'	3:C:1224:G:C8	2.39	0.56
3:C:1594:G:H2'	3:C:1595:G:C8	2.40	0.56
17:Q:39:VAL:HA	17:Q:103:ASP:HB3	1.87	0.56
2:B:65:ARG:H	2:B:65:ARG:HE	1.52	0.56
3:C:929:C:H1'	3:C:1339:G:N2	2.21	0.56
3:C:1704:U:H2'	3:C:1705:C:C6	2.40	0.56
7:G:19:ILE:HD13	7:G:180:LEU:HD22	1.87	0.56
18:R:23:ASP:OD1	18:R:88:ARG:HA	2.05	0.56
33:g:25:VAL:CG1	33:g:34:GLN:HB3	2.35	0.56
2:B:34:ILE:HD12	3:C:1588:G:N2	2.20	0.56
3:C:2:A:H2'	3:C:3:A:H8	1.70	0.56
3:C:162:A:O2'	9:I:118:GLN:OE1	2.21	0.56
15:O:30:GLY:H	15:O:105:GLU:CD	2.14	0.56
16:P:26:THR:HG23	16:P:75:VAL:HG21	1.87	0.56
24:X:16:ARG:CG	24:X:48:GLU:HG3	2.36	0.56
3:C:80:G:OP1	23:W:94:LYS:NZ	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:2971:G:O6	3:C:2979:C:H5''	2.06	0.56
3:C:964:C:H2'	3:C:965:U:H6	1.71	0.56
3:C:2340:A:N6	3:C:2394:A:H61	2.03	0.56
20:T:60:VAL:HG22	20:T:102:ILE:HG12	1.87	0.56
3:C:639:C:O2'	3:C:640:G:O5'	2.24	0.56
3:C:1202:A:N3	3:C:1223:U:O2'	2.27	0.56
3:C:1554:U:OP1	3:C:1616:A:N6	2.38	0.56
3:C:3014:A:H62	3:C:3113:A:H2	1.51	0.56
6:F:30:ASN:O	6:F:34:MET:HG2	2.05	0.56
30:d:42:CYS:HB3	30:d:45:CYS:HB2	1.87	0.56
3:C:137:G:H2'	3:C:138:A:C8	2.41	0.55
3:C:344:G:O5'	3:C:344:G:H8	1.89	0.55
3:C:2144:AI5:C19	3:C:2144:AI5:C42	2.84	0.55
3:C:723:C:O2	3:C:733:U:O2'	2.24	0.55
3:C:772:U:H2'	3:C:773:G:C8	2.41	0.55
3:C:2558:C:N4	25:Y:75:ARG:HD2	2.20	0.55
23:W:12:ILE:HG22	23:W:70:ASN:C	2.31	0.55
3:C:2968:G:OP1	8:H:151:ARG:NH2	2.39	0.55
35:i:1:G:H2'	35:i:2:U:C6	2.41	0.55
3:C:29:C:N4	3:C:535:A:OP2	2.38	0.55
3:C:1137:U:H2'	3:C:1138:A:C8	2.41	0.55
3:C:1598:U:N3	3:C:1600:G:N7	2.55	0.55
3:C:1606:G:H2'	3:C:1607:C:C6	2.41	0.55
3:C:2968:G:H4'	8:H:151:ARG:HH12	1.72	0.55
13:M:63:VAL:HB	13:M:102:VAL:HG13	1.89	0.55
21:U:79:ALA:HB2	21:U:115:GLU:HG3	1.88	0.55
3:C:356:G:H21	3:C:362:A:N6	2.05	0.55
3:C:615:A:OP2	12:L:116:ARG:NH1	2.39	0.55
3:C:1111:G:OP2	19:S:51:ARG:NH2	2.39	0.55
3:C:1213:A:N3	3:C:1213:A:H2'	2.22	0.55
3:C:1543:A:H2'	3:C:1544:U:C6	2.41	0.55
19:S:91:ASP:OD1	19:S:94:ASN:ND2	2.36	0.55
3:C:928:U:H2'	3:C:929:C:C6	2.42	0.55
6:F:4:LYS:HE3	6:F:17:SER:HB2	1.89	0.55
12:L:67:ASP:OD2	12:L:71:LYS:HE3	2.06	0.55
3:C:1180:G:O2'	3:C:1181:G:OP1	2.20	0.55
3:C:1530:G:H2'	3:C:1531:C:C5	2.41	0.55
3:C:2772:G:N3	13:M:23:ARG:NH2	2.54	0.55
8:H:97:VAL:HG22	8:H:106:PHE:CD1	2.42	0.55
11:K:102:VAL:HG13	11:K:141:VAL:HG13	1.89	0.55
3:C:1754:G:H8	3:C:1754:G:OP2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:42:LEU:HD11	6:F:186:TYR:CE1	2.42	0.55
28:b:11:SER:HB3	28:b:31:ILE:HD11	1.89	0.55
2:B:34:ILE:HD12	3:C:1588:G:H22	1.72	0.55
2:B:34:ILE:HD13	2:B:50:THR:HB	1.88	0.55
2:B:177:ILE:HB	2:B:243:LEU:HB2	1.89	0.55
3:C:162:A:O3'	9:I:118:GLN:NE2	2.39	0.55
3:C:2136:A:H2'	3:C:2136:A:N3	2.21	0.55
5:E:37:THR:HG22	5:E:75:VAL:HG21	1.89	0.55
13:M:107:ARG:HG2	13:M:107:ARG:HH11	1.72	0.55
3:C:1160:G:H2'	3:C:1161:C:H6	1.71	0.54
9:I:4:ILE:HG13	9:I:39:ALA:HB2	1.89	0.54
9:I:32:PRO:HB3	26:Z:64:ALA:HA	1.90	0.54
15:O:54:ILE:O	15:O:58:ILE:HG12	2.08	0.54
25:Y:20:ARG:O	25:Y:24:LYS:NZ	2.40	0.54
3:C:1971:C:H5	18:R:93:ARG:NH2	2.04	0.54
11:K:112:GLU:HG3	11:K:115:LYS:HZ2	1.72	0.54
14:N:44:LYS:HG3	14:N:45:ASN:H	1.72	0.54
15:O:46:GLN:HG2	15:O:126:PRO:HD3	1.90	0.54
3:C:835:C:H2'	3:C:836:G:H8	1.72	0.54
3:C:1206:A:N6	11:K:136:SER:HB3	2.23	0.54
3:C:1379:G:OP1	29:c:16:ARG:NH2	2.40	0.54
8:H:22:GLN:HG3	8:H:37:VAL:HB	1.90	0.54
13:M:87:ILE:HA	13:M:93:PRO:HA	1.88	0.54
17:Q:4:LYS:HD2	17:Q:5:PRO:HD2	1.88	0.54
3:C:89:A:H2'	3:C:90:C:C6	2.43	0.54
3:C:384:G:H2'	3:C:385:G:C8	2.41	0.54
3:C:1288:A:H2'	3:C:1289:A:C8	2.42	0.54
3:C:1550:G:O6	3:C:1620:U:O4	2.26	0.54
3:C:2345:U:H2'	3:C:2346:G:C8	2.43	0.54
9:I:2:LYS:HB3	9:I:20:GLU:OE1	2.07	0.54
9:I:29:TYR:CD1	9:I:30:LEU:HD12	2.41	0.54
15:O:51:ARG:HD3	15:O:66:ILE:HD11	1.90	0.54
3:C:361:A:H8	3:C:361:A:H5''	1.72	0.54
3:C:2155:U:C5'	3:C:2155:U:H6	2.21	0.54
5:E:40:ARG:HD2	5:E:47:TYR:CZ	2.42	0.54
10:J:17:PHE:HD1	10:J:81:PHE:HE2	1.56	0.54
35:i:35:G:O2'	35:i:45:G:N7	2.33	0.54
3:C:313:G:H2'	3:C:314:G:C8	2.43	0.54
3:C:429:A:H2'	3:C:430:A:C8	2.42	0.54
3:C:2781:G:H2'	3:C:2782:C:C6	2.42	0.54
3:C:2922:U:H2'	3:C:2923:C:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:143:HIS:ND1	4:D:194:GLY:O	2.40	0.54
11:K:62:VAL:HA	11:K:68:PHE:HA	1.89	0.54
2:B:59:GLU:H	2:B:59:GLU:CD	2.16	0.54
3:C:1204:A:O2'	3:C:1205:G:N7	2.41	0.54
3:C:1546:A:H2'	3:C:1547:G:C8	2.43	0.54
3:C:1546:A:H2'	3:C:1547:G:H8	1.73	0.54
3:C:1790:A:H5'	4:D:36:PRO:HB3	1.89	0.54
3:C:2096:G:H2'	3:C:2097:G:C8	2.42	0.54
3:C:1160:G:H2'	3:C:1161:C:C6	2.43	0.54
3:C:1568:C:N3	3:C:1604:G:N1	2.55	0.54
3:C:2095:G:O2'	3:C:2096:G:H8	1.89	0.54
3:C:2778:U:H2'	3:C:2779:U:C6	2.43	0.54
6:F:41:GLN:HE22	6:F:184:ASN:HB2	1.72	0.54
12:L:49:ASP:OD1	12:L:121:LYS:NZ	2.38	0.54
17:Q:73:ILE:HD11	17:Q:83:ARG:HG2	1.90	0.54
3:C:751:A:H2'	3:C:752:C:C6	2.42	0.54
3:C:2611:U:O4'	25:Y:41:ARG:NH1	2.41	0.54
4:D:65:ILE:HD13	4:D:88:ARG:CZ	2.37	0.54
12:L:57:ILE:HD11	12:L:130:HIS:HB3	1.90	0.54
2:B:65:ARG:CZ	3:C:2146:A:H5''	2.31	0.53
3:C:364:A:H2'	3:C:365:U:O4'	2.07	0.53
15:O:30:GLY:N	15:O:105:GLU:OE2	2.41	0.53
3:C:293:G:H2'	3:C:294:G:H8	1.72	0.53
3:C:2145:C:H4'	3:C:2145:C:OP2	2.08	0.53
7:G:11:LEU:HD21	7:G:180:LEU:HD12	1.89	0.53
3:C:1206:A:H62	11:K:136:SER:HB3	1.74	0.53
3:C:1564:A:H5'	3:C:1565:A:OP2	2.09	0.53
7:G:67:ILE:HG23	7:G:68:THR:HG23	1.90	0.53
18:R:73:PHE:HB3	18:R:80:ILE:HD11	1.90	0.53
3:C:1180:G:H2'	3:C:1181:G:C8	2.43	0.53
3:C:1468:A:H2'	3:C:1469:A:C8	2.44	0.53
4:D:76:ASN:HB2	4:D:98:LEU:HD23	1.91	0.53
10:J:41:ARG:NE	11:K:119:ASN:OD1	2.41	0.53
13:M:78:LYS:HB3	18:R:70:GLU:HB2	1.90	0.53
15:O:15:PRO:HG3	15:O:72:ARG:HE	1.74	0.53
3:C:818:U:H2'	3:C:819:G:O4'	2.08	0.53
3:C:1210:C:H2'	3:C:1211:G:O4'	2.08	0.53
3:C:2081:U:OP1	3:C:2634:G:O2'	2.25	0.53
8:H:35:LEU:HD11	8:H:72:LEU:HB3	1.89	0.53
10:J:27:GLU:HB3	10:J:104:VAL:HG22	1.90	0.53
24:X:16:ARG:HH12	24:X:19:THR:HG23	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1884:G:O2'	13:M:6:SER:OG	2.24	0.53
3:C:2043:C:OP2	4:D:222:ARG:HB2	2.09	0.53
17:Q:46:HIS:CE1	17:Q:66:ILE:HG22	2.43	0.53
17:Q:71:ARG:NH2	35:i:28:A:OP1	2.42	0.53
28:b:17:TRP:HD1	28:b:20:ARG:NH2	2.05	0.53
3:C:615:A:H5''	12:L:116:ARG:NH1	2.23	0.53
3:C:763:G:H2'	3:C:764:U:C6	2.44	0.53
3:C:1201:G:O3'	3:C:1202:A:H8	1.92	0.53
24:X:68:THR:HB	24:X:75:GLU:OE2	2.07	0.53
3:C:1214:A:H8	3:C:1214:A:OP2	1.91	0.53
7:G:40:LYS:HG2	7:G:164:VAL:HB	1.90	0.53
18:R:100:ARG:O	18:R:103:ARG:NH1	2.37	0.53
19:S:48:ARG:NE	19:S:49:ASP:OD1	2.40	0.53
23:W:75:ASP:HA	23:W:105:ILE:HG21	1.91	0.53
24:X:157:ILE:HA	24:X:161:GLN:NE2	2.24	0.53
3:C:1033:A:N3	35:i:81:U:O2'	2.42	0.53
3:C:1221:A:OP2	3:C:1222:C:N4	2.42	0.53
3:C:2367:G:N3	3:C:2369:C:H1'	2.24	0.53
22:V:69:THR:HG23	22:V:72:GLY:H	1.73	0.53
24:X:131:ILE:HD11	24:X:178:VAL:HG22	1.91	0.53
34:h:42:HIS:HB3	34:h:45:TYR:HD2	1.74	0.53
3:C:1214:A:H8	3:C:1214:A:P	2.32	0.53
3:C:2011:U:H2'	3:C:2012:C:H6	1.73	0.53
3:C:2030:C:H5''	4:D:40:LYS:HD2	1.90	0.53
3:C:26:U:H2'	3:C:27:G:H8	1.74	0.52
3:C:247:G:OP2	3:C:249:C:N4	2.36	0.52
3:C:971:G:H2'	3:C:972:A:C8	2.44	0.52
3:C:1529:U:H3'	3:C:1530:G:C8	2.43	0.52
3:C:1615:G:O5'	3:C:1615:G:H8	1.92	0.52
3:C:2256:G:N2	3:C:2796:A:OP2	2.41	0.52
9:I:2:LYS:HD2	9:I:39:ALA:HB3	1.91	0.52
2:B:34:ILE:HD11	3:C:1588:G:N2	2.23	0.52
3:C:1758:G:H2'	3:C:1759:A:C8	2.44	0.52
3:C:2275:A:H5'	3:C:2802:G:O4'	2.09	0.52
12:L:21:SER:HA	12:L:61:LYS:HB2	1.91	0.52
15:O:29:PHE:N	15:O:105:GLU:OE2	2.42	0.52
16:P:75:VAL:HA	16:P:78:THR:HG22	1.90	0.52
2:B:34:ILE:CD1	3:C:1588:G:H21	2.22	0.52
9:I:137:HIS:HB2	9:I:140:VAL:HG12	1.91	0.52
3:C:1229:A:H8	3:C:1230:G:H1'	1.74	0.52
3:C:1563:A:O2'	3:C:1564:A:O5'	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:103:ASN:OD1	8:H:117:GLU:HG2	2.09	0.52
3:C:3034:C:H2'	3:C:3035:C:H6	1.74	0.52
7:G:129:PHE:HD2	7:G:133:GLY:HA2	1.75	0.52
11:K:44:TYR:OH	11:K:56:ILE:O	2.27	0.52
35:i:18:C:H2'	35:i:19:G:O4'	2.10	0.52
3:C:81:A:N1	3:C:96:G:O2'	2.43	0.52
3:C:1568:C:H2'	3:C:1569:A:C8	2.45	0.52
15:O:12:GLN:OE1	15:O:73:PRO:HD2	2.10	0.52
22:V:27:ASN:HD21	22:V:90:SER:HA	1.75	0.52
3:C:312:G:H2'	3:C:313:G:H5'	1.92	0.52
22:V:53:LYS:NZ	22:V:54:VAL:O	2.42	0.52
3:C:1564:A:H5''	3:C:1565:A:N7	2.24	0.52
3:C:1710:A:O2'	3:C:1711:G:H5''	2.10	0.52
4:D:65:ILE:HD13	4:D:88:ARG:NH2	2.23	0.52
6:F:143:THR:O	6:F:147:THR:HG23	2.10	0.52
9:I:98:ALA:HB2	9:I:114:LYS:HZ3	1.74	0.52
3:C:361:A:N1	3:C:440:U:O2'	2.42	0.52
3:C:661:U:O2'	3:C:1101:A:N1	2.38	0.52
3:C:2698:C:O2'	3:C:2699:C:OP1	2.27	0.52
3:C:1076:A:H2'	3:C:1077:A:C8	2.45	0.51
3:C:2709:G:OP1	15:O:46:GLN:NE2	2.43	0.51
4:D:64:VAL:O	4:D:104:TYR:HB2	2.10	0.51
19:S:24:TYR:HB2	19:S:29:SER:HB3	1.91	0.51
20:T:43:VAL:HG22	20:T:48:VAL:HG12	1.92	0.51
24:X:136:GLU:OE1	24:X:138:LEU:N	2.35	0.51
3:C:1220:C:H2'	3:C:1221:A:H8	1.74	0.51
3:C:1575:A:H61	3:C:1596:C:N4	2.08	0.51
3:C:1611:A:H2	4:D:134:ARG:HH21	1.56	0.51
2:B:33:ARG:HG2	2:B:34:ILE:H	1.75	0.51
3:C:1025:A:H2'	3:C:1026:A:C8	2.45	0.51
3:C:1509:U:H2'	3:C:1510:A:O4'	2.10	0.51
3:C:1675:U:O2'	3:C:1676:G:N7	2.44	0.51
3:C:2070:A:N3	3:C:2457:U:O2'	2.42	0.51
3:C:2406:U:H2'	3:C:2407:C:C6	2.44	0.51
3:C:3032:G:H5''	5:E:63:ILE:CG2	2.40	0.51
3:C:1087:G:H2'	3:C:1088:U:C6	2.46	0.51
3:C:1146:A:N6	3:C:1243:G:H2'	2.26	0.51
3:C:1205:G:O6	3:C:1207:G:N2	2.44	0.51
3:C:2729:G:O6	3:C:2800:G:H2'	2.10	0.51
11:K:15:ILE:HG23	11:K:19:GLN:HE21	1.76	0.51
12:L:15:TRP:CE3	12:L:55:ILE:HD11	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:ARG:O	2:B:4:ARG:NE	2.44	0.51
3:C:1706:A:H2'	3:C:1707:G:C8	2.46	0.51
8:H:120:GLU:N	8:H:120:GLU:OE1	2.44	0.51
10:J:32:THR:OG1	10:J:35:ASN:OD1	2.21	0.51
21:U:71:LEU:HD13	21:U:116:SER:HB2	1.93	0.51
3:C:1295:U:H2'	3:C:1296:G:H8	1.74	0.51
3:C:1620:U:H2'	3:C:1621:C:C6	2.45	0.51
3:C:2913:U:O2'	16:P:14:SER:OG	2.24	0.51
4:D:72:LYS:NZ	4:D:101:GLU:OE1	2.41	0.51
7:G:125:SER:HA	7:G:185:LYS:HB2	1.93	0.51
16:P:51:LEU:HD22	16:P:66:VAL:HG23	1.92	0.51
25:Y:33:ALA:HB2	25:Y:64:PRO:HD3	1.91	0.51
2:B:167:LEU:C	2:B:167:LEU:HD12	2.36	0.51
3:C:1163:A:OP1	10:J:6:LYS:NZ	2.43	0.51
3:C:2902:A:H2'	3:C:2903:A:H8	1.76	0.51
7:G:117:ARG:HD2	7:G:146:HIS:CE1	2.46	0.51
12:L:37:ARG:NH1	12:L:110:PRO:HG2	2.25	0.51
15:O:43:THR:HG22	15:O:94:VAL:HG22	1.93	0.51
18:R:90:ASP:OD2	18:R:113:ARG:NH1	2.44	0.51
20:T:39:VAL:HG11	20:T:42:VAL:HG23	1.93	0.51
32:f:26:LYS:HE3	32:f:48:THR:HB	1.92	0.51
1:3:3:LYS:HE2	3:C:1252:G:N7	2.26	0.51
3:C:624:G:H5''	12:L:5:THR:HG21	1.93	0.51
3:C:834:C:H2'	3:C:835:C:C6	2.45	0.51
3:C:1562:C:H2'	3:C:1563:A:C8	2.45	0.51
3:C:1732:U:H2'	3:C:1733:C:H6	1.76	0.51
3:C:1815:G:H5'	3:C:1816:C:OP1	2.11	0.51
3:C:2639:G:H2'	3:C:2640:G:C8	2.45	0.51
3:C:2736:C:H2'	3:C:2737:G:O4'	2.11	0.51
3:C:356:G:H21	3:C:362:A:H61	1.58	0.51
3:C:582:G:H5''	21:U:11:THR:HG23	1.93	0.51
3:C:681:C:H2'	3:C:682:A:C8	2.46	0.51
3:C:1291:G:H2'	3:C:1292:U:C6	2.46	0.51
3:C:2175:U:N3	3:C:2178:G:OP2	2.33	0.51
3:C:2224:C:O2'	3:C:2913:U:OP2	2.29	0.51
3:C:2936:C:OP1	3:C:2938:G:H4'	2.11	0.51
3:C:2968:G:H4'	8:H:151:ARG:HH22	1.74	0.51
3:C:3034:C:H2'	3:C:3035:C:C6	2.46	0.51
19:S:77:ASN:OD1	19:S:78:ARG:N	2.42	0.51
32:f:24:ARG:O	32:f:47:ARG:HG3	2.10	0.51
3:C:681:C:H2'	3:C:682:A:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1235:U:H2'	3:C:1236:G:H8	1.74	0.51
8:H:8:PRO:HB2	8:H:50:ALA:HB1	1.93	0.51
23:W:30:ARG:HG3	23:W:30:ARG:HH11	1.76	0.51
3:C:334:G:C2	3:C:335:G:C8	2.99	0.50
3:C:574:C:O2'	21:U:67:ASN:OD1	2.29	0.50
3:C:1704:U:H2'	3:C:1705:C:H6	1.76	0.50
3:C:1791:A:H2'	3:C:1792:A:C8	2.46	0.50
3:C:2366:C:H2'	3:C:2367:G:O4'	2.10	0.50
14:N:121:LYS:HE3	14:N:141:GLY:HA3	1.92	0.50
25:Y:49:VAL:HG12	25:Y:79:ASN:HB3	1.93	0.50
3:C:879:A:H5''	4:D:210:GLY:CA	2.42	0.50
3:C:1250:U:H6	12:L:84:LEU:HD11	1.76	0.50
6:F:31:ILE:HD11	14:N:4:ILE:HD13	1.92	0.50
9:I:9:VAL:HB	9:I:12:LEU:HB3	1.92	0.50
9:I:126:SER:O	9:I:130:HIS:NE2	2.43	0.50
24:X:152:GLU:HG2	24:X:153:ALA:H	1.75	0.50
27:a:29:LEU:HA	27:a:32:LEU:HD23	1.93	0.50
35:i:113:G:H2'	35:i:114:A:H8	1.77	0.50
3:C:773:G:H21	6:F:106:MET:HE3	1.77	0.50
3:C:979:G:H2'	3:C:980:C:C6	2.46	0.50
3:C:1295:U:H2'	3:C:1296:G:C8	2.46	0.50
3:C:2011:U:H2'	3:C:2012:C:C6	2.47	0.50
3:C:2043:C:O2'	3:C:2195:U:OP2	2.28	0.50
3:C:2691:C:H2'	3:C:2692:A:O4'	2.12	0.50
7:G:12:LYS:HB2	7:G:104:TRP:CD1	2.47	0.50
16:P:97:ILE:HG12	16:P:113:ILE:HG12	1.92	0.50
34:h:16:CYS:SG	34:h:38:CYS:SG	3.10	0.50
3:C:263:G:C6	3:C:264:G:C6	2.99	0.50
3:C:1627:U:H2'	3:C:1628:A:H8	1.76	0.50
3:C:1679:A:H4'	3:C:1679:A:OP1	2.12	0.50
12:L:42:PRO:HB3	19:S:68:ALA:HB2	1.93	0.50
17:Q:12:GLU:CG	35:i:60:G:H4'	2.40	0.50
19:S:108:ALA:O	19:S:112:VAL:HG23	2.11	0.50
3:C:1173:G:N1	3:C:1223:U:O4	2.44	0.50
3:C:1112:C:O2	20:T:12:LYS:HE3	2.12	0.50
3:C:1122:C:H2'	3:C:1129:G:H2'	1.94	0.50
3:C:1603:G:H2'	3:C:1604:G:C8	2.47	0.50
3:C:2026:A:H8	3:C:2026:A:OP2	1.94	0.50
3:C:2085:C:H2'	3:C:2086:U:C6	2.47	0.50
3:C:2128:G:H8	3:C:2128:G:H5''	1.76	0.50
3:C:2387:U:H3'	3:C:2388:G:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:89:GLU:HG2	8:H:131:LYS:HG2	1.94	0.50
10:J:15:GLU:HA	10:J:18:LYS:HG2	1.93	0.50
15:O:2:LEU:HD12	15:O:69:PHE:CE1	2.47	0.50
2:B:35:ASP:OD1	3:C:1588:G:N2	2.45	0.50
3:C:1625:G:H2'	3:C:1626:G:C8	2.47	0.50
3:C:2128:G:H5''	3:C:2128:G:C8	2.46	0.50
3:C:2164:U:H1'	3:C:2166:C:N4	2.26	0.50
6:F:188:VAL:HG23	6:F:194:VAL:HG21	1.94	0.50
12:L:4:TYR:OH	12:L:10:ASP:OD2	2.22	0.50
3:C:1006:G:H2'	3:C:1007:G:C8	2.47	0.50
3:C:1756:G:H8	3:C:1756:G:OP2	1.94	0.50
3:C:1996:U:OP2	3:C:2001:A:N6	2.28	0.50
3:C:3009:U:H2'	3:C:3010:U:H6	1.76	0.50
3:C:1507:G:O6	22:V:18:GLU:HG3	2.12	0.49
3:C:1610:C:H2'	3:C:1611:A:H8	1.73	0.49
11:K:11:ILE:HG13	11:K:60:ILE:HB	1.94	0.49
12:L:76:ARG:NE	12:L:87:ARG:HH21	2.10	0.49
3:C:279:U:H2'	3:C:280:G:H8	1.77	0.49
3:C:978:A:H2'	3:C:979:G:C8	2.46	0.49
3:C:2767:G:H2'	3:C:2768:G:C8	2.47	0.49
4:D:127:PRO:HA	4:D:193:VAL:HG23	1.93	0.49
15:O:27:VAL:CG1	15:O:134:ARG:HA	2.43	0.49
15:O:77:LYS:NZ	15:O:82:ARG:O	2.27	0.49
21:U:63:ALA:O	21:U:66:GLN:HB2	2.11	0.49
3:C:284:G:O3'	3:C:285:U:H3'	2.13	0.49
3:C:946:G:O2'	14:N:40:THR:OG1	2.22	0.49
3:C:1188:A:H3'	3:C:1189:G:H3'	1.93	0.49
3:C:1393:C:H2'	3:C:1394:A:C8	2.48	0.49
3:C:2238:A:P	21:U:104:ARG:HH12	2.34	0.49
3:C:2261:U:H2'	3:C:2262:C:C6	2.47	0.49
12:L:120:LYS:O	12:L:123:LYS:NZ	2.45	0.49
27:a:36:MET:HE2	27:a:41:LEU:HD23	1.93	0.49
27:a:45:ARG:HH22	27:a:48:ARG:HH21	1.59	0.49
28:b:16:ARG:NH1	35:i:83:C:OP1	2.26	0.49
3:C:1214:A:P	3:C:1214:A:H3'	2.52	0.49
3:C:2155:U:C5'	3:C:2155:U:C6	2.95	0.49
3:C:1124:C:H1'	12:L:108:MET:HB3	1.94	0.49
3:C:1212:U:H1'	3:C:1216:A:N6	2.27	0.49
3:C:1294:U:H2'	3:C:1295:U:C6	2.48	0.49
8:H:53:VAL:HG21	8:H:70:ARG:HB2	1.95	0.49
24:X:47:LEU:HD11	24:X:71:ILE:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:66:ILE:HD13	24:X:79:LEU:HD13	1.94	0.49
35:i:26:A:H2'	35:i:27:A:C8	2.47	0.49
3:C:166:A:H2'	3:C:167:G:O4'	2.13	0.49
3:C:1542:A:N6	3:C:1628:A:H1'	2.28	0.49
3:C:1678:U:H5'	3:C:1679:A:OP2	2.13	0.49
3:C:2238:A:H2'	3:C:2239:A:C8	2.48	0.49
3:C:2357:A:C2	3:C:2358:A:H1'	2.48	0.49
3:C:2569:G:N3	3:C:2605:C:H2'	2.28	0.49
3:C:2746:U:O2'	3:C:2871:U:OP1	2.23	0.49
8:H:54:THR:HA	8:H:66:HIS:HE1	1.76	0.49
11:K:16:GLN:HA	11:K:55:VAL:HB	1.94	0.49
14:N:118:LEU:HD22	14:N:137:ILE:HD13	1.95	0.49
24:X:122:THR:HA	24:X:184:ALA:H	1.77	0.49
3:C:844:G:O2'	3:C:878:G:H4'	2.12	0.49
3:C:879:A:N3	4:D:213:ARG:HD2	2.28	0.49
3:C:1131:G:H1'	12:L:147:GLN:HE21	1.77	0.49
3:C:1211:G:N2	3:C:1216:A:H62	2.09	0.49
3:C:1525:U:H2'	3:C:1526:A:C8	2.47	0.49
3:C:2639:G:H2'	3:C:2640:G:H8	1.77	0.49
5:E:157:PRO:HG3	5:E:161:PHE:CZ	2.48	0.49
11:K:14:GLN:HA	11:K:57:PRO:HA	1.95	0.49
12:L:129:ASP:N	12:L:129:ASP:OD1	2.45	0.49
2:B:262:ARG:HG3	2:B:262:ARG:NH1	2.26	0.49
3:C:441:G:H2'	3:C:442:U:C6	2.47	0.49
3:C:1512:U:OP2	3:C:1513:C:N4	2.38	0.49
3:C:2401:U:H2'	3:C:2402:C:H5	1.78	0.49
3:C:2861:U:H2'	3:C:2862:G:O4'	2.12	0.49
6:F:154:VAL:HG22	6:F:175:VAL:HG22	1.94	0.49
7:G:107:LEU:O	7:G:111:ILE:HG12	2.13	0.49
35:i:1:G:H2'	35:i:2:U:H6	1.77	0.49
3:C:1907:A:H61	3:C:1915:G:H2'	1.78	0.49
9:I:26:GLY:O	9:I:31:LEU:HD22	2.13	0.49
10:J:59:ARG:O	10:J:62:SER:OG	2.26	0.49
3:C:619:C:OP1	3:C:653:G:N2	2.38	0.48
3:C:1343:G:H2'	3:C:1345:G:C8	2.47	0.48
3:C:1533:U:H3'	3:C:1534:C:H5''	1.95	0.48
3:C:1715:A:N3	3:C:1798:U:O2'	2.37	0.48
3:C:3017:C:H2'	3:C:3018:U:C6	2.48	0.48
9:I:90:LYS:HE2	9:I:125:LYS:HG3	1.94	0.48
17:Q:4:LYS:NZ	17:Q:5:PRO:O	2.45	0.48
3:C:345:G:H8	3:C:345:G:OP2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:444:U:O3'	3:C:446:G:H4'	2.13	0.48
3:C:502:C:H2'	3:C:503:A:C8	2.47	0.48
3:C:1393:C:H2'	3:C:1394:A:H8	1.77	0.48
3:C:1605:G:H2'	3:C:1606:G:C5	2.48	0.48
3:C:2761:U:H2'	3:C:2762:C:C6	2.48	0.48
7:G:178:ARG:HE	7:G:184:PHE:HD2	1.59	0.48
12:L:125:TYR:OH	12:L:132:HIS:NE2	2.37	0.48
24:X:37:LEU:O	24:X:44:PRO:HA	2.14	0.48
34:h:38:CYS:H	34:h:41:CYS:HB2	1.78	0.48
2:B:64:SER:HB3	2:B:95:GLY:HA2	1.95	0.48
3:C:175:G:O2'	3:C:176:G:H5'	2.13	0.48
3:C:462:A:H1'	3:C:489:A:N6	2.28	0.48
3:C:1531:C:O2'	3:C:1636:A:H4'	2.14	0.48
3:C:1689:U:H2'	3:C:1744:A:N6	2.28	0.48
2:B:60:ARG:C	2:B:62:TRP:H	2.22	0.48
3:C:404:A:OP1	6:F:170:ARG:HD2	2.14	0.48
3:C:740:A:O2'	3:C:741:G:OP2	2.27	0.48
3:C:977:G:H2'	3:C:978:A:O4'	2.12	0.48
3:C:2584:A:OP1	32:f:24:ARG:NH1	2.46	0.48
3:C:3009:U:H5'	5:E:38:ARG:HH22	1.78	0.48
5:E:51:GLN:HA	5:E:83:GLU:HB3	1.96	0.48
7:G:142:GLN:NE2	7:G:155:ARG:O	2.36	0.48
11:K:14:GLN:HG2	11:K:57:PRO:HB3	1.95	0.48
12:L:65:SER:O	12:L:68:LYS:HE3	2.14	0.48
13:M:106:LEU:HB3	13:M:111:PHE:HB2	1.96	0.48
19:S:94:ASN:O	19:S:98:LEU:HD23	2.13	0.48
3:C:725:A:OP1	32:f:47:ARG:NH1	2.43	0.48
3:C:1558:C:H2'	3:C:1559:A:C8	2.49	0.48
3:C:1728:U:H4'	3:C:1729:A:H5'	1.94	0.48
3:C:1907:A:H2'	3:C:1908:A:C8	2.49	0.48
3:C:3010:U:H2'	3:C:3011:C:H6	1.78	0.48
5:E:154:CYS:C	5:E:156:THR:H	2.18	0.48
9:I:63:GLU:HA	9:I:137:HIS:CD2	2.48	0.48
18:R:28:HIS:HD2	18:R:82:HIS:HB3	1.79	0.48
3:C:897:A:C2	4:D:226:MET:SD	3.07	0.48
3:C:1720:G:N2	4:D:99:ASP:O	2.45	0.48
3:C:1975:A:H3'	3:C:1976:A:C8	2.48	0.48
3:C:2321:U:H2'	3:C:2322:C:C6	2.49	0.48
26:Z:39:VAL:HG21	26:Z:64:ALA:HB3	1.95	0.48
3:C:289:A:H62	3:C:299:G:H22	1.61	0.48
3:C:821:A:O2'	4:D:4:ARG:NH2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1015:A:H2'	3:C:1016:C:O4'	2.13	0.48
3:C:1640:A:H2'	3:C:1642:G:N7	2.28	0.48
7:G:53:ASP:HB2	7:G:56:LEU:HD23	1.96	0.48
8:H:90:ILE:HD12	8:H:163:VAL:HG22	1.96	0.48
3:C:5:U:C2'	3:C:6:G:H5'	2.44	0.48
3:C:251:A:C5	3:C:252:G:H1'	2.48	0.48
3:C:940:A:H2'	3:C:941:U:O4'	2.13	0.48
3:C:3086:U:OP2	3:C:3087:G:O2'	2.19	0.48
4:D:3:ILE:HD12	4:D:204:ILE:CG2	2.43	0.48
4:D:259:LYS:HD3	4:D:260:PRO:HD2	1.94	0.48
7:G:23:LEU:HD13	7:G:36:PRO:HG2	1.94	0.48
33:g:4:ASN:O	33:g:36:GLN:HA	2.14	0.48
33:g:14:CYS:SG	33:g:27:CYS:HB2	2.53	0.48
3:C:263:G:H2'	3:C:264:G:O4'	2.14	0.48
3:C:2309:U:H2'	3:C:2310:G:C8	2.49	0.48
3:C:49:A:H2'	3:C:50:A:C8	2.49	0.48
3:C:196:A:H62	3:C:2654:A:H2'	1.78	0.48
3:C:729:C:O2'	3:C:733:U:OP1	2.25	0.48
3:C:1075:U:O4	15:O:17:GLN:HB3	2.14	0.48
3:C:2094:G:HO2'	3:C:2095:G:H8	1.54	0.48
22:V:14:PRO:HD3	27:a:34:PHE:CD1	2.48	0.48
3:C:164:A:H2'	3:C:165:U:C6	2.48	0.47
3:C:604:C:O2'	21:U:25:ARG:NH2	2.39	0.47
3:C:972:A:H5''	25:Y:69:PHE:CD2	2.49	0.47
4:D:8:PRO:HB3	4:D:14:ARG:HD3	1.96	0.47
15:O:71:ASP:N	15:O:71:ASP:OD1	2.46	0.47
28:b:3:GLU:HA	28:b:39:ASP:HB2	1.96	0.47
3:C:736:G:O2'	3:C:738:A:N7	2.43	0.47
3:C:868:C:H5'	31:e:2:ALA:HA	1.96	0.47
3:C:1648:A:H4'	3:C:1649:C:O5'	2.14	0.47
3:C:2754:G:N7	8:H:173:LYS:NZ	2.58	0.47
3:C:3055:G:H2'	3:C:3100:A:H61	1.78	0.47
8:H:16:ASP:OD1	8:H:27:LYS:HB2	2.13	0.47
24:X:136:GLU:OE1	24:X:137:ALA:N	2.47	0.47
29:c:49:LEU:HG	29:c:51:LEU:HD13	1.96	0.47
3:C:410:U:H4'	23:W:67:HIS:CD2	2.48	0.47
3:C:619:C:O2	19:S:28:ARG:NH2	2.47	0.47
3:C:1434:G:H2'	3:C:1435:C:C6	2.50	0.47
3:C:2349:A:H1'	3:C:2350:G:N9	2.30	0.47
3:C:2530:C:H5''	3:C:2531:G:H2'	1.95	0.47
4:D:145:VAL:HG22	4:D:155:LEU:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:128:THR:OG1	6:F:129:GLU:OE1	2.19	0.47
9:I:84:ALA:HB2	9:I:91:LEU:HG	1.94	0.47
35:i:4:A:N6	35:i:23:G:HO2'	2.11	0.47
3:C:285:U:C2	3:C:287:A:H4'	2.49	0.47
3:C:1500:A:O2'	3:C:1511:U:O2	2.32	0.47
7:G:63:ASP:HB2	7:G:148:ILE:CD1	2.44	0.47
15:O:21:ALA:HB2	15:O:98:LYS:HB2	1.96	0.47
22:V:18:GLU:HG2	22:V:19:LYS:H	1.76	0.47
2:B:59:GLU:CD	2:B:59:GLU:N	2.73	0.47
3:C:965:U:H2'	3:C:966:U:C6	2.50	0.47
3:C:1690:A:OP2	3:C:1744:A:N6	2.48	0.47
3:C:1698:A:N6	3:C:1736:G:O2'	2.43	0.47
3:C:1886:A:H4'	3:C:1887:A:O5'	2.15	0.47
4:D:3:ILE:HG23	4:D:204:ILE:HG22	1.96	0.47
4:D:273:ARG:HH11	4:D:275:GLY:N	2.08	0.47
8:H:149:ILE:HG22	8:H:163:VAL:HG11	1.96	0.47
12:L:106:ILE:HD12	12:L:119:GLN:HG2	1.97	0.47
14:N:56:PRO:O	14:N:60:ARG:HG2	2.14	0.47
27:a:43:ASN:CG	27:a:46:ARG:HG3	2.40	0.47
33:g:2:LYS:NZ	33:g:31:ARG:O	2.47	0.47
3:C:312:G:C2'	3:C:313:G:H5'	2.45	0.47
3:C:2347:G:H2'	3:C:2348:G:H5'	1.97	0.47
3:C:2531:G:N2	3:C:2535:A:O2'	2.47	0.47
5:E:160:VAL:HG12	5:E:160:VAL:O	2.14	0.47
7:G:33:MET:CE	35:i:55:G:H21	2.28	0.47
7:G:128:GLN:HB3	7:G:135:TYR:HE1	1.79	0.47
10:J:6:LYS:HG2	10:J:56:LEU:HD11	1.95	0.47
17:Q:69:ASP:OD1	17:Q:69:ASP:N	2.47	0.47
23:W:32:LYS:HD3	23:W:65:PRO:HB2	1.97	0.47
24:X:157:ILE:HA	24:X:161:GLN:HE21	1.80	0.47
3:C:1060:U:OP1	14:N:37:THR:HG22	2.15	0.47
3:C:1301:G:H2'	3:C:1302:G:O4'	2.13	0.47
3:C:1531:C:N4	3:C:1532:G:C2	2.82	0.47
3:C:1732:U:H2'	3:C:1733:C:C6	2.50	0.47
3:C:1937:U:H2'	3:C:1938:G:O4'	2.15	0.47
3:C:2144:AI5:C19	3:C:2144:AI5:C01	2.92	0.47
3:C:2297:U:H2'	3:C:2298:U:C6	2.50	0.47
3:C:2343:G:H2'	3:C:2344:G:C8	2.49	0.47
3:C:2367:G:C2	3:C:2369:C:H1'	2.50	0.47
3:C:2516:U:H2'	3:C:2517:C:C6	2.49	0.47
3:C:3096:U:H4'	18:R:3:THR:HG23	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:23:ALA:N	11:K:24:PRO:HD2	2.30	0.47
11:K:115:LYS:HA	11:K:118:LEU:HD12	1.95	0.47
14:N:64:LEU:HD23	32:f:25:GLN:HG3	1.96	0.47
17:Q:40:VAL:HG22	17:Q:49:VAL:HG12	1.95	0.47
24:X:78:ALA:HB1	24:X:97:LEU:HD12	1.97	0.47
34:h:40:GLN:C	34:h:48:LYS:HZ1	2.22	0.47
35:i:10:G:O2'	35:i:11:U:OP1	2.32	0.47
3:C:341:C:N4	3:C:342:C:H42	2.12	0.47
3:C:1271:C:O3'	19:S:80:ILE:HD11	2.15	0.47
3:C:1578:G:C6	3:C:1594:G:N1	2.83	0.47
3:C:2971:G:H5'	8:H:71:THR:HG21	1.96	0.47
13:M:101:PRO:HB2	13:M:122:LEU:HD23	1.97	0.47
19:S:47:TYR:OH	19:S:51:ARG:NH1	2.47	0.47
21:U:78:VAL:HA	21:U:114:VAL:HG12	1.97	0.47
22:V:11:ILE:HG22	22:V:33:VAL:HG12	1.95	0.47
26:Z:6:ASP:HB2	26:Z:50:ASN:O	2.14	0.47
3:C:348:G:C6	3:C:349:G:C6	3.03	0.47
3:C:761:G:H2'	3:C:762:U:C6	2.50	0.47
3:C:1479:G:HO2'	3:C:2025:C:H5	1.63	0.47
3:C:1603:G:H2'	3:C:1604:G:H8	1.80	0.47
3:C:1616:A:O5'	3:C:1616:A:C8	2.66	0.47
3:C:1888:C:O2	5:E:139:HIS:NE2	2.46	0.47
21:U:72:ASP:OD2	21:U:74:SER:OG	2.33	0.47
3:C:348:G:H2'	3:C:349:G:C8	2.50	0.47
3:C:608:C:H2'	3:C:609:G:C8	2.48	0.47
3:C:1568:C:N4	3:C:1604:G:O6	2.49	0.47
3:C:1589:G:H2'	3:C:1590:G:O4'	2.15	0.47
3:C:1636:A:N6	3:C:1802:G:H21	2.03	0.47
3:C:1970:G:H5''	18:R:92:ARG:HD3	1.97	0.47
3:C:2094:G:O2'	3:C:2095:G:H8	1.98	0.47
3:C:2098:U:H2'	3:C:2099:G:O4'	2.14	0.47
3:C:2353:U:N3	3:C:2354:G:N7	2.63	0.47
6:F:123:ARG:HD2	6:F:193:ASP:OD1	2.14	0.47
6:F:167:LYS:HD3	6:F:170:ARG:NH2	2.30	0.47
10:J:48:THR:O	10:J:80:ALA:HA	2.15	0.47
14:N:57:ILE:O	14:N:61:LEU:HD13	2.15	0.47
3:C:217:G:H22	3:C:235:U:H4'	1.80	0.46
3:C:2756:G:O2'	3:C:2881:A:N1	2.41	0.46
5:E:70:PHE:HD1	5:E:75:VAL:HG23	1.80	0.46
2:B:17:ALA:HB1	2:B:22:GLN:HB2	1.97	0.46
3:C:782:U:H2'	3:C:783:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1231:U:H2'	3:C:1232:G:C8	2.51	0.46
3:C:2253:A:N6	3:C:2257:A:OP2	2.46	0.46
3:C:2277:G:H5'	5:E:155:ALA:H	1.80	0.46
3:C:2693:A:H2'	3:C:2694:G:O4'	2.15	0.46
3:C:2971:G:OP1	8:H:75:ASN:ND2	2.24	0.46
11:K:111:ALA:O	11:K:115:LYS:N	2.44	0.46
13:M:4:GLN:NE2	13:M:22:ILE:O	2.49	0.46
2:B:180:LEU:HG	2:B:180:LEU:O	2.15	0.46
3:C:567:A:H4'	3:C:568:A:OP1	2.14	0.46
3:C:830:A:H3'	3:C:831:A:H8	1.80	0.46
3:C:929:C:H2'	3:C:930:C:H6	1.80	0.46
3:C:966:U:H2'	3:C:967:G:H8	1.81	0.46
4:D:20:ASP:O	4:D:22:ALA:N	2.48	0.46
8:H:97:VAL:HG22	8:H:106:PHE:HD1	1.81	0.46
9:I:77:ASP:OD2	9:I:147:ASN:ND2	2.49	0.46
12:L:96:HIS:HA	12:L:97:PRO:HD3	1.75	0.46
3:C:351:G:H3'	3:C:352:G:H8	1.80	0.46
3:C:502:C:H2'	3:C:503:A:H8	1.80	0.46
3:C:586:U:H2'	3:C:587:G:O4'	2.16	0.46
3:C:1437:A:C5	3:C:1438:G:N7	2.84	0.46
3:C:1869:G:H2'	3:C:1870:U:O4'	2.16	0.46
3:C:2084:A:H2'	3:C:2085:C:O4'	2.15	0.46
3:C:2094:G:O2'	3:C:2095:G:C8	2.64	0.46
3:C:2113:A:H2'	3:C:2114:A:C8	2.50	0.46
3:C:2351:A:N3	3:C:2396:A:O2'	2.45	0.46
3:C:2569:G:H4'	3:C:2570:A:H5''	1.97	0.46
3:C:2623:A:H2'	3:C:2624:C:H6	1.81	0.46
3:C:2785:A:H2'	3:C:2786:U:O4'	2.15	0.46
11:K:125:ALA:O	11:K:129:ILE:HG23	2.15	0.46
15:O:63:LYS:HG2	15:O:65:TRP:CZ2	2.51	0.46
21:U:11:THR:O	21:U:64:ASN:ND2	2.49	0.46
3:C:662:G:H2'	3:C:2254:A:N7	2.31	0.46
3:C:1523:U:H2'	3:C:1524:G:C8	2.50	0.46
3:C:1593:U:H2'	3:C:1594:G:H8	1.81	0.46
3:C:1885:G:O2'	3:C:2215:U:O4	2.23	0.46
3:C:2144:AI5:O16	3:C:2144:AI5:C17	2.63	0.46
24:X:80:THR:HG21	24:X:83:LEU:CD1	2.43	0.46
3:C:334:G:C6	3:C:348:G:C6	3.03	0.46
3:C:356:G:H4'	3:C:358:G:C4	2.51	0.46
3:C:1119:A:H2'	3:C:1120:G:O4'	2.15	0.46
3:C:2375:G:H2'	3:C:2376:G:C4	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:2686:U:H2'	3:C:2687:U:C6	2.50	0.46
31:e:27:THR:O	31:e:31:ARG:HG3	2.16	0.46
35:i:14:A:N1	35:i:70:G:O2'	2.41	0.46
3:C:302:U:O2'	3:C:303:G:H5'	2.15	0.46
3:C:639:C:O2'	3:C:640:G:H8	1.98	0.46
3:C:947:U:H2'	3:C:948:G:C8	2.50	0.46
3:C:1651:C:H2'	3:C:1652:A:C8	2.51	0.46
3:C:2007:C:H2'	3:C:2008:A:C5	2.51	0.46
3:C:2329:G:O6	3:C:2406:U:O4	2.34	0.46
6:F:124:ILE:HD13	6:F:194:VAL:HB	1.97	0.46
6:F:156:VAL:HG12	6:F:158:ILE:HG12	1.97	0.46
7:G:126:PRO:O	7:G:174:ARG:NH1	2.47	0.46
10:J:25:VAL:HG13	10:J:106:LYS:HB2	1.96	0.46
10:J:64:ALA:HB3	10:J:66:ILE:HG23	1.97	0.46
35:i:27:A:C2	35:i:28:A:H1'	2.50	0.46
3:C:954:U:H2'	3:C:955:C:C6	2.50	0.46
3:C:1549:G:O2'	3:C:1550:G:H8	1.99	0.46
3:C:2170:U:H2'	3:C:2171:C:C6	2.51	0.46
3:C:2532:G:H1	3:C:2535:A:N6	2.06	0.46
5:E:60:ARG:HG2	5:E:60:ARG:NH1	2.30	0.46
10:J:37:ALA:HB1	11:K:119:ASN:OD1	2.15	0.46
13:M:71:ARG:HH22	13:M:122:LEU:C	2.23	0.46
13:M:86:ILE:HG22	13:M:94:ARG:HD3	1.98	0.46
27:a:29:LEU:HD13	27:a:50:VAL:HG13	1.98	0.46
2:B:182:LYS:HB3	2:B:185:PHE:HD2	1.81	0.46
3:C:449:G:O5'	3:C:449:G:C8	2.64	0.46
3:C:673:C:H2'	3:C:674:U:C6	2.51	0.46
3:C:1258:C:OP2	12:L:68:LYS:NZ	2.46	0.46
3:C:1672:C:O2'	3:C:1679:A:N6	2.49	0.46
3:C:2075:G:O2'	3:C:2107:G:N1	2.46	0.46
3:C:2339:G:O6	3:C:2387:U:N3	2.40	0.46
3:C:2363:A:H2'	3:C:2364:C:C6	2.51	0.46
3:C:2955:G:O2'	3:C:2956:G:H5'	2.16	0.46
6:F:76:GLN:HE21	6:F:84:PHE:HE1	1.61	0.46
7:G:38:VAL:HA	7:G:165:THR:HG22	1.98	0.46
10:J:55:THR:HA	10:J:58:LYS:HG3	1.98	0.46
15:O:75:THR:HA	15:O:90:PRO:HA	1.98	0.46
21:U:66:GLN:OE1	21:U:73:PRO:HD3	2.16	0.46
3:C:262:A:H62	3:C:263:G:N2	2.05	0.46
3:C:336:C:H3'	3:C:337:U:C6	2.51	0.46
3:C:1501:C:H2'	3:C:1502:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1543:A:O5'	3:C:1543:A:H8	1.99	0.46
3:C:1653:G:H2'	3:C:1654:G:O4'	2.16	0.46
3:C:1784:C:H2'	3:C:1785:C:C6	2.50	0.46
3:C:2288:C:H2'	3:C:2289:C:H6	1.79	0.46
3:C:2623:A:H2'	3:C:2624:C:C6	2.51	0.46
3:C:2861:U:H5'	5:E:47:TYR:CE2	2.50	0.46
7:G:76:ARG:HD3	7:G:89:GLY:HA2	1.98	0.46
8:H:77:VAL:O	8:H:80:VAL:HG12	2.16	0.46
21:U:25:ARG:HA	21:U:28:ILE:HB	1.98	0.46
34:h:42:HIS:CD2	34:h:43:PRO:HD2	2.51	0.46
35:i:114:A:H2'	35:i:115:A:H8	1.76	0.46
3:C:442:U:H2'	3:C:443:C:C6	2.51	0.45
3:C:462:A:H1'	3:C:489:A:H61	1.79	0.45
3:C:1576:C:H2'	3:C:1577:C:O4'	2.15	0.45
3:C:2640:G:H5''	14:N:65:LYS:HB2	1.98	0.45
3:C:2901:G:H2'	3:C:2902:A:C8	2.51	0.45
5:E:13:MET:HB2	5:E:26:VAL:O	2.16	0.45
10:J:23:THR:OG1	10:J:109:TYR:O	2.34	0.45
10:J:51:VAL:HG12	10:J:78:ALA:HB2	1.97	0.45
21:U:52:GLU:HB2	21:U:53:PRO:HD3	1.97	0.45
28:b:5:LYS:HE2	28:b:57:GLU:OE2	2.16	0.45
3:C:388:U:H2'	3:C:389:G:O4'	2.16	0.45
3:C:499:G:OP2	3:C:2630:A:O2'	2.34	0.45
3:C:1131:G:H2'	3:C:1132:U:H6	1.80	0.45
3:C:1790:A:H2'	3:C:1791:A:C8	2.51	0.45
3:C:1971:C:C5	18:R:93:ARG:NH2	2.85	0.45
3:C:2909:G:P	18:R:48:ARG:HH22	2.39	0.45
3:C:3017:C:H2'	3:C:3018:U:H6	1.81	0.45
3:C:3040:G:H2'	3:C:3042:A:N7	2.31	0.45
7:G:47:VAL:O	7:G:49:ASP:N	2.47	0.45
9:I:118:GLN:CG	9:I:133:THR:HG23	2.42	0.45
10:J:13:ILE:O	10:J:16:GLN:HG3	2.17	0.45
10:J:100:ASN:C	10:J:102:ALA:H	2.24	0.45
21:U:23:LYS:HG2	29:c:20:TRP:HH2	1.80	0.45
2:B:11:LEU:C	2:B:11:LEU:HD23	2.41	0.45
3:C:760:U:H2'	3:C:761:G:H8	1.81	0.45
3:C:1174:G:N1	3:C:1220:C:OP2	2.43	0.45
3:C:2600:A:N3	17:Q:121:ARG:NH2	2.65	0.45
5:E:115:THR:HG21	5:E:174:ARG:HH11	1.82	0.45
8:H:158:TYR:O	8:H:172:ARG:NH2	2.45	0.45
20:T:33:ALA:O	20:T:64:VAL:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:89:A:H2'	3:C:90:C:H6	1.79	0.45
3:C:2723:C:H6	3:C:2723:C:O5'	1.99	0.45
7:G:129:PHE:CD2	7:G:133:GLY:HA2	2.52	0.45
2:B:236:ASN:CG	2:B:236:ASN:O	2.59	0.45
3:C:422:A:H2'	3:C:423:C:O4'	2.17	0.45
3:C:864:A:H8	3:C:864:A:OP1	2.00	0.45
3:C:1160:G:H1	3:C:1231:U:H3	1.64	0.45
3:C:1203:A:H2'	3:C:1204:A:C5	2.51	0.45
3:C:1788:G:H5'	4:D:60:ARG:HA	1.99	0.45
3:C:2791:G:H2'	3:C:2792:C:C6	2.52	0.45
30:d:38:ILE:CD1	30:d:40:LYS:HD3	2.46	0.45
3:C:97:U:OP1	3:C:98:U:O2'	2.32	0.45
3:C:2904:C:H5'	5:E:199:PRO:HA	1.99	0.45
3:C:2922:U:H2'	3:C:2923:C:H6	1.82	0.45
16:P:79:LEU:HD23	16:P:83:ILE:HD12	1.99	0.45
35:i:110:G:H2'	35:i:111:C:C6	2.52	0.45
3:C:1380:A:H3'	29:c:16:ARG:NH2	2.32	0.45
3:C:1619:U:H2'	3:C:1620:U:O4'	2.16	0.45
3:C:2145:C:OP2	3:C:2145:C:C4'	2.64	0.45
3:C:2558:C:H5'	17:Q:20:ARG:NH2	2.32	0.45
6:F:132:GLU:H	6:F:132:GLU:CD	2.25	0.45
10:J:57:VAL:HG23	10:J:73:PHE:HZ	1.81	0.45
3:C:284:G:HO2'	3:C:285:U:P	2.34	0.45
3:C:336:C:H3'	3:C:337:U:H6	1.80	0.45
3:C:1033:A:H5''	35:i:95:G:O2'	2.17	0.45
3:C:1131:G:H2'	3:C:1132:U:C6	2.52	0.45
3:C:2016:G:C5	4:D:177:MET:HG3	2.52	0.45
3:C:2165:C:H2'	3:C:2166:C:O4'	2.16	0.45
3:C:2589:G:OP1	25:Y:55:GLY:N	2.50	0.45
3:C:2635:A:H2'	3:C:2636:A:C8	2.52	0.45
7:G:63:ASP:HB2	7:G:148:ILE:HD13	1.97	0.45
11:K:88:GLN:OE1	11:K:89:LYS:HG2	2.16	0.45
16:P:49:GLU:OE1	16:P:95:THR:OG1	2.35	0.45
27:a:6:THR:CG2	27:a:9:GLU:HG2	2.47	0.45
3:C:193:G:H2'	3:C:194:A:O4'	2.17	0.45
3:C:339:U:H2'	3:C:340:A:C8	2.52	0.45
3:C:992:C:H2'	3:C:993:G:O4'	2.16	0.45
3:C:1562:C:H2'	3:C:1563:A:H8	1.82	0.45
3:C:2255:A:C6	3:C:2722:C:H1'	2.52	0.45
10:J:22:ALA:HB3	10:J:82:VAL:HB	1.99	0.45
10:J:24:VAL:HG21	10:J:93:ILE:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:X:71:ILE:O	24:X:74:THR:OG1	2.33	0.45
3:C:69:U:C6	27:a:58:TYR:HD2	2.34	0.45
3:C:402:G:N2	6:F:171:ASN:O	2.49	0.45
3:C:784:G:N3	3:C:784:G:H2'	2.31	0.45
9:I:105:LYS:HG3	9:I:109:GLY:O	2.16	0.45
24:X:177:LEU:HD21	24:X:180:ASN:HB2	1.99	0.45
2:B:133:ARG:HH11	2:B:133:ARG:CG	2.30	0.44
3:C:181:A:H2'	3:C:182:C:C6	2.52	0.44
3:C:378:G:OP1	23:W:94:LYS:NZ	2.50	0.44
3:C:672:C:H2'	3:C:673:C:H6	1.82	0.44
3:C:736:G:H1'	3:C:740:A:N6	2.33	0.44
3:C:998:G:H2'	3:C:999:C:H6	1.82	0.44
3:C:1158:U:O5'	24:X:52:ARG:NH2	2.50	0.44
3:C:2006:A:H2'	3:C:2007:C:O4'	2.16	0.44
3:C:2074:G:H5'	3:C:2075:G:OP2	2.17	0.44
3:C:2865:G:OP1	12:L:76:ARG:NH1	2.44	0.44
9:I:91:LEU:HB2	9:I:125:LYS:HA	1.98	0.44
12:L:31:ALA:O	12:L:35:LEU:HD23	2.17	0.44
13:M:92:ASP:N	13:M:92:ASP:OD1	2.50	0.44
16:P:44:LEU:HD23	16:P:113:ILE:HD12	1.98	0.44
25:Y:36:ILE:HG22	25:Y:60:PHE:HB3	1.98	0.44
34:h:16:CYS:HB2	34:h:20:HIS:H	1.82	0.44
2:B:180:LEU:C	2:B:180:LEU:HD12	2.42	0.44
3:C:920:G:H22	3:C:943:U:H5''	1.82	0.44
7:G:57:ILE:O	7:G:61:ILE:HG23	2.17	0.44
9:I:73:GLU:C	9:I:75:LEU:H	2.25	0.44
11:K:63:TYR:HB2	11:K:67:SER:OG	2.18	0.44
13:M:120:GLU:HG2	18:R:65:TYR:HE2	1.81	0.44
16:P:10:LEU:HD21	16:P:40:LYS:HA	1.99	0.44
2:B:8:ASP:OD1	2:B:8:ASP:N	2.50	0.44
3:C:21:G:O2'	21:U:85:GLU:O	2.34	0.44
3:C:929:C:H2'	3:C:930:C:C6	2.53	0.44
3:C:2155:U:C6	3:C:2155:U:H5'	2.52	0.44
3:C:2171:C:H2'	3:C:2172:G:H8	1.82	0.44
3:C:2411:U:H2'	3:C:2412:U:C6	2.52	0.44
3:C:2530:C:H3'	3:C:2531:G:H8	1.82	0.44
3:C:2717:U:C4	3:C:2718:G:C8	3.05	0.44
10:J:13:ILE:HD11	10:J:79:ILE:HD11	1.98	0.44
16:P:61:HIS:O	16:P:65:GLU:HG2	2.16	0.44
17:Q:87:LEU:HD23	17:Q:87:LEU:HA	1.85	0.44
28:b:6:ILE:HG13	28:b:56:VAL:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:264:G:O2'	3:C:516:G:N2	2.37	0.44
3:C:1138:A:N1	3:C:1259:U:H2'	2.32	0.44
3:C:1474:A:OP2	3:C:1486:G:N1	2.41	0.44
3:C:1550:G:O2'	3:C:1551:U:H2'	2.17	0.44
3:C:1806:A:H2'	3:C:1807:C:C6	2.53	0.44
3:C:2531:G:H5'	3:C:2532:G:C5	2.52	0.44
3:C:2537:C:H4'	7:G:95:ARG:HD3	1.99	0.44
25:Y:24:LYS:O	25:Y:25:ARG:NH1	2.49	0.44
3:C:5:U:O2'	3:C:6:G:H5'	2.17	0.44
3:C:247:G:H4'	3:C:474:G:C5	2.52	0.44
3:C:453:U:H2'	3:C:454:U:C6	2.52	0.44
3:C:487:U:H2'	3:C:488:G:O4'	2.18	0.44
3:C:1164:A:C2	10:J:59:ARG:HD2	2.52	0.44
3:C:1201:G:O3'	3:C:1202:A:C8	2.70	0.44
5:E:154:CYS:O	5:E:156:THR:N	2.47	0.44
7:G:139:LEU:HD21	7:G:159:MET:HB2	1.99	0.44
9:I:9:VAL:HG22	9:I:35:LEU:HD12	2.00	0.44
12:L:62:ILE:HD12	12:L:62:ILE:HA	1.78	0.44
18:R:4:LEU:O	18:R:7:VAL:HG22	2.18	0.44
18:R:102:LEU:HD12	18:R:106:LYS:HB2	2.00	0.44
19:S:120:ASP:HB3	19:S:123:ALA:HB2	2.00	0.44
3:C:998:G:H2'	3:C:999:C:C6	2.53	0.44
3:C:2579:C:H4'	25:Y:24:LYS:HG2	1.99	0.44
9:I:135:LYS:HE2	9:I:135:LYS:HB3	1.78	0.44
10:J:61:ALA:C	10:J:66:ILE:HG13	2.43	0.44
12:L:95:LYS:HG3	12:L:96:HIS:HD1	1.81	0.44
15:O:20:ILE:HD13	15:O:99:PRO:HG2	1.98	0.44
20:T:43:VAL:HG13	20:T:48:VAL:HG12	2.00	0.44
21:U:34:LYS:O	21:U:78:VAL:HG22	2.16	0.44
21:U:50:ALA:O	21:U:53:PRO:HD2	2.18	0.44
2:B:209:LEU:HD12	2:B:260:VAL:HG21	1.99	0.44
3:C:293:G:C6	3:C:294:G:O6	2.71	0.44
3:C:1130:C:O2	12:L:27:ARG:NH1	2.50	0.44
3:C:1754:G:H1	3:C:1759:A:H61	1.65	0.44
3:C:2011:U:H1'	3:C:2124:A:C2	2.53	0.44
3:C:2274:C:H2'	3:C:2275:A:O4'	2.17	0.44
3:C:2588:C:H2'	3:C:2589:G:O4'	2.18	0.44
34:h:40:GLN:O	34:h:48:LYS:NZ	2.39	0.44
35:i:5:C:O2'	35:i:27:A:N1	2.39	0.44
3:C:2085:C:H2'	3:C:2086:U:H6	1.83	0.44
3:C:2144:AI5:O16	3:C:2144:AI5:C48	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:2235:C:H2'	3:C:2236:G:O4'	2.17	0.44
6:F:111:LEU:HD21	6:F:184:ASN:HA	2.00	0.44
7:G:150:VAL:O	7:G:153:ILE:HG12	2.17	0.44
9:I:109:GLY:N	9:I:110:PRO:HD2	2.33	0.44
13:M:114:ILE:H	13:M:114:ILE:HD12	1.83	0.44
15:O:17:GLN:CG	15:O:39:HIS:HB3	2.48	0.44
19:S:50:ARG:O	19:S:54:LYS:NZ	2.51	0.44
25:Y:38:VAL:CG1	25:Y:59:LEU:HB2	2.48	0.44
2:B:60:ARG:HA	2:B:60:ARG:HE	1.81	0.44
3:C:1594:G:C2	3:C:1595:G:C5	3.06	0.44
3:C:3008:C:H2'	3:C:3009:U:O4'	2.18	0.44
4:D:266:LYS:HE2	4:D:266:LYS:HB2	1.87	0.44
8:H:81:THR:OG1	8:H:82:GLU:N	2.50	0.44
8:H:122:ILE:HD13	8:H:136:GLY:HA3	1.99	0.44
23:W:35:VAL:HG13	23:W:38:VAL:HG22	1.99	0.44
33:g:27:CYS:SG	33:g:28:SER:N	2.91	0.44
3:C:217:G:N2	3:C:235:U:H4'	2.33	0.43
3:C:548:A:H2'	3:C:549:C:O4'	2.18	0.43
3:C:1538:G:H2'	3:C:1539:A:C8	2.53	0.43
5:E:4:LYS:HE2	5:E:4:LYS:HB3	1.81	0.43
7:G:124:LEU:HD22	7:G:182:PHE:CZ	2.52	0.43
10:J:43:LEU:HD21	10:J:80:ALA:HB1	1.99	0.43
13:M:77:ILE:HD13	18:R:71:ARG:HD3	1.99	0.43
19:S:11:GLN:OE1	19:S:14:ARG:NH1	2.50	0.43
3:C:89:A:O2'	3:C:90:C:OP1	2.31	0.43
3:C:284:G:N1	3:C:300:G:C5	2.86	0.43
3:C:638:U:C2	3:C:639:C:C5	3.06	0.43
3:C:1290:C:N4	3:C:1291:G:C2	2.87	0.43
3:C:1338:U:H4'	20:T:89:GLY:O	2.18	0.43
3:C:1509:U:H4'	3:C:1821:A:H4'	2.00	0.43
3:C:1529:U:H2'	3:C:1530:G:O4'	2.18	0.43
3:C:1550:G:H1'	3:C:1551:U:C5	2.53	0.43
3:C:1600:G:H2'	3:C:1601:G:H8	1.83	0.43
3:C:2016:G:O2'	4:D:181:GLU:OE1	2.29	0.43
3:C:2279:C:H2'	3:C:2728:U:H4'	1.98	0.43
3:C:2349:A:H1'	3:C:2350:G:C8	2.53	0.43
3:C:2800:G:H5'	3:C:2802:G:N7	2.33	0.43
11:K:13:LEU:HD21	11:K:29:ALA:HB1	1.99	0.43
18:R:13:ARG:HD3	18:R:76:HIS:HA	2.01	0.43
24:X:126:GLN:HB3	24:X:179:VAL:HG12	2.00	0.43
35:i:104:G:H2'	35:i:105:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:33:ARG:HD3	2:B:36:GLY:O	2.17	0.43
3:C:332:C:H42	3:C:350:A:H61	1.66	0.43
3:C:752:C:H2'	3:C:753:A:O4'	2.17	0.43
3:C:1510:A:HO2'	3:C:1511:U:P	2.40	0.43
3:C:1975:A:H3'	3:C:1976:A:H8	1.83	0.43
3:C:2029:A:H2'	3:C:2030:C:C6	2.54	0.43
3:C:2487:C:N4	25:Y:15:ASP:OD1	2.50	0.43
5:E:89:GLU:HA	5:E:92:VAL:HG22	1.99	0.43
3:C:256:A:H2'	3:C:257:A:C8	2.53	0.43
3:C:353:G:O6	3:C:442:U:O4	2.36	0.43
3:C:406:A:H2'	3:C:407:C:O4'	2.18	0.43
3:C:1000:C:O2'	3:C:1001:C:OP1	2.34	0.43
3:C:1990:A:H2'	3:C:1991:C:H5'	2.00	0.43
3:C:2048:G:H2'	3:C:2049:C:C6	2.54	0.43
6:F:38:VAL:HG12	6:F:185:THR:HG23	2.00	0.43
12:L:13:ARG:NH1	12:L:121:LYS:HD3	2.33	0.43
3:C:639:C:HO2'	3:C:640:G:C5'	2.30	0.43
3:C:1578:G:H2'	3:C:1579:C:O4'	2.18	0.43
3:C:2006:A:OP2	4:D:222:ARG:NH1	2.51	0.43
15:O:58:ILE:O	15:O:59:LYS:HG2	2.18	0.43
16:P:10:LEU:HD21	16:P:40:LYS:HG2	1.99	0.43
21:U:58:ILE:HD13	21:U:112:VAL:HG11	2.01	0.43
3:C:441:G:H2'	3:C:442:U:H6	1.84	0.43
3:C:738:A:H2'	3:C:740:A:C8	2.53	0.43
3:C:1545:C:H3'	3:C:1546:A:C8	2.54	0.43
3:C:1555:A:H5'	3:C:1556:A:OP2	2.19	0.43
3:C:2150:U:H6	3:C:2150:U:O5'	2.02	0.43
3:C:2316:G:H4'	9:I:24:GLY:HA3	2.01	0.43
3:C:2574:C:H2'	3:C:2575:G:O4'	2.18	0.43
4:D:129:ASN:O	4:D:193:VAL:HG22	2.18	0.43
11:K:43:ALA:HB1	11:K:70:PHE:CE2	2.53	0.43
22:V:24:ILE:HD13	22:V:28:VAL:O	2.19	0.43
25:Y:17:ALA:O	25:Y:19:GLN:NE2	2.52	0.43
3:C:32:G:H1'	3:C:542:A:C4	2.53	0.43
3:C:943:U:H2'	3:C:944:A:C8	2.53	0.43
3:C:1236:G:H2'	3:C:1237:U:O4'	2.18	0.43
3:C:1690:A:H2'	3:C:1691:A:C8	2.54	0.43
3:C:1941:A:H2'	3:C:1942:G:O4'	2.19	0.43
3:C:2070:A:H2'	3:C:2071:A:C8	2.54	0.43
3:C:2248:C:H2'	3:C:2249:G:C8	2.53	0.43
3:C:2398:C:H2'	3:C:2399:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:2886:A:O5'	3:C:2886:A:H8	2.00	0.43
6:F:25:PHE:HE2	6:F:205:ILE:HD11	1.83	0.43
12:L:64:VAL:CG1	12:L:68:LYS:HB2	2.48	0.43
15:O:28:SER:C	15:O:134:ARG:HH12	2.27	0.43
2:B:239:TYR:HE1	2:B:267:GLY:HA3	1.83	0.43
3:C:345:G:C8	3:C:345:G:H5''	2.54	0.43
3:C:611:U:H2'	3:C:612:U:C6	2.54	0.43
3:C:722:G:H2'	3:C:723:C:C6	2.54	0.43
3:C:1638:C:H2'	3:C:1639:G:O4'	2.18	0.43
3:C:2090:U:H2'	3:C:2091:U:H4'	2.00	0.43
3:C:2107:G:H4'	3:C:2107:G:OP1	2.18	0.43
3:C:2376:G:C4	3:C:2377:G:N7	2.87	0.43
3:C:2932:G:H5'	16:P:68:LYS:HG3	2.01	0.43
3:C:3022:G:H2'	3:C:3023:G:O4'	2.18	0.43
4:D:145:VAL:HG12	4:D:191:ALA:HB1	2.00	0.43
4:D:156:ALA:HB2	4:D:163:ILE:HG13	2.01	0.43
14:N:22:VAL:HG22	14:N:33:ALA:HA	2.01	0.43
20:T:61:THR:HG23	20:T:100:THR:OG1	2.19	0.43
27:a:22:LEU:HD13	27:a:57:VAL:HB	2.00	0.43
2:B:164:LEU:HD22	2:B:214:ARG:HG3	2.01	0.43
3:C:4:G:H2'	3:C:5:U:H6	1.83	0.43
3:C:296:A:H2'	3:C:297:G:C8	2.53	0.43
3:C:462:A:H2'	3:C:463:G:O4'	2.18	0.43
3:C:485:U:H5''	26:Z:32:ASN:HB2	2.01	0.43
3:C:506:C:H2'	3:C:507:G:H8	1.84	0.43
3:C:1093:A:H1'	3:C:1108:A:C2	2.53	0.43
3:C:1118:A:C6	3:C:1119:A:C6	3.06	0.43
3:C:2404:G:H2'	3:C:2404:G:N3	2.34	0.43
3:C:2524:C:H2'	3:C:2525:C:C6	2.54	0.43
3:C:2524:C:H2'	3:C:2525:C:H6	1.83	0.43
3:C:2579:C:O4'	25:Y:36:ILE:HD11	2.18	0.43
3:C:3118:U:H2'	3:C:3119:A:C8	2.54	0.43
5:E:18:ASP:OD2	5:E:19:GLU:N	2.46	0.43
14:N:94:GLY:N	14:N:97:GLU:OE2	2.46	0.43
28:b:51:HIS:HD1	28:b:51:HIS:H	1.66	0.43
35:i:116:C:C4	35:i:118:C:N4	2.87	0.43
3:C:273:A:N6	3:C:313:G:C2	2.84	0.43
3:C:278:A:H2'	3:C:279:U:C6	2.54	0.43
3:C:301:U:H6	3:C:303:G:OP1	2.02	0.43
3:C:1290:C:C2	3:C:1291:G:H1'	2.53	0.43
3:C:1555:A:OP2	3:C:1617:C:N4	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1872:A:O2'	5:E:123:PHE:O	2.32	0.43
3:C:2712:U:H2'	3:C:2713:G:H8	1.84	0.43
3:C:2792:C:H2'	3:C:2793:G:O4'	2.19	0.43
6:F:154:VAL:CG2	6:F:175:VAL:HG22	2.48	0.43
7:G:52:ARG:HH21	7:G:85:LYS:HG3	1.84	0.43
23:W:35:VAL:HG13	23:W:38:VAL:CG2	2.49	0.43
25:Y:46:HIS:CE1	25:Y:75:ARG:HH21	2.37	0.43
3:C:327:U:H2'	3:C:328:C:C6	2.53	0.42
3:C:380:A:N3	3:C:401:C:O2'	2.48	0.42
3:C:483:G:H2'	3:C:484:C:C6	2.54	0.42
3:C:854:A:H1'	3:C:855:C:H5	1.84	0.42
3:C:912:C:OP1	6:F:63:LYS:HG3	2.18	0.42
3:C:2498:A:O2'	3:C:2500:G:OP1	2.25	0.42
3:C:2519:C:OP2	17:Q:24:ARG:NH2	2.51	0.42
7:G:123:GLY:C	7:G:185:LYS:HG3	2.43	0.42
11:K:104:TRP:HZ3	11:K:131:ALA:HB2	1.84	0.42
35:i:58:A:H2'	35:i:59:A:O4'	2.18	0.42
35:i:113:G:H2'	35:i:114:A:C8	2.54	0.42
3:C:412:A:H8	3:C:1324:G:C5	2.37	0.42
3:C:730:G:N1	14:N:77:VAL:HG11	2.33	0.42
3:C:1110:C:OP1	19:S:47:TYR:OH	2.34	0.42
3:C:2132:U:H2'	3:C:2133:G:C8	2.54	0.42
9:I:100:VAL:O	9:I:104:ILE:HG23	2.18	0.42
10:J:41:ARG:HH21	11:K:119:ASN:HD21	1.68	0.42
16:P:72:ASP:O	16:P:76:VAL:HG23	2.19	0.42
18:R:30:LYS:HG2	18:R:79:ASN:O	2.19	0.42
23:W:77:ASP:OD1	23:W:77:ASP:N	2.45	0.42
24:X:191:GLU:OE1	24:X:191:GLU:N	2.51	0.42
27:a:43:ASN:HB3	27:a:46:ARG:HD3	2.01	0.42
35:i:1:G:H21	35:i:117:A:H62	1.67	0.42
3:C:857:U:H2'	3:C:858:A:H8	1.82	0.42
3:C:975:U:H4'	3:C:2491:A:H5'	2.00	0.42
3:C:1146:A:H61	3:C:1243:G:H2'	1.84	0.42
3:C:1194:C:O2'	11:K:93:GLU:OE2	2.30	0.42
3:C:1577:C:H2'	3:C:1578:G:H8	1.83	0.42
3:C:1651:C:H2'	3:C:1652:A:H8	1.82	0.42
3:C:1729:A:H2'	3:C:1731:A:C8	2.54	0.42
3:C:2778:U:H2'	3:C:2779:U:H6	1.84	0.42
3:C:3071:A:N7	3:C:3089:A:O2'	2.45	0.42
4:D:222:ARG:O	4:D:225:VAL:HG22	2.20	0.42
8:H:150:ARG:HD2	8:H:163:VAL:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:23:THR:OG1	10:J:23:THR:O	2.38	0.42
13:M:88:LYS:HG3	13:M:94:ARG:HG3	2.00	0.42
14:N:51:GLU:CD	32:f:57:ARG:HH12	2.27	0.42
15:O:35:GLN:HA	15:O:102:VAL:HA	2.02	0.42
16:P:41:ALA:HA	16:P:113:ILE:HD11	2.01	0.42
17:Q:77:LYS:HB2	35:i:51:G:OP1	2.20	0.42
24:X:109:GLU:HB2	24:X:130:THR:CG2	2.49	0.42
26:Z:41:ARG:HG2	26:Z:43:GLY:H	1.84	0.42
33:g:24:MET:HE2	33:g:26:ILE:HD11	2.00	0.42
2:B:20:ARG:HD2	3:C:2149:C:OP2	2.19	0.42
3:C:74:C:H2'	3:C:75:U:C6	2.54	0.42
3:C:298:G:C6	3:C:299:G:C2	3.08	0.42
3:C:1489:G:OP1	3:C:2435:U:O2'	2.32	0.42
3:C:1617:C:O2	3:C:1617:C:H2'	2.19	0.42
3:C:1645:G:H2'	3:C:1646:U:O4'	2.19	0.42
3:C:1727:A:O5'	3:C:1727:A:H8	2.02	0.42
3:C:2379:G:O5'	3:C:2379:G:H8	2.02	0.42
6:F:191:ALA:HB1	6:F:193:ASP:O	2.20	0.42
7:G:90:MET:O	7:G:92:ILE:HG12	2.20	0.42
10:J:10:VAL:HG13	10:J:60:ALA:CB	2.41	0.42
3:C:1374:G:H2'	3:C:1375:G:C8	2.55	0.42
3:C:1882:A:H2	13:M:1:MET:HE1	1.85	0.42
3:C:2145:C:O2	3:C:2145:C:H2'	2.20	0.42
3:C:2349:A:N6	3:C:2385:G:H1'	2.35	0.42
3:C:2712:U:H2'	3:C:2713:G:C8	2.55	0.42
3:C:2925:C:H3'	3:C:2926:A:H5''	2.01	0.42
3:C:2995:U:H5''	5:E:212:ILE:HD12	2.00	0.42
15:O:39:HIS:HA	15:O:97:VAL:O	2.20	0.42
22:V:95:LEU:HB3	27:a:34:PHE:HD2	1.84	0.42
23:W:12:ILE:HD12	23:W:12:ILE:HA	1.82	0.42
3:C:568:A:O2'	23:W:42:LYS:O	2.38	0.42
3:C:663:A:N3	3:C:663:A:H2'	2.35	0.42
3:C:979:G:H2'	3:C:980:C:H6	1.84	0.42
3:C:1174:G:O2'	3:C:1204:A:H1'	2.19	0.42
3:C:2097:G:H2'	3:C:2098:U:C6	2.55	0.42
3:C:2425:U:O2'	3:C:2427:G:OP1	2.31	0.42
3:C:3033:G:H2'	3:C:3034:C:C6	2.55	0.42
3:C:3033:G:H2'	3:C:3034:C:H6	1.84	0.42
4:D:77:ALA:HB2	4:D:97:TYR:CD2	2.53	0.42
4:D:85:ASP:OD1	4:D:87:ASN:N	2.53	0.42
8:H:165:TYR:HB2	8:H:168:GLU:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:29:SER:O	13:M:29:SER:OG	2.34	0.42
13:M:63:VAL:HG23	13:M:64:ARG:HG2	2.01	0.42
2:B:26:LEU:HA	2:B:31:LYS:HD2	2.01	0.42
2:B:54:VAL:HG13	2:B:56:THR:H	1.84	0.42
3:C:890:G:OP1	3:C:892:G:O2'	2.32	0.42
3:C:1198:C:H2'	3:C:1199:U:H6	1.84	0.42
3:C:2365:A:C6	3:C:2373:G:O6	2.73	0.42
3:C:2603:G:H2'	3:C:2604:U:C6	2.55	0.42
10:J:43:LEU:HD12	10:J:92:ALA:HB3	2.02	0.42
11:K:24:PRO:CG	11:K:25:PRO:HD3	2.47	0.42
16:P:65:GLU:O	16:P:68:LYS:HB3	2.19	0.42
23:W:41:ILE:O	23:W:61:THR:HA	2.20	0.42
35:i:1:G:H21	35:i:117:A:N6	2.18	0.42
35:i:61:C:H2'	35:i:62:C:O4'	2.20	0.42
3:C:997:G:H2'	3:C:998:G:H8	1.85	0.42
3:C:1011:A:H5''	3:C:1011:A:N3	2.35	0.42
3:C:1487:U:H2'	3:C:1488:A:O4'	2.20	0.42
3:C:1558:C:H2'	3:C:1559:A:H8	1.84	0.42
4:D:158:SER:O	4:D:161:VAL:HG22	2.19	0.42
6:F:163:GLU:OE2	6:F:167:LYS:NZ	2.41	0.42
7:G:151:ASP:OD1	7:G:151:ASP:N	2.51	0.42
9:I:33:ARG:HB3	9:I:35:LEU:CD2	2.50	0.42
14:N:80:VAL:HG22	14:N:118:LEU:HB2	2.01	0.42
14:N:92:THR:HA	14:N:123:ASP:HB2	2.01	0.42
18:R:94:ALA:O	18:R:95:LYS:HG3	2.20	0.42
35:i:75:U:H2'	35:i:76:G:O4'	2.20	0.42
3:C:166:A:C2	3:C:167:G:H1'	2.54	0.42
3:C:356:G:N2	3:C:357:U:O4	2.53	0.42
3:C:826:G:H2'	3:C:827:G:C8	2.55	0.42
3:C:1024:A:H2'	3:C:1027:C:C5	2.55	0.42
3:C:1179:U:OP1	11:K:74:THR:HG21	2.20	0.42
3:C:1260:C:O2'	12:L:27:ARG:NH2	2.53	0.42
3:C:1446:C:H2'	3:C:1448:C:C5	2.55	0.42
3:C:1614:G:H2'	3:C:1615:G:C8	2.55	0.42
3:C:1624:U:O2'	3:C:1625:G:N7	2.50	0.42
3:C:2407:C:H2'	3:C:2408:G:C8	2.55	0.42
3:C:2505:C:O2'	3:C:2506:G:H5'	2.20	0.42
4:D:211:ARG:HG3	4:D:214:TRP:CE3	2.54	0.42
8:H:84:TYR:CZ	8:H:139:LYS:HD2	2.55	0.42
11:K:56:ILE:HG22	11:K:57:PRO:O	2.20	0.42
13:M:104:ARG:HB2	13:M:122:LEU:C	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:113:LYS:O	13:M:116:SER:OG	2.31	0.42
27:a:6:THR:HG23	27:a:9:GLU:HG2	2.02	0.42
34:h:14:VAL:HB	34:h:22:PHE:HB2	2.00	0.42
34:h:15:GLN:O	34:h:34:VAL:HA	2.19	0.42
3:C:322:A:H2'	3:C:323:C:H6	1.84	0.42
3:C:1314:C:H2'	3:C:1315:C:H6	1.85	0.42
3:C:2579:C:C1'	25:Y:36:ILE:HD11	2.50	0.42
3:C:3071:A:H2'	3:C:3072:A:C8	2.55	0.42
23:W:75:ASP:OD2	23:W:100:THR:OG1	2.34	0.42
26:Z:39:VAL:HG11	26:Z:44:GLY:HA2	2.02	0.42
3:C:289:A:O2'	3:C:300:G:N2	2.50	0.41
3:C:320:G:H2'	3:C:321:G:H8	1.85	0.41
3:C:1136:C:O3'	3:C:1238:G:N2	2.54	0.41
4:D:30:GLU:HG2	4:D:33:LEU:HD12	2.02	0.41
4:D:68:ARG:O	4:D:70:HIS:N	2.53	0.41
11:K:103:THR:HA	11:K:142:GLU:C	2.44	0.41
16:P:104:LYS:HE3	16:P:104:LYS:HB2	1.96	0.41
34:h:28:LYS:HA	34:h:28:LYS:HD3	1.85	0.41
2:B:123:ARG:NH1	2:B:123:ARG:HG3	2.35	0.41
3:C:1443:G:H2'	3:C:1445:C:C4	2.55	0.41
3:C:1530:G:H5''	3:C:1531:C:OP1	2.20	0.41
3:C:1606:G:O2'	3:C:1607:C:O4'	2.25	0.41
3:C:3009:U:OP1	5:E:44:ARG:NH2	2.52	0.41
4:D:53:HIS:CE1	4:D:220:THR:HG23	2.55	0.41
7:G:105:GLU:OE1	34:h:25:ARG:N	2.52	0.41
10:J:47:ALA:HB2	10:J:82:VAL:HG22	2.02	0.41
10:J:56:LEU:HD23	10:J:56:LEU:HA	1.88	0.41
11:K:26:VAL:HA	11:K:29:ALA:HB2	2.02	0.41
11:K:122:ASP:OD1	11:K:122:ASP:N	2.53	0.41
21:U:78:VAL:O	21:U:78:VAL:HG23	2.20	0.41
2:B:153:ALA:HB3	2:B:179:PRO:HA	2.01	0.41
3:C:109:U:H2'	3:C:110:G:O4'	2.21	0.41
3:C:296:A:C6	3:C:340:A:N6	2.88	0.41
3:C:643:G:O2'	3:C:644:G:OP1	2.21	0.41
3:C:911:U:H2'	3:C:912:C:C6	2.55	0.41
3:C:1197:C:H2'	11:K:135:ARG:HH21	1.85	0.41
3:C:1453:G:O2'	22:V:18:GLU:OE2	2.38	0.41
3:C:1568:C:H2'	3:C:1569:A:H8	1.83	0.41
3:C:1600:G:H2'	3:C:1601:G:C8	2.54	0.41
3:C:2089:C:C4	3:C:2090:U:C4	3.08	0.41
3:C:2418:U:H2'	3:C:2419:C:C6	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:15:U:OP2	35:i:71:C:O2'	2.33	0.41
3:C:658:U:OP1	14:N:31:LYS:HE2	2.21	0.41
3:C:733:U:H2'	3:C:734:C:C6	2.56	0.41
3:C:1208:U:N3	3:C:1209:G:N7	2.67	0.41
3:C:2318:U:O3'	9:I:11:HIS:ND1	2.54	0.41
3:C:2804:U:H2'	3:C:2805:G:O4'	2.21	0.41
10:J:53:LYS:HB3	10:J:56:LEU:HB2	2.03	0.41
11:K:13:LEU:HD23	11:K:13:LEU:HA	1.96	0.41
11:K:59:GLU:OE1	11:K:73:LYS:HD2	2.21	0.41
19:S:11:GLN:O	19:S:15:ARG:HG3	2.21	0.41
3:C:80:G:N2	3:C:100:A:OP2	2.53	0.41
3:C:313:G:O2'	3:C:314:G:O5'	2.33	0.41
3:C:503:A:H2'	3:C:504:C:C6	2.55	0.41
3:C:1220:C:H2'	3:C:1221:A:C8	2.54	0.41
3:C:1296:G:H2'	3:C:1297:G:C8	2.54	0.41
3:C:1660:A:H2'	3:C:1661:G:O4'	2.20	0.41
3:C:1857:U:O2'	3:C:2923:C:H4'	2.20	0.41
3:C:2083:A:N6	3:C:2099:G:O2'	2.50	0.41
3:C:2106:A:H3'	3:C:2107:G:H5''	2.03	0.41
3:C:2467:U:H2'	3:C:2468:U:H6	1.82	0.41
3:C:2630:A:N7	14:N:70:ARG:NH2	2.69	0.41
9:I:84:ALA:O	9:I:151:GLN:HB2	2.20	0.41
13:M:20:LEU:HD13	13:M:44:LYS:HE3	2.03	0.41
20:T:77:LYS:HB2	20:T:86:LYS:HB3	2.02	0.41
21:U:34:LYS:HD3	21:U:38:GLU:OE2	2.20	0.41
24:X:146:VAL:HG12	24:X:162:ILE:HG23	2.02	0.41
3:C:195:A:C2	14:N:50:PHE:HZ	2.39	0.41
3:C:450:G:C8	3:C:450:G:H5''	2.55	0.41
3:C:1849:G:H1'	3:C:1853:A:N6	2.35	0.41
3:C:1900:C:H2'	3:C:1901:C:C6	2.56	0.41
3:C:2035:U:O2'	4:D:154:LYS:O	2.34	0.41
3:C:2362:C:H2'	3:C:2363:A:H8	1.80	0.41
3:C:2778:U:C2	3:C:2779:U:C5	3.08	0.41
3:C:2873:U:H2'	3:C:2874:C:C6	2.55	0.41
6:F:37:VAL:O	6:F:41:GLN:HG3	2.20	0.41
7:G:135:TYR:HB3	7:G:163:VAL:CG1	2.50	0.41
15:O:52:ILE:O	15:O:56:ARG:HG2	2.21	0.41
17:Q:42:ARG:HD2	17:Q:112:ARG:HD3	2.02	0.41
18:R:43:LYS:O	18:R:62:LYS:HG3	2.20	0.41
28:b:26:LEU:O	28:b:37:ARG:NH2	2.53	0.41
34:h:16:CYS:HB3	34:h:38:CYS:SG	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:6:ARG:O	2:B:9:ALA:HB3	2.20	0.41
3:C:351:G:O6	3:C:444:U:C2	2.74	0.41
3:C:1191:A:H3'	3:C:1192:G:H8	1.86	0.41
3:C:2885:G:H2'	3:C:2886:A:C8	2.56	0.41
3:C:2955:G:H2'	3:C:2956:G:C8	2.55	0.41
8:H:70:ARG:NH1	8:H:74:ALA:HB2	2.35	0.41
9:I:21:VAL:HG22	9:I:22:LYS:N	2.36	0.41
9:I:25:TYR:C	9:I:27:ARG:H	2.28	0.41
11:K:96:LYS:HA	11:K:96:LYS:HD3	1.74	0.41
23:W:104:ASP:O	23:W:105:ILE:HB	2.20	0.41
2:B:85:ARG:HH22	2:B:109:VAL:HG23	1.85	0.41
3:C:759:G:H1	25:Y:64:PRO:HB3	1.85	0.41
3:C:1108:A:N1	20:T:79:LYS:NZ	2.66	0.41
3:C:1175:A:N6	3:C:1176:G:O6	2.54	0.41
3:C:1568:C:C2	3:C:1604:G:N1	2.89	0.41
3:C:2787:U:H2'	3:C:2789:A:OP2	2.21	0.41
3:C:2861:U:P	5:E:85:ARG:HH21	2.43	0.41
7:G:45:MET:HE1	7:G:60:ALA:HA	2.02	0.41
7:G:113:ILE:HD12	34:h:35:VAL:HG21	2.01	0.41
10:J:57:VAL:HG23	10:J:73:PHE:CZ	2.55	0.41
10:J:109:TYR:CE2	10:J:112:GLY:HA2	2.55	0.41
24:X:33:VAL:HG23	24:X:51:ALA:HA	2.03	0.41
24:X:108:VAL:HG22	24:X:109:GLU:N	2.34	0.41
27:a:32:LEU:HD21	27:a:50:VAL:HG11	2.03	0.41
30:d:15:CYS:SG	30:d:17:VAL:HG22	2.61	0.41
2:B:133:ARG:NH1	2:B:133:ARG:HG3	2.35	0.41
3:C:263:G:H3'	3:C:263:G:H8	1.86	0.41
3:C:324:C:O2	3:C:324:C:H2'	2.20	0.41
3:C:856:U:H2'	3:C:857:U:O4'	2.20	0.41
3:C:864:A:H4'	3:C:1386:G:N3	2.36	0.41
3:C:911:U:H5''	6:F:63:LYS:NZ	2.36	0.41
3:C:1213:A:N3	3:C:1213:A:C2'	2.83	0.41
3:C:1561:C:H2'	3:C:1562:C:H6	1.86	0.41
3:C:2171:C:H2'	3:C:2172:G:C8	2.56	0.41
3:C:2448:G:H4'	3:C:2450:C:C2	2.55	0.41
3:C:2481:U:O2'	3:C:2482:U:H5'	2.21	0.41
3:C:2857:A:H2'	3:C:2858:G:C8	2.55	0.41
3:C:2862:G:HO2'	3:C:2863:A:H8	1.62	0.41
6:F:152:LYS:HD3	6:F:152:LYS:HA	1.77	0.41
7:G:23:LEU:O	7:G:27:PHE:HB2	2.21	0.41
7:G:81:ILE:HD12	7:G:81:ILE:HA	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:80:VAL:N	14:N:113:LEU:O	2.54	0.41
16:P:117:ARG:HE	16:P:117:ARG:HB3	1.61	0.41
30:d:44:ASN:OD1	30:d:45:CYS:N	2.53	0.41
2:B:100:LEU:HB3	2:B:105:ALA:HB2	2.03	0.41
3:C:2:A:C6	3:C:3119:A:C2	3.09	0.41
3:C:181:A:H2'	3:C:182:C:H6	1.86	0.41
3:C:461:U:C2	3:C:462:A:C8	3.09	0.41
3:C:668:U:H2'	3:C:669:G:C8	2.56	0.41
3:C:1064:A:H2'	3:C:1065:C:C6	2.56	0.41
3:C:1164:A:H5''	10:J:59:ARG:NH2	2.36	0.41
3:C:1259:U:OP2	12:L:65:SER:OG	2.28	0.41
3:C:1703:G:C2	3:C:1727:A:C2	3.09	0.41
3:C:2331:U:H1'	3:C:2404:G:N2	2.25	0.41
3:C:2471:A:H2'	3:C:2472:C:H6	1.85	0.41
3:C:2519:C:OP1	17:Q:21:ARG:NH1	2.54	0.41
3:C:2873:U:H2'	3:C:2874:C:H6	1.85	0.41
4:D:60:ARG:HD3	4:D:87:ASN:OD1	2.21	0.41
4:D:72:LYS:O	4:D:119:SER:HB2	2.21	0.41
4:D:97:TYR:HE1	4:D:103:ARG:HB2	1.85	0.41
6:F:137:SER:H	6:F:168:SER:HB2	1.86	0.41
7:G:113:ILE:C	7:G:116:PRO:HD2	2.46	0.41
8:H:30:LYS:HZ1	8:H:82:GLU:C	2.29	0.41
9:I:72:LEU:O	9:I:75:LEU:HG	2.21	0.41
12:L:96:HIS:CD2	12:L:99:ARG:NE	2.89	0.41
16:P:56:LYS:HE2	16:P:56:LYS:HB3	1.77	0.41
25:Y:38:VAL:HG12	25:Y:59:LEU:HB2	2.02	0.41
27:a:45:ARG:NH2	27:a:48:ARG:HH21	2.19	0.41
30:d:27:LYS:NZ	30:d:32:ASP:O	2.49	0.41
3:C:700:U:H5''	3:C:713:G:O6	2.22	0.40
3:C:841:G:HO2'	3:C:842:A:P	2.42	0.40
3:C:975:U:H1'	3:C:2492:A:H5'	2.02	0.40
3:C:1146:A:N3	3:C:2710:G:O2'	2.49	0.40
3:C:1880:U:H2'	3:C:1881:U:O4'	2.20	0.40
3:C:1964:U:H2'	3:C:1965:G:C8	2.56	0.40
3:C:2342:A:N6	3:C:2390:U:H2'	2.36	0.40
8:H:4:ILE:HG13	8:H:5:GLY:N	2.36	0.40
8:H:41:ILE:HD13	8:H:66:HIS:HA	2.03	0.40
10:J:39:LEU:HD11	10:J:43:LEU:HD13	2.03	0.40
13:M:44:LYS:HD3	13:M:44:LYS:HA	1.73	0.40
21:U:18:ARG:HA	21:U:107:THR:HG22	2.03	0.40
3:C:254:G:H4'	3:C:472:C:H4'	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:296:A:C2	3:C:297:G:C5	3.10	0.40
3:C:363:A:H2'	3:C:364:A:C8	2.56	0.40
3:C:580:G:H2'	3:C:581:G:O4'	2.21	0.40
3:C:1334:C:H2'	3:C:1335:G:O4'	2.21	0.40
3:C:1650:G:H2'	3:C:1651:C:C6	2.56	0.40
3:C:1999:U:H1'	3:C:2833:U:H5''	2.02	0.40
3:C:2241:U:O2	29:c:7:ARG:HB2	2.22	0.40
3:C:2965:A:H2'	3:C:2966:C:O4'	2.21	0.40
12:L:95:LYS:HG3	12:L:96:HIS:ND1	2.36	0.40
22:V:6:ASP:HB2	22:V:7:PRO:HD2	2.03	0.40
2:B:19:SER:HB3	2:B:22:GLN:HG2	2.03	0.40
3:C:279:U:C2	3:C:280:G:C8	3.09	0.40
3:C:774:G:H21	6:F:36:GLN:NE2	2.20	0.40
3:C:831:A:C2	3:C:832:G:H1'	2.56	0.40
3:C:1129:G:N3	12:L:147:GLN:NE2	2.66	0.40
3:C:1696:G:O2'	3:C:1736:G:O6	2.38	0.40
3:C:2016:G:N7	4:D:177:MET:HG3	2.36	0.40
3:C:2505:C:C2'	3:C:2506:G:H5'	2.51	0.40
8:H:97:VAL:HG13	8:H:104:LEU:HD21	2.03	0.40
10:J:9:ALA:O	10:J:13:ILE:HG22	2.21	0.40
24:X:135:ALA:HB2	24:X:168:VAL:HG12	2.02	0.40
29:c:8:MET:HE1	29:c:16:ARG:NE	2.36	0.40
2:B:9:ALA:O	2:B:13:ARG:HG3	2.20	0.40
2:B:192:VAL:HG21	3:C:2143:A:C8	2.56	0.40
2:B:244:ARG:HE	2:B:245:THR:H	1.70	0.40
3:C:262:A:N7	3:C:263:G:N2	2.70	0.40
3:C:303:G:H2'	3:C:304:U:O4'	2.21	0.40
3:C:316:U:O2'	3:C:317:G:OP1	2.30	0.40
3:C:363:A:H2'	3:C:364:A:H8	1.85	0.40
3:C:1535:C:H2'	3:C:1536:A:O4'	2.22	0.40
3:C:1550:G:N2	3:C:1620:U:O2	2.31	0.40
3:C:2331:U:O2'	3:C:2404:G:N2	2.54	0.40
3:C:2338:G:C6	3:C:2340:A:H3'	2.56	0.40
3:C:3082:U:H2'	3:C:3083:A:C8	2.57	0.40
4:D:111:LEU:HD11	4:D:117:ILE:HD11	2.04	0.40
9:I:8:GLU:OE1	9:I:14:ALA:HA	2.22	0.40
11:K:104:TRP:O	11:K:107:VAL:HB	2.21	0.40
24:X:18:ARG:NH1	24:X:23:ALA:HB2	2.36	0.40
25:Y:85:ARG:HA	25:Y:86:PRO:HD3	1.93	0.40
27:a:20:ASP:O	27:a:24:GLU:HG2	2.22	0.40
32:f:62:LEU:HA	32:f:62:LEU:HD23	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:249:ARG:HD2	2:B:249:ARG:HA	1.78	0.40
3:C:341:C:N4	3:C:342:C:H41	2.13	0.40
3:C:748:U:H2'	3:C:749:C:C6	2.57	0.40
3:C:940:A:H4'	3:C:2652:G:C5	2.57	0.40
3:C:1559:A:H2'	3:C:1560:U:H6	1.85	0.40
3:C:2105:G:H2'	3:C:2106:A:C8	2.57	0.40
7:G:183:PRO:HG3	34:h:45:TYR:CE1	2.56	0.40
13:M:52:VAL:HG22	13:M:94:ARG:HH21	1.86	0.40
14:N:122:VAL:O	14:N:142:GLY:HA3	2.22	0.40
30:d:13:LEU:HB3	30:d:51:HIS:HB3	2.04	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	3	21/23 (91%)	19 (90%)	2 (10%)	0	100	100
2	B	263/284 (93%)	229 (87%)	34 (13%)	0	100	100
4	D	273/275 (99%)	255 (93%)	18 (7%)	0	100	100
5	E	212/214 (99%)	200 (94%)	12 (6%)	0	100	100
6	F	207/210 (99%)	203 (98%)	4 (2%)	0	100	100
7	G	180/182 (99%)	159 (88%)	21 (12%)	0	100	100
8	H	174/176 (99%)	168 (97%)	6 (3%)	0	100	100
9	I	149/151 (99%)	134 (90%)	15 (10%)	0	100	100
10	J	124/126 (98%)	113 (91%)	11 (9%)	0	100	100
11	K	131/133 (98%)	119 (91%)	12 (9%)	0	100	100
12	L	144/146 (99%)	137 (95%)	7 (5%)	0	100	100
13	M	120/122 (98%)	116 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	N	143/145 (99%)	129 (90%)	14 (10%)	0	100	100
15	O	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
16	P	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
17	Q	124/126 (98%)	118 (95%)	6 (5%)	0	100	100
18	R	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
19	S	122/124 (98%)	116 (95%)	6 (5%)	0	100	100
20	T	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
21	U	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
22	V	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
23	W	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
24	X	190/192 (99%)	181 (95%)	9 (5%)	0	100	100
25	Y	77/79 (98%)	73 (95%)	4 (5%)	0	100	100
26	Z	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
27	a	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
28	b	57/59 (97%)	53 (93%)	4 (7%)	0	100	100
29	c	52/54 (96%)	52 (100%)	0	0	100	100
30	d	47/49 (96%)	46 (98%)	1 (2%)	0	100	100
31	e	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
32	f	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
33	g	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
34	h	46/48 (96%)	43 (94%)	3 (6%)	0	100	100
All	All	3878/3974 (98%)	3637 (94%)	241 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	3	18/18 (100%)	18 (100%)	0	100	100
2	B	197/212 (93%)	161 (82%)	36 (18%)	2	7
4	D	215/215 (100%)	214 (100%)	1 (0%)	81	82
5	E	160/160 (100%)	160 (100%)	0	100	100
6	F	169/170 (99%)	169 (100%)	0	100	100
7	G	151/151 (100%)	150 (99%)	1 (1%)	76	80
8	H	148/148 (100%)	148 (100%)	0	100	100
9	I	90/116 (78%)	90 (100%)	0	100	100
10	J	89/89 (100%)	89 (100%)	0	100	100
11	K	102/102 (100%)	102 (100%)	0	100	100
12	L	119/119 (100%)	118 (99%)	1 (1%)	73	79
13	M	100/100 (100%)	100 (100%)	0	100	100
14	N	112/112 (100%)	112 (100%)	0	100	100
15	O	114/114 (100%)	114 (100%)	0	100	100
16	P	97/97 (100%)	97 (100%)	0	100	100
17	Q	93/93 (100%)	93 (100%)	0	100	100
18	R	100/100 (100%)	100 (100%)	0	100	100
19	S	97/97 (100%)	97 (100%)	0	100	100
20	T	81/81 (100%)	81 (100%)	0	100	100
21	U	90/90 (100%)	90 (100%)	0	100	100
22	V	83/83 (100%)	83 (100%)	0	100	100
23	W	81/86 (94%)	81 (100%)	0	100	100
24	X	155/155 (100%)	155 (100%)	0	100	100
25	Y	58/58 (100%)	58 (100%)	0	100	100
26	Z	50/50 (100%)	50 (100%)	0	100	100
27	a	58/58 (100%)	58 (100%)	0	100	100
28	b	52/52 (100%)	52 (100%)	0	100	100
29	c	43/43 (100%)	43 (100%)	0	100	100
30	d	47/47 (100%)	47 (100%)	0	100	100
31	e	35/35 (100%)	35 (100%)	0	100	100
32	f	53/53 (100%)	53 (100%)	0	100	100
33	g	35/35 (100%)	35 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	h	43/43 (100%)	43 (100%)	0	100	100
All	All	3135/3182 (98%)	3096 (99%)	39 (1%)	61	75

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	4	ARG
2	B	6	ARG
2	B	8	ASP
2	B	18	ARG
2	B	22	GLN
2	B	33	ARG
2	B	34	ILE
2	B	37	LEU
2	B	40	VAL
2	B	41	LYS
2	B	55	VAL
2	B	59	GLU
2	B	60	ARG
2	B	65	ARG
2	B	127	ARG
2	B	133	ARG
2	B	151	VAL
2	B	155	LEU
2	B	158	ILE
2	B	160	LEU
2	B	163	VAL
2	B	167	LEU
2	B	178	VAL
2	B	180	LEU
2	B	187	VAL
2	B	189	LYS
2	B	218	LEU
2	B	241	LEU
2	B	242	TRP
2	B	244	ARG
2	B	246	GLN
2	B	247	THR
2	B	258	ASP
2	B	260	VAL
2	B	262	ARG
2	B	266	GLU

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Mol	Chain	Res	Type
4	D	157	ARG
7	G	140	ASN
12	L	91	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	53	HIS
4	D	109	GLN
4	D	113	GLN
4	D	130	ASN
5	E	183	HIS
6	F	76	GLN
7	G	24	GLN
7	G	70	GLN
10	J	16	GLN
11	K	19	GLN
15	O	9	HIS
15	O	17	GLN
17	Q	53	ASN
19	S	27	GLN
19	S	39	GLN
24	X	9	ASN
24	X	126	GLN
27	a	43	ASN
29	c	36	GLN
32	f	59	ASN
34	h	6	HIS
34	h	20	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C	3117/3120 (99%)	673 (21%)	28 (0%)
35	i	117/118 (99%)	20 (17%)	0
All	All	3234/3238 (99%)	693 (21%)	28 (0%)

All (693) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	C	6	G
3	C	10	A
3	C	11	A
3	C	12	G
3	C	20	G
3	C	31	U
3	C	33	G
3	C	40	G
3	C	55	G
3	C	58	G
3	C	60	A
3	C	61	G
3	C	68	A
3	C	71	A
3	C	72	G
3	C	83	C
3	C	88	A
3	C	90	C
3	C	93	A
3	C	94	G
3	C	99	G
3	C	115	A
3	C	116	A
3	C	117	U
3	C	125	C
3	C	136	U
3	C	148	A
3	C	153	G
3	C	162	A
3	C	164	A
3	C	180	A
3	C	195	A
3	C	198	A
3	C	212	A
3	C	214	G
3	C	215	A
3	C	221	A
3	C	227	A
3	C	229	U
3	C	230	G
3	C	231	U
3	C	233	A
3	C	248	G

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Mol	Chain	Res	Type
3	C	250	G
3	C	264	G
3	C	270	U
3	C	273	A
3	C	278	A
3	C	282	A
3	C	284	G
3	C	285	U
3	C	286	G
3	C	288	U
3	C	290	C
3	C	292	G
3	C	300	G
3	C	301	U
3	C	302	U
3	C	303	G
3	C	311	G
3	C	312	G
3	C	313	G
3	C	314	G
3	C	315	U
3	C	317	G
3	C	318	U
3	C	319	G
3	C	324	C
3	C	328	C
3	C	330	U
3	C	331	U
3	C	336	C
3	C	338	C
3	C	339	U
3	C	342	C
3	C	343	U
3	C	344	G
3	C	345	G
3	C	348	G
3	C	351	G
3	C	352	G
3	C	355	A
3	C	357	U
3	C	358	G
3	C	361	A

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Mol	Chain	Res	Type
3	C	362	A
3	C	366	G
3	C	367	U
3	C	370	U
3	C	384	G
3	C	399	G
3	C	400	C
3	C	404	A
3	C	412	A
3	C	413	G
3	C	416	C
3	C	425	U
3	C	428	A
3	C	434	G
3	C	445	U
3	C	446	G
3	C	447	A
3	C	450	G
3	C	452	G
3	C	453	U
3	C	454	U
3	C	460	G
3	C	472	C
3	C	473	C
3	C	474	G
3	C	477	G
3	C	489	A
3	C	490	A
3	C	491	U
3	C	494	G
3	C	505	C
3	C	512	G
3	C	514	C
3	C	531	A
3	C	544	U
3	C	554	A
3	C	555	G
3	C	569	G
3	C	581	G
3	C	591	G
3	C	592	A
3	C	594	U

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Mol	Chain	Res	Type
3	C	595	A
3	C	596	C
3	C	605	G
3	C	614	C
3	C	617	U
3	C	618	C
3	C	619	C
3	C	620	G
3	C	635	G
3	C	636	U
3	C	637	G
3	C	638	U
3	C	639	C
3	C	640	G
3	C	642	G
3	C	644	G
3	C	655	G
3	C	658	U
3	C	665	G
3	C	666	A
3	C	667	A
3	C	679	G
3	C	683	G
3	C	684	G
3	C	685	G
3	C	696	A
3	C	706	G
3	C	707	G
3	C	708	G
3	C	709	U
3	C	714	U
3	C	721	A
3	C	725	A
3	C	728	G
3	C	731	A
3	C	738	A
3	C	740	A
3	C	742	G
3	C	747	A
3	C	756	A
3	C	757	G
3	C	759	G

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Mol	Chain	Res	Type
3	C	760	U
3	C	764	U
3	C	765	G
3	C	766	G
3	C	768	G
3	C	784	G
3	C	785	A
3	C	801	U
3	C	809	U
3	C	819	G
3	C	832	G
3	C	838	G
3	C	845	C
3	C	862	U
3	C	863	G
3	C	868	C
3	C	878	G
3	C	879	A
3	C	880	G
3	C	890	G
3	C	891	G
3	C	897	A
3	C	899	G
3	C	900	G
3	C	902	C
3	C	904	A
3	C	907	A
3	C	908	A
3	C	920	G
3	C	927	C
3	C	942	U
3	C	944	A
3	C	972	A
3	C	974	G
3	C	981	U
3	C	982	A
3	C	994	A
3	C	996	G
3	C	1001	C
3	C	1002	C
3	C	1003	A
3	C	1006	G

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Mol	Chain	Res	Type
3	C	1008	G
3	C	1009	U
3	C	1011	A
3	C	1012	C
3	C	1014	G
3	C	1017	G
3	C	1022	C
3	C	1025	A
3	C	1030	C
3	C	1046	C
3	C	1047	A
3	C	1048	A
3	C	1049	G
3	C	1063	G
3	C	1076	A
3	C	1078	G
3	C	1085	G
3	C	1092	G
3	C	1098	A
3	C	1101	A
3	C	1103	C
3	C	1114	G
3	C	1119	A
3	C	1131	G
3	C	1140	G
3	C	1144	A
3	C	1151	U
3	C	1163	A
3	C	1164	A
3	C	1165	G
3	C	1166	A
3	C	1171	C
3	C	1173	G
3	C	1174	G
3	C	1179	U
3	C	1181	G
3	C	1182	C
3	C	1183	U
3	C	1188	A
3	C	1189	G
3	C	1191	A
3	C	1192	G

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Mol	Chain	Res	Type
3	C	1195	A
3	C	1196	C
3	C	1200	U
3	C	1201	G
3	C	1202	A
3	C	1203	A
3	C	1205	G
3	C	1206	A
3	C	1207	G
3	C	1208	U
3	C	1212	U
3	C	1213	A
3	C	1214	A
3	C	1215	U
3	C	1219	U
3	C	1222	C
3	C	1223	U
3	C	1228	A
3	C	1230	G
3	C	1234	U
3	C	1235	U
3	C	1237	U
3	C	1238	G
3	C	1240	G
3	C	1248	U
3	C	1250	U
3	C	1251	A
3	C	1253	C
3	C	1254	G
3	C	1260	C
3	C	1261	A
3	C	1262	A
3	C	1287	C
3	C	1293	G
3	C	1294	U
3	C	1298	C
3	C	1314	C
3	C	1316	U
3	C	1332	G
3	C	1335	G
3	C	1344	A
3	C	1347	G

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Mol	Chain	Res	Type
3	C	1352	A
3	C	1353	G
3	C	1365	G
3	C	1368	A
3	C	1370	U
3	C	1371	G
3	C	1384	G
3	C	1385	C
3	C	1386	G
3	C	1387	A
3	C	1389	U
3	C	1390	A
3	C	1403	C
3	C	1415	A
3	C	1416	A
3	C	1427	U
3	C	1429	C
3	C	1447	G
3	C	1448	C
3	C	1465	C
3	C	1467	U
3	C	1480	A
3	C	1482	A
3	C	1494	U
3	C	1499	A
3	C	1501	C
3	C	1510	A
3	C	1511	U
3	C	1522	G
3	C	1531	C
3	C	1532	G
3	C	1533	U
3	C	1534	C
3	C	1538	G
3	C	1539	A
3	C	1540	U
3	C	1541	G
3	C	1542	A
3	C	1548	C
3	C	1549	G
3	C	1550	G
3	C	1552	A

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Mol	Chain	Res	Type
3	C	1553	C
3	C	1554	U
3	C	1555	A
3	C	1563	A
3	C	1564	A
3	C	1565	A
3	C	1567	C
3	C	1573	U
3	C	1575	A
3	C	1578	G
3	C	1579	C
3	C	1581	C
3	C	1585	U
3	C	1586	C
3	C	1587	G
3	C	1588	G
3	C	1593	U
3	C	1597	G
3	C	1598	U
3	C	1599	U
3	C	1600	G
3	C	1604	G
3	C	1605	G
3	C	1613	G
3	C	1618	C
3	C	1625	G
3	C	1628	A
3	C	1629	G
3	C	1630	U
3	C	1631	A
3	C	1638	C
3	C	1639	G
3	C	1640	A
3	C	1641	U
3	C	1648	A
3	C	1649	C
3	C	1656	A
3	C	1670	G
3	C	1672	C
3	C	1676	G
3	C	1679	A
3	C	1680	A

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Mol	Chain	Res	Type
3	C	1681	U
3	C	1686	G
3	C	1688	G
3	C	1703	G
3	C	1710	A
3	C	1711	G
3	C	1713	U
3	C	1714	A
3	C	1717	U
3	C	1720	G
3	C	1724	G
3	C	1729	A
3	C	1730	U
3	C	1731	A
3	C	1737	A
3	C	1738	G
3	C	1744	A
3	C	1746	G
3	C	1753	C
3	C	1754	G
3	C	1755	A
3	C	1756	G
3	C	1769	G
3	C	1786	G
3	C	1787	A
3	C	1789	A
3	C	1798	U
3	C	1803	A
3	C	1810	A
3	C	1825	C
3	C	1826	A
3	C	1847	U
3	C	1852	A
3	C	1863	G
3	C	1864	U
3	C	1866	C
3	C	1871	G
3	C	1872	A
3	C	1892	G
3	C	1893	C
3	C	1895	A
3	C	1932	U

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Mol	Chain	Res	Type
3	C	1947	U
3	C	1949	C
3	C	1950	G
3	C	1961	G
3	C	1963	G
3	C	1973	C
3	C	1974	A
3	C	1975	A
3	C	1977	C
3	C	1981	U
3	C	1990	A
3	C	1999	U
3	C	2003	A
3	C	2004	A
3	C	2017	C
3	C	2018	G
3	C	2026	A
3	C	2033	U
3	C	2046	A
3	C	2051	U
3	C	2054	C
3	C	2065	A
3	C	2074	G
3	C	2075	G
3	C	2085	C
3	C	2086	U
3	C	2088	C
3	C	2089	C
3	C	2091	U
3	C	2092	U
3	C	2093	G
3	C	2094	G
3	C	2095	G
3	C	2097	G
3	C	2100	A
3	C	2105	G
3	C	2106	A
3	C	2107	G
3	C	2127	G
3	C	2128	G
3	C	2130	G
3	C	2137	A

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Mol	Chain	Res	Type
3	C	2138	C
3	C	2139	U
3	C	2141	U
3	C	2142	A
3	C	2143	A
3	C	2146	A
3	C	2147	U
3	C	2151	A
3	C	2153	G
3	C	2154	G
3	C	2155	U
3	C	2156	A
3	C	2161	A
3	C	2163	U
3	C	2164	U
3	C	2168	U
3	C	2179	U
3	C	2191	C
3	C	2194	A
3	C	2195	U
3	C	2196	G
3	C	2197	G
3	C	2215	U
3	C	2217	U
3	C	2221	A
3	C	2244	A
3	C	2245	C
3	C	2247	A
3	C	2255	A
3	C	2256	G
3	C	2257	A
3	C	2260	C
3	C	2263	G
3	C	2267	C
3	C	2279	C
3	C	2280	G
3	C	2284	A
3	C	2285	G
3	C	2286	A
3	C	2294	A
3	C	2316	G
3	C	2319	G

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Mol	Chain	Res	Type
3	C	2320	C
3	C	2324	A
3	C	2325	U
3	C	2328	G
3	C	2329	G
3	C	2331	U
3	C	2332	U
3	C	2333	G
3	C	2334	U
3	C	2335	G
3	C	2336	U
3	C	2337	A
3	C	2338	G
3	C	2339	G
3	C	2340	A
3	C	2341	U
3	C	2342	A
3	C	2343	G
3	C	2345	U
3	C	2348	G
3	C	2349	A
3	C	2351	A
3	C	2353	U
3	C	2355	U
3	C	2356	G
3	C	2357	A
3	C	2359	G
3	C	2368	C
3	C	2369	C
3	C	2370	A
3	C	2373	G
3	C	2374	U
3	C	2377	G
3	C	2378	U
3	C	2380	G
3	C	2381	A
3	C	2382	G
3	C	2386	U
3	C	2387	U
3	C	2388	G
3	C	2389	U
3	C	2390	U

Continued on next page...

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Mol	Chain	Res	Type
3	C	2391	G
3	C	2393	A
3	C	2394	A
3	C	2395	U
3	C	2396	A
3	C	2399	A
3	C	2402	C
3	C	2404	G
3	C	2405	A
3	C	2406	U
3	C	2407	C
3	C	2408	G
3	C	2409	U
3	C	2414	G
3	C	2421	A
3	C	2427	G
3	C	2447	G
3	C	2449	A
3	C	2454	G
3	C	2455	C
3	C	2462	G
3	C	2463	G
3	C	2467	U
3	C	2491	A
3	C	2492	A
3	C	2503	G
3	C	2506	G
3	C	2507	C
3	C	2511	A
3	C	2529	A
3	C	2531	G
3	C	2532	G
3	C	2534	A
3	C	2536	U
3	C	2543	U
3	C	2545	G
3	C	2548	U
3	C	2549	G
3	C	2558	C
3	C	2559	A
3	C	2568	U
3	C	2569	G

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Mol	Chain	Res	Type
3	C	2571	C
3	C	2574	C
3	C	2582	A
3	C	2607	G
3	C	2609	A
3	C	2627	C
3	C	2630	A
3	C	2643	U
3	C	2647	U
3	C	2649	A
3	C	2652	G
3	C	2653	G
3	C	2654	A
3	C	2655	U
3	C	2659	A
3	C	2665	C
3	C	2671	G
3	C	2672	A
3	C	2677	A
3	C	2688	C
3	C	2694	G
3	C	2699	C
3	C	2700	A
3	C	2705	G
3	C	2715	U
3	C	2726	G
3	C	2729	G
3	C	2741	C
3	C	2742	A
3	C	2744	C
3	C	2749	G
3	C	2752	U
3	C	2753	G
3	C	2759	G
3	C	2778	U
3	C	2783	C
3	C	2785	A
3	C	2786	U
3	C	2790	A
3	C	2791	G
3	C	2806	G
3	C	2826	A

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Mol	Chain	Res	Type
3	C	2827	G
3	C	2833	U
3	C	2834	C
3	C	2837	U
3	C	2839	U
3	C	2855	G
3	C	2862	G
3	C	2870	C
3	C	2911	U
3	C	2912	A
3	C	2913	U
3	C	2915	C
3	C	2926	A
3	C	2936	C
3	C	2938	G
3	C	2948	C
3	C	2950	C
3	C	2956	G
3	C	2957	A
3	C	2972	A
3	C	2976	C
3	C	2981	A
3	C	2982	A
3	C	2985	G
3	C	2986	G
3	C	3002	A
3	C	3014	A
3	C	3015	C
3	C	3020	U
3	C	3021	A
3	C	3022	G
3	C	3042	A
3	C	3045	C
3	C	3075	C
3	C	3082	U
3	C	3088	C
3	C	3093	A
3	C	3101	C
3	C	3104	A
3	C	3105	C
3	C	3112	A
3	C	3114	A

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Mol	Chain	Res	Type
35	i	4	A
35	i	5	C
35	i	11	U
35	i	13	C
35	i	25	G
35	i	30	G
35	i	36	U
35	i	43	C
35	i	51	G
35	i	57	U
35	i	58	A
35	i	67	A
35	i	70	G
35	i	87	U
35	i	88	C
35	i	94	G
35	i	103	G
35	i	107	A
35	i	112	C
35	i	117	A

All (28) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	C	89	A
3	C	284	G
3	C	316	U
3	C	643	G
3	C	899	G
3	C	980	C
3	C	981	U
3	C	1000	C
3	C	1010	U
3	C	1046	C
3	C	1077	A
3	C	1084	U
3	C	1178	U
3	C	1180	G
3	C	1213	A
3	C	1214	A
3	C	1234	U
3	C	1510	A

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Mol	Chain	Res	Type
3	C	2094	G
3	C	2145	C
3	C	2154	G
3	C	2155	U
3	C	2254	A
3	C	2350	G
3	C	2398	C
3	C	2698	C
3	C	2980	U
3	C	3002	A

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
3	AI5	C	2144	3	49,53,53	3.36	23 (46%)	66,76,76	2.17	17 (25%)

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
3	AI5	C	2144	3	-	9/31/65/65	0/5/5/5

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2144	AI5	C48-C17	-10.84	1.29	1.53
3	C	2144	AI5	O25-C26	8.19	1.60	1.42
3	C	2144	AI5	O25-C24	-7.40	1.28	1.45
3	C	2144	AI5	C39-C37	-6.61	1.35	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2144	AI5	C26-N27	-5.06	1.32	1.46
3	C	2144	AI5	C39-C24	4.92	1.65	1.53
3	C	2144	AI5	C32-N33	4.79	1.46	1.34
3	C	2144	AI5	O07-C08	-4.78	1.31	1.42
3	C	2144	AI5	O07-C01	4.27	1.54	1.45
3	C	2144	AI5	O3'-C48	3.96	1.52	1.43
3	C	2144	AI5	C12-N13	3.76	1.43	1.33
3	C	2144	AI5	O18-C17	3.50	1.49	1.43
3	C	2144	AI5	C02-C01	-3.45	1.41	1.51
3	C	2144	AI5	C36-N27	-3.32	1.31	1.37
3	C	2144	AI5	C14-C12	-2.99	1.36	1.42
3	C	2144	AI5	C15-N09	-2.90	1.31	1.38
3	C	2144	AI5	P-O03	2.90	1.71	1.62
3	C	2144	AI5	C10-N09	-2.83	1.34	1.40
3	C	2144	AI5	C17-C08	2.79	1.60	1.53
3	C	2144	AI5	O38-C37	2.49	1.49	1.43
3	C	2144	AI5	C34-N35	-2.33	1.34	1.39
3	C	2144	AI5	O16-C10	-2.33	1.19	1.23
3	C	2144	AI5	C20-N21	2.09	1.52	1.47

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2144	AI5	C34-C28-N29	-6.69	117.51	126.72
3	C	2144	AI5	N29-C28-N27	5.20	136.01	127.17
3	C	2144	AI5	N31-C30-N29	-4.93	121.12	128.58
3	C	2144	AI5	C08-N09-C10	4.42	128.20	118.44
3	C	2144	AI5	N13-C12-N11	4.36	125.71	117.91
3	C	2144	AI5	C30-N29-C28	4.27	122.25	111.83
3	C	2144	AI5	O16-C10-N11	-4.12	115.83	122.33
3	C	2144	AI5	C08-N09-C15	-4.05	112.11	120.78
3	C	2144	AI5	N27-C36-N35	-3.50	108.97	113.94
3	C	2144	AI5	C34-N35-C36	3.45	108.87	103.45
3	C	2144	AI5	C28-C34-N35	-3.29	106.82	110.58
3	C	2144	AI5	C28-N27-C36	2.97	108.85	105.74
3	C	2144	AI5	C15-C14-C12	2.92	122.31	117.53
3	C	2144	AI5	C14-C12-N13	-2.47	116.31	120.63
3	C	2144	AI5	C14-C15-N09	-2.33	118.05	121.84
3	C	2144	AI5	N09-C10-N11	2.20	122.63	118.80
3	C	2144	AI5	C01-O07-C08	-2.05	104.93	109.47

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2144	AI5	C48-C17-O18-C19
3	C	2144	AI5	C41-C42-C43-N44
3	C	2144	AI5	C17-C08-N09-C15
3	C	2144	AI5	C17-C08-N09-C10
3	C	2144	AI5	O18-C19-C20-N21
3	C	2144	AI5	C22-C23-C24-O25
3	C	2144	AI5	C22-C23-C24-C39
3	C	2144	AI5	C41-C42-C43-C45
3	C	2144	AI5	N21-C22-C23-C24

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2144	AI5	5	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 406 ligands modelled in this entry, 406 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

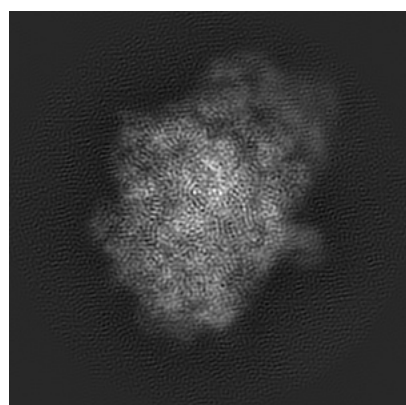
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24792. These allow visual inspection of the internal detail of the map and identification of artifacts.

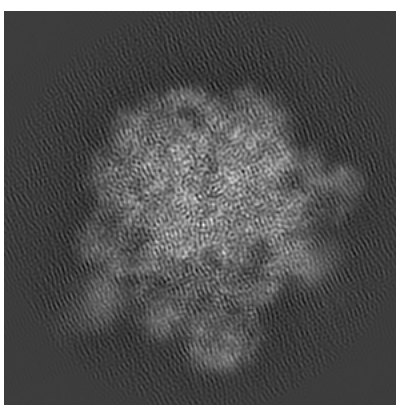
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

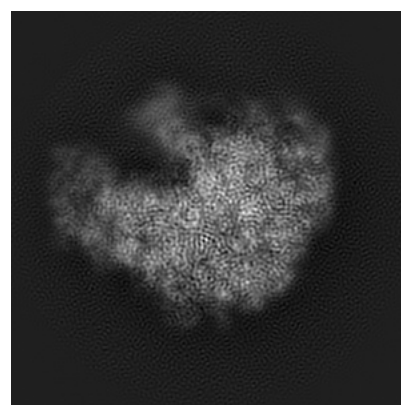
6.1.1 Primary map



X



Y

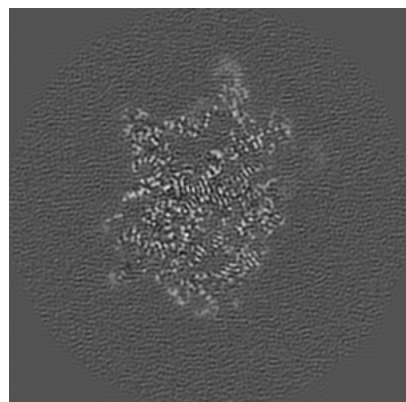


Z

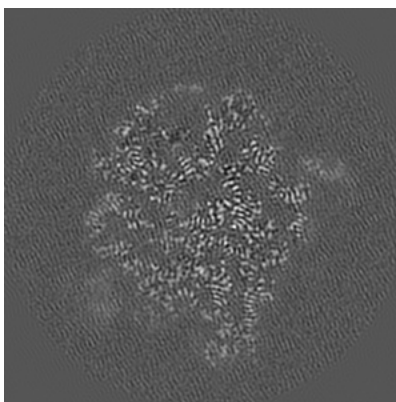
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

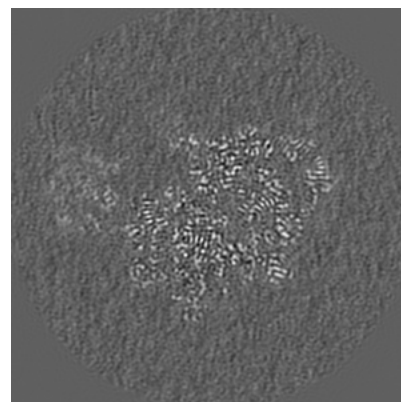
6.2.1 Primary map



X Index: 140



Y Index: 140

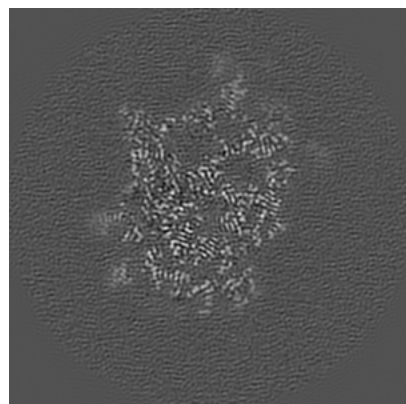


Z Index: 140

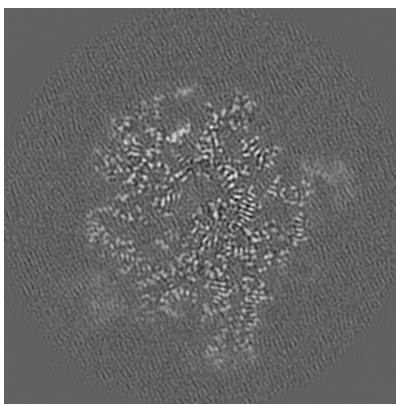
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

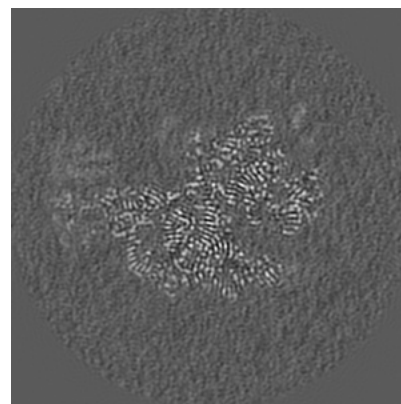
6.3.1 Primary map



X Index: 145



Y Index: 142

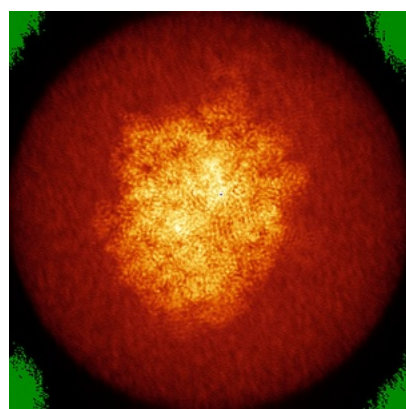


Z Index: 152

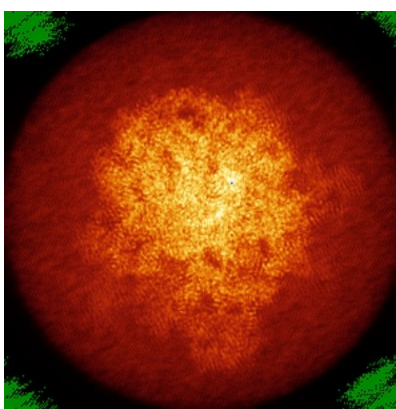
The images above show the largest variance slices of the map in three orthogonal directions.

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

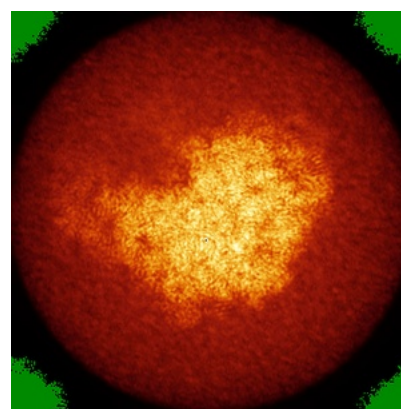
6.4.1 Primary map



X



Y

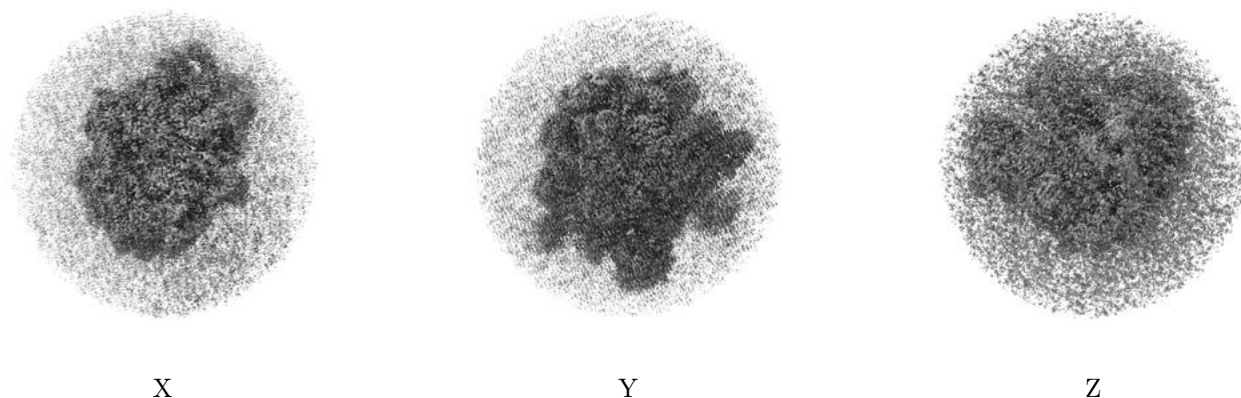


Z

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 0.0179. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

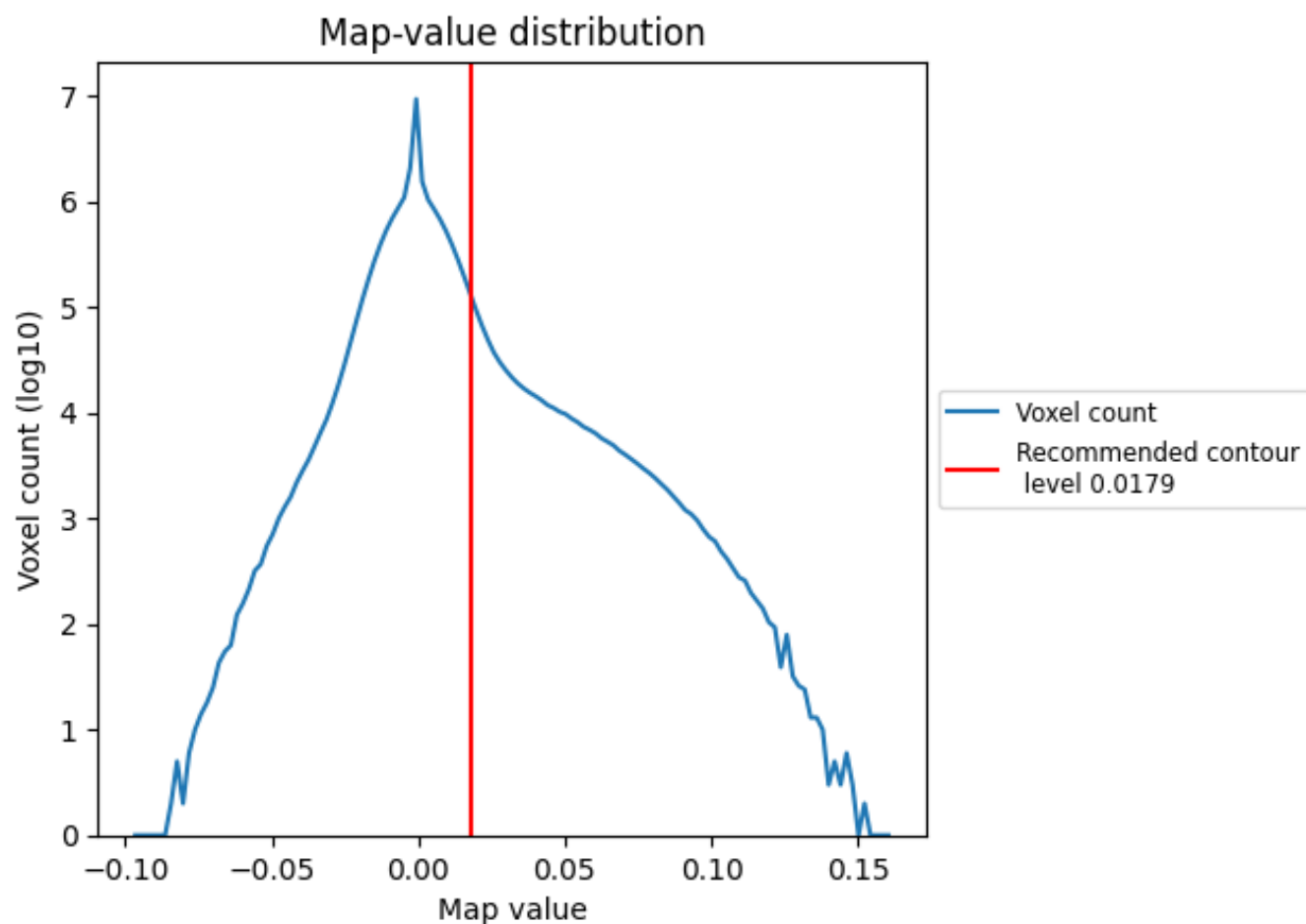
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

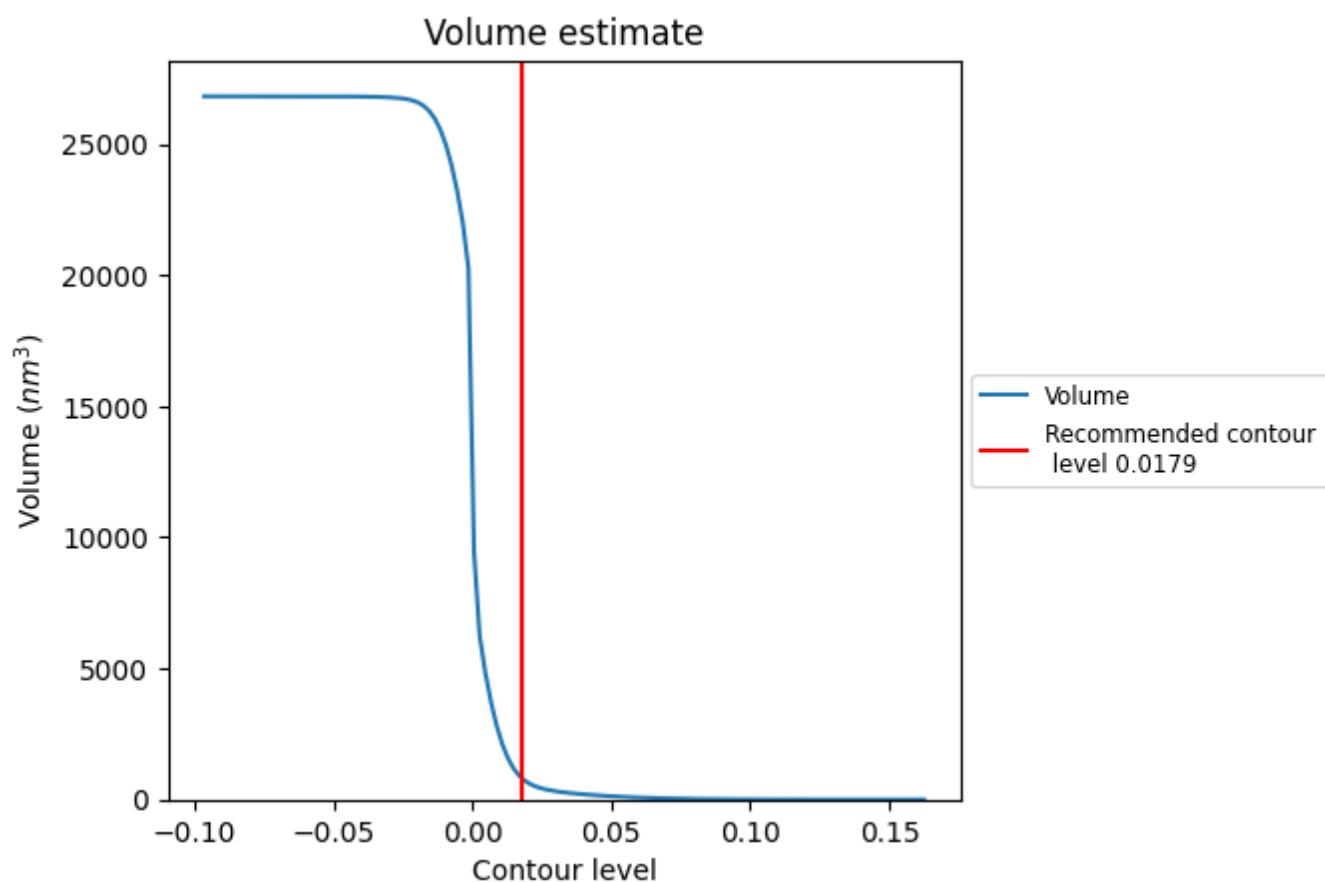
This section contains the results of statistical analysis of the map.

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.

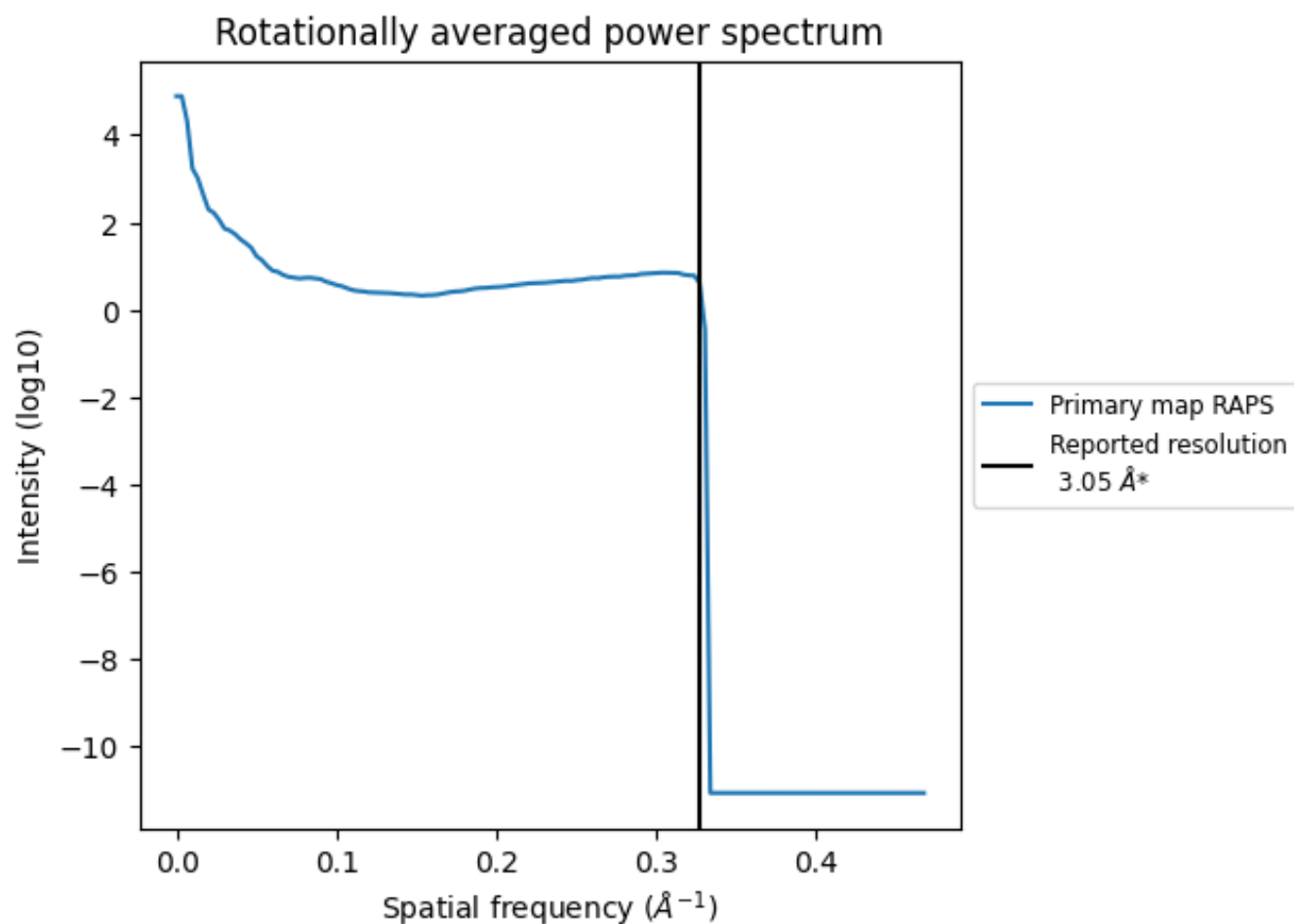
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 809 nm^3 ; this corresponds to an approximate mass of 731 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 ⓘ

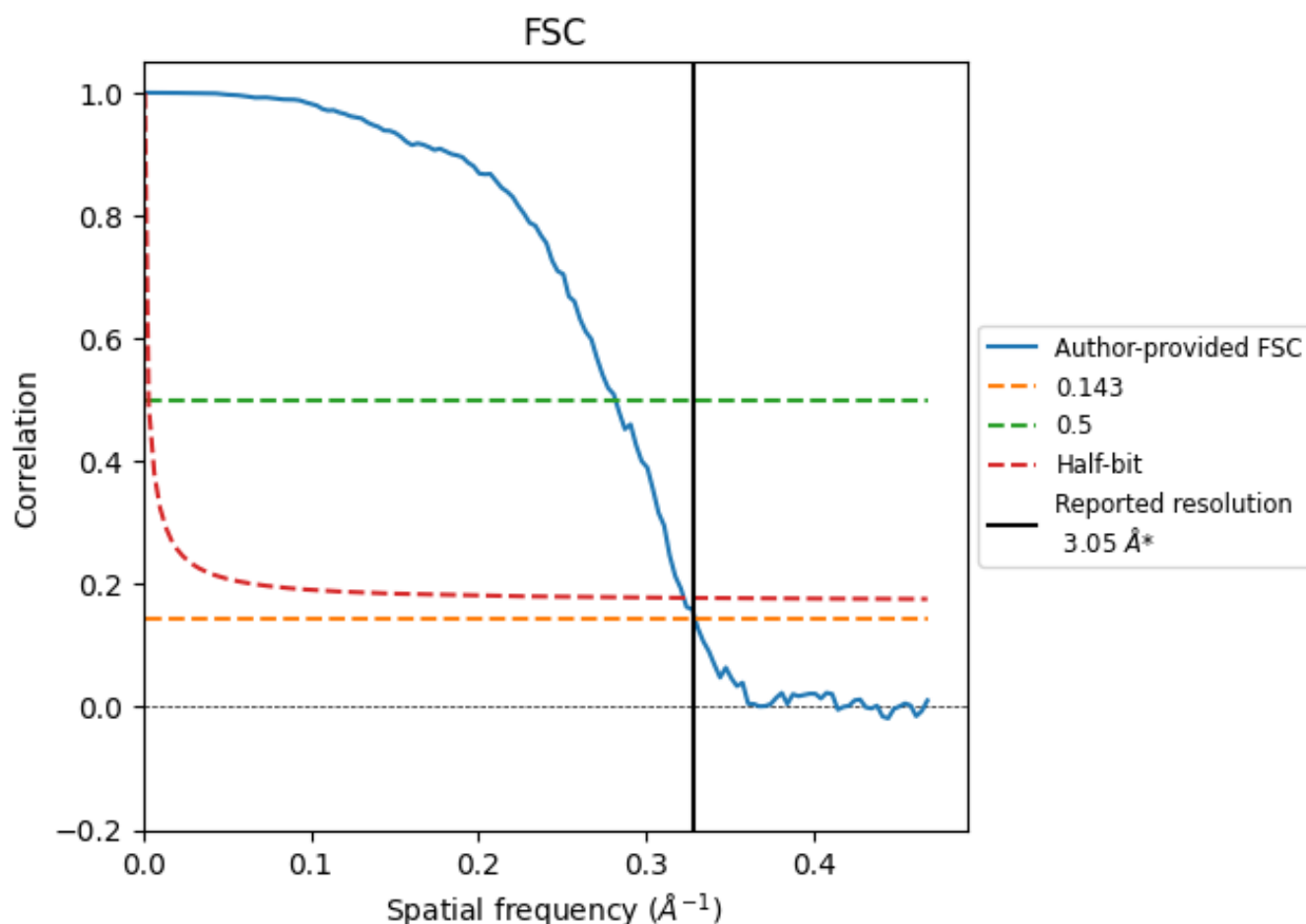


*Reported resolution corresponds to spatial frequency of 0.328 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.328 Å⁻¹

8.2 Resolution estimates [i](#)

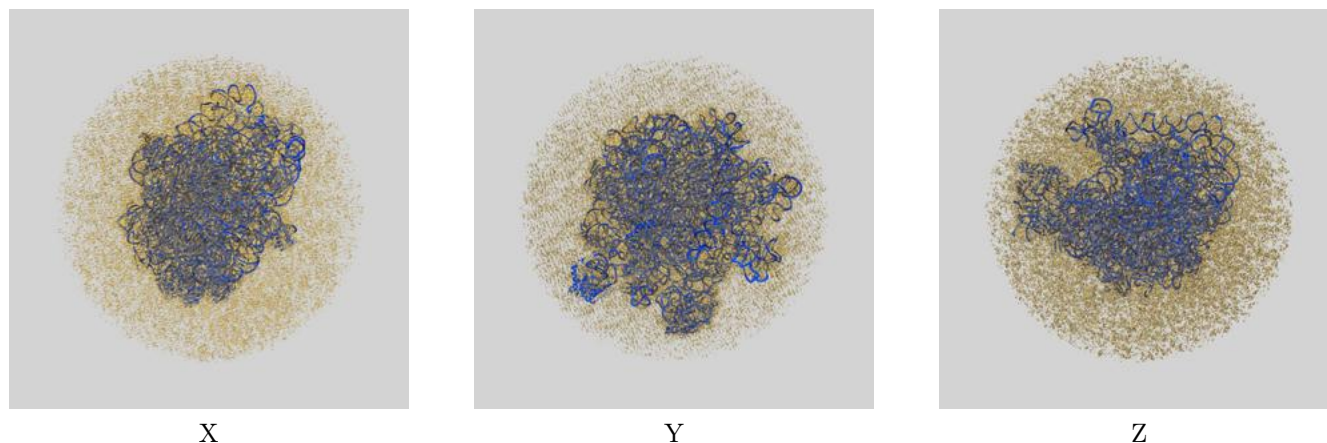
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.05	-	-
Author-provided FSC curve	3.04	3.55	3.10
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

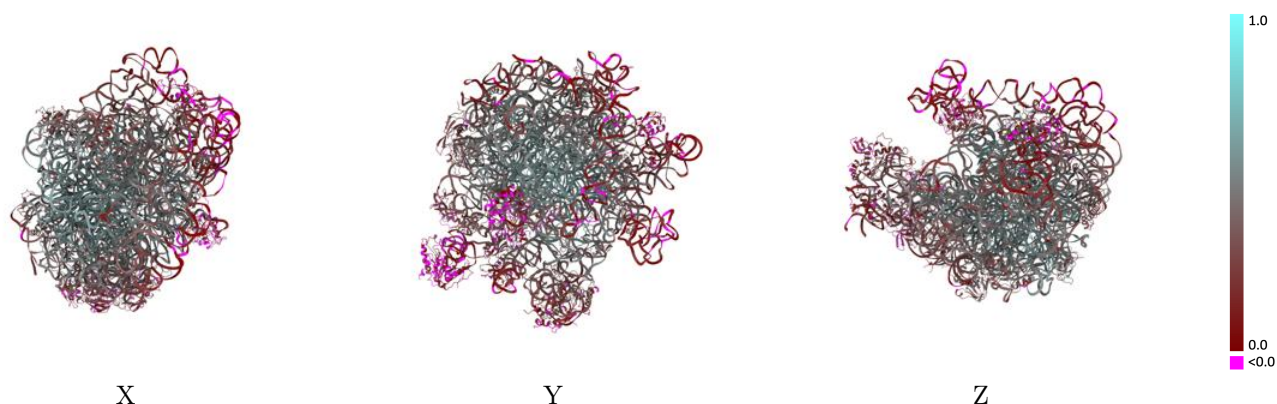
This section contains information regarding the fit between EMDB map EMD-24792 and PDB model 7S0S. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



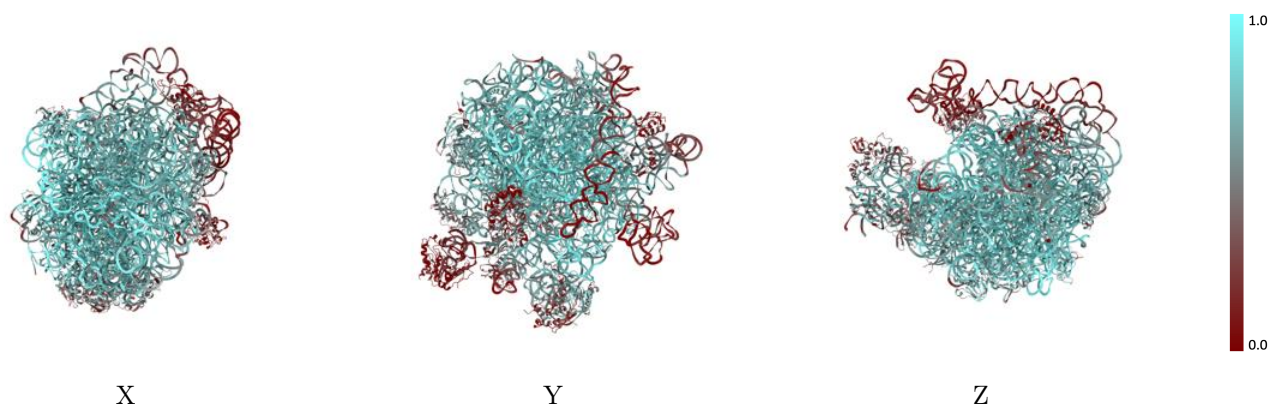
The images above show the 3D surface view of the map at the recommended contour level 0.0179 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



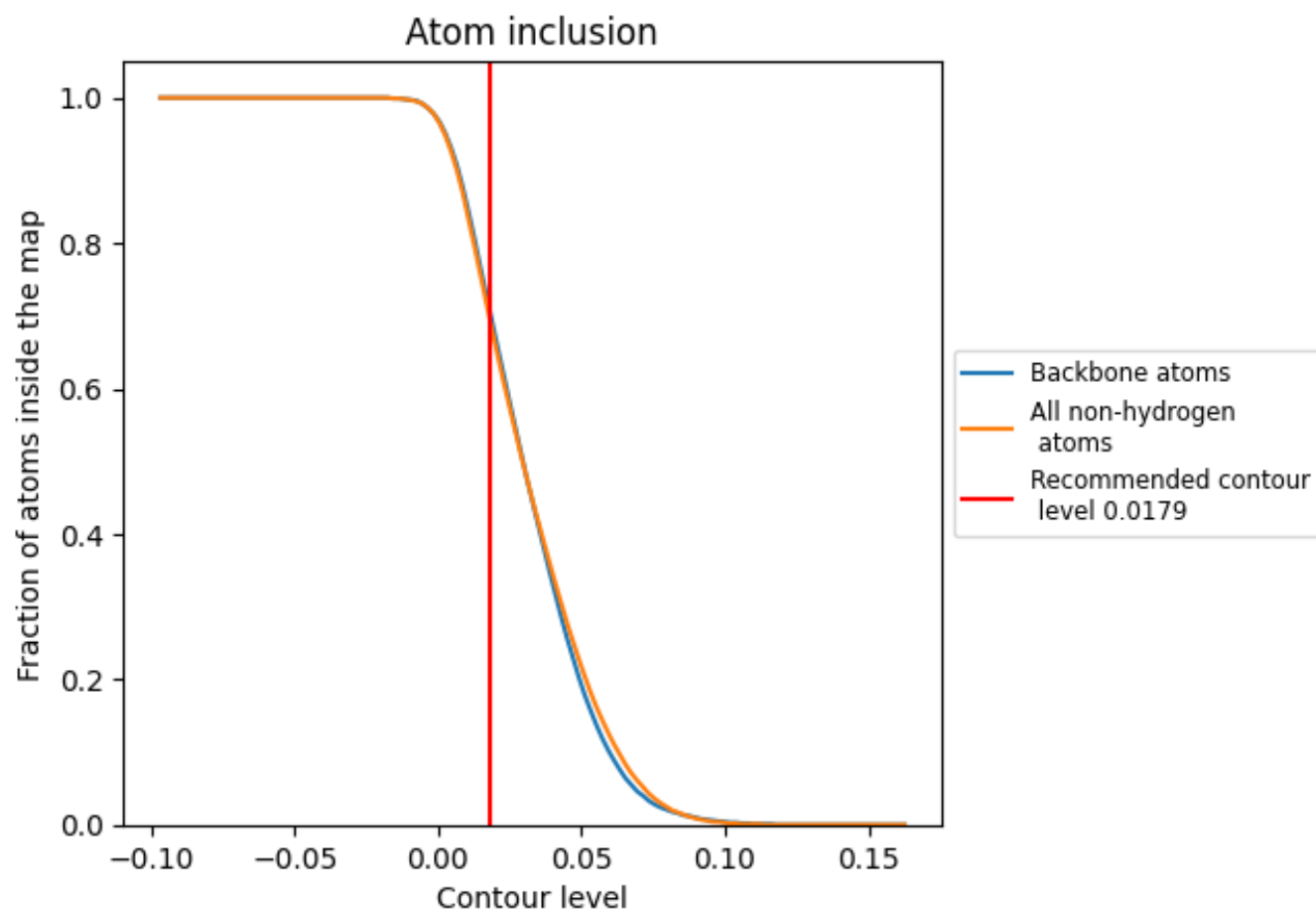
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0179).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 70% 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 (0.0179) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6990	 0.3830
3	 0.7320	 0.4390
B	 0.1620	 0.0740
C	 0.7590	 0.4130
D	 0.7740	 0.4540
E	 0.7320	 0.4120
F	 0.7290	 0.4170
G	 0.3590	 0.2190
H	 0.3810	 0.1650
I	 0.1990	 0.1710
J	 0.0430	 0.0460
K	 0.0420	 0.0630
L	 0.7120	 0.3830
M	 0.6540	 0.3610
N	 0.7480	 0.4230
O	 0.6490	 0.3660
P	 0.8130	 0.4790
Q	 0.5350	 0.2300
R	 0.5610	 0.2960
S	 0.7520	 0.4290
T	 0.7140	 0.3920
U	 0.8670	 0.5750
V	 0.6680	 0.3910
W	 0.7070	 0.4300
X	 0.3210	 0.1470
Y	 0.7240	 0.3960
Z	 0.7340	 0.4330
a	 0.6470	 0.3290
b	 0.6780	 0.3390
c	 0.8380	 0.5420
d	 0.7850	 0.4530
e	 0.8570	 0.5370
f	 0.8420	 0.4900
g	 0.5970	 0.2840
h	 0.2100	 0.1460
i	 0.6500	 0.3020

