



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 09:38 PM UTC

PDB ID : 6S12 / pdb_00006s12
EMDB ID : EMD-10078
Title : Erythromycin Resistant Staphylococcus aureus 50S ribosome (delta R88 A89 uL22).
Authors : Halfon, Y.; Matozv, D.; Eyal, Z.; Bashan, A.; Zimmerman, E.; Kjeldgaard, J.; Ingmer, H.; Yonath, A.
Deposited on : 2019-06-18
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

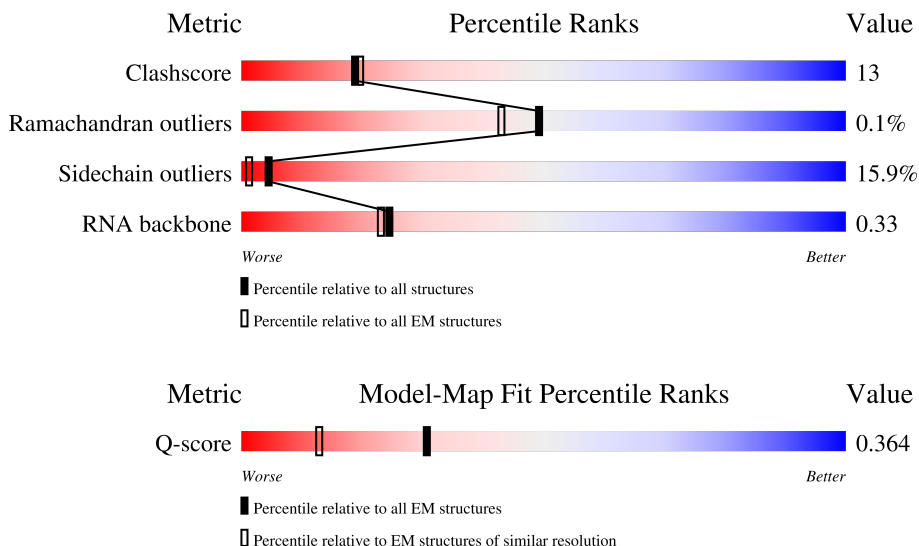
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	A	2905	
2	B	115	
3	C	274	

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Mol	Chain	Length	Quality of chain
4	D	215	
5	E	206	
6	F	175	
7	G	175	
8	H	145	
9	I	122	
10	J	146	
11	K	137	
12	L	120	
13	M	119	
14	N	114	
15	O	116	
16	P	102	
17	Q	110	
18	R	89	
19	S	103	
20	T	94	
21	U	82	
22	V	58	
23	W	67	
24	X	58	
25	Y	59	
26	Z	48	
27	1	47	
28	2	43	

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Mol	Chain	Length	Quality of chain
29	3	64	52% 42% 6%
30	4	37	35% 59% 35% • •

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 146017 atoms, of which 57352 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 RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2905	Total	C	H	N	O	P	0	0
			93573	27803	31296	11387	20182	2905		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	115	Total	C	H	N	O	P	0	0
			3685	1094	1240	436	801	114		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	274	Total	C	H	N	O	S	0	0
			4291	1301	2201	415	369	5		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	215	Total	C	H	N	O	S	0	0
			3294	1018	1667	299	305	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	206	Total	C	H	N	O	S	0	0
			3192	986	1620	288	296	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	175	Total	C	H	N	O	S	0	0
			2667	837	1342	227	255	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	175	Total	C	H	N	O	S	0	0
			2488	790	1225	239	231	3		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	145	Total	C	H	N	O	S	0	0
			2277	714	1134	208	218	3		

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	122	Total	C	H	N	O	S	0	0
			1899	572	981	174	168	4		

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	146	Total	C	H	N	O	S	0	0
			2211	674	1125	214	197	1		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	137	Total	C	H	N	O	S	0	0
			2194	689	1123	203	175	4		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	120	Total	C	H	N	O	S	0	0
			1915	576	983	182	173	1		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	119	Total	C	H	N	O	S	0	0
			1816	557	925	174	159	1		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	114	Total	C	H	N	O	0	0
			1826	563	937	175	151		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	116	Total	C	H	N	O	S	0	0
			1956	593	1014	189	156	4		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	102	Total	C	H	N	O	S	0	0
			1620	503	830	142	144	1		

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	110	Total	C	H	N	O	S	0	0
			1724	523	887	158	153	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	?	-	ARG	deletion	UNP A0A077UKF9
Q	?	-	ALA	deletion	UNP A0A077UKF9

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	89	Total	C	H	N	O	S	0	0
			1463	453	748	127	131	4		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	S	103	Total	C	H	N	O	S	0	0
			1579	486	809	142	141	1		

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	94	Total	C	H	N	O	0	0
			1488	463	766	130	129		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	82	Total	C	H	N	O	0	0
			1265	385	643	122	115		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	58	Total	C	H	N	O	0	0
			911	277	466	96	72		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	67	Total	C	H	N	O	0	0
			1104	333	563	102	106		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	58	Total	C	H	N	O	0	0
			940	280	491	85	84		

- Molecule 25 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Y	59	Total	C	H	N	O	S	0	0
			613	225	243	68	76	1		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
26	Z	48	Total	C	H	N	O	S	0	0
			718	222	358	77	59	2		

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	1	47	Total	C	H	N	O	S	0	0
			784	238	394	78	70	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	2	43	Total	C	H	N	O	S	0	0
			782	225	415	89	52	1		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	3	64	Total	C	H	N	O	S	0	0
			1107	324	586	113	82	2		

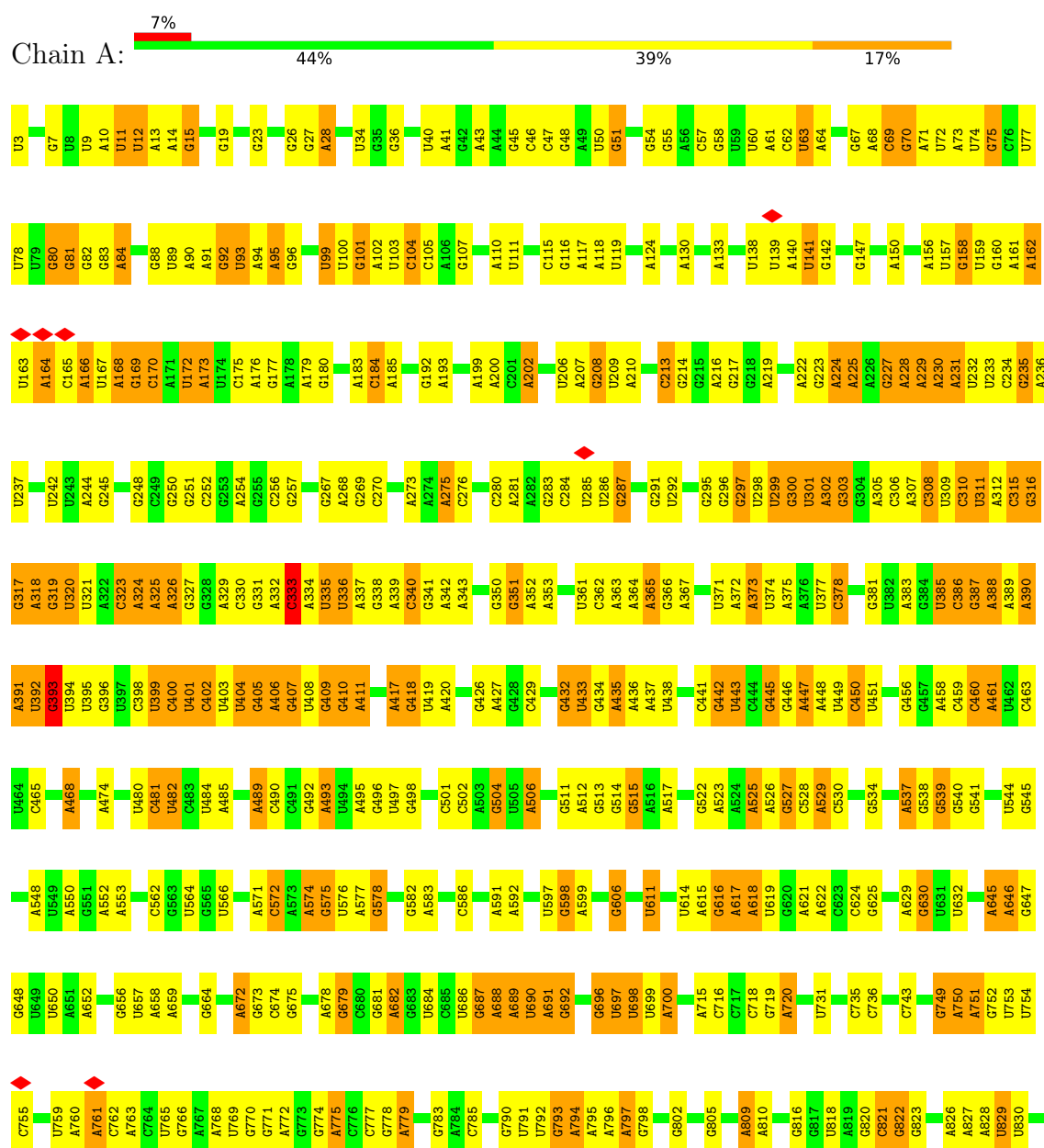
- Molecule 30 is a protein called 50S ribosomal protein L36.

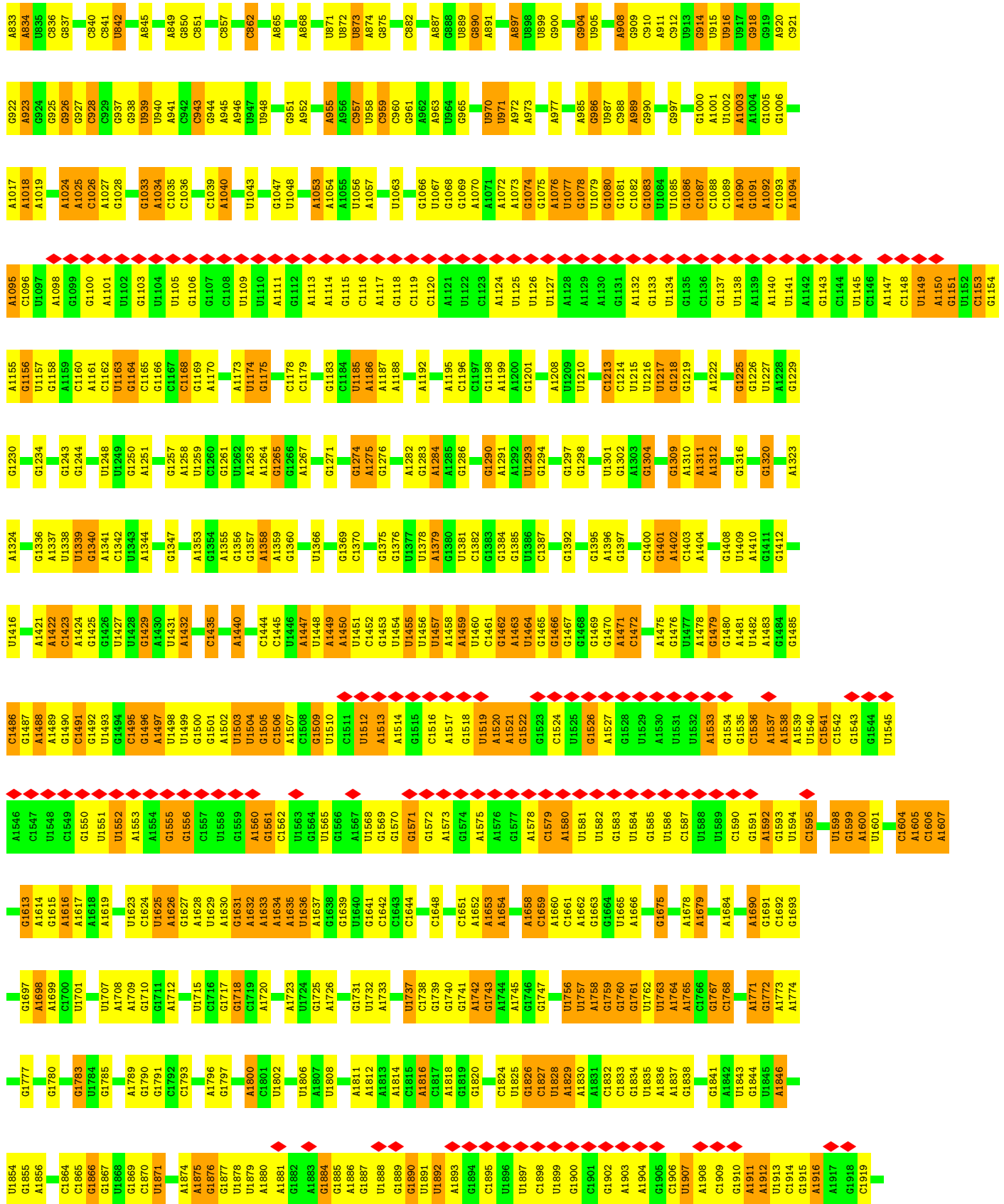
Mol	Chain	Residues	Atoms						AltConf	Trace
30	4	37	Total	C	H	N	O	S	0	0
			635	186	340	60	44	5		

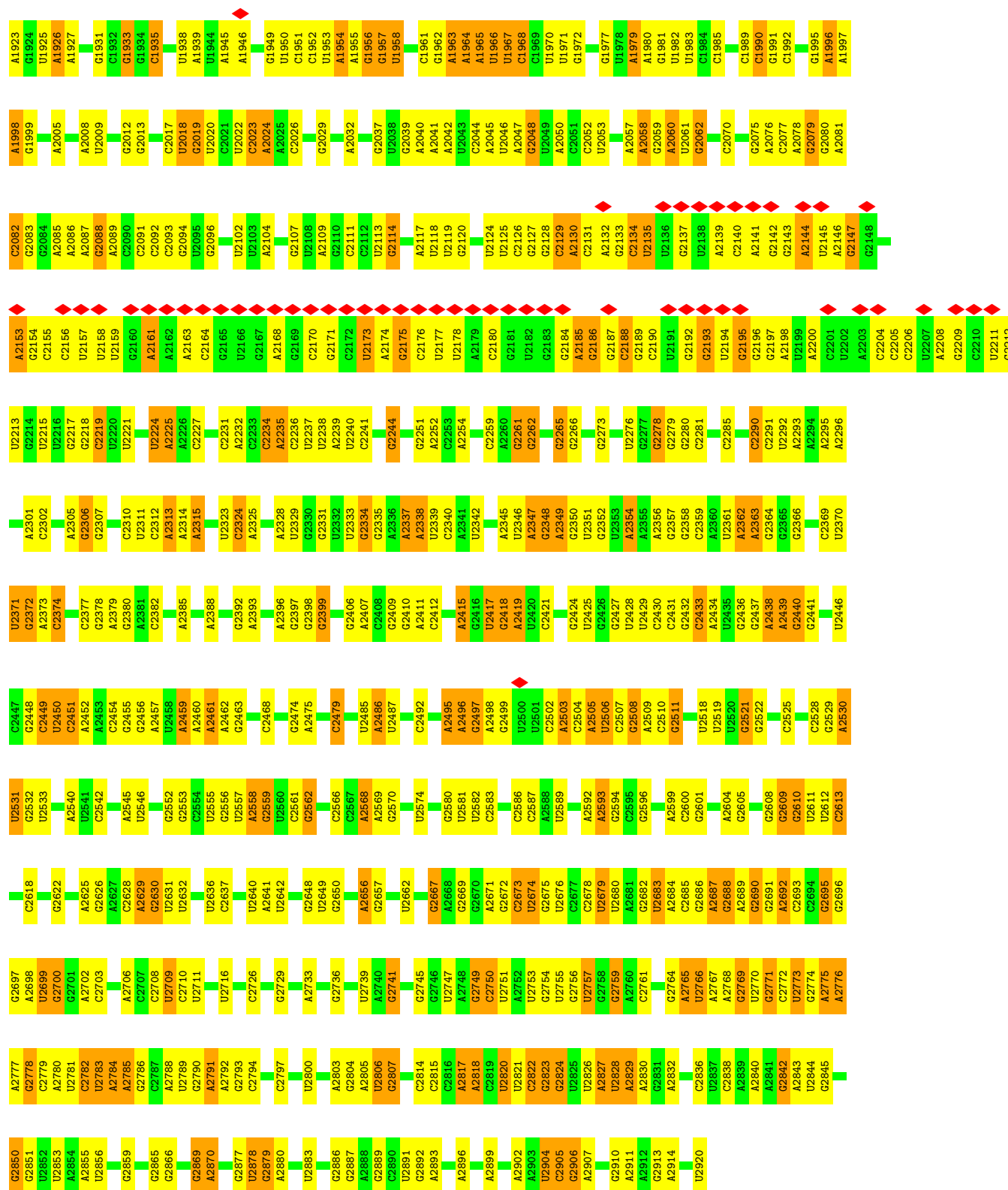
3 Residue-property plots [i](#)

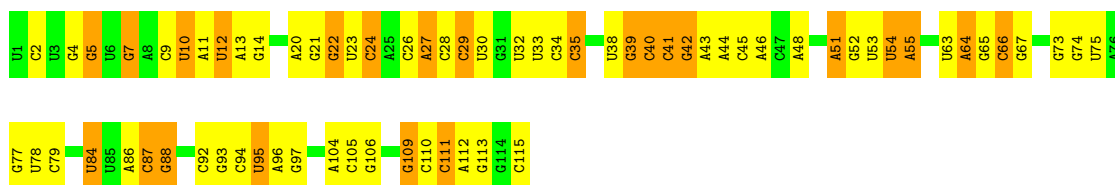
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 23S ribosomal RNA



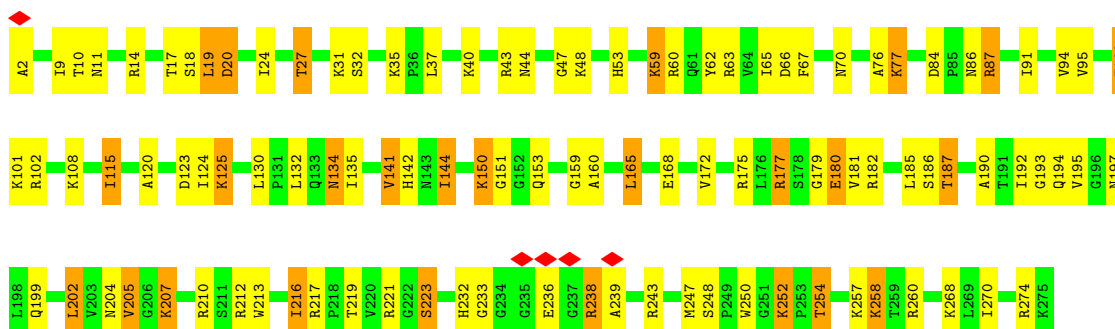






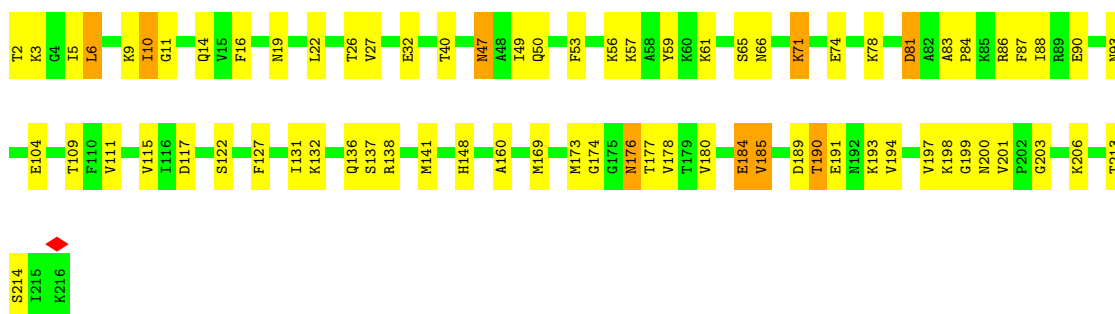
• Molecule 3: 50S ribosomal protein L2

Chain C: 61% 29% 9%



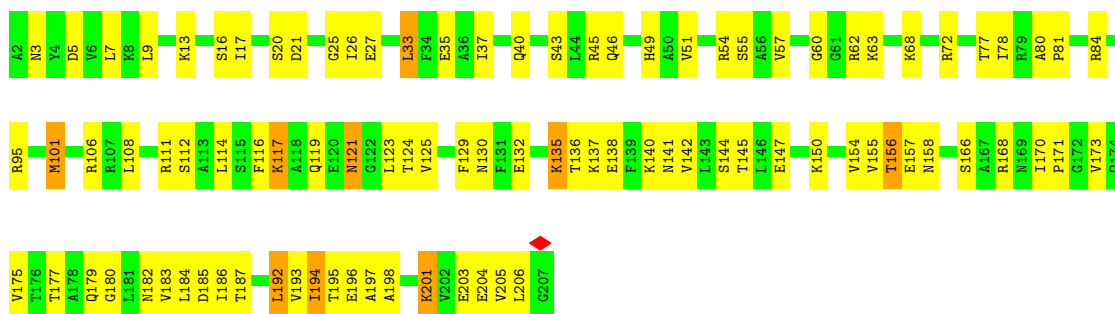
• Molecule 4: 50S ribosomal protein L3

Chain D: 66% 30% 4%

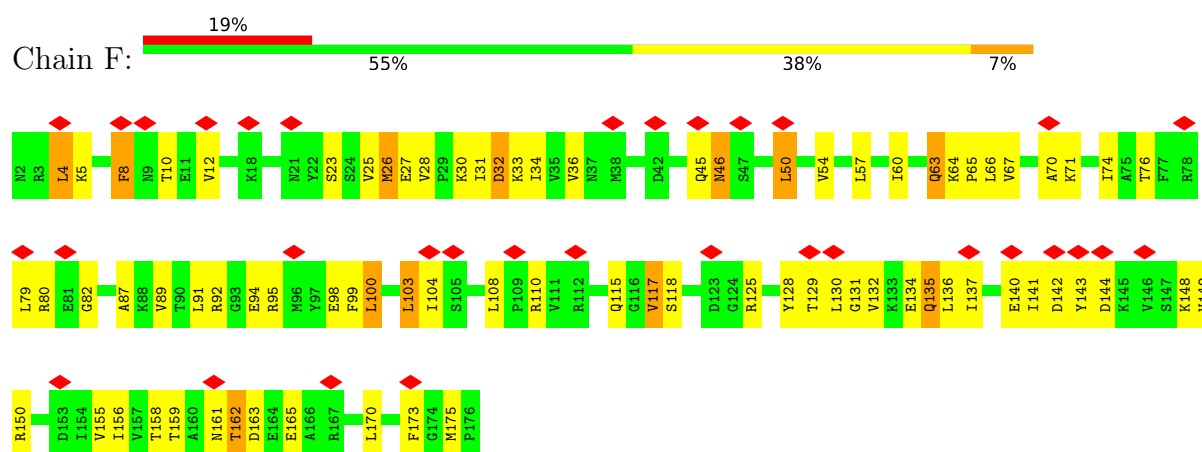


• Molecule 5: 50S ribosomal protein L4

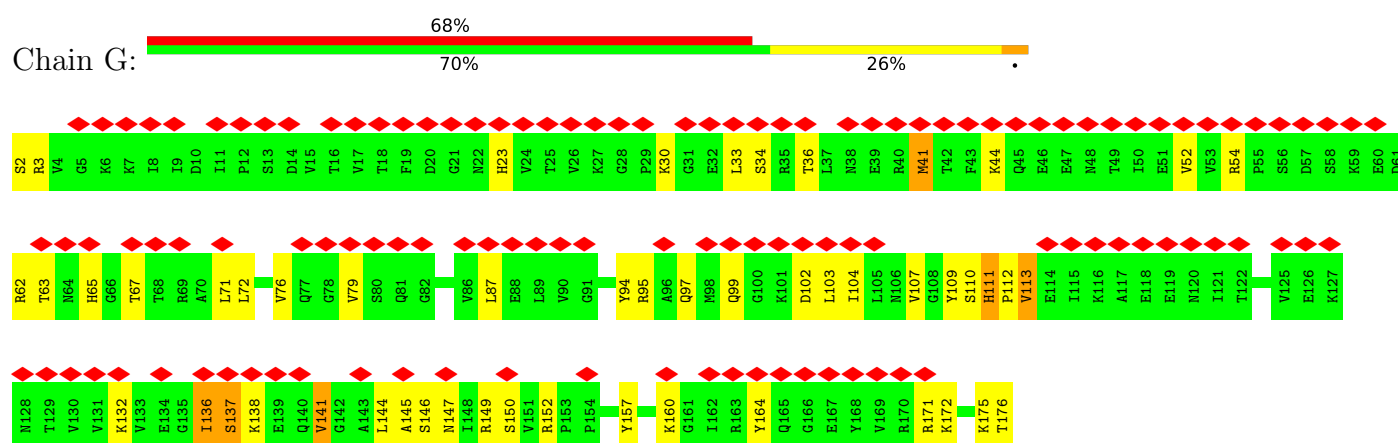
Chain E: 54% 41% 5%



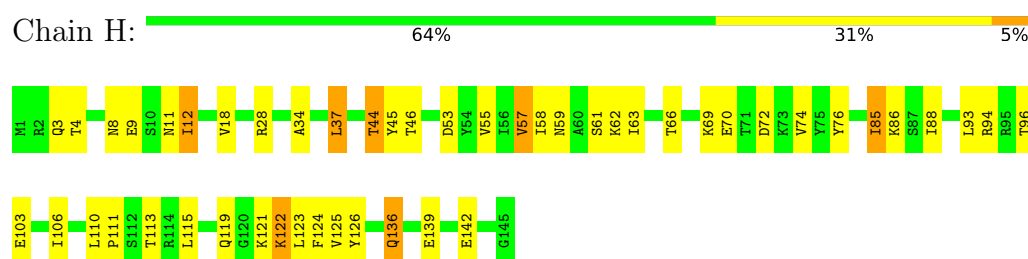
• Molecule 6: 50S ribosomal protein L5



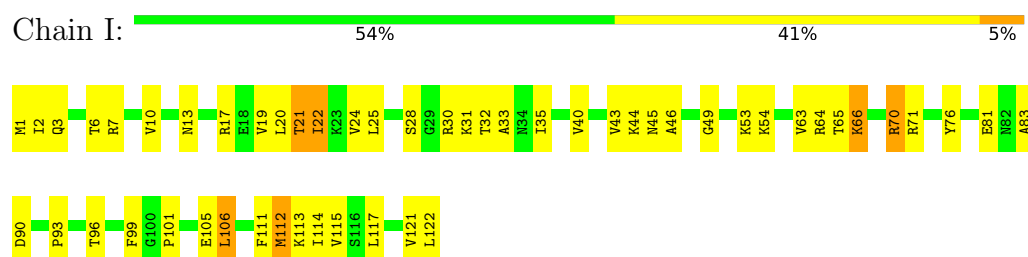
- Molecule 7: 50S ribosomal protein L6



- Molecule 8: 50S ribosomal protein L13

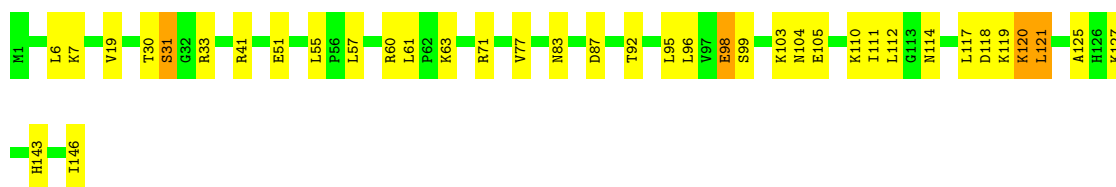


- Molecule 9: 50S ribosomal protein L14



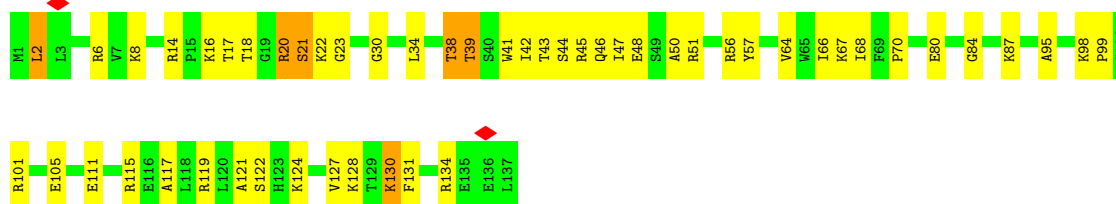
- Molecule 10: 50S ribosomal protein L15

Chain J:  74% 23% .



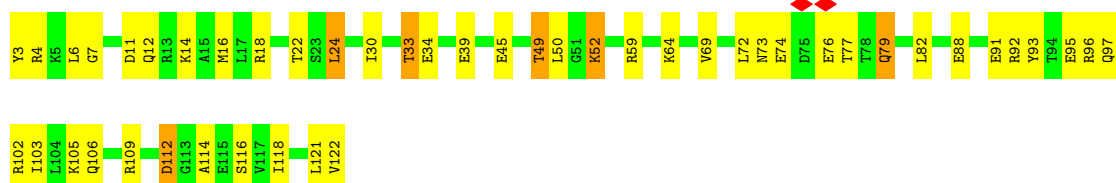
- Molecule 11: 50S ribosomal protein L16

Chain K:  62% 34% .



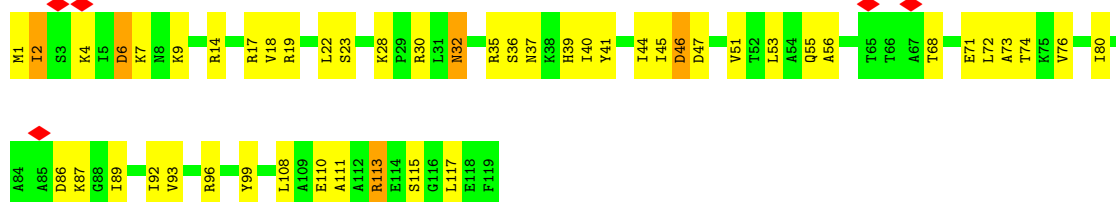
- Molecule 12: 50S ribosomal protein L17

Chain L:  61% 34% 5%



- Molecule 13: 50S ribosomal protein L18

Chain M:  58% 38% .



- Molecule 14: 50S ribosomal protein L19

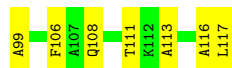
Chain N:  67% 31% .





• Molecule 15: 50S ribosomal protein L20

Chain O: 61% 35% .



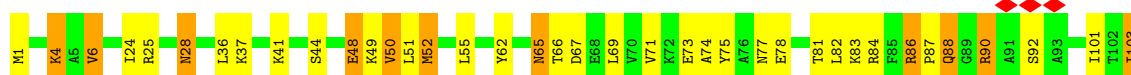
• Molecule 16: 50S ribosomal protein L21

Chain P: 61% 37% .



• Molecule 17: 50S ribosomal protein L22

Chain Q: 63% 27% 10%



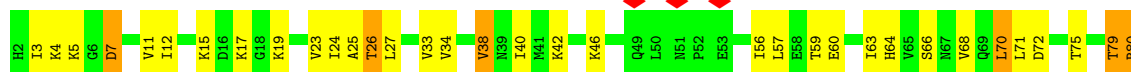
• Molecule 18: 50S ribosomal protein L23

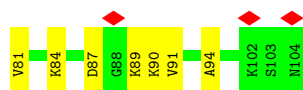
Chain R: 60% 35% 6%



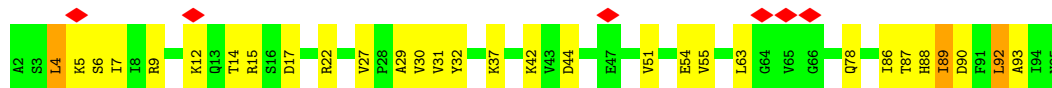
• Molecule 19: 50S ribosomal protein L24

Chain S: 6% 60% 34% 6%

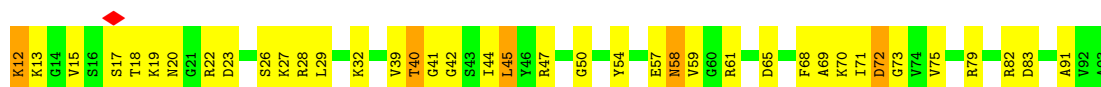




- Molecule 20: 50S ribosomal protein L25



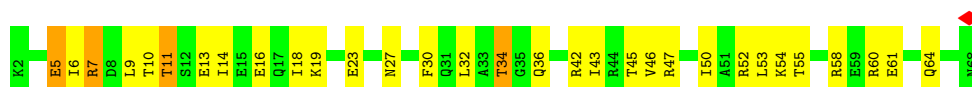
- Molecule 21: 50S ribosomal protein L27



- Molecule 22: 50S ribosomal protein L28



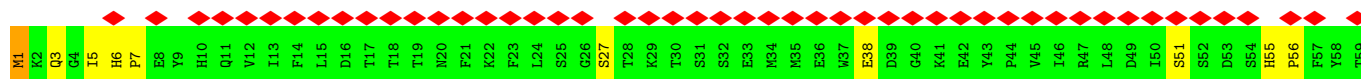
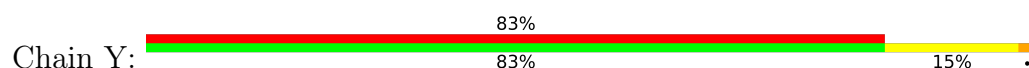
- Molecule 23: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L30



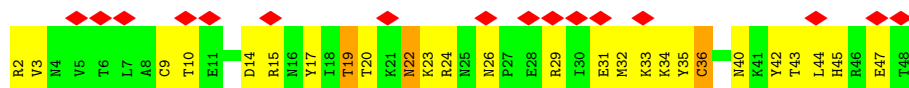
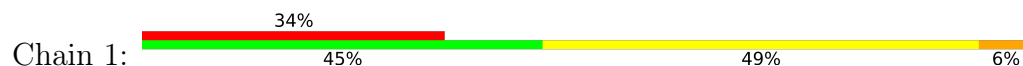
- Molecule 25: 50S ribosomal protein L31 type B



- Molecule 26: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L33



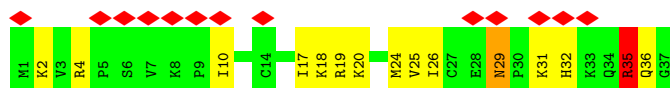
- Molecule 28: 50S ribosomal protein L34



- Molecule 29: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	145897	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.076	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.288	Depositor
Minimum map value	-0.161	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	426.80002, 426.80002, 426.80002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.067, 1.067, 1.067	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.80	10/69739 (0.0%)	0.58	9/108751 (0.0%)
2	B	0.49	0/2733	0.54	0/4257
3	C	0.79	1/2125 (0.0%)	0.70	0/2853
4	D	0.84	0/1651	0.64	0/2215
5	E	0.83	0/1595	0.70	0/2154
6	F	0.33	0/1339	0.65	0/1805
7	G	0.30	0/1281	0.56	0/1736
8	H	0.83	0/1165	0.70	0/1570
9	I	0.80	0/925	0.74	1/1242 (0.1%)
10	J	0.75	0/1100	0.65	0/1467
11	K	0.60	0/1095	0.62	0/1472
12	L	0.81	0/936	0.68	0/1253
13	M	0.47	0/900	0.66	0/1205
14	N	0.76	0/901	0.71	0/1209
15	O	0.94	0/954	0.70	1/1264 (0.1%)
16	P	0.83	0/800	0.67	0/1070
17	Q	0.79	0/845	0.74	0/1140
18	R	0.69	0/723	0.64	0/966
19	S	0.57	0/779	0.60	0/1043
20	T	0.40	0/730	0.56	0/981
21	U	0.79	0/628	0.72	0/833
22	V	0.55	0/451	0.68	0/603
23	W	0.56	0/542	0.64	0/722
24	X	0.87	0/451	0.65	0/606
25	Y	0.23	0/378	0.51	0/521
26	Z	0.71	0/366	0.77	0/489
27	1	0.33	0/395	0.55	0/530
28	2	0.89	0/371	0.68	0/484
29	3	0.70	0/526	0.71	0/690
30	4	0.55	0/298	0.88	0/392
All	All	0.77	11/96722 (0.0%)	0.60	11/145523 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	1
8	H	0	1
16	P	0	2
23	W	0	1
30	4	0	1
All	All	0	6

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	393	G	C1'-N9	67.78	2.49	1.48
1	A	333	C	C2-N3	43.34	2.22	1.35
1	A	333	C	N3-C4	41.31	2.16	1.33
1	A	333	C	N1-C6	41.23	2.19	1.37
1	A	333	C	N1-C2	40.50	2.21	1.40
1	A	333	C	C4-C5	37.62	2.18	1.43
1	A	333	C	C5-C6	35.02	2.04	1.34
1	A	393	G	N9-C4	14.22	1.66	1.38
1	A	393	G	N9-C8	12.16	1.62	1.37
1	A	393	G	N7-C5	-6.43	1.26	1.39
3	C	216	ILE	C-N	-5.27	1.26	1.32

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	393	G	C8-N9-C4	-13.52	65.85	106.40
1	A	393	G	N9-C1'-C2'	12.72	131.09	112.00
1	A	393	G	N7-C8-N9	10.66	145.09	113.10
1	A	393	G	O4'-C1'-N9	8.11	120.67	108.50
1	A	393	G	C4-N9-C1'	7.35	148.54	126.50
1	A	393	G	O4'-C1'-C2'	-7.32	100.28	107.60
1	A	393	G	N9-C4-C5	7.16	126.89	105.40
1	A	393	G	N3-C4-C5	-6.93	107.82	128.60
1	A	393	G	C8-N9-C1'	6.19	145.56	127.00
15	O	34	VAL	N-CA-C	-5.78	107.27	112.12
9	I	22	ILE	N-CA-C	-5.75	107.08	111.62

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	4	35	ARG	Peptide
4	D	173	MET	Peptide
8	H	11	ASN	Peptide
16	P	50	ALA	Peptide
16	P	77	LYS	Peptide
23	W	34	THR	Peptide

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	A	62277	31296	31303	1059	0
2	B	2445	1240	1240	65	0
3	C	2090	2201	2201	73	0
4	D	1627	1667	1667	47	0
5	E	1572	1620	1619	58	0
6	F	1325	1342	1342	54	0
7	G	1263	1225	1225	39	0
8	H	1143	1134	1134	31	0
9	I	918	981	981	39	0
10	J	1086	1125	1125	23	0
11	K	1071	1123	1123	36	0
12	L	932	983	983	30	0
13	M	891	925	925	33	0
14	N	889	937	937	18	0
15	O	942	1014	1014	35	0
16	P	790	830	830	18	0
17	Q	837	887	887	25	0
18	R	715	748	748	23	0
19	S	770	809	809	27	0
20	T	722	766	766	19	0
21	U	622	643	643	25	0
22	V	445	466	466	15	0
23	W	541	563	563	22	0
24	X	449	491	491	9	0
25	Y	370	243	243	13	0
26	Z	360	358	358	22	0
27	1	390	394	394	24	0
28	2	367	415	415	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	3	521	586	586	25	0
30	4	295	340	340	18	0
All	All	88665	57352	57358	1627	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 13.

All (1627) 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)
1:A:333:C:C5	1:A:333:C:C6	2.04	1.45
1:A:2432:G:N2	1:A:2439:A:N7	1.69	1.35
1:A:333:C:C5	1:A:333:C:C4	2.18	1.31
1:A:1675:G:N3	1:A:1679:A:N6	1.87	1.22
1:A:1663:G:HO2'	28:2:2:VAL:N	1.39	1.18
1:A:2496:A:N7	1:A:2508:G:C2	2.12	1.17
1:A:333:C:N1	1:A:393:G:H1'	1.60	1.15
1:A:333:C:C4	1:A:333:C:N3	2.16	1.14
1:A:2496:A:C8	1:A:2508:G:N2	2.17	1.12
1:A:333:C:C6	1:A:333:C:N1	2.19	1.10
1:A:2379:A:N7	1:A:2392:G:N2	1.97	1.10
1:A:333:C:N1	1:A:333:C:C2	2.21	1.08
1:A:333:C:N3	1:A:333:C:C2	2.22	1.07
1:A:420:A:N7	1:A:446:G:N2	2.02	1.07
1:A:2774:G:C2	1:A:2784:A:N6	2.24	1.06
1:A:159:U:N3	1:A:169:G:O6	1.93	1.01
1:A:2774:G:N2	1:A:2784:A:C6	2.32	0.96
1:A:751:A:N6	1:A:770:G:N3	2.12	0.96
1:A:1731:G:N2	1:A:1745:A:N7	2.14	0.96
1:A:749:G:N2	1:A:772:A:H62	1.62	0.96
1:A:752:G:C6	1:A:769:U:O2	2.22	0.92
1:A:159:U:C4	1:A:169:G:O6	2.21	0.92
1:A:2125:U:O2	1:A:2218:G:N1	2.02	0.92
1:A:333:C:C2	1:A:393:G:N9	2.38	0.92
1:A:1451:U:N3	1:A:1633:A:N7	2.20	0.89
1:A:2618:C:O2	1:A:2630:G:N2	2.06	0.88
1:A:336:U:O4	1:A:388:A:C6	2.25	0.88
1:A:749:G:H21	1:A:772:A:H62	1.19	0.88
30:4:35:ARG:NH1	30:4:36:GLN:O	2.06	0.88
1:A:1725:G:HO2'	1:A:1789:A:HO2'	1.11	0.86
1:A:1450:A:OP2	1:A:1452:C:N4	2.08	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2774:G:C2	1:A:2784:A:C6	2.64	0.86
1:A:1261:G:OP1	16:P:67:ARG:NH2	2.09	0.86
1:A:2378:G:N7	29:3:42:ARG:NH1	2.23	0.85
1:A:84:A:N6	1:A:101:G:C2	2.44	0.85
1:A:1301:U:HO2'	26:Z:8:THR:HG1	1.21	0.85
29:3:32:LEU:O	29:3:36:LYS:NZ	2.10	0.85
1:A:790:G:N2	1:A:795:A:H61	1.74	0.85
1:A:2496:A:N6	1:A:2508:G:C4	2.45	0.85
1:A:562:C:OP2	26:Z:10:LYS:NZ	2.09	0.84
1:A:2499:G:N2	1:A:2504:C:OP1	2.10	0.84
1:A:1709:A:O2'	9:I:1:MET:N	2.10	0.84
1:A:749:G:O2'	1:A:771:G:N2	2.10	0.84
1:A:1538:A:N3	1:A:1625:U:O2'	2.10	0.83
13:M:56:ALA:HB2	13:M:80:ILE:HD13	1.59	0.83
1:A:1466:G:N2	1:A:1541:C:O2	2.11	0.83
1:A:1725:G:O2'	1:A:1789:A:O2'	1.93	0.83
1:A:2124:U:O4	1:A:2219:C:N4	2.08	0.83
2:B:77:G:N1	2:B:95:U:O2	2.11	0.83
1:A:1215:U:O2'	1:A:1217:U:OP2	1.95	0.83
1:A:679:G:N7	10:J:71:ARG:NH2	2.26	0.83
1:A:1083:G:N2	1:A:1160:C:O2	2.12	0.82
1:A:1708:A:H61	1:A:2023:C:H42	1.25	0.82
1:A:1708:A:H61	1:A:2023:C:N4	1.76	0.82
1:A:2361:U:O4	1:A:2363:A:N7	2.12	0.82
11:K:18:THR:O	11:K:98:LYS:NZ	2.10	0.82
1:A:333:C:C5	1:A:393:G:N9	2.47	0.82
1:A:574:A:N3	1:A:575:G:N2	2.27	0.82
1:A:1887:G:N2	1:A:1909:C:O2	2.12	0.82
1:A:1854:U:OP1	1:A:1998:A:O2'	1.98	0.81
22:V:45:LYS:NZ	22:V:46:LYS:O	2.13	0.81
1:A:333:C:OP2	1:A:393:G:N2	2.13	0.81
1:A:2125:U:N3	1:A:2218:G:O6	2.13	0.81
1:A:2772:C:N4	1:A:2782:C:O2'	2.14	0.81
1:A:333:C:C4	1:A:393:G:N9	2.47	0.81
1:A:1263:A:O3'	16:P:85:LYS:NZ	2.14	0.81
1:A:333:C:N1	1:A:393:G:N9	2.29	0.81
1:A:1229:G:OP1	10:J:30:THR:OG1	1.99	0.81
1:A:2628:C:O2'	1:A:2629:A:O4'	1.97	0.81
1:A:333:C:C2	1:A:393:G:C1'	2.63	0.81
1:A:1404:A:O3'	28:2:26:LYS:NZ	2.14	0.81
1:A:2088:G:OP1	5:E:68:LYS:NZ	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:G:N2	18:R:40:MET:SD	2.52	0.81
1:A:336:U:O4	1:A:388:A:C5	2.34	0.80
1:A:916:U:O2	1:A:951:G:N2	2.14	0.80
1:A:2279:G:N7	21:U:12:LYS:N	2.29	0.80
1:A:2292:U:O2	1:A:2301:A:N6	2.14	0.80
4:D:56:LYS:NZ	4:D:66:ASN:O	2.12	0.80
11:K:20:ARG:NH1	11:K:99:PRO:O	2.14	0.80
1:A:829:U:O2'	1:A:837:G:N7	2.13	0.80
1:A:1880:A:N6	1:A:2114:G:O2'	2.13	0.80
1:A:333:C:C6	1:A:393:G:N9	2.50	0.80
1:A:333:C:C4	1:A:393:G:C1'	2.65	0.80
1:A:606:G:O3'	15:O:41:LYS:NZ	2.14	0.80
22:V:27:ARG:NH1	22:V:28:ARG:O	2.13	0.80
1:A:2555:U:O2	1:A:2562:G:O6	1.99	0.80
16:P:99:LYS:NZ	16:P:100:ILE:O	2.11	0.80
1:A:333:C:N3	1:A:393:G:N9	2.30	0.80
1:A:2278:G:N7	21:U:12:LYS:NZ	2.29	0.80
1:A:351:G:O2'	19:S:15:LYS:NZ	2.15	0.80
1:A:790:G:H21	1:A:795:A:N6	1.78	0.80
1:A:1827:C:OP2	3:C:182:ARG:NH2	2.15	0.80
1:A:540:G:OP1	17:Q:4:LYS:NZ	2.14	0.80
15:O:50:ARG:O	15:O:54:LYS:NZ	2.15	0.80
1:A:2736:G:OP1	12:L:14:LYS:NZ	2.10	0.80
1:A:493:A:OP1	15:O:5:LYS:NZ	2.14	0.80
2:B:78:U:O4	20:T:15:ARG:NH2	2.15	0.79
1:A:1890:G:O2'	1:A:2438:A:O2'	1.97	0.79
1:A:1935:C:O2	1:A:1949:G:N2	2.15	0.79
1:A:1495:C:N3	1:A:1504:U:O4	2.16	0.79
2:B:29:C:O2	2:B:51:A:N6	2.15	0.79
1:A:184:C:N4	1:A:214:G:N7	2.29	0.79
11:K:130:LYS:NZ	11:K:131:PHE:O	2.16	0.79
1:A:230:A:H61	1:A:456:G:H21	1.28	0.79
1:A:333:C:C6	1:A:393:G:C1'	2.66	0.79
2:B:41:C:O2'	25:Y:1:MET:SD	2.40	0.79
1:A:1875:A:O2'	1:A:1876:G:N7	2.16	0.79
1:A:1828:U:OP2	3:C:150:LYS:NZ	2.16	0.78
1:A:1916:A:N3	1:A:2113:U:O2'	2.16	0.78
1:A:306:C:O2	1:A:411:A:N6	2.15	0.78
1:A:1222:A:O3'	24:X:29:LYS:NZ	2.16	0.78
1:A:1324:A:O4'	12:L:109:ARG:NH1	2.15	0.78
1:A:1979:A:OP1	9:I:44:LYS:NZ	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2775:A:N6	30:4:18:LYS:O	2.15	0.78
1:A:9:U:O2	1:A:2656:A:N7	2.16	0.78
1:A:2113:U:N3	1:A:2261:G:C6	2.52	0.78
1:A:1889:G:O6	1:A:1907:U:N3	2.17	0.78
1:A:2678:C:O2	1:A:2696:G:N2	2.16	0.78
2:B:5:G:O2'	13:M:32:ASN:ND2	2.17	0.78
9:I:112:MET:N	9:I:112:MET:SD	2.56	0.78
1:A:158:G:O6	1:A:170:C:N4	2.16	0.78
1:A:352:A:N6	1:A:1248:U:O2	2.16	0.78
1:A:752:G:O6	1:A:769:U:O2	2.01	0.78
1:A:1087:C:O2'	1:A:1092:A:O3'	2.01	0.78
1:A:1522:G:O3'	1:A:1607:A:O2'	2.02	0.78
1:A:1891:U:O2'	1:A:2436:G:N2	2.17	0.78
1:A:2372:G:O6	1:A:2398:G:N2	2.14	0.78
1:A:1520:A:O2'	1:A:1561:G:O6	2.02	0.78
1:A:2558:A:N6	1:A:2688:G:O6	2.16	0.78
2:B:53:U:O2'	2:B:55:A:N7	2.16	0.78
1:A:446:G:N7	22:V:55:LYS:NZ	2.31	0.78
1:A:2425:U:O2	27:1:15:ARG:NH2	2.17	0.77
1:A:273:A:N7	1:A:298:U:O2	2.16	0.77
1:A:460:C:O2	1:A:1891:U:O2'	2.03	0.77
1:A:752:G:O6	1:A:769:U:C2	2.38	0.77
1:A:1024:A:OP1	1:A:1026:C:N4	2.17	0.77
1:A:2905:C:N4	26:Z:29:GLU:O	2.18	0.77
1:A:674:C:O2	1:A:684:U:O2'	2.03	0.77
1:A:675:G:N2	1:A:678:A:OP2	2.15	0.77
1:A:1761:G:N2	1:A:1767:G:OP2	2.18	0.77
1:A:2126:C:O2	1:A:2217:G:N2	2.14	0.77
1:A:2817:A:N3	1:A:2818:A:N6	2.33	0.77
1:A:2828:U:O2	1:A:2911:A:N6	2.15	0.77
1:A:2130:A:O2'	1:A:2213:U:O4	2.01	0.77
2:B:42:G:OP1	25:Y:3:GLN:NE2	2.18	0.77
1:A:1035:C:O2'	16:P:84:ARG:NH1	2.18	0.77
1:A:61:A:N6	1:A:93:U:O2	2.18	0.77
1:A:429:C:N4	1:A:432:G:OP2	2.18	0.77
11:K:30:GLY:O	11:K:134:ARG:NH1	2.18	0.77
1:A:1968:C:N4	1:A:1992:C:O4'	2.18	0.77
1:A:2392:G:N7	29:3:39:LYS:NZ	2.33	0.77
1:A:2776:A:N7	1:A:2780:A:N6	2.31	0.77
1:A:445:G:N7	22:V:52:ARG:NH2	2.33	0.76
1:A:2692:A:N6	7:G:107:VAL:O	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:23:GLU:O	23:W:27:ASN:ND2	2.18	0.76
1:A:1424:A:O2'	1:A:1571:G:N2	2.17	0.76
12:L:52:LYS:NZ	12:L:93:TYR:O	2.18	0.76
1:A:332:A:N6	1:A:333:C:O2	2.19	0.76
1:A:928:C:N4	1:A:938:G:OP2	2.18	0.76
1:A:1708:A:N6	1:A:2023:C:H42	1.83	0.76
1:A:1966:U:OP1	1:A:2631:U:O2'	2.04	0.76
1:A:309:U:O2	1:A:406:A:O2'	2.04	0.76
1:A:1464:U:O2'	1:A:1465:G:O4'	2.03	0.76
1:A:1658:A:N6	17:Q:86:ARG:O	2.18	0.76
1:A:2766:U:O2	1:A:2791:A:N6	2.19	0.76
1:A:333:C:C2	1:A:393:G:H1'	2.21	0.76
1:A:418:G:O2'	1:A:446:G:O6	2.03	0.76
1:A:1463:A:N6	1:A:1537:A:N1	2.31	0.76
1:A:162:A:O4'	1:A:2235:A:O2'	2.04	0.76
1:A:375:A:O2'	1:A:377:U:OP2	2.04	0.76
1:A:2044:C:O2'	26:Z:6:ARG:NH1	2.19	0.76
1:A:2334:G:O2'	1:A:2337:A:OP2	2.04	0.76
13:M:55:GLN:O	13:M:83:LYS:NZ	2.19	0.76
18:R:9:ARG:NH1	18:R:10:PRO:O	2.19	0.76
1:A:441:C:O3'	22:V:10:ARG:NH1	2.19	0.76
1:A:2305:A:OP2	21:U:20:ASN:ND2	2.19	0.76
1:A:2747:U:O4	1:A:2893:A:N6	2.19	0.76
6:F:60:ILE:O	6:F:95:ARG:NH1	2.18	0.76
1:A:230:A:N6	1:A:456:G:H21	1.83	0.75
1:A:1448:U:O3'	1:A:1449:A:OP1	2.04	0.75
2:B:29:C:O2'	2:B:51:A:N1	2.19	0.75
1:A:62:C:O2	1:A:92:G:N2	2.19	0.75
1:A:333:C:N3	1:A:393:G:C1'	2.49	0.75
1:A:1470:G:OP2	1:A:1471:A:O2'	2.02	0.75
1:A:2497:G:O6	1:A:2503:A:O2'	2.03	0.75
14:N:16:ARG:NH2	14:N:80:THR:O	2.20	0.75
1:A:897:A:N6	1:A:971:U:O4	2.18	0.75
1:A:1763:U:O2	1:A:1765:A:O2'	2.03	0.75
1:A:2046:U:OP2	26:Z:6:ARG:NH1	2.20	0.75
1:A:2142:G:N2	1:A:2188:C:OP1	2.19	0.75
1:A:2313:A:N6	27:1:19:THR:OG1	2.20	0.75
1:A:2818:A:N6	1:A:2826:U:O4	2.20	0.75
12:L:73:ASN:N	12:L:77:THR:O	2.20	0.75
1:A:302:A:O2'	1:A:410:G:N1	2.19	0.75
1:A:2324:C:O2	1:A:2348:G:N2	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:84:U:O2	2:B:88:G:N2	2.19	0.75
1:A:393:G:N9	1:A:393:G:C1'	2.49	0.75
1:A:1490:G:O2'	1:A:1491:C:O4'	2.05	0.75
1:A:1490:G:O2'	1:A:1491:C:O5'	2.03	0.75
1:A:1865:C:N4	1:A:1926:A:O4'	2.20	0.75
1:A:2783:U:O2'	1:A:2785:A:OP2	2.05	0.75
7:G:95:ARG:O	7:G:97:GLN:NE2	2.20	0.75
1:A:749:G:H21	1:A:772:A:N6	1.84	0.75
1:A:809:A:N3	3:C:212:ARG:NH1	2.35	0.75
1:A:43:A:N6	1:A:482:U:O4	2.13	0.75
1:A:1096:C:O2	1:A:1151:G:N2	2.20	0.75
1:A:752:G:N1	1:A:769:U:O2	2.19	0.74
1:A:914:G:O2'	11:K:8:LYS:NZ	2.20	0.74
17:Q:83:LYS:O	17:Q:84:ARG:NE	2.20	0.74
1:A:1085:U:O2	1:A:1158:G:O6	2.05	0.74
1:A:1095:A:N6	1:A:1153:C:O2	2.19	0.74
1:A:1435:C:O3'	18:R:24:LYS:NZ	2.19	0.74
1:A:1933:G:N2	1:A:1951:C:O2	2.18	0.74
13:M:6:ASP:OD1	13:M:9:LYS:NZ	2.19	0.74
1:A:84:A:N6	1:A:101:G:N2	2.34	0.74
1:A:2530:A:O2'	1:A:2532:G:OP2	2.05	0.74
1:A:2686:G:N2	1:A:2689:A:OP2	2.20	0.74
1:A:2830:A:H62	1:A:2910:G:H21	1.32	0.74
2:B:24:C:OP1	2:B:26:C:N4	2.19	0.74
11:K:67:LYS:NZ	11:K:105:GLU:OE2	2.20	0.74
1:A:2313:A:OP2	27:1:22:ASN:ND2	2.20	0.74
29:3:9:GLY:O	29:3:13:ARG:NH1	2.20	0.74
1:A:1360:G:OP1	17:Q:84:ARG:NH1	2.21	0.74
1:A:1648:C:O2'	1:A:1654:A:N6	2.20	0.74
7:G:145:ALA:O	7:G:164:TYR:OH	2.03	0.74
1:A:299:U:O2	1:A:300:G:N2	2.21	0.74
1:A:1091:G:H1	1:A:1154:G:HO2'	1.33	0.74
1:A:2022:U:O2'	9:I:31:LYS:NZ	2.14	0.74
5:E:3:ASN:ND2	5:E:17:ILE:O	2.21	0.74
1:A:1977:G:N2	1:A:1983:U:O4	2.18	0.74
1:A:1780:G:N2	1:A:1783:G:OP2	2.17	0.74
1:A:2496:A:C5	1:A:2508:G:C2	2.76	0.74
1:A:2555:U:O2	1:A:2562:G:C6	2.40	0.74
11:K:21:SER:OG	11:K:99:PRO:O	2.06	0.74
1:A:159:U:O4	1:A:169:G:O6	2.05	0.74
1:A:2366:G:O3'	2:B:39:G:N2	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1979:A:N3	1:A:2587:C:O2'	2.16	0.73
1:A:2877:G:N2	1:A:2880:A:OP2	2.20	0.73
2:B:46:A:OP1	13:M:35:ARG:NH1	2.21	0.73
30:4:17:ILE:O	30:4:24:MET:N	2.21	0.73
1:A:333:C:N4	1:A:393:G:OP2	2.20	0.73
1:A:1915:G:N2	1:A:1915:G:OP2	2.20	0.73
1:A:2495:A:N1	1:A:2508:G:O2'	2.19	0.73
5:E:137:LYS:O	5:E:141:ASN:ND2	2.22	0.73
1:A:301:U:O2'	1:A:302:A:O5'	2.03	0.73
1:A:1793:C:O2	1:A:2013:G:N2	2.20	0.73
1:A:1885:G:O4'	1:A:1911:A:N6	2.21	0.73
4:D:117:ASP:OD1	4:D:214:SER:OG	2.06	0.73
8:H:53:ASP:O	8:H:122:LYS:NZ	2.21	0.73
24:X:6:ILE:O	24:X:34:SER:OG	2.05	0.73
1:A:350:G:O2'	1:A:352:A:N7	2.19	0.73
5:E:158:ASN:O	5:E:177:THR:OG1	2.06	0.73
11:K:111:GLU:OE2	11:K:115:ARG:NE	2.22	0.73
1:A:160:G:O2'	1:A:168:A:N1	2.18	0.73
1:A:1579:C:OP2	1:A:1587:C:N4	2.21	0.73
1:A:2398:G:N2	27:1:42:TYR:OH	2.20	0.73
1:A:2865:G:N2	1:A:2891:U:O2	2.19	0.73
1:A:2421:C:N3	1:A:2459:A:N6	2.36	0.73
1:A:2675:G:N1	1:A:2699:U:O2	2.20	0.73
1:A:2783:U:O2'	1:A:2786:G:OP2	2.07	0.73
1:A:1033:G:OP1	24:X:31:THR:OG1	2.07	0.73
1:A:248:G:N7	29:3:8:ARG:NH2	2.36	0.73
1:A:1085:U:O2	1:A:1158:G:C6	2.42	0.73
1:A:1261:G:N7	16:P:70:LYS:NZ	2.36	0.73
1:A:1301:U:O2'	26:Z:8:THR:OG1	2.06	0.73
1:A:1478:A:O2'	1:A:1522:G:OP1	2.05	0.73
1:A:2499:G:C2	1:A:2505:A:N6	2.57	0.73
1:A:1826:G:N2	1:A:1846:A:OP2	2.20	0.72
1:A:495:A:O2'	15:O:3:ARG:NH1	2.21	0.72
1:A:2347:A:O2'	1:A:2349:A:N6	2.21	0.72
1:A:1480:G:N2	1:A:1561:G:N3	2.37	0.72
1:A:515:G:N7	28:2:38:LYS:NZ	2.35	0.72
1:A:1489:A:N1	1:A:1506:C:N4	2.37	0.72
1:A:1796:A:O2'	1:A:1985:C:OP1	2.07	0.72
4:D:26:THR:OG1	4:D:199:GLY:O	2.07	0.72
1:A:341:G:O2'	1:A:365:A:N1	2.20	0.72
1:A:688:A:O2'	1:A:689:A:O5'	2.08	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:823:G:OP1	3:C:48:LYS:NZ	2.23	0.72
1:A:2178:U:OP1	1:A:2187:G:N2	2.22	0.72
1:A:2324:C:N3	1:A:2348:G:N1	2.38	0.72
1:A:2622:G:N2	1:A:2625:A:OP2	2.19	0.72
1:A:834:A:N6	1:A:1658:A:OP2	2.22	0.72
1:A:1763:U:O2'	1:A:1767:G:O6	2.08	0.72
1:A:1520:A:N6	1:A:1562:C:O4'	2.23	0.72
1:A:2129:C:O2'	1:A:2130:A:O3'	2.08	0.72
1:A:1039:C:O2'	15:O:93:LYS:NZ	2.22	0.72
1:A:1402:A:O4'	22:V:28:ARG:NH2	2.22	0.72
1:A:2851:G:N2	1:A:2904:U:OP2	2.22	0.72
1:A:1869:G:O6	1:A:1925:U:O2	2.08	0.71
1:A:2153:A:O2'	1:A:2189:G:N2	2.23	0.71
1:A:2709:U:O2'	4:D:14:GLN:OE1	2.08	0.71
1:A:165:C:OP2	1:A:166:A:N6	2.23	0.71
1:A:273:A:OP2	1:A:297:G:N2	2.23	0.71
1:A:365:A:OP1	5:E:168:ARG:NE	2.21	0.71
1:A:378:C:OP2	19:S:80:ARG:NH1	2.24	0.71
29:3:54:ASP:OD1	29:3:57:ARG:NH1	2.24	0.71
1:A:60:U:O4	1:A:63:U:O2'	2.09	0.71
1:A:284:C:O2'	1:A:287:G:N2	2.14	0.71
1:A:316:G:O6	1:A:403:U:O2'	2.08	0.71
1:A:795:A:OP2	17:Q:88:GLN:NE2	2.24	0.71
1:A:2450:U:O2'	1:A:2451:C:O5'	2.08	0.71
9:I:64:ARG:NH1	9:I:101:PRO:O	2.24	0.71
13:M:96:ARG:NH2	13:M:99:TYR:O	2.24	0.71
1:A:1000:G:N7	11:K:14:ARG:NH2	2.38	0.71
1:A:1759:G:N2	1:A:1771:A:O3'	2.24	0.71
1:A:229:A:O2'	1:A:231:A:O4'	2.07	0.70
1:A:448:A:N1	1:A:468:A:N6	2.39	0.70
1:A:630:G:N1	10:J:31:SER:OG	2.23	0.70
1:A:1470:G:N7	3:C:31:LYS:NZ	2.30	0.70
1:A:2113:U:C2	1:A:2261:G:N1	2.58	0.70
1:A:1053:A:O2'	1:A:1054:A:O4'	2.07	0.70
1:A:1448:U:N3	1:A:1635:A:C6	2.59	0.70
1:A:2195:G:N2	1:A:2197:G:O6	2.24	0.70
5:E:40:GLN:O	5:E:43:SER:OG	2.10	0.70
14:N:95:ARG:O	14:N:96:ARG:NH1	2.25	0.70
1:A:230:A:H61	1:A:456:G:N2	1.88	0.70
1:A:1068:G:O2'	1:A:1188:A:O2'	2.08	0.70
1:A:1376:G:O3'	18:R:15:LYS:NZ	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2134:C:N4	1:A:2208:A:OP2	2.24	0.70
20:T:14:THR:N	20:T:17:ASP:OD1	2.25	0.70
1:A:1074:G:OP2	11:K:128:LYS:NZ	2.20	0.70
1:A:162:A:O2'	1:A:2234:C:O2	2.10	0.70
1:A:794:A:O2'	1:A:1309:G:N2	2.25	0.70
1:A:1448:U:N3	1:A:1635:A:N1	2.39	0.70
1:A:1449:A:O2'	1:A:1450:A:O4'	2.10	0.70
1:A:2005:A:N3	3:C:11:ASN:ND2	2.39	0.70
1:A:1616:A:O5'	3:C:59:LYS:NZ	2.25	0.70
3:C:35:LYS:O	3:C:62:TYR:N	2.25	0.70
27:1:19:THR:OG1	27:1:20:THR:N	2.24	0.70
29:3:16:ARG:NH1	29:3:20:GLY:O	2.25	0.70
1:A:928:C:O2'	1:A:939:U:O4	2.09	0.69
1:A:1091:G:O2'	1:A:1155:A:N6	2.25	0.69
1:A:2504:C:OP2	30:4:4:ARG:NH2	2.26	0.69
3:C:159:GLY:O	3:C:177:ARG:NH2	2.24	0.69
1:A:333:C:C5	1:A:393:G:C1'	2.75	0.69
1:A:743:C:O2'	1:A:779:A:N6	2.24	0.69
1:A:2499:G:O2'	1:A:2505:A:N1	2.18	0.69
2:B:112:A:O2'	13:M:55:GLN:NE2	2.25	0.69
12:L:92:ARG:NH2	12:L:93:TYR:OH	2.25	0.69
1:A:2251:G:OP1	3:C:268:LYS:NZ	2.26	0.69
1:A:2685:C:OP1	7:G:160:LYS:NZ	2.20	0.69
3:C:18:SER:OG	3:C:19:LEU:N	2.25	0.69
23:W:45:THR:HG23	23:W:46:VAL:HG23	1.75	0.69
1:A:2175:G:O2'	1:A:2176:C:O4'	2.10	0.69
1:A:1466:G:O2'	1:A:1535:G:N3	2.26	0.69
1:A:252:C:O2	10:J:63:LYS:NZ	2.25	0.69
27:1:22:ASN:OD1	27:1:22:ASN:N	2.25	0.69
1:A:9:U:C2	1:A:2656:A:N7	2.61	0.69
1:A:442:G:O4'	22:V:10:ARG:NH2	2.25	0.69
1:A:1422:A:O4'	1:A:1513:A:O2'	2.10	0.69
1:A:1555:G:N2	1:A:1556:G:O6	2.26	0.69
1:A:2113:U:C2	1:A:2261:G:C2	2.81	0.69
2:B:109:G:O2'	2:B:110:C:O4'	2.08	0.69
1:A:1501:G:N2	1:A:1504:U:O4'	2.26	0.69
1:A:1757:U:O2'	1:A:1758:A:O5'	2.11	0.69
1:A:2869:G:O3'	1:A:2886:G:N2	2.26	0.69
18:R:7:LEU:HA	18:R:29:VAL:HG12	1.74	0.69
1:A:28:A:N3	15:O:11:ARG:NH2	2.41	0.68
1:A:2496:A:C5	1:A:2508:G:N3	2.61	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2559:G:N1	1:A:2689:A:N1	2.40	0.68
1:A:562:C:O2'	17:Q:78:GLU:OE2	2.04	0.68
4:D:2:THR:O	4:D:213:THR:OG1	2.06	0.68
5:E:20:SER:N	5:E:203:GLU:OE2	2.25	0.68
14:N:64:ARG:NH1	14:N:73:GLU:OE2	2.25	0.68
1:A:1248:U:O4'	1:A:1275:A:N6	2.27	0.68
1:A:1756:U:O4	1:A:1774:A:N6	2.26	0.68
3:C:100:GLU:OE2	3:C:102:ARG:NH2	2.26	0.68
1:A:1077:U:O4	1:A:1162:C:N4	2.26	0.68
1:A:2137:G:OP1	1:A:2170:C:O2'	2.07	0.68
1:A:2780:A:C2	30:4:17:ILE:HG21	2.28	0.68
1:A:1427:U:O2	1:A:1432:A:N7	2.27	0.68
23:W:60:ARG:O	23:W:64:GLN:NE2	2.27	0.68
1:A:1448:U:O3'	1:A:1449:A:O4'	2.10	0.68
1:A:1509:G:O2'	1:A:1595:C:N4	2.26	0.68
1:A:2212:G:O2'	1:A:2213:U:O4'	2.12	0.68
1:A:2312:C:OP2	27:1:24:ARG:NH2	2.27	0.68
1:A:2314:A:O2'	1:A:2315:A:OP2	2.12	0.68
1:A:1066:G:O6	8:H:69:LYS:NZ	2.25	0.68
1:A:1491:C:O2'	1:A:1492:G:O4'	2.06	0.68
4:D:19:ASN:O	14:N:82:LYS:NZ	2.26	0.68
1:A:418:G:N2	1:A:447:A:OP2	2.26	0.68
1:A:2144:A:N6	1:A:2188:C:OP2	2.27	0.68
17:Q:74:ALA:HB2	17:Q:103:ILE:HD13	1.74	0.68
1:A:2078:A:O2'	1:A:2079:G:OP2	2.12	0.68
1:A:2608:G:N2	1:A:2608:G:OP2	2.23	0.68
1:A:383:A:O2'	5:E:168:ARG:NH1	2.28	0.67
1:A:409:G:H22	1:A:411:A:H62	1.41	0.67
1:A:1378:U:O2'	18:R:54:ASN:OD1	2.05	0.67
11:K:16:LYS:NZ	11:K:18:THR:OG1	2.27	0.67
21:U:26:SER:O	21:U:28:ARG:NH2	2.27	0.67
1:A:2044:C:O3'	26:Z:6:ARG:NH1	2.27	0.67
1:A:1663:G:O2'	28:2:2:VAL:N	2.20	0.67
1:A:2684:A:HO2'	7:G:94:TYR:HH	1.38	0.67
1:A:2817:A:O4'	1:A:2827:A:N6	2.28	0.67
1:A:1347:G:OP2	28:2:10:LYS:NZ	2.20	0.67
9:I:88:ARG:NH1	9:I:93:PRO:O	2.28	0.67
1:A:303:G:OP2	1:A:410:G:N1	2.27	0.67
1:A:350:G:OP2	1:A:350:G:N2	2.24	0.67
13:M:68:THR:OG1	13:M:71:GLU:N	2.28	0.67
1:A:1196:C:OP1	15:O:84:LYS:NZ	2.23	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1501:G:H22	1:A:2729:G:H22	1.43	0.67
1:A:1698:A:O2'	4:D:127:PHE:O	2.10	0.67
1:A:2851:G:OP2	4:D:65:SER:OG	2.05	0.67
7:G:147:ASN:O	7:G:150:SER:OG	2.10	0.67
1:A:2618:C:OP1	3:C:238:ARG:NH1	2.28	0.67
1:A:1379:A:O2'	1:A:1381:U:OP2	2.12	0.67
1:A:1401:G:O2'	1:A:1404:A:N6	2.28	0.67
1:A:2859:G:N2	12:L:97:GLN:O	2.24	0.67
1:A:80:G:N2	1:A:105:C:O2	2.20	0.66
1:A:750:A:N6	1:A:771:G:O4'	2.27	0.66
1:A:1214:C:O2	1:A:1219:G:N2	2.26	0.66
1:A:1710:G:N3	9:I:3:GLN:NE2	2.42	0.66
2:B:73:G:N2	20:T:78:GLN:OE1	2.28	0.66
10:J:83:ASN:ND2	10:J:117:LEU:O	2.28	0.66
1:A:213:C:O2'	1:A:1403:C:O2	2.14	0.66
1:A:1455:U:O2'	1:A:1631:G:OP2	2.08	0.66
1:A:2135:U:OP2	1:A:2205:C:N4	2.28	0.66
1:A:2695:G:O4'	7:G:111:HIS:NE2	2.29	0.66
18:R:13:THR:OG1	18:R:14:GLU:OE1	2.10	0.66
1:A:333:C:N1	1:A:393:G:C1'	2.49	0.66
1:A:775:A:OP1	1:A:1802:U:O2'	2.13	0.66
1:A:1423:C:O2'	1:A:1512:U:O2	2.11	0.66
2:B:27:A:OP2	13:M:37:ASN:ND2	2.28	0.66
1:A:12:U:O2	1:A:571:A:N7	2.28	0.66
1:A:2842:G:O2'	1:A:2844:U:OP2	2.04	0.66
3:C:199:GLN:HA	3:C:202:LEU:HD21	1.78	0.66
5:E:132:GLU:OE1	5:E:132:GLU:N	2.28	0.66
1:A:458:A:N1	1:A:1890:G:O2'	2.29	0.66
1:A:336:U:C4	1:A:388:A:C6	2.83	0.66
1:A:496:G:OP1	1:A:1286:G:N2	2.28	0.66
2:B:42:G:OP2	2:B:44:A:N6	2.29	0.66
4:D:174:GLY:O	4:D:176:ASN:ND2	2.28	0.66
1:A:386:C:N4	1:A:387:G:O6	2.29	0.66
1:A:1094:A:N1	1:A:1153:C:O2'	2.27	0.66
19:S:79:THR:OG1	19:S:80:ARG:O	2.14	0.66
1:A:410:G:O2'	1:A:411:A:N7	2.28	0.66
1:A:480:U:O2	1:A:481:C:N4	2.28	0.66
1:A:2312:C:OP2	27:1:2:ARG:NH2	2.29	0.66
3:C:130:LEU:HB2	3:C:135:ILE:HD11	1.78	0.66
6:F:30:LYS:N	6:F:159:THR:OG1	2.28	0.66
1:A:1889:G:O6	1:A:1907:U:C4	2.49	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2757:U:OP1	4:D:198:LYS:NZ	2.29	0.66
1:A:138:U:N3	1:A:141:U:OP2	2.28	0.65
1:A:1153:C:O3'	1:A:2778:G:O6	2.11	0.65
1:A:2147:G:N2	1:A:2205:C:O2	2.28	0.65
1:A:2329:U:O2	6:F:125:ARG:NH1	2.28	0.65
1:A:2499:G:N2	1:A:2505:A:N6	2.45	0.65
11:K:119:ARG:O	11:K:122:SER:OG	2.14	0.65
2:B:77:G:C2	2:B:95:U:O2	2.50	0.65
9:I:88:ARG:NH2	9:I:90:ASP:OD2	2.30	0.65
1:A:1886:A:C5	1:A:1910:G:N2	2.65	0.65
15:O:99:ALA:HB2	15:O:106:PHE:CE1	2.31	0.65
1:A:1149:U:O2'	1:A:1150:A:O4'	2.10	0.65
1:A:2782:C:O2'	1:A:2783:U:OP2	2.15	0.65
1:A:865:A:N3	1:A:987:U:O2'	2.28	0.65
1:A:1448:U:C2	1:A:1635:A:N6	2.64	0.65
2:B:53:U:O2	2:B:55:A:N6	2.29	0.65
29:3:54:ASP:O	29:3:58:VAL:HG22	1.96	0.65
5:E:147:GLU:OE1	5:E:147:GLU:N	2.30	0.65
1:A:1440:A:O2'	1:A:1514:A:O4'	2.13	0.65
1:A:2496:A:O2'	11:K:56:ARG:NH1	2.30	0.65
1:A:2498:A:N6	1:A:2503:A:O2'	2.29	0.65
2:B:64:A:O2'	2:B:104:A:N6	2.30	0.65
4:D:56:LYS:N	4:D:84:PRO:O	2.29	0.65
8:H:99:GLU:OE1	8:H:99:GLU:N	2.30	0.65
21:U:57:GLU:N	21:U:57:GLU:OE1	2.29	0.65
1:A:1024:A:O2'	1:A:1025:A:OP1	2.13	0.64
1:A:1304:G:O2'	1:A:2039:G:O6	2.14	0.64
1:A:2561:C:N4	1:A:2562:G:O6	2.29	0.64
1:A:1312:A:O4'	12:L:12:GLN:NE2	2.30	0.64
1:A:1496:G:OP1	1:A:1497:A:N6	2.30	0.64
5:E:157:GLU:OE1	5:E:198:ALA:N	2.31	0.64
10:J:33:ARG:NH1	10:J:41:ARG:O	2.30	0.64
19:S:79:THR:OG1	19:S:94:ALA:O	2.15	0.64
29:3:16:ARG:NE	29:3:65:LYS:O	2.30	0.64
1:A:3:U:O2	1:A:2920:U:O2'	2.13	0.64
1:A:333:C:C5	1:A:393:G:O4'	2.51	0.64
2:B:77:G:N2	2:B:95:U:O2	2.31	0.64
1:A:1072:A:H61	1:A:1169:G:H2'	1.62	0.64
1:A:1369:G:N7	1:A:1653:A:O2'	2.30	0.64
9:I:30:ARG:NE	9:I:32:THR:O	2.27	0.64
1:A:300:G:O2'	1:A:301:U:OP2	2.15	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:79:GLN:NE2	12:L:88:GLU:OE2	2.29	0.64
1:A:1465:G:O2'	1:A:1536:C:O2'	2.02	0.64
1:A:1539:A:N3	1:A:1624:C:O2'	2.28	0.64
1:A:335:U:O2'	1:A:336:U:O5'	2.15	0.64
1:A:1472:C:O2'	1:A:1616:A:OP2	2.08	0.64
29:3:55:MET:O	29:3:55:MET:HE3	1.98	0.64
1:A:2510:C:N3	11:K:124:LYS:NZ	2.34	0.64
1:A:250:G:OP2	1:A:252:C:N4	2.31	0.64
1:A:1079:U:O2	1:A:1164:G:O6	2.16	0.64
1:A:1485:G:O2'	1:A:1599:G:N1	2.31	0.64
1:A:2089:A:N6	1:A:2530:A:N7	2.45	0.64
21:U:45:LEU:HD21	21:U:69:ALA:H	1.63	0.64
1:A:319:G:O4'	1:A:325:A:N6	2.30	0.63
1:A:1615:G:OP2	3:C:63:ARG:NH2	2.31	0.63
1:A:2711:U:OP2	14:N:53:ARG:NH2	2.32	0.63
1:A:2883:U:OP1	14:N:93:LYS:NZ	2.22	0.63
5:E:135:LYS:N	5:E:166:SER:OG	2.30	0.63
1:A:648:G:N7	10:J:103:LYS:NZ	2.46	0.63
1:A:687:G:N1	1:A:690:U:OP2	2.30	0.63
1:A:2667:G:OP1	8:H:100:ARG:NH1	2.30	0.63
1:A:206:U:OP2	1:A:207:A:O2'	2.17	0.63
1:A:1496:G:O2'	1:A:1497:A:O5'	2.16	0.63
1:A:1957:G:O2'	1:A:1995:G:O6	2.12	0.63
1:A:2261:G:O2'	1:A:2262:G:OP1	2.10	0.63
2:B:12:U:O2'	2:B:104:A:O2'	2.12	0.63
4:D:59:TYR:N	4:D:74:GLU:OE2	2.30	0.63
5:E:182:ASN:OD1	5:E:184:LEU:N	2.32	0.63
25:Y:51:SER:O	25:Y:55:HIS:NE2	2.32	0.63
1:A:1800:A:N6	3:C:11:ASN:O	2.30	0.63
2:B:35:C:N3	2:B:46:A:O2'	2.23	0.63
3:C:243:ARG:NH2	3:C:247:MET:SD	2.71	0.63
1:A:1451:U:C2	1:A:1633:A:N7	2.66	0.63
23:W:5:GLU:OE1	23:W:5:GLU:N	2.32	0.63
30:4:10:ILE:HD12	30:4:29:ASN:HB2	1.81	0.63
1:A:84:A:H62	1:A:101:G:N2	1.96	0.63
1:A:301:U:HO2'	1:A:302:A:P	2.22	0.63
1:A:1217:U:O2	1:A:1218:G:N1	2.32	0.63
1:A:2448:G:N7	29:3:31:HIS:NE2	2.47	0.63
1:A:2499:G:N2	1:A:2505:A:H62	1.96	0.63
12:L:95:GLU:O	12:L:97:GLN:NE2	2.32	0.63
1:A:1521:A:N6	1:A:1560:A:O2'	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:120:ALA:O	3:C:134:ASN:ND2	2.31	0.62
5:E:141:ASN:O	5:E:145:THR:HG23	1.98	0.62
1:A:202:A:O3'	22:V:23:ASN:ND2	2.32	0.62
1:A:753:U:N3	1:A:769:U:O2	2.32	0.62
1:A:1478:A:N6	1:A:1605:A:N7	2.37	0.62
1:A:1962:G:N1	1:A:1989:C:O2'	2.31	0.62
1:A:2324:C:O2	1:A:2348:G:C2	2.52	0.62
19:S:11:VAL:HG23	19:S:17:LYS:HA	1.82	0.62
6:F:70:ALA:N	6:F:82:GLY:O	2.32	0.62
1:A:583:A:O3'	8:H:8:ASN:ND2	2.31	0.62
24:X:9:THR:OG1	24:X:55:THR:OG1	2.14	0.62
1:A:342:A:N3	1:A:362:C:O2'	2.23	0.62
1:A:1505:G:O4'	1:A:2729:G:N2	2.27	0.62
1:A:2302:C:O2'	11:K:84:GLY:O	2.15	0.62
1:A:299:U:O2'	1:A:300:G:N2	2.32	0.62
1:A:1213:C:H42	1:A:1219:G:H22	1.46	0.62
1:A:1485:G:HO2'	1:A:1599:G:H1	1.46	0.62
1:A:504:G:O2'	1:A:515:G:O6	2.08	0.62
1:A:2060:A:O2'	1:A:2062:G:OP2	2.17	0.62
1:A:2196:G:O2'	1:A:2197:G:O4'	2.13	0.62
1:A:2546:U:O2'	1:A:2568:A:N6	2.33	0.62
13:M:74:THR:HG23	13:M:111:ALA:HB2	1.82	0.62
1:A:1199:A:O3'	15:O:55:ARG:NH2	2.32	0.62
1:A:2171:G:N2	1:A:2173:U:O4'	2.33	0.62
6:F:32:ASP:N	6:F:32:ASP:OD1	2.33	0.62
8:H:37:LEU:HD12	8:H:37:LEU:O	1.99	0.62
8:H:85:ILE:HD12	8:H:86:LYS:N	2.14	0.61
1:A:227:G:H22	1:A:235:G:H21	1.46	0.61
1:A:1448:U:C2	1:A:1635:A:C6	2.87	0.61
1:A:2558:A:N7	1:A:2687:A:N6	2.48	0.61
1:A:2800:U:O3'	4:D:177:THR:OG1	2.18	0.61
4:D:16:PHE:O	14:N:14:GLN:NE2	2.33	0.61
19:S:5:LYS:O	19:S:23:VAL:HG13	1.99	0.61
1:A:333:C:N3	1:A:393:G:C8	2.68	0.61
1:A:442:G:O2'	22:V:30:ASN:O	2.18	0.61
1:A:517:A:OP1	5:E:84:ARG:NH1	2.33	0.61
1:A:1652:A:N7	1:A:1665:U:O2	2.33	0.61
10:J:51:GLU:OE2	29:3:57:ARG:NE	2.33	0.61
1:A:1067:U:OP2	1:A:1069:G:O2'	2.18	0.61
1:A:1079:U:C2	1:A:1164:G:O6	2.53	0.61
23:W:11:THR:OG1	23:W:60:ARG:NH2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:A:O2'	1:A:402:C:N4	2.33	0.61
1:A:2557:U:OP1	1:A:2562:G:N2	2.32	0.61
1:A:2672:G:O2'	1:A:2673:C:OP1	2.11	0.61
12:L:4:ARG:NH1	12:L:39:GLU:OE2	2.33	0.61
1:A:84:A:N6	1:A:99:U:O4'	2.34	0.61
1:A:2224:U:O2'	1:A:2225:A:N3	2.21	0.61
1:A:2259:C:OP2	22:V:27:ARG:NH2	2.33	0.61
1:A:2555:U:C2	1:A:2562:G:O6	2.53	0.61
1:A:2774:G:N3	1:A:2784:A:N6	2.49	0.61
1:A:2906:G:O2'	26:Z:29:GLU:OE1	2.11	0.61
2:B:10:U:O5'	2:B:13:A:N6	2.34	0.61
15:O:89:ASP:O	16:P:11:GLN:NE2	2.34	0.61
1:A:1476:G:O6	1:A:1607:A:N6	2.34	0.61
1:A:2776:A:OP1	7:G:3:ARG:N	2.34	0.61
1:A:333:C:C6	1:A:393:G:H1'	2.35	0.61
1:A:434:G:O2'	1:A:435:A:O5'	2.15	0.61
11:K:70:PRO:HA	11:K:95:ALA:HB2	1.81	0.61
1:A:2710:C:N3	1:A:2754:G:O2'	2.32	0.61
1:A:963:A:OP2	1:A:2295:A:N6	2.34	0.60
1:A:335:U:HO2'	1:A:336:U:H6	1.48	0.60
1:A:1039:C:N3	8:H:4:THR:OG1	2.28	0.60
1:A:2433:C:OP1	1:A:2438:A:N6	2.34	0.60
2:B:64:A:N6	2:B:105:C:O5'	2.32	0.60
1:A:84:A:O5'	19:S:4:LYS:NZ	2.32	0.60
1:A:1185:U:OP2	8:H:66:THR:OG1	2.19	0.60
1:A:1462:G:N2	1:A:1463:A:N7	2.49	0.60
1:A:224:A:O2'	1:A:269:G:N7	2.33	0.60
1:A:672:A:N6	1:A:682:A:O4'	2.33	0.60
1:A:1486:C:O2	1:A:1598:U:N3	2.35	0.60
6:F:4:LEU:HD22	6:F:100:LEU:HD11	1.83	0.60
6:F:108:LEU:HD21	25:Y:56:PRO:HD2	1.84	0.60
7:G:157:TYR:O	7:G:171:ARG:NH1	2.35	0.60
1:A:124:A:O4'	28:2:15:LYS:NZ	2.34	0.60
1:A:1953:U:O2'	1:A:1954:A:N7	2.34	0.60
1:A:1963:A:N6	1:A:1990:C:O2	2.20	0.60
1:A:111:U:OP1	23:W:58:ARG:NH1	2.35	0.60
1:A:461:A:O2'	1:A:1892:U:O3'	2.19	0.60
1:A:621:A:OP1	1:A:1293:U:O2'	2.18	0.60
1:A:1874:A:N6	1:A:1876:G:O6	2.35	0.60
5:E:80:ALA:HB1	5:E:81:PRO:HD2	1.84	0.60
1:A:1533:A:N7	3:C:100:GLU:N	2.44	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:A:N6	1:A:101:G:H21	1.98	0.60
1:A:526:A:O2'	19:S:42:LYS:O	2.18	0.60
6:F:140:GLU:HB2	6:F:141:ILE:HD12	1.83	0.60
11:K:44:SER:HA	11:K:47:ILE:HD11	1.83	0.60
21:U:50:GLY:N	21:U:65:ASP:OD2	2.35	0.60
19:S:3:ILE:HD12	19:S:4:LYS:N	2.17	0.60
5:E:101:MET:O	5:E:106:ARG:NH1	2.35	0.59
1:A:7:G:O4'	8:H:136:GLN:NE2	2.35	0.59
1:A:78:U:O2	1:A:107:G:N2	2.24	0.59
1:A:2774:G:H2'	7:G:67:THR:HG22	1.84	0.59
3:C:141:VAL:HG12	3:C:192:ILE:HA	1.82	0.59
17:Q:36:LEU:O	17:Q:44:SER:OG	2.17	0.59
1:A:1712:A:H61	1:A:1720:A:H61	1.48	0.59
1:A:1952:C:N4	1:A:1956:G:H22	2.00	0.59
1:A:2496:A:C6	1:A:2508:G:N3	2.70	0.59
6:F:94:GLU:OE1	6:F:94:GLU:N	2.34	0.59
9:I:87:ILE:HD12	9:I:89:ASP:H	1.66	0.59
5:E:33:LEU:HD21	5:E:183:VAL:HG21	1.83	0.59
1:A:1081:G:N2	1:A:1163:U:O2'	2.36	0.59
1:A:1086:G:N2	1:A:1157:U:O2	2.36	0.59
1:A:1226:G:O2'	1:A:1227:U:O2	2.20	0.59
1:A:2771:G:O2'	7:G:149:ARG:NH1	2.35	0.59
3:C:179:GLY:O	3:C:274:ARG:NH1	2.35	0.59
1:A:522:G:N1	1:A:525:A:OP2	2.36	0.59
19:S:25:ALA:HB3	19:S:34:VAL:HG12	1.84	0.59
1:A:697:U:O2'	1:A:698:U:OP1	2.11	0.59
1:A:1085:U:C2	1:A:1158:G:O6	2.55	0.59
1:A:1257:G:O5'	15:O:19:LYS:NZ	2.36	0.59
1:A:1356:G:H21	1:A:1358:A:N6	2.01	0.59
1:A:1712:A:N6	1:A:1720:A:H61	2.01	0.59
1:A:2077:C:O2	4:D:169:MET:HE1	2.01	0.59
1:A:2113:U:O2	1:A:2261:G:C2	2.56	0.59
6:F:161:ASN:ND2	6:F:165:GLU:OE2	2.36	0.59
10:J:118:ASP:O	10:J:119:LYS:NZ	2.26	0.59
1:A:1076:A:N6	1:A:1163:U:O4	2.31	0.59
5:E:157:GLU:CD	5:E:197:ALA:HB3	2.28	0.59
7:G:2:SER:O	7:G:54:ARG:NH1	2.35	0.59
1:A:72:U:OP1	23:W:54:LYS:NZ	2.33	0.58
1:A:2306:G:N7	21:U:22:ARG:NH1	2.51	0.58
3:C:65:ILE:HD11	3:C:67:PHE:CE2	2.38	0.58
27:1:36:CYS:SG	27:1:45:HIS:NE2	2.75	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:751:A:H61	1:A:770:G:C1'	2.16	0.58
1:A:2593:A:N1	9:I:28:SER:OG	2.31	0.58
3:C:65:ILE:HD11	3:C:67:PHE:CD2	2.38	0.58
1:A:460:C:O4'	1:A:1890:G:N2	2.36	0.58
1:A:1173:A:O2'	1:A:2542:C:O2	2.20	0.58
1:A:1963:A:OP2	1:A:1989:C:N4	2.36	0.58
13:M:28:LYS:HB3	13:M:93:VAL:HG23	1.84	0.58
1:A:489:A:N6	1:A:1283:G:O2'	2.37	0.58
1:A:514:G:O2'	5:E:62:ARG:NH1	2.35	0.58
1:A:1764:A:N7	1:A:1765:A:N6	2.52	0.58
23:W:50:ILE:HA	23:W:53:LEU:HD12	1.86	0.58
13:M:44:ILE:O	13:M:53:LEU:N	2.35	0.58
27:1:9:CYS:SG	27:1:10:THR:N	2.76	0.58
1:A:69:C:O2'	1:A:70:G:OP1	2.19	0.58
1:A:1282:A:OP1	10:J:7:LYS:NZ	2.36	0.58
1:A:333:C:C4	1:A:393:G:C8	2.91	0.58
1:A:418:G:N7	22:V:56:SER:OG	2.26	0.58
1:A:427:A:OP1	22:V:18:ARG:NH2	2.36	0.58
10:J:87:ASP:OD1	10:J:120:LYS:N	2.36	0.58
1:A:1096:C:O2'	1:A:1151:G:N2	2.36	0.57
1:A:1301:U:OP1	26:Z:13:LYS:NZ	2.37	0.57
1:A:1385:G:H22	1:A:1642:C:H42	1.52	0.57
1:A:2785:A:N1	7:G:71:LEU:HD11	2.18	0.57
3:C:233:GLY:HA2	3:C:239:ALA:HB1	1.85	0.57
29:3:58:VAL:HB	29:3:61:LEU:HD12	1.85	0.57
1:A:1063:U:H3	1:A:1186:A:H62	1.52	0.57
1:A:1737:U:O2	3:C:14:ARG:NH2	2.37	0.57
1:A:2521:G:O2'	11:K:80:GLU:O	2.22	0.57
1:A:2618:C:C2	1:A:2630:G:N2	2.65	0.57
1:A:2774:G:OP1	7:G:138:LYS:NZ	2.31	0.57
2:B:77:G:O6	20:T:15:ARG:NH2	2.37	0.57
1:A:427:A:N6	1:A:433:U:O4	2.37	0.57
6:F:134:GLU:CB	6:F:137:ILE:HD11	2.34	0.57
9:I:49:GLY:O	9:I:53:LYS:NZ	2.36	0.57
21:U:44:ILE:C	21:U:45:LEU:HD23	2.28	0.57
1:A:310:C:O3'	1:A:405:G:N2	2.35	0.57
1:A:1397:G:N2	1:A:2241:C:C4	2.73	0.57
1:A:1466:G:N3	1:A:1535:G:N2	2.52	0.57
1:A:1887:G:N1	1:A:1909:C:N3	2.52	0.57
3:C:151:GLY:O	3:C:153:GLN:NE2	2.37	0.57
19:S:72:ASP:OD2	19:S:75:THR:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:G:O2'	1:A:236:A:N3	2.29	0.57
1:A:228:A:N6	1:A:465:C:O2'	2.38	0.57
1:A:351:G:O3'	19:S:15:LYS:NZ	2.34	0.57
1:A:1002:U:C2	11:K:17:THR:HG21	2.40	0.57
1:A:1489:A:P	1:A:1492:G:H22	2.28	0.57
1:A:1832:C:OP1	3:C:252:LYS:NZ	2.31	0.57
1:A:2104:A:OP1	1:A:2265:G:N2	2.34	0.57
1:A:2807:G:OP1	8:H:121:LYS:NZ	2.26	0.57
1:A:332:A:O5'	1:A:393:G:N2	2.38	0.57
1:A:1079:U:O2	1:A:1164:G:C6	2.58	0.57
1:A:1173:A:N1	1:A:2596:G:O2'	2.36	0.57
20:T:4:LEU:HD23	20:T:5:LYS:H	1.69	0.57
3:C:100:GLU:OE1	3:C:101:LYS:N	2.38	0.57
1:A:13:A:O2'	1:A:15:G:N7	2.37	0.57
1:A:678:A:OP1	10:J:71:ARG:NE	2.31	0.57
1:A:681:G:O6	10:J:110:LYS:NZ	2.37	0.57
1:A:795:A:OP1	1:A:1659:C:N4	2.38	0.57
1:A:2093:C:N4	1:A:2094:G:O6	2.38	0.57
1:A:2285:C:O2'	1:A:2454:C:OP2	2.21	0.57
1:A:2511:G:OP1	11:K:45:ARG:NH2	2.38	0.57
3:C:204:ASN:OD1	3:C:205:VAL:N	2.36	0.57
5:E:195:THR:OG1	5:E:196:GLU:N	2.37	0.57
9:I:115:VAL:HG13	9:I:121:VAL:HG21	1.86	0.57
1:A:2342:U:H5''	13:M:2:ILE:HD12	1.86	0.57
1:A:2710:C:OP1	14:N:53:ARG:NH2	2.38	0.57
1:A:2672:G:HO2'	1:A:2673:C:P	2.26	0.56
19:S:33:VAL:O	19:S:63:ILE:N	2.38	0.56
1:A:1458:A:H2	1:A:1631:G:H21	1.52	0.56
1:A:2113:U:N3	1:A:2261:G:N1	2.52	0.56
17:Q:65:ASN:ND2	17:Q:67:ASP:OD1	2.39	0.56
1:A:1957:G:N2	1:A:1958:U:O4	2.34	0.56
1:A:2682:G:O2'	1:A:2691:G:O6	2.09	0.56
3:C:223:SER:O	3:C:239:ALA:HB2	2.06	0.56
14:N:31:HIS:NE2	14:N:87:GLU:OE2	2.37	0.56
18:R:82:LEU:HD12	18:R:83:LYS:N	2.21	0.56
1:A:1956:G:O2'	1:A:1957:G:OP2	2.20	0.56
1:A:2485:U:O2'	1:A:2487:U:O4	2.15	0.56
3:C:27:THR:O	3:C:27:THR:OG1	2.18	0.56
18:R:84:GLU:OE1	18:R:84:GLU:N	2.38	0.56
1:A:2769:G:N2	1:A:2789:U:O2	2.35	0.56
3:C:168:GLU:N	3:C:168:GLU:OE1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:14:GLN:HB2	4:D:22:LEU:HD11	1.88	0.56
19:S:66:SER:O	19:S:66:SER:OG	2.21	0.56
1:A:1467:G:H21	1:A:1542:C:C4'	2.19	0.56
24:X:5:GLN:HB2	24:X:36:VAL:HG22	1.87	0.56
1:A:332:A:N6	1:A:395:U:O2	2.39	0.56
1:A:2499:G:H2'	1:A:2505:A:H61	1.69	0.56
1:A:2649:U:O3'	1:A:2845:G:N2	2.33	0.56
3:C:254:THR:O	3:C:254:THR:OG1	2.24	0.56
17:Q:25:ARG:NH1	17:Q:74:ALA:O	2.35	0.56
23:W:6:ILE:HG23	23:W:9:LEU:HD12	1.88	0.56
1:A:2380:G:N2	21:U:42:GLY:O	2.33	0.56
1:A:2662:U:O2'	4:D:50:GLN:NE2	2.39	0.56
1:A:2830:A:H62	1:A:2910:G:N2	2.04	0.56
15:O:59:LYS:HA	15:O:62:ILE:HD12	1.88	0.56
17:Q:103:ILE:HD12	17:Q:104:VAL:N	2.21	0.56
18:R:24:LYS:HG2	18:R:81:THR:HG23	1.88	0.56
1:A:1073:A:H61	1:A:1169:G:H1'	1.70	0.55
1:A:1086:G:N1	1:A:1157:U:C2	2.74	0.55
19:S:89:LYS:O	19:S:91:VAL:HG13	2.06	0.55
1:A:193:A:H61	1:A:210:A:H1'	1.70	0.55
1:A:2359:C:OP1	21:U:54:TYR:OH	2.25	0.55
4:D:81:ASP:N	4:D:81:ASP:OD1	2.36	0.55
4:D:87:PHE:C	4:D:88:ILE:HD12	2.31	0.55
14:N:27:THR:C	14:N:28:LEU:HD12	2.31	0.55
1:A:1869:G:C6	1:A:1925:U:O2	2.59	0.55
4:D:27:VAL:HG11	14:N:7:ILE:HD11	1.89	0.55
1:A:315:C:O2	1:A:317:G:N2	2.40	0.55
1:A:320:U:OP1	1:A:323:C:N4	2.40	0.55
1:A:926:G:H21	1:A:941:A:H62	1.55	0.55
1:A:2048:G:OP1	26:Z:9:SER:OG	2.17	0.55
1:A:2896:A:OP1	14:N:3:ASN:ND2	2.40	0.55
2:B:32:U:O2'	2:B:42:G:N7	2.34	0.55
9:I:114:ILE:HA	9:I:117:LEU:HD12	1.87	0.55
1:A:458:A:OP2	1:A:2433:C:N4	2.39	0.55
1:A:928:C:N4	1:A:937:G:OP1	2.40	0.55
1:A:1187:A:OP1	8:H:28:ARG:NH1	2.39	0.55
27:1:22:ASN:O	27:1:26:ASN:N	2.39	0.55
1:A:1039:C:O2	15:O:93:LYS:NZ	2.32	0.55
1:A:1086:G:C2	1:A:1157:U:O2	2.60	0.55
1:A:1080:G:H1	1:A:1163:U:HO2'	1.55	0.55
1:A:2276:U:N3	1:A:2280:G:OP2	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:60:GLY:HA2	5:E:78:ILE:HG22	1.87	0.55
29:3:31:HIS:CG	29:3:32:LEU:HD23	2.42	0.55
1:A:227:G:N2	1:A:235:G:H21	2.05	0.55
1:A:1302:G:N1	1:A:2041:A:OP2	2.38	0.55
1:A:2374:C:O3'	27:1:17:TYR:OH	2.18	0.55
1:A:2774:G:N7	30:4:19:ARG:NE	2.55	0.55
19:S:70:LEU:HD23	19:S:71:LEU:H	1.71	0.55
21:U:72:ASP:N	21:U:72:ASP:OD1	2.38	0.55
1:A:1103:G:O6	1:A:1124:A:N6	2.39	0.55
2:B:53:U:O2'	2:B:54:U:O4'	2.24	0.55
1:A:751:A:H61	1:A:770:G:C2'	2.20	0.55
1:A:2558:A:OP1	7:G:176:THR:OG1	2.25	0.55
1:A:2612:U:O2'	1:A:2613:C:OP2	2.19	0.55
10:J:55:LEU:HD23	10:J:60:ARG:HG2	1.88	0.55
1:A:1520:A:H62	1:A:1562:C:C1'	2.19	0.54
1:A:1931:G:O2'	1:A:1955:A:N1	2.31	0.54
9:I:81:GLU:OE1	9:I:81:GLU:N	2.39	0.54
1:A:790:G:N2	1:A:795:A:N6	2.40	0.54
1:A:11:U:O2'	1:A:12:U:OP1	2.21	0.54
1:A:1134:U:O4	1:A:1145:U:N3	2.41	0.54
1:A:1579:C:O2	1:A:1580:A:N6	2.31	0.54
1:A:1715:U:O2'	1:A:1717:G:N7	2.34	0.54
11:K:38:THR:HG22	11:K:39:THR:H	1.71	0.54
1:A:1448:U:O2	1:A:1450:A:N6	2.40	0.54
1:A:2129:C:H42	1:A:2213:U:H3'	1.72	0.54
1:A:2558:A:OP2	7:G:176:THR:N	2.40	0.54
2:B:52:G:N2	6:F:26:MET:SD	2.77	0.54
3:C:185:LEU:HD13	3:C:186:SER:N	2.23	0.54
13:M:110:GLU:OE2	13:M:113:ARG:NH1	2.40	0.54
1:A:625:G:OP1	15:O:14:ARG:NH1	2.41	0.54
1:A:2374:C:C3'	27:1:17:TYR:HH	2.19	0.54
1:A:2546:U:O4'	1:A:2569:A:N6	2.40	0.54
1:A:333:C:N3	1:A:393:G:C2'	2.70	0.54
1:A:1466:G:H2'	1:A:1467:G:C8	2.43	0.54
1:A:2052:C:HO2'	1:A:2053:U:H5'	1.73	0.54
1:A:2397:G:O2'	27:1:35:TYR:OH	2.25	0.54
1:A:94:A:OP2	1:A:95:A:N6	2.41	0.54
1:A:1869:G:O6	1:A:1925:U:C2	2.60	0.54
1:A:2815:C:O2'	1:A:2829:A:N3	2.37	0.54
4:D:184:GLU:OE1	4:D:185:VAL:N	2.41	0.54
6:F:33:LYS:C	6:F:34:ILE:HD12	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:99:GLN:OE1	7:G:104:ILE:HD11	2.07	0.54
17:Q:52:MET:N	17:Q:52:MET:SD	2.81	0.54
1:A:652:A:N6	1:A:664:G:O2'	2.33	0.54
1:A:1884:G:O2'	1:A:1912:A:N6	2.38	0.54
6:F:30:LYS:NZ	6:F:31:ILE:O	2.40	0.54
1:A:1265:G:N7	15:O:16:LYS:NZ	2.56	0.54
1:A:2026:C:OP1	4:D:132:LYS:NZ	2.41	0.54
2:B:73:G:O2'	20:T:88:HIS:NE2	2.32	0.54
4:D:6:LEU:HD12	4:D:53:PHE:HB2	1.89	0.54
8:H:74:VAL:HG23	8:H:76:TYR:HE2	1.72	0.54
1:A:47:C:N4	1:A:48:G:O6	2.41	0.54
1:A:447:A:H61	1:A:468:A:H61	1.55	0.54
1:A:922:G:H22	1:A:945:A:H2	1.54	0.54
1:A:1459:A:N6	1:A:1631:G:O4'	2.41	0.54
10:J:111:ILE:O	10:J:112:LEU:HD23	2.07	0.54
11:K:41:TRP:C	11:K:42:ILE:HD12	2.32	0.54
13:M:14:ARG:O	13:M:18:VAL:HG23	2.07	0.54
1:A:250:G:O6	29:3:12:LYS:NZ	2.26	0.53
1:A:443:U:O3'	22:V:32:ASN:ND2	2.41	0.53
1:A:527:G:O2'	1:A:552:A:N6	2.41	0.53
1:A:529:A:O5'	19:S:46:LYS:NZ	2.40	0.53
1:A:2618:C:N3	1:A:2630:G:N1	2.51	0.53
14:N:55:GLY:O	14:N:58:SER:OG	2.24	0.53
1:A:2555:U:OP1	7:G:172:LYS:NZ	2.18	0.53
1:A:2680:U:N3	7:G:110:SER:OG	2.41	0.53
1:A:2878:U:O2'	1:A:2879:G:OP1	2.23	0.53
3:C:65:ILE:HD12	3:C:66:ASP:N	2.23	0.53
4:D:104:GLU:N	4:D:104:GLU:OE1	2.42	0.53
1:A:333:C:C6	1:A:393:G:C4	2.95	0.53
1:A:2354:A:N7	1:A:2415:A:N6	2.56	0.53
2:B:4:G:O6	2:B:111:C:N4	2.41	0.53
6:F:66:LEU:HD13	25:Y:5:ILE:HG21	1.91	0.53
1:A:970:U:H3'	1:A:971:U:H4'	1.90	0.53
2:B:42:G:O4'	2:B:45:C:N4	2.42	0.53
29:3:22:LEU:O	29:3:49:LEU:HD23	2.08	0.53
1:A:1261:G:N2	1:A:1264:A:OP2	2.40	0.53
1:A:1465:G:C2'	1:A:1537:A:H62	2.22	0.53
1:A:1504:U:O2'	1:A:1505:G:OP2	2.26	0.53
1:A:1697:G:O6	12:L:7:GLY:N	2.40	0.53
1:A:736:C:O4'	3:C:43:ARG:NH2	2.40	0.53
1:A:564:U:O2'	17:Q:73:GLU:OE2	2.25	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:797:A:OP1	28:2:4:ARG:NH2	2.40	0.53
1:A:1561:G:O4'	1:A:1604:C:O2'	2.26	0.53
1:A:1935:C:N3	1:A:1949:G:N1	2.47	0.53
4:D:10:ILE:HG12	4:D:27:VAL:HG13	1.90	0.53
1:A:388:A:O2'	1:A:390:A:N6	2.40	0.53
1:A:2566:C:O2'	1:A:2768:A:O2'	2.25	0.53
4:D:9:LYS:NZ	4:D:203:GLY:O	2.40	0.53
12:L:109:ARG:NH2	12:L:112:ASP:OD2	2.41	0.53
29:3:37:SER:O	29:3:41:LYS:NZ	2.39	0.53
1:A:632:U:O3'	5:E:95:ARG:NH1	2.42	0.53
1:A:699:U:O2'	1:A:700:A:O5'	2.26	0.53
1:A:1395:G:O2'	1:A:1410:A:N6	2.39	0.53
1:A:2324:C:C2	1:A:2348:G:N2	2.77	0.53
1:A:2495:A:N7	1:A:2504:C:C4	2.77	0.53
1:A:1088:C:N4	1:A:1156:G:O6	2.42	0.52
1:A:2674:U:O4	1:A:2700:G:O6	2.26	0.52
13:M:28:LYS:CB	13:M:93:VAL:HG23	2.39	0.52
18:R:34:ASN:OD1	18:R:36:THR:N	2.42	0.52
23:W:61:GLU:OE1	23:W:61:GLU:N	2.42	0.52
1:A:688:A:O2'	1:A:689:A:O4'	2.28	0.52
1:A:750:A:H61	1:A:771:G:C4'	2.22	0.52
1:A:2141:A:N3	1:A:2193:G:O2'	2.42	0.52
6:F:99:PHE:CE2	6:F:103:LEU:HD22	2.44	0.52
17:Q:66:THR:HA	17:Q:69:LEU:HD12	1.91	0.52
1:A:791:U:H1'	1:A:793:G:H21	1.74	0.52
1:A:1723:A:O4'	1:A:2017:C:O2'	2.25	0.52
1:A:2496:A:N6	1:A:2508:G:N9	2.57	0.52
1:A:2778:G:H21	1:A:2778:G:P	2.32	0.52
7:G:23:HIS:NE2	7:G:34:SER:OG	2.33	0.52
27:1:29:ARG:NH2	27:1:47:GLU:O	2.41	0.52
1:A:1018:A:O4'	1:A:1225:G:N2	2.43	0.52
1:A:1080:G:N1	1:A:1164:G:N7	2.57	0.52
5:E:21:ASP:O	5:E:25:GLY:N	2.38	0.52
8:H:37:LEU:HD11	8:H:119:GLN:HB3	1.91	0.52
18:R:6:ILE:CG1	18:R:7:LEU:HD12	2.40	0.52
1:A:302:A:N7	1:A:450:C:O2'	2.40	0.52
1:A:904:G:O2'	1:A:961:G:O6	2.24	0.52
1:A:1981:G:O2'	1:A:1983:U:O4	2.13	0.52
1:A:2417:U:N3	1:A:2452:A:N7	2.57	0.52
1:A:2662:U:O2'	4:D:90:GLU:OE2	2.11	0.52
1:A:2706:A:N3	4:D:200:ASN:ND2	2.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:44:ASN:O	3:C:47:GLY:N	2.41	0.52
5:E:157:GLU:OE2	5:E:195:THR:OG1	2.23	0.52
1:A:352:A:N6	1:A:1248:U:C2	2.68	0.52
1:A:1965:A:N3	1:A:2632:U:O2'	2.40	0.52
1:A:2125:U:C2	1:A:2218:G:N1	2.69	0.52
1:A:2783:U:O2'	1:A:2783:U:O2	2.28	0.52
1:A:84:A:C5	1:A:101:G:N2	2.78	0.52
1:A:616:G:N2	1:A:2058:A:OP1	2.43	0.52
9:I:17:ARG:NH2	9:I:46:ALA:O	2.41	0.52
15:O:99:ALA:HB2	15:O:106:PHE:HE1	1.75	0.52
1:A:207:A:O2'	1:A:208:G:OP2	2.27	0.52
1:A:1336:G:N1	1:A:1684:A:OP2	2.40	0.52
1:A:1400:C:O2'	1:A:1836:A:N3	2.43	0.52
1:A:1482:U:OP2	1:A:1600:A:O2'	2.27	0.52
1:A:333:C:C2	1:A:393:G:C2'	2.93	0.52
1:A:2905:C:H42	26:Z:37:LYS:NZ	2.08	0.52
5:E:77:THR:OG1	5:E:78:ILE:N	2.42	0.52
6:F:30:LYS:O	6:F:159:THR:OG1	2.21	0.52
6:F:108:LEU:HD21	25:Y:56:PRO:CD	2.40	0.52
23:W:45:THR:HG23	23:W:46:VAL:CG2	2.39	0.52
1:A:2774:G:N2	1:A:2784:A:N1	2.58	0.52
1:A:2822:C:O2'	1:A:2824:G:O6	2.11	0.52
13:M:36:SER:OG	13:M:37:ASN:N	2.41	0.52
15:O:116:ALA:C	15:O:117:LEU:HD23	2.35	0.52
18:R:24:LYS:CG	18:R:81:THR:HG23	2.40	0.52
1:A:1072:A:H62	1:A:1170:A:H62	1.57	0.51
1:A:1385:G:N2	1:A:1642:C:H42	2.08	0.51
1:A:1470:G:O2'	1:A:1619:A:N6	2.37	0.51
1:A:1496:G:HO2'	1:A:1497:A:C5'	2.22	0.51
1:A:2421:C:H42	1:A:2459:A:H62	1.57	0.51
1:A:2817:A:N7	1:A:2822:C:O2'	2.43	0.51
7:G:33:LEU:HD11	7:G:136:ILE:HG13	1.91	0.51
19:S:7:ASP:O	19:S:23:VAL:HG12	2.09	0.51
20:T:22:ARG:NE	20:T:87:THR:O	2.36	0.51
1:A:2907:A:H1'	26:Z:28:THR:HG22	1.93	0.51
4:D:14:GLN:OE1	4:D:14:GLN:N	2.43	0.51
10:J:120:LYS:C	10:J:121:LEU:HD23	2.35	0.51
23:W:7:ARG:O	23:W:60:ARG:NH1	2.43	0.51
1:A:75:G:H22	1:A:110:A:H2	1.58	0.51
1:A:2019:G:N2	1:A:2023:C:O2'	2.42	0.51
4:D:11:GLY:O	4:D:27:VAL:HG12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:18:ARG:NH2	12:L:64:LYS:O	2.43	0.51
1:A:1675:G:H1'	1:A:1679:A:H61	1.75	0.51
1:A:2092:C:H5'	1:A:2278:G:H21	1.75	0.51
11:K:43:THR:OG1	11:K:46:GLN:OE1	2.25	0.51
12:L:72:LEU:HD21	12:L:76:GLU:HA	1.92	0.51
16:P:68:GLY:O	16:P:89:ARG:NE	2.41	0.51
1:A:1880:A:N6	1:A:2114:G:HO2'	2.09	0.51
1:A:2702:A:N6	1:A:2759:G:N1	2.57	0.51
3:C:159:GLY:H	3:C:195:VAL:HG23	1.75	0.51
9:I:24:VAL:HG11	9:I:33:ALA:HB2	1.92	0.51
9:I:112:MET:SD	9:I:113:LYS:N	2.81	0.51
28:2:33:ALA:O	28:2:37:ARG:N	2.43	0.51
1:A:254:A:OP1	29:3:7:HIS:NE2	2.41	0.51
1:A:1710:G:OP1	9:I:66:LYS:NZ	2.44	0.51
1:A:2418:G:O2'	1:A:2419:A:OP2	2.22	0.51
5:E:117:LYS:CD	5:E:192:LEU:HD23	2.40	0.51
17:Q:28:ASN:N	17:Q:28:ASN:OD1	2.44	0.51
1:A:1592:A:O2'	1:A:1593:G:O4'	2.28	0.51
16:P:31:ASP:N	16:P:31:ASP:OD1	2.44	0.51
18:R:90:PHE:HD2	23:W:34:THR:HG21	1.74	0.51
25:Y:38:GLU:OE1	25:Y:38:GLU:N	2.43	0.51
5:E:138:GLU:O	5:E:142:VAL:HG23	2.10	0.51
8:H:34:ALA:HB1	8:H:110:LEU:HD21	1.92	0.51
8:H:123:LEU:HD12	8:H:124:PHE:H	1.76	0.51
1:A:84:A:C6	1:A:101:G:N2	2.73	0.51
1:A:297:G:O2'	1:A:298:U:O5'	2.27	0.51
1:A:1293:U:N3	5:E:72:ARG:O	2.41	0.51
12:L:59:ARG:CD	12:L:82:LEU:HD21	2.41	0.51
1:A:81:G:H1	1:A:104:C:H42	1.56	0.51
1:A:1213:C:N4	1:A:1219:G:H22	2.09	0.51
1:A:1396:A:OP2	1:A:1408:G:N1	2.43	0.51
1:A:1731:G:H21	1:A:1745:A:H62	1.57	0.51
1:A:2479:C:N3	1:A:2531:U:O4	2.44	0.51
1:A:252:C:O2'	10:J:63:LYS:NZ	2.21	0.50
1:A:1251:A:OP2	1:A:1274:G:N2	2.38	0.50
1:A:2324:C:C2	1:A:2348:G:N1	2.79	0.50
1:A:2499:G:H21	1:A:2505:A:N6	2.08	0.50
1:A:2555:U:O2'	1:A:2557:U:OP1	2.25	0.50
2:B:7:G:H1'	2:B:110:C:H42	1.76	0.50
1:A:23:G:H21	17:Q:77:ASN:ND2	2.08	0.50
1:A:1891:U:C5'	1:A:2437:G:H21	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:45:GLN:O	6:F:45:GLN:NE2	2.42	0.50
6:F:162:THR:OG1	6:F:163:ASP:N	2.44	0.50
8:H:9:GLU:HA	8:H:12:ILE:HD11	1.92	0.50
1:A:909:G:N7	11:K:22:LYS:NZ	2.57	0.50
1:A:1833:C:OP1	3:C:250:TRP:NE1	2.39	0.50
1:A:1891:U:H5'	1:A:2437:G:H21	1.76	0.50
1:A:774:G:O4'	3:C:207:LYS:NZ	2.42	0.50
1:A:1613:G:OP1	3:C:210:ARG:NE	2.43	0.50
7:G:146:SER:O	7:G:149:ARG:NH1	2.43	0.50
8:H:63:ILE:O	8:H:94:ARG:NH2	2.44	0.50
12:L:22:THR:HG21	12:L:69:VAL:HG21	1.92	0.50
1:A:1490:G:N2	1:A:1490:G:OP1	2.45	0.50
1:A:1864:C:O3'	1:A:1954:A:O2'	2.23	0.50
1:A:2499:G:N2	1:A:2506:U:O4	2.45	0.50
4:D:47:ASN:OD1	4:D:47:ASN:N	2.45	0.50
21:U:58:ASN:N	21:U:58:ASN:OD1	2.43	0.50
7:G:99:GLN:N	7:G:102:ASP:O	2.40	0.50
9:I:70:ARG:NH1	9:I:76:TYR:OH	2.44	0.50
1:A:1035:C:HO2'	16:P:84:ARG:NH1	2.08	0.50
1:A:2102:U:OP2	1:A:2265:G:O2'	2.27	0.50
5:E:9:LEU:HD11	5:E:129:PHE:HD1	1.77	0.50
12:L:33:THR:OG1	12:L:34:GLU:N	2.44	0.50
15:O:82:GLY:HA2	15:O:117:LEU:HD21	1.92	0.50
1:A:1401:G:N2	1:A:1404:A:OP2	2.39	0.50
1:A:1472:C:N4	1:A:1617:A:OP2	2.25	0.50
1:A:1879:U:O2	1:A:1916:A:N7	2.44	0.50
3:C:134:ASN:N	3:C:134:ASN:OD1	2.45	0.50
5:E:33:LEU:HD21	5:E:183:VAL:CG2	2.42	0.50
9:I:17:ARG:NH2	9:I:45:ASN:OD1	2.45	0.50
1:A:163:U:O2'	1:A:164:A:OP2	2.25	0.50
1:A:583:A:O2'	8:H:8:ASN:OD1	2.26	0.50
1:A:1353:A:O4'	1:A:1429:G:N2	2.41	0.50
1:A:1397:G:N2	1:A:2241:C:N3	2.59	0.50
1:A:2749:G:O2'	1:A:2750:C:OP1	2.26	0.50
12:L:72:LEU:HD22	12:L:77:THR:O	2.11	0.50
15:O:35:ALA:O	15:O:39:VAL:HG23	2.12	0.50
1:A:340:C:OP1	19:S:90:LYS:NZ	2.31	0.49
1:A:1889:G:C6	1:A:1907:U:N3	2.79	0.49
4:D:189:ASP:OD1	4:D:190:THR:N	2.45	0.49
17:Q:48:GLU:OE1	17:Q:49:LYS:N	2.44	0.49
1:A:2669:G:OP2	8:H:86:LYS:NZ	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:64:A:H1'	2:B:66:C:H41	1.77	0.49
5:E:123:LEU:HD12	5:E:124:THR:N	2.28	0.49
10:J:125:ALA:O	10:J:146:ILE:N	2.44	0.49
1:A:245:G:O2'	1:A:257:G:O6	2.27	0.49
1:A:1465:G:H2'	1:A:1537:A:H62	1.77	0.49
1:A:2739:U:OP1	1:A:2741:G:O2'	2.26	0.49
4:D:213:THR:HG22	4:D:214:SER:O	2.12	0.49
6:F:50:LEU:O	6:F:54:VAL:HG23	2.11	0.49
6:F:142:ASP:OD1	6:F:143:TYR:N	2.42	0.49
6:F:156:ILE:CG2	6:F:158:THR:HG23	2.42	0.49
9:I:20:LEU:HD12	9:I:21:THR:N	2.28	0.49
1:A:434:G:HO2'	1:A:435:A:P	2.34	0.49
1:A:1302:G:O2'	1:A:2042:A:N6	2.34	0.49
1:A:1067:U:O2'	1:A:1166:G:OP1	2.29	0.49
1:A:1467:G:O5'	1:A:1535:G:O2'	2.26	0.49
2:B:40:C:C1'	6:F:66:LEU:HD22	2.43	0.49
6:F:148:LYS:NZ	6:F:149:VAL:O	2.46	0.49
1:A:673:G:O2'	1:A:696:G:O2'	2.31	0.49
1:A:2780:A:H2	30:4:17:ILE:HG21	1.72	0.49
5:E:121:ASN:OD1	5:E:121:ASN:N	2.45	0.49
1:A:1175:G:O2'	1:A:2052:C:O2'	2.24	0.49
1:A:1198:G:OP2	15:O:58:ARG:NH2	2.44	0.49
4:D:9:LYS:NZ	4:D:201:VAL:O	2.45	0.49
14:N:107:GLY:O	14:N:110:ALA:N	2.45	0.49
1:A:1091:G:N1	1:A:1154:G:O2'	2.33	0.49
1:A:1885:G:N2	1:A:1911:A:OP2	2.45	0.49
1:A:1952:C:H42	1:A:1956:G:N2	2.11	0.49
1:A:2185:A:O2'	1:A:2186:G:O5'	2.28	0.49
1:A:2770:U:O5'	1:A:2782:C:N4	2.46	0.49
3:C:205:VAL:HG13	3:C:210:ARG:HD3	1.94	0.49
6:F:117:VAL:HG13	6:F:175:MET:HE2	1.94	0.49
23:W:19:LYS:NZ	23:W:23:GLU:OE2	2.45	0.49
1:A:82:G:N1	1:A:101:G:O3'	2.43	0.49
1:A:302:A:O2'	1:A:303:G:N7	2.27	0.49
1:A:333:C:N1	1:A:393:G:C4	2.81	0.49
3:C:160:ALA:H	3:C:195:VAL:HG22	1.78	0.49
11:K:57:TYR:CD2	11:K:117:ALA:HB2	2.48	0.49
1:A:1448:U:C4	1:A:1635:A:N1	2.80	0.49
1:A:1731:G:N2	1:A:1745:A:H62	2.10	0.49
1:A:2189:G:O2'	1:A:2200:A:N7	2.40	0.49
1:A:2557:U:O2'	1:A:2561:C:N4	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:108:LYS:N	3:C:194:GLN:O	2.41	0.49
3:C:123:ASP:OD1	3:C:125:LYS:NZ	2.42	0.49
17:Q:86:ARG:O	17:Q:92:SER:OG	2.29	0.49
1:A:82:G:H22	1:A:102:A:P	2.35	0.48
1:A:1000:G:OP2	11:K:87:LYS:NZ	2.46	0.48
1:A:2161:A:H61	1:A:2184:G:C2'	2.25	0.48
1:A:2672:G:H1	1:A:2797:C:H42	1.60	0.48
6:F:8:PHE:O	6:F:12:VAL:HG22	2.13	0.48
7:G:111:HIS:O	7:G:113:VAL:HG13	2.12	0.48
13:M:73:ALA:HB1	13:M:108:LEU:HB2	1.95	0.48
17:Q:1:MET:SD	17:Q:1:MET:N	2.85	0.48
1:A:2703:C:O2	1:A:2759:G:N2	2.43	0.48
8:H:142:GLU:N	8:H:142:GLU:OE1	2.46	0.48
9:I:35:ILE:HD11	9:I:65:THR:H	1.77	0.48
18:R:47:ASN:O	18:R:47:ASN:ND2	2.46	0.48
1:A:672:A:O2'	1:A:681:G:N2	2.42	0.48
1:A:749:G:N2	1:A:772:A:N6	2.43	0.48
1:A:751:A:H61	1:A:770:G:H1'	1.77	0.48
1:A:1518:G:HO2'	1:A:1519:U:H6	1.60	0.48
3:C:77:LYS:N	3:C:95:VAL:O	2.46	0.48
15:O:108:GLN:O	15:O:111:THR:OG1	2.29	0.48
1:A:2361:U:O4	1:A:2363:A:C5	2.66	0.48
6:F:110:ARG:O	6:F:135:GLN:NE2	2.47	0.48
7:G:72:LEU:O	7:G:76:VAL:HG22	2.14	0.48
21:U:58:ASN:O	21:U:70:LYS:N	2.42	0.48
1:A:19:G:OP1	15:O:23:GLY:N	2.42	0.48
1:A:392:U:N3	1:A:393:G:O6	2.47	0.48
1:A:918:G:N7	11:K:2:LEU:HD23	2.28	0.48
1:A:1501:G:N2	1:A:2729:G:H22	2.09	0.48
1:A:2044:C:HO2'	26:Z:6:ARG:HH11	1.60	0.48
1:A:2559:G:N3	1:A:2690:G:N2	2.57	0.48
5:E:111:ARG:HG2	5:E:206:LEU:HD23	1.95	0.48
21:U:39:VAL:HG22	21:U:73:GLY:O	2.12	0.48
1:A:616:G:O2'	1:A:618:A:OP1	2.20	0.48
1:A:821:C:O2'	1:A:822:G:OP1	2.28	0.48
1:A:973:A:O2'	24:X:40:ASN:ND2	2.47	0.48
1:A:1396:A:N7	1:A:1409:U:O4	2.46	0.48
1:A:1881:A:N1	1:A:2114:G:O2'	2.32	0.48
1:A:2281:C:H42	21:U:15:VAL:CG2	2.26	0.48
5:E:201:LYS:O	5:E:205:VAL:HG23	2.13	0.48
17:Q:55:LEU:CD2	17:Q:105:VAL:HG11	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:513:G:OP1	28:2:34:ARG:NH2	2.47	0.48
1:A:2421:C:N4	1:A:2459:A:H62	2.10	0.48
1:A:2485:U:O2	1:A:2486:A:N6	2.45	0.48
1:A:2784:A:N1	7:G:67:THR:HG21	2.28	0.48
3:C:144:ILE:HG23	3:C:190:ALA:HB2	1.95	0.48
18:R:34:ASN:N	18:R:37:GLN:OE1	2.45	0.48
1:A:390:A:H3'	1:A:391:A:H4'	1.96	0.48
1:A:2559:G:N2	1:A:2690:G:N3	2.62	0.48
8:H:123:LEU:HD12	8:H:124:PHE:N	2.28	0.48
12:L:24:LEU:HD13	12:L:24:LEU:C	2.38	0.48
15:O:62:ILE:HG23	15:O:76:TYR:CE1	2.49	0.48
1:A:311:U:O2	1:A:405:G:O2'	2.13	0.48
1:A:364:A:OP2	5:E:135:LYS:NZ	2.39	0.48
1:A:774:G:O5'	3:C:207:LYS:NZ	2.47	0.48
1:A:882:C:H5	1:A:986:G:H22	1.61	0.48
1:A:2171:G:N2	1:A:2174:A:N7	2.62	0.48
5:E:170:ILE:HG22	5:E:171:PRO:O	2.13	0.48
12:L:59:ARG:HD2	12:L:82:LEU:HD21	1.96	0.48
27:1:14:ASP:OD1	27:1:14:ASP:N	2.46	0.48
1:A:545:G:N1	1:A:548:A:OP2	2.43	0.47
1:A:1083:G:N2	1:A:1160:C:C2	2.63	0.47
1:A:1290:G:O4'	15:O:33:LYS:NZ	2.25	0.47
1:A:1892:U:P	1:A:2436:G:H21	2.36	0.47
1:A:2780:A:O2'	30:4:26:ILE:HG21	2.14	0.47
5:E:37:ILE:HG23	5:E:184:LEU:CD1	2.43	0.47
5:E:123:LEU:HD12	5:E:124:THR:H	1.77	0.47
29:3:63:ALA:HB3	29:3:64:TYR:CD2	2.49	0.47
1:A:223:G:N1	1:A:474:A:OP2	2.44	0.47
1:A:915:U:OP1	11:K:6:ARG:NH1	2.47	0.47
1:A:2024:A:OP1	4:D:137:SER:OG	2.32	0.47
6:F:130:LEU:HD23	6:F:131:GLY:N	2.29	0.47
30:4:31:LYS:O	30:4:32:HIS:ND1	2.47	0.47
1:A:40:U:O4	1:A:41:A:N6	2.47	0.47
1:A:1536:C:O2'	1:A:1537:A:N7	2.43	0.47
1:A:1731:G:H21	1:A:1745:A:N6	2.11	0.47
8:H:45:TYR:O	15:O:64:ARG:NH2	2.41	0.47
9:I:21:THR:OG1	9:I:22:ILE:N	2.48	0.47
13:M:73:ALA:O	13:M:108:LEU:HD13	2.14	0.47
19:S:38:VAL:N	19:S:60:GLU:OE1	2.47	0.47
24:X:4:LEU:HD23	24:X:58:GLU:HA	1.96	0.47
1:A:323:C:O2	1:A:324:A:N6	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1339:U:HO2'	1:A:1340:G:P	2.37	0.47
6:F:31:ILE:HA	6:F:158:THR:HG22	1.97	0.47
6:F:134:GLU:HB2	6:F:137:ILE:HD11	1.95	0.47
23:W:14:ILE:HG22	23:W:18:ILE:HD11	1.96	0.47
3:C:2:ALA:N	3:C:20:ASP:OD1	2.47	0.47
4:D:3:LYS:HE3	4:D:109:THR:HG22	1.96	0.47
9:I:111:PHE:O	9:I:114:ILE:N	2.47	0.47
26:Z:18:THR:HG23	26:Z:19:HIS:H	1.79	0.47
1:A:1320:G:N2	1:A:1323:A:OP2	2.47	0.47
1:A:2125:U:N3	1:A:2218:G:C6	2.77	0.47
1:A:2338:A:OP1	1:A:2340:C:N4	2.45	0.47
1:A:2710:C:H42	1:A:2754:G:C2'	2.28	0.47
3:C:66:ASP:N	3:C:66:ASP:OD1	2.47	0.47
4:D:83:ALA:HB1	4:D:84:PRO:CD	2.45	0.47
9:I:3:GLN:O	9:I:6:THR:OG1	2.30	0.47
16:P:1:MET:HE2	16:P:43:GLY:HA2	1.96	0.47
26:Z:28:THR:HG21	26:Z:39:SER:OG	2.15	0.47
1:A:1034:A:O2'	1:A:1036:C:OP2	2.32	0.47
1:A:1726:A:P	1:A:1743:G:H22	2.37	0.47
2:B:74:G:OP1	20:T:9:ARG:NH2	2.47	0.47
6:F:104:ILE:HD12	6:F:173:PHE:CB	2.45	0.47
1:A:333:C:H41	1:A:392:U:H3'	1.79	0.47
1:A:2775:A:H62	1:A:2781:U:H3	1.63	0.47
1:A:2870:A:P	1:A:2886:G:H22	2.37	0.47
13:M:56:ALA:CB	13:M:80:ILE:HD13	2.37	0.47
1:A:690:U:O2'	1:A:691:A:O4'	2.33	0.47
1:A:1636:U:O4	1:A:1637:A:N6	2.48	0.47
1:A:1758:A:O2'	1:A:1759:G:OP2	2.25	0.47
1:A:2775:A:O2'	7:G:62:ARG:O	2.32	0.47
1:A:2878:U:HO2'	1:A:2879:G:P	2.39	0.47
13:M:92:ILE:HD12	13:M:93:VAL:N	2.30	0.47
1:A:19:G:O3'	15:O:22:LYS:NZ	2.49	0.46
1:A:943:C:N4	1:A:944:G:O6	2.49	0.46
1:A:1712:A:O2'	1:A:1718:G:N7	2.45	0.46
1:A:2142:G:O2'	1:A:2192:G:N2	2.46	0.46
1:A:2774:G:C2'	7:G:67:THR:HG22	2.45	0.46
3:C:142:HIS:ND1	3:C:193:GLY:O	2.48	0.46
12:L:11:ASP:OD1	12:L:12:GLN:N	2.48	0.46
1:A:275:A:H61	1:A:296:G:C2'	2.29	0.46
1:A:1675:G:N2	1:A:1679:A:H62	2.11	0.46
1:A:2776:A:N6	30:4:18:LYS:O	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:124:ILE:HD12	3:C:124:ILE:N	2.30	0.46
4:D:189:ASP:OD1	4:D:191:GLU:N	2.47	0.46
19:S:7:ASP:OD1	19:S:7:ASP:N	2.44	0.46
1:A:1397:G:C2	1:A:2241:C:N3	2.84	0.46
1:A:1425:G:C4'	1:A:1571:G:H21	2.28	0.46
12:L:52:LYS:NZ	12:L:96:ARG:O	2.43	0.46
1:A:275:A:H61	1:A:296:G:H2'	1.80	0.46
1:A:1250:G:O2'	1:A:1274:G:N1	2.48	0.46
1:A:1699:A:N6	1:A:2032:A:O2'	2.43	0.46
1:A:2311:U:H3	1:A:2411:A:H62	1.62	0.46
1:A:2698:A:H3'	1:A:2699:U:H5''	1.96	0.46
1:A:2710:C:O2	9:I:76:TYR:OH	2.33	0.46
1:A:2828:U:N3	1:A:2911:A:N7	2.60	0.46
3:C:202:LEU:N	3:C:202:LEU:HD23	2.31	0.46
7:G:52:VAL:O	7:G:65:HIS:NE2	2.48	0.46
12:L:106:GLN:NE2	12:L:118:ILE:HD12	2.30	0.46
1:A:228:A:O2'	1:A:229:A:O4'	2.28	0.46
1:A:385:U:O2'	1:A:386:C:OP1	2.29	0.46
1:A:2496:A:C6	1:A:2508:G:C4	3.03	0.46
2:B:74:G:O2'	20:T:78:GLN:NE2	2.42	0.46
3:C:165:LEU:HD21	3:C:175:ARG:NH1	2.31	0.46
1:A:333:C:C2	1:A:393:G:H2'	2.51	0.46
1:A:1526:G:N2	1:A:1552:U:O4	2.48	0.46
1:A:1844:G:OP1	3:C:87:ARG:NH2	2.49	0.46
1:A:2504:C:OP1	30:4:2:LYS:NZ	2.46	0.46
1:A:2866:G:OP1	14:N:54:GLY:N	2.49	0.46
29:3:55:MET:HE3	29:3:55:MET:C	2.41	0.46
1:A:720:A:OP1	5:E:63:LYS:NZ	2.43	0.46
1:A:1827:C:OP1	3:C:260:ARG:NH2	2.46	0.46
4:D:141:MET:HE1	4:D:148:HIS:ND1	2.30	0.46
6:F:23:SER:N	6:F:27:GLU:OE2	2.49	0.46
8:H:58:ILE:HD12	8:H:59:ASN:N	2.30	0.46
19:S:11:VAL:HG22	19:S:19:LYS:O	2.16	0.46
20:T:6:SER:C	20:T:7:ILE:HD12	2.41	0.46
1:A:1834:G:N2	1:A:1837:A:OP2	2.39	0.46
1:A:2504:C:O2'	1:A:2506:U:OP2	2.34	0.46
4:D:9:LYS:O	4:D:206:LYS:N	2.46	0.46
19:S:25:ALA:HB3	19:S:34:VAL:CG1	2.45	0.46
1:A:1962:G:H22	1:A:1991:G:P	2.39	0.46
23:W:14:ILE:HG22	23:W:18:ILE:CD1	2.46	0.46
1:A:82:G:N2	1:A:102:A:OP2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:106:LEU:N	9:I:106:LEU:HD23	2.31	0.46
1:A:394:U:O2'	1:A:395:U:O2	2.25	0.45
1:A:2048:G:OP2	26:Z:12:ARG:NH2	2.49	0.45
1:A:2774:G:O6	30:4:20:LYS:NZ	2.45	0.45
2:B:43:A:O4'	6:F:92:ARG:NE	2.49	0.45
2:B:64:A:H61	2:B:105:C:C5'	2.29	0.45
6:F:4:LEU:HD21	6:F:173:PHE:CB	2.46	0.45
16:P:53:VAL:HG21	16:P:56:ALA:HB3	1.97	0.45
5:E:185:ASP:OD1	5:E:186:ILE:N	2.49	0.45
6:F:118:SER:OG	6:F:128:TYR:OH	2.33	0.45
23:W:11:THR:HA	23:W:14:ILE:HD12	1.98	0.45
1:A:611:U:N3	1:A:614:U:OP2	2.48	0.45
1:A:1475:A:N6	1:A:1606:C:O2	2.49	0.45
1:A:2782:C:O5'	30:4:19:ARG:NH1	2.46	0.45
5:E:141:ASN:O	5:E:144:SER:OG	2.28	0.45
1:A:1644:C:OP1	18:R:76:ARG:NH1	2.49	0.45
2:B:12:U:OP2	21:U:82:ARG:NH1	2.50	0.45
2:B:21:G:N1	2:B:22:G:O6	2.50	0.45
3:C:180:GLU:OE1	3:C:180:GLU:N	2.49	0.45
5:E:5:ASP:HB2	5:E:7:LEU:HD21	1.98	0.45
5:E:33:LEU:HD22	5:E:37:ILE:HD11	1.97	0.45
7:G:137:SER:O	7:G:141:VAL:N	2.45	0.45
8:H:93:LEU:HD23	8:H:96:THR:O	2.17	0.45
24:X:18:THR:HG22	24:X:49:LYS:NZ	2.32	0.45
1:A:572:C:N4	1:A:2806:U:OP2	2.50	0.45
1:A:1304:G:OP1	26:Z:16:ARG:NE	2.44	0.45
1:A:2507:C:N4	1:A:2508:G:O6	2.49	0.45
1:A:2686:G:O2'	1:A:2688:G:N7	2.37	0.45
1:A:2767:A:OP2	1:A:2790:G:N1	2.47	0.45
1:A:2773:U:O4	30:4:20:LYS:NZ	2.50	0.45
1:A:2820:U:O2'	1:A:2823:G:N7	2.45	0.45
5:E:108:LEU:HD12	5:E:108:LEU:O	2.16	0.45
6:F:98:GLU:OE1	6:F:98:GLU:N	2.50	0.45
1:A:213:C:OP2	28:2:30:LYS:NZ	2.48	0.45
1:A:333:C:C6	1:A:393:G:N3	2.85	0.45
1:A:2091:C:O2'	1:A:2278:G:N2	2.49	0.45
1:A:2177:U:OP2	1:A:2187:G:O2'	2.29	0.45
1:A:2338:A:O3'	6:F:74:ILE:HD12	2.17	0.45
1:A:2372:G:N7	27:1:42:TYR:OH	2.47	0.45
9:I:13:ASN:OD1	9:I:96:THR:N	2.50	0.45
13:M:92:ILE:HD12	13:M:93:VAL:C	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:111:ALA:O	13:M:115:SER:OG	2.30	0.45
1:A:923:A:H2	1:A:944:G:H22	1.65	0.45
2:B:77:G:N1	2:B:95:U:C2	2.77	0.45
6:F:134:GLU:OE2	6:F:150:ARG:N	2.50	0.45
23:W:34:THR:O	23:W:36:GLN:N	2.44	0.45
1:A:64:A:O2'	18:R:68:TYR:O	2.34	0.45
1:A:222:A:N3	1:A:237:U:O2'	2.45	0.45
1:A:373:A:H2	1:A:1248:U:HO2'	1.62	0.45
1:A:862:C:N3	1:A:1230:G:N1	2.65	0.45
1:A:1375:G:O6	18:R:61:LYS:NZ	2.21	0.45
1:A:1891:U:C4'	1:A:2437:G:H21	2.30	0.45
1:A:2125:U:O2	1:A:2218:G:C2	2.69	0.45
1:A:319:G:C4'	1:A:325:A:H62	2.30	0.45
2:B:29:C:OP1	13:M:4:LYS:NZ	2.41	0.45
3:C:185:LEU:HD12	3:C:187:THR:O	2.17	0.45
6:F:128:TYR:O	6:F:129:THR:OG1	2.35	0.45
6:F:142:ASP:O	6:F:144:ASP:N	2.49	0.45
21:U:45:LEU:HD23	21:U:45:LEU:N	2.32	0.45
1:A:777:C:H2'	1:A:778:G:O4'	2.17	0.45
1:A:1284:A:O2'	5:E:45:ARG:NH1	2.49	0.45
1:A:2017:C:H2'	1:A:2018:U:O4'	2.17	0.45
2:B:87:C:H1'	11:K:18:THR:HG22	1.99	0.45
20:T:92:LEU:HD13	20:T:93:ALA:N	2.32	0.45
1:A:988:C:O2'	1:A:989:A:OP1	2.32	0.44
1:A:2044:C:O2'	1:A:2046:U:OP2	2.27	0.44
12:L:114:ALA:O	12:L:116:SER:N	2.50	0.44
13:M:89:ILE:HA	13:M:117:LEU:HD22	1.98	0.44
15:O:39:VAL:O	15:O:42:SER:OG	2.32	0.44
1:A:312:A:O2'	1:A:404:U:OP2	2.20	0.44
1:A:336:U:C4	1:A:388:A:N1	2.85	0.44
1:A:401:U:H2'	1:A:402:C:H6	1.81	0.44
25:Y:6:HIS:ND1	25:Y:7:PRO:O	2.50	0.44
1:A:225:A:O2'	1:A:227:G:N7	2.49	0.44
1:A:417:A:H61	1:A:447:A:H3'	1.80	0.44
1:A:534:G:N2	1:A:537:A:OP2	2.50	0.44
1:A:1290:G:N3	15:O:33:LYS:NZ	2.66	0.44
1:A:2726:C:N4	1:A:2736:G:O6	2.50	0.44
3:C:132:LEU:HD12	3:C:185:LEU:O	2.17	0.44
6:F:63:GLN:CG	6:F:89:VAL:HG13	2.47	0.44
13:M:30:ARG:NH2	13:M:47:ASP:OD1	2.50	0.44
1:A:842:U:OP1	5:E:62:ARG:NH2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1094:A:H62	1:A:2778:G:H2'	1.81	0.44
1:A:1733:A:OP2	1:A:1742:A:N6	2.43	0.44
1:A:2424:G:N2	1:A:2446:U:O2	2.44	0.44
1:A:2682:G:N2	1:A:2683:U:O4	2.36	0.44
1:A:2781:U:H1'	30:4:26:ILE:HD11	1.98	0.44
2:B:38:U:H1'	2:B:43:A:H61	1.81	0.44
1:A:1479:G:H2'	1:A:1480:G:C8	2.53	0.44
1:A:2580:G:H21	1:A:2609:G:N2	2.16	0.44
2:B:40:C:N1	6:F:66:LEU:HD22	2.33	0.44
16:P:65:GLN:HG2	16:P:93:THR:HG22	1.99	0.44
29:3:21:GLN:HB3	29:3:49:LEU:HD22	1.98	0.44
1:A:1452:C:O2'	1:A:1631:G:N2	2.50	0.44
1:A:2113:U:C4	1:A:2261:G:O6	2.70	0.44
1:A:2765:A:N1	1:A:2793:G:C6	2.86	0.44
1:A:2905:C:H42	26:Z:37:LYS:HZ3	1.65	0.44
5:E:136:THR:HG22	5:E:170:ILE:HD11	2.00	0.44
6:F:46:ASN:OD1	6:F:46:ASN:N	2.49	0.44
6:F:60:ILE:HG22	6:F:99:PHE:CE1	2.53	0.44
7:G:107:VAL:HG23	7:G:109:TYR:CD1	2.53	0.44
9:I:101:PRO:HD2	14:N:70:VAL:HG21	2.00	0.44
1:A:2710:C:H42	1:A:2754:G:H2'	1.81	0.44
2:B:73:G:H1'	20:T:30:VAL:HG21	2.00	0.44
6:F:50:LEU:HD13	6:F:54:VAL:HG23	1.99	0.44
9:I:7:ARG:HE	9:I:20:LEU:HD23	1.83	0.44
9:I:113:LYS:CE	9:I:117:LEU:HD11	2.47	0.44
10:J:55:LEU:HD23	10:J:60:ARG:CG	2.47	0.44
11:K:34:LEU:HD12	11:K:130:LYS:O	2.18	0.44
1:A:905:U:OP2	1:A:961:G:N1	2.44	0.44
1:A:1076:A:C8	30:4:36:GLN:HB3	2.52	0.44
1:A:1397:G:C2	1:A:2241:C:C2	3.06	0.44
1:A:1449:A:O2'	1:A:1450:A:N3	2.41	0.44
1:A:1964:A:H62	1:A:1967:U:H5	1.65	0.44
1:A:2382:C:O3'	21:U:32:LYS:NZ	2.42	0.44
1:A:2775:A:H1'	7:G:67:THR:HG23	2.00	0.44
1:A:2814:C:O3'	4:D:71:LYS:NZ	2.47	0.44
2:B:27:A:H2'	2:B:28:C:C2	2.52	0.44
28:2:10:LYS:O	28:2:14:SER:OG	2.36	0.44
1:A:921:C:H42	1:A:946:A:N6	2.16	0.44
1:A:1457:U:OP2	1:A:1628:A:N6	2.42	0.44
1:A:2430:C:H2'	1:A:2431:C:C6	2.53	0.44
1:A:2850:G:OP2	4:D:86:ARG:NH1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:57:LEU:HD12	6:F:65:PRO:HG3	1.99	0.44
15:O:88:ILE:HD13	15:O:88:ILE:N	2.33	0.44
16:P:57:THR:OG1	16:P:58:VAL:N	2.50	0.44
1:A:334:A:H3'	1:A:335:U:C4'	2.48	0.43
1:A:443:U:O5'	22:V:32:ASN:ND2	2.51	0.43
1:A:1537:A:H2	1:A:1626:A:H1'	1.83	0.43
1:A:1816:A:OP2	3:C:221:ARG:NH2	2.49	0.43
1:A:1980:A:O2'	1:A:2586:C:O2'	2.22	0.43
1:A:2374:C:HO2'	27:1:17:TYR:HH	1.47	0.43
2:B:34:C:H42	2:B:48:A:C1'	2.30	0.43
2:B:79:C:H41	2:B:92:C:H42	1.65	0.43
2:B:94:C:OP2	20:T:12:LYS:NZ	2.50	0.43
9:I:43:VAL:HG23	9:I:54:LYS:HA	1.99	0.43
9:I:87:ILE:HD12	9:I:88:ARG:N	2.33	0.43
21:U:83:ASP:N	21:U:83:ASP:OD1	2.49	0.43
1:A:544:U:H2'	1:A:545:G:O4'	2.18	0.43
1:A:617:A:H62	1:A:2081:A:H4'	1.82	0.43
1:A:2290:C:N4	21:U:23:ASP:OD2	2.51	0.43
1:A:2902:A:OP1	12:L:102:ARG:NH1	2.46	0.43
2:B:7:G:H21	2:B:110:C:H41	1.66	0.43
5:E:16:SER:OG	5:E:17:ILE:N	2.51	0.43
11:K:50:ALA:HB1	11:K:121:ALA:HB1	2.00	0.43
1:A:318:A:H1'	1:A:402:C:H42	1.82	0.43
1:A:325:A:H2'	1:A:326:A:C4	2.53	0.43
1:A:1316:G:H5'	12:L:30:ILE:HG22	2.00	0.43
1:A:1533:A:H62	3:C:100:GLU:N	2.16	0.43
1:A:1989:C:O2'	1:A:1991:G:OP2	2.31	0.43
15:O:116:ALA:O	15:O:117:LEU:HD23	2.18	0.43
21:U:71:ILE:HD13	21:U:91:ALA:HB2	2.00	0.43
25:Y:1:MET:O	25:Y:3:GLN:N	2.51	0.43
1:A:401:U:O2'	1:A:402:C:O4'	2.30	0.43
1:A:718:C:OP1	5:E:54:ARG:NH2	2.44	0.43
1:A:1024:A:HO2'	1:A:1025:A:P	2.37	0.43
1:A:1465:G:O2'	1:A:1537:A:N7	2.51	0.43
1:A:2431:C:H42	1:A:2440:G:H1	1.66	0.43
2:B:29:C:H1'	2:B:51:A:H61	1.83	0.43
20:T:4:LEU:HD23	20:T:5:LYS:N	2.32	0.43
27:1:32:MET:O	27:1:44:LEU:HD12	2.18	0.43
1:A:72:U:P	23:W:54:LYS:HZ2	2.41	0.43
1:A:597:U:H2'	1:A:598:G:O4'	2.19	0.43
1:A:794:A:C3'	1:A:1309:G:H21	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:955:A:N3	1:A:2291:C:O2'	2.50	0.43
1:A:2557:U:HO2'	1:A:2561:C:N4	2.17	0.43
7:G:94:TYR:OH	7:G:152:ARG:NH2	2.51	0.43
18:R:6:ILE:HG12	18:R:7:LEU:HD12	1.99	0.43
20:T:51:VAL:O	20:T:55:VAL:HG12	2.18	0.43
1:A:889:U:H2'	1:A:890:G:O4'	2.19	0.43
1:A:1463:A:O2'	1:A:1464:U:O5'	2.30	0.43
1:A:1875:A:N1	1:A:1919:C:N4	2.67	0.43
1:A:2449:C:N4	1:A:2450:U:O4	2.51	0.43
2:B:73:G:H2'	2:B:74:G:O4'	2.18	0.43
18:R:87:ILE:HG22	18:R:89:LEU:HD21	2.01	0.43
19:S:26:THR:HA	19:S:33:VAL:HG12	2.01	0.43
1:A:1767:G:OP2	1:A:1768:C:N4	2.50	0.43
1:A:2399:G:O3'	27:1:33:LYS:NZ	2.51	0.43
5:E:179:GLN:OE1	5:E:180:GLY:N	2.51	0.43
6:F:140:GLU:OE1	25:Y:27:SER:N	2.51	0.43
11:K:39:THR:HG23	11:K:98:LYS:HA	2.01	0.43
1:A:162:A:H2'	1:A:2244:G:H21	1.83	0.43
1:A:908:A:O3'	2:B:97:G:N2	2.44	0.43
1:A:1074:G:H2'	1:A:1075:G:C1'	2.48	0.43
1:A:1168:C:H3'	1:A:1169:G:C8	2.54	0.43
1:A:1816:A:P	3:C:221:ARG:HE	2.41	0.43
30:4:19:ARG:HD3	30:4:20:LYS:HZ3	1.83	0.43
1:A:193:A:H61	1:A:210:A:C1'	2.32	0.43
1:A:352:A:HO2'	1:A:372:A:C2'	2.30	0.43
1:A:1447:A:N6	1:A:1637:A:N1	2.67	0.43
1:A:1760:G:O6	1:A:1761:G:N2	2.45	0.43
1:A:2629:A:O2'	1:A:2631:U:OP2	2.34	0.43
3:C:84:ASP:OD2	3:C:86:ASN:N	2.50	0.43
5:E:21:ASP:O	5:E:25:GLY:C	2.62	0.43
8:H:57:VAL:O	8:H:126:TYR:N	2.48	0.43
1:A:308:C:O2'	1:A:407:G:N2	2.48	0.43
1:A:1018:A:O2'	1:A:1033:G:N2	2.50	0.43
1:A:1311:A:N7	1:A:1690:A:O2'	2.50	0.43
1:A:2037:G:OP2	17:Q:41:LYS:NZ	2.52	0.43
6:F:134:GLU:HB3	6:F:137:ILE:HD11	2.00	0.43
1:A:26:G:H2'	1:A:27:G:O4'	2.19	0.42
1:A:796:A:OP2	17:Q:90:ARG:NE	2.52	0.42
1:A:1465:G:N3	1:A:1537:A:N6	2.67	0.42
1:A:1632:A:H2'	1:A:1633:A:N3	2.34	0.42
4:D:141:MET:HE1	4:D:148:HIS:CG	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:46:ASP:N	13:M:51:VAL:O	2.50	0.42
28:2:31:VAL:HG12	28:2:34:ARG:NH2	2.34	0.42
1:A:645:A:O2'	1:A:646:A:O5'	2.37	0.42
1:A:719:G:H2'	1:A:849:A:H61	1.84	0.42
1:A:1079:U:N3	1:A:1080:G:N7	2.67	0.42
1:A:1829:A:OP2	1:A:1841:G:N1	2.47	0.42
2:B:40:C:O5'	25:Y:5:ILE:HG23	2.19	0.42
3:C:185:LEU:HD13	3:C:187:THR:N	2.34	0.42
8:H:97:ASN:OD1	8:H:100:ARG:NE	2.48	0.42
13:M:19:ARG:NH2	13:M:23:SER:OG	2.48	0.42
26:Z:15:LYS:O	26:Z:18:THR:HG22	2.19	0.42
1:A:10:A:N6	1:A:2656:A:O4'	2.52	0.42
1:A:362:C:H2'	1:A:363:A:O4'	2.19	0.42
1:A:926:G:N1	1:A:939:U:OP1	2.52	0.42
1:A:1174:U:N3	4:D:160:ALA:HB2	2.34	0.42
1:A:1309:G:O6	1:A:1659:C:O2	2.37	0.42
1:A:1614:A:OP1	3:C:60:ARG:NH2	2.52	0.42
1:A:2349:A:H2'	1:A:2350:G:O4'	2.19	0.42
1:A:2496:A:N6	1:A:2508:G:O4'	2.52	0.42
2:B:75:U:H3	2:B:96:A:H62	1.67	0.42
3:C:165:LEU:HD21	3:C:175:ARG:HH12	1.84	0.42
4:D:93:ASN:OD1	4:D:93:ASN:N	2.51	0.42
7:G:41:MET:N	7:G:41:MET:SD	2.92	0.42
9:I:19:VAL:HG23	9:I:43:VAL:HA	2.01	0.42
16:P:4:ILE:HG22	16:P:39:LEU:HD12	2.00	0.42
18:R:18:GLU:O	18:R:21:ALA:HB3	2.19	0.42
23:W:6:ILE:HA	23:W:9:LEU:HD12	2.00	0.42
28:2:9:ASN:OD1	28:2:12:LYS:N	2.46	0.42
1:A:1290:G:N7	15:O:36:LYS:NZ	2.54	0.42
1:A:1455:U:O2	1:A:1457:U:N3	2.46	0.42
1:A:1503:U:O2'	1:A:1504:U:OP2	2.36	0.42
1:A:1633:A:H1'	1:A:1634:A:C8	2.55	0.42
1:A:2307:G:N7	21:U:22:ARG:NH2	2.67	0.42
27:1:31:GLU:HB2	27:1:44:LEU:HD11	2.01	0.42
1:A:50:U:O2'	1:A:51:G:OP1	2.35	0.42
1:A:172:U:O4	1:A:173:A:N6	2.53	0.42
1:A:317:G:H22	1:A:402:C:H2'	1.85	0.42
1:A:333:C:N4	1:A:392:U:H3'	2.34	0.42
1:A:484:U:O4	1:A:485:A:N6	2.53	0.42
1:A:645:A:O2'	1:A:700:A:N1	2.50	0.42
1:A:873:U:O2'	1:A:874:A:O4'	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2362:A:O5'	13:M:17:ARG:NH2	2.52	0.42
1:A:578:G:O2'	15:O:38:GLN:OE1	2.35	0.42
1:A:912:C:N3	1:A:957:C:O2'	2.52	0.42
1:A:1039:C:O2'	1:A:1040:A:OP2	2.25	0.42
2:B:7:G:N2	2:B:109:G:N7	2.67	0.42
6:F:74:ILE:N	6:F:79:LEU:HD21	2.34	0.42
8:H:37:LEU:HD11	8:H:119:GLN:CB	2.50	0.42
8:H:44:THR:O	8:H:44:THR:OG1	2.27	0.42
9:I:13:ASN:OD1	9:I:13:ASN:N	2.53	0.42
24:X:43:ILE:HD13	24:X:46:GLN:OE1	2.20	0.42
1:A:54:G:H1	1:A:115:C:H42	1.67	0.42
1:A:248:G:O6	29:3:8:ARG:NE	2.52	0.42
1:A:926:G:N2	1:A:941:A:H62	2.16	0.42
1:A:1854:U:H2'	1:A:1855:G:O4'	2.19	0.42
1:A:1866:G:O2'	1:A:1954:A:OP1	2.20	0.42
1:A:2042:A:C2	26:Z:3:VAL:HG12	2.55	0.42
1:A:2836:C:O3'	12:L:105:LYS:NZ	2.49	0.42
1:A:2844:U:H2'	1:A:2845:G:O4'	2.20	0.42
5:E:155:VAL:HG12	5:E:156:THR:O	2.20	0.42
1:A:506:A:H2	1:A:515:G:H21	1.68	0.42
1:A:624:C:H5'	15:O:31:LEU:HD22	2.01	0.42
1:A:1090:A:O2'	1:A:1091:G:OP1	2.37	0.42
1:A:2371:U:O2'	27:1:32:MET:SD	2.66	0.42
1:A:2372:G:O6	1:A:2398:G:C2	2.71	0.42
1:A:2378:G:N2	1:A:2393:A:OP2	2.51	0.42
2:B:40:C:O2'	25:Y:5:ILE:HD11	2.20	0.42
8:H:57:VAL:HG23	8:H:125:VAL:HG23	2.02	0.42
8:H:111:PRO:HB2	8:H:113:THR:HG23	2.02	0.42
10:J:61:LEU:O	29:3:13:ARG:NE	2.48	0.42
17:Q:88:GLN:O	17:Q:90:ARG:NE	2.53	0.42
19:S:3:ILE:HD12	19:S:4:LYS:O	2.20	0.42
1:A:116:G:OP2	1:A:118:A:O2'	2.38	0.42
1:A:1952:C:H42	1:A:1956:G:H22	1.65	0.42
1:A:399:U:H3'	1:A:400:C:O4'	2.19	0.42
1:A:2347:A:H4'	1:A:2348:G:O5'	2.19	0.42
1:A:2610:G:O2'	1:A:2611:U:O4'	2.37	0.42
1:A:2684:A:N6	1:A:2691:G:O2'	2.52	0.42
12:L:45:GLU:O	12:L:49:THR:OG1	2.38	0.42
12:L:74:GLU:O	12:L:77:THR:OG1	2.33	0.42
13:M:86:ASP:OD1	13:M:86:ASP:N	2.53	0.42
1:A:323:C:H2'	1:A:324:A:C5	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1092:A:N6	1:A:1155:A:O4'	2.52	0.41
1:A:1226:G:O2'	1:A:1227:U:O5'	2.37	0.41
1:A:2225:A:C5'	1:A:2227:C:H41	2.33	0.41
1:A:2371:U:H2'	27:1:32:MET:HB2	2.01	0.41
3:C:216:ILE:HG22	3:C:217:ARG:N	2.35	0.41
4:D:131:ILE:HG22	4:D:136:GLN:O	2.19	0.41
5:E:21:ASP:O	5:E:25:GLY:CA	2.68	0.41
6:F:65:PRO:CB	6:F:87:ALA:HB1	2.50	0.41
21:U:18:THR:OG1	21:U:19:LYS:N	2.53	0.41
1:A:343:A:O2'	1:A:361:U:O2	2.31	0.41
1:A:575:G:N2	1:A:2050:A:OP2	2.53	0.41
1:A:1078:G:H2'	1:A:1079:U:O4'	2.20	0.41
1:A:2397:G:O3'	27:1:40:ASN:ND2	2.48	0.41
3:C:53:HIS:CD2	3:C:219:THR:HG22	2.55	0.41
6:F:89:VAL:CG1	6:F:91:LEU:HD21	2.49	0.41
15:O:96:SER:OG	15:O:97:GLU:N	2.53	0.41
16:P:97:ILE:H	16:P:97:ILE:HD12	1.86	0.41
20:T:44:ASP:N	20:T:44:ASP:OD1	2.53	0.41
1:A:9:U:O2	1:A:2656:A:C5	2.74	0.41
1:A:622:A:O2'	1:A:2046:U:OP1	2.38	0.41
1:A:958:U:O2	1:A:959:C:N4	2.50	0.41
1:A:2080:G:N7	1:A:2604:A:N6	2.68	0.41
1:A:2082:C:OP1	26:Z:5:LYS:NZ	2.53	0.41
1:A:2350:G:H2'	1:A:2351:U:O4'	2.20	0.41
16:P:25:LEU:HD22	16:P:93:THR:HG21	2.01	0.41
1:A:2479:C:C4	1:A:2531:U:O4	2.73	0.41
1:A:2693:C:N4	7:G:109:TYR:HA	2.35	0.41
6:F:25:VAL:O	6:F:28:VAL:HG13	2.21	0.41
11:K:66:ILE:HG22	11:K:68:ILE:H	1.85	0.41
15:O:83:LEU:HD12	15:O:113:ALA:HB2	2.02	0.41
19:S:89:LYS:O	19:S:91:VAL:N	2.53	0.41
26:Z:18:THR:HG23	26:Z:19:HIS:N	2.35	0.41
1:A:1871:U:H4'	3:C:257:LYS:HZ1	1.85	0.41
6:F:60:ILE:HG22	6:F:99:PHE:HE1	1.85	0.41
7:G:136:ILE:H	7:G:141:VAL:HG11	1.85	0.41
9:I:105:GLU:N	9:I:106:LEU:HD23	2.36	0.41
13:M:32:ASN:HB3	13:M:45:ILE:HD12	2.01	0.41
17:Q:50:VAL:CG1	17:Q:103:ILE:HG21	2.51	0.41
1:A:678:A:P	10:J:71:ARG:HE	2.41	0.41
1:A:794:A:H61	1:A:798:G:H1'	1.85	0.41
2:B:22:G:N7	2:B:54:U:H2'	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:156:THR:OG1	5:E:157:GLU:N	2.52	0.41
7:G:30:LYS:O	7:G:79:VAL:HG13	2.20	0.41
21:U:40:THR:HG22	21:U:41:GLY:H	1.86	0.41
1:A:73:A:O5'	23:W:47:ARG:NH1	2.54	0.41
1:A:89:U:N3	1:A:90:A:O2'	2.54	0.41
1:A:342:A:N6	1:A:365:A:O2'	2.48	0.41
1:A:2828:U:H3	1:A:2911:A:H62	1.68	0.41
1:A:2851:G:H21	1:A:2904:U:P	2.42	0.41
2:B:42:G:O5'	25:Y:1:MET:HE1	2.21	0.41
9:I:63:VAL:HG23	9:I:83:ALA:HB3	2.02	0.41
1:A:77:U:OP1	23:W:52:ARG:NE	2.47	0.41
1:A:1957:G:N1	1:A:1996:A:OP2	2.48	0.41
1:A:2024:A:OP2	4:D:138:ARG:NH1	2.53	0.41
2:B:64:A:O2'	2:B:67:G:O6	2.33	0.41
5:E:136:THR:CG2	5:E:170:ILE:HD11	2.51	0.41
7:G:94:TYR:HH	7:G:152:ARG:HH22	1.67	0.41
16:P:88:HIS:NE2	16:P:90:GLN:OE1	2.47	0.41
20:T:90:ASP:OD1	20:T:90:ASP:N	2.52	0.41
29:3:19:SER:OG	29:3:20:GLY:N	2.53	0.41
1:A:200:A:H2	1:A:2461:A:H61	1.68	0.41
1:A:325:A:N1	1:A:402:C:N4	2.69	0.41
1:A:606:G:H1	1:A:621:A:H61	1.69	0.41
1:A:686:U:O4	1:A:692:G:O6	2.38	0.41
1:A:818:U:O2	1:A:823:G:O2'	2.38	0.41
1:A:1002:U:H3	2:B:87:C:H41	1.68	0.41
1:A:1073:A:H62	1:A:1169:G:N2	2.19	0.41
1:A:1488:A:N7	1:A:1490:G:N1	2.69	0.41
1:A:1488:A:H2'	1:A:1489:A:H3'	2.03	0.41
1:A:1502:A:N3	1:A:1504:U:N3	2.69	0.41
1:A:2313:A:C5	1:A:2373:A:C6	3.09	0.41
1:A:2348:G:OP1	1:A:2359:C:N4	2.54	0.41
1:A:2676:U:N3	1:A:2699:U:O2	2.54	0.41
1:A:2829:A:H62	1:A:2910:G:H2'	1.85	0.41
7:G:103:LEU:O	7:G:104:ILE:HD13	2.21	0.41
22:V:36:VAL:O	22:V:47:VAL:N	2.48	0.41
1:A:192:G:H21	1:A:210:A:H62	1.68	0.41
1:A:760:A:O2'	1:A:761:A:OP2	2.28	0.41
1:A:909:G:H2'	1:A:910:C:C6	2.56	0.41
1:A:1162:C:H3'	1:A:1163:U:H5''	2.02	0.41
1:A:1462:G:H22	1:A:1625:U:H2'	1.86	0.41
1:A:1652:A:N7	1:A:1665:U:C2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1759:G:H21	1:A:1772:G:P	2.44	0.41
2:B:9:C:H3'	2:B:10:U:C5'	2.51	0.41
10:J:95:LEU:HD13	10:J:96:LEU:HD12	2.02	0.41
10:J:98:GLU:OE1	10:J:99:SER:N	2.54	0.41
11:K:48:GLU:O	11:K:51:ARG:NH2	2.54	0.41
16:P:35:PHE:O	16:P:57:THR:OG1	2.39	0.41
18:R:87:ILE:HG22	18:R:89:LEU:CD2	2.51	0.41
29:3:52:LYS:HA	29:3:55:MET:HB2	2.03	0.41
1:A:1500:G:H2'	1:A:1501:G:O4'	2.21	0.40
1:A:1911:A:O2'	1:A:1912:A:OP2	2.33	0.40
1:A:2628:C:H2'	1:A:2629:A:C8	2.56	0.40
5:E:123:LEU:HD11	5:E:194:ILE:HD11	2.03	0.40
11:K:23:GLY:O	11:K:101:ARG:NE	2.54	0.40
13:M:74:THR:CG2	13:M:111:ALA:HB2	2.50	0.40
28:2:16:VAL:HG23	28:2:17:HIS:CD2	2.55	0.40
28:2:31:VAL:HG12	28:2:34:ARG:HH21	1.87	0.40
1:A:1304:G:N2	1:A:2040:A:OP2	2.54	0.40
1:A:1824:C:O3'	3:C:258:LYS:HB3	2.22	0.40
1:A:2137:G:O6	1:A:2206:C:N4	2.54	0.40
14:N:49:VAL:O	14:N:99:LEU:HD12	2.21	0.40
1:A:921:C:H42	1:A:946:A:H61	1.68	0.40
1:A:2678:C:H2'	1:A:2679:U:C6	2.57	0.40
1:A:2902:A:OP1	12:L:102:ARG:NH2	2.51	0.40
5:E:54:ARG:O	5:E:57:VAL:HG22	2.21	0.40
9:I:76:TYR:HB2	14:N:75:THR:HB	2.03	0.40
11:K:34:LEU:HD12	11:K:130:LYS:C	2.46	0.40
20:T:29:ALA:HB2	20:T:89:ILE:HG23	2.04	0.40
1:A:193:A:H62	1:A:209:U:H3	1.70	0.40
1:A:539:G:H4'	17:Q:6:VAL:HG23	2.03	0.40
1:A:1864:C:O2'	1:A:1954:A:N3	2.41	0.40
1:A:2709:U:O4	1:A:2755:U:O2'	2.20	0.40
1:A:2772:C:H3'	1:A:2773:U:C5	2.57	0.40
3:C:76:ALA:O	3:C:115:ILE:HG22	2.20	0.40
13:M:76:VAL:O	13:M:80:ILE:HG22	2.22	0.40
1:A:371:U:O2'	19:S:64:HIS:ND1	2.41	0.40
1:A:1003:A:N6	1:A:2522:G:O2'	2.51	0.40
1:A:1243:G:H2'	1:A:1244:G:O4'	2.22	0.40
2:B:73:G:O3'	20:T:9:ARG:NH1	2.43	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	
3	C	272/274 (99%)	218 (80%)	54 (20%)	0	100	100
4	D	213/215 (99%)	179 (84%)	34 (16%)	0	100	100
5	E	204/206 (99%)	176 (86%)	28 (14%)	0	100	100
6	F	173/175 (99%)	142 (82%)	31 (18%)	0	100	100
7	G	173/175 (99%)	155 (90%)	18 (10%)	0	100	100
8	H	143/145 (99%)	126 (88%)	17 (12%)	0	100	100
9	I	120/122 (98%)	102 (85%)	18 (15%)	0	100	100
10	J	144/146 (99%)	123 (85%)	21 (15%)	0	100	100
11	K	135/137 (98%)	117 (87%)	18 (13%)	0	100	100
12	L	118/120 (98%)	105 (89%)	13 (11%)	0	100	100
13	M	117/119 (98%)	100 (86%)	17 (14%)	0	100	100
14	N	112/114 (98%)	97 (87%)	14 (12%)	1 (1%)	14	47
15	O	114/116 (98%)	107 (94%)	7 (6%)	0	100	100
16	P	100/102 (98%)	89 (89%)	10 (10%)	1 (1%)	12	45
17	Q	108/110 (98%)	94 (87%)	13 (12%)	1 (1%)	14	47
18	R	87/89 (98%)	72 (83%)	15 (17%)	0	100	100
19	S	101/103 (98%)	83 (82%)	18 (18%)	0	100	100
20	T	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
21	U	80/82 (98%)	68 (85%)	12 (15%)	0	100	100
22	V	56/58 (97%)	48 (86%)	8 (14%)	0	100	100
23	W	65/67 (97%)	57 (88%)	8 (12%)	0	100	100
24	X	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
25	Y	57/59 (97%)	48 (84%)	9 (16%)	0	100	100
26	Z	46/48 (96%)	33 (72%)	13 (28%)	0	100	100
27	1	45/47 (96%)	41 (91%)	4 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	2	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
29	3	62/64 (97%)	52 (84%)	10 (16%)	0	100	100
30	4	35/37 (95%)	25 (71%)	10 (29%)	0	100	100
All	All	3069/3125 (98%)	2632 (86%)	434 (14%)	3 (0%)	49	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	Q	87	PRO
16	P	51	PRO
14	N	54	GLY

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	
3	C	220/221 (100%)	177 (80%)	43 (20%)	1	8
4	D	173/173 (100%)	149 (86%)	24 (14%)	3	17
5	E	168/168 (100%)	137 (82%)	31 (18%)	1	9
6	F	141/154 (92%)	116 (82%)	25 (18%)	2	10
7	G	124/153 (81%)	110 (89%)	14 (11%)	5	24
8	H	122/123 (99%)	102 (84%)	20 (16%)	2	12
9	I	100/100 (100%)	87 (87%)	13 (13%)	4	20
10	J	109/112 (97%)	95 (87%)	14 (13%)	4	20
11	K	108/114 (95%)	100 (93%)	8 (7%)	13	43
12	L	96/101 (95%)	82 (85%)	14 (15%)	3	16
13	M	86/95 (90%)	73 (85%)	13 (15%)	3	14
14	N	93/100 (93%)	78 (84%)	15 (16%)	2	13
15	O	96/96 (100%)	87 (91%)	9 (9%)	8	33
16	P	84/86 (98%)	70 (83%)	14 (17%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	Q	88/90 (98%)	67 (76%)	21 (24%)	1	4
18	R	78/80 (98%)	64 (82%)	14 (18%)	2	9
19	S	81/88 (92%)	64 (79%)	17 (21%)	1	6
20	T	78/82 (95%)	67 (86%)	11 (14%)	3	17
21	U	63/64 (98%)	48 (76%)	15 (24%)	1	4
22	V	44/49 (90%)	34 (77%)	10 (23%)	1	5
23	W	58/60 (97%)	47 (81%)	11 (19%)	1	9
24	X	52/52 (100%)	43 (83%)	9 (17%)	2	10
25	Y	23/56 (41%)	22 (96%)	1 (4%)	26	59
26	Z	35/44 (80%)	28 (80%)	7 (20%)	1	7
27	1	44/45 (98%)	37 (84%)	7 (16%)	2	13
28	2	39/39 (100%)	33 (85%)	6 (15%)	2	14
29	3	55/55 (100%)	47 (86%)	8 (14%)	3	16
30	4	35/35 (100%)	32 (91%)	3 (9%)	10	36
All	All	2493/2635 (95%)	2096 (84%)	397 (16%)	4	13

All (397) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	9	ILE
3	C	10	THR
3	C	17	THR
3	C	19	LEU
3	C	20	ASP
3	C	24	ILE
3	C	27	THR
3	C	32	SER
3	C	37	LEU
3	C	40	LYS
3	C	59	LYS
3	C	70	ASN
3	C	77	LYS
3	C	87	ARG
3	C	91	ILE
3	C	94	VAL
3	C	100	GLU
3	C	115	ILE

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Mol	Chain	Res	Type
3	C	125	LYS
3	C	134	ASN
3	C	141	VAL
3	C	144	ILE
3	C	150	LYS
3	C	165	LEU
3	C	172	VAL
3	C	177	ARG
3	C	180	GLU
3	C	181	VAL
3	C	187	THR
3	C	197	ASN
3	C	202	LEU
3	C	205	VAL
3	C	207	LYS
3	C	213	TRP
3	C	223	SER
3	C	232	HIS
3	C	236	GLU
3	C	238	ARG
3	C	248	SER
3	C	252	LYS
3	C	254	THR
3	C	258	LYS
3	C	270	ILE
4	D	5	ILE
4	D	6	LEU
4	D	10	ILE
4	D	32	GLU
4	D	40	THR
4	D	47	ASN
4	D	49	ILE
4	D	57	LYS
4	D	61	LYS
4	D	71	LYS
4	D	78	LYS
4	D	81	ASP
4	D	111	VAL
4	D	115	VAL
4	D	122	SER
4	D	176	ASN
4	D	178	VAL

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Mol	Chain	Res	Type
4	D	180	VAL
4	D	184	GLU
4	D	185	VAL
4	D	190	THR
4	D	193	LYS
4	D	194	VAL
4	D	197	VAL
5	E	13	LYS
5	E	26	ILE
5	E	27	GLU
5	E	33	LEU
5	E	35	GLU
5	E	46	GLN
5	E	49	HIS
5	E	51	VAL
5	E	55	SER
5	E	101	MET
5	E	112	SER
5	E	114	LEU
5	E	116	PHE
5	E	117	LYS
5	E	119	GLN
5	E	121	ASN
5	E	125	VAL
5	E	130	ASN
5	E	135	LYS
5	E	140	LYS
5	E	150	LYS
5	E	154	VAL
5	E	156	THR
5	E	173	VAL
5	E	175	VAL
5	E	187	THR
5	E	192	LEU
5	E	193	VAL
5	E	194	ILE
5	E	201	LYS
5	E	204	GLU
6	F	4	LEU
6	F	5	LYS
6	F	8	PHE
6	F	10	THR

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Mol	Chain	Res	Type
6	F	26	MET
6	F	32	ASP
6	F	36	VAL
6	F	46	ASN
6	F	50	LEU
6	F	63	GLN
6	F	64	LYS
6	F	67	VAL
6	F	71	LYS
6	F	76	THR
6	F	80	ARG
6	F	100	LEU
6	F	103	LEU
6	F	115	GLN
6	F	117	VAL
6	F	132	VAL
6	F	135	GLN
6	F	136	LEU
6	F	155	VAL
6	F	162	THR
6	F	170	LEU
7	G	36	THR
7	G	41	MET
7	G	44	LYS
7	G	63	THR
7	G	87	LEU
7	G	111	HIS
7	G	112	PRO
7	G	113	VAL
7	G	132	LYS
7	G	136	ILE
7	G	137	SER
7	G	141	VAL
7	G	144	LEU
7	G	175	LYS
8	H	3	GLN
8	H	12	ILE
8	H	18	VAL
8	H	37	LEU
8	H	44	THR
8	H	46	THR
8	H	55	VAL

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Mol	Chain	Res	Type
8	H	57	VAL
8	H	61	SER
8	H	62	LYS
8	H	70	GLU
8	H	72	ASP
8	H	85	ILE
8	H	88	ILE
8	H	103	GLU
8	H	106	ILE
8	H	115	LEU
8	H	122	LYS
8	H	136	GLN
8	H	139	GLU
9	I	2	ILE
9	I	10	VAL
9	I	21	THR
9	I	25	LEU
9	I	40	VAL
9	I	66	LYS
9	I	70	ARG
9	I	71	ARG
9	I	86	ILE
9	I	99	PHE
9	I	106	LEU
9	I	112	MET
9	I	122	LEU
10	J	6	LEU
10	J	19	VAL
10	J	31	SER
10	J	57	LEU
10	J	77	VAL
10	J	92	THR
10	J	98	GLU
10	J	104	ASN
10	J	105	GLU
10	J	114	ASN
10	J	120	LYS
10	J	121	LEU
10	J	127	LYS
10	J	143	HIS
11	K	2	LEU
11	K	20	ARG

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Mol	Chain	Res	Type
11	K	21	SER
11	K	38	THR
11	K	39	THR
11	K	64	VAL
11	K	127	VAL
11	K	130	LYS
12	L	3	TYR
12	L	6	LEU
12	L	16	MET
12	L	24	LEU
12	L	33	THR
12	L	49	THR
12	L	50	LEU
12	L	52	LYS
12	L	79	GLN
12	L	91	GLU
12	L	103	ILE
12	L	112	ASP
12	L	121	LEU
12	L	122	VAL
13	M	1	MET
13	M	2	ILE
13	M	6	ASP
13	M	7	LYS
13	M	22	LEU
13	M	32	ASN
13	M	39	HIS
13	M	40	ILE
13	M	41	TYR
13	M	46	ASP
13	M	72	LEU
13	M	87	LYS
13	M	113	ARG
14	N	2	THR
14	N	6	LEU
14	N	19	LEU
14	N	32	VAL
14	N	42	ILE
14	N	43	GLN
14	N	44	VAL
14	N	48	VAL
14	N	52	ARG

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Mol	Chain	Res	Type
14	N	53	ARG
14	N	66	ILE
14	N	78	LEU
14	N	80	THR
14	N	89	LYS
14	N	98	LYS
15	O	4	VAL
15	O	9	VAL
15	O	10	THR
15	O	11	ARG
15	O	34	VAL
15	O	51	ARG
15	O	80	MET
15	O	84	LYS
15	O	88	ILE
16	P	5	ILE
16	P	10	LYS
16	P	13	LYS
16	P	20	ILE
16	P	21	PHE
16	P	24	LYS
16	P	25	LEU
16	P	31	ASP
16	P	34	THR
16	P	48	VAL
16	P	59	THR
16	P	75	THR
16	P	76	TYR
16	P	96	THR
17	Q	4	LYS
17	Q	6	VAL
17	Q	24	ILE
17	Q	28	ASN
17	Q	37	LYS
17	Q	48	GLU
17	Q	50	VAL
17	Q	51	LEU
17	Q	52	MET
17	Q	62	TYR
17	Q	65	ASN
17	Q	71	VAL
17	Q	75	TYR

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Mol	Chain	Res	Type
17	Q	81	THR
17	Q	82	LEU
17	Q	86	ARG
17	Q	88	GLN
17	Q	90	ARG
17	Q	101	ILE
17	Q	103	ILE
17	Q	109	LYS
18	R	9	ARG
18	R	11	VAL
18	R	31	THR
18	R	33	VAL
18	R	35	LYS
18	R	44	GLU
18	R	50	VAL
18	R	53	VAL
18	R	56	MET
18	R	65	MET
18	R	83	LYS
18	R	84	GLU
18	R	87	ILE
18	R	90	PHE
19	S	7	ASP
19	S	12	ILE
19	S	24	ILE
19	S	26	THR
19	S	27	LEU
19	S	38	VAL
19	S	40	ILE
19	S	56	ILE
19	S	57	LEU
19	S	59	THR
19	S	68	VAL
19	S	70	LEU
19	S	79	THR
19	S	80	ARG
19	S	81	VAL
19	S	84	LYS
19	S	87	ASP
20	T	4	LEU
20	T	27	VAL
20	T	31	VAL

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Mol	Chain	Res	Type
20	T	32	TYR
20	T	37	LYS
20	T	42	LYS
20	T	54	GLU
20	T	63	LEU
20	T	86	ILE
20	T	89	ILE
20	T	92	LEU
21	U	12	LYS
21	U	13	LYS
21	U	17	SER
21	U	27	LYS
21	U	29	LEU
21	U	40	THR
21	U	45	LEU
21	U	47	ARG
21	U	58	ASN
21	U	59	VAL
21	U	61	ARG
21	U	68	PHE
21	U	72	ASP
21	U	75	VAL
21	U	79	ARG
22	V	3	LYS
22	V	11	LYS
22	V	29	TRP
22	V	32	ASN
22	V	33	LEU
22	V	36	VAL
22	V	38	ILE
22	V	40	VAL
22	V	52	ARG
22	V	54	LEU
23	W	5	GLU
23	W	7	ARG
23	W	10	THR
23	W	11	THR
23	W	13	GLU
23	W	16	GLU
23	W	30	PHE
23	W	32	LEU
23	W	42	ARG

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Mol	Chain	Res	Type
23	W	43	ILE
23	W	55	THR
24	X	3	LYS
24	X	7	THR
24	X	9	THR
24	X	12	VAL
24	X	29	LYS
24	X	48	ASN
24	X	55	THR
24	X	56	VAL
24	X	57	GLU
25	Y	1	MET
26	Z	8	THR
26	Z	11	THR
26	Z	16	ARG
26	Z	22	ILE
26	Z	29	GLU
26	Z	30	CYS
26	Z	37	LYS
27	1	3	VAL
27	1	19	THR
27	1	22	ASN
27	1	23	LYS
27	1	34	LYS
27	1	36	CYS
27	1	43	THR
28	2	11	ARG
28	2	14	SER
28	2	15	LYS
28	2	16	VAL
28	2	25	THR
28	2	37	ARG
29	3	3	LYS
29	3	6	THR
29	3	32	LEU
29	3	41	LYS
29	3	44	LEU
29	3	52	LYS
29	3	55	MET
29	3	56	LYS
30	4	25	VAL
30	4	29	ASN

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Mol	Chain	Res	Type
30	4	35	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	15	ASN
3	C	90	ASN
4	D	50	GLN
4	D	103	GLN
4	D	128	GLN
4	D	176	ASN
5	E	3	ASN
5	E	46	GLN
5	E	119	GLN
8	H	68	ASN
8	H	119	GLN
9	I	82	ASN
12	L	106	GLN
13	M	32	ASN
13	M	55	GLN
15	O	44	GLN
16	P	81	ASN
17	Q	65	ASN
19	S	67	ASN
20	T	84	ASN
24	X	32	ASN
24	X	40	ASN
24	X	48	ASN
29	3	40	GLN
29	3	43	GLN
29	3	60	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2897/2905 (99%)	1041 (35%)	36 (1%)
2	B	114/115 (99%)	38 (33%)	0
All	All	3011/3020 (99%)	1079 (35%)	36 (1%)

All (1079) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	12	U
1	A	14	A
1	A	15	G
1	A	28	A
1	A	34	U
1	A	36	G
1	A	45	G
1	A	46	C
1	A	51	G
1	A	55	G
1	A	57	C
1	A	58	G
1	A	63	U
1	A	67	G
1	A	68	A
1	A	70	G
1	A	71	A
1	A	74	U
1	A	75	G
1	A	80	G
1	A	81	G
1	A	83	G
1	A	84	A
1	A	88	G
1	A	91	A
1	A	92	G
1	A	93	U
1	A	95	A
1	A	96	G
1	A	99	U
1	A	100	U
1	A	101	G
1	A	103	U
1	A	104	C
1	A	117	A
1	A	119	U
1	A	130	A
1	A	133	A
1	A	139	U
1	A	140	A
1	A	141	U
1	A	147	G
1	A	150	A

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Mol	Chain	Res	Type
1	A	156	A
1	A	157	U
1	A	158	G
1	A	161	A
1	A	162	A
1	A	164	A
1	A	166	A
1	A	167	U
1	A	168	A
1	A	169	G
1	A	170	C
1	A	172	U
1	A	173	A
1	A	175	C
1	A	176	A
1	A	177	G
1	A	179	A
1	A	180	G
1	A	183	A
1	A	184	C
1	A	185	A
1	A	199	A
1	A	202	A
1	A	208	G
1	A	213	C
1	A	216	A
1	A	217	G
1	A	219	A
1	A	224	A
1	A	225	A
1	A	227	G
1	A	228	A
1	A	229	A
1	A	230	A
1	A	231	A
1	A	232	U
1	A	233	U
1	A	234	C
1	A	235	G
1	A	242	U
1	A	244	A
1	A	251	G

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Mol	Chain	Res	Type
1	A	256	C
1	A	268	A
1	A	270	C
1	A	275	A
1	A	276	C
1	A	280	C
1	A	281	A
1	A	283	G
1	A	285	U
1	A	286	U
1	A	287	G
1	A	292	U
1	A	295	G
1	A	297	G
1	A	299	U
1	A	300	G
1	A	301	U
1	A	302	A
1	A	303	G
1	A	305	A
1	A	307	A
1	A	308	C
1	A	310	C
1	A	311	U
1	A	315	C
1	A	316	G
1	A	317	G
1	A	318	A
1	A	319	G
1	A	320	U
1	A	321	U
1	A	323	C
1	A	324	A
1	A	325	A
1	A	326	A
1	A	327	G
1	A	329	A
1	A	330	C
1	A	331	G
1	A	333	C
1	A	335	U
1	A	336	U

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Mol	Chain	Res	Type
1	A	338	G
1	A	339	A
1	A	340	C
1	A	351	G
1	A	353	A
1	A	365	A
1	A	366	G
1	A	367	A
1	A	373	A
1	A	374	U
1	A	378	C
1	A	381	G
1	A	386	C
1	A	387	G
1	A	388	A
1	A	389	A
1	A	390	A
1	A	391	A
1	A	392	U
1	A	393	G
1	A	396	G
1	A	398	C
1	A	399	U
1	A	400	C
1	A	401	U
1	A	402	C
1	A	404	U
1	A	405	G
1	A	406	A
1	A	407	G
1	A	408	U
1	A	409	G
1	A	410	G
1	A	411	A
1	A	417	A
1	A	418	G
1	A	419	U
1	A	426	G
1	A	432	G
1	A	433	U
1	A	435	A
1	A	436	A

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Mol	Chain	Res	Type
1	A	437	A
1	A	438	U
1	A	442	G
1	A	443	U
1	A	445	G
1	A	447	A
1	A	449	U
1	A	450	C
1	A	451	U
1	A	459	C
1	A	460	C
1	A	461	A
1	A	463	C
1	A	468	A
1	A	481	C
1	A	482	U
1	A	489	A
1	A	490	C
1	A	492	G
1	A	493	A
1	A	497	U
1	A	498	G
1	A	501	C
1	A	502	C
1	A	504	G
1	A	506	A
1	A	511	G
1	A	512	A
1	A	515	G
1	A	523	A
1	A	525	A
1	A	527	G
1	A	528	C
1	A	529	A
1	A	530	C
1	A	537	A
1	A	538	G
1	A	539	G
1	A	541	G
1	A	550	A
1	A	553	A
1	A	566	U

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Mol	Chain	Res	Type
1	A	572	C
1	A	574	A
1	A	575	G
1	A	576	U
1	A	577	A
1	A	578	G
1	A	582	G
1	A	586	C
1	A	591	A
1	A	592	A
1	A	598	G
1	A	599	A
1	A	606	G
1	A	611	U
1	A	615	A
1	A	616	G
1	A	617	A
1	A	618	A
1	A	619	U
1	A	629	A
1	A	630	G
1	A	645	A
1	A	646	A
1	A	647	G
1	A	650	U
1	A	656	G
1	A	657	U
1	A	658	A
1	A	659	A
1	A	672	A
1	A	679	G
1	A	682	A
1	A	687	G
1	A	688	A
1	A	689	A
1	A	690	U
1	A	691	A
1	A	692	G
1	A	696	G
1	A	697	U
1	A	698	U
1	A	700	A

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Mol	Chain	Res	Type
1	A	715	A
1	A	716	C
1	A	720	A
1	A	731	U
1	A	735	C
1	A	749	G
1	A	750	A
1	A	751	A
1	A	754	U
1	A	755	C
1	A	759	U
1	A	761	A
1	A	762	C
1	A	763	A
1	A	765	U
1	A	766	G
1	A	768	A
1	A	775	A
1	A	779	A
1	A	783	G
1	A	785	C
1	A	792	U
1	A	793	G
1	A	794	A
1	A	797	A
1	A	802	G
1	A	805	G
1	A	809	A
1	A	810	A
1	A	816	G
1	A	820	G
1	A	821	C
1	A	822	G
1	A	826	A
1	A	827	A
1	A	828	A
1	A	829	U
1	A	830	U
1	A	833	A
1	A	834	A
1	A	836	C
1	A	841	C

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Mol	Chain	Res	Type
1	A	842	U
1	A	845	A
1	A	850	G
1	A	851	C
1	A	857	C
1	A	862	C
1	A	868	A
1	A	871	U
1	A	872	U
1	A	873	U
1	A	875	G
1	A	887	A
1	A	891	A
1	A	897	A
1	A	899	U
1	A	900	G
1	A	904	G
1	A	908	A
1	A	911	A
1	A	914	G
1	A	916	U
1	A	918	G
1	A	920	A
1	A	923	A
1	A	925	G
1	A	926	G
1	A	927	G
1	A	928	C
1	A	939	U
1	A	940	U
1	A	943	C
1	A	948	U
1	A	952	A
1	A	955	A
1	A	957	C
1	A	959	C
1	A	960	C
1	A	965	G
1	A	970	U
1	A	971	U
1	A	972	A
1	A	977	A

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Mol	Chain	Res	Type
1	A	985	A
1	A	986	G
1	A	989	A
1	A	990	G
1	A	997	G
1	A	1001	A
1	A	1003	A
1	A	1005	G
1	A	1006	G
1	A	1017	A
1	A	1018	A
1	A	1019	A
1	A	1024	A
1	A	1025	A
1	A	1027	A
1	A	1028	G
1	A	1033	G
1	A	1034	A
1	A	1040	A
1	A	1043	U
1	A	1047	G
1	A	1048	U
1	A	1053	A
1	A	1056	U
1	A	1057	A
1	A	1070	A
1	A	1074	G
1	A	1076	A
1	A	1077	U
1	A	1078	G
1	A	1080	G
1	A	1082	C
1	A	1083	G
1	A	1086	G
1	A	1087	C
1	A	1089	C
1	A	1090	A
1	A	1091	G
1	A	1092	A
1	A	1093	C
1	A	1094	A
1	A	1095	A

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Mol	Chain	Res	Type
1	A	1098	A
1	A	1100	G
1	A	1101	A
1	A	1105	U
1	A	1106	G
1	A	1109	U
1	A	1111	A
1	A	1113	A
1	A	1114	A
1	A	1115	G
1	A	1116	C
1	A	1117	A
1	A	1118	G
1	A	1119	C
1	A	1120	C
1	A	1125	U
1	A	1126	U
1	A	1127	U
1	A	1132	A
1	A	1133	G
1	A	1137	G
1	A	1138	U
1	A	1140	A
1	A	1141	U
1	A	1143	G
1	A	1147	A
1	A	1148	C
1	A	1149	U
1	A	1150	A
1	A	1151	G
1	A	1153	C
1	A	1156	G
1	A	1161	A
1	A	1163	U
1	A	1164	G
1	A	1165	C
1	A	1168	C
1	A	1174	U
1	A	1175	G
1	A	1178	C
1	A	1179	C
1	A	1183	G

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Mol	Chain	Res	Type
1	A	1185	U
1	A	1186	A
1	A	1192	A
1	A	1195	A
1	A	1201	G
1	A	1208	A
1	A	1210	U
1	A	1213	C
1	A	1216	U
1	A	1217	U
1	A	1218	G
1	A	1225	G
1	A	1234	G
1	A	1258	A
1	A	1259	U
1	A	1265	G
1	A	1267	A
1	A	1271	G
1	A	1274	G
1	A	1275	A
1	A	1276	G
1	A	1284	A
1	A	1290	G
1	A	1291	A
1	A	1293	U
1	A	1294	G
1	A	1297	G
1	A	1298	G
1	A	1304	G
1	A	1309	G
1	A	1310	A
1	A	1311	A
1	A	1312	A
1	A	1320	G
1	A	1337	A
1	A	1338	U
1	A	1339	U
1	A	1340	G
1	A	1341	A
1	A	1342	C
1	A	1344	A
1	A	1355	A

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Mol	Chain	Res	Type
1	A	1357	G
1	A	1358	A
1	A	1359	A
1	A	1366	U
1	A	1370	C
1	A	1379	A
1	A	1382	C
1	A	1384	G
1	A	1387	C
1	A	1392	G
1	A	1401	G
1	A	1402	A
1	A	1412	G
1	A	1416	U
1	A	1421	A
1	A	1422	A
1	A	1423	C
1	A	1429	G
1	A	1431	U
1	A	1432	A
1	A	1435	C
1	A	1440	A
1	A	1444	C
1	A	1445	C
1	A	1447	A
1	A	1449	A
1	A	1450	A
1	A	1453	G
1	A	1454	U
1	A	1455	U
1	A	1456	U
1	A	1457	U
1	A	1459	A
1	A	1460	U
1	A	1461	C
1	A	1462	G
1	A	1463	A
1	A	1464	U
1	A	1466	G
1	A	1469	G
1	A	1471	A
1	A	1472	C

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Mol	Chain	Res	Type
1	A	1479	G
1	A	1481	A
1	A	1483	A
1	A	1486	C
1	A	1487	G
1	A	1488	A
1	A	1491	C
1	A	1493	U
1	A	1495	C
1	A	1496	G
1	A	1497	A
1	A	1498	U
1	A	1499	U
1	A	1503	U
1	A	1504	U
1	A	1505	G
1	A	1506	C
1	A	1507	A
1	A	1509	G
1	A	1510	U
1	A	1512	U
1	A	1513	A
1	A	1516	C
1	A	1517	A
1	A	1519	U
1	A	1520	A
1	A	1521	A
1	A	1522	G
1	A	1524	C
1	A	1526	G
1	A	1527	A
1	A	1533	A
1	A	1534	G
1	A	1536	C
1	A	1537	A
1	A	1538	A
1	A	1540	U
1	A	1541	C
1	A	1543	G
1	A	1545	U
1	A	1550	G
1	A	1551	U

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Mol	Chain	Res	Type
1	A	1552	U
1	A	1553	A
1	A	1555	G
1	A	1556	G
1	A	1560	A
1	A	1561	G
1	A	1565	U
1	A	1568	U
1	A	1569	G
1	A	1570	G
1	A	1571	G
1	A	1572	G
1	A	1573	A
1	A	1575	A
1	A	1578	A
1	A	1579	C
1	A	1580	A
1	A	1581	U
1	A	1582	U
1	A	1583	G
1	A	1584	U
1	A	1585	G
1	A	1586	U
1	A	1590	C
1	A	1591	G
1	A	1592	A
1	A	1594	U
1	A	1595	C
1	A	1598	U
1	A	1599	G
1	A	1600	A
1	A	1601	U
1	A	1604	C
1	A	1605	A
1	A	1606	C
1	A	1607	A
1	A	1613	G
1	A	1616	A
1	A	1623	U
1	A	1625	U
1	A	1626	A
1	A	1627	G

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Mol	Chain	Res	Type
1	A	1629	U
1	A	1630	A
1	A	1631	G
1	A	1632	A
1	A	1633	A
1	A	1634	A
1	A	1635	A
1	A	1636	U
1	A	1639	G
1	A	1641	G
1	A	1651	C
1	A	1653	A
1	A	1654	A
1	A	1658	A
1	A	1659	C
1	A	1660	A
1	A	1661	C
1	A	1662	A
1	A	1666	A
1	A	1675	G
1	A	1678	A
1	A	1679	A
1	A	1690	A
1	A	1691	G
1	A	1692	C
1	A	1693	G
1	A	1698	A
1	A	1701	U
1	A	1707	U
1	A	1718	G
1	A	1732	U
1	A	1737	U
1	A	1738	C
1	A	1739	G
1	A	1740	G
1	A	1741	G
1	A	1742	A
1	A	1743	G
1	A	1747	G
1	A	1757	U
1	A	1758	A
1	A	1759	G

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Mol	Chain	Res	Type
1	A	1760	G
1	A	1761	G
1	A	1762	U
1	A	1763	U
1	A	1764	A
1	A	1765	A
1	A	1767	G
1	A	1768	C
1	A	1771	A
1	A	1772	G
1	A	1773	A
1	A	1777	G
1	A	1783	G
1	A	1785	G
1	A	1790	G
1	A	1791	G
1	A	1797	G
1	A	1800	A
1	A	1806	U
1	A	1808	U
1	A	1811	A
1	A	1812	A
1	A	1814	A
1	A	1816	A
1	A	1818	A
1	A	1820	G
1	A	1825	U
1	A	1826	G
1	A	1827	C
1	A	1828	U
1	A	1829	A
1	A	1830	A
1	A	1835	U
1	A	1838	G
1	A	1843	U
1	A	1846	A
1	A	1856	A
1	A	1866	G
1	A	1867	G
1	A	1870	C
1	A	1871	U
1	A	1875	A

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Mol	Chain	Res	Type
1	A	1876	G
1	A	1877	G
1	A	1878	U
1	A	1884	G
1	A	1888	U
1	A	1890	G
1	A	1892	U
1	A	1893	A
1	A	1895	C
1	A	1897	U
1	A	1898	C
1	A	1899	U
1	A	1900	G
1	A	1902	G
1	A	1903	A
1	A	1904	A
1	A	1906	C
1	A	1907	U
1	A	1908	A
1	A	1911	A
1	A	1912	A
1	A	1913	U
1	A	1914	C
1	A	1916	A
1	A	1923	A
1	A	1926	A
1	A	1927	A
1	A	1933	G
1	A	1935	C
1	A	1938	U
1	A	1939	A
1	A	1945	A
1	A	1946	A
1	A	1950	U
1	A	1954	A
1	A	1956	G
1	A	1957	G
1	A	1958	U
1	A	1961	C
1	A	1963	A
1	A	1964	A
1	A	1965	A

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Mol	Chain	Res	Type
1	A	1966	U
1	A	1967	U
1	A	1968	C
1	A	1970	U
1	A	1971	U
1	A	1972	G
1	A	1979	A
1	A	1982	U
1	A	1990	C
1	A	1996	A
1	A	1997	A
1	A	1998	A
1	A	1999	G
1	A	2008	A
1	A	2009	U
1	A	2012	G
1	A	2018	U
1	A	2019	G
1	A	2020	U
1	A	2023	C
1	A	2024	A
1	A	2029	G
1	A	2045	A
1	A	2047	A
1	A	2048	G
1	A	2057	A
1	A	2058	A
1	A	2059	G
1	A	2060	A
1	A	2061	U
1	A	2062	G
1	A	2070	C
1	A	2075	G
1	A	2076	A
1	A	2079	G
1	A	2082	C
1	A	2083	G
1	A	2085	A
1	A	2086	A
1	A	2087	A
1	A	2088	G
1	A	2096	G

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Mol	Chain	Res	Type
1	A	2107	G
1	A	2109	A
1	A	2111	C
1	A	2114	G
1	A	2117	A
1	A	2118	U
1	A	2119	U
1	A	2120	G
1	A	2127	G
1	A	2128	G
1	A	2129	C
1	A	2130	A
1	A	2131	C
1	A	2132	A
1	A	2133	G
1	A	2134	C
1	A	2135	U
1	A	2139	A
1	A	2140	C
1	A	2143	G
1	A	2144	A
1	A	2145	U
1	A	2146	A
1	A	2147	G
1	A	2153	A
1	A	2154	G
1	A	2155	C
1	A	2156	C
1	A	2157	U
1	A	2158	U
1	A	2159	U
1	A	2161	A
1	A	2163	A
1	A	2164	C
1	A	2168	A
1	A	2173	U
1	A	2175	G
1	A	2180	C
1	A	2185	A
1	A	2186	G
1	A	2188	C
1	A	2190	C

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Mol	Chain	Res	Type
1	A	2193	G
1	A	2194	U
1	A	2195	G
1	A	2198	A
1	A	2204	C
1	A	2209	G
1	A	2211	U
1	A	2215	U
1	A	2219	C
1	A	2221	U
1	A	2224	U
1	A	2225	A
1	A	2231	C
1	A	2232	A
1	A	2234	C
1	A	2235	A
1	A	2236	C
1	A	2237	U
1	A	2238	U
1	A	2239	A
1	A	2240	U
1	A	2244	G
1	A	2252	A
1	A	2254	A
1	A	2261	G
1	A	2262	G
1	A	2265	G
1	A	2266	G
1	A	2273	G
1	A	2278	G
1	A	2290	C
1	A	2293	A
1	A	2296	A
1	A	2306	G
1	A	2310	C
1	A	2313	A
1	A	2315	A
1	A	2323	U
1	A	2324	C
1	A	2325	A
1	A	2328	A
1	A	2331	G

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Mol	Chain	Res	Type
1	A	2333	U
1	A	2334	G
1	A	2335	G
1	A	2337	A
1	A	2338	A
1	A	2339	U
1	A	2345	A
1	A	2346	U
1	A	2347	A
1	A	2348	G
1	A	2349	A
1	A	2352	G
1	A	2354	A
1	A	2356	A
1	A	2357	G
1	A	2358	G
1	A	2362	A
1	A	2363	A
1	A	2364	G
1	A	2369	C
1	A	2370	U
1	A	2371	U
1	A	2372	G
1	A	2374	C
1	A	2377	C
1	A	2385	A
1	A	2388	A
1	A	2396	A
1	A	2399	G
1	A	2406	G
1	A	2407	A
1	A	2409	G
1	A	2410	G
1	A	2412	C
1	A	2415	A
1	A	2417	U
1	A	2418	G
1	A	2419	A
1	A	2427	G
1	A	2429	U
1	A	2433	C
1	A	2434	A

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Mol	Chain	Res	Type
1	A	2438	A
1	A	2439	A
1	A	2440	G
1	A	2441	G
1	A	2449	C
1	A	2450	U
1	A	2451	C
1	A	2456	G
1	A	2457	A
1	A	2459	A
1	A	2460	A
1	A	2461	A
1	A	2463	G
1	A	2468	C
1	A	2474	G
1	A	2475	A
1	A	2479	C
1	A	2486	A
1	A	2492	C
1	A	2495	A
1	A	2496	A
1	A	2497	G
1	A	2502	C
1	A	2503	A
1	A	2505	A
1	A	2506	U
1	A	2508	G
1	A	2509	A
1	A	2511	G
1	A	2518	U
1	A	2519	U
1	A	2521	G
1	A	2525	C
1	A	2528	C
1	A	2529	G
1	A	2530	A
1	A	2531	U
1	A	2533	U
1	A	2540	A
1	A	2545	A
1	A	2552	G
1	A	2553	G

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Mol	Chain	Res	Type
1	A	2556	G
1	A	2558	A
1	A	2559	G
1	A	2562	G
1	A	2568	A
1	A	2570	G
1	A	2574	U
1	A	2581	U
1	A	2582	U
1	A	2583	C
1	A	2589	U
1	A	2592	A
1	A	2593	A
1	A	2594	G
1	A	2599	A
1	A	2600	C
1	A	2601	G
1	A	2605	G
1	A	2609	G
1	A	2610	G
1	A	2613	C
1	A	2626	G
1	A	2629	A
1	A	2630	G
1	A	2636	U
1	A	2637	C
1	A	2640	U
1	A	2641	A
1	A	2642	U
1	A	2648	G
1	A	2650	G
1	A	2656	A
1	A	2657	G
1	A	2667	G
1	A	2671	A
1	A	2673	C
1	A	2674	U
1	A	2679	U
1	A	2683	U
1	A	2687	A
1	A	2688	G
1	A	2690	G

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Mol	Chain	Res	Type
1	A	2692	A
1	A	2695	G
1	A	2697	G
1	A	2699	U
1	A	2700	G
1	A	2708	C
1	A	2709	U
1	A	2716	U
1	A	2733	A
1	A	2741	G
1	A	2745	G
1	A	2750	C
1	A	2751	U
1	A	2753	U
1	A	2756	G
1	A	2757	U
1	A	2759	G
1	A	2761	C
1	A	2764	G
1	A	2765	A
1	A	2766	U
1	A	2769	G
1	A	2771	G
1	A	2773	U
1	A	2775	A
1	A	2776	A
1	A	2777	A
1	A	2778	G
1	A	2779	C
1	A	2782	C
1	A	2783	U
1	A	2784	A
1	A	2785	A
1	A	2788	A
1	A	2791	A
1	A	2792	A
1	A	2794	C
1	A	2803	A
1	A	2804	G
1	A	2805	A
1	A	2806	U
1	A	2807	G

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Mol	Chain	Res	Type
1	A	2817	A
1	A	2818	A
1	A	2820	U
1	A	2821	U
1	A	2822	C
1	A	2823	G
1	A	2824	G
1	A	2827	A
1	A	2828	U
1	A	2829	A
1	A	2832	A
1	A	2838	C
1	A	2840	A
1	A	2842	G
1	A	2843	A
1	A	2850	G
1	A	2853	U
1	A	2855	A
1	A	2856	U
1	A	2869	G
1	A	2870	A
1	A	2878	U
1	A	2879	G
1	A	2887	G
1	A	2889	G
1	A	2892	G
1	A	2899	A
1	A	2904	U
1	A	2905	C
1	A	2906	G
1	A	2913	G
1	A	2914	A
2	B	2	C
2	B	5	G
2	B	7	G
2	B	10	U
2	B	11	A
2	B	12	U
2	B	14	G
2	B	20	A
2	B	22	G
2	B	23	U

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Mol	Chain	Res	Type
2	B	24	C
2	B	27	A
2	B	29	C
2	B	30	U
2	B	33	U
2	B	35	C
2	B	39	G
2	B	40	C
2	B	41	C
2	B	42	G
2	B	51	A
2	B	54	U
2	B	55	A
2	B	63	U
2	B	64	A
2	B	65	G
2	B	66	C
2	B	84	U
2	B	86	A
2	B	87	C
2	B	88	G
2	B	93	G
2	B	95	U
2	B	106	G
2	B	109	G
2	B	111	C
2	B	113	G
2	B	115	C

All (36) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	11	U
1	A	69	C
1	A	157	U
1	A	169	G
1	A	227	G
1	A	267	G
1	A	291	G
1	A	335	U
1	A	337	A
1	A	385	U

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Mol	Chain	Res	Type
1	A	576	U
1	A	657	U
1	A	688	A
1	A	697	U
1	A	809	A
1	A	840	C
1	A	890	G
1	A	1024	A
1	A	1026	C
1	A	1503	U
1	A	1520	A
1	A	1521	A
1	A	1632	A
1	A	1658	A
1	A	1756	U
1	A	2117	A
1	A	2127	G
1	A	2237	U
1	A	2261	G
1	A	2428	U
1	A	2450	U
1	A	2455	G
1	A	2462	A
1	A	2749	G
1	A	2782	C
1	A	2878	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	8

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2207:U	O3'	2208:A	P	11.16
1	A	1939:A	O3'	1944:U	P	10.86
1	A	929:C	O3'	937:G	P	10.36
1	A	1096:C	O3'	1097:U	P	7.19
1	A	1153:C	O3'	1154:G	P	7.11
1	A	770:G	O3'	771:G	P	3.87
1	A	2217:G	O3'	2218:G	P	3.68
1	A	1448:U	O3'	1449:A	P	3.05

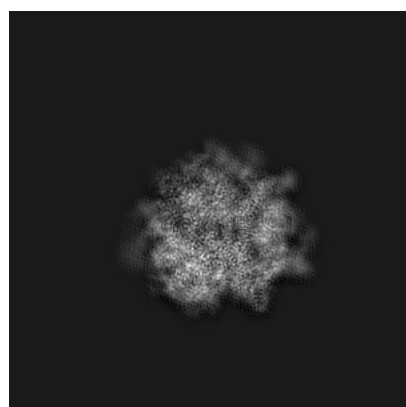
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10078. These allow visual inspection of the internal detail of the map and identification of artifacts.

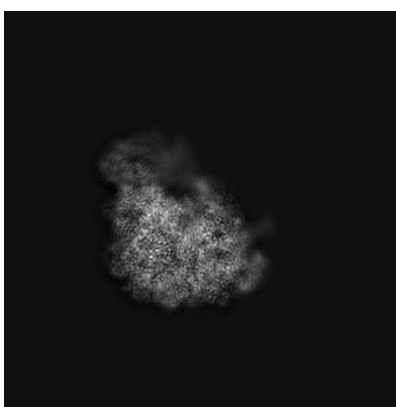
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

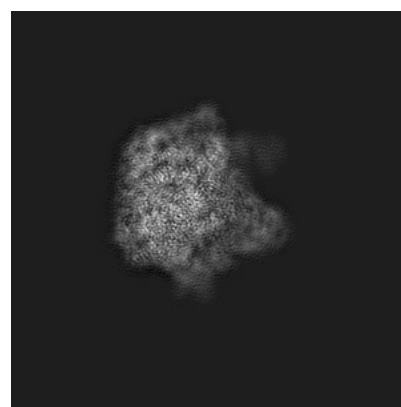
6.1.1 Primary map



X



Y

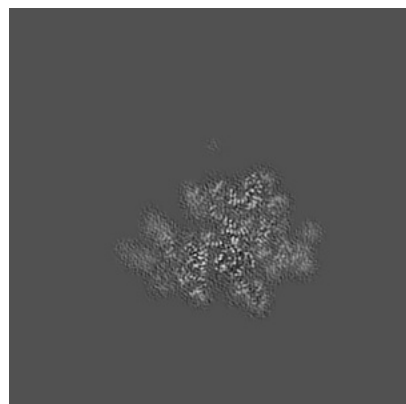


Z

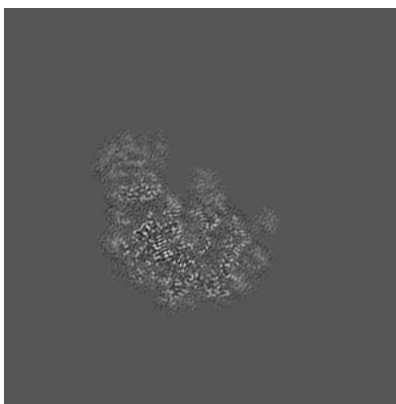
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

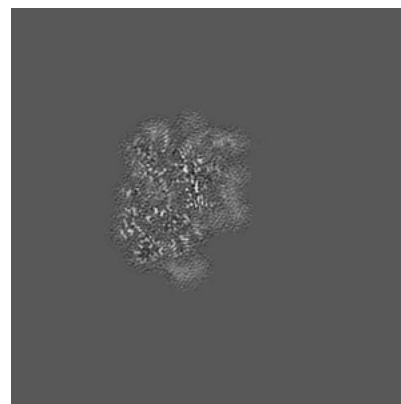
6.2.1 Primary map



X Index: 200



Y Index: 200

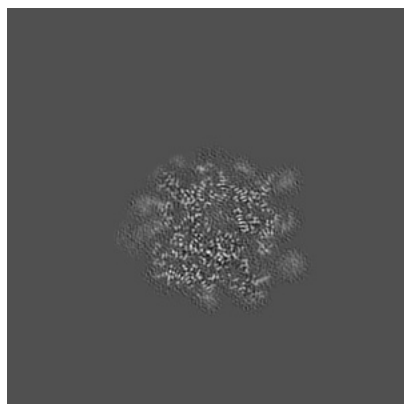


Z Index: 200

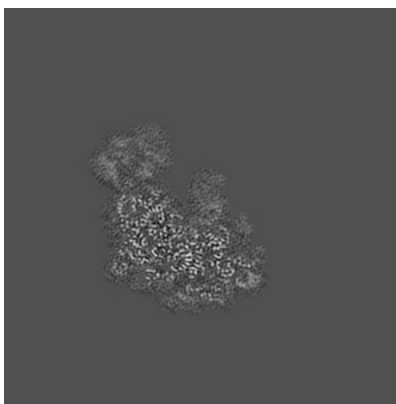
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

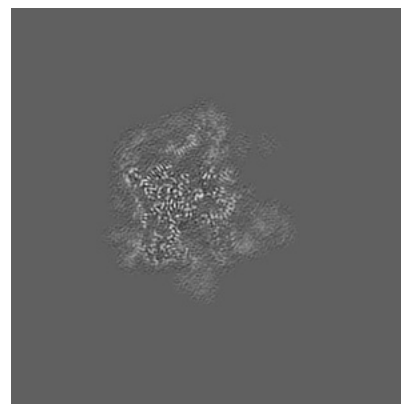
6.3.1 Primary map



X Index: 164



Y Index: 185

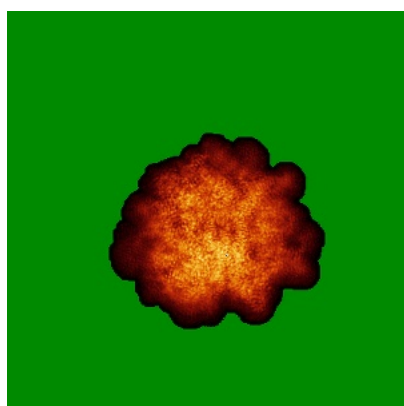


Z Index: 154

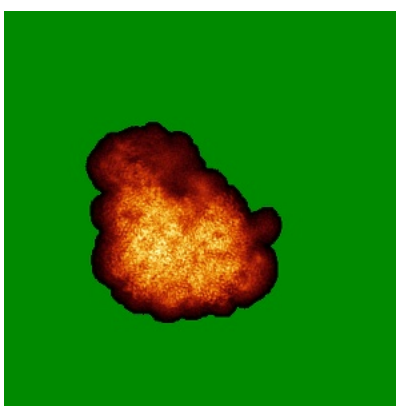
The images above show the largest variance slices of the map in three orthogonal directions.

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

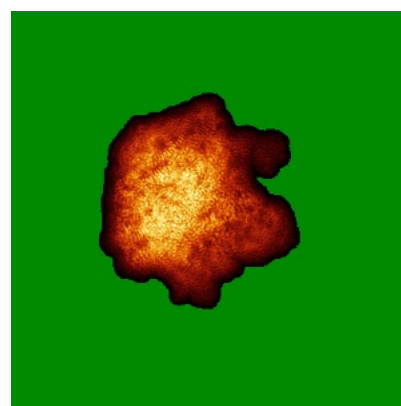
6.4.1 Primary map



X



Y

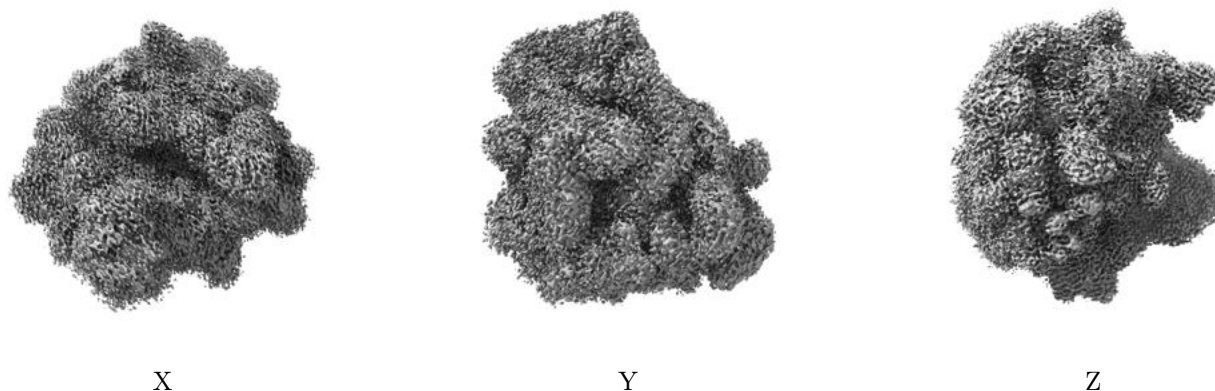


Z

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

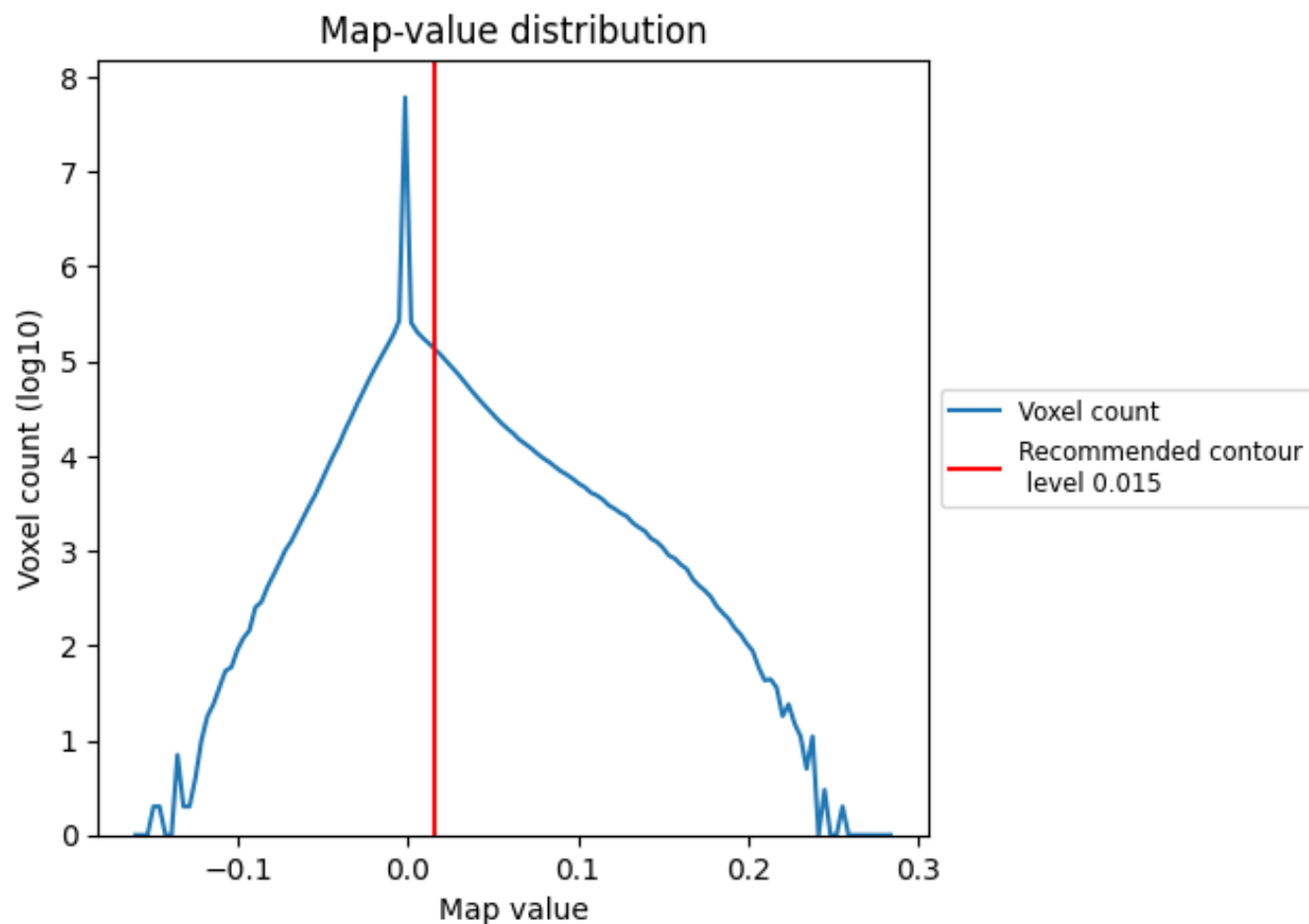
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

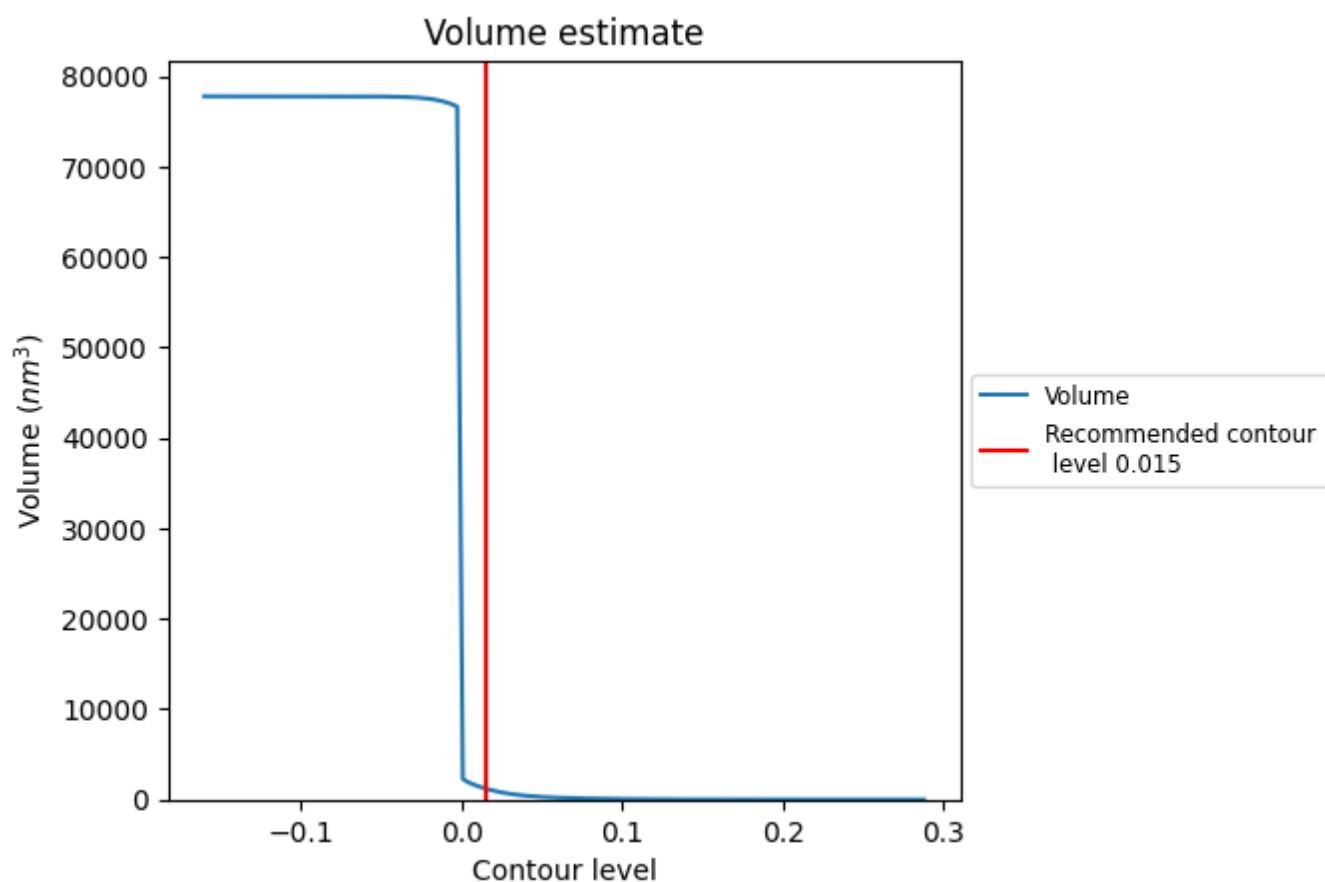
This section contains the results of statistical analysis of the map.

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.

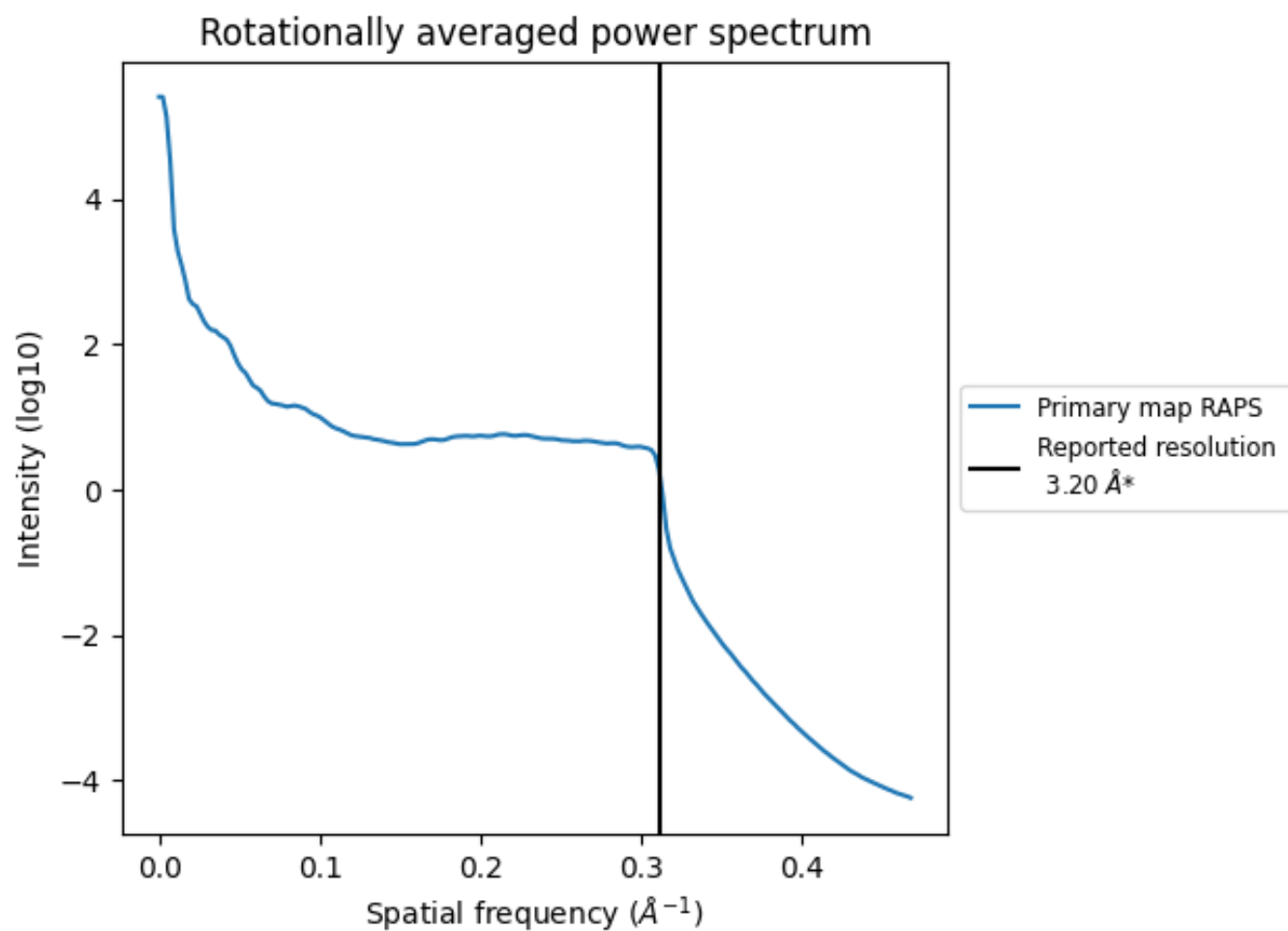
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1203 nm^3 ; this corresponds to an approximate mass of 1087 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 0.312 Å⁻¹

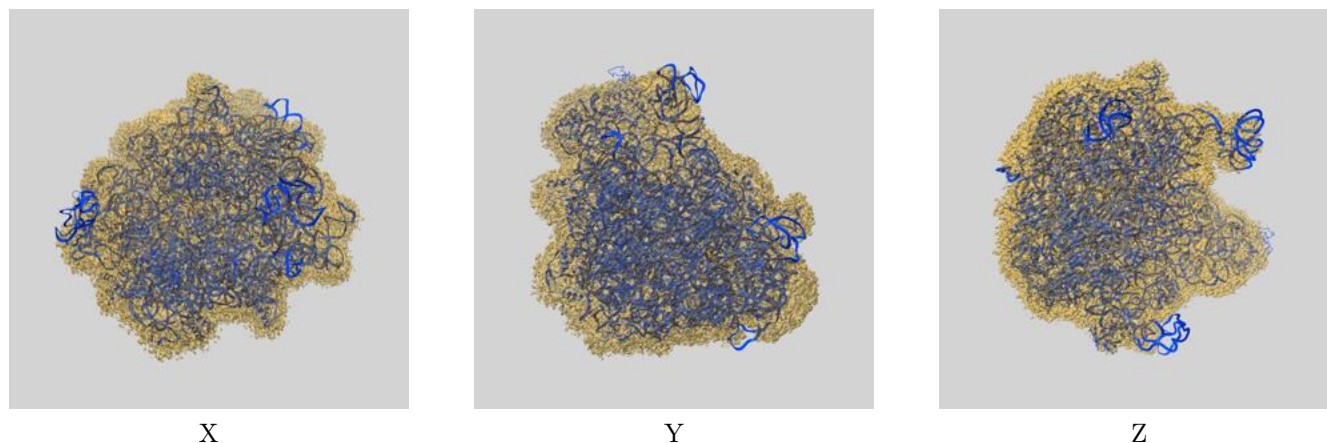
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

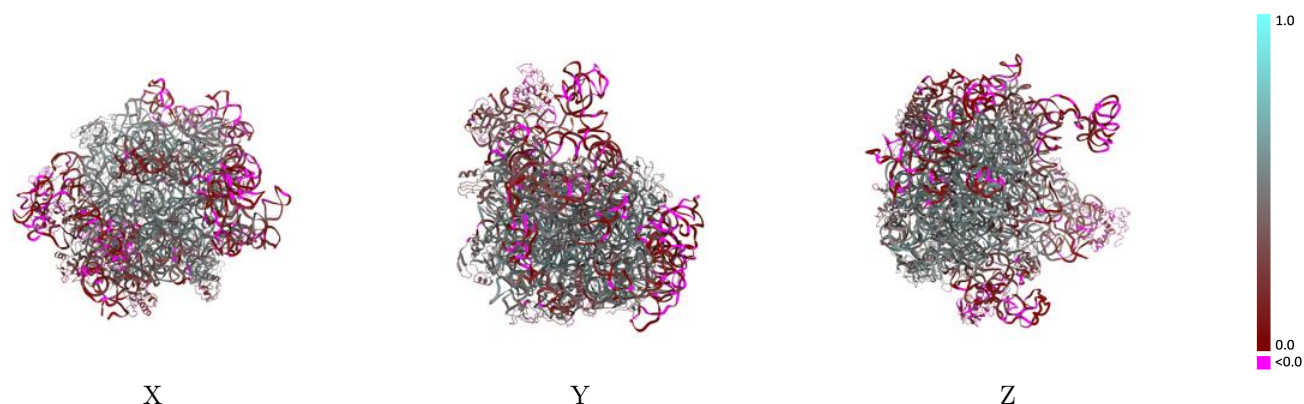
This section contains information regarding the fit between EMDB map EMD-10078 and PDB model 6S12. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



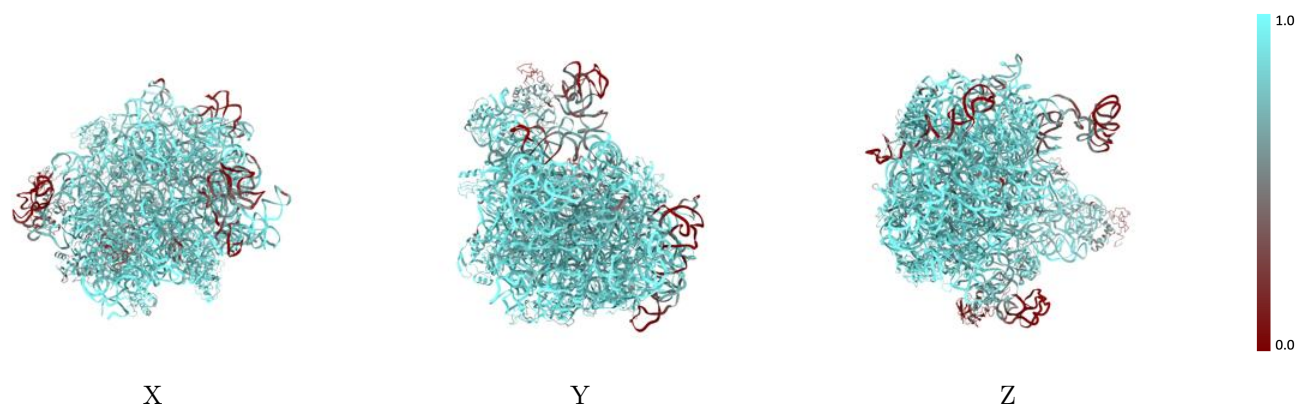
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



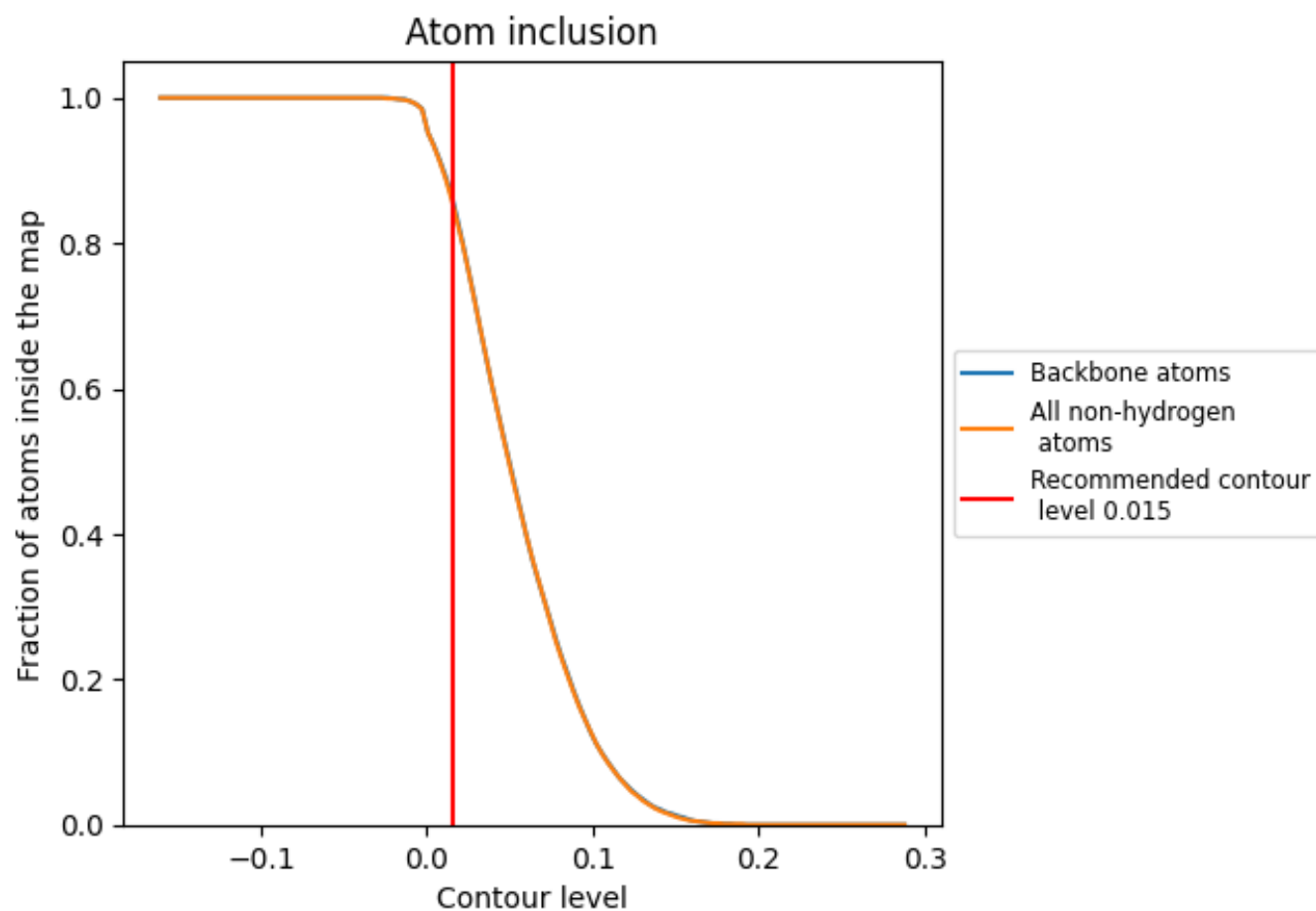
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8590	 0.3640
1	 0.5010	 0.1650
2	 0.9020	 0.4630
3	 0.8980	 0.4510
4	 0.5050	 0.0530
A	 0.8760	 0.3690
B	 0.9060	 0.2130
C	 0.8870	 0.4390
D	 0.9270	 0.4850
E	 0.9040	 0.4640
F	 0.6080	 0.0970
G	 0.3130	 0.0670
H	 0.9140	 0.4760
I	 0.8750	 0.4380
J	 0.9000	 0.4190
K	 0.8670	 0.3600
L	 0.8990	 0.4580
M	 0.8390	 0.2650
N	 0.9220	 0.4640
O	 0.9090	 0.4850
P	 0.9140	 0.4630
Q	 0.8700	 0.4230
R	 0.8860	 0.3960
S	 0.8390	 0.3390
T	 0.7120	 0.2510
U	 0.8890	 0.4270
V	 0.7740	 0.3170
W	 0.8440	 0.2920
X	 0.9090	 0.4770
Y	 0.2120	 0.0390
Z	 0.8470	 0.3190

