



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 05:12 AM UTC

PDB ID : 5LMT / pdb_00005lmt
EMDB ID : EMD-4079
Title : Structure of bacterial 30S-IF1-IF3-mRNA-tRNA translation pre-initiation complex(state-3)
Authors : Hussain, T.; Llacer, J.L.; Wimberly, B.T.; Ramakrishnan, V.
Deposited on : 2016-08-01
Resolution : 4.15 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

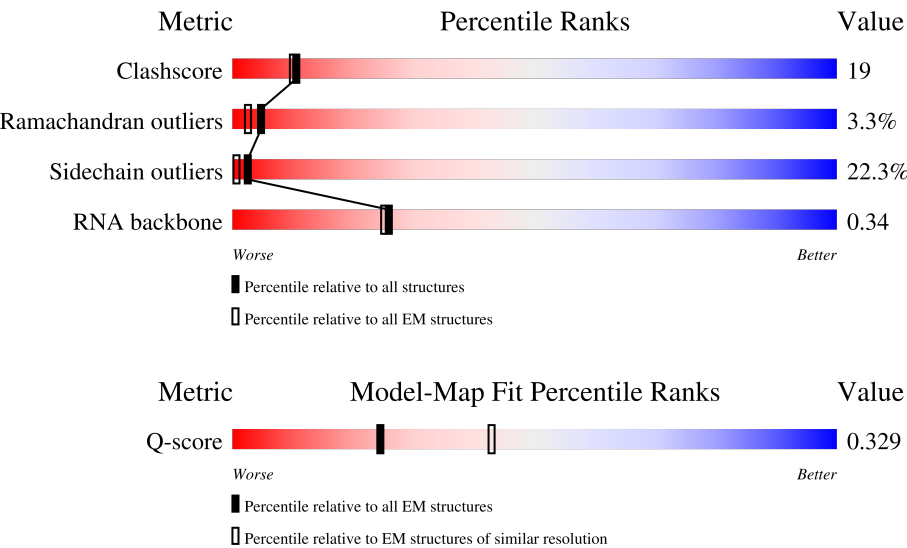
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.15 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	5475 (3.66 - 4.65)

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	1522	27% 52% 18% .
2	B	256	56% 46% 34% 10% . 9%
3	C	239	43% 36% 6% . 14%

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	132	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	V	27	
22	W	72	
23	X	171	
24	Y	42	
25	Z	77	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
27	ZN	D	300	-	-	X	-

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 55776 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1515	Total	C	N	O	P	0	0
			32544	14490	6021	10521	1512		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	234	Total	C	N	O	S	0	0
			1900	1213	341	341	5		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	206	Total	C	N	O	S	0	0
			1612	1016	314	281	1		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	150	Total	C	N	O	S	0	0
			1146	724	217	201	4		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	127	Total	C	N	O	0	0
			1010	639	197	174		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	98	Total	C	N	O	S	0	0
			792	498	156	137	1		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	119	Total	C	N	O	S	0	0
			885	549	168	165	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	124	Total	C	N	O	S	0	0
			970	611	195	163	1		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	119	Total	C	N	O	S	0	0
			946	585	195	164	2		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	83	Total	C	N	O	S	0	0
			700	443	139	117	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	99	Total	C	N	O	S	0	0
			823	528	151	142	2		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	73	Total	C	N	O	0	0
			598	381	118	99		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	82	Total	C	N	O	S	0	0
			655	419	120	114	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

- Molecule 21 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	V	24	Total	C	N	O	0	0
			208	128	50	30		

- Molecule 22 is a protein called Translation initiation factor IF-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	71	Total	C	N	O	S	0	0
			570	362	103	103	2		

- Molecule 23 is a protein called Translation initiation factor IF-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	164	Total	C	N	O	S	0	0
			1336	841	245	241	9		

- Molecule 24 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	20	Total	C	N	O	P	0	0
			439	196	89	134	20		

- Molecule 25 is a RNA chain called tRNAi.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Z	77	Total	C	N	O	P	S	0	0
			1646	735	297	536	77	1		

- Molecule 26 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
26	A	83	Total	Mg	0
			83	83	
26	E	1	Total	Mg	0
			1	1	
26	W	1	Total	Mg	0
			1	1	
26	Z	1	Total	Mg	0
			1	1	

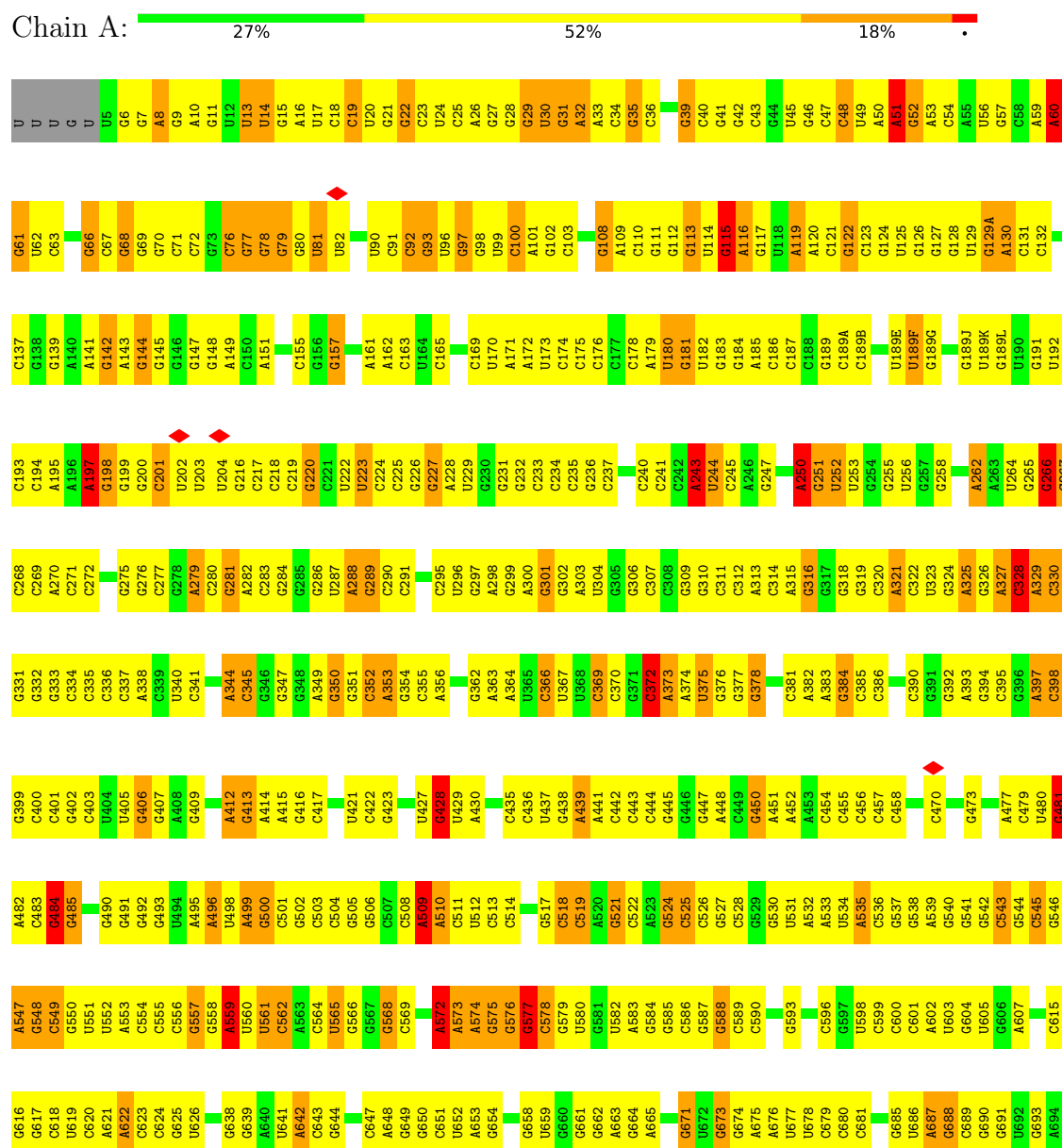
- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
27	D	1	Total 1	Zn 1	0
27	N	1	Total 1	Zn 1	0

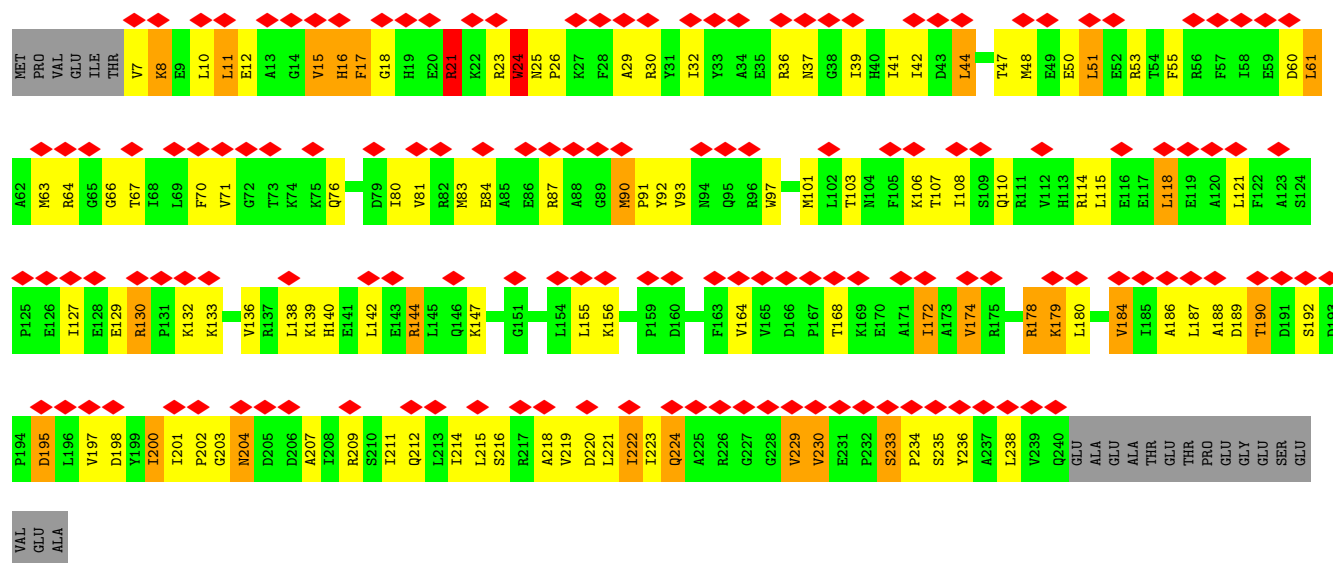
3 Residue-property plots

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

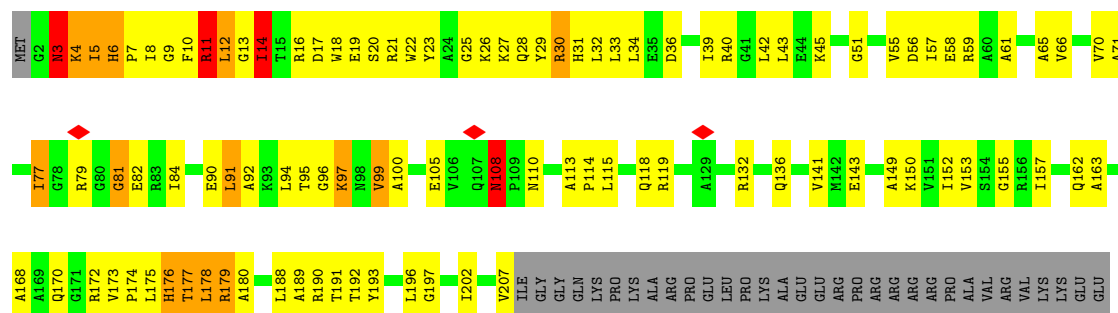
• Molecule 1: 16S ribosomal RNA



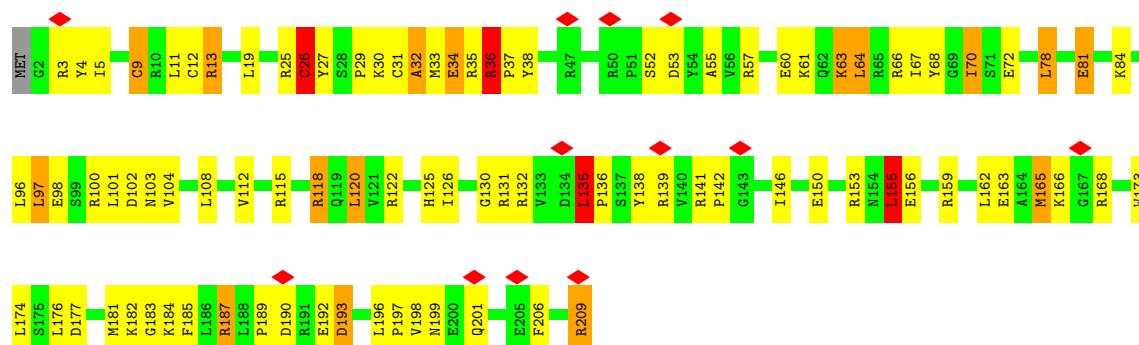




• Molecule 3: 30S ribosomal protein S3

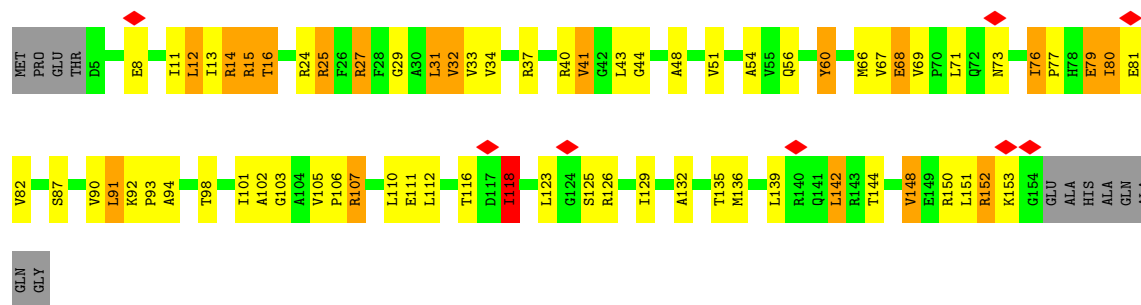


• Molecule 4: 30S ribosomal protein S4

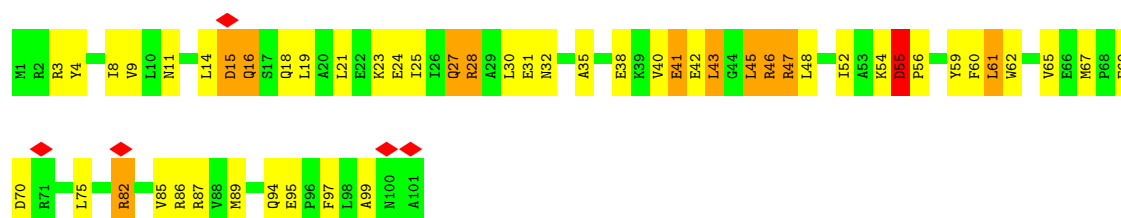


• Molecule 5: 30S ribosomal protein S5

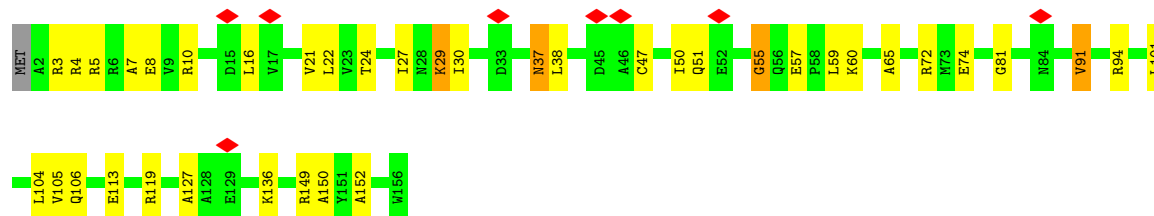
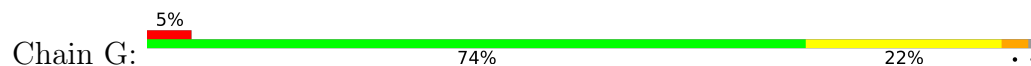




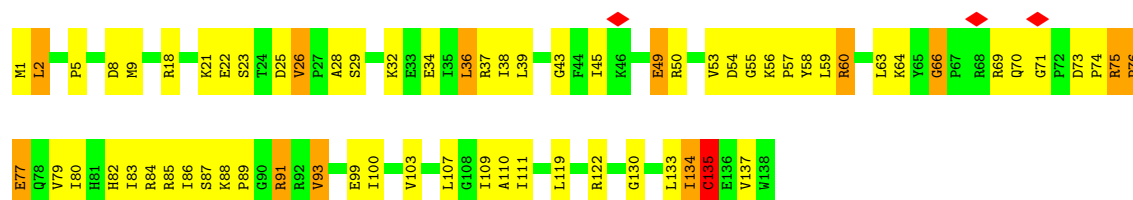
• Molecule 6: 30S ribosomal protein S6



• Molecule 7: 30S ribosomal protein S7



• Molecule 8: 30S ribosomal protein S8

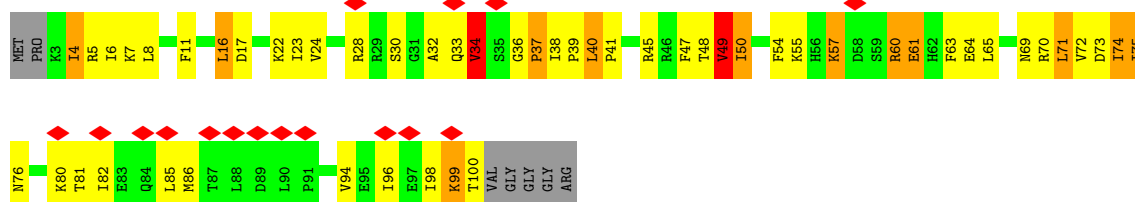
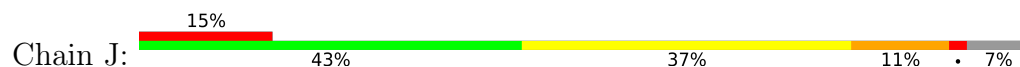


• Molecule 9: 30S ribosomal protein S9

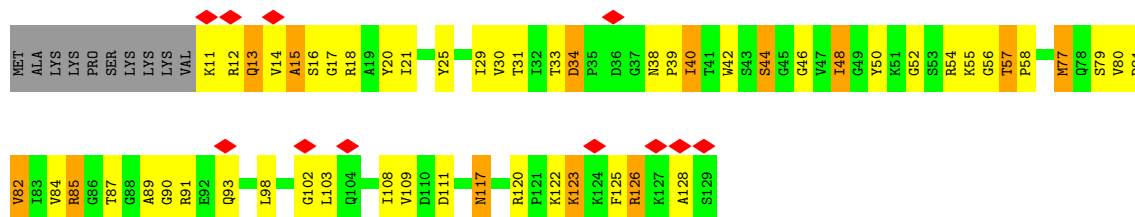




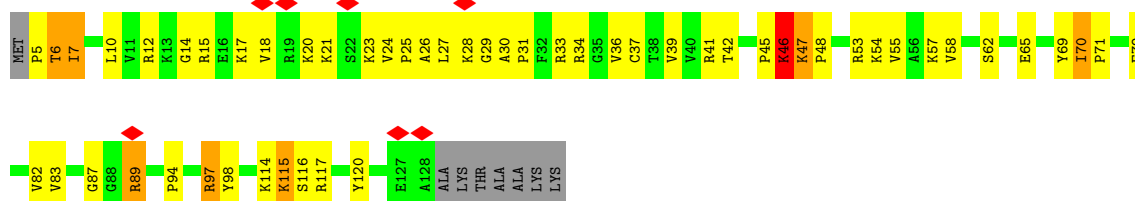
• Molecule 10: 30S ribosomal protein S10



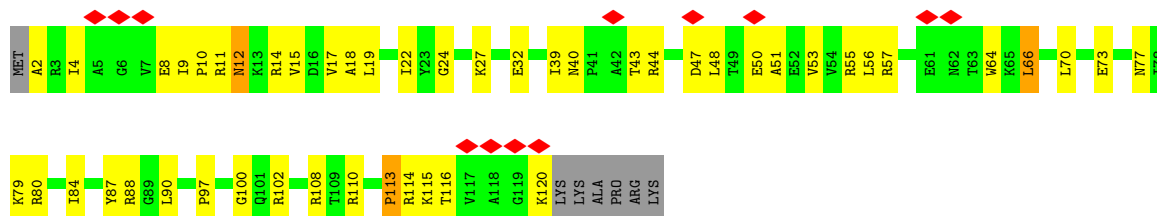
• Molecule 11: 30S ribosomal protein S11



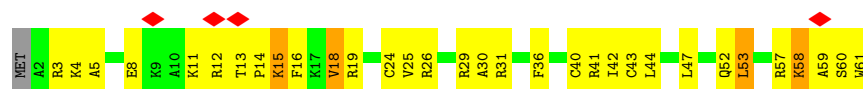
• Molecule 12: 30S ribosomal protein S12



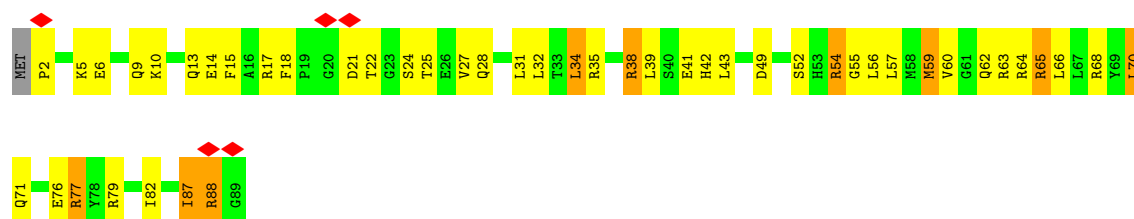
• Molecule 13: 30S ribosomal protein S13



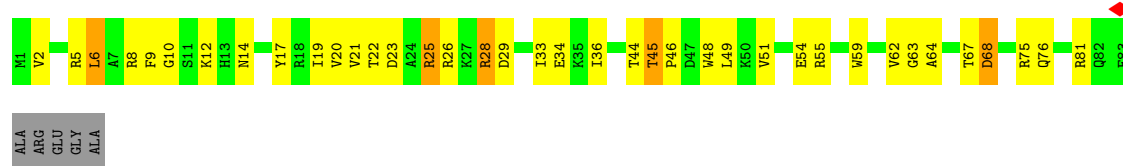
• Molecule 14: 30S ribosomal protein S14 type Z



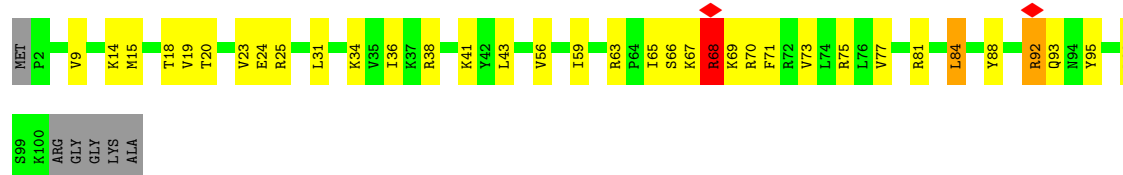
• Molecule 15: 30S ribosomal protein S15



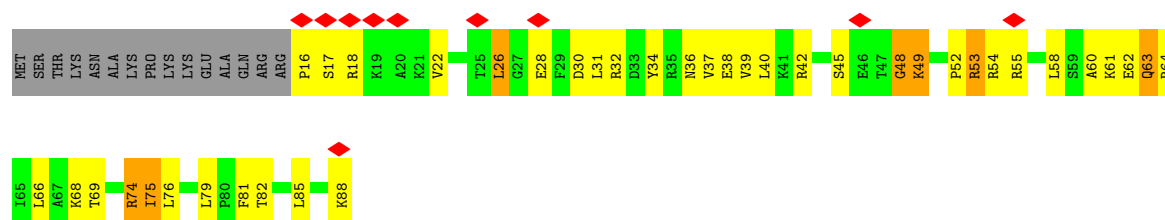
• Molecule 16: 30S ribosomal protein S16



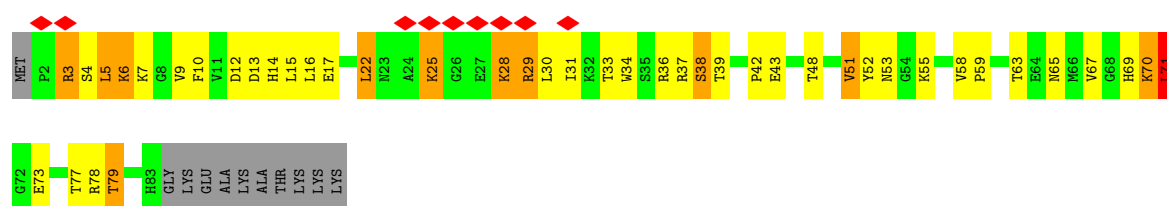
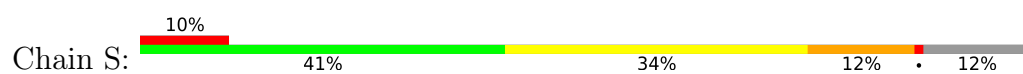
• Molecule 17: 30S ribosomal protein S17



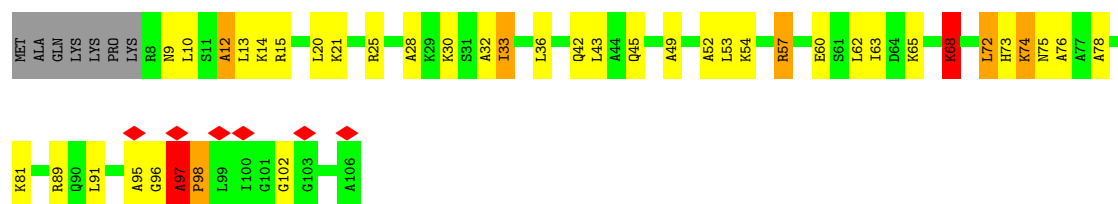
• Molecule 18: 30S ribosomal protein S18



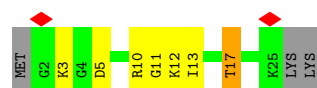
• Molecule 19: 30S ribosomal protein S19



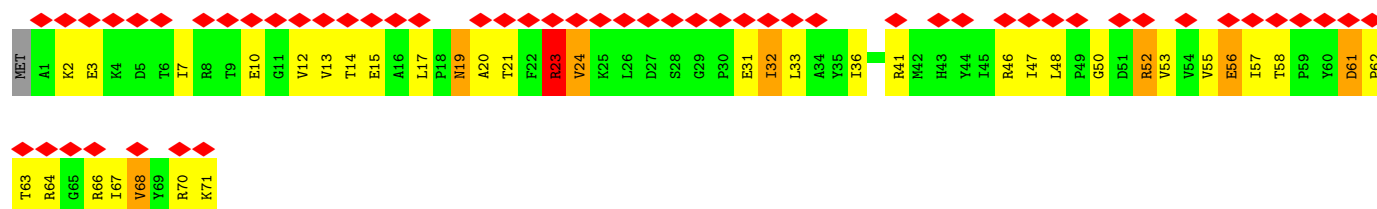
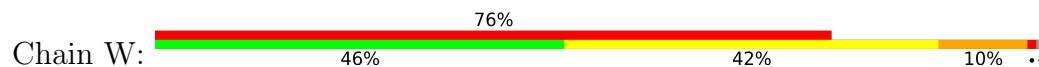
- Molecule 20: 30S ribosomal protein S20



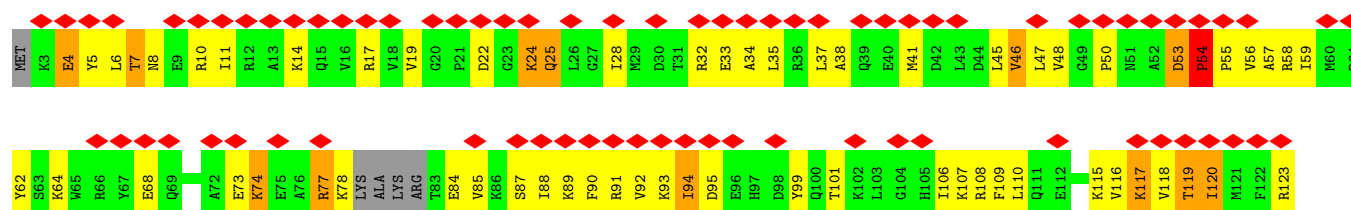
- Molecule 21: 30S ribosomal protein Thx

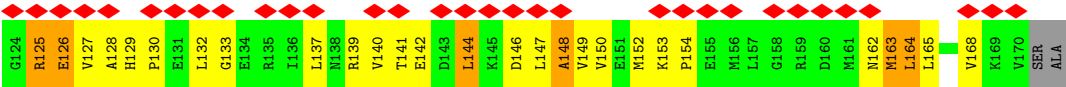


- Molecule 22: Translation initiation factor IF-1

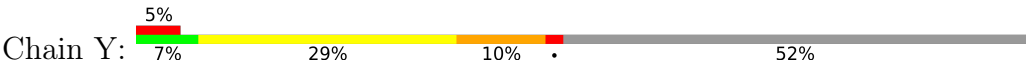


- Molecule 23: Translation initiation factor IF-3

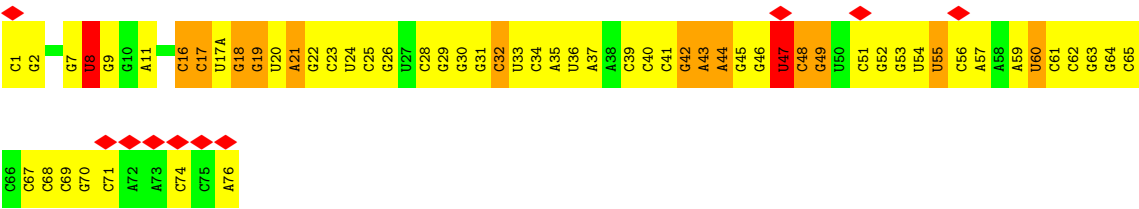




• Molecule 24: mRNA



• Molecule 25: tRNAi



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24771	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	OTHER	Depositor
Maximum map value	0.574	Depositor
Minimum map value	-0.157	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.08	Depositor
Map size ($\text{\AA}$)	348.4, 348.4, 348.4	wwPDB
Map dimensions	260, 260, 260	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PSU, OMC, ZN, 4SU, 5MU, G7M, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.44	2/36419 (0.0%)	0.85	90/56821 (0.2%)
2	B	0.73	0/1935	1.22	9/2609 (0.3%)
3	C	0.59	0/1636	1.10	3/2205 (0.1%)
4	D	0.59	0/1733	1.18	7/2318 (0.3%)
5	E	0.60	0/1162	1.28	8/1564 (0.5%)
6	F	0.56	0/856	1.09	3/1154 (0.3%)
7	G	0.57	0/1276	1.13	0/1709
8	H	0.56	0/1136	1.10	6/1527 (0.4%)
9	I	0.58	0/1029	1.14	3/1379 (0.2%)
10	J	0.73	0/805	1.10	2/1082 (0.2%)
11	K	0.64	0/900	1.12	2/1213 (0.2%)
12	L	0.56	0/986	1.05	3/1320 (0.2%)
13	M	0.69	0/956	1.20	4/1281 (0.3%)
14	N	0.54	0/501	1.03	0/664
15	O	0.61	0/745	1.20	0/992
16	P	0.52	0/716	1.01	0/963
17	Q	0.52	0/836	1.04	1/1117 (0.1%)
18	R	0.64	0/604	1.12	0/801
19	S	0.66	0/670	1.13	4/903 (0.4%)
20	T	0.64	0/765	1.37	5/1007 (0.5%)
21	V	0.56	0/212	0.99	0/277
22	W	0.77	0/580	1.32	5/782 (0.6%)
23	X	0.83	0/1354	1.24	6/1813 (0.3%)
24	Y	0.49	0/492	0.85	1/762 (0.1%)
25	Z	0.57	2/1720 (0.1%)	0.88	2/2678 (0.1%)
All	All	0.52	4/60024 (0.0%)	0.96	164/88941 (0.2%)

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
1	A	0	1
14	N	0	1
19	S	0	1
23	X	0	1
All	All	0	4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	Z	8	4SU	O3'-P	6.95	1.63	1.56
25	Z	46	G7M	O3'-P	6.13	1.62	1.56
1	A	1001	A	O3'-P	-6.12	1.53	1.61
1	A	999	C	O3'-P	-5.38	1.53	1.61

All (164) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	7	THR	CB-CA-C	-18.79	78.91	111.22
5	E	15	ARG	N-CA-C	-18.37	78.97	109.46
22	W	23	ARG	N-CA-C	-16.27	83.88	109.76
1	A	575	G	C2'-C3'-O3'	12.32	127.98	109.50
4	D	36	ARG	N-CA-C	12.05	136.45	109.81
1	A	266	G	C2'-C3'-O3'	11.81	127.22	109.50
1	A	1145	C	C2'-C3'-O3'	11.33	126.49	109.50
1	A	328	C	C2'-C3'-O3'	11.28	126.42	109.50
1	A	181	G	C2'-C3'-O3'	10.57	125.36	109.50
1	A	197	A	C2'-C3'-O3'	10.46	125.19	109.50
1	A	1301	U	C2'-C3'-O3'	10.32	124.98	109.50
1	A	1498	U	C2'-C3'-O3'	10.31	124.96	109.50
5	E	15	ARG	CB-CA-C	-10.18	93.11	109.80
22	W	24	VAL	N-CA-CB	-10.17	97.37	111.41
1	A	51	A	C4'-C3'-O3'	10.12	124.58	109.40
1	A	1279	A	C2'-C3'-O3'	-10.00	98.70	113.70
1	A	792	A	C2'-C3'-O3'	9.78	124.16	109.50
1	A	1534	A	C2'-C3'-O3'	9.58	128.07	113.70
1	A	1067	A	C2'-C3'-O3'	9.41	123.62	109.50
25	Z	47	U	C2'-C3'-O3'	9.31	123.46	109.50
10	J	49	VAL	N-CA-C	9.11	121.05	107.75
1	A	1346	A	C2'-C3'-O3'	9.04	123.07	109.50
1	A	115	G	C4'-C3'-O3'	8.90	122.76	109.40
1	A	1001	A	C4'-C3'-O3'	-8.80	99.80	113.00
1	A	572	A	C4'-C3'-O3'	-8.78	99.83	113.00
5	E	16	THR	N-CA-CB	-8.70	95.25	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1200	C	C4'-C3'-O3'	-8.46	100.31	113.00
1	A	559	A	C2'-C3'-O3'	8.14	121.71	109.50
1	A	965	A	C2'-C3'-O3'	8.05	121.57	109.50
1	A	960	U	C2'-C3'-O3'	8.02	121.53	109.50
1	A	1001	A	O4'-C4'-C3'	-8.02	95.98	104.00
11	K	17	GLY	N-CA-C	7.85	121.18	110.58
4	D	36	ARG	N-CA-CB	-7.80	96.48	110.37
1	A	1049	U	C4'-C3'-O3'	7.76	121.05	109.40
1	A	1380	U	C2'-C3'-O3'	7.73	121.10	109.50
8	H	119	LEU	N-CA-C	7.66	118.00	107.73
10	J	80	LYS	N-CA-C	-7.65	103.91	113.55
1	A	687	A	C2'-C3'-O3'	7.63	120.95	109.50
1	A	181	G	C4'-C3'-O3'	7.54	120.70	109.40
12	L	30	ALA	CA-C-N	7.38	128.03	119.47
12	L	30	ALA	C-N-CA	7.38	128.03	119.47
17	Q	65	ILE	N-CA-C	-7.35	106.73	113.71
19	S	71	LEU	N-CA-C	7.31	119.24	111.28
1	A	60	A	C2'-C3'-O3'	7.27	120.41	109.50
1	A	1182	G	C2'-C3'-O3'	7.25	120.38	109.50
22	W	23	ARG	CB-CA-C	-6.96	98.49	109.84
2	B	90	MET	CA-C-N	6.91	128.48	119.84
2	B	90	MET	C-N-CA	6.91	128.48	119.84
13	M	50	GLU	N-CA-C	6.90	118.45	111.07
24	Y	32	A	C4'-C3'-O3'	6.88	119.72	109.40
1	A	992	U	C2'-C3'-O3'	6.80	119.70	109.50
1	A	748	C	C2'-C3'-O3'	6.75	119.63	109.50
1	A	428	G	C2'-C3'-O3'	6.72	119.58	109.50
1	A	687	A	C4'-C3'-O3'	6.72	119.48	109.40
2	B	25	ASN	CA-C-N	6.70	128.21	119.84
2	B	25	ASN	C-N-CA	6.70	128.21	119.84
4	D	155	LEU	N-CA-C	6.69	120.00	109.96
5	E	51	VAL	O-C-N	6.69	124.70	120.42
1	A	1380	U	C4'-C3'-O3'	6.64	119.36	109.40
1	A	496	A	C4'-C3'-O3'	6.63	119.35	109.40
20	T	74	LYS	N-CA-C	6.56	118.51	111.36
1	A	812	C	C2'-C3'-O3'	6.46	123.39	113.70
1	A	509	A	C4'-C3'-O3'	6.46	122.68	113.00
1	A	481	G	C2'-C3'-O3'	6.45	119.17	109.50
1	A	484	G	C4'-C3'-O3'	6.42	119.03	109.40
23	X	148	ALA	N-CA-C	6.38	118.80	108.41
1	A	1145	C	C4'-C3'-O3'	-6.36	99.86	109.40
1	A	372	C	C2'-C3'-O3'	6.35	119.02	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	S	10	PHE	N-CA-C	6.34	119.84	109.76
1	A	115	G	C2'-C3'-O3'	6.33	118.99	109.50
1	A	281	G	C2'-C3'-O3'	6.32	123.18	113.70
1	A	113	G	C4'-C3'-O3'	-6.32	103.53	113.00
8	H	75	ARG	CA-C-N	6.30	127.71	119.84
8	H	75	ARG	C-N-CA	6.30	127.71	119.84
1	A	1285	A	C4'-C3'-O3'	6.27	118.81	109.40
2	B	24	TRP	N-CA-C	6.25	124.11	110.80
1	A	250	A	C2'-C3'-O3'	6.23	118.84	109.50
9	I	91	ASP	N-CA-C	-6.22	106.91	114.75
1	A	1101	A	C4'-C3'-O3'	6.21	118.71	109.40
1	A	1190	G	C2'-C3'-O3'	6.20	123.00	113.70
3	C	192	THR	N-CA-C	6.19	118.83	111.71
23	X	53	ASP	CA-C-N	6.17	126.74	120.38
23	X	53	ASP	C-N-CA	6.17	126.74	120.38
23	X	7	THR	N-CA-C	6.16	119.50	109.59
1	A	1541	U	C4'-C3'-O3'	6.13	122.20	113.00
1	A	1493	A	C4'-C3'-O3'	6.13	122.19	113.00
1	A	1347	G	C1'-C2'-O2'	-6.09	102.67	111.80
1	A	1065	U	C4'-C3'-O3'	6.07	118.51	109.40
1	A	1201	A	C2'-C3'-O3'	6.03	118.55	109.50
1	A	577	G	C4'-C3'-O3'	-6.01	103.98	113.00
1	A	1201	A	C4'-C3'-O3'	5.98	118.37	109.40
1	A	1357	A	C4'-C3'-O3'	-5.97	104.05	113.00
9	I	70	LYS	N-CA-C	5.92	117.40	111.07
1	A	243	A	C4'-C3'-O3'	5.90	118.25	109.40
19	S	38	SER	N-CA-C	5.84	119.47	110.42
12	L	20	LYS	N-CA-C	5.79	118.17	108.73
1	A	499	A	C4'-C3'-O3'	5.73	118.00	109.40
20	T	97	ALA	CA-C-N	5.73	127.00	119.84
20	T	97	ALA	C-N-CA	5.73	127.00	119.84
1	A	484	G	C2'-C3'-O3'	5.72	118.08	109.50
2	B	222	ILE	N-CA-CB	5.68	117.20	110.55
1	A	960	U	C4'-C3'-O3'	5.64	117.86	109.40
1	A	546	G	C4'-C3'-O3'	-5.60	104.59	113.00
22	W	61	ASP	CA-C-N	5.58	125.25	119.56
22	W	61	ASP	C-N-CA	5.58	125.25	119.56
1	A	1356	G	C4'-C3'-O3'	-5.57	104.64	113.00
11	K	80	VAL	N-CA-C	5.55	116.05	107.78
1	A	1305	G	C4'-C3'-O3'	-5.54	104.68	113.00
1	A	1513	A	C4'-C3'-O3'	-5.54	104.69	113.00
5	E	92	LYS	CA-C-N	5.54	125.48	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	92	LYS	C-N-CA	5.54	125.48	119.78
13	M	4	ILE	N-CA-C	5.53	116.31	110.72
1	A	1101	A	C2'-C3'-O3'	5.52	117.78	109.50
1	A	508	C	C4'-C3'-O3'	5.52	117.68	109.40
20	T	33	ILE	N-CA-C	-5.51	104.95	110.30
23	X	54	PRO	N-CA-C	5.50	117.41	110.70
1	A	243	A	C2'-C3'-O3'	5.49	117.74	109.50
1	A	1397	C	C2'-C3'-O3'	5.49	117.73	109.50
1	A	1504	G	C2'-C3'-O3'	5.48	117.72	109.50
23	X	4	GLU	N-CA-C	5.47	118.27	107.98
1	A	557	G	C4'-C3'-O3'	-5.46	104.80	113.00
2	B	179	LYS	N-CA-C	5.43	117.62	111.11
4	D	63	LYS	N-CA-C	-5.43	104.40	111.02
4	D	135	LEU	CA-C-N	5.42	125.13	119.82
4	D	135	LEU	C-N-CA	5.42	125.13	119.82
6	F	43	LEU	N-CA-C	-5.39	106.47	113.16
1	A	549	C	C4'-C3'-O3'	-5.39	104.92	113.00
1	A	1397	C	C4'-C3'-O3'	5.38	117.48	109.40
1	A	1347	G	C2'-C3'-O3'	5.36	117.55	109.50
3	C	6	HIS	CA-C-N	5.35	124.86	119.19
3	C	6	HIS	C-N-CA	5.35	124.86	119.19
1	A	1125	U	C4'-C3'-O3'	-5.34	104.99	113.00
2	B	201	ILE	CA-C-N	5.34	126.52	119.84
2	B	201	ILE	C-N-CA	5.34	126.52	119.84
25	Z	60	U	C2'-C3'-O3'	5.34	117.51	109.50
1	A	1065	U	C2'-C3'-O3'	5.29	117.44	109.50
13	M	40	ASN	CA-C-N	5.29	124.95	119.56
13	M	40	ASN	C-N-CA	5.29	124.95	119.56
6	F	55	ASP	CA-C-N	5.28	126.22	120.83
6	F	55	ASP	C-N-CA	5.28	126.22	120.83
1	A	372	C	C4'-C3'-O3'	5.28	117.31	109.40
1	A	1346	A	C4'-C3'-O3'	5.26	117.29	109.40
5	E	118	ILE	N-CA-C	5.25	115.13	107.88
1	A	119	A	C2'-C3'-O3'	5.25	117.37	109.50
1	A	1498	U	C4'-C3'-O3'	5.23	117.25	109.40
1	A	964	A	C4'-C3'-O3'	-5.20	105.20	113.00
8	H	66	GLY	CA-C-N	5.19	126.33	119.84
8	H	66	GLY	C-N-CA	5.19	126.33	119.84
1	A	48	C	C4'-C3'-O3'	5.19	117.18	109.40
8	H	135	CYS	N-CA-C	5.18	116.94	108.76
1	A	944	G	C4'-C3'-O3'	-5.17	105.25	113.00
1	A	1347	G	C4'-C3'-O3'	5.16	117.14	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1506	U	C1'-C2'-O2'	-5.12	104.12	111.80
1	A	975	A	C2'-C3'-O3'	5.11	117.17	109.50
1	A	35	G	C4'-C3'-O3'	-5.10	105.35	113.00
4	D	125	HIS	N-CA-C	-5.07	107.48	113.97
1	A	1300	G	C2'-C3'-O3'	5.06	121.29	113.70
20	T	12	ALA	N-CA-C	-5.04	106.91	113.16
1	A	1366	C	C4'-C3'-O3'	-5.03	105.45	113.00
1	A	1147	C	C3'-C2'-O2'	5.03	118.24	110.70
1	A	428	G	C4'-C3'-O3'	5.03	116.94	109.40
5	E	41	VAL	N-CA-C	5.02	115.88	108.45
19	S	4	SER	N-CA-C	5.02	117.76	107.37
1	A	1459	C	C2'-C3'-O3'	-5.01	106.19	113.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1209	C	Sidechain
14	N	30	ALA	Peptide
19	S	3	ARG	Peptide
23	X	53	ASP	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	32544	0	16441	1101	0
2	B	1900	0	1951	51	0
3	C	1612	0	1675	70	0
4	D	1703	0	1765	79	0
5	E	1146	0	1207	39	0
6	F	843	0	857	31	0
7	G	1257	0	1296	17	0
8	H	1116	0	1177	28	0
9	I	1010	0	1037	34	0
10	J	792	0	835	46	0
11	K	885	0	904	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L	970	0	1057	32	0
13	M	946	0	1008	22	0
14	N	492	0	530	25	0
15	O	734	0	771	17	0
16	P	700	0	720	20	0
17	Q	823	0	891	22	0
18	R	598	0	670	29	0
19	S	655	0	672	35	0
20	T	763	0	861	43	0
21	V	208	0	221	3	0
22	W	570	0	599	46	0
23	X	1336	0	1389	64	0
24	Y	439	0	220	18	0
25	Z	1646	0	844	54	0
26	A	83	0	0	3	0
26	E	1	0	0	0	0
26	W	1	0	0	0	0
26	Z	1	0	0	0	0
27	D	1	0	0	4	0
27	N	1	0	0	0	0
All	All	55776	0	39598	1779	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 19.

All (1779) 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)
22:W:23:ARG:NH2	22:W:33:LEU:HG	1.33	1.38
20:T:30:LYS:NZ	20:T:72:LEU:HD21	1.28	1.38
11:K:56:GLY:O	11:K:89:ALA:HB3	1.26	1.34
19:S:36:ARG:HA	19:S:71:LEU:CD1	1.55	1.34
20:T:30:LYS:HE2	20:T:72:LEU:CD2	1.55	1.34
1:A:413:G:O6	4:D:35:ARG:NH1	1.61	1.32
1:A:412:A:N3	4:D:35:ARG:NH2	1.78	1.32
22:W:23:ARG:NH2	22:W:33:LEU:CG	1.94	1.30
20:T:30:LYS:CE	20:T:72:LEU:CD2	2.09	1.29
11:K:56:GLY:O	11:K:89:ALA:CB	1.80	1.29
10:J:38:ILE:HG23	10:J:71:LEU:O	1.25	1.26
20:T:30:LYS:CE	20:T:72:LEU:HD21	1.64	1.25
1:A:1358:U:H3	1:A:1363(A):A:N6	1.38	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1459:C:OP1	20:T:28:ALA:HA	1.38	1.21
1:A:1358:U:O4	1:A:1363(A):A:N1	1.71	1.21
10:J:38:ILE:CG2	10:J:71:LEU:O	1.90	1.18
1:A:413:G:C6	4:D:35:ARG:NH1	2.13	1.17
1:A:439:A:OP2	1:A:493:G:N1	1.77	1.16
19:S:36:ARG:CA	19:S:71:LEU:CD1	2.25	1.15
1:A:1256:A:H62	1:A:1278:U:H1'	1.09	1.12
19:S:36:ARG:HA	19:S:71:LEU:HD13	1.34	1.10
22:W:23:ARG:HH21	22:W:33:LEU:CG	1.58	1.09
20:T:30:LYS:HE2	20:T:72:LEU:HD23	1.20	1.07
20:T:30:LYS:NZ	20:T:72:LEU:CD2	2.18	1.07
19:S:36:ARG:CA	19:S:71:LEU:HD12	1.86	1.06
22:W:23:ARG:CZ	22:W:33:LEU:HD11	1.86	1.06
20:T:30:LYS:CE	20:T:72:LEU:HD23	1.80	1.04
22:W:23:ARG:CZ	22:W:33:LEU:CD1	2.39	1.01
22:W:23:ARG:NH2	22:W:33:LEU:CD1	2.23	1.00
1:A:99:U:H2'	1:A:100:C:C6	1.96	1.00
4:D:31:CYS:SG	27:D:300:ZN:ZN	1.50	0.98
19:S:36:ARG:C	19:S:71:LEU:CD1	2.36	0.98
3:C:57:ILE:HG23	3:C:65:ALA:O	1.63	0.98
1:A:266:G:C8	1:A:266:G:H5''	2.01	0.95
10:J:16:LEU:HD23	10:J:70:ARG:HG2	1.48	0.94
19:S:70:LYS:O	19:S:73:GLU:HG2	1.67	0.93
1:A:1358:U:N3	1:A:1363(A):A:N6	2.04	0.93
1:A:439:A:OP2	1:A:493:G:C2	2.22	0.92
1:A:864:A:H2'	1:A:865:A:C8	2.04	0.92
1:A:1255:G:H2'	1:A:1279:A:N6	1.85	0.92
23:X:41:MET:HG3	23:X:59:ILE:HG21	1.52	0.92
1:A:149:A:C1'	1:A:149:A:C8	2.54	0.90
19:S:36:ARG:HA	19:S:71:LEU:HD12	1.44	0.90
1:A:80:G:H3'	1:A:81:U:H5''	1.51	0.90
19:S:36:ARG:C	19:S:71:LEU:HD11	1.97	0.90
1:A:149:A:C1'	1:A:149:A:C4	2.54	0.90
3:C:26:LYS:HD3	14:N:36:PHE:HE1	1.34	0.89
1:A:413:G:C5	4:D:35:ARG:NH1	2.35	0.89
25:Z:16:C:H3'	25:Z:17:C:H5'	1.55	0.88
1:A:1218:C:H2'	1:A:1219:U:C6	2.08	0.88
1:A:69:G:H1	1:A:100:C:H42	1.22	0.87
3:C:26:LYS:HD3	14:N:36:PHE:CE1	2.09	0.87
1:A:736:C:H2'	1:A:737:A:C8	2.08	0.87
19:S:36:ARG:C	19:S:71:LEU:HD12	1.99	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:U:H2'	1:A:57:G:H8	1.36	0.87
1:A:224:C:P	20:T:74:LYS:HZ1	1.97	0.87
1:A:1348:U:H2'	1:A:1349:A:H8	1.39	0.86
1:A:439:A:OP2	1:A:493:G:N2	2.09	0.86
1:A:413:G:N7	4:D:35:ARG:NH1	2.22	0.86
20:T:30:LYS:HZ3	20:T:72:LEU:HD21	1.04	0.85
1:A:1358:U:H3	1:A:1363(A):A:H61	0.90	0.85
4:D:31:CYS:HG	27:D:300:ZN:ZN	0.58	0.85
1:A:1507:A:H2'	1:A:1508:G:C8	2.11	0.84
1:A:56:U:H2'	1:A:57:G:C8	2.11	0.84
1:A:1457:G:H5''	1:A:1457:G:C8	2.12	0.84
6:F:43:LEU:HB2	6:F:60:PHE:HB2	1.58	0.84
9:I:114:TYR:CE2	10:J:60:ARG:O	2.31	0.84
1:A:543:C:H2'	1:A:544:G:H8	1.43	0.83
11:K:56:GLY:O	11:K:89:ALA:HB2	1.77	0.83
1:A:1459:C:OP1	20:T:28:ALA:CA	2.26	0.83
1:A:1513:A:H2'	1:A:1514:C:C6	2.13	0.83
6:F:97:PHE:HB2	18:R:32:ARG:NE	1.94	0.83
1:A:1001:A:H2'	1:A:1001(A):G:C8	2.14	0.83
1:A:398:C:H2'	1:A:399:G:H8	1.43	0.83
1:A:1256:A:N6	1:A:1278:U:H1'	1.93	0.83
1:A:736:C:H2'	1:A:737:A:H8	1.43	0.82
5:E:87:SER:HA	5:E:125:SER:HB3	1.62	0.82
1:A:412:A:H1'	4:D:35:ARG:NH2	1.95	0.81
3:C:92:ALA:O	3:C:95:THR:O	1.99	0.81
16:P:59:TRP:O	16:P:62:VAL:HG23	1.80	0.81
1:A:926:G:H3'	1:A:1505:G:H21	1.43	0.81
1:A:1255:G:H2'	1:A:1279:A:H62	1.44	0.81
23:X:19:VAL:HG21	23:X:56:VAL:HG13	1.63	0.80
1:A:1025:U:H2'	1:A:1026:G:C8	2.16	0.80
1:A:662:G:H2'	1:A:663:A:H8	1.47	0.80
13:M:22:ILE:HG22	13:M:24:GLY:H	1.47	0.79
1:A:1410:G:H2'	1:A:1411:C:C6	2.16	0.79
1:A:1106:G:H5''	3:C:172:ARG:HG2	1.64	0.79
9:I:8:GLY:HA2	9:I:79:LEU:HD12	1.63	0.79
4:D:163:GLU:HA	4:D:166:LYS:HD2	1.63	0.79
2:B:71:VAL:HA	2:B:93:VAL:HG12	1.65	0.78
16:P:59:TRP:O	16:P:62:VAL:CG2	2.30	0.78
25:Z:16:C:C3'	25:Z:17:C:H5'	2.14	0.78
5:E:16:THR:HB	5:E:27:ARG:O	1.82	0.78
11:K:15:ALA:HA	11:K:77:MET:HA	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:662:G:H2'	1:A:663:A:C8	2.19	0.78
20:T:72:LEU:O	20:T:76:ALA:HB3	1.84	0.77
1:A:129(A):G:H4'	1:A:130:A:O5'	1.83	0.77
4:D:78:LEU:HD21	4:D:96:LEU:HB3	1.66	0.77
10:J:30:SER:HB2	10:J:81:THR:HA	1.65	0.77
1:A:579:G:H2'	1:A:580:U:C6	2.20	0.77
13:M:108:ARG:HH21	13:M:114:ARG:HA	1.50	0.77
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.66	0.77
1:A:21:G:H21	1:A:914:A:H62	1.32	0.76
1:A:1128:C:H2'	1:A:1139:G:N7	2.01	0.76
1:A:880:C:H2'	1:A:881:G:H8	1.51	0.76
1:A:1127:G:H21	1:A:1147:C:H41	1.32	0.76
1:A:269:C:H2'	1:A:270:A:C8	2.20	0.76
20:T:65:LYS:O	20:T:68:LYS:HB3	1.85	0.76
22:W:23:ARG:HH21	22:W:33:LEU:HG	0.69	0.76
1:A:521:G:N2	1:A:522:C:C2	2.54	0.75
1:A:1542:U:H4'	18:R:18:ARG:H	1.52	0.75
1:A:543:C:H2'	1:A:544:G:C8	2.20	0.75
1:A:814:A:H2'	1:A:816:A:H5''	1.68	0.74
1:A:952:U:H2'	1:A:953:G:H8	1.52	0.74
3:C:57:ILE:HA	3:C:65:ALA:O	1.87	0.74
10:J:38:ILE:HG22	10:J:71:LEU:O	1.87	0.74
1:A:34:C:H2'	1:A:35:G:C8	2.23	0.74
1:A:170:U:H2'	1:A:171:A:H8	1.52	0.74
4:D:9:CYS:SG	27:D:300:ZN:ZN	1.75	0.74
1:A:1456:G:H3'	1:A:1457:G:O4'	1.86	0.74
1:A:78:G:H2'	1:A:79:G:O4'	1.86	0.74
1:A:946:A:H2'	1:A:947:G:C8	2.22	0.74
23:X:11:ILE:HD13	23:X:45:LEU:HD23	1.68	0.74
23:X:89:LYS:HA	23:X:119:THR:O	1.88	0.74
14:N:24:CYS:HB3	14:N:29:ARG:H	1.53	0.74
1:A:224:C:OP1	20:T:74:LYS:HE3	1.87	0.74
1:A:1099:G:C6	1:A:1100:C:N3	2.56	0.73
1:A:1508:G:OP1	26:A:1608:MG:MG	1.29	0.73
1:A:1493:A:C2	22:W:46:ARG:HA	2.23	0.73
1:A:299:G:H2'	1:A:300:A:C8	2.24	0.73
1:A:562:C:H5	1:A:884:U:H2'	1.54	0.73
3:C:23:TYR:HA	10:J:11:PHE:HE2	1.54	0.73
1:A:1446:U:O2'	1:A:1456:G:O6	2.07	0.73
1:A:313:A:H2'	1:A:314:C:C6	2.24	0.73
18:R:52:PRO:HD2	18:R:55:ARG:HB2	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Z:36:U:H2'	25:Z:37:A:C8	2.24	0.72
6:F:97:PHE:HB2	18:R:32:ARG:HE	1.54	0.72
15:O:18:PHE:O	15:O:21:ASP:HB3	1.90	0.71
1:A:436:C:H2'	1:A:437:U:H6	1.55	0.71
22:W:47:ILE:HD13	22:W:67:ILE:HD13	1.72	0.71
1:A:266:G:H5''	1:A:266:G:H8	1.52	0.71
1:A:745:C:H2'	1:A:746:A:C8	2.25	0.71
1:A:524:G:C6	1:A:525:C:N4	2.58	0.71
1:A:224:C:OP1	20:T:74:LYS:CE	2.39	0.71
23:X:106:ILE:HG23	23:X:116:VAL:HG11	1.71	0.71
1:A:769:G:N2	1:A:770:C:C2	2.59	0.71
1:A:839:U:O2	1:A:839:U:H2'	1.89	0.71
8:H:9:MET:HG3	8:H:26:VAL:HG21	1.70	0.71
1:A:69:G:H1	1:A:100:C:N4	1.88	0.70
1:A:720:C:H2'	1:A:721:G:C8	2.26	0.70
3:C:141:VAL:HG11	3:C:149:ALA:HB2	1.71	0.70
1:A:481:G:O2'	1:A:483:C:N4	2.24	0.70
1:A:1219:U:H2'	1:A:1220:G:C8	2.26	0.70
1:A:90:U:H2'	1:A:91:C:C6	2.26	0.70
1:A:1409:C:H2'	1:A:1410:G:C8	2.25	0.70
1:A:1507:A:H2'	1:A:1508:G:H8	1.52	0.70
14:N:15:LYS:HB3	14:N:19:ARG:HH12	1.55	0.70
1:A:1102:A:H2'	1:A:1103:C:C6	2.26	0.70
12:L:46:LYS:HB3	12:L:48:PRO:HD2	1.73	0.70
1:A:303:A:H2'	1:A:304:U:H6	1.57	0.70
1:A:34:C:H2'	1:A:35:G:H8	1.55	0.69
1:A:436:C:H2'	1:A:437:U:C6	2.27	0.69
1:A:170:U:H2'	1:A:171:A:C8	2.27	0.69
1:A:1391:U:H2'	1:A:1392:G:C8	2.27	0.69
6:F:27:GLN:HA	6:F:30:LEU:HD12	1.74	0.69
1:A:671:G:N2	1:A:736:C:C2	2.60	0.69
1:A:1234:C:H2'	1:A:1235:U:C6	2.27	0.69
1:A:1354:C:H2'	1:A:1355:G:H8	1.56	0.69
1:A:674:G:H2'	1:A:675:A:H8	1.56	0.69
1:A:1351:U:H2'	1:A:1352:C:H6	1.57	0.69
20:T:30:LYS:HZ1	20:T:72:LEU:HD21	1.53	0.69
1:A:1225:A:H2'	1:A:1225:A:N3	2.07	0.69
1:A:1264:C:H2'	1:A:1265:G:H8	1.56	0.69
1:A:1356:G:H2'	1:A:1357:A:C8	2.28	0.69
4:D:81:GLU:HA	4:D:84:LYS:HE3	1.74	0.69
22:W:23:ARG:NH2	22:W:33:LEU:HD11	1.97	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:C:H2'	1:A:225:C:C6	2.28	0.69
1:A:269:C:H2'	1:A:270:A:H8	1.57	0.69
1:A:576:G:H3'	1:A:577:G:H5''	1.75	0.68
1:A:412:A:N3	4:D:35:ARG:CZ	2.55	0.68
1:A:1256:A:H62	1:A:1278:U:C1'	1.98	0.68
1:A:1358:U:C4	1:A:1363(A):A:N1	2.59	0.68
1:A:521:G:N1	1:A:522:C:C4	2.61	0.68
1:A:13:U:H5'	1:A:14:U:H5	1.58	0.68
23:X:149:VAL:HG13	23:X:168:VAL:HG22	1.74	0.68
1:A:740:U:OP2	15:O:2:PRO:N	2.27	0.68
4:D:9:CYS:HG	4:D:31:CYS:HG	1.39	0.68
1:A:552:U:H2'	1:A:553:A:C8	2.29	0.68
2:B:87:ARG:HG3	2:B:234:PRO:HG3	1.75	0.68
12:L:24:VAL:HG12	12:L:26:ALA:H	1.58	0.68
1:A:309:G:H2'	1:A:310:G:H8	1.59	0.67
1:A:61:G:H2'	1:A:62:U:O4'	1.93	0.67
23:X:120:ILE:HD12	23:X:133:GLY:HA2	1.75	0.67
23:X:41:MET:CG	23:X:59:ILE:HG21	2.23	0.67
1:A:728:A:H2'	1:A:729:A:H8	1.58	0.67
20:T:30:LYS:HA	20:T:33:ILE:HD12	1.76	0.67
1:A:1022:G:H2'	1:A:1023:G:H8	1.58	0.67
1:A:1367:C:H4'	10:J:48:THR:HG21	1.76	0.67
11:K:87:THR:HG23	11:K:91:ARG:HD3	1.77	0.67
4:D:201:GLN:NE2	5:E:116:THR:OG1	2.28	0.67
19:S:36:ARG:O	19:S:71:LEU:HD12	1.94	0.67
1:A:671:G:C2	1:A:736:C:N3	2.63	0.67
19:S:70:LYS:O	19:S:73:GLU:CG	2.40	0.67
6:F:47:ARG:HB2	6:F:47:ARG:HH11	1.59	0.67
1:A:45:U:H2'	1:A:46:G:C8	2.30	0.66
1:A:999:C:O2'	1:A:1000:U:H5'	1.95	0.66
1:A:513:C:H2'	1:A:514:C:C6	2.30	0.66
1:A:920:U:H2'	1:A:921:U:C6	2.31	0.66
1:A:1445:C:C2	1:A:1458:G:C2	2.83	0.66
1:A:743:U:H2'	1:A:744:C:C6	2.31	0.66
16:P:67:THR:HG22	16:P:68:ASP:H	1.60	0.66
4:D:120:LEU:HD23	4:D:126:ILE:HD11	1.76	0.66
1:A:952:U:H2'	1:A:953:G:C8	2.30	0.66
2:B:218:ALA:O	2:B:222:ILE:HG13	1.95	0.66
9:I:13:ALA:HB2	9:I:68:GLY:HA3	1.77	0.66
11:K:18:ARG:HG3	11:K:81:ASP:HB3	1.77	0.66
1:A:524:G:C2	1:A:525:C:N3	2.64	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:C:P	20:T:74:LYS:NZ	2.68	0.66
1:A:689:C:OP1	11:K:44:SER:OG	2.13	0.66
1:A:1022:G:H2'	1:A:1023:G:C8	2.30	0.66
3:C:66:VAL:HG21	3:C:91:LEU:HD11	1.76	0.66
1:A:792:A:H4'	1:A:793:U:H5''	1.78	0.66
1:A:1126:U:O2	1:A:1126:U:H2'	1.95	0.66
1:A:1348:U:H2'	1:A:1349:A:C8	2.27	0.66
6:F:28:ARG:HH11	6:F:28:ARG:HB2	1.60	0.66
25:Z:49:G:H1	25:Z:65:C:H42	1.41	0.66
1:A:398:C:H2'	1:A:399:G:C8	2.30	0.65
25:Z:23:C:H2'	25:Z:24:U:C6	2.31	0.65
1:A:1493:A:H2'	22:W:20:ALA:N	2.11	0.65
1:A:20:U:H2'	1:A:21:G:O4'	1.97	0.65
3:C:23:TYR:HA	10:J:11:PHE:CE2	2.32	0.65
6:F:43:LEU:HB2	6:F:60:PHE:CB	2.27	0.65
9:I:7:THR:O	9:I:83:ARG:NH1	2.29	0.65
1:A:29:G:N2	1:A:555:C:C2	2.65	0.65
7:G:150:ALA:HB1	11:K:57:THR:HG21	1.79	0.65
1:A:312:C:H2'	1:A:313:A:C8	2.32	0.65
6:F:45:LEU:HD12	6:F:59:TYR:HD2	1.61	0.65
22:W:33:LEU:O	22:W:64:ARG:HA	1.97	0.65
1:A:397:A:H3'	1:A:397:A:N3	2.12	0.65
1:A:725:G:N2	1:A:726:C:C2	2.65	0.65
25:Z:8:4SU:H5''	25:Z:49:G:H5'	1.79	0.65
1:A:917:G:H2'	1:A:918:A:C8	2.31	0.64
1:A:60:A:H4'	1:A:61:G:O5'	1.97	0.64
25:Z:43:A:H2'	25:Z:44:A:C8	2.32	0.64
1:A:99:U:H2'	1:A:100:C:H6	1.55	0.64
10:J:57:LYS:O	10:J:60:ARG:NE	2.31	0.64
11:K:123:LYS:HA	11:K:126:ARG:HB2	1.80	0.64
1:A:1430:C:H2'	1:A:1431:C:C6	2.32	0.64
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.78	0.64
20:T:54:LYS:HA	20:T:57:ARG:HD3	1.78	0.64
1:A:1097:C:H2'	1:A:1098:C:C6	2.32	0.64
1:A:558:G:OP1	26:A:1678:MG:MG	1.38	0.64
1:A:1135:U:H4'	1:A:1136:U:H5	1.63	0.64
1:A:1414:U:H2'	1:A:1415:G:C8	2.33	0.64
2:B:24:TRP:CZ3	2:B:26:PRO:HA	2.33	0.64
22:W:23:ARG:NH2	22:W:33:LEU:CD2	2.60	0.64
1:A:15:G:H2'	1:A:16:A:C8	2.32	0.64
1:A:1475:G:H2'	1:A:1476:G:C8	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:9:VAL:HG21	17:Q:84:LEU:HD23	1.79	0.64
2:B:29:ALA:HA	2:B:32:ILE:HD12	1.80	0.64
1:A:412:A:H1'	4:D:35:ARG:HH22	1.62	0.64
1:A:522:C:H41	12:L:53:ARG:HH21	1.44	0.64
1:A:1056:U:H5'	3:C:163:ALA:HB2	1.80	0.64
1:A:1137:C:H4'	1:A:1138:G:C2	2.33	0.64
13:M:108:ARG:NH2	13:M:114:ARG:HA	2.13	0.64
25:Z:24:U:H2'	25:Z:25:C:C6	2.32	0.64
1:A:21:G:H2'	1:A:22:G:C8	2.32	0.63
1:A:926:G:H3'	1:A:1505:G:N2	2.13	0.63
1:A:1202:G:H8	1:A:1202:G:OP1	1.81	0.63
1:A:1459:C:P	20:T:28:ALA:HA	2.38	0.63
3:C:33:LEU:HD11	14:N:53:LEU:HD22	1.80	0.63
3:C:91:LEU:HD21	3:C:99:VAL:CG2	2.29	0.63
1:A:579:G:H2'	1:A:580:U:H6	1.61	0.63
3:C:174:PRO:C	3:C:176:HIS:H	2.07	0.63
5:E:25:ARG:HH11	5:E:25:ARG:HB2	1.63	0.63
10:J:7:LYS:HG3	10:J:71:LEU:HD23	1.80	0.63
1:A:1135:U:H4'	1:A:1136:U:C5	2.33	0.63
1:A:1425:U:H2'	1:A:1426:C:C6	2.34	0.63
1:A:1493:A:H2'	22:W:20:ALA:H	1.61	0.63
1:A:1540:U:H3	24:Y:25:A:H61	1.45	0.63
1:A:234:C:H2'	1:A:235:C:C6	2.34	0.63
1:A:262:A:H5''	20:T:76:ALA:HB2	1.80	0.63
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.34	0.63
1:A:1132:C:H2'	1:A:1133:G:C8	2.33	0.63
1:A:1406:U:H2'	1:A:1407:C:C6	2.34	0.63
6:F:41:GLU:HB2	6:F:62:TRP:HE3	1.64	0.63
1:A:562:C:C5	1:A:884:U:H2'	2.34	0.62
1:A:588:G:N2	1:A:589:C:C2	2.67	0.62
15:O:24:SER:HB3	15:O:27:VAL:HG23	1.81	0.62
1:A:1492:A:H2'	22:W:19:ASN:HA	1.81	0.62
9:I:112:LYS:HA	9:I:119:ALA:HB2	1.79	0.62
1:A:59:A:H3'	1:A:331:G:H22	1.64	0.62
1:A:988:G:N1	1:A:989:C:C2	2.68	0.62
1:A:1504:G:H4'	1:A:1505:G:O5'	2.00	0.62
4:D:11:LEU:HD13	4:D:66:ARG:HG2	1.80	0.62
23:X:34:ALA:HB1	23:X:45:LEU:HD22	1.82	0.62
1:A:328:C:H4'	1:A:329:A:H5'	1.82	0.62
1:A:1127:G:H21	1:A:1147:C:N4	1.97	0.62
6:F:43:LEU:HB3	6:F:46:ARG:HG3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:23:ARG:NE	22:W:33:LEU:HD12	2.13	0.62
1:A:174:C:H2'	1:A:175:C:C6	2.34	0.62
1:A:413:G:O2'	1:A:428:G:N2	2.33	0.62
1:A:1219:U:H2'	1:A:1220:G:H8	1.63	0.62
1:A:1354:C:H2'	1:A:1355:G:C8	2.33	0.62
23:X:34:ALA:HB1	23:X:45:LEU:CD2	2.29	0.62
1:A:947:G:H2'	1:A:948:C:O4'	1.98	0.62
1:A:224:C:OP1	20:T:74:LYS:NZ	2.32	0.62
1:A:559:A:H1'	1:A:561:U:H2'	1.81	0.62
1:A:874:G:N2	1:A:875:C:C2	2.67	0.62
1:A:1151:A:HO2'	1:A:1152:A:H8	1.45	0.62
3:C:77:ILE:HG22	3:C:81:GLY:HA2	1.81	0.62
4:D:25:ARG:C	4:D:27:TYR:H	2.07	0.62
1:A:1264:C:H2'	1:A:1265:G:C8	2.33	0.62
1:A:1308:U:OP1	13:M:97:PRO:HA	1.99	0.62
12:L:47:LYS:H	12:L:48:PRO:HD2	1.65	0.62
19:S:28:LYS:HD3	19:S:29:ARG:H	1.65	0.62
23:X:85:VAL:HG22	23:X:115:LYS:HB2	1.82	0.62
1:A:1106:G:N2	1:A:1107:C:C2	2.67	0.62
1:A:600:C:H2'	1:A:601:C:C6	2.35	0.62
1:A:335:C:H2'	1:A:336:C:C6	2.35	0.61
1:A:512:U:H2'	1:A:513:C:C6	2.36	0.61
1:A:664:G:H22	1:A:741:G:H1	1.48	0.61
1:A:729:A:H2'	1:A:730:G:H8	1.64	0.61
1:A:1422:G:H1	1:A:1478:C:H42	1.45	0.61
2:B:15:VAL:HG11	2:B:209:ARG:HB3	1.82	0.61
2:B:178:ARG:HA	2:B:178:ARG:HH11	1.64	0.61
1:A:1262:C:H42	1:A:1273:G:H1	1.48	0.61
1:A:1347:G:O2'	1:A:1348:U:OP2	2.16	0.61
1:A:1386:G:H2'	1:A:1387:G:H8	1.65	0.61
1:A:1525:G:H2'	1:A:1526:G:H8	1.65	0.61
4:D:9:CYS:HG	27:D:300:ZN:ZN	1.11	0.61
1:A:303:A:H2'	1:A:304:U:C6	2.34	0.61
1:A:578:C:OP1	26:A:1674:MG:MG	1.42	0.61
1:A:1028:C:H2'	1:A:1029:C:O4'	2.00	0.61
1:A:1353:G:N2	1:A:1354:C:C2	2.69	0.61
1:A:1430:C:H2'	1:A:1431:C:H6	1.65	0.61
23:X:150:VAL:HG11	23:X:163:MET:HE2	1.82	0.61
1:A:552:U:H2'	1:A:553:A:H8	1.64	0.61
1:A:992:U:H1'	1:A:993:G:C2	2.35	0.61
1:A:344:A:H4'	1:A:345:C:OP2	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:491:G:H2'	1:A:492:G:O4'	2.01	0.61
10:J:61:GLU:HG2	10:J:63:PHE:CE2	2.35	0.61
1:A:1534:A:H61	24:Y:31:U:H3	1.48	0.61
8:H:49:GLU:HG3	8:H:60:ARG:HB2	1.83	0.61
1:A:316:G:H1	1:A:337:C:H42	1.47	0.60
1:A:457:C:H2'	1:A:458:C:C6	2.36	0.60
1:A:1443:G:C6	1:A:1444:C:N4	2.69	0.60
19:S:34:TRP:HA	19:S:52:TYR:HB2	1.83	0.60
1:A:132:C:H5''	20:T:75:ASN:ND2	2.16	0.60
1:A:695:A:H2'	1:A:696:A:C8	2.36	0.60
1:A:112:G:H21	1:A:354:G:H5'	1.66	0.60
1:A:1343:G:H4'	9:I:122:ALA:HB3	1.83	0.60
1:A:741:G:H5'	15:O:39:LEU:HD21	1.83	0.60
1:A:1281:U:H4'	1:A:1282:C:OP2	2.01	0.60
1:A:15:G:H2'	1:A:16:A:H8	1.67	0.60
1:A:457:C:H2'	1:A:458:C:H6	1.66	0.60
3:C:30:ARG:HH11	3:C:30:ARG:CG	2.14	0.60
4:D:36:ARG:HG3	4:D:38:TYR:CZ	2.36	0.60
1:A:551:U:H2'	1:A:552:U:C6	2.37	0.60
1:A:584:G:H2'	1:A:585:G:H8	1.67	0.60
1:A:602:A:H2'	1:A:603:U:O4'	2.01	0.60
10:J:38:ILE:O	10:J:71:LEU:N	2.30	0.60
1:A:108:G:H1	20:T:15:ARG:HE	1.49	0.60
1:A:123:C:H2'	1:A:124:G:H8	1.66	0.60
1:A:340:U:H2'	1:A:341:C:H6	1.66	0.60
1:A:349:A:H2'	1:A:350:G:O4'	2.02	0.60
1:A:748:C:H1'	1:A:749:C:H5	1.66	0.60
1:A:769:G:N1	1:A:770:C:C4	2.69	0.60
1:A:686:U:O4	1:A:703:G:O2'	2.17	0.60
1:A:279:A:H3'	17:Q:95:TYR:HE1	1.67	0.60
1:A:652:U:O4	1:A:752:G:O2'	2.15	0.60
22:W:55:VAL:HA	22:W:66:ARG:O	2.01	0.60
3:C:150:LYS:HE2	3:C:152:ILE:HD11	1.83	0.60
1:A:275:G:H5'	17:Q:14:LYS:HD3	1.84	0.59
1:A:673:G:H2'	1:A:674:G:C8	2.37	0.59
23:X:38:ALA:HB2	23:X:45:LEU:HB2	1.83	0.59
1:A:1235:U:H2'	1:A:1236:A:O4'	2.02	0.59
3:C:66:VAL:O	3:C:66:VAL:HG12	2.02	0.59
1:A:148:G:H2'	1:A:149:A:C8	2.37	0.59
1:A:373:A:H2'	1:A:374:A:H8	1.67	0.59
1:A:911:U:H2'	1:A:912:C:C6	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:X:19:VAL:HG13	23:X:25:GLN:HG2	1.84	0.59
1:A:1218:C:H2'	1:A:1219:U:C5	2.36	0.59
3:C:11:ARG:O	3:C:13:GLY:N	2.35	0.59
1:A:551:U:H2'	1:A:552:U:H6	1.67	0.59
10:J:49:VAL:CG1	14:N:41:ARG:HB2	2.33	0.59
12:L:10:LEU:O	12:L:14:GLY:N	2.35	0.59
15:O:35:ARG:HE	15:O:59:MET:HE1	1.66	0.59
23:X:7:THR:HA	23:X:45:LEU:O	2.03	0.59
1:A:1405:G:H2'	1:A:1406:U:C6	2.37	0.59
1:A:1488:G:H2'	1:A:1489:G:H8	1.68	0.59
1:A:1515:C:H2'	1:A:1516:G:C8	2.37	0.59
4:D:35:ARG:O	4:D:37:PRO:CD	2.51	0.59
1:A:98:G:H2'	1:A:99:U:C6	2.38	0.59
1:A:354:G:N2	1:A:355:C:C2	2.71	0.59
2:B:80:ILE:HG21	2:B:212:GLN:HA	1.85	0.59
1:A:24:U:H2'	1:A:25:C:C6	2.37	0.59
1:A:473:G:OP2	16:P:75:ARG:HD2	2.02	0.59
1:A:1157:A:H4'	1:A:1158:C:O5'	2.03	0.59
22:W:55:VAL:HG13	22:W:66:ARG:H	1.66	0.59
25:Z:24:U:H2'	25:Z:25:C:H6	1.65	0.59
1:A:270:A:H2'	1:A:271:C:C6	2.37	0.59
1:A:1266:G:N2	1:A:1270:C:C2	2.71	0.58
1:A:132:C:C2	1:A:231:G:N2	2.71	0.58
4:D:64:LEU:HA	4:D:67:ILE:HD12	1.85	0.58
1:A:674:G:H2'	1:A:675:A:C8	2.37	0.58
1:A:718:G:H21	18:R:49:LYS:HE3	1.67	0.58
1:A:883:C:H2'	1:A:884:U:C6	2.38	0.58
1:A:1464:G:N2	1:A:1465:C:C2	2.71	0.58
1:A:362:G:N2	1:A:364:A:H3'	2.18	0.58
1:A:1505:G:H4'	1:A:1506:U:H5''	1.85	0.58
20:T:45:GLN:HA	20:T:91:LEU:HD22	1.85	0.58
1:A:621:A:H2'	1:A:622:A:C8	2.39	0.58
1:A:1125:U:H5'	1:A:1126:U:H5	1.69	0.58
1:A:1291:G:O3'	9:I:39:GLY:HA3	2.03	0.58
1:A:129(A):G:O2'	1:A:189(F):U:H2'	2.04	0.58
1:A:337:C:H2'	1:A:338:A:H8	1.68	0.58
1:A:793:U:H3	23:X:108:ARG:CZ	2.16	0.58
1:A:1070:U:H2'	1:A:1071:C:H6	1.68	0.58
1:A:1218:C:H2'	1:A:1219:U:H6	1.67	0.58
2:B:36:ARG:O	2:B:37:ASN:HB2	2.03	0.58
4:D:176:LEU:HA	4:D:183:GLY:HA2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:111:ARG:HH12	14:N:61:TRP:H	1.52	0.58
10:J:37:PRO:HA	10:J:72:VAL:HG22	1.86	0.58
12:L:28:LYS:HB2	12:L:33:ARG:HH21	1.68	0.58
4:D:13:ARG:HH21	4:D:36:ARG:CZ	2.16	0.58
6:F:9:VAL:HB	6:F:87:ARG:HB2	1.84	0.58
1:A:80:G:H3'	1:A:81:U:C5'	2.29	0.58
1:A:674:G:O5'	1:A:674:G:H8	1.86	0.58
1:A:718:G:H5'	11:K:117:ASN:CG	2.28	0.58
1:A:880:C:H2'	1:A:881:G:C8	2.35	0.58
1:A:1070:U:H2'	1:A:1071:C:C6	2.38	0.58
3:C:25:GLY:O	3:C:29:TYR:HB2	2.04	0.58
1:A:662:G:C2	1:A:744:C:O2	2.57	0.58
5:E:102:ALA:O	5:E:107:ARG:NH1	2.37	0.58
22:W:32:ILE:H	22:W:32:ILE:CD1	2.17	0.58
1:A:545:C:O2'	1:A:549:C:H5''	2.03	0.57
2:B:32:ILE:HA	2:B:42:ILE:HA	1.86	0.57
20:T:60:GLU:HG3	20:T:81:LYS:HE3	1.85	0.57
22:W:23:ARG:NE	22:W:33:LEU:CD1	2.67	0.57
25:Z:42:G:H2'	25:Z:43:A:C8	2.39	0.57
1:A:939:G:H2'	1:A:940:C:C6	2.39	0.57
1:A:974:A:H8	1:A:974:A:OP1	1.87	0.57
1:A:1457:G:C8	1:A:1457:G:C5'	2.85	0.57
11:K:122:LYS:O	11:K:126:ARG:N	2.37	0.57
1:A:67:C:H2'	1:A:68:G:C8	2.40	0.57
1:A:172:A:H2'	1:A:174:C:H5	1.69	0.57
1:A:450:G:H5''	1:A:451:A:H3'	1.86	0.57
1:A:1048:G:H5''	14:N:3:ARG:HG2	1.86	0.57
4:D:98:GLU:HG2	4:D:189:PRO:HG3	1.85	0.57
10:J:36:GLY:O	10:J:72:VAL:HG13	2.04	0.57
1:A:222:U:H2'	1:A:223:U:C6	2.40	0.57
1:A:538:G:H5''	12:L:114:LYS:HB2	1.87	0.57
1:A:568:G:N2	1:A:883:C:C2	2.72	0.57
4:D:173:TRP:HB2	4:D:187:ARG:O	2.04	0.57
17:Q:66:SER:HB3	17:Q:69:LYS:HB3	1.85	0.57
25:Z:18:G:O2'	25:Z:19:G:O5'	2.23	0.57
1:A:255:G:H2'	1:A:256:U:C6	2.39	0.57
1:A:412:A:C2	4:D:35:ARG:NE	2.70	0.57
1:A:513:C:H2'	1:A:514:C:H6	1.70	0.57
1:A:1251:A:H4'	9:I:12:GLU:OE1	2.04	0.57
3:C:20:SER:OG	3:C:40:ARG:NH2	2.37	0.57
24:Y:32:A:H4'	24:Y:33:A:OP2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:779:C:H2'	1:A:780:A:O4'	2.05	0.57
1:A:1194:U:H2'	1:A:1195:C:C6	2.40	0.57
4:D:31:CYS:C	4:D:33:MET:H	2.13	0.57
5:E:135:THR:O	5:E:139:LEU:HG	2.05	0.57
7:G:101:LEU:HA	7:G:104:LEU:HD12	1.87	0.57
12:L:27:LEU:HG	12:L:28:LYS:H	1.70	0.57
1:A:137:C:H1'	16:P:63:GLY:HA3	1.85	0.57
1:A:392:G:H2'	1:A:393:A:C8	2.40	0.57
1:A:991:U:C4	1:A:1212:U:H1'	2.40	0.57
1:A:1518:A:H2'	1:A:1519:A:H8	1.69	0.57
25:Z:18:G:O2'	25:Z:19:G:P	2.62	0.57
1:A:123:C:H5''	1:A:311:C:O2'	2.05	0.57
1:A:792:A:H4'	1:A:793:U:C5'	2.35	0.57
1:A:1457:G:H5''	1:A:1457:G:H8	1.64	0.57
9:I:50:LEU:HB3	9:I:56:LEU:H	1.68	0.57
23:X:152:MET:SD	25:Z:11:A:H4'	2.44	0.57
1:A:45:U:H2'	1:A:46:G:H8	1.69	0.57
1:A:589:C:O2	1:A:651:C:O2	2.22	0.57
1:A:784:C:C2	1:A:799:G:N2	2.73	0.57
1:A:914:A:C4	1:A:915:A:N7	2.73	0.57
1:A:922:G:H2'	1:A:923:A:C8	2.40	0.57
1:A:793:U:H3'	1:A:794:A:H5''	1.87	0.56
4:D:57:ARG:HH11	4:D:57:ARG:HG3	1.69	0.56
18:R:48:GLY:HA3	18:R:82:THR:HA	1.86	0.56
1:A:824:C:H2'	1:A:825:G:H8	1.70	0.56
1:A:1283:G:N2	1:A:1284:C:C2	2.73	0.56
1:A:132:C:C5'	20:T:75:ASN:ND2	2.69	0.56
1:A:583:A:H2'	1:A:584:G:O4'	2.06	0.56
1:A:688:G:H2'	1:A:689:C:C6	2.41	0.56
1:A:1095:U:OP1	1:A:1108:G:N2	2.38	0.56
1:A:1368:G:N2	1:A:1369:C:C2	2.73	0.56
4:D:26:CYS:HA	4:D:31:CYS:HB2	1.86	0.56
11:K:52:GLY:H	11:K:55:LYS:HE3	1.70	0.56
17:Q:56:VAL:HG13	17:Q:77:VAL:HB	1.86	0.56
25:Z:49:G:H1	25:Z:65:C:N4	2.03	0.56
1:A:186:C:H5'	20:T:78:ALA:HB1	1.87	0.56
1:A:525:C:H2'	1:A:526:C:C6	2.40	0.56
1:A:553:A:O2'	12:L:29:GLY:O	2.23	0.56
1:A:1511:G:H2'	1:A:1512:U:O4'	2.06	0.56
10:J:5:ARG:HG3	10:J:71:LEU:HD11	1.86	0.56
10:J:50:ILE:HD13	14:N:41:ARG:HH11	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:91:ARG:HG3	18:R:88:LYS:HZ1	1.70	0.56
4:D:162:LEU:HB3	4:D:166:LYS:HE3	1.88	0.56
1:A:101:A:H2'	1:A:102:G:H8	1.69	0.56
1:A:370:C:C2	1:A:392:G:N2	2.73	0.56
1:A:729:A:H2'	1:A:730:G:C8	2.39	0.56
25:Z:41:C:H2'	25:Z:42:G:C8	2.40	0.56
1:A:522:C:N4	1:A:528:C:H42	2.03	0.56
1:A:728:A:H2'	1:A:729:A:C8	2.41	0.56
1:A:876:G:H2'	1:A:877:C:C6	2.41	0.56
8:H:28:ALA:HB3	8:H:57:PRO:HB2	1.86	0.56
17:Q:41:LYS:HE2	17:Q:88:TYR:HE1	1.71	0.56
2:B:174:VAL:HG22	2:B:184:VAL:HG21	1.88	0.56
3:C:57:ILE:CG2	3:C:65:ALA:O	2.46	0.56
1:A:255:G:C2	1:A:272:C:C2	2.94	0.56
1:A:838:G:C2	1:A:849:C:C2	2.94	0.56
3:C:9:GLY:HA2	3:C:12:LEU:HD12	1.87	0.56
1:A:13:U:H5'	1:A:14:U:C5	2.41	0.56
1:A:96:U:H2'	1:A:97:G:C8	2.41	0.56
1:A:1493:A:H2'	22:W:20:ALA:CA	2.36	0.56
1:A:1515:C:H2'	1:A:1516:G:H8	1.71	0.56
14:N:43:CYS:O	14:N:47:LEU:HG	2.06	0.56
16:P:59:TRP:O	16:P:62:VAL:HG22	2.05	0.56
1:A:745:C:H2'	1:A:746:A:H8	1.70	0.55
1:A:931:C:O2	1:A:1387:G:C2	2.59	0.55
10:J:57:LYS:O	10:J:60:ARG:CZ	2.54	0.55
23:X:7:THR:HG21	23:X:62:TYR:CB	2.36	0.55
1:A:443:C:C2	1:A:492:G:N2	2.74	0.55
1:A:1435:G:H2'	1:A:1436:U:C6	2.42	0.55
3:C:30:ARG:HG2	3:C:30:ARG:NH1	2.19	0.55
3:C:189:ALA:HB3	3:C:196:LEU:HB2	1.88	0.55
1:A:17:U:H2'	1:A:18:C:C6	2.41	0.55
1:A:128:G:C2	1:A:234:C:C2	2.95	0.55
4:D:35:ARG:O	4:D:37:PRO:N	2.39	0.55
10:J:30:SER:CB	10:J:81:THR:HA	2.34	0.55
13:M:80:ARG:O	13:M:84:ILE:HG12	2.07	0.55
18:R:40:LEU:HB3	18:R:79:LEU:HD11	1.87	0.55
1:A:123:C:H2'	1:A:124:G:C8	2.40	0.55
1:A:1241:G:N2	1:A:1242:C:C2	2.75	0.55
15:O:34:LEU:O	15:O:38:ARG:HG2	2.06	0.55
1:A:96:U:H2'	1:A:97:G:H8	1.70	0.55
1:A:145:G:N2	1:A:178:C:C2	2.75	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:946:A:H2'	1:A:947:G:H8	1.72	0.55
1:A:1525:G:C5	1:A:1526:G:N7	2.74	0.55
1:A:309:G:H2'	1:A:310:G:C8	2.40	0.55
1:A:774:G:N2	1:A:806:C:C2	2.74	0.55
3:C:95:THR:HB	3:C:97:LYS:HE3	1.89	0.55
6:F:23:LYS:HE2	6:F:61:LEU:HD21	1.88	0.55
23:X:125:ARG:C	23:X:127:VAL:H	2.14	0.55
1:A:1082:G:H2'	1:A:1083:U:O4'	2.06	0.55
1:A:1095:U:H2'	1:A:1096:C:C6	2.42	0.55
1:A:1312:G:N2	1:A:1326:C:C2	2.74	0.55
1:A:1493:A:H2	22:W:47:ILE:H	1.55	0.55
8:H:87:SER:HA	8:H:93:VAL:HG23	1.88	0.55
1:A:216:G:C6	1:A:217:C:N4	2.75	0.55
2:B:21:ARG:HA	2:B:39:ILE:HA	1.88	0.55
1:A:874:G:N1	1:A:875:C:C4	2.74	0.55
2:B:118:LEU:HD21	2:B:138:LEU:HB3	1.89	0.55
25:Z:1:C:H2'	25:Z:2:G:H8	1.72	0.55
1:A:124:G:H2'	1:A:125:U:O4'	2.06	0.54
1:A:228:A:H2'	1:A:229:U:C6	2.42	0.54
1:A:761:G:C2	1:A:762:C:C2	2.95	0.54
1:A:1323:G:H2'	1:A:1324:A:C8	2.41	0.54
1:A:1343:G:H2'	1:A:1344:C:O4'	2.06	0.54
3:C:28:GLN:O	3:C:32:LEU:HG	2.07	0.54
1:A:127:G:N2	1:A:235:C:C2	2.76	0.54
1:A:235:C:H2'	1:A:236:G:H8	1.72	0.54
1:A:1424:C:H42	1:A:1476:G:H1	1.56	0.54
11:K:16:SER:HA	11:K:79:SER:HB3	1.88	0.54
25:Z:16:C:H3'	25:Z:17:C:C5'	2.31	0.54
13:M:22:ILE:HG22	13:M:24:GLY:N	2.21	0.54
5:E:139:LEU:HA	5:E:142:LEU:HD12	1.89	0.54
13:M:11:ARG:HG3	13:M:12:ASN:HD22	1.73	0.54
17:Q:41:LYS:HZ3	17:Q:92:ARG:HH21	1.53	0.54
25:Z:51:C:H42	25:Z:63:G:H1	1.55	0.54
1:A:93:G:H2'	1:A:96:U:O4'	2.07	0.54
1:A:685:G:H4'	11:K:40:ILE:O	2.07	0.54
6:F:47:ARG:HB2	6:F:47:ARG:NH1	2.23	0.54
23:X:125:ARG:HD3	23:X:128:ALA:HB3	1.89	0.54
23:X:148:ALA:HB1	23:X:165:LEU:HD22	1.90	0.54
1:A:947:G:C2	1:A:948:C:C2	2.95	0.54
1:A:977:A:H1'	1:A:982:U:O4	2.08	0.54
1:A:1189:C:H5''	3:C:5:ILE:HG12	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1518:A:H2'	1:A:1519:A:C8	2.41	0.54
2:B:47:THR:HG23	2:B:202:PRO:HD2	1.88	0.54
4:D:25:ARG:C	4:D:27:TYR:N	2.66	0.54
25:Z:8:4SU:O2	25:Z:21:A:H2	1.90	0.54
1:A:122:G:C6	1:A:123:C:C4	2.95	0.54
1:A:811:C:H5''	1:A:812:C:OP2	2.08	0.54
1:A:939:G:C6	1:A:940:C:N4	2.76	0.54
1:A:962:C:H1'	1:A:1201:A:N6	2.22	0.54
1:A:1351:U:H2'	1:A:1352:C:C6	2.40	0.54
19:S:36:ARG:O	19:S:71:LEU:CD1	2.51	0.54
25:Z:36:U:H2'	25:Z:37:A:H8	1.70	0.54
3:C:29:TYR:CD1	3:C:29:TYR:C	2.86	0.54
3:C:30:ARG:HG3	3:C:31:HIS:N	2.21	0.54
4:D:13:ARG:NH1	4:D:38:TYR:O	2.40	0.54
13:M:44:ARG:H	13:M:47:ASP:HB3	1.73	0.54
1:A:51:A:H4'	1:A:52:G:C5'	2.38	0.54
1:A:558:G:H3'	1:A:559:A:H5''	1.89	0.54
1:A:1023:G:H2'	1:A:1023:G:N3	2.23	0.54
1:A:1086:U:H3	1:A:1099:G:H22	1.55	0.54
1:A:1343:G:C5	1:A:1344:C:C4	2.95	0.54
1:A:1458:G:OP1	20:T:32:ALA:HA	2.08	0.54
6:F:25:ILE:HG21	6:F:82:ARG:HD2	1.89	0.54
1:A:891:U:H2'	1:A:892:A:H8	1.72	0.54
1:A:1343:G:C6	1:A:1344:C:N3	2.75	0.54
4:D:102:ASP:HB3	4:D:136:PRO:HB3	1.89	0.54
9:I:18:PHE:HB3	9:I:20:ARG:HH21	1.72	0.54
25:Z:28:C:H2'	25:Z:29:G:C8	2.42	0.54
1:A:41:G:H2'	1:A:42:G:H8	1.72	0.53
1:A:171:A:H2'	1:A:172:A:C8	2.43	0.53
1:A:289:G:N2	1:A:290:C:C2	2.75	0.53
1:A:1129:C:O2'	1:A:1132:C:OP2	2.25	0.53
1:A:344:A:H5''	1:A:345:C:H5	1.73	0.53
1:A:509:A:H4'	1:A:510:A:OP1	2.07	0.53
1:A:1010:G:H2'	1:A:1011:G:H8	1.72	0.53
1:A:1493:A:H2	22:W:46:ARG:HA	1.70	0.53
6:F:97:PHE:HD2	18:R:32:ARG:HH21	1.55	0.53
7:G:113:GLU:HG2	7:G:119:ARG:HG2	1.91	0.53
11:K:85:ARG:HA	11:K:111:ASP:O	2.08	0.53
16:P:48:TRP:CD1	16:P:48:TRP:H	2.26	0.53
1:A:1106:G:N1	1:A:1107:C:C4	2.77	0.53
2:B:184:VAL:HG13	2:B:198:ASP:H	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:11:ILE:HG22	5:E:12:LEU:HB2	1.90	0.53
10:J:50:ILE:HG13	10:J:60:ARG:HH21	1.73	0.53
1:A:536:C:H2'	1:A:537:G:C8	2.44	0.53
1:A:568:G:C2	1:A:883:C:N3	2.76	0.53
1:A:1010:G:H2'	1:A:1011:G:C8	2.43	0.53
1:A:1068:G:N2	1:A:1069:C:C2	2.76	0.53
1:A:1340:A:H2'	1:A:1341:U:O4'	2.07	0.53
1:A:1312:G:C2	1:A:1326:C:C2	2.96	0.53
1:A:1422:G:H1	1:A:1478:C:N4	2.07	0.53
23:X:110:LEU:HD13	23:X:147:LEU:HB2	1.89	0.53
1:A:1233:G:C6	1:A:1234:C:N4	2.77	0.53
4:D:30:LYS:C	4:D:32:ALA:H	2.16	0.53
1:A:189(K):U:H2'	1:A:189(L):G:C8	2.44	0.53
1:A:1074:G:C2	1:A:1075:C:C2	2.97	0.53
6:F:99:ALA:HB2	18:R:31:LEU:HG	1.90	0.53
1:A:725:G:N1	1:A:726:C:C4	2.77	0.53
1:A:973:G:H3'	1:A:974:A:H5''	1.91	0.53
1:A:1464:G:N1	1:A:1465:C:C4	2.77	0.53
1:A:1475:G:H2'	1:A:1476:G:H8	1.70	0.53
1:A:1481:U:H2'	1:A:1482:G:O4'	2.09	0.53
1:A:1485:U:H2'	1:A:1486:G:H8	1.74	0.53
25:Z:18:G:H1	25:Z:55:PSU:H1'	1.74	0.53
1:A:377:G:H2'	1:A:378:G:C8	2.44	0.53
1:A:622:A:H3'	1:A:623:C:H6	1.74	0.53
3:C:6:HIS:HD2	3:C:9:GLY:H	1.56	0.53
3:C:26:LYS:CD	14:N:36:PHE:CE1	2.90	0.53
5:E:148:VAL:O	5:E:152:ARG:HG2	2.08	0.53
1:A:872:A:C4	1:A:874:G:N7	2.77	0.53
2:B:235:SER:HA	2:B:238:LEU:HD13	1.91	0.53
19:S:5:LEU:HD13	19:S:9:VAL:HA	1.89	0.53
22:W:13:VAL:HG22	22:W:24:VAL:HG22	1.91	0.53
23:X:7:THR:H	23:X:10:ARG:HD2	1.74	0.53
1:A:234:C:H2'	1:A:235:C:H6	1.73	0.52
1:A:522:C:H42	1:A:528:C:H42	1.55	0.52
1:A:1320:C:OP1	19:S:70:LYS:HG3	2.09	0.52
4:D:142:PRO:HA	4:D:185:PHE:CD2	2.45	0.52
18:R:40:LEU:C	18:R:42:ARG:H	2.17	0.52
19:S:36:ARG:CA	19:S:71:LEU:HD11	2.27	0.52
25:Z:64:G:C2	25:Z:65:C:C2	2.98	0.52
1:A:381:C:H2'	1:A:382:A:O4'	2.09	0.52
3:C:10:PHE:HA	14:N:58:LYS:HE2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:G:O2'	20:T:102:GLY:O	2.23	0.52
1:A:258:G:N2	1:A:269:C:C2	2.77	0.52
1:A:587:G:OP1	8:H:89:PRO:HB3	2.09	0.52
1:A:695:A:H2'	1:A:696:A:H8	1.74	0.52
1:A:504:C:C2	1:A:542:G:N2	2.77	0.52
1:A:998:G:N2	1:A:999:C:C2	2.78	0.52
1:A:1256:A:N6	1:A:1278:U:C2	2.77	0.52
1:A:763:G:H2'	1:A:764:C:C6	2.45	0.52
1:A:876:G:C6	1:A:877:C:N4	2.77	0.52
1:A:1008:C:N3	1:A:1022:G:N2	2.57	0.52
1:A:1080:A:C8	1:A:1081:G:H1'	2.44	0.52
1:A:1127:G:H1	1:A:1145:C:N4	2.07	0.52
1:A:1127:G:N2	1:A:1145:C:C2	2.76	0.52
3:C:91:LEU:HD21	3:C:99:VAL:HG21	1.91	0.52
5:E:33:VAL:HG13	5:E:112:LEU:HD22	1.92	0.52
22:W:10:GLU:HB3	22:W:52:ARG:HD2	1.90	0.52
23:X:154:PRO:HD3	23:X:163:MET:HE3	1.90	0.52
1:A:755:G:N2	1:A:756:C:C2	2.77	0.52
5:E:40:ARG:HB3	5:E:66:MET:SD	2.50	0.52
1:A:676:A:H2'	1:A:677:U:H6	1.74	0.52
1:A:1007:C:H42	1:A:1022:G:H1	1.58	0.52
1:A:1216:G:N2	1:A:1217:C:C2	2.78	0.52
1:A:1233:G:N2	1:A:1234:C:C2	2.78	0.52
4:D:68:TYR:HB2	4:D:70:ILE:HD11	1.91	0.52
16:P:21:VAL:HG12	16:P:34:GLU:HB3	1.92	0.52
19:S:67:VAL:C	19:S:69:HIS:H	2.17	0.52
1:A:21:G:C2	1:A:22:G:C5	2.97	0.52
9:I:28:VAL:HG22	9:I:63:ILE:HB	1.92	0.52
14:N:26:ARG:HH11	14:N:47:LEU:HD21	1.74	0.52
17:Q:41:LYS:HE2	17:Q:88:TYR:CE1	2.44	0.52
1:A:250:A:H4'	1:A:251:G:O5'	2.10	0.52
3:C:36:ASP:HA	3:C:39:ILE:HD12	1.92	0.52
7:G:150:ALA:C	7:G:152:ALA:H	2.17	0.52
1:A:30:U:H4'	1:A:31:G:OP2	2.10	0.51
1:A:122:G:C2	1:A:123:C:C2	2.97	0.51
1:A:794:A:H2'	1:A:795:C:C6	2.45	0.51
1:A:1233:G:H2'	1:A:1234:C:C6	2.44	0.51
1:A:1347:G:HO2'	1:A:1373:G:H1	1.57	0.51
19:S:30:LEU:H	19:S:48:THR:HB	1.75	0.51
1:A:18:C:H2'	1:A:19:C:O4'	2.09	0.51
1:A:568:G:C6	1:A:569:C:N4	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:839:U:O2	1:A:839:U:C2'	2.58	0.51
3:C:14:ILE:HD13	3:C:14:ILE:N	2.25	0.51
5:E:43:LEU:HB2	5:E:136:MET:HG3	1.91	0.51
1:A:33:A:H2'	1:A:34:C:C6	2.46	0.51
1:A:823:G:N2	1:A:824:C:C2	2.78	0.51
1:A:1416:G:H2'	1:A:1417:G:O4'	2.09	0.51
23:X:77:ARG:HH12	25:Z:23:C:H4'	1.76	0.51
1:A:251:G:C2	1:A:266:G:C6	2.99	0.51
1:A:1048:G:N2	1:A:1210:C:C2	2.78	0.51
1:A:1365:G:C2	1:A:1366:C:C2	2.99	0.51
1:A:1444:C:H2'	1:A:1445:C:C6	2.45	0.51
1:A:333:G:N2	1:A:334:C:C2	2.78	0.51
1:A:558:G:H3'	1:A:559:A:C5'	2.40	0.51
1:A:1310:G:N2	1:A:1328:C:C2	2.79	0.51
1:A:1444:C:H2'	1:A:1445:C:H6	1.75	0.51
10:J:47:PHE:HB2	10:J:63:PHE:HB2	1.93	0.51
18:R:74:ARG:HE	18:R:81:PHE:HA	1.75	0.51
25:Z:55:PSU:O2'	25:Z:57:A:N7	2.40	0.51
1:A:113:G:H2'	1:A:114:U:C6	2.46	0.51
1:A:588:G:N1	1:A:589:C:C4	2.78	0.51
1:A:1057:G:H2'	1:A:1058:G:H8	1.75	0.51
1:A:1149:C:H2'	1:A:1150:U:C6	2.45	0.51
1:A:1488:G:H2'	1:A:1489:G:C8	2.46	0.51
3:C:99:VAL:CG2	3:C:100:ALA:N	2.73	0.51
9:I:4:TYR:CE1	9:I:88:TYR:HD1	2.27	0.51
20:T:43:LEU:HB3	20:T:52:ALA:HB2	1.93	0.51
1:A:566:G:H8	1:A:566:G:O5'	1.93	0.51
1:A:872:A:C8	1:A:874:G:C8	2.99	0.51
1:A:1278:U:H5'	1:A:1279:A:O4'	2.11	0.51
6:F:41:GLU:HB2	6:F:62:TRP:CE3	2.46	0.51
23:X:74:LYS:O	23:X:77:ARG:HB2	2.09	0.51
23:X:141:THR:HG22	23:X:165:LEU:HD21	1.93	0.51
1:A:579:G:H1	1:A:762:C:H42	1.59	0.51
1:A:761:G:C6	1:A:762:C:C4	2.99	0.51
1:A:1266:G:C2	1:A:1270:C:N3	2.79	0.51
25:Z:40:C:H2'	25:Z:41:C:C6	2.46	0.51
1:A:145:G:C2	1:A:178:C:N3	2.79	0.51
1:A:324:G:N2	1:A:327:A:OP2	2.42	0.51
1:A:861:G:N2	1:A:862:C:C2	2.79	0.51
1:A:1017:G:C2	1:A:1018:C:C2	2.99	0.51
1:A:1241:G:C6	1:A:1242:C:N4	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1540:U:H3	24:Y:25:A:N6	2.09	0.51
6:F:4:TYR:HB2	6:F:65:VAL:HG23	1.91	0.51
1:A:22:G:C6	1:A:23:C:C4	2.99	0.51
1:A:504:C:N3	1:A:542:G:C2	2.79	0.51
1:A:1525:G:C4	1:A:1526:G:C8	2.99	0.51
2:B:71:VAL:HB	2:B:164:VAL:HA	1.93	0.51
3:C:97:LYS:NZ	3:C:97:LYS:HB3	2.25	0.51
4:D:60:GLU:CD	4:D:199:ASN:H	2.19	0.51
8:H:83:ILE:HD12	8:H:137:VAL:HG13	1.91	0.51
1:A:1040:U:H2'	1:A:1041:A:C8	2.46	0.50
1:A:1162:C:C2	1:A:1175:G:N2	2.79	0.50
1:A:1232:U:H5''	9:I:124:GLN:O	2.11	0.50
6:F:94:GLN:HB3	18:R:32:ARG:HH11	1.76	0.50
1:A:725:G:C2	1:A:726:C:C4	2.99	0.50
4:D:3:ARG:HD2	4:D:118:ARG:NE	2.27	0.50
18:R:53:ARG:HE	18:R:60:ALA:HA	1.75	0.50
19:S:28:LYS:HA	19:S:29:ARG:CZ	2.41	0.50
25:Z:8:4SU:O2	25:Z:21:A:C2	2.64	0.50
25:Z:28:C:H2'	25:Z:29:G:H8	1.75	0.50
1:A:109:A:H5'	1:A:110:C:C5	2.47	0.50
1:A:1405:G:H2'	1:A:1406:U:H6	1.75	0.50
10:J:6:ILE:HD11	10:J:23:ILE:HG21	1.94	0.50
22:W:53:VAL:HG12	22:W:71:LYS:HA	1.92	0.50
23:X:19:VAL:CG2	23:X:56:VAL:HG13	2.35	0.50
1:A:41:G:H2'	1:A:42:G:C8	2.46	0.50
1:A:174:C:H2'	1:A:175:C:H6	1.74	0.50
1:A:681:C:C2	1:A:710:G:N2	2.79	0.50
1:A:1004:A:H5''	1:A:1025:U:C5	2.46	0.50
13:M:2:ALA:HB1	13:M:57:ARG:HH22	1.77	0.50
1:A:522:C:H41	12:L:53:ARG:NH2	2.08	0.50
1:A:810:C:H2'	1:A:811:C:O4'	2.11	0.50
1:A:1412:C:H2'	1:A:1413:A:O4'	2.11	0.50
2:B:178:ARG:NH2	8:H:74:PRO:HB3	2.27	0.50
3:C:30:ARG:HH11	3:C:30:ARG:HG2	1.76	0.50
5:E:40:ARG:HG2	5:E:68:GLU:CG	2.42	0.50
1:A:405:U:H5''	1:A:406:G:O4'	2.11	0.50
1:A:1347:G:O2'	1:A:1373:G:N1	2.44	0.50
3:C:179:ARG:HD3	3:C:207:VAL:HG22	1.93	0.50
4:D:29:PRO:HA	4:D:34:GLU:HG2	1.93	0.50
4:D:155:LEU:O	4:D:159:ARG:HD2	2.12	0.50
5:E:98:THR:HG22	5:E:101:ILE:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:64:LYS:HB3	8:H:79:VAL:HG11	1.94	0.50
12:L:87:GLY:HA2	12:L:98:TYR:HA	1.94	0.50
20:T:30:LYS:HE2	20:T:72:LEU:CG	2.34	0.50
24:Y:23:C:H2'	24:Y:24:A:O4'	2.12	0.50
24:Y:27:G:H2'	24:Y:28:A:O4'	2.12	0.50
1:A:366:C:H1'	1:A:394:G:H22	1.77	0.50
1:A:1074:G:C6	1:A:1075:C:C4	3.00	0.50
1:A:1347:G:O6	9:I:10:ARG:NH2	2.44	0.50
9:I:113:LYS:H	9:I:119:ALA:HA	1.77	0.50
1:A:132:C:N3	1:A:231:G:C2	2.80	0.50
1:A:509:A:C2	1:A:510:A:C2	3.00	0.50
1:A:834:C:C2	1:A:853:G:C2	3.00	0.50
1:A:992:U:O2	1:A:992:U:H2'	2.11	0.50
1:A:1487:G:H2'	1:A:1488:G:C8	2.46	0.50
2:B:80:ILE:HG22	2:B:84:GLU:HG3	1.93	0.50
3:C:30:ARG:CG	3:C:30:ARG:NH1	2.73	0.50
5:E:103:GLY:O	5:E:106:PRO:HD2	2.11	0.50
10:J:45:ARG:HB2	10:J:65:LEU:HB3	1.94	0.50
11:K:122:LYS:HB2	11:K:125:PHE:HD2	1.77	0.50
16:P:8:ARG:HB3	16:P:28:ARG:CZ	2.42	0.50
23:X:48:VAL:HG21	23:X:58:ARG:HE	1.77	0.50
1:A:734:G:C2	1:A:735:C:C2	3.00	0.50
1:A:957:U:H4'	19:S:79:THR:HG23	1.94	0.50
1:A:1216:G:H5''	14:N:5:ALA:HB2	1.92	0.50
1:A:1517:G:H1'	23:X:101:THR:OG1	2.12	0.50
2:B:17:PHE:HD1	2:B:18:GLY:H	1.60	0.50
2:B:36:ARG:HG3	2:B:41:ILE:HD12	1.93	0.50
1:A:66:G:N2	1:A:67:C:C2	2.79	0.49
1:A:363:A:OP2	12:L:34:ARG:HG2	2.12	0.49
1:A:590:C:N3	1:A:650:G:C2	2.79	0.49
1:A:625:G:OP1	16:P:9:PHE:HB3	2.12	0.49
1:A:688:G:C6	1:A:689:C:N4	2.79	0.49
1:A:793:U:H3'	1:A:794:A:C5'	2.42	0.49
2:B:220:ASP:HA	2:B:230:VAL:HG12	1.93	0.49
24:Y:28:A:H3'	24:Y:29:G:C8	2.46	0.49
1:A:1220:G:H2'	1:A:1221:G:O4'	2.12	0.49
1:A:1508:G:H2'	1:A:1509:C:O4'	2.13	0.49
4:D:201:GLN:CD	5:E:116:THR:OG1	2.55	0.49
5:E:110:LEU:HB3	5:E:118:ILE:HD12	1.94	0.49
1:A:219:C:H2'	1:A:220:G:O4'	2.12	0.49
1:A:584:G:H2'	1:A:585:G:C8	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:662:G:C6	1:A:744:C:N3	2.80	0.49
1:A:799:G:H3'	1:A:800:G:H8	1.77	0.49
1:A:947:G:C6	1:A:948:C:C4	3.00	0.49
1:A:1353:G:N1	1:A:1354:C:C4	2.80	0.49
1:A:1526:G:N2	1:A:1527:C:C2	2.80	0.49
3:C:91:LEU:CD2	3:C:99:VAL:HG21	2.43	0.49
1:A:572:A:N1	1:A:864:A:C5	2.80	0.49
1:A:786:G:N2	1:A:797:C:C2	2.81	0.49
1:A:1092:A:H5''	7:G:4:ARG:CZ	2.41	0.49
1:A:1361:G:C6	1:A:1362:C:N3	2.81	0.49
4:D:9:CYS:SG	4:D:26:CYS:SG	3.11	0.49
18:R:16:PRO:HD3	24:Y:24:A:N3	2.28	0.49
21:V:5:ASP:O	21:V:11:GLY:HA3	2.13	0.49
12:L:42:THR:HG23	12:L:54:LYS:HG3	1.94	0.49
1:A:279:A:H3'	17:Q:95:TYR:CE1	2.45	0.49
1:A:297:G:N2	1:A:301:G:N7	2.60	0.49
1:A:824:C:H2'	1:A:825:G:C8	2.47	0.49
1:A:878:G:H2'	1:A:879:C:C6	2.48	0.49
1:A:1008:C:H2'	1:A:1009:G:O4'	2.12	0.49
1:A:1162:C:C2	1:A:1175:G:C2	3.01	0.49
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.94	0.49
5:E:87:SER:CA	5:E:125:SER:HB3	2.36	0.49
7:G:51:GLN:O	7:G:55:GLY:HA2	2.13	0.49
1:A:189:G:C2	1:A:189(A):C:C2	3.01	0.49
1:A:688:G:H5'	11:K:46:GLY:C	2.38	0.49
1:A:1414:U:H2'	1:A:1415:G:H8	1.77	0.49
6:F:11:ASN:HB3	6:F:14:LEU:HG	1.94	0.49
1:A:264:U:H2'	1:A:265:G:O4'	2.13	0.49
1:A:277:C:H5'	17:Q:68:ARG:NH2	2.28	0.49
1:A:548:G:C6	1:A:549:C:N4	2.80	0.49
1:A:599:C:H4'	8:H:130:GLY:C	2.37	0.49
1:A:1438:G:N2	1:A:1439:C:C2	2.80	0.49
1:A:1506:U:O2'	1:A:1507:A:H5'	2.12	0.49
4:D:3:ARG:HD2	4:D:118:ARG:CZ	2.43	0.49
16:P:6:LEU:HG	16:P:17:TYR:HB3	1.95	0.49
24:Y:36:A:H2'	24:Y:37:U:O4'	2.12	0.49
1:A:399:G:N2	1:A:400:C:C2	2.81	0.49
1:A:803:G:H2'	1:A:804:U:O4'	2.13	0.49
1:A:862:C:H2'	1:A:863:U:O4'	2.13	0.49
1:A:1536:C:N4	24:Y:29:G:H1	2.11	0.49
13:M:14:ARG:HA	13:M:43:THR:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:30:LYS:HE3	20:T:72:LEU:HD23	1.85	0.49
23:X:17:ARG:HG2	23:X:25:GLN:HE22	1.78	0.49
1:A:216:G:C2	1:A:217:C:N3	2.81	0.49
1:A:437:U:H3'	1:A:438:G:H8	1.78	0.49
1:A:573:A:H2'	1:A:574:A:O4'	2.12	0.49
1:A:590:C:H42	1:A:649:G:H1	1.61	0.49
1:A:982:U:H4'	1:A:983:A:O4'	2.13	0.49
1:A:1095:U:P	1:A:1108:G:H1	2.36	0.49
1:A:1333:A:H2'	1:A:1334:G:O4'	2.12	0.49
7:G:74:GLU:HG2	7:G:91:VAL:HG22	1.94	0.49
13:M:32:GLU:OE1	13:M:64:TRP:HH2	1.96	0.49
1:A:35:G:C6	1:A:36:C:N4	2.81	0.48
1:A:316:G:H1	1:A:337:C:N4	2.11	0.48
1:A:399:G:C6	1:A:400:C:N4	2.81	0.48
1:A:1130:A:N6	1:A:1144:G:H21	2.10	0.48
1:A:1245:A:H2'	1:A:1246:C:C6	2.48	0.48
1:A:1418:A:N6	1:A:1482:G:O2'	2.46	0.48
1:A:1507:A:H2'	1:A:1508:G:O4'	2.12	0.48
1:A:1365:G:C6	1:A:1366:C:C4	3.01	0.48
1:A:321:A:H2'	1:A:322:C:C6	2.47	0.48
1:A:585:G:O3'	17:Q:34:LYS:NZ	2.45	0.48
1:A:638:G:H2'	1:A:639:G:O4'	2.14	0.48
23:X:7:THR:HG21	23:X:62:TYR:HB2	1.94	0.48
1:A:127:G:C2	1:A:235:C:N3	2.81	0.48
1:A:189(K):U:H2'	1:A:189(L):G:H8	1.78	0.48
1:A:715:A:H2'	1:A:716:A:C8	2.47	0.48
1:A:977:A:H2'	1:A:978:A:H5''	1.95	0.48
1:A:1025:U:H2'	1:A:1026:G:H8	1.76	0.48
1:A:376:G:H2'	1:A:377:G:H8	1.79	0.48
1:A:1050:G:C6	1:A:1051:C:N4	2.81	0.48
7:G:65:ALA:HB1	7:G:127:ALA:HB3	1.95	0.48
19:S:71:LEU:H	19:S:71:LEU:HG	1.41	0.48
1:A:71:C:H2'	1:A:72:C:O4'	2.14	0.48
1:A:192:U:H2'	1:A:193:C:C6	2.48	0.48
1:A:988:G:C6	1:A:989:C:N3	2.81	0.48
1:A:1536:C:H42	24:Y:29:G:H1	1.60	0.48
3:C:6:HIS:HA	3:C:7:PRO:HD3	1.73	0.48
5:E:48:ALA:HB3	5:E:54:ALA:HB2	1.94	0.48
25:Z:40:C:H2'	25:Z:41:C:H6	1.79	0.48
25:Z:49:G:H8	25:Z:49:G:O5'	1.97	0.48
1:A:183:G:H2'	1:A:184:G:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:C:N3	1:A:191:G:C2	2.82	0.48
1:A:576:G:H3'	1:A:577:G:C5'	2.44	0.48
1:A:1050:G:N2	1:A:1051:C:C2	2.81	0.48
1:A:1119:C:H42	1:A:1154:G:H1	1.61	0.48
2:B:7:VAL:HA	2:B:221:LEU:HD23	1.95	0.48
12:L:27:LEU:HG	12:L:28:LYS:N	2.29	0.48
23:X:7:THR:HG22	23:X:46:VAL:HG22	1.95	0.48
1:A:784:C:H42	1:A:798:G:H1	1.62	0.48
2:B:51:LEU:HD23	2:B:55:PHE:CE1	2.48	0.48
5:E:13:ILE:HA	5:E:29:GLY:O	2.14	0.48
8:H:103:VAL:HG21	8:H:110:ALA:HB2	1.95	0.48
1:A:130:A:H8	1:A:130:A:OP1	1.97	0.48
1:A:499:A:N6	1:A:547:A:C8	2.82	0.48
1:A:540:G:H2'	1:A:541:G:C8	2.49	0.48
1:A:1015:A:H2'	1:A:1016:A:C8	2.49	0.48
1:A:1129:C:O5'	1:A:1130:A:H5'	2.14	0.48
1:A:1321:C:H4'	13:M:87:TYR:CZ	2.48	0.48
1:A:1363(A):A:H1'	1:A:1365:G:N7	2.29	0.48
11:K:120:ARG:HH11	11:K:126:ARG:HE	1.61	0.48
23:X:33:GLU:O	23:X:37:LEU:HG	2.14	0.48
1:A:192:U:H2'	1:A:193:C:H6	1.77	0.48
1:A:524:G:C2	1:A:525:C:C4	3.02	0.48
1:A:734:G:C6	1:A:735:C:C4	3.02	0.48
1:A:777:A:H2'	1:A:778:G:C8	2.49	0.48
1:A:968:A:C8	1:A:1062:U:H4'	2.49	0.48
1:A:975:A:H4'	1:A:976:G:C5'	2.44	0.48
1:A:1445:C:O2	1:A:1458:G:C2	2.67	0.48
1:A:287:U:H2'	1:A:288:A:H8	1.78	0.47
1:A:708:C:H2'	1:A:709:G:H8	1.79	0.47
1:A:799:G:H3'	1:A:800:G:C8	2.49	0.47
1:A:1317:C:H2'	1:A:1318:A:C8	2.49	0.47
1:A:1346:A:C8	1:A:1348:U:C2	3.02	0.47
1:A:1464:G:C2	1:A:1465:C:C4	3.02	0.47
2:B:223:ILE:HD12	2:B:230:VAL:HG11	1.95	0.47
10:J:4:ILE:N	10:J:73:ASP:OD1	2.47	0.47
1:A:1050:G:C2	1:A:1209:C:C2	3.02	0.47
1:A:1410:G:C6	1:A:1411:C:N4	2.83	0.47
1:A:1458:G:H5''	20:T:32:ALA:HB2	1.96	0.47
23:X:5:TYR:HD1	23:X:48:VAL:HA	1.78	0.47
1:A:276:G:C2	1:A:277:C:C2	3.02	0.47
1:A:509:A:H5'	4:D:55:ALA:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:577:G:N2	1:A:578:C:C2	2.82	0.47
1:A:621:A:H2'	1:A:622:A:H8	1.78	0.47
1:A:774:G:C2	1:A:806:C:N3	2.82	0.47
1:A:779:C:O2'	11:K:120:ARG:HD2	2.13	0.47
20:T:63:ILE:HG21	20:T:81:LYS:HG3	1.97	0.47
21:V:10:ARG:HA	21:V:13:ILE:HD12	1.97	0.47
22:W:57:ILE:HG23	22:W:62:PRO:HA	1.96	0.47
23:X:50:PRO:HA	23:X:55:PRO:HB3	1.97	0.47
25:Z:40:C:H2'	25:Z:41:C:O4'	2.14	0.47
1:A:35:G:H2'	1:A:36:C:C6	2.49	0.47
1:A:236:G:C2	1:A:237:C:C2	3.02	0.47
1:A:974:A:H4'	1:A:975:A:H3'	1.95	0.47
1:A:1404:C:H2'	1:A:1405:G:C8	2.49	0.47
3:C:77:ILE:HA	3:C:84:ILE:HB	1.96	0.47
4:D:97:LEU:O	4:D:100:ARG:HB2	2.15	0.47
8:H:49:GLU:HG3	8:H:60:ARG:CB	2.45	0.47
10:J:40:LEU:HD23	10:J:41:PRO:HD2	1.96	0.47
22:W:32:ILE:HD13	22:W:32:ILE:N	2.29	0.47
1:A:10:A:H2'	1:A:11:G:C8	2.49	0.47
1:A:46:G:H2'	1:A:366:C:C5	2.50	0.47
1:A:77:G:H3'	1:A:77:G:C8	2.49	0.47
1:A:329:A:H4'	1:A:330:C:OP1	2.12	0.47
1:A:616:G:H1	1:A:624:C:H42	1.62	0.47
1:A:1105:A:H2'	1:A:1106:G:H8	1.79	0.47
1:A:1190:G:H5'	3:C:176:HIS:CE1	2.50	0.47
1:A:1287:A:H2'	1:A:1288:A:C8	2.49	0.47
3:C:19:GLU:O	3:C:56:ASP:HA	2.15	0.47
8:H:32:LYS:O	8:H:36:LEU:HD12	2.15	0.47
23:X:123:ARG:C	23:X:129:HIS:HE1	2.22	0.47
1:A:8:A:C5	4:D:209:ARG:HB3	2.50	0.47
1:A:451:A:C6	1:A:480:U:H2'	2.50	0.47
1:A:553:A:H2'	1:A:554:C:C6	2.49	0.47
1:A:590:C:C2	1:A:650:G:C2	3.02	0.47
1:A:701:C:H1'	1:A:703:G:C5	2.50	0.47
1:A:737:A:H2'	1:A:738:C:C6	2.50	0.47
1:A:1163:C:H2'	1:A:1164:G:H8	1.80	0.47
1:A:1371:G:OP1	9:I:68:GLY:HA2	2.15	0.47
10:J:5:ARG:HD2	10:J:99:LYS:HB2	1.95	0.47
23:X:90:PHE:HD1	23:X:94:ILE:HG21	1.80	0.47
1:A:132:C:H5'	20:T:75:ASN:HD22	1.80	0.47
1:A:173:U:H5'	1:A:197:A:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:C:C4	1:A:356:A:N7	2.83	0.47
1:A:499:A:C6	1:A:547:A:C8	3.03	0.47
1:A:556:C:H2'	1:A:557:G:O4'	2.14	0.47
1:A:568:G:C2	1:A:883:C:C2	3.02	0.47
1:A:975:A:H4'	1:A:976:G:O5'	2.13	0.47
1:A:1076:C:H2'	1:A:1077:G:H8	1.80	0.47
1:A:1097:C:H5''	2:B:140:HIS:CE1	2.49	0.47
1:A:1258:G:C6	1:A:1259:C:N4	2.83	0.47
1:A:1399:C:C2	1:A:1502:A:N6	2.83	0.47
1:A:1469:G:H2'	1:A:1470:G:H8	1.79	0.47
1:A:1500:A:H5''	1:A:1508:G:H5''	1.96	0.47
2:B:188:ALA:HB1	2:B:192:SER:HB3	1.96	0.47
4:D:57:ARG:HG3	4:D:57:ARG:NH1	2.30	0.47
5:E:110:LEU:HB3	5:E:118:ILE:CD1	2.45	0.47
11:K:21:ILE:HG23	11:K:30:VAL:HG22	1.96	0.47
11:K:82:VAL:HB	11:K:108:ILE:HA	1.95	0.47
13:M:77:ASN:HA	13:M:80:ARG:NH1	2.30	0.47
15:O:63:ARG:HA	15:O:66:LEU:HD12	1.97	0.47
23:X:45:LEU:HD21	23:X:57:ALA:HB1	1.95	0.47
24:Y:33:A:H2'	24:Y:33:A:N3	2.30	0.47
1:A:216:G:H2'	1:A:217:C:C6	2.50	0.47
1:A:241:C:C2	1:A:286:G:N2	2.83	0.47
1:A:604:G:H2'	1:A:605:U:O4'	2.15	0.47
1:A:778:G:C6	1:A:779:C:C4	3.03	0.47
1:A:1006:C:N3	1:A:1024:G:H1'	2.30	0.47
1:A:1049:U:O2'	14:N:3:ARG:HD2	2.15	0.47
1:A:1118:C:P	9:I:9:ARG:HH21	2.38	0.47
2:B:220:ASP:O	2:B:224:GLN:HB2	2.14	0.47
10:J:81:THR:HG22	10:J:85:LEU:HD12	1.96	0.47
17:Q:75:ARG:HH12	17:Q:77:VAL:HA	1.79	0.47
1:A:39:G:C6	1:A:40:C:C4	3.03	0.47
1:A:918:A:H2'	1:A:919:A:O4'	2.15	0.47
7:G:24:THR:HA	7:G:27:ILE:HD12	1.96	0.47
10:J:50:ILE:CG1	10:J:60:ARG:HH21	2.27	0.47
12:L:23:LYS:HE2	12:L:89:ARG:HE	1.80	0.47
15:O:14:GLU:HG2	15:O:15:PHE:CD1	2.49	0.47
16:P:2:VAL:HG13	16:P:64:ALA:HA	1.97	0.47
19:S:22:LEU:HA	19:S:25:LYS:HB2	1.97	0.47
25:Z:30:G:N2	25:Z:41:C:C2	2.83	0.47
1:A:501:C:H2'	1:A:502:G:C8	2.50	0.47
1:A:505:G:H2'	1:A:506:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:536:C:H2'	1:A:537:G:H8	1.80	0.47
1:A:778:G:C2	1:A:779:C:C2	3.03	0.47
1:A:910:C:H5''	12:L:97:ARG:HH21	1.78	0.47
1:A:1057:G:H2'	1:A:1058:G:C8	2.50	0.47
4:D:25:ARG:HG3	4:D:30:LYS:HB3	1.97	0.47
5:E:80:ILE:HD11	5:E:142:LEU:HG	1.97	0.47
20:T:12:ALA:O	20:T:15:ARG:HB2	2.15	0.47
23:X:64:LYS:O	23:X:68:GLU:HG2	2.15	0.47
25:Z:43:A:H2'	25:Z:44:A:H8	1.79	0.47
1:A:144:G:H1	1:A:178:C:H42	1.63	0.46
1:A:542:G:C6	1:A:543:C:N4	2.83	0.46
1:A:855:G:C6	1:A:856:C:C4	3.03	0.46
1:A:1006:C:N4	1:A:1023:G:O6	2.48	0.46
1:A:1424:C:N4	1:A:1476:G:H1	2.12	0.46
2:B:91:PRO:HB3	2:B:155:LEU:HD11	1.95	0.46
3:C:174:PRO:C	3:C:176:HIS:N	2.73	0.46
5:E:60:TYR:CD1	5:E:60:TYR:C	2.93	0.46
14:N:47:LEU:HB3	14:N:53:LEU:HD21	1.97	0.46
15:O:62:GLN:HA	15:O:65:ARG:NH1	2.31	0.46
22:W:36:ILE:HD13	22:W:41:ARG:HG3	1.97	0.46
1:A:142:G:H2'	1:A:143:A:C8	2.51	0.46
1:A:172:A:H2'	1:A:174:C:C5	2.50	0.46
1:A:200:G:C2	1:A:218:C:C2	3.03	0.46
1:A:518:C:H5''	1:A:519:C:C6	2.50	0.46
1:A:577:G:C2	1:A:578:C:C2	3.03	0.46
1:A:696:A:N3	1:A:786:G:O2'	2.41	0.46
1:A:876:G:C2	1:A:877:C:N3	2.83	0.46
1:A:1284:C:H2'	1:A:1285:A:C8	2.50	0.46
2:B:44:LEU:HA	2:B:47:THR:HB	1.98	0.46
10:J:24:VAL:CG1	10:J:28:ARG:HE	2.28	0.46
11:K:14:VAL:HG21	11:K:34:ASP:HB2	1.97	0.46
1:A:22:G:C2	1:A:23:C:C2	3.04	0.46
1:A:108:G:H5'	1:A:109:A:H5''	1.97	0.46
1:A:109:A:H5'	1:A:110:C:H5	1.79	0.46
1:A:988:G:C6	1:A:989:C:C2	3.03	0.46
3:C:8:ILE:HG23	3:C:16:ARG:HG2	1.96	0.46
3:C:174:PRO:O	3:C:176:HIS:N	2.48	0.46
4:D:57:ARG:HB3	4:D:206:PHE:HB2	1.97	0.46
4:D:173:TRP:HA	4:D:187:ARG:HB3	1.98	0.46
4:D:177:ASP:HB3	4:D:182:LYS:HB2	1.97	0.46
15:O:70:LEU:HD11	15:O:77:ARG:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:59:ILE:HD13	17:Q:73:VAL:HA	1.96	0.46
22:W:13:VAL:HA	22:W:24:VAL:HA	1.97	0.46
1:A:1126:U:O2	1:A:1126:U:C2'	2.63	0.46
16:P:12:LYS:C	16:P:14:ASN:H	2.24	0.46
17:Q:92:ARG:O	17:Q:95:TYR:HB2	2.16	0.46
23:X:126:GLU:HA	23:X:129:HIS:HB2	1.96	0.46
1:A:318:G:N2	1:A:336:C:C2	2.84	0.46
1:A:518:C:O2'	1:A:519:C:OP2	2.30	0.46
1:A:590:C:C2	1:A:650:G:N2	2.83	0.46
1:A:922:G:C2	1:A:923:A:C4	3.03	0.46
1:A:975:A:H5''	1:A:975:A:C8	2.50	0.46
1:A:1358:U:O4	1:A:1363(A):A:C2	2.61	0.46
1:A:1469:G:H2'	1:A:1470:G:C8	2.51	0.46
1:A:1514:C:H2'	1:A:1515:C:C6	2.50	0.46
2:B:61:LEU:HD13	2:B:66:GLY:HA3	1.97	0.46
11:K:58:PRO:HA	11:K:90:GLY:HA3	1.98	0.46
13:M:51:ALA:O	13:M:55:ARG:HG3	2.15	0.46
18:R:26:LEU:HD11	18:R:39:VAL:HG23	1.97	0.46
19:S:22:LEU:HD11	19:S:31:ILE:HD11	1.97	0.46
1:A:1493:A:H4'	1:A:1494:G:OP1	2.15	0.46
1:A:1508:G:C2	1:A:1509:C:C2	3.04	0.46
9:I:114:TYR:CG	10:J:60:ARG:HB2	2.51	0.46
13:M:48:LEU:HD13	13:M:53:VAL:HG22	1.98	0.46
23:X:38:ALA:HA	23:X:59:ILE:HG23	1.98	0.46
1:A:169:C:H2'	1:A:170:U:C6	2.51	0.46
1:A:401:C:H2'	1:A:402:G:H8	1.81	0.46
1:A:601:C:H2'	1:A:602:A:H8	1.80	0.46
1:A:914:A:N6	1:A:915:A:N6	2.64	0.46
1:A:999:C:O2	1:A:1043:C:O2	2.34	0.46
1:A:1144:G:N2	1:A:1146:A:H62	2.13	0.46
1:A:1487:G:C2'	1:A:1488:G:C8	2.99	0.46
4:D:108:LEU:HD11	4:D:146:ILE:HD13	1.97	0.46
25:Z:64:G:C6	25:Z:65:C:C4	3.04	0.46
1:A:715:A:H2'	1:A:716:A:H8	1.81	0.46
1:A:725:G:C6	1:A:726:C:N4	2.84	0.46
1:A:1144:G:H22	1:A:1146:A:H62	1.63	0.46
1:A:1534:A:N6	24:Y:31:U:H3	2.13	0.46
5:E:37:ARG:HH12	5:E:111:GLU:HB3	1.80	0.46
7:G:29:LYS:HB3	7:G:105:VAL:HG21	1.97	0.46
8:H:86:ILE:HB	8:H:133:LEU:HD22	1.97	0.46
9:I:48:GLU:N	9:I:49:PRO:HD2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:369:C:H2'	1:A:370:C:C6	2.51	0.46
1:A:763:G:C2	1:A:764:C:C2	3.03	0.46
1:A:965:A:H4'	1:A:966:G:O5'	2.16	0.46
1:A:1076:C:H2'	1:A:1077:G:C8	2.51	0.46
9:I:22:GLY:HA3	9:I:60:ASP:HB2	1.96	0.46
9:I:46:ALA:HA	9:I:78:LYS:HB2	1.97	0.46
10:J:16:LEU:HD23	10:J:70:ARG:CG	2.33	0.46
15:O:76:GLU:HA	15:O:79:ARG:HH11	1.81	0.46
1:A:23:C:C4	1:A:24:U:C4	3.04	0.46
1:A:443:C:N3	1:A:492:G:C2	2.84	0.46
1:A:522:C:OP2	12:L:69:TYR:OH	2.33	0.46
1:A:693:G:H1'	7:G:81:GLY:O	2.16	0.46
1:A:1099:G:C2	1:A:1100:C:O2	2.69	0.46
1:A:1102:A:H2'	1:A:1103:C:H6	1.80	0.46
1:A:1353:G:C2	1:A:1354:C:C4	3.04	0.46
1:A:1419:G:C2	1:A:1420:C:C2	3.04	0.46
7:G:47:CYS:HA	7:G:50:ILE:HD12	1.99	0.46
14:N:41:ARG:HE	14:N:42:ILE:HG13	1.81	0.46
1:A:252:U:H2'	1:A:253:U:C5	2.51	0.45
8:H:111:ILE:HG22	8:H:134:ILE:HD12	1.98	0.45
20:T:10:LEU:HG	20:T:12:ALA:H	1.80	0.45
22:W:32:ILE:CD1	22:W:32:ILE:N	2.78	0.45
1:A:189:G:C6	1:A:189(A):C:C4	3.04	0.45
1:A:323:U:H2'	1:A:324:G:O4'	2.16	0.45
1:A:659:U:H5''	15:O:9:GLN:HE21	1.81	0.45
1:A:832:C:C2	1:A:855:G:C2	3.04	0.45
1:A:1493:A:H2'	22:W:20:ALA:HA	1.98	0.45
1:A:1494:G:C6	1:A:1495:U:C4	3.04	0.45
4:D:4:TYR:HB3	4:D:115:ARG:HH22	1.81	0.45
4:D:196:LEU:C	4:D:198:VAL:H	2.25	0.45
8:H:79:VAL:HG13	8:H:80:ILE:HG13	1.98	0.45
10:J:70:ARG:HD3	10:J:70:ARG:HA	1.79	0.45
1:A:312:C:H2'	1:A:313:A:H8	1.77	0.45
1:A:548:G:C2	1:A:549:C:C2	3.05	0.45
1:A:585:G:C2	1:A:586:C:C2	3.04	0.45
1:A:601:C:H2'	1:A:602:A:C8	2.51	0.45
2:B:186:ALA:HB3	2:B:200:ILE:HA	1.98	0.45
4:D:35:ARG:HG3	4:D:36:ARG:N	2.31	0.45
5:E:91:LEU:HD11	5:E:110:LEU:HD11	1.99	0.45
10:J:38:ILE:HG23	10:J:71:LEU:C	2.26	0.45
19:S:36:ARG:CB	19:S:71:LEU:HD12	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:15:GLU:HB3	22:W:23:ARG:HB2	1.98	0.45
1:A:530:G:H2'	1:A:530:G:N3	2.32	0.45
1:A:643:C:H2'	1:A:644:G:H8	1.82	0.45
1:A:865:A:C2	1:A:866:C:C2	3.05	0.45
1:A:1457:G:C5'	1:A:1457:G:H8	2.25	0.45
1:A:1489:G:C2	1:A:1490:C:C2	3.05	0.45
6:F:97:PHE:O	18:R:30:ASP:HA	2.16	0.45
1:A:564:C:C5	17:Q:31:LEU:HD11	2.52	0.45
1:A:914:A:C6	1:A:915:A:N6	2.84	0.45
1:A:914:A:H2'	1:A:915:A:C8	2.52	0.45
1:A:1111:A:N1	3:C:177:THR:HB	2.32	0.45
1:A:1151:A:O2'	1:A:1152:A:H8	1.98	0.45
1:A:1162:C:H2'	1:A:1163:C:C6	2.52	0.45
1:A:1502:A:H2'	1:A:1504:G:N7	2.31	0.45
1:A:1542:U:H4'	18:R:18:ARG:N	2.28	0.45
4:D:142:PRO:HA	4:D:185:PHE:HD2	1.82	0.45
9:I:17:VAL:HG22	9:I:63:ILE:HG12	1.98	0.45
16:P:22:THR:HA	16:P:33:ILE:HD13	1.96	0.45
18:R:61:LYS:HA	18:R:64:ARG:NH1	2.31	0.45
22:W:23:ARG:HH22	22:W:33:LEU:CD2	2.30	0.45
1:A:6:G:O6	5:E:94:ALA:HA	2.17	0.45
1:A:600:C:H2'	1:A:601:C:H6	1.81	0.45
1:A:623:C:H2'	1:A:624:C:O4'	2.16	0.45
1:A:902:G:H2'	1:A:903:G:H8	1.81	0.45
1:A:914:A:H2'	1:A:915:A:H8	1.81	0.45
1:A:1048:G:H2'	1:A:1050:G:H8	1.81	0.45
1:A:354:G:N1	1:A:355:C:C4	2.85	0.45
1:A:502:G:C2	1:A:503:C:C2	3.05	0.45
1:A:786:G:C2	1:A:797:C:C2	3.05	0.45
1:A:918:A:H2'	1:A:919:A:C8	2.51	0.45
1:A:1129:C:H1'	1:A:1132:C:H5	1.80	0.45
1:A:1339:A:H1'	25:Z:41:C:H1'	1.99	0.45
1:A:1418:A:H2'	1:A:1418:A:N3	2.31	0.45
3:C:22:TRP:HB3	3:C:59:ARG:H	1.81	0.45
5:E:81:GLU:HG3	5:E:90:VAL:HG22	1.98	0.45
10:J:33:GLN:HB3	10:J:75:ILE:HD12	1.99	0.45
19:S:70:LYS:N	19:S:73:GLU:OE2	2.50	0.45
25:Z:22:G:C6	25:Z:23:C:N4	2.85	0.45
1:A:108:G:H22	20:T:15:ARG:HH21	1.65	0.45
1:A:384:G:C2	1:A:385:C:C2	3.05	0.45
1:A:501:C:H2'	1:A:502:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:916:G:H2'	1:A:917:G:H8	1.82	0.45
1:A:945:G:H2'	1:A:945:G:N3	2.31	0.45
1:A:1353:G:C6	1:A:1354:C:N4	2.84	0.45
3:C:19:GLU:HB2	14:N:52:GLN:HA	1.98	0.45
14:N:47:LEU:CB	14:N:53:LEU:HD21	2.47	0.45
1:A:184:G:H2'	1:A:185:A:C8	2.52	0.45
1:A:412:A:C4	4:D:35:ARG:NH2	2.71	0.45
1:A:484:G:H8	1:A:484:G:OP1	2.00	0.45
1:A:499:A:C5	1:A:547:A:N7	2.85	0.45
1:A:707:C:H4'	11:K:20:TYR:CD2	2.52	0.45
1:A:746:A:H2'	1:A:747:C:C6	2.52	0.45
1:A:788:U:H2'	1:A:789:U:O4'	2.17	0.45
1:A:1114:C:C2	1:A:1187:G:C2	3.05	0.45
1:A:1409:C:H2'	1:A:1410:G:H8	1.79	0.45
2:B:178:ARG:NH1	8:H:71:GLY:H	2.15	0.45
3:C:18:TRP:HZ2	14:N:57:ARG:HG3	1.82	0.45
8:H:91:ARG:HB2	12:L:7:ILE:HG13	1.99	0.45
12:L:47:LYS:N	12:L:48:PRO:HD2	2.30	0.45
1:A:42:G:C2	1:A:43:C:C2	3.05	0.45
1:A:382:A:H2'	1:A:383:A:C8	2.52	0.45
1:A:895:G:C2	1:A:896:C:C2	3.05	0.45
1:A:1143:G:H2'	1:A:1144:G:O4'	2.17	0.45
1:A:1314:C:H2'	1:A:1315:U:C6	2.51	0.45
1:A:1386:G:H2'	1:A:1387:G:C8	2.50	0.45
2:B:24:TRP:CZ2	2:B:26:PRO:HG3	2.52	0.45
5:E:151:LEU:HB3	8:H:79:VAL:HG23	1.99	0.45
1:A:116:A:C4	1:A:117:G:C8	3.06	0.44
1:A:236:G:C6	1:A:237:C:C4	3.05	0.44
1:A:538:G:OP2	12:L:115:LYS:HB2	2.17	0.44
1:A:615:C:H2'	1:A:616:G:H8	1.81	0.44
1:A:767:A:H2'	1:A:768:A:O4'	2.16	0.44
1:A:985:C:C2	1:A:1221:G:N2	2.85	0.44
1:A:1017:G:C6	1:A:1018:C:C4	3.05	0.44
1:A:1537:U:H3	24:Y:28:A:H61	1.65	0.44
9:I:10:ARG:HD3	9:I:105:ASP:HB3	1.99	0.44
23:X:91:ARG:HB2	23:X:94:ILE:HB	1.99	0.44
24:Y:28:A:H3'	24:Y:29:G:H8	1.82	0.44
1:A:414:A:H2'	1:A:415:A:O4'	2.18	0.44
1:A:585:G:C6	1:A:586:C:C4	3.05	0.44
1:A:917:G:H2'	1:A:918:A:H8	1.77	0.44
1:A:1118:C:H2'	1:A:1119:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1207:G:C2	1:A:1208:C:C2	3.05	0.44
1:A:1372:U:H2'	1:A:1373:G:O4'	2.17	0.44
3:C:108:ASN:HD21	3:C:110:ASN:HB2	1.82	0.44
6:F:48:LEU:HD13	6:F:52:ILE:HD12	1.99	0.44
8:H:86:ILE:H	8:H:135:CYS:HA	1.82	0.44
10:J:5:ARG:CG	10:J:71:LEU:HD11	2.47	0.44
1:A:277:C:H5'	17:Q:68:ARG:HH22	1.82	0.44
1:A:321:A:H2'	1:A:322:C:H6	1.83	0.44
1:A:376:G:H5''	16:P:5:ARG:HB2	1.98	0.44
1:A:455:C:H2'	1:A:456:C:C6	2.51	0.44
1:A:502:G:C6	1:A:503:C:C4	3.05	0.44
1:A:680:C:C2	1:A:711:G:C2	3.05	0.44
1:A:688:G:C2	1:A:689:C:N3	2.85	0.44
1:A:823:G:N1	1:A:824:C:C4	2.86	0.44
1:A:868:C:H2'	1:A:869:G:O4'	2.18	0.44
1:A:1163:C:C2	1:A:1174:G:N2	2.85	0.44
1:A:1164:G:N2	1:A:1165:C:C2	2.85	0.44
1:A:1282:C:C2	1:A:1283:G:C8	3.05	0.44
2:B:172:ILE:H	2:B:172:ILE:HG13	1.25	0.44
7:G:27:ILE:HA	7:G:30:ILE:HD12	2.00	0.44
22:W:13:VAL:HG21	22:W:47:ILE:CG2	2.47	0.44
1:A:27:G:H2'	1:A:28:G:O4'	2.17	0.44
1:A:109:A:H2'	1:A:326:G:N2	2.32	0.44
1:A:114:U:H2'	1:A:115:G:C8	2.52	0.44
1:A:302:G:H2'	1:A:303:A:C8	2.52	0.44
1:A:340:U:H2'	1:A:341:C:C6	2.48	0.44
1:A:931:C:C2	1:A:1387:G:N1	2.85	0.44
1:A:998:G:N1	1:A:999:C:C4	2.85	0.44
1:A:1179:A:OP2	9:I:93:ARG:NH2	2.50	0.44
1:A:1253:G:C2	1:A:1254:C:C2	3.06	0.44
3:C:71:ALA:HB2	3:C:115:LEU:HD13	1.98	0.44
5:E:32:VAL:HG12	5:E:44:GLY:HA3	2.00	0.44
6:F:97:PHE:HB2	18:R:32:ARG:CD	2.47	0.44
8:H:34:GLU:O	8:H:37:ARG:HB3	2.18	0.44
9:I:128:ARG:NH1	25:Z:35:A:OP1	2.50	0.44
12:L:54:LYS:HB3	12:L:70:ILE:HD12	2.00	0.44
1:A:988:G:C6	1:A:989:C:C4	3.06	0.44
1:A:1262:C:N4	1:A:1273:G:H1	2.15	0.44
2:B:17:PHE:HB2	2:B:41:ILE:HG23	1.99	0.44
2:B:90:MET:HA	2:B:91:PRO:HD2	1.74	0.44
8:H:66:GLY:HA3	8:H:77:GLU:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:53:ASN:C	19:S:55:LYS:H	2.26	0.44
1:A:370:C:N3	1:A:392:G:C2	2.86	0.44
1:A:711:G:H2'	1:A:712:A:H8	1.83	0.44
1:A:932:C:H5'	7:G:3:ARG:HB2	1.98	0.44
1:A:1147:C:H2'	1:A:1148:U:C6	2.53	0.44
1:A:1257:U:H4'	1:A:1258:G:O5'	2.17	0.44
1:A:306:G:C6	1:A:307:C:C4	3.06	0.44
1:A:310:G:C2	1:A:311:C:C2	3.05	0.44
1:A:402:G:N2	1:A:403:C:C2	2.86	0.44
1:A:413:G:N7	4:D:35:ARG:NH2	2.66	0.44
1:A:522:C:H42	1:A:528:C:N4	2.14	0.44
1:A:625:G:H2'	1:A:626:U:C6	2.53	0.44
1:A:866:C:C4	1:A:867:G:H1'	2.53	0.44
1:A:1360:A:H2'	1:A:1361:G:C8	2.53	0.44
2:B:115:LEU:HD12	2:B:142:LEU:HD23	1.99	0.44
16:P:45:THR:HA	16:P:46:PRO:HD2	1.87	0.44
16:P:59:TRP:CE3	16:P:62:VAL:HG21	2.53	0.44
1:A:147:G:C2	1:A:176:C:C2	3.06	0.44
1:A:540:G:H2'	1:A:541:G:H8	1.82	0.44
1:A:975:A:H4'	1:A:976:G:H5'	1.99	0.44
1:A:1517:G:C8	23:X:101:THR:HG23	2.53	0.44
6:F:45:LEU:HD12	6:F:59:TYR:CD2	2.49	0.44
22:W:23:ARG:HH22	22:W:33:LEU:HD21	1.82	0.44
25:Z:70:G:C2	25:Z:71:C:C2	3.06	0.44
1:A:179:A:H2'	1:A:180:U:C6	2.52	0.44
1:A:276:G:C6	1:A:277:C:C4	3.06	0.44
1:A:352:C:H4'	1:A:354:G:OP1	2.17	0.44
1:A:416:G:C6	1:A:417:C:C4	3.06	0.44
1:A:662:G:O2'	1:A:836:G:H5'	2.18	0.44
1:A:1498:U:H4'	1:A:1519:A:H2	1.83	0.44
4:D:98:GLU:CD	4:D:103:ASN:HD21	2.26	0.44
12:L:39:VAL:HG22	12:L:57:LYS:HB2	2.00	0.44
17:Q:18:THR:HG23	17:Q:69:LYS:HE3	2.00	0.44
19:S:12:ASP:C	19:S:14:HIS:H	2.26	0.44
25:Z:39:C:H2'	25:Z:40:C:C6	2.52	0.44
1:A:42:G:C6	1:A:43:C:C4	3.06	0.43
1:A:300:A:H1'	1:A:565:U:O2	2.18	0.43
1:A:616:G:H2'	1:A:617:G:H8	1.82	0.43
1:A:886:G:C2	1:A:912:C:O2	2.71	0.43
1:A:1001(A):G:N2	1:A:1040:U:C2	2.86	0.43
1:A:1241:G:C2	1:A:1242:C:C4	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1291:G:H4'	9:I:38:GLN:O	2.18	0.43
1:A:1431:C:C2	1:A:1470:G:N2	2.86	0.43
2:B:16:HIS:NE2	2:B:203:GLY:HA3	2.33	0.43
5:E:151:LEU:HD22	8:H:79:VAL:HA	2.00	0.43
6:F:19:LEU:HD11	6:F:59:TYR:CE2	2.53	0.43
11:K:33:THR:HA	11:K:39:PRO:HA	1.99	0.43
17:Q:59:ILE:HG23	17:Q:71:PHE:HB3	2.00	0.43
23:X:88:ILE:HD11	23:X:109:PHE:CD2	2.52	0.43
24:Y:38:G:H1	25:Z:34:C:H42	1.66	0.43
1:A:29:G:C2	1:A:555:C:N3	2.87	0.43
1:A:1106:G:C2	1:A:1107:C:C4	3.07	0.43
1:A:1196:U:H5'	1:A:1197:G:H5'	2.00	0.43
15:O:54:ARG:HG3	15:O:55:GLY:N	2.32	0.43
25:Z:29:G:C2	25:Z:42:G:C2	3.06	0.43
25:Z:47:U:C2	25:Z:48:C:H5	2.37	0.43
1:A:39:G:C2	1:A:40:C:C2	3.06	0.43
1:A:110:C:H2'	1:A:111:G:O4'	2.18	0.43
1:A:122:G:N1	1:A:123:C:C2	2.86	0.43
1:A:505:G:H2'	1:A:506:G:C8	2.53	0.43
1:A:661:G:C2	1:A:745:C:N3	2.87	0.43
1:A:876:G:C2	1:A:877:C:C2	3.06	0.43
1:A:976:G:C5	1:A:1363(A):A:N6	2.86	0.43
1:A:1018:C:H2'	1:A:1019:C:C6	2.54	0.43
1:A:1050:G:N1	1:A:1051:C:C4	2.86	0.43
1:A:1207:G:C6	1:A:1208:C:C4	3.07	0.43
1:A:1412:C:H2'	1:A:1413:A:C8	2.53	0.43
6:F:89:MET:HE2	18:R:76:LEU:HD21	2.00	0.43
10:J:8:LEU:O	10:J:69:ASN:HA	2.17	0.43
16:P:21:VAL:CG1	16:P:34:GLU:HB3	2.48	0.43
17:Q:20:THR:HG23	17:Q:43:LEU:HD23	2.01	0.43
23:X:148:ALA:CB	23:X:165:LEU:HD22	2.47	0.43
25:Z:17:C:O2	25:Z:17:C:C2'	2.66	0.43
1:A:101:A:C4	1:A:102:G:C8	3.06	0.43
1:A:252:U:H2'	1:A:253:U:C6	2.53	0.43
1:A:289:G:C2	1:A:290:C:C2	3.07	0.43
1:A:711:G:H2'	1:A:712:A:C8	2.53	0.43
1:A:1103:C:H2'	1:A:1104:G:O4'	2.18	0.43
1:A:1325:C:H4'	21:V:17:THR:HG21	1.99	0.43
1:A:1347:G:N2	1:A:1373:G:H2'	2.33	0.43
1:A:1387:G:C2	1:A:1388:C:C2	3.06	0.43
16:P:28:ARG:HH11	16:P:29:ASP:CG	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:X:116:VAL:O	23:X:164:LEU:HA	2.19	0.43
1:A:128:G:N2	1:A:234:C:C2	2.87	0.43
1:A:310:G:C6	1:A:311:C:C4	3.06	0.43
1:A:374:A:C6	1:A:375:U:C4	3.06	0.43
1:A:412:A:N3	4:D:35:ARG:NE	2.65	0.43
1:A:447:G:H3'	1:A:485:G:H22	1.83	0.43
1:A:598:U:H2'	1:A:599:C:C6	2.54	0.43
1:A:724:G:H2'	1:A:725:G:H8	1.83	0.43
1:A:855:G:C2	1:A:856:C:C2	3.06	0.43
1:A:869:G:O2'	1:A:872:A:N7	2.51	0.43
1:A:929:G:C6	1:A:930:C:C4	3.07	0.43
1:A:1361:G:C2	1:A:1362:C:O2	2.72	0.43
1:A:1427:U:H2'	1:A:1428:A:C8	2.53	0.43
3:C:153:VAL:HA	3:C:197:GLY:O	2.19	0.43
6:F:55:ASP:HA	6:F:56:PRO:HD2	1.89	0.43
8:H:75:ARG:HA	8:H:76:PRO:HD2	1.77	0.43
12:L:116:SER:O	12:L:120:TYR:HD2	2.01	0.43
23:X:120:ILE:HD11	23:X:137:LEU:HG	2.00	0.43
1:A:193:C:H2'	1:A:194:C:C6	2.54	0.43
1:A:502:G:H2'	1:A:503:C:O4'	2.19	0.43
1:A:874:G:C2	1:A:875:C:C4	3.07	0.43
1:A:881:G:C2	1:A:882:C:C2	3.06	0.43
1:A:927:G:O2'	1:A:1503:A:N7	2.38	0.43
1:A:1368:G:N1	1:A:1369:C:C4	2.86	0.43
2:B:144:ARG:O	2:B:147:LYS:HB3	2.18	0.43
3:C:30:ARG:HH11	3:C:30:ARG:CB	2.32	0.43
10:J:38:ILE:HA	10:J:39:PRO:HD3	1.89	0.43
23:X:34:ALA:CB	23:X:45:LEU:HD22	2.47	0.43
1:A:864:A:C2	1:A:865:A:C2	3.07	0.43
1:A:885:G:C2	1:A:886:G:C5	3.06	0.43
1:A:1130:A:C6	1:A:1146:A:C5	3.06	0.43
1:A:1283:G:N1	1:A:1284:C:C4	2.86	0.43
1:A:1309:G:H2'	1:A:1310:G:O4'	2.19	0.43
1:A:1464:G:C2	1:A:1465:C:N3	2.87	0.43
4:D:60:GLU:OE1	4:D:198:VAL:HA	2.19	0.43
8:H:85:ARG:HH11	8:H:88:LYS:HA	1.83	0.43
10:J:4:ILE:HA	10:J:100:THR:HA	1.99	0.43
13:M:8:GLU:HG3	13:M:22:ILE:HA	2.01	0.43
13:M:66:LEU:HA	13:M:70:LEU:HD12	2.01	0.43
1:A:32:A:H2'	1:A:33:A:C8	2.53	0.43
1:A:126:G:H2'	1:A:127:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:662:G:N1	1:A:744:C:C2	2.86	0.43
1:A:903:G:C2	1:A:904:C:C2	3.07	0.43
1:A:1346:A:H2'	7:G:10:ARG:HH22	1.84	0.43
1:A:1407:C:H2'	1:A:1408:A:H8	1.84	0.43
1:A:1508:G:C6	1:A:1509:C:C4	3.07	0.43
3:C:29:TYR:C	3:C:29:TYR:HD1	2.25	0.43
19:S:58:VAL:HA	19:S:59:PRO:HD3	1.85	0.43
25:Z:64:G:C5	25:Z:65:C:C4	3.07	0.43
1:A:52:G:C6	1:A:53:A:C5	3.07	0.43
1:A:394:G:C2	1:A:395:C:C2	3.06	0.43
1:A:394:G:N2	1:A:395:C:C2	2.87	0.43
1:A:501:C:OP1	12:L:117:ARG:NH2	2.51	0.43
1:A:676:A:H2'	1:A:677:U:C6	2.54	0.43
1:A:748:C:H4'	1:A:749:C:O5'	2.19	0.43
1:A:828:A:H2'	1:A:829:G:O4'	2.18	0.43
1:A:971:G:H1'	1:A:1365:G:O2'	2.18	0.43
1:A:1030:C:H2'	1:A:1030(A):G:C8	2.53	0.43
1:A:1233:G:C2	1:A:1234:C:C2	3.07	0.43
4:D:35:ARG:O	4:D:37:PRO:HD3	2.18	0.43
11:K:31:THR:HG23	11:K:42:TRP:HB3	2.01	0.43
22:W:32:ILE:H	22:W:32:ILE:HD13	1.83	0.43
23:X:37:LEU:O	23:X:41:MET:HG2	2.19	0.43
23:X:125:ARG:C	23:X:127:VAL:N	2.77	0.43
1:A:798:G:H2'	1:A:799:G:O4'	2.19	0.43
1:A:917:G:C6	1:A:918:A:C6	3.07	0.43
1:A:1443:G:C2	1:A:1444:C:N3	2.86	0.43
25:Z:31:G:C2	25:Z:40:C:C2	3.07	0.43
25:Z:32:OMC:HM22	25:Z:33:U:H5'	2.01	0.43
1:A:70:G:C2	1:A:100:C:C2	3.07	0.42
1:A:327:A:N3	1:A:329:A:H1'	2.34	0.42
1:A:615:C:H2'	1:A:616:G:C8	2.54	0.42
1:A:999:C:C2'	1:A:1000:U:H5'	2.49	0.42
1:A:1117:G:N1	1:A:1184:G:C6	2.87	0.42
2:B:15:VAL:HG21	2:B:209:ARG:HG2	2.00	0.42
20:T:72:LEU:HD22	20:T:72:LEU:HA	1.83	0.42
22:W:32:ILE:HD13	22:W:32:ILE:O	2.18	0.42
1:A:287:U:H2'	1:A:288:A:C8	2.54	0.42
1:A:313:A:H2'	1:A:314:C:H6	1.76	0.42
1:A:548:G:H2'	1:A:549:C:C6	2.54	0.42
1:A:1270:C:H2'	1:A:1271:G:H8	1.84	0.42
1:A:1499:A:C4	1:A:1500:A:C8	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:92:ALA:HA	3:C:99:VAL:HG11	2.01	0.42
7:G:37:ASN:HD21	9:I:41:VAL:H	1.68	0.42
8:H:2:LEU:HD11	8:H:8:ASP:CG	2.43	0.42
18:R:53:ARG:HH21	18:R:60:ALA:HB2	1.84	0.42
23:X:129:HIS:N	23:X:130:PRO:HD2	2.34	0.42
1:A:161:A:H2'	1:A:162:A:C8	2.54	0.42
1:A:245:C:C2	1:A:284:G:C2	3.07	0.42
1:A:325:A:H2'	1:A:326:G:O4'	2.19	0.42
1:A:372:C:H4'	1:A:373:A:O5'	2.18	0.42
1:A:399:G:C2	1:A:400:C:C2	3.07	0.42
1:A:406:G:C4	1:A:407:G:C8	3.06	0.42
1:A:538:G:H2'	1:A:539:A:C8	2.55	0.42
1:A:741:G:H2'	1:A:742:G:O4'	2.19	0.42
1:A:784:C:N3	1:A:799:G:C2	2.87	0.42
1:A:790:A:C6	1:A:791:G:C6	3.07	0.42
1:A:900:A:H2'	1:A:901:A:C8	2.54	0.42
1:A:1266:G:N2	1:A:1270:C:N3	2.67	0.42
1:A:1410:G:C2	1:A:1491:G:C2	3.07	0.42
1:A:1537:U:H2'	1:A:1538:C:C6	2.53	0.42
1:A:1541:U:C4	1:A:1542:U:C5	3.07	0.42
3:C:29:TYR:CD1	3:C:29:TYR:O	2.71	0.42
3:C:113:ALA:N	3:C:114:PRO:CD	2.82	0.42
17:Q:15:MET:HB2	17:Q:18:THR:HB	2.00	0.42
19:S:13:ASP:HA	19:S:16:LEU:HB3	2.02	0.42
23:X:87:SER:HA	23:X:117:LYS:O	2.19	0.42
1:A:92:C:H2'	1:A:93:G:C8	2.54	0.42
1:A:306:G:C2	1:A:307:C:C2	3.06	0.42
1:A:402:G:C2	1:A:403:C:C2	3.07	0.42
1:A:406:G:H2'	1:A:407:G:O4'	2.19	0.42
1:A:413:G:O6	4:D:35:ARG:CZ	2.55	0.42
1:A:427:U:O2'	1:A:541:G:OP1	2.34	0.42
1:A:499:A:H4'	1:A:500:G:H5'	2.01	0.42
1:A:539:A:H2'	1:A:540:G:C8	2.54	0.42
1:A:677:U:H3	1:A:713:G:H22	1.67	0.42
1:A:689:C:H2'	1:A:690:G:O4'	2.20	0.42
1:A:717:C:H2'	1:A:734:G:H5'	2.02	0.42
1:A:900:A:H2'	1:A:901:A:H8	1.84	0.42
1:A:992:U:H4'	1:A:993:G:O5'	2.19	0.42
1:A:1115:C:C2	1:A:1186:G:N2	2.88	0.42
1:A:1198:G:C5	1:A:1199:U:C4	3.07	0.42
1:A:1464:G:N2	1:A:1465:C:N3	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1492:A:H8	22:W:19:ASN:HB3	1.84	0.42
1:A:1526:G:C2	1:A:1527:C:C2	3.07	0.42
1:A:26:A:O2'	4:D:209:ARG:NH2	2.53	0.42
1:A:184:G:H2'	1:A:185:A:H8	1.84	0.42
1:A:290:C:H2'	1:A:291:C:O4'	2.19	0.42
1:A:1241:G:N1	1:A:1242:C:C4	2.88	0.42
1:A:1419:G:C6	1:A:1420:C:C4	3.07	0.42
1:A:1464:G:C6	1:A:1465:C:N4	2.88	0.42
4:D:101:LEU:HB2	4:D:138:TYR:HB3	2.01	0.42
19:S:70:LYS:N	19:S:70:LYS:CD	2.80	0.42
23:X:24:LYS:HA	25:Z:56:C:N4	2.34	0.42
1:A:328:C:H4'	1:A:329:A:C5'	2.50	0.42
1:A:579:G:H5'	1:A:728:A:H1'	2.01	0.42
1:A:622:A:H3'	1:A:623:C:C6	2.54	0.42
1:A:722:A:H2'	1:A:724:G:C8	2.55	0.42
1:A:763:G:C6	1:A:764:C:N4	2.88	0.42
1:A:1201:A:H4'	1:A:1202:G:O5'	2.19	0.42
1:A:1270:C:H2'	1:A:1271:G:C8	2.54	0.42
1:A:1387:G:C6	1:A:1388:C:C4	3.07	0.42
3:C:97:LYS:HE2	3:C:97:LYS:N	2.35	0.42
5:E:14:ARG:HG2	5:E:29:GLY:HA3	2.02	0.42
18:R:58:LEU:HD23	18:R:62:GLU:HB3	2.02	0.42
22:W:53:VAL:CG1	22:W:71:LYS:HA	2.50	0.42
1:A:132:C:C5'	20:T:75:ASN:HD22	2.32	0.42
1:A:243:A:H4'	1:A:244:U:O5'	2.20	0.42
1:A:394:G:C6	1:A:395:C:C4	3.07	0.42
2:B:70:PHE:H	2:B:92:TYR:HA	1.84	0.42
4:D:173:TRP:CD2	4:D:189:PRO:HB3	2.54	0.42
8:H:36:LEU:HD13	8:H:59:LEU:HD22	2.01	0.42
1:A:51:A:C6	1:A:353:A:C2	3.08	0.42
1:A:232:G:H2'	1:A:233:C:C6	2.55	0.42
1:A:270:A:H2'	1:A:271:C:H6	1.83	0.42
1:A:444:C:H2'	1:A:445:G:H8	1.84	0.42
1:A:823:G:C6	1:A:824:C:N4	2.87	0.42
1:A:985:C:C2	1:A:1221:G:C2	3.08	0.42
1:A:1068:G:N1	1:A:1069:C:C4	2.87	0.42
1:A:1258:G:C2	1:A:1259:C:N3	2.88	0.42
3:C:45:LYS:HA	3:C:45:LYS:HD3	1.80	0.42
4:D:190:ASP:H	4:D:193:ASP:HB2	1.84	0.42
9:I:11:LYS:H	9:I:104:ARG:HH12	1.67	0.42
23:X:47:LEU:HD11	23:X:55:PRO:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:G:C2	1:A:175:C:C2	3.08	0.42
1:A:157:G:C6	1:A:165:C:N3	2.88	0.42
1:A:578:C:H42	1:A:763:G:H1	1.68	0.42
1:A:763:G:C6	1:A:764:C:C4	3.08	0.42
1:A:892:A:C6	1:A:893:C:C4	3.07	0.42
1:A:960:U:H4'	1:A:961:U:H5''	2.01	0.42
1:A:987:G:C2	1:A:988:G:C5	3.08	0.42
4:D:63:LYS:O	4:D:67:ILE:HG13	2.20	0.42
5:E:152:ARG:HB3	8:H:43:GLY:O	2.19	0.42
15:O:49:ASP:OD2	15:O:52:SER:HB2	2.20	0.42
1:A:201:C:H42	1:A:216:G:H1	1.67	0.42
1:A:377:G:H2'	1:A:378:G:H8	1.83	0.42
1:A:402:G:C6	1:A:403:C:C4	3.08	0.42
1:A:545:C:H5'	4:D:72:GLU:HB2	2.02	0.42
1:A:680:C:C2	1:A:711:G:N2	2.88	0.42
1:A:865:A:H2'	1:A:866:C:C6	2.55	0.42
1:A:971:G:N1	1:A:1363(A):A:OP2	2.52	0.42
1:A:1253:G:C6	1:A:1254:C:C4	3.08	0.42
1:A:1520:G:H2'	1:A:1521:G:C8	2.55	0.42
2:B:186:ALA:HB2	2:B:197:VAL:HG11	2.02	0.42
3:C:3:ASN:HB2	3:C:4:LYS:H	1.76	0.42
4:D:19:LEU:HD22	4:D:67:ILE:HG12	2.01	0.42
9:I:7:THR:HB	9:I:83:ARG:HH11	1.82	0.42
11:K:18:ARG:HA	11:K:81:ASP:H	1.85	0.42
22:W:32:ILE:HB	22:W:63:THR:O	2.19	0.42
1:A:490:G:H2'	1:A:491:G:C8	2.55	0.41
1:A:577:G:C6	1:A:578:C:C4	3.08	0.41
1:A:620:C:C4	4:D:135:LEU:HD22	2.54	0.41
1:A:678:U:H2'	1:A:679:C:C6	2.54	0.41
1:A:702:A:H8	1:A:702:A:OP1	2.03	0.41
1:A:954:G:H21	1:A:1227:A:H62	1.68	0.41
1:A:1060:C:C2	1:A:1198:G:C2	3.08	0.41
1:A:1285:A:H4'	1:A:1286:A:O5'	2.19	0.41
1:A:1405:G:N2	1:A:1517:G:H22	2.18	0.41
1:A:400:C:H2'	1:A:401:C:O4'	2.20	0.41
1:A:582:U:C2	1:A:760:G:C6	3.08	0.41
1:A:763:G:N2	1:A:764:C:C2	2.88	0.41
1:A:881:G:C6	1:A:882:C:C4	3.08	0.41
1:A:920:U:H2'	1:A:921:U:H6	1.83	0.41
1:A:1029:C:H2'	1:A:1030:C:C6	2.55	0.41
1:A:1347:G:HO2'	1:A:1348:U:P	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:13:ARG:HD2	4:D:38:TYR:O	2.20	0.41
9:I:96:LEU:HG	9:I:101:PHE:HB2	2.02	0.41
13:M:113:PRO:HB2	13:M:114:ARG:H	1.68	0.41
1:A:19:C:O2	1:A:917:G:C2	2.73	0.41
1:A:22:G:OP1	1:A:885:G:H5'	2.20	0.41
1:A:128:G:C6	1:A:129:U:C4	3.08	0.41
1:A:416:G:C2	1:A:417:C:C2	3.09	0.41
1:A:435:C:H2'	1:A:436:C:C6	2.56	0.41
1:A:477:A:H2'	1:A:479:C:C6	2.55	0.41
1:A:688:G:C2	1:A:689:C:C2	3.08	0.41
2:B:195:ASP:O	8:H:74:PRO:HG2	2.20	0.41
13:M:19:LEU:O	13:M:22:ILE:HG13	2.19	0.41
22:W:23:ARG:HG2	22:W:31:GLU:OE2	2.20	0.41
23:X:137:LEU:HB3	23:X:163:MET:SD	2.60	0.41
25:Z:16:C:C3'	25:Z:17:C:C5'	2.92	0.41
1:A:189:G:C6	1:A:189(L):G:C6	3.09	0.41
1:A:289:G:N1	1:A:290:C:C4	2.88	0.41
1:A:363:A:C6	12:L:31:PRO:HD2	2.56	0.41
1:A:397:A:H5'	1:A:398:C:OP1	2.20	0.41
1:A:443:C:C2	1:A:492:G:C2	3.09	0.41
1:A:538:G:H2'	1:A:539:A:H8	1.84	0.41
1:A:689:C:H3'	1:A:690:G:H8	1.85	0.41
1:A:748:C:H1'	1:A:749:C:C5	2.50	0.41
1:A:768:A:C5	1:A:769:G:C8	3.08	0.41
1:A:823:G:C2	1:A:824:C:C2	3.09	0.41
1:A:1171:G:C2	1:A:1172:C:C2	3.07	0.41
1:A:1358:U:N3	1:A:1363(A):A:C6	2.81	0.41
2:B:83:MET:HG3	2:B:238:LEU:HD22	2.02	0.41
2:B:87:ARG:HE	2:B:219:VAL:HG11	1.85	0.41
2:B:216:SER:HB2	2:B:233:SER:HB2	2.02	0.41
3:C:91:LEU:HD21	3:C:99:VAL:HG22	2.00	0.41
12:L:28:LYS:HB2	12:L:33:ARG:NH2	2.35	0.41
12:L:46:LYS:HB3	12:L:47:LYS:H	1.59	0.41
18:R:63:GLN:HE21	18:R:66:LEU:HD23	1.86	0.41
1:A:76:C:C2'	1:A:77:G:H5'	2.50	0.41
1:A:324:G:N2	1:A:326:G:H3'	2.35	0.41
1:A:333:G:C2	1:A:334:C:C2	3.08	0.41
1:A:877:C:H2'	1:A:878:G:C8	2.55	0.41
1:A:931:C:N3	1:A:1387:G:C6	2.89	0.41
1:A:939:G:H1'	1:A:1375:A:C2	2.56	0.41
1:A:1216:G:N1	1:A:1217:C:C4	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1222:G:N2	1:A:1223:C:C2	2.88	0.41
10:J:32:ALA:CB	10:J:74:ILE:HG23	2.51	0.41
13:M:88:ARG:HD2	19:S:3:ARG:HH21	1.85	0.41
15:O:82:ILE:HD13	15:O:88:ARG:HH22	1.85	0.41
23:X:90:PHE:HB2	23:X:120:ILE:HG12	2.03	0.41
25:Z:31:G:N2	25:Z:40:C:C2	2.88	0.41
1:A:76:C:H2'	1:A:77:G:H5'	2.02	0.41
1:A:77:G:C8	1:A:77:G:C3'	3.03	0.41
1:A:447:G:H2'	1:A:485:G:N2	2.35	0.41
1:A:548:G:N2	1:A:549:C:C2	2.88	0.41
1:A:590:C:N4	1:A:649:G:H1	2.19	0.41
1:A:966:G:C2	25:Z:34:C:H5'	2.56	0.41
1:A:1476:G:C2	1:A:1477:C:C2	3.09	0.41
2:B:42:ILE:HD11	2:B:190:THR:HB	2.01	0.41
3:C:115:LEU:HA	3:C:118:GLN:HE21	1.86	0.41
4:D:165:MET:HA	4:D:168:ARG:HG2	2.03	0.41
5:E:11:ILE:HB	5:E:31:LEU:HD12	2.02	0.41
5:E:79:GLU:CD	5:E:79:GLU:H	2.27	0.41
5:E:132:ALA:O	5:E:136:MET:HG2	2.20	0.41
10:J:61:GLU:OE2	14:N:58:LYS:HG2	2.19	0.41
25:Z:42:G:H3'	25:Z:43:A:H8	1.85	0.41
1:A:241:C:C2	1:A:286:G:C2	3.09	0.41
1:A:642:A:C5	1:A:643:C:C5	3.08	0.41
1:A:664:G:N2	1:A:741:G:H1	2.15	0.41
1:A:774:G:C2	1:A:806:C:C2	3.08	0.41
1:A:939:G:C2	1:A:940:C:N3	2.89	0.41
1:A:972:C:P	10:J:57:LYS:HD2	2.61	0.41
1:A:1295:G:C6	1:A:1296:C:C4	3.08	0.41
1:A:1310:G:C2	1:A:1328:C:N3	2.88	0.41
3:C:96:GLY:C	3:C:97:LYS:HE2	2.45	0.41
3:C:178:LEU:C	3:C:180:ALA:H	2.29	0.41
16:P:25:ARG:H	16:P:25:ARG:HG3	1.68	0.41
18:R:31:LEU:HD22	18:R:66:LEU:HB2	2.03	0.41
22:W:56:GLU:HB2	22:W:68:VAL:HG22	2.03	0.41
23:X:54:PRO:HA	23:X:55:PRO:HD3	1.91	0.41
1:A:384:G:C6	1:A:385:C:C4	3.09	0.41
1:A:392:G:H2'	1:A:393:A:H8	1.83	0.41
1:A:500:G:C6	1:A:501:C:N4	2.89	0.41
1:A:588:G:C2	1:A:589:C:C4	3.09	0.41
1:A:648:A:H2'	1:A:649:G:H8	1.86	0.41
1:A:926:G:C6	1:A:1505:G:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:929:G:C2	1:A:930:C:C2	3.09	0.41
1:A:932:C:C2	1:A:1386:G:C2	3.09	0.41
1:A:1132:C:H2'	1:A:1133:G:H8	1.84	0.41
1:A:1280:A:H3'	1:A:1281:U:H5''	2.03	0.41
1:A:1407:C:H2'	1:A:1408:A:C8	2.56	0.41
1:A:1440:C:H3'	1:A:1441:G:H8	1.86	0.41
1:A:1536:C:N3	24:Y:30:G:C2	2.89	0.41
2:B:224:GLN:HG3	2:B:229:VAL:HG22	2.02	0.41
5:E:126:ARG:HA	5:E:126:ARG:HD3	1.89	0.41
6:F:8:ILE:HG23	6:F:85:VAL:HG13	2.03	0.41
11:K:40:ILE:H	11:K:40:ILE:HG13	1.63	0.41
19:S:78:ARG:HE	19:S:78:ARG:HB3	1.70	0.41
23:X:17:ARG:HG3	23:X:28:ILE:HG13	2.03	0.41
25:Z:47:U:H4'	25:Z:48:C:H5'	2.03	0.41
1:A:21:G:C2	1:A:22:G:C6	3.09	0.41
1:A:70:G:C2	1:A:100:C:O2	2.74	0.41
1:A:102:G:C2	1:A:103:C:C2	3.09	0.41
1:A:217:C:H2'	1:A:218:C:C6	2.56	0.41
1:A:267:C:H2'	1:A:268:C:C6	2.56	0.41
1:A:295:C:C4	1:A:296:U:C4	3.08	0.41
1:A:333:G:N1	1:A:334:C:C4	2.89	0.41
1:A:542:G:N2	1:A:543:C:C2	2.89	0.41
1:A:542:G:C2	1:A:543:C:C2	3.09	0.41
1:A:550:G:H2'	1:A:551:U:C6	2.56	0.41
1:A:588:G:C6	1:A:589:C:N4	2.89	0.41
1:A:671:G:C6	1:A:736:C:N4	2.89	0.41
1:A:867:G:C2	1:A:868:C:C2	3.09	0.41
1:A:903:G:C6	1:A:904:C:C4	3.09	0.41
1:A:1005:A:OP1	1:A:1006:C:OP2	2.37	0.41
1:A:1048:G:C2	1:A:1210:C:N3	2.89	0.41
1:A:1363(A):A:H1'	1:A:1365:G:C5	2.56	0.41
1:A:1443:G:N2	1:A:1444:C:C2	2.89	0.41
1:A:1521:G:H2'	1:A:1522:U:C6	2.56	0.41
3:C:58:GLU:H	3:C:65:ALA:HB3	1.85	0.41
3:C:193:TYR:CE1	3:C:196:LEU:HD11	2.56	0.41
6:F:35:ALA:HA	6:F:67:MET:HB3	2.02	0.41
9:I:89:ASN:HB3	9:I:92:TYR:CE2	2.55	0.41
10:J:64:GLU:HB3	14:N:59:ALA:HB2	2.03	0.41
22:W:52:ARG:HB2	22:W:52:ARG:HH11	1.85	0.41
1:A:251:G:N1	1:A:266:G:C6	2.89	0.41
1:A:319:G:C2	1:A:320:C:C2	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:G:N7	4:D:35:ARG:CZ	2.82	0.41
1:A:533:A:O2'	1:A:535:A:OP2	2.39	0.41
1:A:671:G:N1	1:A:736:C:C4	2.89	0.41
1:A:691:G:O6	11:K:52:GLY:HA2	2.21	0.41
1:A:895:G:C6	1:A:896:C:C4	3.09	0.41
1:A:926:G:H2'	1:A:1505:G:N3	2.36	0.41
1:A:1116:C:H3'	1:A:1117:G:H5''	2.03	0.41
1:A:1225:A:H4'	19:S:78:ARG:HD3	2.03	0.41
5:E:79:GLU:HG3	5:E:93:PRO:HD2	2.03	0.41
10:J:34:VAL:HG13	10:J:74:ILE:HG13	2.02	0.41
11:K:38:ASN:HA	11:K:39:PRO:HD3	1.80	0.41
14:N:16:PHE:HB2	14:N:18:VAL:HG23	2.03	0.41
19:S:33:THR:HG23	19:S:51:VAL:HG13	2.02	0.41
23:X:17:ARG:HA	23:X:28:ILE:HA	2.03	0.41
1:A:137:C:C2	1:A:227:G:C2	3.09	0.40
1:A:189(B):C:C2	1:A:189(J):G:N2	2.89	0.40
1:A:198:G:H2'	1:A:199:G:C8	2.56	0.40
1:A:399:G:H2'	1:A:400:C:C6	2.55	0.40
1:A:593:G:N1	1:A:647:C:C2	2.90	0.40
1:A:791:G:N2	1:A:1497:G:H4'	2.36	0.40
1:A:1003:G:C2	1:A:1004:A:H1'	2.56	0.40
2:B:10:LEU:HD12	2:B:48:MET:HG3	2.03	0.40
5:E:105:VAL:HB	5:E:106:PRO:HD3	2.02	0.40
10:J:54:PHE:H	14:N:41:ARG:NH2	2.18	0.40
11:K:126:ARG:C	11:K:128:ALA:H	2.28	0.40
12:L:5:PRO:HB2	12:L:6:THR:H	1.65	0.40
12:L:36:VAL:HG22	12:L:82:VAL:HG22	2.03	0.40
13:M:79:LYS:HA	13:M:79:LYS:HD3	1.92	0.40
15:O:42:HIS:CD2	15:O:42:HIS:C	2.99	0.40
15:O:87:ILE:HG22	15:O:88:ARG:H	1.85	0.40
23:X:107:LYS:HG3	23:X:144:LEU:HD23	2.02	0.40
23:X:107:LYS:HE3	23:X:144:LEU:HD23	2.03	0.40
24:Y:21:G:H2'	24:Y:22:G:H8	1.85	0.40
1:A:103:C:OP2	20:T:14:LYS:HG3	2.21	0.40
1:A:130:A:OP1	1:A:130:A:C8	2.75	0.40
1:A:289:G:C6	1:A:290:C:C4	3.10	0.40
1:A:320:C:HO2'	1:A:1435:G:HO2'	1.66	0.40
1:A:385:C:N4	1:A:386:C:N4	2.69	0.40
1:A:521:G:C2	1:A:522:C:C4	3.08	0.40
1:A:533:A:C5	1:A:536:C:C4	3.09	0.40
1:A:835:U:OP1	18:R:61:LYS:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:886:G:N1	1:A:912:C:C2	2.88	0.40
1:A:992:U:O2	1:A:992:U:C2'	2.69	0.40
1:A:1068:G:C2	1:A:1069:C:C2	3.10	0.40
1:A:1086:U:H3	1:A:1099:G:N2	2.19	0.40
1:A:1434:A:H2'	1:A:1435:G:O4'	2.21	0.40
4:D:98:GLU:CD	4:D:103:ASN:ND2	2.80	0.40
5:E:76:ILE:HG13	5:E:77:PRO:HD2	2.03	0.40
7:G:150:ALA:C	7:G:152:ALA:N	2.78	0.40
10:J:74:ILE:HG21	10:J:81:THR:HG21	2.02	0.40
20:T:97:ALA:HA	20:T:98:PRO:HD2	1.93	0.40
25:Z:31:G:H2'	25:Z:32:OMC:O4'	2.21	0.40
25:Z:53:G:N2	25:Z:62:C:C2	2.90	0.40
1:A:79:G:H2'	1:A:80:G:H8	1.86	0.40
1:A:237:C:H5''	17:Q:25:ARG:CZ	2.51	0.40
1:A:335:C:H2'	1:A:336:C:H6	1.86	0.40
1:A:617:G:N1	1:A:618:C:C4	2.89	0.40
1:A:1237:C:H5''	1:A:1238:A:O4'	2.21	0.40
1:A:1411:C:O2'	12:L:94:PRO:HG2	2.20	0.40
1:A:1438:G:C2	1:A:1439:C:C2	3.09	0.40
4:D:163:GLU:HA	4:D:166:LYS:HB2	2.04	0.40
22:W:13:VAL:O	23:X:125:ARG:NH1	2.54	0.40
23:X:6:LEU:HB3	23:X:10:ARG:HB3	2.03	0.40
1:A:79:G:N1	1:A:91:C:C2	2.89	0.40
1:A:225:C:H2'	1:A:226:G:H8	1.87	0.40
1:A:881:G:P	12:L:12:ARG:HH22	2.44	0.40
1:A:1433:A:H2'	1:A:1434:A:O4'	2.21	0.40
6:F:30:LEU:HB3	6:F:35:ALA:HB3	2.02	0.40
6:F:87:ARG:NE	18:R:75:ILE:O	2.54	0.40
12:L:37:CYS:HA	12:L:58:VAL:HA	2.03	0.40
18:R:22:VAL:HG23	18:R:55:ARG:O	2.21	0.40
1:A:277:C:P	17:Q:68:ARG:HH22	2.45	0.40
1:A:505:G:C6	1:A:535:A:C2	3.09	0.40
1:A:658:G:H2'	1:A:659:U:C6	2.56	0.40
1:A:744:C:H2'	1:A:745:C:C6	2.57	0.40
1:A:820:U:H4'	1:A:821:G:OP2	2.21	0.40
1:A:924:C:H2'	1:A:925:G:C8	2.57	0.40
1:A:1048:G:P	14:N:4:LYS:HD2	2.62	0.40
1:A:1233:G:C2	1:A:1234:C:C4	3.09	0.40
1:A:1255:G:O2'	1:A:1258:G:N3	2.54	0.40
1:A:1489:G:C6	1:A:1490:C:C4	3.09	0.40
9:I:3:GLN:HG3	9:I:20:ARG:HE	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:29:ILE:HG13	11:K:44:SER:HB2	2.03	0.40
18:R:26:LEU:HD13	18:R:42:ARG:HH21	1.87	0.40
22:W:13:VAL:O	22:W:50:GLY:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	232/256 (91%)	187 (81%)	33 (14%)	12 (5%)	1	16
3	C	204/239 (85%)	172 (84%)	20 (10%)	12 (6%)	1	14
4	D	206/209 (99%)	177 (86%)	22 (11%)	7 (3%)	3	21
5	E	148/162 (91%)	126 (85%)	20 (14%)	2 (1%)	9	38
6	F	99/101 (98%)	89 (90%)	7 (7%)	3 (3%)	3	23
7	G	153/156 (98%)	134 (88%)	17 (11%)	2 (1%)	9	41
8	H	136/138 (99%)	118 (87%)	12 (9%)	6 (4%)	2	18
9	I	125/128 (98%)	103 (82%)	21 (17%)	1 (1%)	16	52
10	J	96/105 (91%)	74 (77%)	17 (18%)	5 (5%)	1	16
11	K	117/129 (91%)	99 (85%)	13 (11%)	5 (4%)	2	18
12	L	122/132 (92%)	99 (81%)	19 (16%)	4 (3%)	3	21
13	M	117/126 (93%)	102 (87%)	13 (11%)	2 (2%)	7	35
14	N	58/61 (95%)	42 (72%)	14 (24%)	2 (3%)	3	21
15	O	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
16	P	81/88 (92%)	73 (90%)	7 (9%)	1 (1%)	10	42
17	Q	97/105 (92%)	83 (86%)	12 (12%)	2 (2%)	5	30
18	R	71/88 (81%)	61 (86%)	8 (11%)	2 (3%)	4	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	S	80/93 (86%)	61 (76%)	17 (21%)	2 (2%)	4	27
20	T	97/106 (92%)	87 (90%)	3 (3%)	7 (7%)	1	11
21	V	22/27 (82%)	21 (96%)	1 (4%)	0	100	100
22	W	69/72 (96%)	56 (81%)	11 (16%)	2 (3%)	3	24
23	X	160/171 (94%)	140 (88%)	14 (9%)	6 (4%)	2	20
All	All	2576/2781 (93%)	2184 (85%)	307 (12%)	85 (3%)	5	21

All (85) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	24	TRP
2	B	132	LYS
3	C	12	LEU
3	C	175	LEU
4	D	36	ARG
7	G	55	GLY
8	H	91	ARG
10	J	34	VAL
10	J	50	ILE
11	K	13	GLN
11	K	50	TYR
13	M	113	PRO
23	X	54	PRO
2	B	17	PHE
2	B	21	ARG
2	B	207	ALA
3	C	3	ASN
3	C	11	ARG
3	C	14	ILE
7	G	7	ALA
8	H	2	LEU
9	I	56	LEU
10	J	55	LYS
10	J	86	MET
12	L	45	PRO
12	L	46	LYS
20	T	68	LYS
23	X	77	ARG
23	X	126	GLU
2	B	11	LEU

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Mol	Chain	Res	Type
3	C	81	GLY
4	D	9	CYS
5	E	24	ARG
5	E	153	LYS
6	F	15	ASP
8	H	5	PRO
17	Q	67	LYS
17	Q	68	ARG
18	R	17	SER
20	T	9	ASN
20	T	49	ALA
20	T	95	ALA
20	T	97	ALA
20	T	98	PRO
22	W	2	LYS
22	W	70	ARG
2	B	130	ARG
2	B	133	LYS
2	B	204	ASN
2	B	229	VAL
3	C	4	LYS
3	C	61	ALA
4	D	32	ALA
6	F	70	ASP
18	R	48	GLY
23	X	8	ASN
23	X	125	ARG
2	B	8	LYS
3	C	108	ASN
4	D	5	ILE
6	F	16	GLN
8	H	55	GLY
12	L	25	PRO
13	M	100	GLY
14	N	15	LYS
16	P	10	GLY
23	X	14	LYS
3	C	168	ALA
4	D	26	CYS
11	K	15	ALA
11	K	102	GLY
19	S	6	LYS

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Mol	Chain	Res	Type
20	T	96	GLY
3	C	51	GLY
8	H	76	PRO
10	J	37	PRO
11	K	48	ILE
12	L	71	PRO
3	C	155	GLY
4	D	197	PRO
14	N	14	PRO
19	S	42	PRO
2	B	233	SER
4	D	130	GLY
8	H	73	ASP

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	
2	B	202/220 (92%)	147 (73%)	55 (27%)	0	3
3	C	160/188 (85%)	120 (75%)	40 (25%)	0	4
4	D	180/181 (99%)	145 (81%)	35 (19%)	1	9
5	E	115/123 (94%)	84 (73%)	31 (27%)	0	3
6	F	90/90 (100%)	65 (72%)	25 (28%)	0	3
7	G	126/127 (99%)	109 (86%)	17 (14%)	4	16
8	H	119/119 (100%)	86 (72%)	33 (28%)	0	3
9	I	98/99 (99%)	82 (84%)	16 (16%)	2	13
10	J	87/92 (95%)	68 (78%)	19 (22%)	1	6
11	K	90/99 (91%)	69 (77%)	21 (23%)	1	5
12	L	104/109 (95%)	86 (83%)	18 (17%)	2	11
13	M	95/101 (94%)	80 (84%)	15 (16%)	2	13
14	N	49/50 (98%)	37 (76%)	12 (24%)	1	5
15	O	79/80 (99%)	52 (66%)	27 (34%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	P	72/74 (97%)	55 (76%)	17 (24%)	1	5
17	Q	94/97 (97%)	81 (86%)	13 (14%)	3	16
18	R	64/77 (83%)	48 (75%)	16 (25%)	0	4
19	S	71/80 (89%)	51 (72%)	20 (28%)	0	3
20	T	76/82 (93%)	63 (83%)	13 (17%)	2	12
21	V	19/22 (86%)	16 (84%)	3 (16%)	2	13
22	W	62/63 (98%)	47 (76%)	15 (24%)	1	5
23	X	145/150 (97%)	115 (79%)	30 (21%)	1	7
All	All	2197/2323 (95%)	1706 (78%)	491 (22%)	2	6

All (491) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	8	LYS
2	B	11	LEU
2	B	12	GLU
2	B	15	VAL
2	B	16	HIS
2	B	21	ARG
2	B	23	ARG
2	B	30	ARG
2	B	44	LEU
2	B	50	GLU
2	B	51	LEU
2	B	53	ARG
2	B	60	ASP
2	B	61	LEU
2	B	63	MET
2	B	64	ARG
2	B	67	THR
2	B	76	GLN
2	B	81	VAL
2	B	97	TRP
2	B	101	MET
2	B	103	THR
2	B	106	LYS
2	B	107	THR
2	B	108	ILE
2	B	110	GLN

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Mol	Chain	Res	Type
2	B	114	ARG
2	B	118	LEU
2	B	121	LEU
2	B	127	ILE
2	B	129	GLU
2	B	130	ARG
2	B	136	VAL
2	B	139	LYS
2	B	144	ARG
2	B	156	LYS
2	B	168	THR
2	B	172	ILE
2	B	174	VAL
2	B	178	ARG
2	B	179	LYS
2	B	180	LEU
2	B	184	VAL
2	B	187	LEU
2	B	189	ASP
2	B	190	THR
2	B	195	ASP
2	B	200	ILE
2	B	204	ASN
2	B	211	ILE
2	B	214	ILE
2	B	215	LEU
2	B	224	GLN
2	B	230	VAL
2	B	236	TYR
3	C	3	ASN
3	C	5	ILE
3	C	11	ARG
3	C	14	ILE
3	C	17	ASP
3	C	21	ARG
3	C	27	LYS
3	C	30	ARG
3	C	34	LEU
3	C	42	LEU
3	C	43	LEU
3	C	55	VAL
3	C	70	VAL

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Mol	Chain	Res	Type
3	C	77	ILE
3	C	79	ARG
3	C	82	GLU
3	C	90	GLU
3	C	91	LEU
3	C	94	LEU
3	C	97	LYS
3	C	99	VAL
3	C	105	GLU
3	C	108	ASN
3	C	119	ARG
3	C	132	ARG
3	C	136	GLN
3	C	143	GLU
3	C	157	ILE
3	C	162	GLN
3	C	167	TRP
3	C	170	GLN
3	C	173	VAL
3	C	176	HIS
3	C	177	THR
3	C	178	LEU
3	C	179	ARG
3	C	188	LEU
3	C	190	ARG
3	C	191	THR
3	C	202	ILE
4	D	12	CYS
4	D	13	ARG
4	D	26	CYS
4	D	34	GLU
4	D	36	ARG
4	D	52	SER
4	D	53	ASP
4	D	61	LYS
4	D	64	LEU
4	D	70	ILE
4	D	78	LEU
4	D	81	GLU
4	D	97	LEU
4	D	104	VAL
4	D	112	VAL

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Mol	Chain	Res	Type
4	D	118	ARG
4	D	120	LEU
4	D	122	ARG
4	D	131	ARG
4	D	132	ARG
4	D	135	LEU
4	D	139	ARG
4	D	141	ARG
4	D	150	GLU
4	D	153	ARG
4	D	155	LEU
4	D	156	GLU
4	D	165	MET
4	D	174	LEU
4	D	181	MET
4	D	184	LYS
4	D	187	ARG
4	D	192	GLU
4	D	193	ASP
4	D	209	ARG
5	E	8	GLU
5	E	12	LEU
5	E	14	ARG
5	E	15	ARG
5	E	25	ARG
5	E	27	ARG
5	E	31	LEU
5	E	32	VAL
5	E	34	VAL
5	E	41	VAL
5	E	56	GLN
5	E	60	TYR
5	E	67	VAL
5	E	68	GLU
5	E	69	VAL
5	E	71	LEU
5	E	73	ASN
5	E	76	ILE
5	E	79	GLU
5	E	80	ILE
5	E	82	VAL
5	E	91	LEU

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Mol	Chain	Res	Type
5	E	107	ARG
5	E	118	ILE
5	E	123	LEU
5	E	129	ILE
5	E	142	LEU
5	E	144	THR
5	E	148	VAL
5	E	150	ARG
5	E	152	ARG
6	F	3	ARG
6	F	15	ASP
6	F	16	GLN
6	F	18	GLN
6	F	21	LEU
6	F	24	GLU
6	F	27	GLN
6	F	28	ARG
6	F	31	GLU
6	F	32	ASN
6	F	38	GLU
6	F	40	VAL
6	F	41	GLU
6	F	42	GLU
6	F	45	LEU
6	F	46	ARG
6	F	47	ARG
6	F	54	LYS
6	F	55	ASP
6	F	61	LEU
6	F	69	GLU
6	F	75	LEU
6	F	82	ARG
6	F	86	ARG
6	F	95	GLU
7	G	5	ARG
7	G	8	GLU
7	G	16	LEU
7	G	21	VAL
7	G	22	LEU
7	G	29	LYS
7	G	37	ASN
7	G	38	LEU

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Mol	Chain	Res	Type
7	G	57	GLU
7	G	59	LEU
7	G	60	LYS
7	G	72	ARG
7	G	91	VAL
7	G	94	ARG
7	G	106	GLN
7	G	136	LYS
7	G	149	ARG
8	H	1	MET
8	H	18	ARG
8	H	21	LYS
8	H	22	GLU
8	H	23	SER
8	H	25	ASP
8	H	26	VAL
8	H	29	SER
8	H	36	LEU
8	H	38	ILE
8	H	39	LEU
8	H	45	ILE
8	H	49	GLU
8	H	50	ARG
8	H	53	VAL
8	H	54	ASP
8	H	56	LYS
8	H	58	TYR
8	H	60	ARG
8	H	63	LEU
8	H	69	ARG
8	H	70	GLN
8	H	77	GLU
8	H	82	HIS
8	H	84	ARG
8	H	93	VAL
8	H	99	GLU
8	H	100	ILE
8	H	107	LEU
8	H	109	ILE
8	H	122	ARG
8	H	134	ILE
8	H	135	CYS

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Mol	Chain	Res	Type
9	I	38	GLN
9	I	40	LEU
9	I	48	GLU
9	I	56	LEU
9	I	60	ASP
9	I	78	LYS
9	I	85	LEU
9	I	95	LYS
9	I	96	LEU
9	I	111	ARG
9	I	112	LYS
9	I	118	LYS
9	I	124	GLN
9	I	125	TYR
9	I	127	LYS
9	I	128	ARG
10	J	4	ILE
10	J	16	LEU
10	J	17	ASP
10	J	22	LYS
10	J	34	VAL
10	J	40	LEU
10	J	49	VAL
10	J	57	LYS
10	J	60	ARG
10	J	61	GLU
10	J	71	LEU
10	J	74	ILE
10	J	75	ILE
10	J	76	ASN
10	J	82	ILE
10	J	94	VAL
10	J	96	ILE
10	J	98	ILE
10	J	99	LYS
11	K	11	LYS
11	K	12	ARG
11	K	13	GLN
11	K	25	TYR
11	K	34	ASP
11	K	40	ILE
11	K	44	SER

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Mol	Chain	Res	Type
11	K	48	ILE
11	K	54	ARG
11	K	57	THR
11	K	77	MET
11	K	82	VAL
11	K	84	VAL
11	K	85	ARG
11	K	93	GLN
11	K	98	LEU
11	K	103	LEU
11	K	109	VAL
11	K	117	ASN
11	K	123	LYS
11	K	126	ARG
12	L	6	THR
12	L	7	ILE
12	L	15	ARG
12	L	17	LYS
12	L	18	VAL
12	L	21	LYS
12	L	41	ARG
12	L	46	LYS
12	L	47	LYS
12	L	55	VAL
12	L	62	SER
12	L	65	GLU
12	L	70	ILE
12	L	79	GLU
12	L	83	VAL
12	L	89	ARG
12	L	97	ARG
12	L	115	LYS
13	M	9	ILE
13	M	12	ASN
13	M	15	VAL
13	M	17	VAL
13	M	27	LYS
13	M	39	ILE
13	M	56	LEU
13	M	66	LEU
13	M	73	GLU
13	M	90	LEU

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Mol	Chain	Res	Type
13	M	102	ARG
13	M	110	ARG
13	M	115	LYS
13	M	116	THR
13	M	120	LYS
14	N	8	GLU
14	N	11	LYS
14	N	12	ARG
14	N	13	THR
14	N	18	VAL
14	N	25	VAL
14	N	31	ARG
14	N	40	CYS
14	N	44	LEU
14	N	53	LEU
14	N	58	LYS
14	N	60	SER
15	O	5	LYS
15	O	6	GLU
15	O	10	LYS
15	O	13	GLN
15	O	17	ARG
15	O	22	THR
15	O	25	THR
15	O	28	GLN
15	O	31	LEU
15	O	32	LEU
15	O	34	LEU
15	O	38	ARG
15	O	41	GLU
15	O	43	LEU
15	O	54	ARG
15	O	56	LEU
15	O	57	LEU
15	O	59	MET
15	O	60	VAL
15	O	64	ARG
15	O	65	ARG
15	O	68	ARG
15	O	70	LEU
15	O	71	GLN
15	O	77	ARG

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Mol	Chain	Res	Type
15	O	87	ILE
15	O	88	ARG
16	P	6	LEU
16	P	19	ILE
16	P	20	VAL
16	P	23	ASP
16	P	25	ARG
16	P	26	ARG
16	P	28	ARG
16	P	36	ILE
16	P	44	THR
16	P	45	THR
16	P	49	LEU
16	P	51	VAL
16	P	54	GLU
16	P	55	ARG
16	P	68	ASP
16	P	76	GLN
16	P	81	ARG
17	Q	19	VAL
17	Q	23	VAL
17	Q	24	GLU
17	Q	36	ILE
17	Q	38	ARG
17	Q	63	ARG
17	Q	68	ARG
17	Q	70	ARG
17	Q	81	ARG
17	Q	84	LEU
17	Q	92	ARG
17	Q	93	GLN
17	Q	98	LEU
18	R	26	LEU
18	R	28	GLU
18	R	34	TYR
18	R	36	ASN
18	R	37	VAL
18	R	38	GLU
18	R	45	SER
18	R	49	LYS
18	R	53	ARG
18	R	54	ARG

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Mol	Chain	Res	Type
18	R	63	GLN
18	R	68	LYS
18	R	69	THR
18	R	74	ARG
18	R	75	ILE
18	R	85	LEU
19	S	5	LEU
19	S	6	LYS
19	S	7	LYS
19	S	15	LEU
19	S	17	GLU
19	S	22	LEU
19	S	25	LYS
19	S	28	LYS
19	S	29	ARG
19	S	37	ARG
19	S	38	SER
19	S	39	THR
19	S	43	GLU
19	S	51	VAL
19	S	63	THR
19	S	65	ASN
19	S	70	LYS
19	S	71	LEU
19	S	77	THR
19	S	79	THR
20	T	13	LEU
20	T	20	LEU
20	T	21	LYS
20	T	25	ARG
20	T	36	LEU
20	T	42	GLN
20	T	53	LEU
20	T	57	ARG
20	T	62	LEU
20	T	68	LYS
20	T	72	LEU
20	T	73	HIS
20	T	89	ARG
21	V	3	LYS
21	V	12	LYS
21	V	17	THR

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Mol	Chain	Res	Type
22	W	3	GLU
22	W	7	ILE
22	W	12	VAL
22	W	14	THR
22	W	17	LEU
22	W	19	ASN
22	W	21	THR
22	W	23	ARG
22	W	32	ILE
22	W	48	LEU
22	W	52	ARG
22	W	56	GLU
22	W	58	THR
22	W	61	ASP
22	W	68	VAL
23	X	4	GLU
23	X	22	ASP
23	X	24	LYS
23	X	25	GLN
23	X	32	ARG
23	X	35	LEU
23	X	46	VAL
23	X	73	GLU
23	X	74	LYS
23	X	78	LYS
23	X	84	GLU
23	X	92	VAL
23	X	93	LYS
23	X	94	ILE
23	X	95	ASP
23	X	99	TYR
23	X	117	LYS
23	X	118	VAL
23	X	119	THR
23	X	120	ILE
23	X	132	LEU
23	X	139	ARG
23	X	140	VAL
23	X	142	GLU
23	X	144	LEU
23	X	146	ASP
23	X	153	LYS

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Mol	Chain	Res	Type
23	X	162	ASN
23	X	163	MET
23	X	164	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	45	GLN
2	B	95	GLN
2	B	104	ASN
2	B	140	HIS
2	B	146	GLN
2	B	204	ASN
3	C	31	HIS
3	C	37	GLN
3	C	108	ASN
3	C	118	GLN
3	C	170	GLN
4	D	125	HIS
4	D	160	GLN
4	D	161	ASN
4	D	201	GLN
5	E	65	ASN
5	E	73	ASN
5	E	130	ASN
6	F	11	ASN
6	F	64	GLN
6	F	100	ASN
7	G	11	GLN
7	G	51	GLN
7	G	96	GLN
7	G	106	GLN
8	H	82	HIS
9	I	31	GLN
9	I	87	GLN
9	I	124	GLN
11	K	13	GLN
11	K	26	ASN
11	K	62	GLN
11	K	93	GLN
12	L	49	ASN
13	M	12	ASN

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Mol	Chain	Res	Type
15	O	9	GLN
15	O	37	ASN
16	P	65	GLN
16	P	76	GLN
18	R	36	ASN
18	R	63	GLN
19	S	14	HIS
19	S	23	ASN
19	S	53	ASN
20	T	9	ASN
20	T	75	ASN
23	X	25	GLN
23	X	114	HIS
23	X	129	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1509/1522 (99%)	423 (28%)	101 (6%)
24	Y	18/42 (42%)	6 (33%)	1 (5%)
25	Z	75/77 (97%)	27 (36%)	4 (5%)
All	All	1602/1641 (97%)	456 (28%)	106 (6%)

All (456) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	8	A
1	A	9	G
1	A	13	U
1	A	14	U
1	A	19	C
1	A	22	G
1	A	29	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	50	A

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Mol	Chain	Res	Type
1	A	51	A
1	A	52	G
1	A	54	C
1	A	61	G
1	A	63	C
1	A	66	G
1	A	68	G
1	A	76	C
1	A	77	G
1	A	78	G
1	A	79	G
1	A	81	U
1	A	82	U
1	A	92	C
1	A	93	G
1	A	97	G
1	A	100	C
1	A	108	G
1	A	115	G
1	A	116	A
1	A	120	A
1	A	121	C
1	A	122	G
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	142	G
1	A	144	G
1	A	151	A
1	A	157	G
1	A	163	C
1	A	180	U
1	A	181	G
1	A	182	U
1	A	189(E)	U
1	A	189(F)	U
1	A	189(G)	G
1	A	195	A
1	A	197	A
1	A	198	G
1	A	201	C
1	A	203	U

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Mol	Chain	Res	Type
1	A	204	U
1	A	220	G
1	A	223	U
1	A	227	G
1	A	240	C
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	262	A
1	A	266	G
1	A	267	C
1	A	280	C
1	A	281	G
1	A	282	A
1	A	283	C
1	A	288	A
1	A	289	G
1	A	298	A
1	A	301	G
1	A	315	A
1	A	316	G
1	A	321	A
1	A	325	A
1	A	327	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	344	A
1	A	345	C
1	A	347	G
1	A	350	G
1	A	351	G
1	A	352	C
1	A	353	A
1	A	366	C
1	A	367	U
1	A	369	C
1	A	372	C
1	A	373	A
1	A	375	U

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Mol	Chain	Res	Type
1	A	378	G
1	A	384	G
1	A	390	C
1	A	397	A
1	A	398	C
1	A	406	G
1	A	409	G
1	A	412	A
1	A	413	G
1	A	421	U
1	A	422	C
1	A	423	G
1	A	428	G
1	A	429	U
1	A	430	A
1	A	439	A
1	A	441	A
1	A	442	C
1	A	448	A
1	A	450	G
1	A	452	A
1	A	454	C
1	A	470	C
1	A	481	G
1	A	482	A
1	A	484	G
1	A	485	G
1	A	495	A
1	A	496	A
1	A	498	U
1	A	500	G
1	A	509	A
1	A	510	A
1	A	511	C
1	A	517	G
1	A	518	C
1	A	519	C
1	A	521	G
1	A	524	G
1	A	525	C
1	A	527	G
1	A	531	U

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Mol	Chain	Res	Type
1	A	532	A
1	A	534	U
1	A	535	A
1	A	543	C
1	A	545	C
1	A	547	A
1	A	548	G
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	565	U
1	A	568	G
1	A	572	A
1	A	573	A
1	A	574	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	578	C
1	A	588	G
1	A	596	C
1	A	607	A
1	A	619	U
1	A	622	A
1	A	641	U
1	A	642	A
1	A	653	A
1	A	654	G
1	A	665	A
1	A	671	G
1	A	673	G
1	A	687	A
1	A	688	G
1	A	695	A
1	A	701	C
1	A	702	A
1	A	703	G
1	A	713	G
1	A	717	C
1	A	718	G
1	A	721	G

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Mol	Chain	Res	Type
1	A	723	U
1	A	728	A
1	A	731	G
1	A	733	A
1	A	734	G
1	A	748	C
1	A	749	C
1	A	755	G
1	A	760	G
1	A	777	A
1	A	785	G
1	A	787	A
1	A	792	A
1	A	793	U
1	A	794	A
1	A	797	C
1	A	799	G
1	A	802	A
1	A	812	C
1	A	813	U
1	A	815	A
1	A	817	C
1	A	819	A
1	A	820	U
1	A	821	G
1	A	826	C
1	A	828	A
1	A	834	C
1	A	836	G
1	A	839	U
1	A	840	C
1	A	841	U
1	A	853	G
1	A	855	G
1	A	864	A
1	A	865	A
1	A	869	G
1	A	872	A
1	A	873	A
1	A	874	G
1	A	876	G
1	A	884	U

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Mol	Chain	Res	Type
1	A	885	G
1	A	891	U
1	A	900	A
1	A	902	G
1	A	914	A
1	A	915	A
1	A	919	A
1	A	922	G
1	A	927	G
1	A	932	C
1	A	934	C
1	A	935	A
1	A	946	A
1	A	950	U
1	A	958	A
1	A	960	U
1	A	961	U
1	A	965	A
1	A	966	G
1	A	968	A
1	A	969	A
1	A	971	G
1	A	972	C
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	980	C
1	A	989	C
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	998	G
1	A	1001	A
1	A	1002	G
1	A	1012	U
1	A	1017	G
1	A	1020	U
1	A	1023	G
1	A	1024	G
1	A	1025	U

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Mol	Chain	Res	Type
1	A	1026	G
1	A	1030	C
1	A	1031	G
1	A	1045	C
1	A	1046	A
1	A	1050	G
1	A	1052	U
1	A	1053	G
1	A	1054	C
1	A	1065	U
1	A	1066	C
1	A	1067	A
1	A	1068	G
1	A	1070	U
1	A	1085	U
1	A	1089	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1104	G
1	A	1108	G
1	A	1117	G
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1128	C
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1134	G
1	A	1135	U
1	A	1136	U
1	A	1138	G
1	A	1139	G
1	A	1145	C
1	A	1146	A
1	A	1152	A
1	A	1154	G
1	A	1157	A
1	A	1158	C

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Mol	Chain	Res	Type
1	A	1159	U
1	A	1163	C
1	A	1165	C
1	A	1182	G
1	A	1183	A
1	A	1184	G
1	A	1187	G
1	A	1188	A
1	A	1191	A
1	A	1193	G
1	A	1195	C
1	A	1196	U
1	A	1197	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1215	G
1	A	1218	C
1	A	1225	A
1	A	1227	A
1	A	1238	A
1	A	1239	A
1	A	1240	U
1	A	1250	A
1	A	1253	G
1	A	1254	C
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1260	C
1	A	1270	C
1	A	1278	U
1	A	1279	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1299	A

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Mol	Chain	Res	Type
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1305	G
1	A	1317	C
1	A	1318	A
1	A	1319	A
1	A	1320	C
1	A	1323	G
1	A	1336	C
1	A	1338	G
1	A	1340	A
1	A	1346	A
1	A	1347	G
1	A	1348	U
1	A	1349	A
1	A	1350	A
1	A	1353	G
1	A	1356	G
1	A	1357	A
1	A	1363	C
1	A	1363(A)	A
1	A	1364	U
1	A	1365	G
1	A	1370	G
1	A	1377	A
1	A	1379	G
1	A	1380	U
1	A	1381	U
1	A	1394	A
1	A	1398	A
1	A	1402	C
1	A	1404	C
1	A	1409	C
1	A	1410	G
1	A	1413	A
1	A	1418	A
1	A	1419	G
1	A	1423	G
1	A	1424	C
1	A	1440	C

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Mol	Chain	Res	Type
1	A	1442	G
1	A	1443	G
1	A	1447	A
1	A	1452	C
1	A	1456	G
1	A	1457	G
1	A	1458	G
1	A	1478	C
1	A	1488	G
1	A	1489	G
1	A	1492	A
1	A	1493	A
1	A	1494	G
1	A	1497	G
1	A	1499	A
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G
1	A	1533	C
1	A	1534	A
1	A	1535	C
1	A	1536	C
1	A	1541	U
24	Y	21	G
24	Y	28	A
24	Y	33	A
24	Y	35	A
24	Y	37	U
24	Y	39	U
25	Z	7	G
25	Z	8	4SU
25	Z	9	G
25	Z	16	C
25	Z	17	C
25	Z	17(A)	U

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Mol	Chain	Res	Type
25	Z	18	G
25	Z	19	G
25	Z	20	U
25	Z	21	A
25	Z	26	G
25	Z	42	G
25	Z	43	A
25	Z	44	A
25	Z	45	G
25	Z	47	U
25	Z	48	C
25	Z	49	G
25	Z	52	G
25	Z	59	A
25	Z	60	U
25	Z	61	C
25	Z	67	C
25	Z	68	C
25	Z	69	C
25	Z	74	C
25	Z	76	A

All (106) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	13	U
1	A	30	U
1	A	48	C
1	A	51	A
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	139	G
1	A	141	A
1	A	155	C
1	A	181	G
1	A	197	A
1	A	202	U
1	A	243	A
1	A	250	A

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Mol	Chain	Res	Type
1	A	251	G
1	A	266	G
1	A	279	A
1	A	281	G
1	A	315	A
1	A	327	A
1	A	328	C
1	A	329	A
1	A	344	A
1	A	351	G
1	A	372	C
1	A	428	G
1	A	429	U
1	A	481	G
1	A	484	G
1	A	495	A
1	A	496	A
1	A	509	A
1	A	518	C
1	A	531	U
1	A	535	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	641	U
1	A	687	A
1	A	701	C
1	A	702	A
1	A	733	A
1	A	748	C
1	A	792	A
1	A	812	C
1	A	832	C
1	A	840	C
1	A	872	A
1	A	884	U
1	A	960	U
1	A	965	A
1	A	968	A
1	A	975	A
1	A	992	U
1	A	993	G

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Mol	Chain	Res	Type
1	A	1001	A
1	A	1049	U
1	A	1053	G
1	A	1065	U
1	A	1067	A
1	A	1101	A
1	A	1145	C
1	A	1154	G
1	A	1157	A
1	A	1182	G
1	A	1187	G
1	A	1190	G
1	A	1196	U
1	A	1200	C
1	A	1201	A
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1239	A
1	A	1257	U
1	A	1279	A
1	A	1285	A
1	A	1286	A
1	A	1298	C
1	A	1299	A
1	A	1300	G
1	A	1301	U
1	A	1346	A
1	A	1347	G
1	A	1364	U
1	A	1380	U
1	A	1397	C
1	A	1442(B)	A
1	A	1447	A
1	A	1457	G
1	A	1488	G
1	A	1493	A
1	A	1498	U
1	A	1503	A
1	A	1504	G
1	A	1533	C
1	A	1534	A

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Mol	Chain	Res	Type
24	Y	32	A
25	Z	9	G
25	Z	47	U
25	Z	60	U
25	Z	68	C

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

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	G7M	Z	46	25	23,26,27	2.44	5 (21%)	34,39,42	2.92	11 (32%)
25	PSU	Z	55	25	18,21,22	1.55	2 (11%)	21,30,33	2.09	6 (28%)
25	5MU	Z	54	25	19,22,23	1.56	4 (21%)	27,32,35	1.78	6 (22%)
25	OMC	Z	32	25	19,22,23	0.86	1 (5%)	25,31,34	1.30	4 (16%)
25	4SU	Z	8	25	18,21,22	1.72	4 (22%)	25,30,33	2.50	9 (36%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	G7M	Z	46	25	-	0/7/25/26	0/3/3/3
25	PSU	Z	55	25	-	0/7/25/26	0/2/2/2
25	5MU	Z	54	25	-	0/7/25/26	0/2/2/2
25	OMC	Z	32	25	-	0/9/27/28	0/2/2/2
25	4SU	Z	8	25	-	2/7/25/26	0/2/2/2

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	Z	46	G7M	C8-N7	7.90	1.46	1.33
25	Z	55	PSU	C6-C5	5.30	1.41	1.35
25	Z	46	G7M	C8-N9	4.58	1.48	1.35
25	Z	8	4SU	C4-S4	-4.36	1.61	1.68
25	Z	46	G7M	C5-C4	4.11	1.48	1.38
25	Z	46	G7M	C5-N7	-3.99	1.34	1.39
25	Z	54	5MU	C6-C5	3.86	1.40	1.34
25	Z	8	4SU	C2-N1	3.41	1.43	1.38
25	Z	54	5MU	C4-C5	3.38	1.50	1.44
25	Z	8	4SU	C4-N3	-2.62	1.34	1.37
25	Z	8	4SU	C6-C5	2.53	1.40	1.35
25	Z	54	5MU	C4-N3	-2.15	1.34	1.38
25	Z	55	PSU	C4-C5	2.13	1.50	1.44
25	Z	46	G7M	C5-C6	2.08	1.49	1.43
25	Z	32	OMC	C6-C5	2.05	1.39	1.35
25	Z	54	5MU	C2-N1	2.04	1.41	1.38

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	Z	46	G7M	CN7-N7-C8	-7.81	112.96	124.79
25	Z	8	4SU	C4-N3-C2	-6.78	120.81	127.31
25	Z	46	G7M	N9-C8-N7	-6.63	96.39	112.48
25	Z	55	PSU	N1-C2-N3	5.90	121.39	115.17
25	Z	46	G7M	N9-C4-N3	5.76	137.46	125.95
25	Z	46	G7M	C8-N7-C5	5.70	114.91	107.78
25	Z	8	4SU	N3-C2-N1	5.59	122.17	114.89
25	Z	46	G7M	C5-C4-N3	-4.74	119.19	128.15
25	Z	54	5MU	N3-C2-N1	4.64	120.93	114.89
25	Z	8	4SU	C5-C4-N3	4.60	119.03	114.75
25	Z	46	G7M	C2-N3-C4	4.39	119.86	112.30
25	Z	46	G7M	C8-N9-C4	4.36	117.89	107.09
25	Z	46	G7M	CN7-N7-C5	4.27	132.12	126.80
25	Z	55	PSU	C4-N3-C2	-3.83	121.10	126.37
25	Z	54	5MU	C4-N3-C2	-3.26	123.07	127.34
25	Z	8	4SU	C6-N1-C2	-3.20	117.10	121.00
25	Z	8	4SU	O4'-C1'-N1	3.14	115.47	108.36
25	Z	32	OMC	C2'-C1'-N1	-3.05	108.46	114.24
25	Z	55	PSU	O3'-C3'-C4'	3.04	119.81	111.08
25	Z	8	4SU	C5-C4-S4	-3.03	120.85	124.31
25	Z	46	G7M	O6-C6-C5	-3.01	121.30	128.01
25	Z	8	4SU	C3'-C2'-C1'	2.82	106.80	101.46
25	Z	55	PSU	O2-C2-N1	-2.78	119.92	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	Z	32	OMC	O2-C2-N3	-2.77	117.96	122.33
25	Z	54	5MU	C5M-C5-C4	2.77	121.74	118.78
25	Z	32	OMC	O4'-C1'-N1	2.72	114.51	108.36
25	Z	8	4SU	O2-C2-N3	-2.71	116.49	121.49
25	Z	54	5MU	C5-C4-N3	2.69	117.66	115.32
25	Z	54	5MU	O2-C2-N1	-2.63	119.38	122.80
25	Z	46	G7M	C1'-N9-C8	-2.62	117.88	126.74
25	Z	55	PSU	O4'-C4'-C3'	-2.49	100.21	105.15
25	Z	55	PSU	C6-C5-C4	-2.39	116.56	118.17
25	Z	8	4SU	C1'-N1-C2	2.37	121.85	117.59
25	Z	54	5MU	C3'-C2'-C1'	2.35	105.90	101.46
25	Z	46	G7M	C5-C6-N1	2.30	116.59	111.84
25	Z	32	OMC	O4'-C4'-C5'	2.11	116.09	109.33

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	Z	8	4SU	O4'-C4'-C5'-O5'
25	Z	8	4SU	C3'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	Z	55	PSU	2	0
25	Z	32	OMC	2	0
25	Z	8	4SU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 88 ligands modelled in this entry, 88 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	5
24	Y	2
25	Z	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	84:U	O3'	88:A	P	5.13
1	A	93:G	O3'	96:U	P	4.66
1	A	204:U	O3'	216:G	P	4.13
1	A	1442(A):G	O3'	1442(B):A	P	4.03
1	A	841:U	O3'	848:C	P	4.00
1	Y	28:A	O3'	29:G	P	3.98
1	Z	71:C	O3'	72:A	P	3.52
1	Y	30:G	O3'	31:U	P	3.26

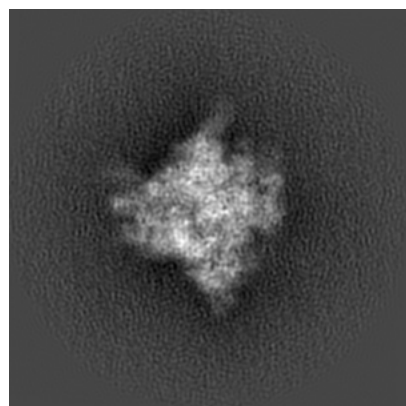
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4079. These allow visual inspection of the internal detail of the map and identification of artifacts.

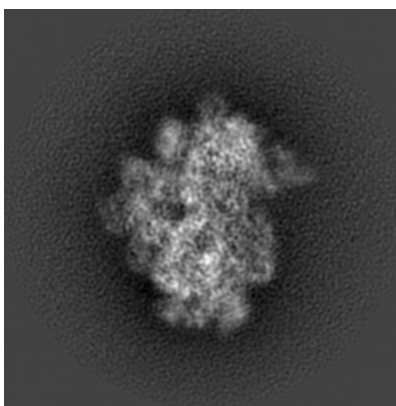
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

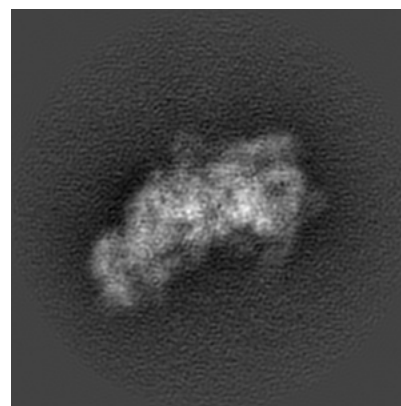
6.1.1 Primary map



X

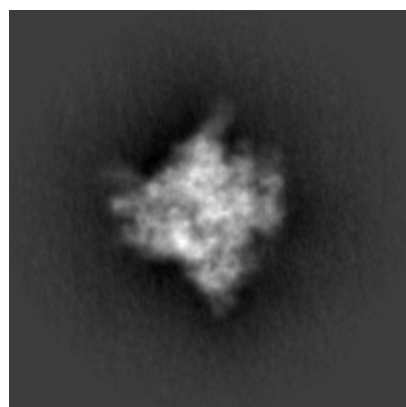


Y

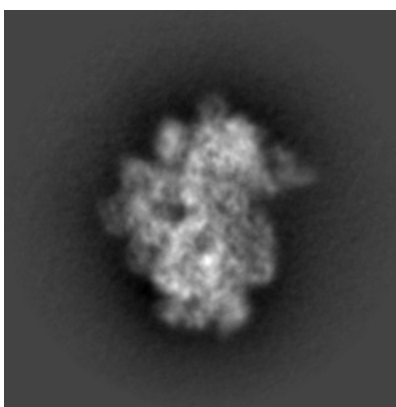


Z

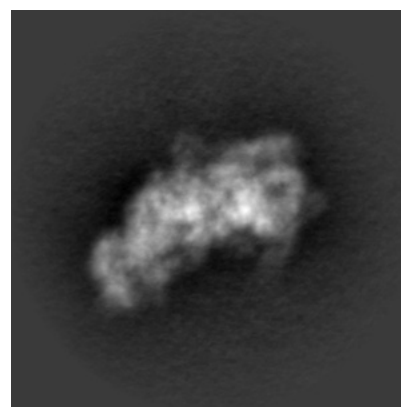
6.1.2 Raw map



X



Y

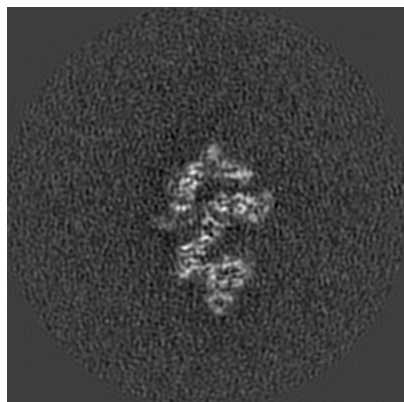


Z

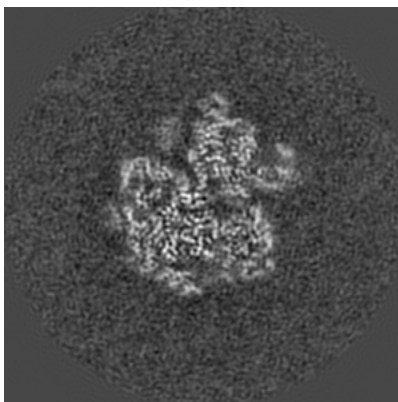
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

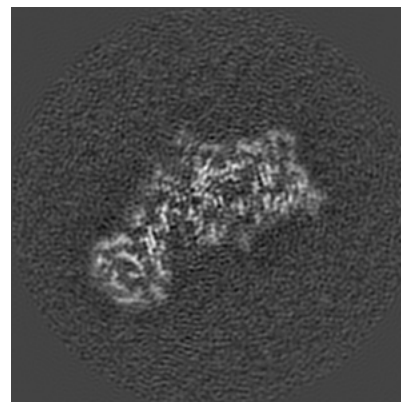
6.2.1 Primary map



X Index: 130

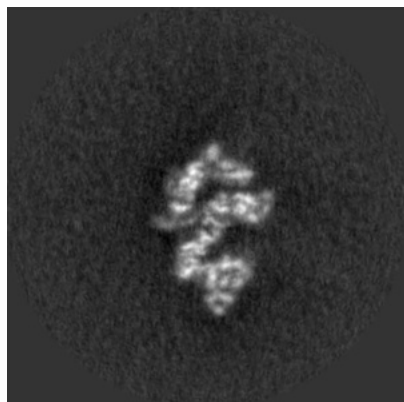


Y Index: 130

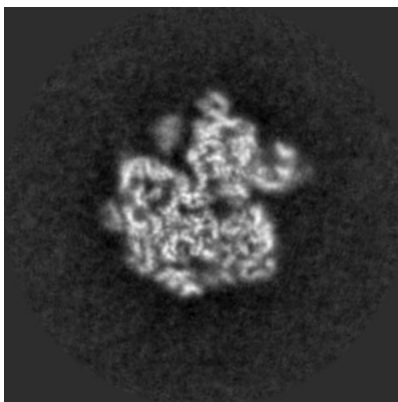


Z Index: 130

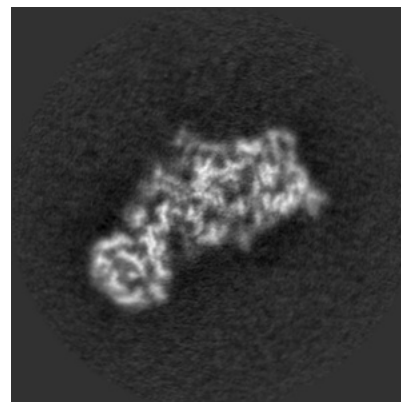
6.2.2 Raw map



X Index: 130



Y Index: 130

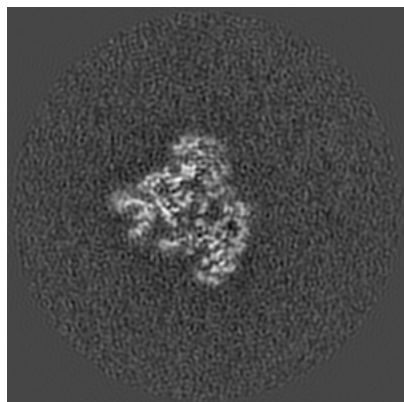


Z Index: 130

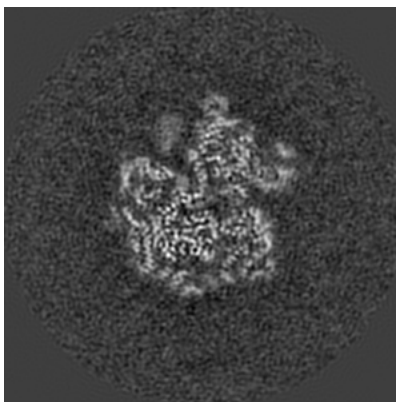
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

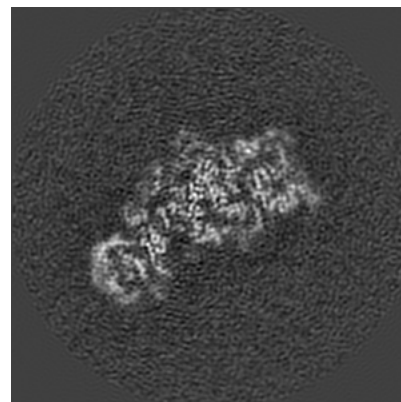
6.3.1 Primary map



X Index: 95

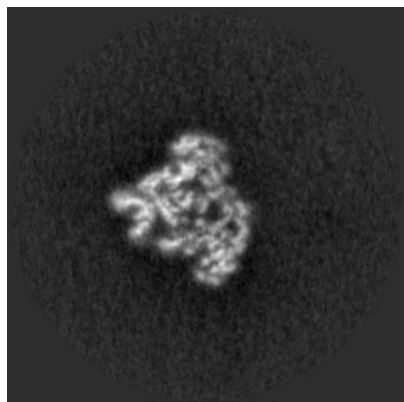


Y Index: 129

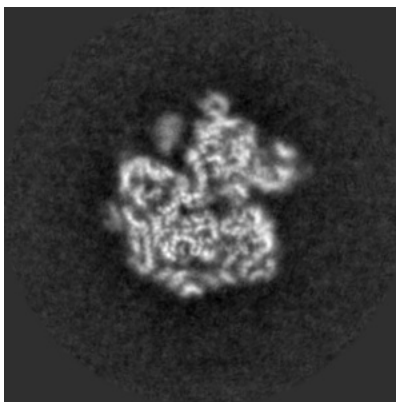


Z Index: 128

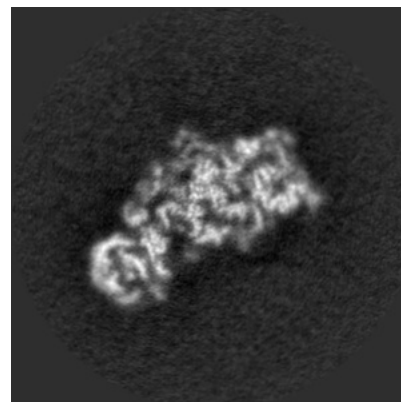
6.3.2 Raw map



X Index: 95



Y Index: 129

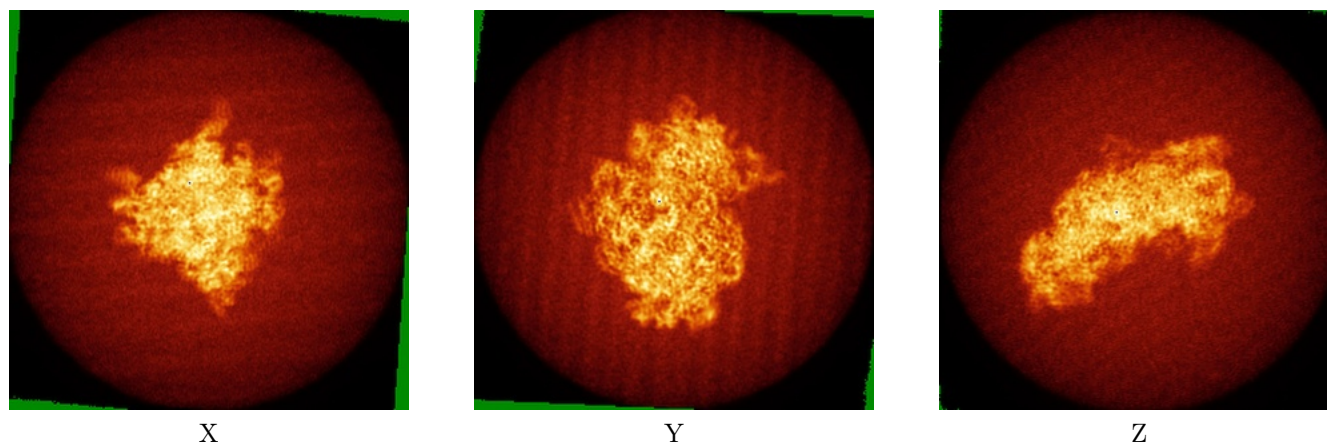


Z Index: 128

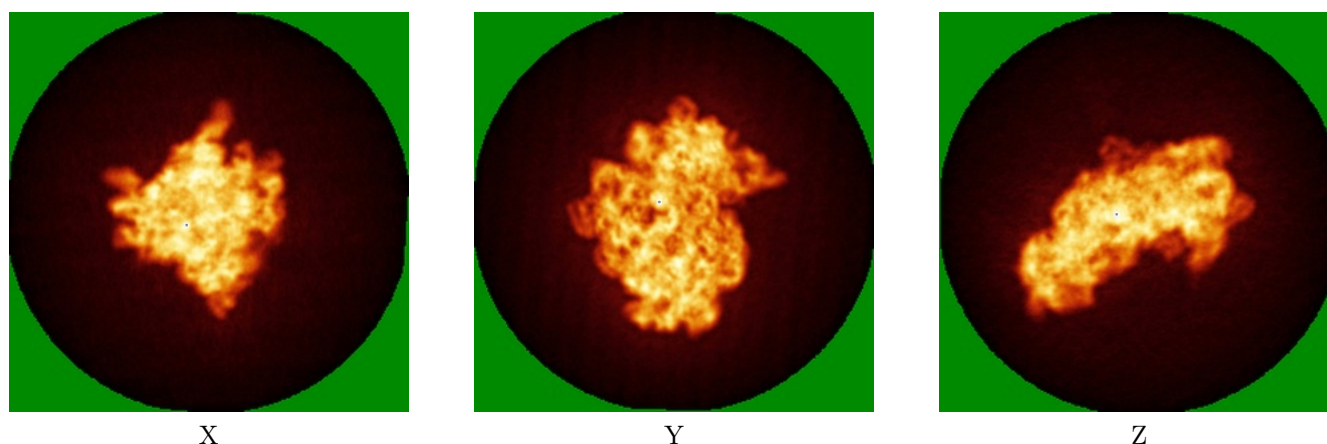
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

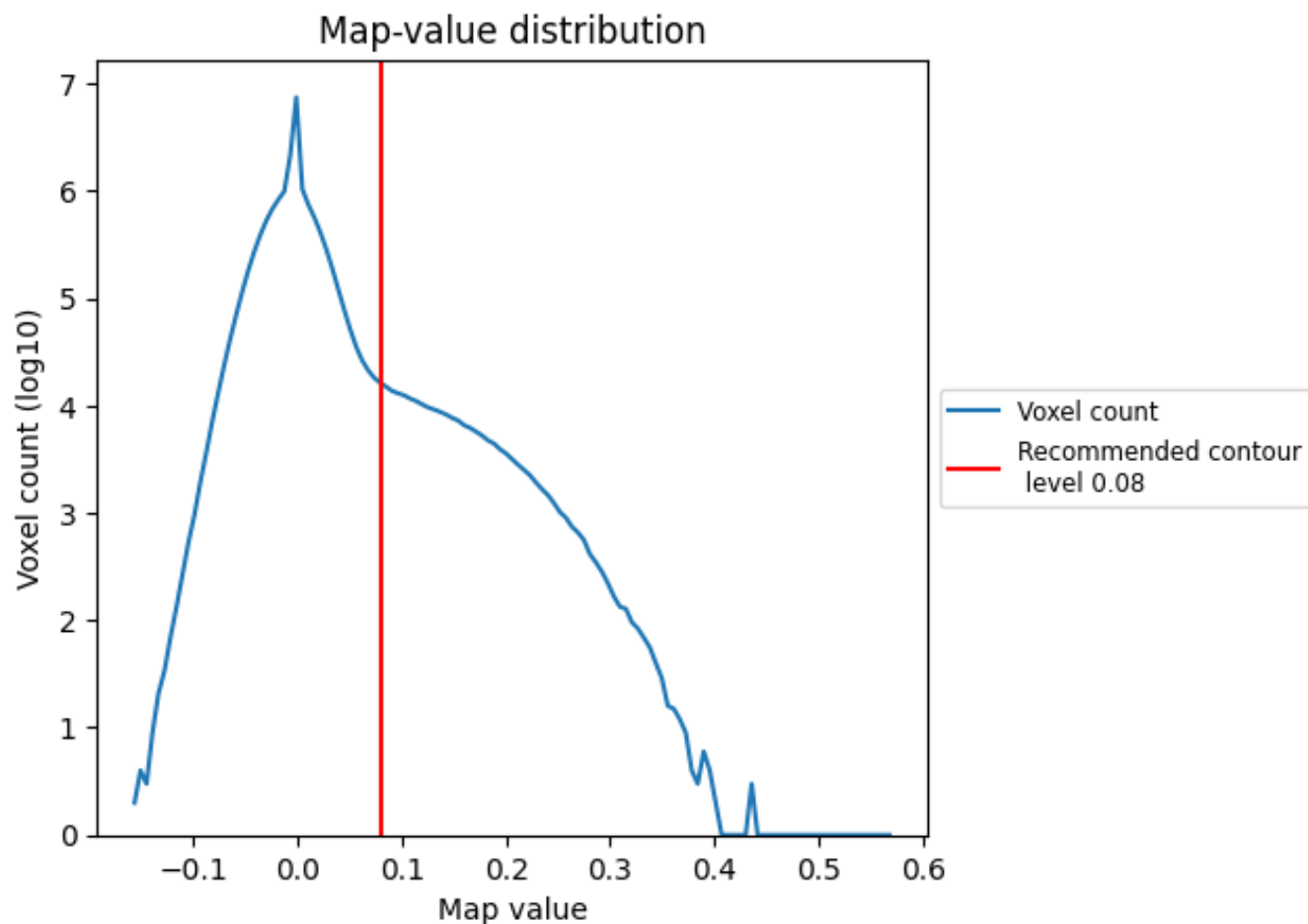
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

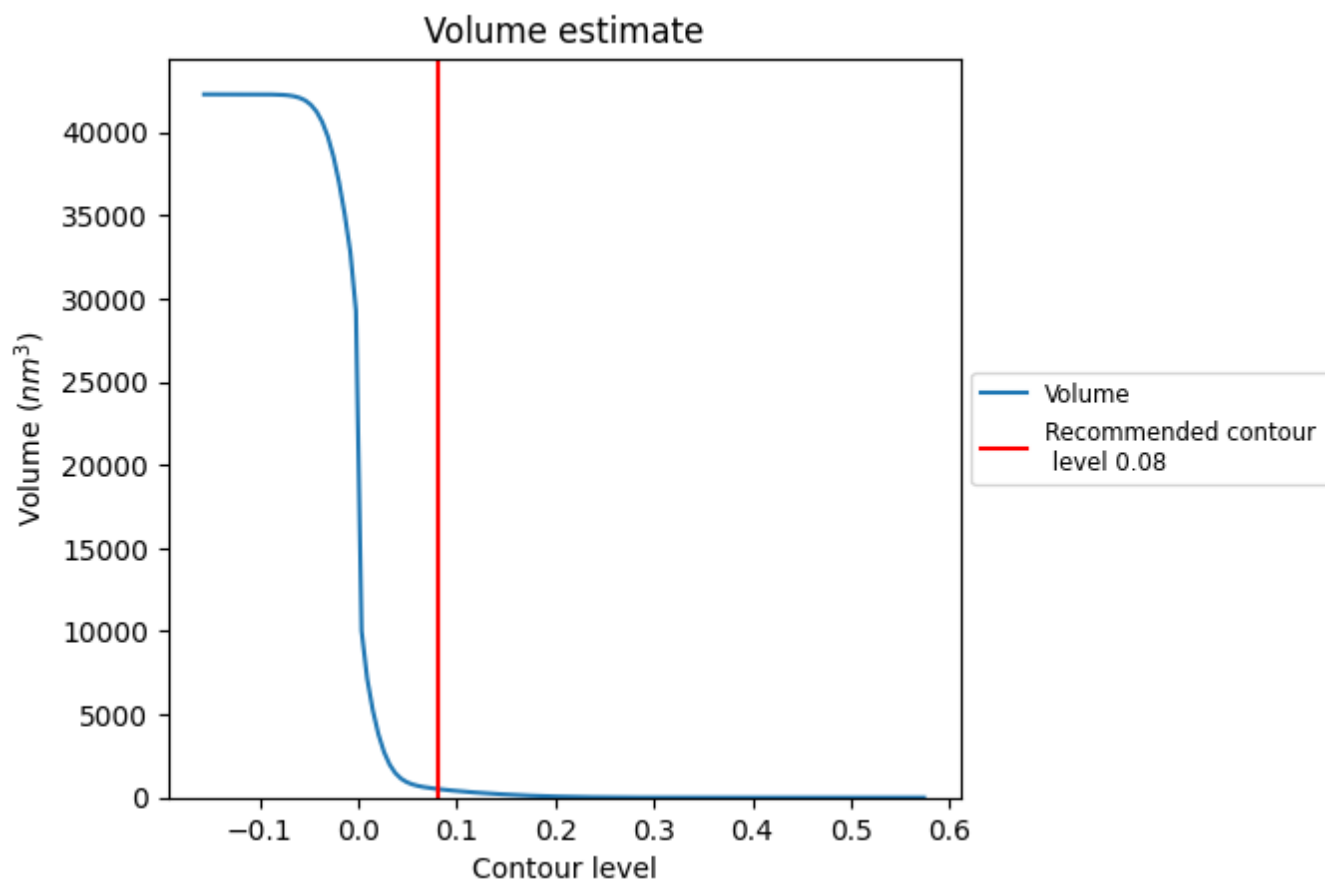
This section contains the results of statistical analysis of the map.

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.

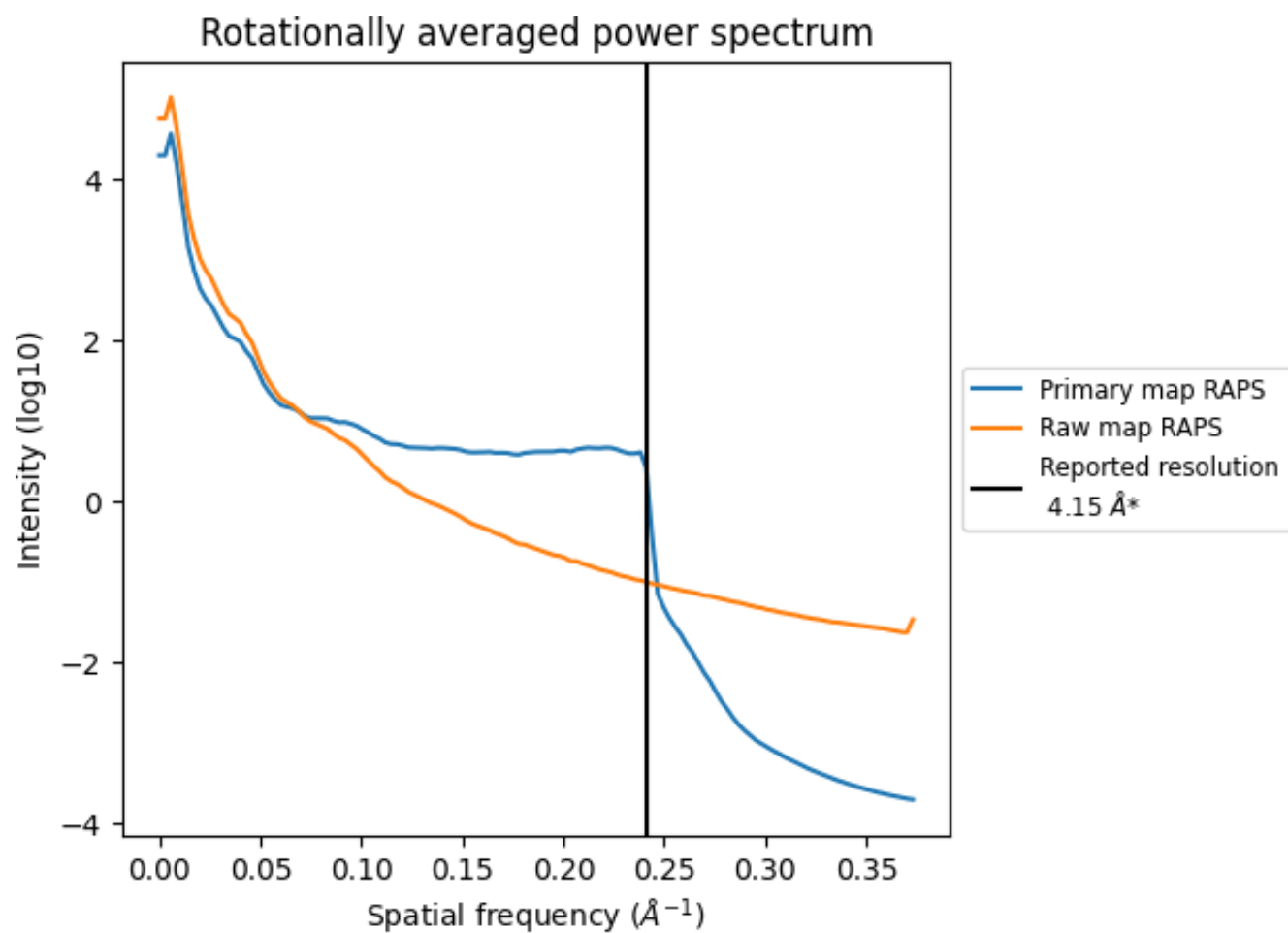
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 519 nm^3 ; this corresponds to an approximate mass of 469 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 ⓘ

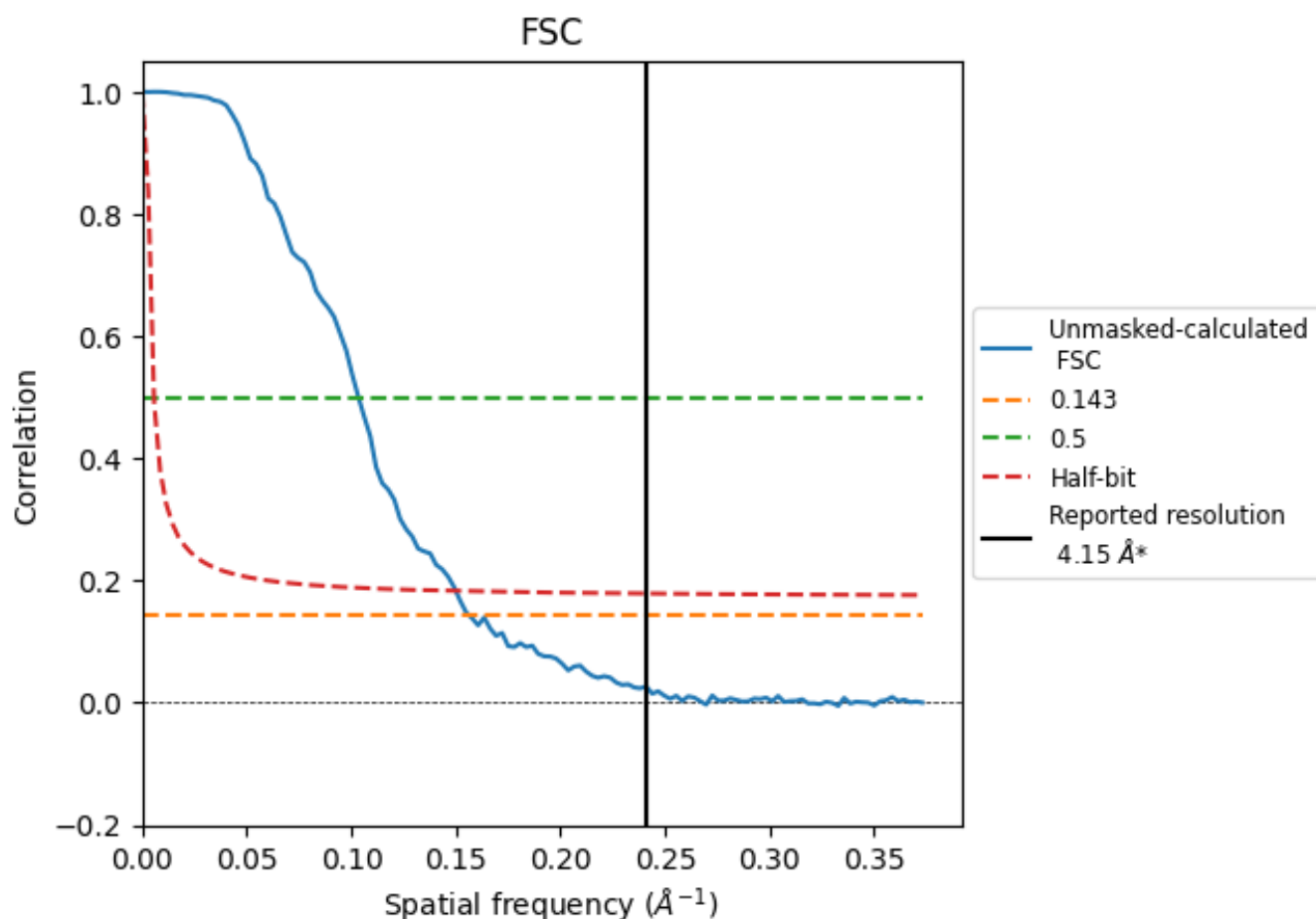


*Reported resolution corresponds to spatial frequency of 0.241 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.241 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

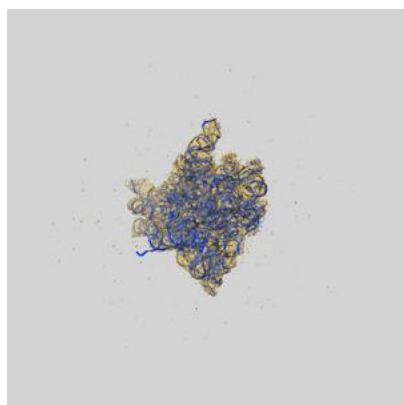
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.15	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.39	9.66	6.67

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.39 differs from the reported value 4.15 by more than 10 %

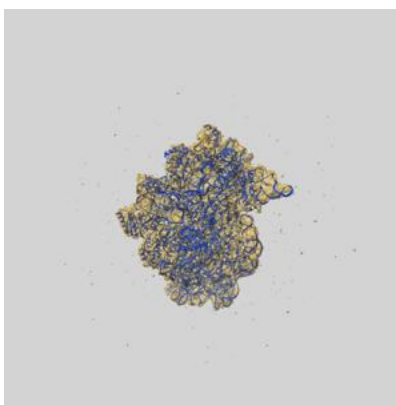
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4079 and PDB model 5LMT. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

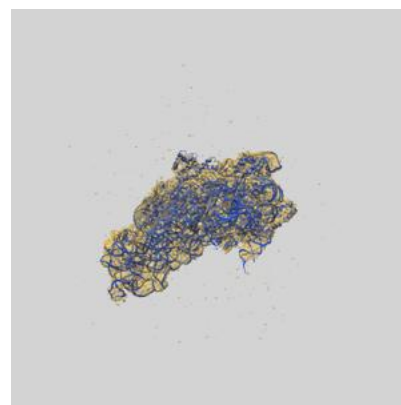
9.1 Map-model overlay [i](#)



X



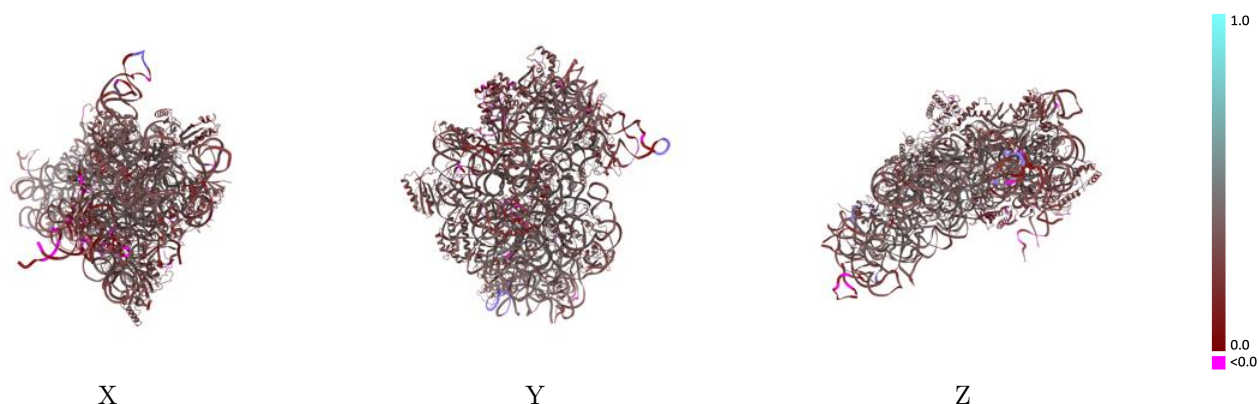
Y



Z

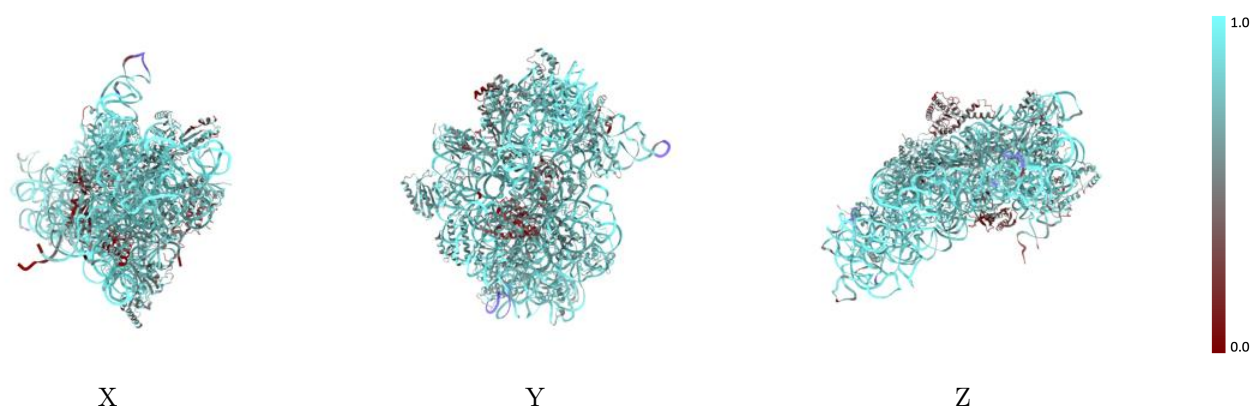
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



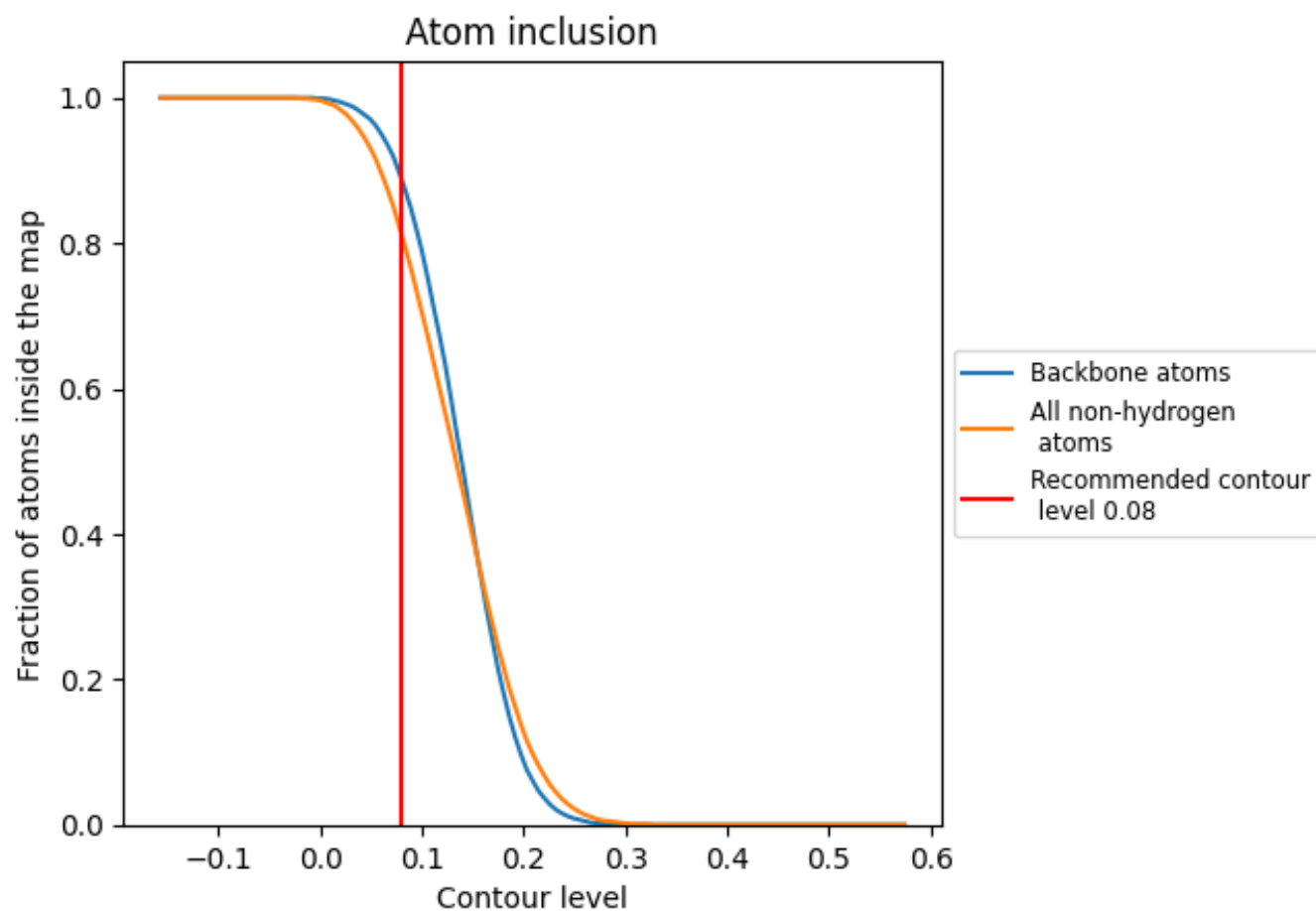
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion ⓘ



At the recommended contour level, 89% of all backbone atoms, 81% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8130	 0.3290
A	 0.9230	 0.3450
B	 0.3440	 0.2630
C	 0.7270	 0.3540
D	 0.7310	 0.3370
E	 0.7100	 0.3660
F	 0.6650	 0.3080
G	 0.7150	 0.3240
H	 0.7390	 0.3570
I	 0.7070	 0.3180
J	 0.6420	 0.3090
K	 0.7070	 0.3200
L	 0.7430	 0.3830
M	 0.6910	 0.2860
N	 0.7760	 0.3770
O	 0.7320	 0.3310
P	 0.7800	 0.3590
Q	 0.7610	 0.3750
R	 0.6710	 0.2900
S	 0.6820	 0.3010
T	 0.6970	 0.3010
V	 0.7380	 0.3450
W	 0.2580	 0.2510
X	 0.3000	 0.1740
Y	 0.7400	 0.2820
Z	 0.7500	 0.1690

