



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 12:53 AM UTC

PDB ID : 9GUW / pdb_00009guw
EMDB ID : EMD-51622
Title : 30S-TEC (TEC in expressome position) Inactive state 2
Authors : Rahil, H.; Weixlbaumer, A.; Webster, M.W.
Deposited on : 2024-09-20
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

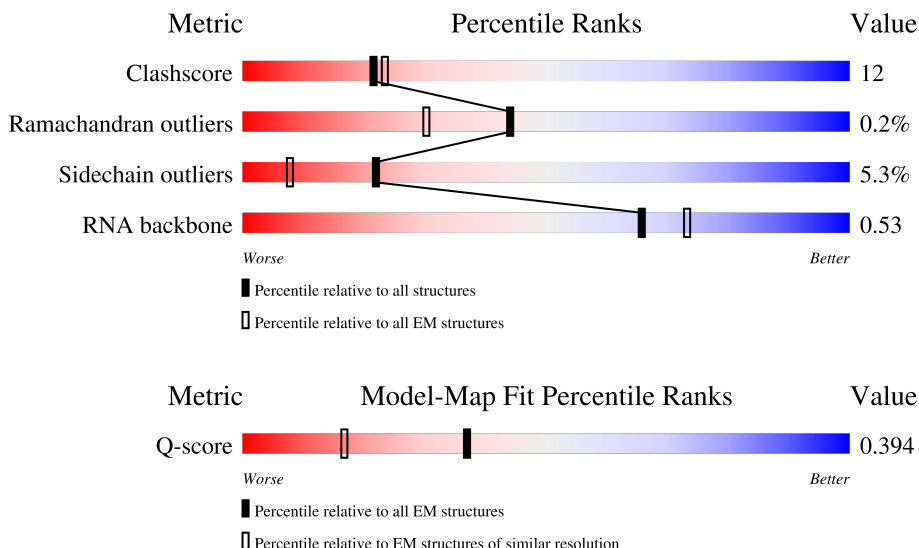
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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.



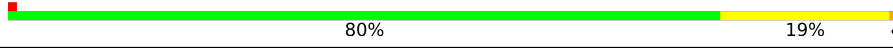
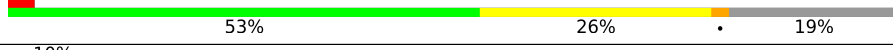
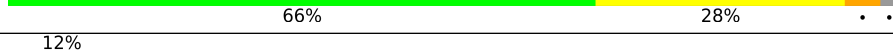
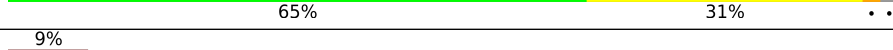
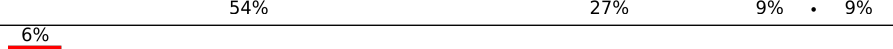
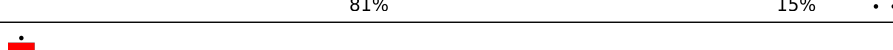
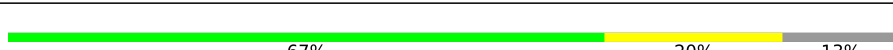
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	1541	
2	B	557	
3	C	241	

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Mol	Chain	Length	Quality of chain
4	D	233	
5	E	206	
6	F	157	
7	G	131	
8	H	156	
9	I	130	
10	J	130	
11	K	103	
12	L	129	
13	M	124	
14	N	118	
15	O	101	
16	P	89	
17	Q	82	
18	R	84	
19	S	75	
20	T	92	
21	U	87	
22	X	53	
23	Z	181	
24	1	329	
24	2	329	
25	3	1342	
26	4	1406	
27	5	91	

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Mol	Chain	Length	Quality of chain
28	6	39	41%5%72%23%
29	7	39	26%33%44%23%

2 Entry composition [i](#)

There are 31 unique types of molecules in this entry. The entry contains 80600 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	1526	Total	C	N	O	P	0	0
			32750	14612	6005	10607	1526		

- Molecule 2 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	173	Total	C	N	O	S	0	0
			1339	843	231	264	1		

- Molecule 3 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 4 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	211	Total	C	N	O	S	0	0
			1655	1047	310	294	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	137	THR	ALA	conflict	UNP C3SQX2

- Molecule 5 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1647	1028	315	300	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	24	ASP	GLY	conflict	UNP C4ZUF1

- Molecule 6 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 7 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 8 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 9 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 10 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	128	Total	C	N	O	S	0	0
			1031	639	207	182	3		

- Molecule 11 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	101	Total	C	N	O	S	0	0
			808	504	155	148	1		

- Molecule 12 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 13 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 14 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 15 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 16 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 17 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 18 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 19 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 20 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 21 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	22	Total	C	N	O	P	0	0
			480	214	98	147	21		

- Molecule 23 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Z	153	Total	C	N	O	S	0	0
			1225	782	209	227	7		

- Molecule 24 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1	229	Total	C	N	O	S	0	0
			1775	1106	313	350	6		
24	2	219	Total	C	N	O	S	0	0
			1684	1051	295	332	6		

- Molecule 25 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3	1320	Total	C	N	O	S	0	0
			10415	6535	1815	2021	44		

- Molecule 26 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	1333	Total	C	N	O	S	0	0
			10375	6518	1851	1956	50		

- Molecule 27 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	5	90	Total	C	N	O	S	0	0
			709	430	136	142	1		

- Molecule 28 is a DNA chain called Non-Template DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	30	Total	C	N	O	P	0	0
			618	294	114	180	30		

- Molecule 29 is a DNA chain called Template DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	7	30	Total	C	N	O	P	0	0
			606	288	105	183	30		

- Molecule 30 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
30	A	116	Total	Mg	0
			116	116	
30	L	1	Total	Mg	0
			1	1	
30	X	1	Total	Mg	0
			1	1	

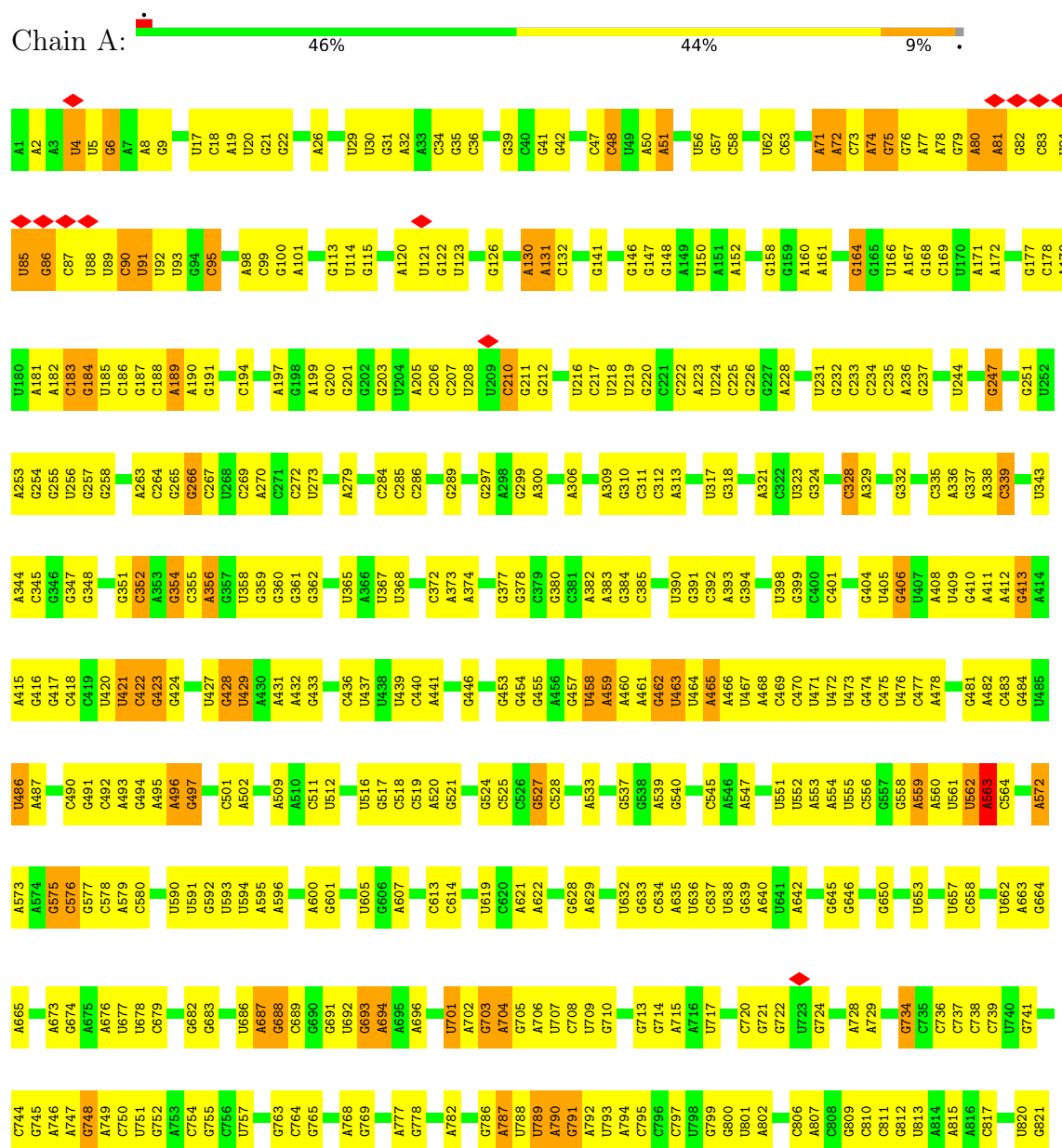
- Molecule 31 is ZINC ION (CCD ID: ZN) (formula: Zn).

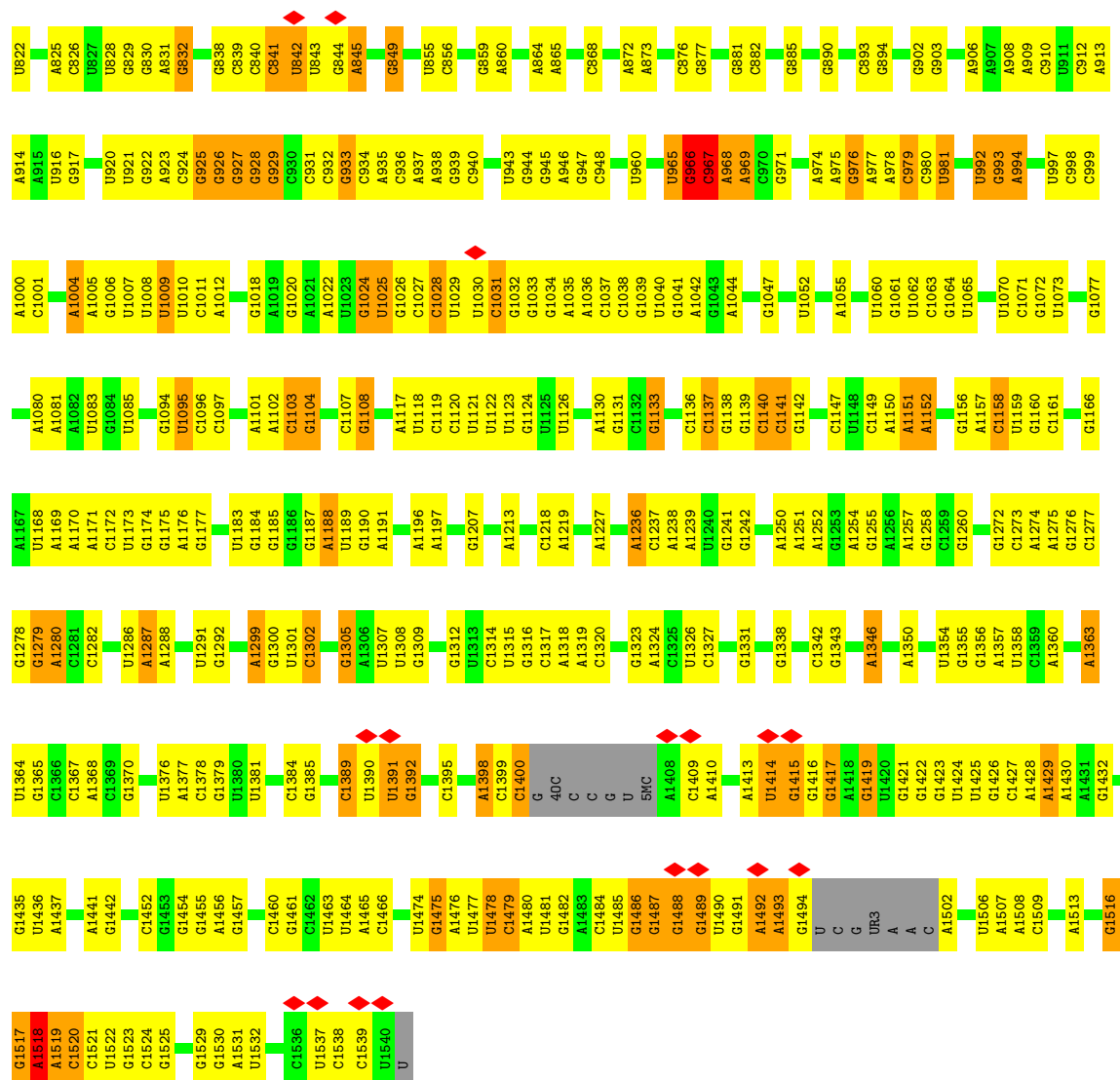
Mol	Chain	Residues	Atoms		AltConf
31	C	1	Total	Zn	0
			1	1	
31	4	2	Total	Zn	0
			2	2	

3 Residue-property plots

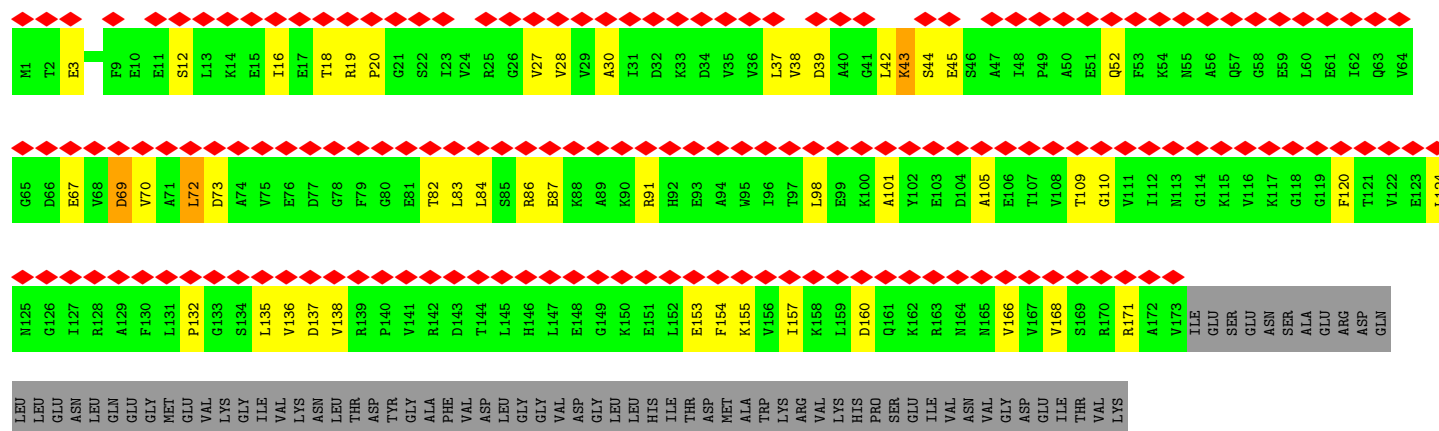
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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



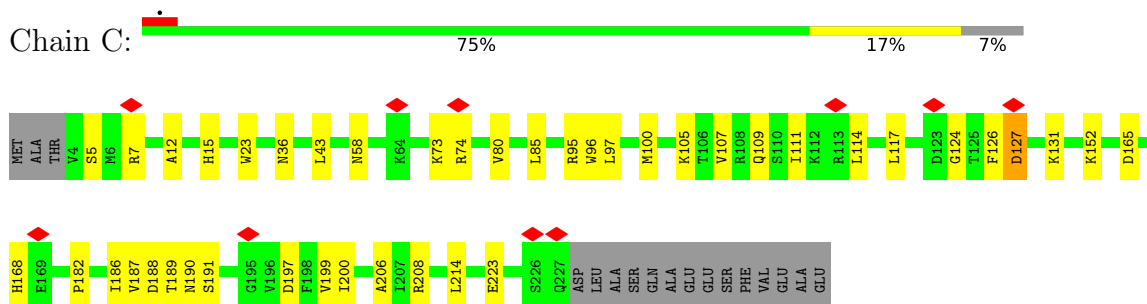


• Molecule 2: 30S ribosomal protein S1

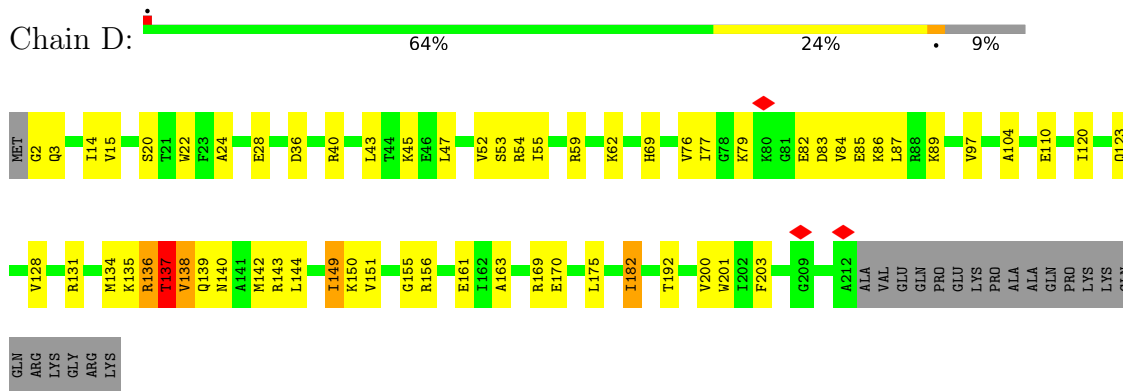


ASN	ALA	ARG	GLU	ASP	HIS	VAL
ALA	ARG	ASP	ARG	ARG	VAL	LEU
MET	GLU	VAL	GLU	VAL	SER	LYS
ALA	VAL	VAL	ILE	GLY	GLU	PHE
ALA	ASP	SER	LEU	LYS	MET	ARG
PHE	ALA	ALA	LEU	ILE	ASP	GLJ
LYS	THR	THR	GLY	LYS	TRP	ARG
ALA	VAL	VAL	VAL	LYS	THR	ARG
LYS	VAL	VAL	GLN	ILE	ASN	VAL
GLY	SER	SER	LEU	ASP	ILE	SER
GLU	VAL	VAL	ALA	PHE	HIS	LEU
	ASP	GLY	GLU	GLY	PRO	GLY
	GLY	GLU	PRO	PHE	SER	LEU
	VAL	VAL	PHE	ILE	LYS	GLN
	ALA	GLU	ASN	LEU	VAL	LEU
	LYS	LYS	ASN	LEU	ASN	GLY
	PHE	THR	VAL	ASP	VAL	GLY
	THR	ALA	GLY	GLY	GLU	ALA
	VAL	ALA	ILE	LEU	VAL	ILE
	ALA	ASN	ILE	HIS	VAL	LYS
	ALA	ARG	VAL	LEU	VAL	ARG
	ILE	ALA	VAL	SER	ASP	TYR
	SER	ILE	THR	ASP	ILE	PRO
	LEU	LEU	GLY	ASP	GLU	GLU
	SER	SER	LYS	SER	GLY	THR
	VAL	VAL	VAL	TRP	GLU	LYS
	ARG	VAL	THR	ASN	ARG	LEU
	ALA	ALA	VAL	VAL	ARG	THR
	LYS	LYS	ASP	ALA	GLY	GLY
	ASP	ASP	ALA	GLY	SER	ARG
	GLU	GLU	LYS	GLU	LEU	THR
	ALA	ALA	GLY	ALA	GLY	VAL
	ASP	ASP	ALA	VAL	LEU	ASN
	GLY	GLY	THR	ARG	LYS	LEU
	LYS	LYS	VAL	GLU	GLN	THR
	ALA	ALA	GLU	TYR	CYS	TYR
	ILE	ILE	ALA	LYS	LYS	GLY
	ALA	THR	GLY	GLY	ASN	CYS
	THR	VAL	GLY	ASP	PRO	PHE
	ASN	ASN	VAL	GLU	TRP	VAL
	VAL	VAL	ILE	ILE	GLN	GLU
	LYS	LYS	GLY	ALA	ILE	GLU
	GLN	GLN	TYR	ALA	PHE	GLJ
	GLU	GLU	LEU	VAL	ALA	GLJ
	ASP	ASP	ARG	VAL	GLY	GLY
	ALA	ALA	ALA	LEU	THR	VAL
	ASN	ASN	SER	GLN	HIS	GLU
	PHE	PHE	GLU	VAL	ASN	GLY
	SER	SER	ALA	ASP	LYS	VAL
	ASN	ASN	SER	ALA	CYS	VAL

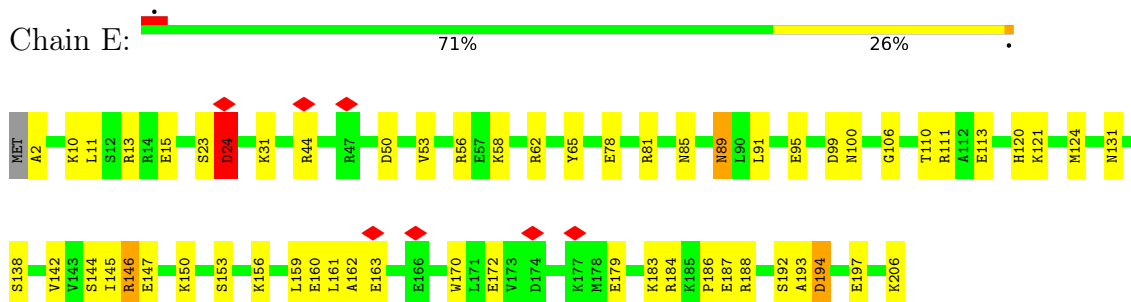
- Molecule 3: 30S ribosomal protein S2



- Molecule 4: Small ribosomal subunit protein uS3



- Molecule 5: Small ribosomal subunit protein uS4



Chain F:

Chain G:

53% 26% 19%

M1 R2 R3 Y4 V10 H11 P12 D13 V18 P19 G20 G21 Y21 T22 E23 A24 Y25 T29 G34 H37 R38 L39 G43 R44 R45 L54 H55 K56 A57 H58 N63 V64 E65 Q68 I71 D72 E75 T76 R79 V84 V89 R90 R91 T92 V96 T97

Chain H:

10% 72% 26%

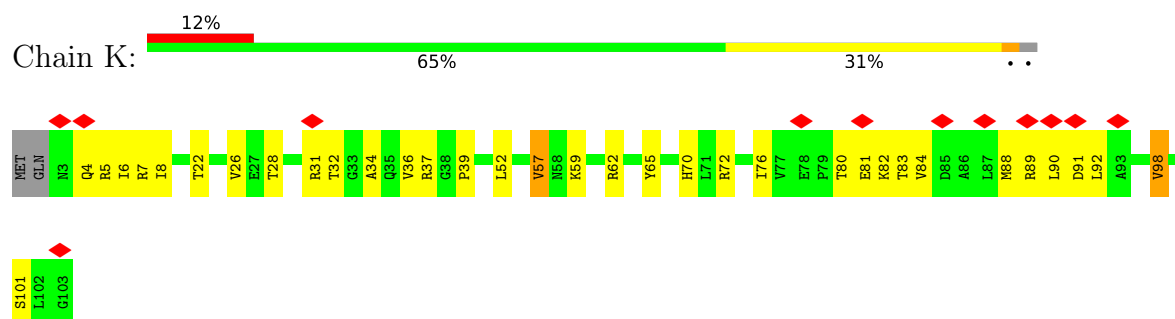
MET P2 R3 R4 R5 G8 G9 R10 R11 K17 F18 G19 S20 N28 M31 V32 D33 S37 S45 A46 L47 E48 T49 L50 S54 G55 K56 S57 E58 L59 E60 A65 N68 V69 E74 V75 R79 V80 G81 G82 S83 P88 R92 P93 R96

I104 L124 L125 D126 E129 N130 K131 G132 T133 A134 V135 R138 E139 H142 E146 A152 H153 Y154 ARG TRP

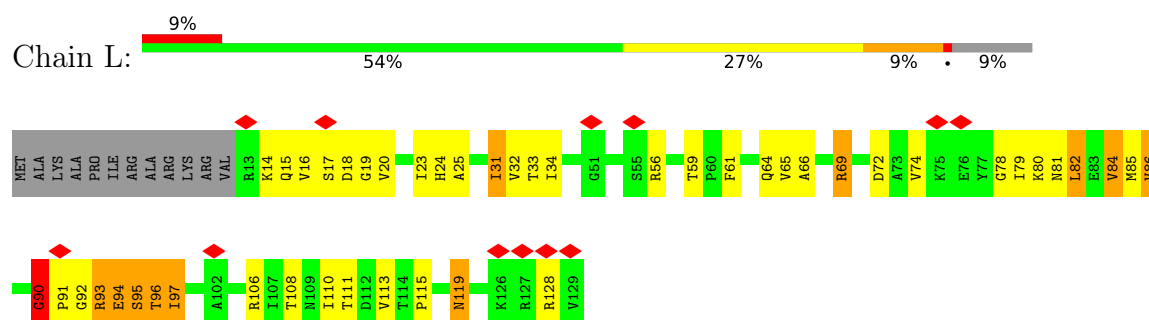
Chain I: 78% 20% ..

Chain J:

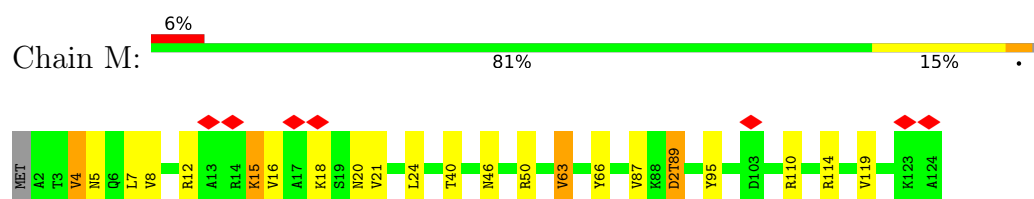
- Molecule 11: 30S ribosomal protein S10



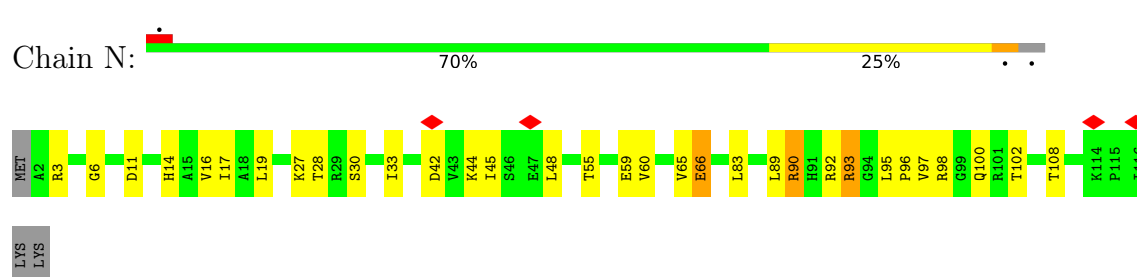
- Molecule 12: 30S ribosomal protein S11



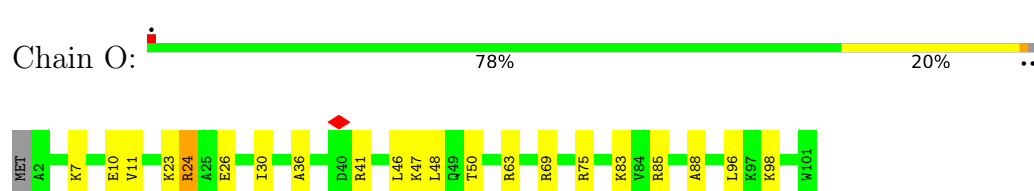
- Molecule 13: 30S ribosomal protein S12



- Molecule 14: 30S ribosomal protein S13

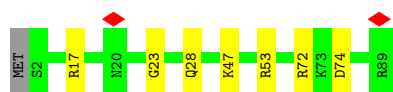


- Molecule 15: 30S ribosomal protein S14



- Molecule 16: Small ribosomal subunit protein uS15

Chain P:  91% 8%



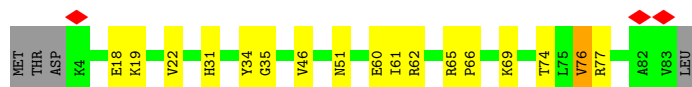
- Molecule 17: 30S ribosomal protein S16

Chain Q:  87% 13%



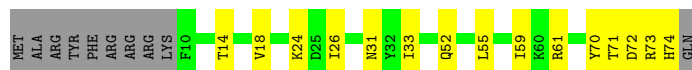
- Molecule 18: 30S ribosomal protein S17

Chain R:  75% 19% 5%



- Molecule 19: 30S ribosomal protein S18

Chain S:  67% 20% 13%



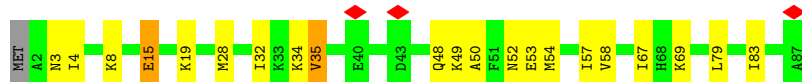
- Molecule 20: 30S ribosomal protein S19

Chain T:  62% 28% 10%



- Molecule 21: 30S ribosomal protein S20

Chain U:  75% 22%

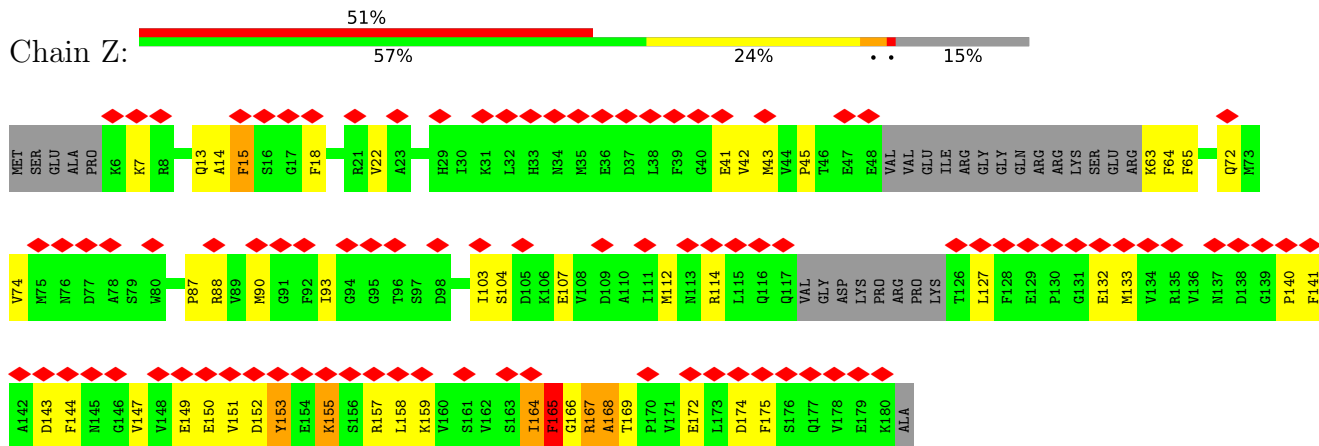


- Molecule 22: mRNA

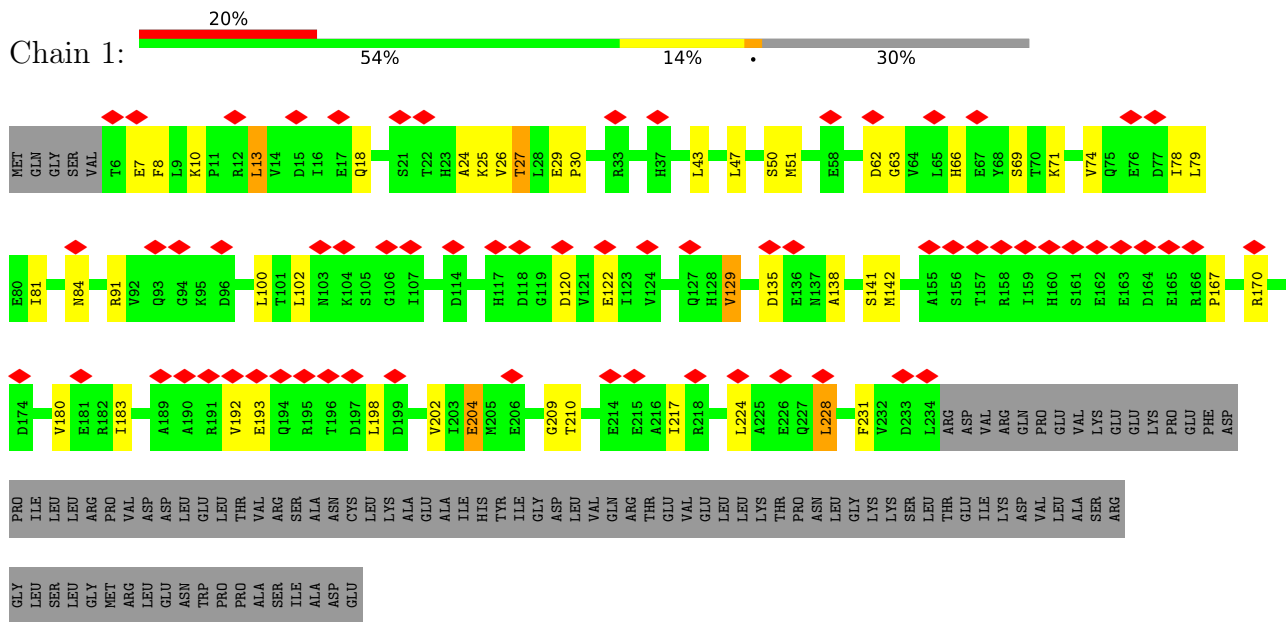
Chain X:  17% 23% 15% 9% 58%



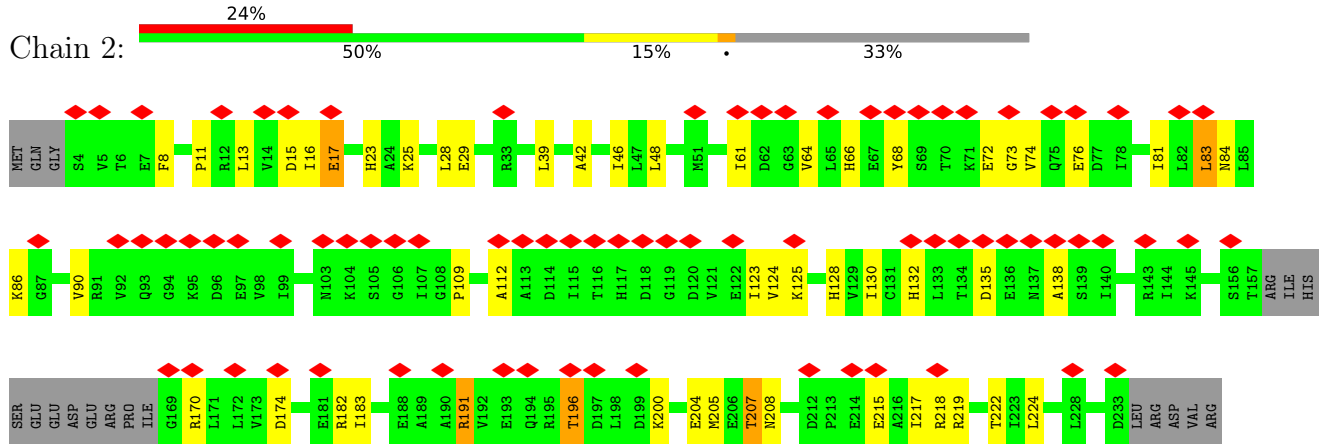
Chain Z:



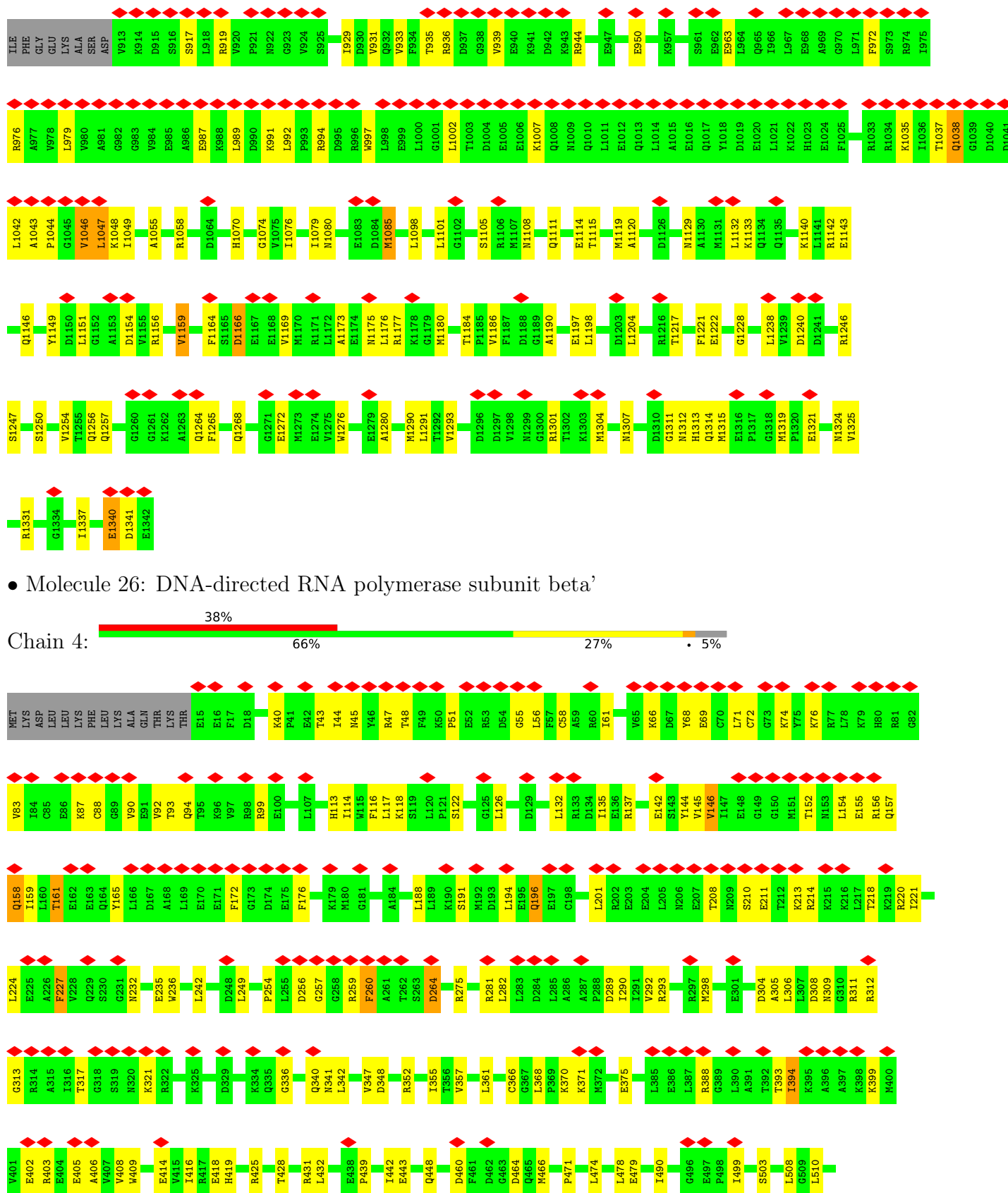
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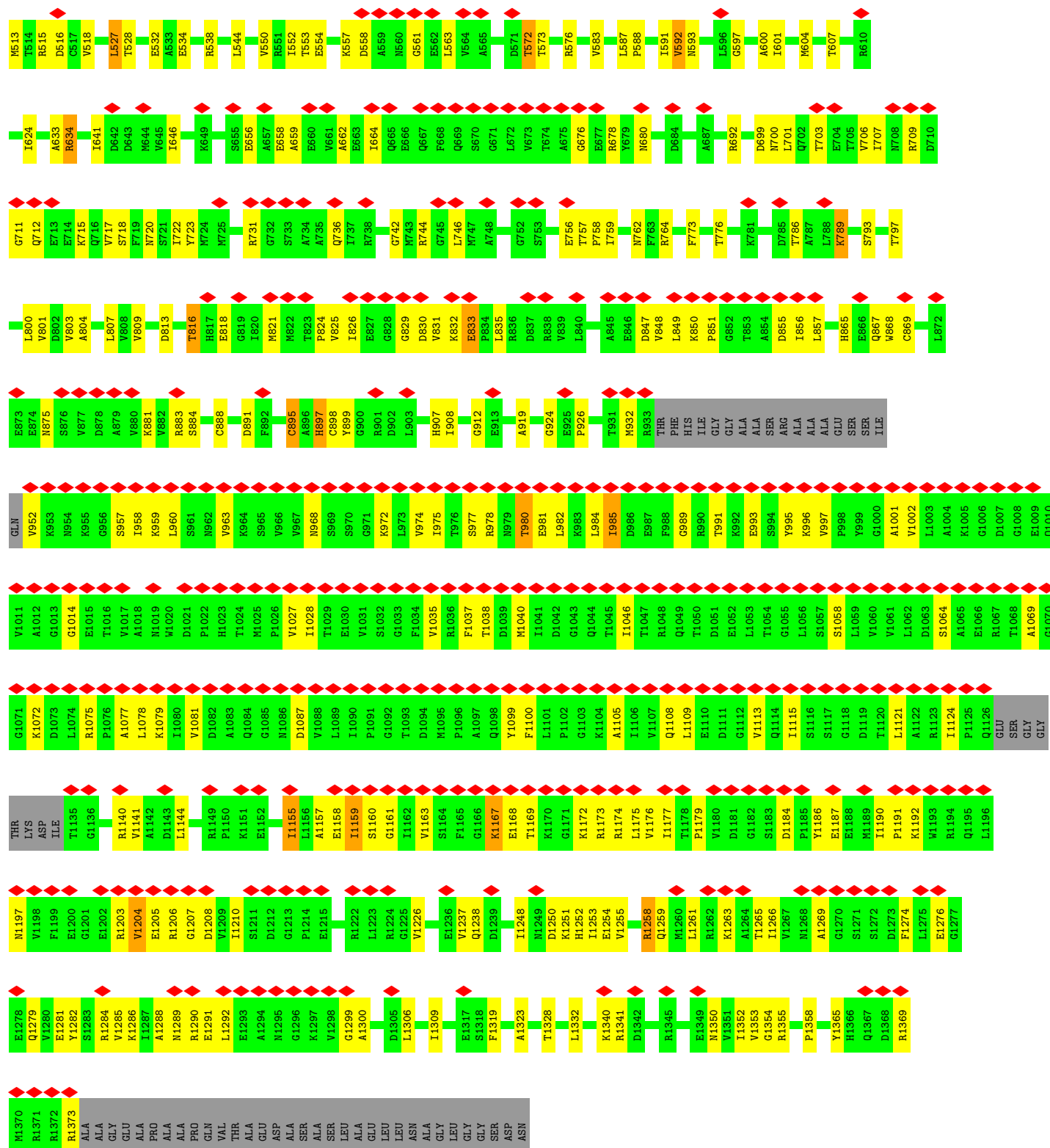


Chain 2:

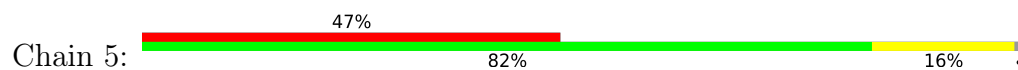


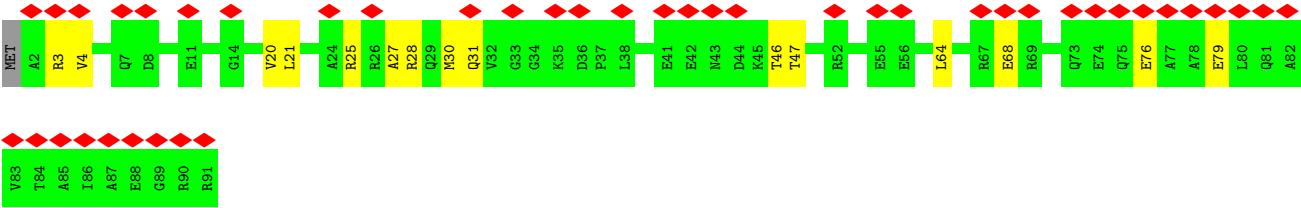




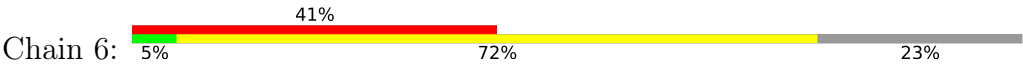


• Molecule 27: DNA-directed RNA polymerase subunit omega





● Molecule 28: Non-Template DNA strand



● Molecule 29: Template DNA strand



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20703	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.95	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	2.717	Depositor
Minimum map value	-0.250	Depositor
Average map value	0.042	Depositor
Map value standard deviation	0.079	Depositor
Recommended contour level	0.411	Depositor
Map size (Å)	503.99997, 503.99997, 503.99997	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, MA6, D2T, G7M, 5MC, PSU, ZN, 2MG

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	0.22	1/36460 (0.0%)	0.35	1/56869 (0.0%)
2	B	0.13	0/1354	0.30	0/1826
3	C	0.16	0/1784	0.36	0/2403
4	D	0.20	0/1682	0.41	2/2266 (0.1%)
5	E	0.20	0/1669	0.34	0/2233
6	F	0.16	0/1169	0.32	0/1573
7	G	0.17	0/881	0.40	0/1189
8	H	0.16	0/1219	0.35	0/1635
9	I	0.15	0/989	0.34	0/1326
10	J	0.18	0/1043	0.37	0/1387
11	K	0.20	0/818	0.37	0/1105
12	L	0.29	0/893	0.58	2/1205 (0.2%)
13	M	0.17	0/960	0.37	0/1286
14	N	0.17	0/900	0.35	0/1204
15	O	0.18	0/817	0.30	0/1088
16	P	0.16	0/722	0.33	0/964
17	Q	0.17	0/659	0.39	0/884
18	R	0.14	0/657	0.35	0/881
19	S	0.14	0/544	0.28	0/731
20	T	0.17	0/680	0.32	0/915
21	U	0.18	0/676	0.35	0/895
22	X	0.23	0/536	0.39	0/834
23	Z	0.25	0/1251	0.52	3/1686 (0.2%)
24	1	0.17	0/1797	0.32	0/2436
24	2	0.14	0/1703	0.29	0/2308
25	3	0.15	0/10581	0.30	0/14275
26	4	0.15	0/10532	0.29	0/14219
27	5	0.17	0/711	0.33	0/956
28	6	0.71	0/693	1.02	1/1068 (0.1%)
29	7	0.69	0/676	0.97	0/1039
All	All	0.21	1/85056 (0.0%)	0.36	9/122686 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	1
12	L	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	G7M	O3'-P	5.21	1.61	1.56

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	Z	164	ILE	CA-C-N	6.46	133.88	121.54
23	Z	164	ILE	C-N-CA	6.46	133.88	121.54
1	A	563	A	C4'-C3'-O3'	-6.35	103.47	113.00
28	6	28	DA	C2'-C3'-O3'	-6.35	101.98	111.50
4	D	137	THR	CA-CB-OG1	-5.99	100.62	109.60
23	Z	65	PHE	CB-CA-C	5.32	115.75	110.33
12	L	90	GLY	CA-C-N	5.23	126.38	119.84
12	L	90	GLY	C-N-CA	5.23	126.38	119.84
4	D	138	VAL	N-CA-C	-5.04	105.80	110.53

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	136	ARG	Sidechain
12	L	90	GLY	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	32750	0	16497	693	0
2	B	1339	0	1364	31	0
3	C	1753	0	1780	29	0
4	D	1655	0	1729	39	0
5	E	1647	0	1708	40	0
6	F	1156	0	1199	19	0
7	G	862	0	864	21	0
8	H	1203	0	1254	25	0
9	I	979	0	1031	14	0
10	J	1031	0	1076	35	0
11	K	808	0	845	35	0
12	L	877	0	887	40	0
13	M	957	0	1017	18	0
14	N	891	0	952	23	0
15	O	805	0	844	16	0
16	P	714	0	734	5	0
17	Q	649	0	666	6	0
18	R	648	0	691	14	0
19	S	535	0	552	8	0
20	T	663	0	688	15	0
21	U	670	0	719	14	0
22	X	480	0	245	14	0
23	Z	1225	0	1203	48	0
24	1	1775	0	1800	30	0
24	2	1684	0	1713	33	0
25	3	10415	0	10432	208	0
26	4	10375	0	10596	246	0
27	5	709	0	719	13	0
28	6	618	0	339	45	0
29	7	606	0	338	23	0
30	A	116	0	0	0	0
30	L	1	0	0	0	0
30	X	1	0	0	0	0
31	4	2	0	0	0	0
31	C	1	0	0	0	0
All	All	80600	0	64482	1665	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 12.

All (1665) 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)
12:L:86:VAL:CG2	12:L:93:ARG:NH2	2.08	1.17
11:K:84:VAL:HG11	23:Z:140:PRO:CB	1.76	1.15
11:K:84:VAL:HG11	23:Z:140:PRO:HB3	1.33	1.09
1:A:925:G:C8	1:A:925:G:H5''	1.86	1.09
12:L:86:VAL:HG21	12:L:93:ARG:NH2	1.67	1.04
12:L:86:VAL:CG2	12:L:93:ARG:HH22	1.72	0.98
1:A:1516:2MG:H2'	1:A:1517:G:H3'	1.46	0.95
1:A:927:G:H1'	1:A:1392:G:H1'	1.50	0.94
12:L:93:ARG:HB3	12:L:93:ARG:CZ	1.97	0.92
28:6:23:DT:C6	28:6:23:DT:H5''	2.07	0.89
11:K:84:VAL:HG11	23:Z:140:PRO:HB2	1.51	0.89
28:6:29:DG:H1'	28:6:30:DA:H5'	1.53	0.89
1:A:1419:G:H1	1:A:1481:U:H3	1.16	0.87
1:A:966:2MG:H5''	1:A:966:2MG:C8	2.11	0.86
1:A:664:G:H22	1:A:741:G:H1	1.24	0.84
1:A:1239:A:H62	1:A:1299:A:H62	1.24	0.84
10:J:88:MET:HE2	10:J:95:ARG:HG2	1.59	0.84
1:A:1400:C:H4'	1:A:1517:G:H1	1.44	0.83
11:K:88:MET:HE3	23:Z:141:PHE:CD1	2.14	0.82
23:Z:167:ARG:HB2	23:Z:167:ARG:CZ	2.08	0.82
26:4:888:CYS:HB2	26:4:898:CYS:SG	2.18	0.82
1:A:859:G:H2'	1:A:860:A:H8	1.45	0.81
12:L:86:VAL:HG22	12:L:93:ARG:NH2	1.95	0.81
26:4:69:GLU:HG3	26:4:76:LYS:HG2	1.63	0.80
1:A:1518:MA6:H102	1:A:1519:MA6:H103	1.62	0.80
1:A:1489:G:OP1	1:A:1489:G:H4'	1.81	0.80
4:D:120:ILE:HD11	4:D:137:THR:HG21	1.62	0.80
25:3:1042:LEU:HB3	25:3:1046:VAL:HG13	1.62	0.80
26:4:137:ARG:HG3	26:4:142:GLU:HB2	1.63	0.79
26:4:275:ARG:HH11	26:4:298:MET:HB3	1.47	0.79
1:A:967:5MC:OP2	1:A:967:5MC:H6	1.66	0.78
26:4:1179:PRO:HD2	26:4:1184:ASP:HA	1.65	0.78
1:A:705:G:H21	12:L:31:ILE:HD11	1.48	0.78
12:L:86:VAL:HG22	12:L:93:ARG:HH22	1.46	0.78
12:L:90:GLY:C	12:L:92:GLY:H	1.91	0.78
1:A:79:G:H2'	1:A:80:A:C8	2.19	0.78
26:4:1350:ASN:HD22	26:4:1358:PRO:HD3	1.48	0.78
1:A:787:A:N3	1:A:787:A:H2'	1.96	0.77
15:O:41:ARG:NH2	20:T:6:LYS:O	2.17	0.77
1:A:152:A:N6	1:A:169:C:O2	2.17	0.77
26:4:211:GLU:HA	26:4:214:ARG:HB2	1.68	0.76
7:G:12:PRO:HD2	7:G:54:LEU:HD21	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:G:O6	1:A:86:G:N2	2.19	0.76
1:A:537:G:OP1	13:M:110:ARG:NH2	2.19	0.76
29:7:3:DC:OP2	29:7:3:DC:H2'	1.85	0.75
1:A:458:U:H6	1:A:458:U:H5''	1.51	0.75
1:A:1489:G:H5''	1:A:1489:G:H8	1.50	0.75
23:Z:41:GLU:H	23:Z:72:GLN:HB3	1.51	0.75
24:1:43:LEU:HD13	24:1:217:ILE:HD11	1.69	0.74
25:3:21:VAL:HG11	25:3:592:ARG:HD2	1.69	0.74
1:A:713:G:H2'	1:A:714:G:C8	2.21	0.74
1:A:966:2MG:H5''	1:A:966:2MG:H8	1.49	0.74
1:A:1377:A:OP1	8:H:92:ARG:NH2	2.21	0.74
1:A:927:G:C8	1:A:927:G:H5''	2.23	0.74
14:N:14:HIS:ND1	14:N:42:ASP:O	2.20	0.73
1:A:113:G:H1'	1:A:354:G:H5'	1.70	0.73
1:A:789:U:H6	1:A:789:U:H5''	1.54	0.73
28:6:33:DT:H2''	28:6:34:DT:H5''	1.71	0.73
25:3:272:ARG:HA	25:3:275:ARG:HD2	1.70	0.73
1:A:1479:C:C5'	1:A:1479:C:H6	2.02	0.72
25:3:1314:GLN:HB2	27:5:28:ARG:HH12	1.54	0.72
28:6:26:DG:H1'	28:6:27:DA:H5'	1.69	0.72
12:L:23:ILE:HG21	12:L:96:THR:HG21	1.71	0.72
25:3:1246:ARG:NH1	25:3:1265:PHE:O	2.22	0.72
1:A:1391:U:O2	1:A:1391:U:H2'	1.87	0.72
25:3:732:ILE:HD11	25:3:769:PRO:HB3	1.70	0.72
1:A:458:U:H5''	1:A:458:U:C6	2.24	0.71
26:4:194:LEU:HD21	26:4:227:PHE:HB3	1.72	0.71
1:A:1381:U:O2'	8:H:79:ARG:O	2.08	0.71
12:L:86:VAL:HG21	12:L:93:ARG:HH22	1.36	0.71
25:3:423:ASP:OD1	25:3:423:ASP:N	2.22	0.71
1:A:1479:C:H6	1:A:1479:C:H5''	1.55	0.71
1:A:676:A:H5''	12:L:115:PRO:HB3	1.72	0.71
22:X:6:G:H5'	22:X:6:G:H8	1.54	0.71
8:H:54:SER:OG	8:H:56:LYS:NZ	2.23	0.71
1:A:736:C:OP1	19:S:61:ARG:NH1	2.23	0.71
1:A:791:G:H8	1:A:791:G:H3'	1.55	0.71
28:6:38:DA:H2'	28:6:38:DA:OP2	1.90	0.71
1:A:1522:U:H2'	1:A:1523:G:H8	1.54	0.70
29:7:3:DC:H2''	29:7:4:DT:C6	2.26	0.70
26:4:155:GLU:HB2	26:4:158:GLN:HB2	1.74	0.70
29:7:8:DT:OP2	29:7:8:DT:H6	1.75	0.70
8:H:69:VAL:HG21	8:H:104:ILE:HD11	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1489:G:H2'	1:A:1490:U:H6	1.57	0.69
25:3:1331:ARG:NH2	25:3:1337:ILE:O	2.24	0.69
1:A:1029:U:O2'	1:A:1032:G:O6	2.10	0.69
1:A:1346:A:H2'	8:H:10:ARG:HH21	1.55	0.69
1:A:790:A:H3'	1:A:790:A:N3	2.08	0.69
26:4:122:SER:HB2	26:4:132:LEU:HD12	1.75	0.69
1:A:1005:A:OP2	1:A:1024:G:N2	2.24	0.69
6:F:45:ARG:NH1	6:F:71:MET:SD	2.66	0.69
11:K:84:VAL:CG1	23:Z:140:PRO:HB2	2.23	0.69
26:4:849:LEU:HA	26:4:856:ILE:HA	1.75	0.69
25:3:936:ARG:NH1	25:3:1042:LEU:O	2.26	0.69
26:4:664:ILE:HG22	26:4:678:ARG:HG2	1.75	0.69
1:A:1491:G:H21	1:A:1492:A:H62	1.41	0.68
5:E:192:SER:OG	5:E:194:ASP:OD1	2.12	0.68
1:A:501:C:OP1	13:M:114:ARG:NH2	2.26	0.68
8:H:93:PRO:HA	8:H:96:ARG:HD2	1.75	0.68
25:3:1002:LEU:HD21	25:3:1007:LYS:HB2	1.76	0.68
1:A:1400:C:H4'	1:A:1517:G:N1	2.08	0.68
1:A:21:G:H2'	1:A:22:G:C8	2.28	0.68
1:A:90:C:H2'	1:A:90:C:OP2	1.94	0.68
4:D:40:ARG:NH1	4:D:55:ILE:O	2.27	0.68
1:A:356:A:N3	1:A:368:U:O2'	2.27	0.68
1:A:1491:G:H21	1:A:1492:A:N6	1.91	0.68
1:A:1140:C:HO2'	1:A:1141:C:H6	1.42	0.67
1:A:421:U:H5''	1:A:422:C:H5	1.59	0.67
25:3:758:ARG:NH2	25:3:762:ASN:OD1	2.28	0.67
26:4:826:ILE:HG12	26:4:831:VAL:HG12	1.75	0.67
26:4:807:LEU:HD12	26:4:1255:VAL:HG13	1.75	0.67
1:A:855:U:H2'	1:A:856:C:H6	1.58	0.67
25:3:678:ARG:NH1	25:3:681:MET:SD	2.67	0.67
18:R:19:LYS:H	18:R:51:ASN:HD21	1.42	0.67
1:A:745:G:H2'	1:A:746:A:H8	1.60	0.67
4:D:123:GLN:HB3	4:D:128:VAL:HG11	1.77	0.67
24:2:191:ARG:HB3	24:2:196:THR:HG23	1.77	0.67
26:4:254:PRO:HA	26:4:260:PHE:HA	1.76	0.67
1:A:859:G:H2'	1:A:860:A:C8	2.28	0.67
7:G:29:ILE:HG22	7:G:34:GLY:HA3	1.76	0.67
1:A:744:C:H2'	1:A:745:G:H8	1.59	0.66
10:J:57:MET:HA	10:J:60:LYS:HE3	1.76	0.66
10:J:118:LEU:HD22	10:J:124:ARG:HG2	1.77	0.66
28:6:32:DA:H1'	28:6:33:DT:H5'	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:7:3:DC:OP2	29:7:3:DC:H6	1.78	0.66
2:B:3:GLU:OE1	3:C:7:ARG:NH2	2.28	0.66
25:3:1166:ASP:HA	25:3:1169:VAL:HB	1.76	0.66
1:A:946:A:H2'	1:A:947:G:H8	1.61	0.66
25:3:1321:GLU:OE2	26:4:99:ARG:NH1	2.29	0.66
28:6:39:DG:H4'	28:6:39:DG:OP1	1.94	0.66
26:4:975:ILE:HG22	26:4:977:SER:H	1.60	0.66
26:4:984:LEU:HB2	26:4:993:GLU:HB2	1.77	0.66
29:7:5:DG:O5'	29:7:5:DG:H8	1.79	0.66
1:A:1478:U:H2'	1:A:1479:C:C6	2.31	0.66
25:3:342:ASP:O	25:3:437:ASN:ND2	2.29	0.66
25:3:230:PHE:HB2	25:3:333:ILE:HG22	1.78	0.65
7:G:45:ARG:O	7:G:56:LYS:HA	1.96	0.65
1:A:927:G:C1'	1:A:1392:G:H1'	2.25	0.65
10:J:39:PHE:O	10:J:45:ARG:NH1	2.29	0.65
25:3:300:ASP:OD1	25:3:313:ALA:N	2.28	0.65
23:Z:13:GLN:HG3	23:Z:93:ILE:HD11	1.79	0.65
26:4:975:ILE:HD13	26:4:980:THR:HG21	1.77	0.65
1:A:492:C:H2'	1:A:493:A:C8	2.31	0.65
1:A:1489:G:H2'	1:A:1490:U:C6	2.32	0.65
12:L:66:ALA:HA	12:L:69:ARG:HD2	1.77	0.65
1:A:1414:U:HO2'	1:A:1415:G:H8	1.44	0.65
6:F:166:GLY:O	9:I:114:ARG:NH2	2.29	0.65
1:A:380:G:N2	1:A:383:A:OP2	2.30	0.65
6:F:13:GLU:HB3	6:F:39:VAL:HG12	1.79	0.65
11:K:88:MET:HE3	23:Z:141:PHE:CE1	2.31	0.65
11:K:88:MET:CE	23:Z:141:PHE:CD1	2.79	0.64
26:4:830:ASP:O	26:4:832:LYS:NZ	2.30	0.64
3:C:97:LEU:H	3:C:100:MET:HE3	1.63	0.64
12:L:93:ARG:HB3	12:L:93:ARG:NH1	2.11	0.64
25:3:1080:ASN:HD22	25:3:1085:MET:HE3	1.62	0.64
1:A:34:C:H2'	1:A:35:G:H8	1.62	0.64
1:A:1038:C:H2'	1:A:1039:G:C8	2.33	0.64
2:B:28:VAL:HG22	2:B:38:VAL:HG22	1.78	0.64
1:A:1415:G:H2'	1:A:1416:G:O4'	1.97	0.64
28:6:13:DC:H2'	28:6:14:DT:C2	2.32	0.64
1:A:1081:A:OP2	6:F:52:LYS:NZ	2.31	0.64
18:R:46:VAL:HG11	18:R:61:ILE:HD12	1.77	0.64
1:A:1518:MA6:H2'	1:A:1519:MA6:C8	2.27	0.64
1:A:362:G:N2	1:A:365:U:OP2	2.29	0.64
1:A:1389:C:H2'	1:A:1390:U:O4'	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:85:ASN:O	5:E:89:ASN:ND2	2.31	0.64
13:M:8:VAL:HG12	18:R:34:TYR:HD2	1.62	0.64
25:3:1105:SER:HB2	26:4:731:ARG:HB3	1.80	0.64
26:4:601:ILE:O	26:4:604:MET:HB3	1.98	0.63
1:A:147:G:H2'	1:A:148:G:C8	2.33	0.63
23:Z:167:ARG:HB2	23:Z:167:ARG:NH1	2.12	0.63
1:A:126:G:OP1	1:A:605:U:O2'	2.16	0.63
1:A:728:A:H2'	1:A:729:A:H8	1.62	0.63
1:A:791:G:H3'	1:A:791:G:C8	2.32	0.63
1:A:855:U:H2'	1:A:856:C:C6	2.33	0.63
9:I:11:LEU:HD22	9:I:75:ILE:HD11	1.79	0.63
14:N:90:ARG:HB2	14:N:97:VAL:HG23	1.81	0.63
25:3:1108:ASN:OD1	25:3:1111:GLN:NE2	2.31	0.63
26:4:210:SER:O	26:4:214:ARG:N	2.28	0.63
1:A:992:U:H4'	1:A:993:G:H5''	1.79	0.63
25:3:742:TYR:HB2	25:3:745:GLU:HB2	1.81	0.63
1:A:1422:G:H2'	1:A:1423:G:H8	1.61	0.63
26:4:957:SER:HB3	26:4:985:ILE:HG23	1.79	0.63
1:A:1518:MA6:H2'	1:A:1519:MA6:H8	1.81	0.63
10:J:84:THR:HG23	10:J:98:LEU:HD13	1.81	0.63
25:3:565:GLU:HG2	25:3:680:LEU:HD21	1.79	0.63
26:4:959:LYS:NZ	26:4:960:LEU:O	2.32	0.63
1:A:203:G:H1'	1:A:465:A:H61	1.64	0.63
1:A:398:U:H2'	1:A:399:G:H8	1.64	0.63
7:G:1:MET:HG3	7:G:65:GLU:HG2	1.80	0.63
26:4:527:LEU:HB2	26:4:550:VAL:HG12	1.80	0.63
26:4:1158:GLU:HG3	26:4:1159:ILE:HG13	1.81	0.63
25:3:617:ALA:HB2	25:3:650:VAL:HG21	1.81	0.62
25:3:935:THR:HG23	25:3:1048:LYS:HB2	1.81	0.62
1:A:843:U:H2'	1:A:844:G:C8	2.33	0.62
24:2:17:GLU:HB3	24:2:25:LYS:HB3	1.81	0.62
25:3:1119:MET:HG3	25:3:1204:LEU:HD13	1.81	0.62
1:A:993:G:H2'	1:A:993:G:N3	2.13	0.62
25:3:1070:HIS:NE2	25:3:1114:GLU:OE1	2.31	0.62
28:6:36:DA:P	28:6:36:DA:H2'	2.40	0.62
26:4:1058:SER:OG	26:4:1108:GLN:NE2	2.32	0.62
1:A:1485:U:H2'	1:A:1486:G:C8	2.34	0.62
9:I:64:LYS:HE2	9:I:71:VAL:HG21	1.82	0.62
25:3:301:TYR:HB3	25:3:330:HIS:CD2	2.35	0.62
25:3:458:GLU:O	25:3:462:ASN:ND2	2.32	0.62
25:3:1222:GLU:HG3	26:4:634:ARG:HH21	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:81:ASN:HD22	12:L:106:ARG:HB3	1.65	0.62
26:4:865:HIS:HD2	26:4:867:GLN:H	1.47	0.62
26:4:975:ILE:HD12	26:4:1001:ALA:HB3	1.82	0.62
28:6:10:DG:H2''	28:6:11:DT:C6	2.34	0.62
1:A:946:A:H2'	1:A:947:G:C8	2.34	0.62
28:6:22:DT:O2	28:6:22:DT:H3'	2.00	0.62
29:7:10:DT:OP2	29:7:10:DT:H73	2.00	0.62
24:2:109:PRO:HA	24:2:132:HIS:HA	1.82	0.62
26:4:1077:ALA:HA	26:4:1100:PHE:HA	1.82	0.62
1:A:1400:C:C4'	1:A:1517:G:H1	2.11	0.62
25:3:197:ARG:HD3	25:3:200:ARG:HA	1.82	0.62
1:A:1083:U:O2'	1:A:1102:A:OP2	2.18	0.61
4:D:110:GLU:HB2	4:D:144:LEU:HD12	1.81	0.61
8:H:135:VAL:O	8:H:139:GLU:HG2	1.99	0.61
20:T:19:VAL:HG11	20:T:44:MET:HG2	1.81	0.61
25:3:201:ARG:NH1	25:3:370:MET:O	2.33	0.61
26:4:1155:ILE:HG13	26:4:1210:ILE:HB	1.82	0.61
1:A:968:A:H8	1:A:968:A:OP1	1.83	0.61
1:A:1250:A:H2'	1:A:1251:A:C8	2.35	0.61
26:4:720:ASN:HD22	26:4:723:TYR:H	1.46	0.61
1:A:745:G:H2'	1:A:746:A:C8	2.34	0.61
4:D:77:ILE:HA	4:D:84:VAL:HG23	1.81	0.61
13:M:46:ASN:ND2	13:M:89:D2T:SB	2.73	0.61
24:1:13:LEU:H	24:1:13:LEU:HD23	1.64	0.61
1:A:1363:A:O2'	1:A:1365:G:N7	2.28	0.61
10:J:21:ILE:HD13	10:J:63:LEU:HB3	1.83	0.61
25:3:848:GLU:HG2	25:3:888:THR:HA	1.83	0.61
26:4:1157:ALA:O	26:4:1207:GLY:N	2.31	0.61
1:A:890:G:O2'	1:A:906:A:N6	2.34	0.61
1:A:683:G:H1	1:A:707:U:H3	1.47	0.61
1:A:71:A:HO2'	1:A:72:A:H8	1.49	0.61
26:4:402:GLU:OE1	26:4:403:ARG:NH1	2.31	0.61
25:3:1314:GLN:OE1	27:5:28:ARG:NH1	2.34	0.61
26:4:72:CYS:HB2	26:4:87:LYS:HD3	1.82	0.61
1:A:1367:C:OP2	10:J:114:LYS:NZ	2.34	0.61
26:4:797:THR:HG22	26:4:924:GLY:HA3	1.82	0.61
1:A:876:C:H2'	1:A:877:G:H8	1.66	0.60
25:3:862:LEU:HD23	25:3:865:LEU:HD12	1.82	0.60
26:4:1027:VAL:HG13	26:4:1121:LEU:HB2	1.84	0.60
5:E:194:ASP:OD1	5:E:194:ASP:N	2.33	0.60
6:F:105:ILE:O	6:F:112:ARG:NH2	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:4:SER:O	25:3:8:LYS:N	2.33	0.60
25:3:13:LYS:NZ	25:3:1149:TYR:O	2.28	0.60
1:A:1291:U:H2'	1:A:1292:G:H8	1.65	0.60
1:A:1479:C:H2'	1:A:1480:A:H8	1.66	0.60
25:3:890:LYS:HB2	25:3:890:LYS:HZ2	1.66	0.60
1:A:337:G:H2'	1:A:338:A:C8	2.35	0.60
1:A:750:C:O3'	16:P:17:ARG:NH2	2.32	0.60
22:X:7:G:H2'	22:X:8:A:C8	2.37	0.60
1:A:51:A:N7	1:A:114:U:O2'	2.35	0.60
1:A:789:U:H2'	1:A:790:A:H5''	1.83	0.60
1:A:1479:C:H2'	1:A:1480:A:C8	2.37	0.60
1:A:1489:G:H8	1:A:1489:G:C5'	2.14	0.60
25:3:1058:ARG:HE	25:3:1238:LEU:HD11	1.66	0.60
27:5:25:ARG:HD3	27:5:64:LEU:HD13	1.84	0.60
1:A:93:U:H6	1:A:93:U:O5'	1.85	0.60
22:X:49:G:O2'	25:3:513:GLN:OE1	2.18	0.60
1:A:1038:C:H2'	1:A:1039:G:H8	1.67	0.60
1:A:93:U:H2'	1:A:95:C:C5	2.37	0.60
1:A:1360:A:OP2	15:O:75:ARG:NH2	2.32	0.60
22:X:50:C:OP2	25:3:540:ARG:NH2	2.35	0.60
1:A:390:U:H2'	1:A:391:G:H8	1.66	0.60
1:A:925:G:H5''	1:A:925:G:N9	2.13	0.60
1:A:728:A:H2'	1:A:729:A:C8	2.37	0.60
1:A:1071:C:H2'	1:A:1072:G:H8	1.65	0.60
1:A:1428:A:H2'	1:A:1429:A:C8	2.37	0.60
25:3:444:ASP:O	25:3:450:ASN:ND2	2.34	0.60
4:D:20:SER:OG	4:D:22:TRP:NE1	2.35	0.59
8:H:28:ASN:HA	8:H:31:MET:HE3	1.84	0.59
26:4:1037:PHE:HB3	26:4:1040:MET:HB2	1.84	0.59
1:A:235:C:H2'	1:A:236:A:H8	1.65	0.59
1:A:791:G:C8	1:A:791:G:C3'	2.84	0.59
24:2:182:ARG:NH1	24:2:204:GLU:OE2	2.35	0.59
11:K:84:VAL:CG1	23:Z:140:PRO:CB	2.68	0.59
25:3:10:ARG:HH11	25:3:791:LEU:HD12	1.67	0.59
25:3:320:ASP:OD1	25:3:320:ASP:N	2.31	0.59
26:4:1177:ILE:HB	26:4:1186:TYR:HD2	1.67	0.59
28:6:19:DA:H2'	28:6:19:DA:N3	2.16	0.59
1:A:787:A:OP2	1:A:787:A:C8	2.56	0.59
10:J:54:LEU:HD23	10:J:98:LEU:HD23	1.85	0.59
26:4:146:VAL:HG11	26:4:154:LEU:HB3	1.84	0.59
26:4:1289:ASN:ND2	26:4:1300:ALA:O	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1011:C:H2'	1:A:1012:A:H8	1.68	0.59
10:J:55:VAL:HG13	10:J:57:MET:H	1.66	0.59
26:4:1078:LEU:N	26:4:1099:TYR:O	2.34	0.59
1:A:1130:A:H2'	1:A:1131:G:H8	1.67	0.59
15:O:10:GLU:HG3	15:O:63:ARG:HD2	1.84	0.59
1:A:1464:U:H2'	1:A:1465:A:H8	1.68	0.59
1:A:865:A:O5'	1:A:865:A:H8	1.85	0.58
11:K:80:THR:HB	11:K:83:THR:HG23	1.85	0.58
12:L:84:VAL:HG23	12:L:110:ILE:HA	1.85	0.58
23:Z:45:PRO:HB2	23:Z:64:PHE:CD2	2.37	0.58
29:7:20:DC:H2'	29:7:21:DG:C8	2.39	0.58
1:A:1356:G:H2'	1:A:1357:A:C8	2.38	0.58
1:A:1428:A:H2'	1:A:1429:A:H8	1.69	0.58
3:C:12:ALA:O	3:C:208:ARG:NE	2.34	0.58
7:G:72:ASP:O	7:G:75:GLU:HG3	2.03	0.58
1:A:999:C:H2'	1:A:1000:A:C8	2.39	0.58
1:A:1537:U:H2'	1:A:1538:C:C6	2.38	0.58
2:B:43:LYS:HB3	2:B:82:THR:HG23	1.86	0.58
6:F:79:GLY:O	6:F:121:HIS:N	2.35	0.58
26:4:388:ARG:NH2	26:4:414:GLU:OE1	2.37	0.58
1:A:754:C:OP1	16:P:72:ARG:NH2	2.36	0.58
1:A:1521:C:H2'	1:A:1522:U:C6	2.38	0.58
26:4:479:GLU:HG3	27:5:20:VAL:HG11	1.85	0.58
1:A:216:U:H2'	1:A:217:C:C6	2.38	0.58
1:A:410:G:OP2	5:E:31:LYS:NZ	2.37	0.58
1:A:787:A:H61	1:A:795:C:H42	1.50	0.58
26:4:256:ASP:O	26:4:259:ARG:NH2	2.35	0.58
1:A:639:G:C2	1:A:640:A:C8	2.92	0.58
1:A:976:G:OP2	1:A:1358:U:O2'	2.21	0.58
1:A:1477:U:H2'	1:A:1478:U:C6	2.39	0.58
4:D:155:GLY:HA2	4:D:163:ALA:HB1	1.85	0.58
5:E:197:GLU:N	5:E:197:GLU:OE1	2.37	0.58
23:Z:14:ALA:HB1	23:Z:22:VAL:HG21	1.86	0.58
23:Z:87:PRO:HA	28:6:19:DA:H8	1.67	0.58
25:3:699:LEU:HG	25:3:799:ASN:HD22	1.68	0.58
26:4:804:ALA:HA	26:4:1259:GLN:HE21	1.67	0.58
1:A:563:A:N3	1:A:563:A:H2'	2.18	0.58
3:C:58:ASN:ND2	3:C:223:GLU:OE1	2.30	0.58
25:3:119:GLU:HG2	25:3:122:VAL:HB	1.86	0.58
25:3:538:LEU:HB3	28:6:25:DG:H1'	1.85	0.58
26:4:1064:SER:OG	26:4:1075:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:6:30:DA:H2''	28:6:31:DG:H5''	1.86	0.58
14:N:17:ILE:HG13	14:N:27:LYS:HE3	1.86	0.58
25:3:247:ARG:HH21	25:3:274:ILE:HD12	1.69	0.58
26:4:604:MET:O	26:4:607:THR:OG1	2.20	0.58
26:4:1281:GLU:HG2	26:4:1284:ARG:HB3	1.85	0.58
1:A:309:A:H2'	1:A:310:G:H8	1.66	0.58
1:A:692:U:O2'	1:A:694:A:N7	2.30	0.58
23:Z:150:GLU:HG3	23:Z:159:LYS:HB3	1.86	0.58
1:A:405:U:O4	5:E:2:ALA:N	2.37	0.57
4:D:143:ARG:HH21	4:D:144:LEU:HG	1.68	0.57
11:K:32:THR:O	11:K:82:LYS:NZ	2.36	0.57
25:3:520:PRO:HG3	25:3:714:VAL:HG11	1.86	0.57
26:4:114:ILE:HG13	26:4:304:ASP:HA	1.85	0.57
1:A:739:C:OP2	7:G:2:ARG:NH2	2.36	0.57
3:C:127:ASP:OD1	3:C:127:ASP:N	2.30	0.57
26:4:891:ASP:OD1	26:4:1286:LYS:NZ	2.37	0.57
1:A:932:C:H2'	1:A:933:G:C8	2.38	0.57
1:A:944:G:N1	1:A:1338:G:OP2	2.35	0.57
1:A:1168:U:O4	3:C:74:ARG:NH1	2.38	0.57
25:3:243:PRO:HB2	25:3:274:ILE:HG23	1.86	0.57
26:4:513:MET:HG3	26:4:544:LEU:HD21	1.86	0.57
1:A:1077:G:N2	1:A:1080:A:OP2	2.30	0.57
24:1:180:VAL:HB	24:1:183:ILE:HD11	1.86	0.57
26:4:474:LEU:HD21	27:5:27:ALA:HB3	1.85	0.57
1:A:1392:G:H4'	1:A:1392:G:OP1	2.03	0.57
25:3:196:VAL:HG11	25:3:209:ILE:HD11	1.86	0.57
26:4:416:ILE:HG12	26:4:439:PRO:HG2	1.87	0.57
1:A:1314:C:H2'	1:A:1315:U:C6	2.39	0.57
11:K:28:THR:HG23	11:K:31:ARG:HH21	1.68	0.57
14:N:33:ILE:HG23	14:N:59:GLU:HB2	1.86	0.57
1:A:4:U:H2'	1:A:5:U:H2'	1.87	0.57
1:A:575:G:H4'	1:A:576:C:H5''	1.86	0.57
1:A:791:G:C8	1:A:791:G:H5''	2.40	0.57
1:A:1004:A:H2'	1:A:1005:A:O4'	2.04	0.57
24:2:205:MET:HE1	24:2:217:ILE:HB	1.87	0.57
25:3:976:ARG:HG3	25:3:989:LEU:HD21	1.87	0.57
1:A:79:G:H21	1:A:90:C:H41	1.52	0.57
18:R:60:GLU:OE1	18:R:77:ARG:NH2	2.38	0.57
24:2:72:GLU:OE1	24:2:73:GLY:N	2.37	0.57
25:3:1256:GLN:HB3	25:3:1301:ARG:HH22	1.70	0.57
26:4:43:THR:HG22	26:4:56:LEU:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:C:H2'	1:A:223:A:H8	1.69	0.56
1:A:517:G:N1	1:A:533:A:OP1	2.35	0.56
1:A:748:G:H2'	1:A:749:A:C8	2.40	0.56
10:J:65:ILE:HG21	10:J:79:ILE:HG12	1.86	0.56
21:U:48:GLN:O	21:U:52:ASN:ND2	2.38	0.56
25:3:406:ASN:ND2	25:3:413:GLU:O	2.38	0.56
25:3:1058:ARG:NH2	25:3:1240:ASP:OD1	2.36	0.56
26:4:419:HIS:NE2	26:4:471:PRO:O	2.30	0.56
29:7:20:DC:H4'	29:7:20:DC:OP1	2.05	0.56
1:A:17:U:H2'	1:A:18:C:C6	2.40	0.56
1:A:552:U:H2'	1:A:553:A:H8	1.69	0.56
1:A:714:G:H2'	1:A:715:A:C8	2.39	0.56
12:L:17:SER:HA	12:L:80:LYS:H	1.69	0.56
25:3:705:GLU:HB3	25:3:794:LEU:H	1.70	0.56
1:A:674:G:N2	1:A:717:U:O2	2.34	0.56
1:A:841:C:H42	1:A:845:A:H62	1.53	0.56
1:A:925:G:H4'	1:A:926:G:OP1	2.04	0.56
1:A:999:C:H2'	1:A:1000:A:H8	1.69	0.56
7:G:43:GLY:HA2	7:G:58:HIS:CE1	2.39	0.56
20:T:50:ALA:HB1	20:T:57:HIS:HB3	1.87	0.56
21:U:28:MET:HE1	21:U:67:ILE:HG21	1.87	0.56
26:4:746:LEU:HD23	26:4:758:PRO:HB3	1.87	0.56
1:A:912:C:H2'	1:A:913:A:C8	2.40	0.56
1:A:553:A:H2'	1:A:554:A:H8	1.69	0.56
1:A:1103:C:OP1	3:C:95:ARG:NH2	2.38	0.56
2:B:18:THR:OG1	3:C:36:ASN:ND2	2.28	0.56
25:3:1142:ARG:NH2	25:3:1166:ASP:OD1	2.29	0.56
2:B:135:LEU:HD13	2:B:171:ARG:HH22	1.70	0.56
7:G:18:VAL:HG22	7:G:19:PRO:HD3	1.86	0.56
26:4:982:LEU:N	26:4:995:TYR:O	2.29	0.56
1:A:199:A:H2'	1:A:200:G:H8	1.71	0.56
1:A:539:A:H2'	1:A:540:G:C8	2.41	0.56
1:A:1239:A:H62	1:A:1299:A:N6	2.00	0.56
7:G:76:THR:HG22	7:G:79:ARG:HH12	1.69	0.56
25:3:56:VAL:HG21	25:3:468:LEU:HB3	1.87	0.56
1:A:1479:C:C5'	1:A:1479:C:C6	2.87	0.56
24:2:219:ARG:O	24:2:222:THR:HB	2.05	0.56
25:3:538:LEU:HD11	25:3:571:LEU:HD22	1.88	0.56
1:A:71:A:H61	1:A:99:C:H1'	1.70	0.56
1:A:410:G:N1	1:A:431:A:OP2	2.35	0.56
1:A:555:U:H2'	1:A:556:C:C6	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:24:HIS:HB3	12:L:31:ILE:HG23	1.88	0.56
22:X:5:A:H2'	22:X:5:A:N3	2.21	0.56
23:Z:18:PHE:CE1	29:7:28:DG:H5''	2.40	0.56
1:A:41:G:H2'	1:A:42:G:H8	1.70	0.55
1:A:790:A:OP1	1:A:790:A:H4'	2.05	0.55
1:A:925:G:OP1	1:A:925:G:C4	2.59	0.55
5:E:153:SER:HA	5:E:156:LYS:HE3	1.86	0.55
24:2:124:VAL:HG23	24:2:125:LYS:HG2	1.88	0.55
25:3:658:GLN:HE21	25:3:1186:VAL:HG23	1.71	0.55
25:3:917:SER:OG	25:3:919:ARG:NH1	2.39	0.55
26:4:982:LEU:O	26:4:995:TYR:N	2.31	0.55
1:A:943:U:H1'	10:J:126:GLN:HE22	1.71	0.55
7:G:19:PRO:O	7:G:23:GLU:HG2	2.06	0.55
11:K:91:ASP:HA	23:Z:165:PHE:HB3	1.88	0.55
25:3:358:ASP:N	25:3:361:SER:OG	2.38	0.55
1:A:312:C:H2'	1:A:313:A:H8	1.70	0.55
1:A:1314:C:H2'	1:A:1315:U:H6	1.71	0.55
1:A:1465:A:H2'	1:A:1466:C:C6	2.41	0.55
24:1:62:ASP:OD1	24:1:63:GLY:N	2.39	0.55
25:3:714:VAL:O	25:3:767:GLN:NE2	2.39	0.55
1:A:235:C:H2'	1:A:236:A:C8	2.41	0.55
25:3:808:ASN:H	26:4:633:ALA:HB2	1.72	0.55
25:3:870:ILE:HB	25:3:944:ARG:HD2	1.88	0.55
1:A:744:C:H2'	1:A:745:G:C8	2.39	0.55
10:J:23:PRO:HA	10:J:61:LEU:HD23	1.89	0.55
28:6:15:DA:H2''	28:6:16:DT:C5	2.41	0.55
1:A:90:C:OP2	1:A:90:C:H6	1.90	0.55
1:A:299:G:H2'	1:A:300:A:C8	2.42	0.55
1:A:992:U:H4'	1:A:993:G:C5'	2.37	0.55
1:A:1384:C:H2'	1:A:1385:G:C8	2.42	0.55
25:3:251:ALA:O	25:3:266:GLY:N	2.31	0.55
28:6:21:DC:H1'	28:6:22:DT:C7	2.37	0.55
1:A:789:U:H3'	1:A:789:U:C6	2.41	0.55
11:K:88:MET:HE1	23:Z:144:PHE:CE2	2.41	0.55
25:3:538:LEU:HA	28:6:25:DG:H2''	1.89	0.55
1:A:91:U:H2'	1:A:92:U:C6	2.42	0.55
25:3:1340:GLU:OE1	25:3:1341:ASP:N	2.39	0.55
25:3:1340:GLU:OE2	26:4:1341:ARG:NH2	2.40	0.55
28:6:15:DA:H2''	28:6:16:DT:C6	2.42	0.55
1:A:1008:U:H2'	1:A:1009:U:C6	2.41	0.55
25:3:1307:ASN:HB3	25:3:1312:ASN:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:C:H2'	1:A:234:C:H6	1.72	0.55
1:A:746:A:H2'	1:A:747:A:C8	2.42	0.55
1:A:1489:G:H5''	1:A:1489:G:C8	2.38	0.55
22:X:44:A:N7	25:3:1264:GLN:NE2	2.54	0.55
24:1:62:ASP:OD1	24:1:71:LYS:NZ	2.36	0.55
26:4:45:ASN:ND2	26:4:48:THR:H	2.04	0.55
1:A:1218:C:H2'	1:A:1219:A:C8	2.42	0.54
21:U:15:GLU:OE1	21:U:19:LYS:NZ	2.39	0.54
1:A:26:A:H61	1:A:558:G:H1'	1.72	0.54
1:A:257:G:H2'	1:A:258:G:H8	1.72	0.54
1:A:1354:U:H2'	1:A:1355:G:H8	1.72	0.54
1:A:1463:U:H2'	1:A:1464:U:C6	2.41	0.54
1:A:337:G:H2'	1:A:338:A:H8	1.71	0.54
1:A:910:C:OP2	13:M:18:LYS:NZ	2.34	0.54
14:N:55:THR:O	14:N:59:GLU:HG2	2.07	0.54
1:A:19:A:O2'	1:A:572:A:N1	2.38	0.54
1:A:255:G:H2'	1:A:256:U:C6	2.42	0.54
1:A:390:U:H2'	1:A:391:G:C8	2.41	0.54
3:C:186:ILE:HD13	3:C:200:ILE:HB	1.88	0.54
12:L:94:GLU:HA	12:L:97:ILE:HG23	1.89	0.54
1:A:673:A:H2'	1:A:674:G:C8	2.43	0.54
26:4:557:LYS:HB3	26:4:563:LEU:HD23	1.88	0.54
26:4:982:LEU:HB3	26:4:995:TYR:HB2	1.90	0.54
29:7:9:DC:H2'	29:7:10:DT:C6	2.43	0.54
1:A:343:U:H2'	1:A:345:C:C4	2.42	0.54
1:A:1008:U:H2'	1:A:1009:U:H6	1.72	0.54
1:A:1287:A:H2'	1:A:1288:A:C8	2.42	0.54
1:A:1427:C:H2'	1:A:1428:A:C8	2.43	0.54
1:A:1427:C:H2'	1:A:1428:A:H8	1.72	0.54
2:B:39:ASP:OD1	3:C:208:ARG:NH1	2.41	0.54
2:B:124:LEU:HD11	2:B:168:VAL:HG11	1.89	0.54
5:E:184:ARG:NH1	5:E:187:GLU:OE1	2.41	0.54
15:O:24:ARG:HD3	15:O:48:LEU:HD11	1.89	0.54
25:3:53:PHE:O	25:3:57:PHE:N	2.41	0.54
1:A:789:U:C6	1:A:789:U:OP1	2.61	0.54
26:4:158:GLN:O	26:4:158:GLN:NE2	2.41	0.54
1:A:1355:G:H2'	1:A:1356:G:H8	1.73	0.54
1:A:1425:U:H2'	1:A:1426:G:H8	1.72	0.54
4:D:150:LYS:HD3	4:D:169:ARG:HD3	1.90	0.54
19:S:33:ILE:HD11	19:S:59:ILE:HD13	1.90	0.54
26:4:144:TYR:OH	26:4:293:ARG:NH2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:763:G:H2'	1:A:764:C:C6	2.43	0.54
26:4:850:LYS:N	26:4:855:ASP:O	2.32	0.54
1:A:553:A:H2'	1:A:554:A:C8	2.43	0.54
1:A:736:C:H2'	1:A:737:C:H6	1.72	0.54
1:A:1120:C:H2'	1:A:1121:U:H6	1.72	0.54
1:A:1275:A:H2'	1:A:1276:G:O4'	2.08	0.54
2:B:70:VAL:HG11	2:B:84:LEU:HB3	1.89	0.54
25:3:162:GLY:HA2	25:3:166:SER:HA	1.89	0.54
26:4:405:GLU:HB2	26:4:408:VAL:HG23	1.90	0.54
1:A:352:C:O2	1:A:355:C:N4	2.35	0.53
1:A:974:A:OP1	15:O:69:ARG:NH2	2.39	0.53
2:B:154:PHE:HB3	2:B:168:VAL:HB	1.90	0.53
26:4:312:ARG:HG2	26:4:313:GLY:H	1.74	0.53
11:K:81:GLU:HA	11:K:84:VAL:HG22	1.89	0.53
17:Q:6:LEU:HB3	17:Q:17:TYR:HB3	1.89	0.53
20:T:63:THR:HG22	20:T:66:MET:HG3	1.89	0.53
25:3:59:ILE:HD12	25:3:472:GLU:HG3	1.89	0.53
1:A:799:G:H2'	1:A:800:G:O4'	2.08	0.53
1:A:1040:U:H2'	1:A:1041:G:C8	2.44	0.53
4:D:47:LEU:HD21	4:D:87:LEU:HD11	1.90	0.53
25:3:135:THR:HG22	25:3:144:VAL:HG22	1.89	0.53
29:7:17:DG:H5''	29:7:17:DG:H8	1.72	0.53
1:A:358:U:H2'	1:A:359:G:H8	1.73	0.53
1:A:501:C:H2'	1:A:502:A:H8	1.72	0.53
1:A:634:C:H2'	1:A:635:A:H8	1.74	0.53
17:Q:12:LYS:HG2	17:Q:13:LYS:HG2	1.90	0.53
26:4:1157:ALA:HB2	26:4:1210:ILE:HD11	1.91	0.53
1:A:902:G:H2'	1:A:903:G:H8	1.73	0.53
1:A:994:A:N1	1:A:1047:G:H4'	2.24	0.53
11:K:81:GLU:O	11:K:84:VAL:HG22	2.09	0.53
25:3:1319:MET:HE3	25:3:1324:ASN:HD21	1.74	0.53
28:6:23:DT:H2''	28:6:24:DC:H5''	1.89	0.53
1:A:459:A:H2'	1:A:460:A:H8	1.73	0.53
1:A:1436:U:H2'	1:A:1437:A:H8	1.73	0.53
1:A:1478:U:C3'	1:A:1479:C:H5''	2.39	0.53
12:L:90:GLY:C	12:L:92:GLY:N	2.61	0.53
26:4:646:ILE:HD12	26:4:762:ASN:HD21	1.73	0.53
26:4:1172:LYS:HE3	26:4:1191:PRO:HA	1.90	0.53
1:A:1175:G:H2'	1:A:1176:A:H8	1.72	0.53
25:3:302:ILE:HG22	25:3:309:LEU:HA	1.91	0.53
25:3:859:GLU:HA	25:3:862:LEU:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:773:PHE:O	26:4:776:THR:OG1	2.25	0.53
1:A:459:A:H2'	1:A:460:A:C8	2.44	0.53
1:A:825:A:H2'	1:A:826:C:H6	1.74	0.53
1:A:841:C:N4	1:A:844:G:OP2	2.42	0.53
6:F:15:LEU:HD21	6:F:18:VAL:HG23	1.91	0.53
26:4:572:THR:OG1	26:4:573:THR:N	2.42	0.53
2:B:12:SER:O	2:B:16:ILE:N	2.42	0.53
2:B:30:ALA:HB3	2:B:37:LEU:HD12	1.91	0.53
2:B:45:GLU:N	2:B:45:GLU:OE1	2.42	0.53
6:F:11:LEU:HD13	6:F:39:VAL:HB	1.91	0.53
25:3:237:LEU:HB3	25:3:292:ILE:HD13	1.91	0.53
26:4:583:VAL:HG13	26:4:587:LEU:HD12	1.90	0.53
1:A:539:A:H2'	1:A:540:G:H8	1.73	0.53
1:A:980:C:O5'	1:A:980:C:H6	1.91	0.53
1:A:1279:G:H2'	1:A:1279:G:N3	2.24	0.53
1:A:1399:C:O2	1:A:1502:A:N6	2.42	0.53
1:A:1516:2MG:C2	1:A:1518:MA6:H5''	2.43	0.53
24:2:86:LYS:HD2	24:2:174:ASP:HB2	1.90	0.53
1:A:93:U:H2'	1:A:95:C:H5	1.74	0.52
14:N:16:VAL:HG13	14:N:17:ILE:HD12	1.90	0.52
14:N:98:ARG:HB2	14:N:100:GLN:HE22	1.74	0.52
23:Z:64:PHE:CE1	23:Z:114:ARG:HB3	2.44	0.52
24:2:215:GLU:O	24:2:218:ARG:HB2	2.09	0.52
25:3:1290:MET:HG3	26:4:347:VAL:HG11	1.90	0.52
1:A:347:G:H8	1:A:347:G:OP2	1.92	0.52
1:A:501:C:H2'	1:A:502:A:C8	2.44	0.52
11:K:81:GLU:HA	11:K:84:VAL:CG2	2.38	0.52
26:4:534:GLU:OE2	26:4:538:ARG:NH2	2.42	0.52
1:A:736:C:H2'	1:A:737:C:C6	2.44	0.52
1:A:927:G:H2'	1:A:927:G:N3	2.23	0.52
25:3:309:LEU:HD21	25:3:312:ALA:HB2	1.90	0.52
1:A:1305:G:N2	1:A:1331:G:H1'	2.24	0.52
1:A:1436:U:H2'	1:A:1437:A:C8	2.45	0.52
3:C:80:VAL:HG22	3:C:214:LEU:HD11	1.90	0.52
22:X:43:A:OP2	25:3:1250:SER:OG	2.26	0.52
26:4:1319:PHE:HB3	26:4:1340:LYS:HD2	1.90	0.52
1:A:1103:C:H2'	1:A:1104:G:O4'	2.10	0.52
26:4:1237:VAL:HG11	26:4:1253:ILE:HG21	1.91	0.52
1:A:56:U:H2'	1:A:57:G:H8	1.75	0.52
1:A:705:G:C4	1:A:706:A:C8	2.98	0.52
5:E:172:GLU:OE1	5:E:183:LYS:HB2	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:73:TYR:HD2	25:3:96:LEU:HD11	1.74	0.52
26:4:968:ASN:OD1	26:4:972:LYS:N	2.42	0.52
1:A:219:U:H2'	1:A:220:G:H8	1.75	0.52
1:A:411:A:H4'	1:A:412:A:H5'	1.92	0.52
1:A:929:G:H8	1:A:929:G:OP2	1.93	0.52
5:E:124:MET:HE3	5:E:146:ARG:HD2	1.92	0.52
25:3:667:LEU:HD23	25:3:704:MET:HB3	1.92	0.52
26:4:1269:ALA:HB2	26:4:1276:GLU:HA	1.91	0.52
1:A:34:C:H2'	1:A:35:G:C8	2.45	0.52
1:A:552:U:C2	1:A:553:A:C8	2.98	0.52
1:A:628:G:H2'	1:A:629:A:C8	2.45	0.52
1:A:926:G:OP1	1:A:926:G:H8	1.92	0.52
12:L:56:ARG:NH1	12:L:59:THR:OG1	2.43	0.52
20:T:3:ARG:NH1	20:T:8:GLY:O	2.37	0.52
1:A:613:C:H2'	1:A:614:C:C6	2.45	0.52
1:A:789:U:C6	1:A:789:U:C3'	2.92	0.52
1:A:1183:U:O2'	1:A:1185:G:OP2	2.28	0.52
25:3:590:PRO:O	25:3:659:GLN:NE2	2.31	0.52
25:3:866:ASP:OD1	25:3:869:GLY:N	2.34	0.52
2:B:110:GLY:HA3	2:B:124:LEU:HD23	1.91	0.52
12:L:69:ARG:HA	12:L:72:ASP:OD2	2.10	0.52
16:P:74:ASP:N	16:P:74:ASP:OD1	2.42	0.52
23:Z:164:ILE:HG22	23:Z:165:PHE:H	1.75	0.52
25:3:478:ARG:NH1	25:3:491:ASP:O	2.41	0.52
26:4:557:LYS:HA	26:4:563:LEU:HA	1.91	0.52
1:A:312:C:H2'	1:A:313:A:C8	2.44	0.51
1:A:1071:C:H2'	1:A:1072:G:C8	2.43	0.51
9:I:96:MET:HE2	9:I:130:ALA:HB1	1.93	0.51
10:J:51:PRO:HD3	10:J:80:ARG:HG3	1.92	0.51
11:K:5:ARG:NH2	11:K:7:ARG:HE	2.07	0.51
11:K:90:LEU:O	23:Z:165:PHE:HB3	2.09	0.51
22:X:46:G:H2'	22:X:47:G:H8	1.74	0.51
23:Z:43:MET:HE1	23:Z:112:MET:HG2	1.92	0.51
24:1:135:ASP:HB3	24:1:138:ALA:HB2	1.93	0.51
25:3:730:SER:O	25:3:753:LEU:N	2.43	0.51
26:4:370:LYS:NZ	26:4:443:GLU:OE2	2.43	0.51
26:4:1163:VAL:HG23	26:4:1177:ILE:HG12	1.91	0.51
10:J:63:LEU:HD12	10:J:65:ILE:HD11	1.92	0.51
25:3:27:LEU:O	25:3:528:ARG:NH1	2.43	0.51
1:A:50:A:O2'	1:A:360:G:N2	2.43	0.51
1:A:167:A:H2'	1:A:168:G:H8	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:U:H2'	1:A:186:C:C6	2.46	0.51
1:A:864:A:O5'	1:A:864:A:H8	1.93	0.51
9:I:7:ILE:O	9:I:11:LEU:HG	2.11	0.51
24:2:61:ILE:HG23	24:2:64:VAL:HB	1.91	0.51
25:3:387:ASN:HA	25:3:391:SER:HB3	1.92	0.51
1:A:1040:U:H2'	1:A:1041:G:H8	1.74	0.51
1:A:1251:A:H2'	1:A:1252:A:C8	2.46	0.51
1:A:1376:U:O4	8:H:10:ARG:NH1	2.44	0.51
13:M:4:VAL:O	13:M:8:VAL:HG13	2.09	0.51
1:A:1319:A:C8	1:A:1323:G:C5	2.99	0.51
1:A:1409:C:N3	1:A:1493:A:N6	2.58	0.51
3:C:23:TRP:HA	3:C:190:ASN:HA	1.92	0.51
12:L:86:VAL:CG2	12:L:93:ARG:HH21	2.17	0.51
21:U:35:VAL:HG11	21:U:79:LEU:HD13	1.92	0.51
26:4:371:LYS:H	26:4:371:LYS:HD2	1.76	0.51
26:4:1292:LEU:HD23	26:4:1299:GLY:HA2	1.92	0.51
1:A:73:C:HO2'	1:A:74:A:H8	1.57	0.51
1:A:462:G:H3'	1:A:463:U:O2	2.10	0.51
10:J:88:MET:HE3	10:J:92:GLU:HA	1.93	0.51
15:O:36:ALA:HB3	15:O:41:ARG:HD2	1.92	0.51
28:6:21:DC:O2	28:6:21:DC:H2'	2.10	0.51
1:A:285:C:H2'	1:A:286:C:C6	2.46	0.51
1:A:297:G:N2	1:A:300:A:OP2	2.26	0.51
2:B:157:ILE:HD11	2:B:171:ARG:HE	1.74	0.51
15:O:88:ALA:HB2	15:O:96:LEU:HD23	1.92	0.51
1:A:201:G:O2'	1:A:469:C:O2'	2.26	0.51
1:A:477:C:H2'	1:A:478:A:C8	2.45	0.51
1:A:795:C:H5''	12:L:128:ARG:HH12	1.75	0.51
2:B:52:GLN:OE1	2:B:86:ARG:N	2.43	0.51
25:3:10:ARG:NH2	25:3:793:GLU:OE1	2.44	0.51
25:3:1101:LEU:HD21	26:4:508:LEU:HD22	1.93	0.51
1:A:338:A:H2'	1:A:339:C:O4'	2.11	0.51
1:A:1422:G:H2'	1:A:1423:G:C8	2.45	0.51
10:J:59:GLU:HG3	10:J:60:LYS:HE2	1.93	0.51
22:X:5:A:P	22:X:5:A:C8	3.03	0.51
23:Z:165:PHE:C	23:Z:167:ARG:H	2.17	0.51
26:4:1109:LEU:HB3	26:4:1115:ILE:HD11	1.93	0.51
1:A:17:U:H2'	1:A:18:C:H6	1.74	0.51
2:B:20:PRO:HA	2:B:72:LEU:HB3	1.93	0.51
4:D:53:SER:N	4:D:69:HIS:O	2.33	0.51
24:2:112:ALA:HB2	24:2:128:HIS:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:929:ILE:HD13	25:3:1055:ALA:HB2	1.93	0.51
1:A:31:G:O2'	1:A:48:C:N4	2.44	0.50
14:N:33:ILE:HD13	14:N:60:VAL:HG22	1.93	0.50
16:P:47:LYS:O	16:P:53:ARG:NH2	2.43	0.50
25:3:557:ARG:NH2	25:3:611:GLU:OE1	2.44	0.50
26:4:1109:LEU:HD12	26:4:1113:VAL:HG11	1.91	0.50
1:A:929:G:OP2	1:A:929:G:C8	2.63	0.50
1:A:1005:A:N6	1:A:1024:G:O2'	2.45	0.50
5:E:58:LYS:HD3	5:E:62:ARG:HD3	1.92	0.50
5:E:100:ASN:HD22	5:E:111:ARG:HE	1.59	0.50
5:E:147:GLU:HA	5:E:150:LYS:HD2	1.91	0.50
25:3:525:THR:HG21	25:3:687:ARG:HD3	1.92	0.50
26:4:71:LEU:H	26:4:90:VAL:HG11	1.75	0.50
26:4:1160:SER:HA	26:4:1205:GLU:HA	1.93	0.50
1:A:19:A:H2'	1:A:20:U:C6	2.45	0.50
1:A:676:A:H2'	1:A:677:U:H6	1.75	0.50
1:A:820:U:H4'	1:A:821:G:OP2	2.11	0.50
4:D:136:ARG:O	4:D:140:ASN:ND2	2.44	0.50
10:J:29:VAL:HG13	10:J:64:TYR:HD1	1.75	0.50
25:3:565:GLU:HA	25:3:569:ILE:HG12	1.93	0.50
26:4:848:VAL:O	26:4:857:LEU:N	2.29	0.50
26:4:883:ARG:NH2	26:4:895:CYS:SG	2.84	0.50
1:A:41:G:H2'	1:A:42:G:C8	2.45	0.50
1:A:545:C:OP1	5:E:58:LYS:NZ	2.44	0.50
5:E:124:MET:HG3	5:E:146:ARG:HG2	1.92	0.50
25:3:192:ASP:HB3	25:3:346:TYR:HD1	1.77	0.50
1:A:440:C:C2	1:A:441:A:C8	3.00	0.50
1:A:926:G:P	1:A:926:G:H2'	2.52	0.50
1:A:945:G:C2	1:A:946:A:C8	2.99	0.50
1:A:1119:C:OP2	10:J:11:ARG:NH2	2.45	0.50
1:A:1426:G:H2'	1:A:1427:C:C6	2.46	0.50
1:A:1538:C:H2'	1:A:1539:C:C6	2.46	0.50
8:H:45:SER:O	8:H:49:THR:HG22	2.11	0.50
25:3:538:LEU:HB3	28:6:25:DG:C1'	2.42	0.50
27:5:30:MET:HE3	27:5:46:THR:HB	1.94	0.50
28:6:22:DT:O2	28:6:22:DT:C3'	2.60	0.50
6:F:151:GLU:H	6:F:151:GLU:CD	2.19	0.50
24:2:135:ASP:HB2	24:2:138:ALA:HB2	1.92	0.50
25:3:145:ILE:HG13	25:3:512:SER:HA	1.94	0.50
25:3:289:VAL:HA	25:3:292:ILE:HD12	1.93	0.50
26:4:66:LYS:HB2	26:4:69:GLU:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:442:ILE:HG13	26:4:448:GLN:HG3	1.94	0.50
1:A:8:A:C5	5:E:206:LYS:HA	2.47	0.50
1:A:460:A:H2'	1:A:461:A:H8	1.77	0.50
1:A:1011:C:H2'	1:A:1012:A:C8	2.47	0.50
2:B:27:VAL:HG22	2:B:67:GLU:HG2	1.93	0.50
8:H:74:GLU:O	8:H:88:PRO:HA	2.12	0.50
24:2:74:VAL:HG21	24:2:81:ILE:HD11	1.92	0.50
25:3:83:GLN:OE1	25:3:83:GLN:N	2.37	0.50
25:3:533:LEU:HD21	25:3:571:LEU:HD13	1.92	0.50
27:5:76:GLU:O	27:5:79:GLU:HB2	2.11	0.50
28:6:22:DT:N3	28:6:22:DT:OP2	2.44	0.50
1:A:131:A:H2'	1:A:132:C:C6	2.47	0.50
1:A:437:U:HO2'	5:E:120:HIS:HD1	1.59	0.50
1:A:696:A:N3	1:A:786:G:O2'	2.38	0.50
1:A:708:C:H2'	1:A:709:U:H6	1.76	0.50
17:Q:74:LEU:O	17:Q:77:GLU:HG3	2.11	0.50
25:3:347:ILE:HD11	25:3:433:ILE:HD11	1.92	0.50
25:3:726:TYR:HB3	25:3:733:VAL:HG13	1.93	0.50
25:3:1276:TRP:CZ2	26:4:801:VAL:HG21	2.47	0.50
1:A:436:C:H2'	1:A:437:U:C6	2.47	0.50
1:A:1010:U:H2'	1:A:1011:C:H6	1.77	0.50
1:A:1152:A:P	11:K:72:ARG:HH22	2.35	0.50
25:3:800:MET:HE1	25:3:822:VAL:HB	1.93	0.50
26:4:963:VAL:HG22	26:4:980:THR:HG23	1.93	0.50
1:A:187:G:N2	1:A:190:A:OP2	2.45	0.49
1:A:231:U:H2'	1:A:232:G:H8	1.75	0.49
1:A:881:G:H2'	1:A:882:C:O4'	2.12	0.49
1:A:1241:G:H2'	1:A:1242:G:H8	1.76	0.49
1:A:1309:G:N7	14:N:98:ARG:NH2	2.60	0.49
21:U:49:LYS:HA	21:U:52:ASN:HD21	1.76	0.49
1:A:638:U:C2	1:A:639:G:C8	3.00	0.49
1:A:1486:G:H1'	1:A:1487:G:H1'	1.94	0.49
4:D:14:ILE:HG22	4:D:15:VAL:HG13	1.94	0.49
23:Z:165:PHE:CD2	23:Z:165:PHE:N	2.79	0.49
26:4:201:LEU:HD22	26:4:220:ARG:HH11	1.76	0.49
26:4:208:THR:O	26:4:214:ARG:NE	2.45	0.49
1:A:782:A:H62	1:A:800:G:H21	1.59	0.49
1:A:920:U:H2'	1:A:921:U:C6	2.47	0.49
1:A:928:G:H2'	1:A:929:G:C8	2.47	0.49
26:4:342:LEU:HD23	26:4:1352:ILE:HG23	1.94	0.49
26:4:789:LYS:HB2	26:4:932:MET:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:1263:LYS:HD3	26:4:1281:GLU:HA	1.93	0.49
1:A:720:C:O2'	19:S:52:GLN:NE2	2.40	0.49
9:I:50:LYS:NZ	9:I:60:GLU:OE1	2.44	0.49
14:N:92:ARG:HD2	14:N:93:ARG:HH21	1.78	0.49
19:S:71:THR:HG23	19:S:73:ARG:H	1.77	0.49
23:Z:15:PHE:CE1	28:6:18:DG:H3'	2.47	0.49
23:Z:167:ARG:O	23:Z:168:ALA:C	2.54	0.49
24:1:231:PHE:HE2	24:2:39:LEU:HD13	1.77	0.49
26:4:985:ILE:HA	26:4:991:THR:HA	1.95	0.49
26:4:1238:GLN:NE2	26:4:1250:ASP:OD1	2.45	0.49
1:A:1027:C:H2'	1:A:1028:C:C6	2.48	0.49
5:E:110:THR:HG23	5:E:113:GLU:H	1.78	0.49
7:G:37:HIS:N	7:G:63:ASN:O	2.45	0.49
25:3:994:ARG:HA	25:3:997:TRP:CE2	2.47	0.49
1:A:1391:U:C6	1:A:1391:U:H5''	2.48	0.49
14:N:11:ASP:HA	14:N:45:ILE:HB	1.95	0.49
26:4:317:THR:HG21	26:4:321:LYS:HA	1.94	0.49
1:A:20:U:H2'	1:A:21:G:O4'	2.13	0.49
1:A:392:C:O2'	1:A:483:C:O2'	2.19	0.49
1:A:413:G:H1'	1:A:428:G:H21	1.78	0.49
1:A:939:G:H2'	1:A:940:C:C6	2.47	0.49
1:A:1060:U:OP1	15:O:85:ARG:NH2	2.46	0.49
1:A:1350:A:O2'	8:H:33:ASP:OD1	2.30	0.49
3:C:114:LEU:HD21	3:C:152:LYS:HD2	1.95	0.49
4:D:24:ALA:HB1	4:D:28:GLU:HG2	1.95	0.49
26:4:1172:LYS:HE3	26:4:1192:LYS:H	1.78	0.49
1:A:1518:MA6:H102	1:A:1518:MA6:N7	2.28	0.49
12:L:56:ARG:HH22	12:L:61:PHE:HD2	1.61	0.49
24:2:109:PRO:HB3	24:2:132:HIS:CE1	2.47	0.49
25:3:1132:LEU:HD11	25:3:1173:ALA:HB1	1.95	0.49
26:4:117:LEU:HG	26:4:118:LYS:HG3	1.94	0.49
28:6:22:DT:O2	28:6:22:DT:C2'	2.60	0.49
1:A:71:A:O2'	1:A:72:A:O4'	2.30	0.49
1:A:74:A:H2'	1:A:75:G:O4'	2.13	0.49
1:A:405:U:OP1	1:A:406:G:O2'	2.30	0.49
1:A:560:A:H4'	1:A:561:U:H5''	1.94	0.49
1:A:927:G:N2	1:A:1391:U:H1'	2.28	0.49
1:A:978:A:C5	1:A:1319:A:C2	3.01	0.49
25:3:314:ASN:O	25:3:352:ARG:NH2	2.31	0.49
26:4:478:LEU:HG	27:5:47:THR:HG23	1.95	0.49
28:6:14:DT:H2'	28:6:15:DA:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:6:35:DC:H2''	28:6:36:DA:C8	2.48	0.49
1:A:722:G:H2'	1:A:724:G:C8	2.48	0.49
1:A:1273:C:H2'	1:A:1274:A:O4'	2.13	0.49
4:D:131:ARG:HA	4:D:134:MET:HE2	1.95	0.49
6:F:150:PRO:HA	6:F:153:VAL:HG22	1.95	0.49
7:G:55:HIS:O	7:G:56:LYS:HG2	2.13	0.49
10:J:45:ARG:O	10:J:49:ARG:HG2	2.13	0.49
24:2:90:VAL:HG13	24:2:123:ILE:HD13	1.95	0.49
1:A:948:C:OP1	14:N:108:THR:HG22	2.13	0.48
1:A:1120:C:H2'	1:A:1121:U:C6	2.47	0.48
10:J:123:ARG:NH1	10:J:124:ARG:O	2.47	0.48
25:3:382:GLU:O	25:3:386:GLU:HG2	2.13	0.48
26:4:242:LEU:HD21	26:4:306:LEU:HD22	1.96	0.48
1:A:384:G:H2'	1:A:385:C:H6	1.78	0.48
1:A:621:A:H2'	1:A:622:A:C8	2.48	0.48
1:A:704:A:C4	1:A:705:G:C8	3.01	0.48
1:A:825:A:H2'	1:A:826:C:C6	2.48	0.48
9:I:48:ASP:OD1	9:I:49:PHE:N	2.41	0.48
15:O:26:GLU:O	15:O:30:ILE:HG22	2.14	0.48
19:S:33:ILE:HD11	19:S:59:ILE:HG21	1.94	0.48
24:1:71:LYS:O	24:1:74:VAL:HG22	2.13	0.48
25:3:213:LEU:HD22	25:3:422:LYS:HE2	1.95	0.48
26:4:368:LEU:HD22	26:4:439:PRO:HB2	1.95	0.48
26:4:851:PRO:HG2	26:4:875:ASN:HB3	1.95	0.48
1:A:71:A:C4	1:A:72:A:C8	3.01	0.48
1:A:178:C:C2	1:A:179:A:C8	3.01	0.48
1:A:790:A:OP1	1:A:790:A:O3'	2.32	0.48
9:I:106:THR:HB	9:I:121:LEU:HD23	1.95	0.48
14:N:89:LEU:O	14:N:93:ARG:HG2	2.13	0.48
1:A:71:A:C6	1:A:100:G:C8	3.02	0.48
1:A:236:A:H2'	1:A:237:G:H8	1.77	0.48
1:A:264:C:O2'	18:R:66:PRO:O	2.30	0.48
1:A:688:G:H2'	1:A:689:C:H6	1.78	0.48
1:A:1052:U:O2'	1:A:1055:A:OP2	2.18	0.48
6:F:115:LEU:HD13	6:F:123:VAL:HG11	1.95	0.48
9:I:29:SER:HB3	9:I:57:PRO:HB2	1.95	0.48
26:4:891:ASP:OD2	26:4:1290:ARG:NH2	2.29	0.48
1:A:26:A:N6	1:A:558:G:H1'	2.29	0.48
1:A:404:G:H2'	1:A:405:U:O4'	2.13	0.48
1:A:965:U:H5''	1:A:966:2MG:OP1	2.14	0.48
23:Z:13:GLN:HB3	28:6:18:DG:H1'	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:939:VAL:HG11	25:3:1047:LEU:HD13	1.96	0.48
25:3:1257:GLN:NE2	26:4:341:ASN:O	2.45	0.48
29:7:18:DC:H2'	29:7:19:DG:C8	2.49	0.48
1:A:460:A:H2'	1:A:461:A:C8	2.49	0.48
1:A:707:U:C2	1:A:708:C:C5	3.02	0.48
1:A:1121:U:H2'	1:A:1122:U:H6	1.78	0.48
1:A:1516:2MG:H3'	1:A:1516:2MG:H8	1.78	0.48
2:B:39:ASP:HB2	2:B:45:GLU:HG3	1.95	0.48
4:D:135:LYS:O	4:D:139:GLN:HG2	2.13	0.48
23:Z:63:LYS:O	23:Z:64:PHE:C	2.56	0.48
25:3:1043:ALA:HB3	25:3:1044:PRO:HD3	1.96	0.48
26:4:393:THR:OG1	26:4:394:ILE:N	2.46	0.48
29:7:8:DT:H2''	29:7:9:DC:C6	2.49	0.48
29:7:21:DG:H2'	29:7:22:DC:C6	2.48	0.48
1:A:789:U:H5''	1:A:789:U:C6	2.41	0.48
1:A:1062:U:H2'	1:A:1063:C:C6	2.48	0.48
1:A:1107:C:C4	1:A:1108:G:C8	3.01	0.48
1:A:1355:G:H2'	1:A:1356:G:C8	2.48	0.48
25:3:820:GLU:N	25:3:1080:ASN:O	2.46	0.48
26:4:44:ILE:HG22	26:4:51:PRO:HA	1.96	0.48
26:4:1353:VAL:HG23	26:4:1355:ARG:HG2	1.96	0.48
1:A:73:C:C2	1:A:74:A:C8	3.02	0.48
1:A:216:U:H4'	1:A:464:U:H4'	1.96	0.48
1:A:1171:A:H2'	1:A:1172:C:H6	1.79	0.48
9:I:78:VAL:HG12	9:I:85:ILE:HD12	1.95	0.48
13:M:21:VAL:HG23	13:M:95:TYR:CE2	2.49	0.48
26:4:756:GLU:HG3	26:4:757:THR:HG23	1.96	0.48
26:4:1159:ILE:O	26:4:1206:ARG:N	2.46	0.48
1:A:420:U:O2'	1:A:423:G:O6	2.27	0.48
1:A:708:C:H2'	1:A:709:U:C6	2.48	0.48
1:A:936:C:C2	1:A:937:A:C8	3.01	0.48
11:K:81:GLU:C	11:K:84:VAL:HG22	2.39	0.48
22:X:5:A:H3'	22:X:6:G:C8	2.49	0.48
24:2:29:GLU:HB2	24:2:200:LYS:HG3	1.96	0.48
25:3:1154:ASP:OD1	25:3:1154:ASP:N	2.43	0.48
29:7:6:DA:H8	29:7:6:DA:OP2	1.96	0.48
1:A:358:U:H2'	1:A:359:G:C8	2.49	0.47
1:A:707:U:H2'	1:A:708:C:H6	1.78	0.47
1:A:1000:A:H2'	1:A:1001:C:C6	2.49	0.47
4:D:182:ILE:HD13	4:D:203:PHE:HB2	1.95	0.47
7:G:37:HIS:NE2	7:G:65:GLU:HB2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:119:GLU:HB2	25:3:489:PRO:HG2	1.96	0.47
25:3:629:PHE:HB2	25:3:647:ARG:HG3	1.96	0.47
26:4:406:ALA:HA	26:4:409:TRP:HD1	1.78	0.47
26:4:821:MET:HA	26:4:881:LYS:HA	1.96	0.47
1:A:1255:G:O2'	1:A:1258:G:N3	2.41	0.47
1:A:1519:MA6:H102	1:A:1519:MA6:N7	2.28	0.47
8:H:68:ASN:ND2	8:H:130:ASN:OD1	2.47	0.47
11:K:81:GLU:O	11:K:84:VAL:CG2	2.62	0.47
24:1:79:LEU:HD13	25:3:693:LEU:HD11	1.96	0.47
25:3:150:HIS:CE1	25:3:454:ARG:HG3	2.49	0.47
1:A:218:U:H2'	1:A:219:U:C6	2.50	0.47
1:A:236:A:H2'	1:A:237:G:C8	2.49	0.47
1:A:765:G:N2	1:A:813:U:OP2	2.47	0.47
1:A:864:A:H2'	1:A:865:A:C8	2.49	0.47
1:A:1072:G:H2'	1:A:1073:U:C6	2.49	0.47
1:A:1435:G:H2'	1:A:1436:U:C6	2.49	0.47
1:A:206:C:H2'	1:A:207:C:C6	2.49	0.47
1:A:707:U:H2'	1:A:708:C:C6	2.50	0.47
1:A:1476:A:H2'	1:A:1477:U:O4'	2.14	0.47
5:E:50:ASP:O	5:E:53:VAL:HG12	2.14	0.47
5:E:160:GLU:O	5:E:163:GLU:HG3	2.14	0.47
10:J:67:VAL:HG21	10:J:79:ILE:HD11	1.96	0.47
11:K:34:ALA:HB2	11:K:83:THR:HG21	1.96	0.47
26:4:425:ARG:HB2	26:4:466:MET:HE2	1.96	0.47
1:A:590:U:H2'	1:A:591:U:H6	1.79	0.47
1:A:810:C:H2'	1:A:811:C:O4'	2.14	0.47
12:L:16:VAL:HG12	12:L:18:ASP:H	1.79	0.47
12:L:34:ILE:HD13	12:L:74:VAL:HG21	1.96	0.47
24:1:78:ILE:HD13	24:1:81:ILE:HD12	1.97	0.47
25:3:727:VAL:HG22	25:3:732:ILE:HG12	1.97	0.47
1:A:269:C:H2'	1:A:270:A:C8	2.50	0.47
1:A:377:G:H2'	1:A:378:G:H8	1.79	0.47
1:A:1039:G:H2'	1:A:1040:U:C6	2.49	0.47
1:A:1140:C:O2'	1:A:1141:C:H6	1.97	0.47
25:3:41:GLN:CD	25:3:41:GLN:H	2.22	0.47
25:3:228:VAL:HB	25:3:245:ARG:HH12	1.79	0.47
26:4:1079:LYS:HE3	26:4:1081:VAL:HG12	1.96	0.47
1:A:247:G:H4'	1:A:247:G:OP1	2.14	0.47
1:A:524:G:H2'	1:A:525:C:C6	2.50	0.47
2:B:43:LYS:NZ	3:C:188:ASP:OD2	2.47	0.47
2:B:135:LEU:HD13	2:B:171:ARG:NH2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:28:ILE:HG12	10:J:63:LEU:HG	1.97	0.47
10:J:55:VAL:HG23	10:J:94:LEU:HD22	1.96	0.47
14:N:14:HIS:HD1	14:N:42:ASP:C	2.21	0.47
20:T:21:LYS:O	20:T:24:GLU:HG3	2.15	0.47
26:4:699:ASP:O	26:4:703:THR:OG1	2.21	0.47
1:A:593:U:H2'	1:A:594:U:C6	2.50	0.47
1:A:634:C:H2'	1:A:635:A:C8	2.50	0.47
1:A:713:G:H2'	1:A:714:G:H8	1.75	0.47
1:A:1323:G:H2'	1:A:1324:A:C8	2.49	0.47
1:A:1516:2MG:HM21	1:A:1520:C:N4	2.30	0.47
7:G:25:TYR:O	7:G:29:ILE:HG12	2.15	0.47
25:3:196:VAL:HG21	25:3:209:ILE:HD11	1.97	0.47
25:3:436:ARG:O	25:3:436:ARG:NH1	2.46	0.47
25:3:1291:LEU:HD11	26:4:1354:GLY:HA2	1.97	0.47
1:A:199:A:H2'	1:A:200:G:C8	2.49	0.47
1:A:763:G:H2'	1:A:764:C:H6	1.80	0.47
1:A:800:G:H2'	1:A:801:U:C5	2.50	0.47
1:A:1126:U:O2	1:A:1280:A:H2'	2.14	0.47
1:A:1173:U:C2	1:A:1174:G:C8	3.02	0.47
4:D:156:ARG:H	4:D:163:ALA:HA	1.80	0.47
12:L:69:ARG:HE	12:L:69:ARG:HB3	1.30	0.47
24:1:91:ARG:NH1	24:1:209:GLY:O	2.48	0.47
25:3:745:GLU:CD	25:3:746:ALA:H	2.23	0.47
25:3:814:ASP:O	25:3:1074:GLY:HA3	2.15	0.47
26:4:899:TYR:O	26:4:1251:LYS:NZ	2.40	0.47
1:A:1137:C:H1'	1:A:1138:G:N2	2.30	0.47
23:Z:64:PHE:HE1	23:Z:114:ARG:HB3	1.80	0.47
26:4:825:VAL:HG12	26:4:833:GLU:HG2	1.97	0.47
26:4:1282:TYR:HA	26:4:1285:VAL:HG12	1.95	0.47
1:A:373:A:C2	1:A:374:A:C8	3.03	0.46
1:A:687:A:N7	1:A:701:U:N3	2.63	0.46
1:A:688:G:H2'	1:A:689:C:C6	2.50	0.46
5:E:170:TRP:CD2	5:E:186:PRO:HB3	2.50	0.46
25:3:10:ARG:HG2	25:3:1175:ASN:HB3	1.98	0.46
26:4:355:ILE:HG12	26:4:464:ASP:O	2.14	0.46
26:4:952:VAL:HG13	26:4:1014:GLY:H	1.80	0.46
1:A:253:A:H2'	1:A:254:G:C8	2.49	0.46
1:A:693:G:HO2'	1:A:694:A:P	2.37	0.46
4:D:120:ILE:HA	4:D:123:GLN:HE21	1.79	0.46
13:M:50:ARG:HB3	13:M:66:TYR:HE1	1.80	0.46
25:3:549:ASP:OD1	25:3:550:VAL:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:3:1184:THR:HG23	25:3:1190:ALA:H	1.79	0.46
26:4:1038:THR:HG21	26:4:1079:LYS:HE2	1.98	0.46
1:A:91:U:H2'	1:A:92:U:H6	1.78	0.46
1:A:893:C:C2	1:A:894:G:C8	3.04	0.46
8:H:65:ALA:O	8:H:69:VAL:HG23	2.16	0.46
12:L:94:GLU:OE1	12:L:94:GLU:N	2.48	0.46
24:1:120:ASP:OD1	24:1:120:ASP:N	2.43	0.46
25:3:447:HIS:CD2	25:3:553:THR:HG21	2.51	0.46
25:3:820:GLU:HA	25:3:1079:ILE:HD11	1.96	0.46
26:4:968:ASN:HD21	26:4:972:LYS:HB2	1.81	0.46
26:4:1072:LYS:HD2	26:4:1168:GLU:HB3	1.98	0.46
1:A:56:U:H2'	1:A:57:G:C8	2.50	0.46
1:A:416:G:H2'	1:A:417:G:H8	1.80	0.46
1:A:916:U:H2'	1:A:917:G:H8	1.81	0.46
1:A:1010:U:H2'	1:A:1011:C:C6	2.50	0.46
13:M:21:VAL:HG21	13:M:24:LEU:HD12	1.98	0.46
25:3:841:ARG:HA	25:3:1046:VAL:HA	1.98	0.46
25:3:987:GLU:O	25:3:991:LYS:HB2	2.15	0.46
25:3:1115:THR:HG23	25:3:1228:GLY:HA3	1.97	0.46
1:A:182:A:O2'	1:A:183:C:H5''	2.16	0.46
1:A:1319:A:C8	1:A:1323:G:C6	3.03	0.46
5:E:99:ASP:OD1	5:E:100:ASN:N	2.48	0.46
10:J:88:MET:SD	10:J:98:LEU:HD12	2.56	0.46
12:L:79:ILE:HD12	12:L:79:ILE:H	1.80	0.46
24:1:167:PRO:HD2	24:1:170:ARG:HD2	1.98	0.46
25:3:80:PHE:HE1	25:3:1035:LYS:HD2	1.81	0.46
26:4:1105:ALA:HA	26:4:1124:ILE:HG13	1.97	0.46
1:A:384:G:H2'	1:A:385:C:C6	2.50	0.46
1:A:490:C:H2'	1:A:491:G:H8	1.81	0.46
1:A:1399:C:H2'	1:A:1400:C:C5	2.51	0.46
2:B:109:THR:HG22	2:B:153:GLU:HG2	1.98	0.46
11:K:7:ARG:HB2	11:K:101:SER:OG	2.16	0.46
21:U:35:VAL:HG23	21:U:50:ALA:HB3	1.96	0.46
25:3:213:LEU:HD22	25:3:422:LYS:HG2	1.98	0.46
25:3:678:ARG:HD3	25:3:678:ARG:HA	1.70	0.46
25:3:1268:GLN:OE1	26:4:352:ARG:NH1	2.47	0.46
26:4:865:HIS:NE2	26:4:867:GLN:HB2	2.31	0.46
28:6:36:DA:H2'	28:6:36:DA:O5'	2.15	0.46
28:6:36:DA:H2''	28:6:37:DG:C8	2.51	0.46
1:A:382:A:H2'	1:A:383:A:C8	2.51	0.46
1:A:635:A:H2'	1:A:636:U:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:936:C:C4	1:A:937:A:N7	2.84	0.46
1:A:1055:A:O2'	4:D:161:GLU:O	2.27	0.46
1:A:1118:U:H2'	1:A:1119:C:C6	2.51	0.46
1:A:1118:U:H2'	1:A:1119:C:H6	1.80	0.46
23:Z:90:MET:HB2	28:6:18:DG:C4'	2.46	0.46
25:3:210:LEU:HA	25:3:213:LEU:HB2	1.98	0.46
26:4:659:ALA:O	26:4:662:ALA:HB3	2.16	0.46
1:A:123:U:H5''	1:A:311:C:O2'	2.16	0.46
1:A:392:C:C2	1:A:393:A:C8	3.04	0.46
1:A:398:U:H2'	1:A:399:G:C8	2.46	0.46
4:D:76:VAL:O	4:D:83:ASP:HB3	2.16	0.46
12:L:19:GLY:O	12:L:82:LEU:HA	2.16	0.46
13:M:4:VAL:HG23	18:R:34:TYR:HB3	1.98	0.46
25:3:1105:SER:OG	26:4:731:ARG:NH2	2.35	0.46
26:4:308:ASP:OD2	26:4:311:ARG:HB2	2.16	0.46
26:4:824:PRO:HG3	26:4:835:LEU:HB2	1.96	0.46
26:4:926:PRO:HG3	26:4:1248:ILE:HD11	1.97	0.46
1:A:431:A:C4	1:A:432:A:C8	3.04	0.46
1:A:745:G:C2	1:A:746:A:C5	3.04	0.46
1:A:1149:C:H2'	1:A:1150:A:C8	2.51	0.46
1:A:1474:U:H5'	1:A:1475:G:OP2	2.16	0.46
11:K:28:THR:O	11:K:32:THR:HG22	2.16	0.46
15:O:7:LYS:O	15:O:11:VAL:HG23	2.16	0.46
25:3:208:ILE:HD11	25:3:365:GLU:HB3	1.97	0.46
25:3:1293:VAL:HG21	25:3:1315:MET:HB2	1.98	0.46
26:4:93:THR:OG1	26:4:94:GLN:N	2.49	0.46
26:4:744:ARG:HB3	26:4:759:ILE:HB	1.98	0.46
2:B:69:ASP:OD1	2:B:69:ASP:N	2.49	0.46
5:E:23:SER:O	5:E:24:ASP:HB3	2.15	0.46
6:F:162:GLU:O	6:F:166:GLY:N	2.49	0.46
8:H:126:ASP:HA	8:H:129:GLU:HG2	1.97	0.46
13:M:5:ASN:O	13:M:8:VAL:HG22	2.16	0.46
17:Q:4:ILE:HG12	17:Q:21:VAL:HG22	1.97	0.46
22:X:6:G:H5'	22:X:6:G:C8	2.43	0.46
26:4:706:VAL:HA	26:4:715:LYS:HA	1.97	0.46
26:4:1109:LEU:HD23	26:4:1121:LEU:HA	1.98	0.46
26:4:1288:ALA:O	26:4:1291:GLU:HG3	2.16	0.46
1:A:591:U:H2'	1:A:592:G:H8	1.82	0.45
6:F:44:GLY:O	6:F:74:VAL:N	2.38	0.45
11:K:22:THR:CG2	11:K:39:PRO:CG	2.93	0.45
25:3:799:ASN:OD1	25:3:799:ASN:N	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:161:THR:O	26:4:165:TYR:N	2.41	0.45
26:4:1161:GLY:HA3	26:4:1179:PRO:HA	1.98	0.45
1:A:73:C:O2'	1:A:74:A:H8	1.99	0.45
1:A:224:U:H2'	1:A:225:C:C6	2.52	0.45
1:A:263:A:H2'	1:A:264:C:C6	2.51	0.45
1:A:657:U:H2'	1:A:658:C:H6	1.80	0.45
1:A:748:G:H2'	1:A:749:A:H8	1.78	0.45
1:A:789:U:H6	1:A:789:U:C5'	2.26	0.45
1:A:1277:C:H2'	1:A:1279:G:H8	1.81	0.45
1:A:1354:U:H2'	1:A:1355:G:C8	2.51	0.45
2:B:42:LEU:HB2	2:B:82:THR:HG21	1.98	0.45
25:3:24:VAL:HG11	25:3:704:MET:HE1	1.98	0.45
26:4:1167:LYS:HD2	26:4:1174:ARG:HD3	1.99	0.45
28:6:11:DT:OP2	28:6:11:DT:H6	2.00	0.45
1:A:328:C:H4'	1:A:329:A:H5'	1.98	0.45
1:A:482:A:H8	1:A:482:A:O5'	1.98	0.45
1:A:486:U:H2'	1:A:487:A:H8	1.80	0.45
1:A:1176:A:H2'	1:A:1177:G:C8	2.51	0.45
1:A:1291:U:H2'	1:A:1292:G:C8	2.49	0.45
1:A:1516:2MG:C8	1:A:1516:2MG:C3'	2.99	0.45
24:2:218:ARG:O	24:2:222:THR:OG1	2.32	0.45
25:3:301:TYR:HB3	25:3:330:HIS:HD2	1.77	0.45
27:5:27:ALA:HA	27:5:30:MET:HE2	1.98	0.45
1:A:114:U:H2'	1:A:115:G:C8	2.52	0.45
1:A:1141:C:O2'	1:A:1142:G:H8	1.99	0.45
1:A:1400:C:H4'	1:A:1517:G:H22	1.81	0.45
2:B:87:GLU:O	2:B:91:ARG:HG3	2.17	0.45
25:3:672:GLU:HG3	25:3:673:HIS:CE1	2.51	0.45
26:4:919:ALA:HA	26:4:1252:HIS:HD2	1.82	0.45
1:A:79:G:N2	1:A:90:C:H41	2.13	0.45
1:A:309:A:O2'	1:A:607:A:N1	2.48	0.45
1:A:768:A:H4'	1:A:1523:G:N2	2.31	0.45
1:A:1096:C:H2'	1:A:1097:C:H6	1.81	0.45
1:A:1516:2MG:H3'	1:A:1516:2MG:C8	2.52	0.45
26:4:432:LEU:HD13	26:4:499:ILE:HG12	1.98	0.45
26:4:907:HIS:ND1	26:4:908:ILE:O	2.37	0.45
26:4:1161:GLY:O	26:4:1204:VAL:N	2.31	0.45
1:A:323:U:H2'	1:A:324:G:O4'	2.17	0.45
1:A:628:G:H2'	1:A:629:A:H8	1.79	0.45
1:A:737:C:H2'	1:A:738:C:C6	2.51	0.45
1:A:1279:G:N3	1:A:1279:G:C2'	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1377:A:H4'	1:A:1378:C:H5	1.81	0.45
10:J:91:ASP:O	10:J:92:GLU:HB2	2.17	0.45
26:4:807:LEU:HD11	26:4:1258:ARG:HG2	1.99	0.45
1:A:264:C:H2'	1:A:265:G:O4'	2.17	0.45
1:A:408:A:H2'	1:A:409:U:C6	2.51	0.45
1:A:471:U:H2'	1:A:472:U:C6	2.52	0.45
8:H:68:ASN:O	8:H:138:ARG:NH2	2.43	0.45
10:J:94:LEU:H	10:J:94:LEU:HG	1.54	0.45
23:Z:127:LEU:HD23	23:Z:127:LEU:H	1.80	0.45
25:3:812:PHE:CZ	26:4:503:SER:HB2	2.51	0.45
25:3:1120:ALA:HB1	25:3:1198:LEU:HG	1.97	0.45
29:7:2:DT:H2''	29:7:3:DC:C5	2.51	0.45
1:A:181:A:O2'	1:A:194:C:N4	2.50	0.45
1:A:335:C:C2	1:A:336:A:C8	3.05	0.45
1:A:931:C:H2'	1:A:932:C:C6	2.52	0.45
1:A:1095:U:H2'	1:A:1096:C:C6	2.52	0.45
3:C:15:HIS:HB3	3:C:43:LEU:HD11	1.98	0.45
3:C:105:LYS:O	3:C:109:GLN:HG2	2.17	0.45
5:E:121:LYS:HG3	5:E:131:ASN:HD21	1.82	0.45
6:F:157:ARG:HH21	9:I:43:GLU:HB3	1.82	0.45
13:M:20:ASN:OD1	13:M:20:ASN:N	2.46	0.45
14:N:19:LEU:HB3	14:N:30:SER:OG	2.17	0.45
26:4:1350:ASN:ND2	26:4:1358:PRO:HD3	2.25	0.45
1:A:255:G:H2'	1:A:256:U:H6	1.81	0.45
1:A:613:C:H2'	1:A:614:C:H6	1.82	0.45
1:A:1299:A:O2'	1:A:1301:U:O4'	2.32	0.45
8:H:58:GLU:OE1	8:H:58:GLU:N	2.50	0.45
11:K:81:GLU:CA	11:K:84:VAL:HG22	2.46	0.45
14:N:65:VAL:O	14:N:66:GLU:HB2	2.16	0.45
16:P:23:GLY:O	16:P:28:GLN:NE2	2.48	0.45
24:1:47:LEU:HA	24:1:51:MET:HG2	1.99	0.45
25:3:812:PHE:HB3	26:4:357:VAL:HG11	1.99	0.45
25:3:819:SER:HB2	25:3:1085:MET:SD	2.57	0.45
25:3:1307:ASN:O	25:3:1311:GLY:N	2.50	0.45
1:A:35:G:H2'	1:A:36:C:C6	2.52	0.45
1:A:201:G:HO2'	1:A:469:C:HO2'	1.64	0.45
1:A:1119:C:OP1	10:J:85:ARG:NH1	2.50	0.45
1:A:1151:A:O2'	1:A:1152:A:O4'	2.34	0.45
1:A:1323:G:H2'	1:A:1324:A:H8	1.82	0.45
1:A:1507:A:H2'	1:A:1508:A:C8	2.52	0.45
4:D:79:LYS:O	4:D:82:GLU:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:2:84:ASN:ND2	24:2:130:ILE:HA	2.32	0.45
29:7:1:DC:H2''	29:7:2:DT:H71	1.99	0.45
29:7:6:DA:OP2	29:7:6:DA:C8	2.70	0.45
1:A:636:U:H2'	1:A:637:C:H6	1.81	0.44
1:A:645:G:C2	1:A:646:G:C8	3.05	0.44
1:A:838:G:H2'	1:A:839:C:H6	1.83	0.44
1:A:925:G:C8	1:A:925:G:C5'	2.78	0.44
1:A:925:G:O4'	1:A:925:G:P	2.75	0.44
1:A:1326:U:H2'	1:A:1327:C:C6	2.52	0.44
3:C:85:LEU:HA	3:C:85:LEU:HD23	1.78	0.44
20:T:17:LYS:O	20:T:21:LYS:HD3	2.17	0.44
22:X:6:G:C8	22:X:6:G:OP2	2.71	0.44
24:2:83:LEU:HD13	26:4:528:THR:HA	1.98	0.44
25:3:240:GLU:HA	25:3:283:LYS:O	2.17	0.44
26:4:656:GLU:OE1	26:4:692:ARG:NH2	2.35	0.44
26:4:809:VAL:O	26:4:912:GLY:N	2.48	0.44
1:A:482:A:H2'	1:A:483:C:O4'	2.17	0.44
1:A:1436:U:C2	1:A:1437:A:C8	3.05	0.44
1:A:1537:U:H2'	1:A:1538:C:H6	1.83	0.44
3:C:187:VAL:HG13	3:C:191:SER:HB2	1.99	0.44
25:3:1132:LEU:HD12	25:3:1177:ARG:HB3	2.00	0.44
26:4:152:THR:HG21	26:4:176:PHE:HB3	1.99	0.44
26:4:829:GLY:O	26:4:993:GLU:HA	2.17	0.44
1:A:978:A:C2'	1:A:979:C:H5'	2.48	0.44
4:D:22:TRP:CD1	4:D:59:ARG:HG3	2.53	0.44
26:4:515:ARG:NH2	26:4:718:SER:O	2.50	0.44
1:A:2:A:H1'	1:A:613:C:O2'	2.18	0.44
1:A:90:C:H2'	1:A:90:C:P	2.57	0.44
1:A:393:A:C2	1:A:394:G:C8	3.05	0.44
1:A:1152:A:OP1	11:K:70:HIS:ND1	2.50	0.44
1:A:1460:C:H2'	1:A:1461:G:H8	1.82	0.44
12:L:86:VAL:HG21	12:L:93:ARG:CZ	2.40	0.44
29:7:8:DT:OP2	29:7:8:DT:C6	2.62	0.44
1:A:993:G:N3	1:A:993:G:C2'	2.80	0.44
1:A:1518:MA6:H8	1:A:1518:MA6:O5'	2.18	0.44
4:D:36:ASP:OD1	4:D:59:ARG:NH1	2.50	0.44
10:J:17:ALA:HB2	10:J:67:VAL:HG13	2.00	0.44
15:O:23:LYS:HE3	15:O:23:LYS:HB3	1.84	0.44
23:Z:7:LYS:HG2	23:Z:74:VAL:HG13	1.99	0.44
26:4:232:ASN:HA	26:4:236:TRP:CZ3	2.53	0.44
28:6:21:DC:H6	28:6:22:DT:H71	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:G:C8	1:A:178:C:C6	3.05	0.44
1:A:272:C:H2'	1:A:273:U:C6	2.53	0.44
1:A:673:A:C6	1:A:734:G:C6	3.05	0.44
1:A:751:U:H2'	1:A:752:G:O4'	2.18	0.44
1:A:790:A:N3	1:A:790:A:C3'	2.79	0.44
1:A:838:G:H2'	1:A:839:C:C6	2.52	0.44
1:A:925:G:OP1	1:A:925:G:N3	2.51	0.44
1:A:1171:A:H2'	1:A:1172:C:C6	2.52	0.44
1:A:1342:C:H2'	1:A:1343:G:C8	2.52	0.44
1:A:1424:U:H2'	1:A:1425:U:O4'	2.17	0.44
20:T:41:PHE:HB2	20:T:44:MET:HE3	1.99	0.44
1:A:130:A:N3	1:A:263:A:O2'	2.39	0.44
1:A:475:C:H2'	1:A:476:U:C6	2.52	0.44
1:A:642:A:N7	9:I:107:SER:HA	2.33	0.44
1:A:923:A:H2'	1:A:924:C:O4'	2.18	0.44
1:A:1096:C:H2'	1:A:1097:C:C6	2.52	0.44
1:A:1147:C:H4'	10:J:7:TYR:CE2	2.53	0.44
1:A:1191:A:OP2	4:D:2:GLY:N	2.50	0.44
4:D:69:HIS:HA	4:D:104:ALA:O	2.17	0.44
4:D:83:ASP:HA	4:D:86:LYS:HG2	1.98	0.44
6:F:148:ASN:ND2	9:I:73:GLU:OE2	2.50	0.44
7:G:68:GLN:O	7:G:71:ILE:HG13	2.18	0.44
12:L:85:MET:SD	12:L:111:THR:OG1	2.73	0.44
25:3:209:ILE:O	25:3:213:LEU:N	2.44	0.44
29:7:6:DA:H8	29:7:6:DA:P	2.40	0.44
1:A:676:A:H2'	1:A:677:U:C6	2.53	0.44
1:A:926:G:N1	1:A:1395:C:H4'	2.32	0.44
1:A:927:G:N2	1:A:1390:U:O2	2.48	0.44
1:A:931:C:H2'	1:A:932:C:H6	1.82	0.44
2:B:137:ASP:OD1	2:B:138:VAL:N	2.51	0.44
5:E:121:LYS:HG3	5:E:131:ASN:ND2	2.33	0.44
5:E:153:SER:O	5:E:156:LYS:HG2	2.17	0.44
6:F:11:LEU:HD11	6:F:68:ARG:NH1	2.32	0.44
25:3:592:ARG:N	25:3:653:MET:O	2.47	0.44
26:4:58:CYS:HB3	26:4:61:ILE:HB	1.99	0.44
26:4:312:ARG:HG2	26:4:313:GLY:N	2.32	0.44
26:4:361:LEU:HD13	26:4:366:CYS:HA	1.98	0.44
1:A:182:A:C4	1:A:184:G:C8	3.06	0.44
1:A:216:U:H2'	1:A:217:C:H6	1.81	0.44
1:A:254:G:O2'	18:R:18:GLU:O	2.36	0.44
1:A:494:G:O2'	1:A:496:A:H1'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1398:A:N3	1:A:1398:A:H2'	2.33	0.44
1:A:1489:G:C5'	1:A:1489:G:C8	2.98	0.44
3:C:124:GLY:C	3:C:126:PHE:H	2.26	0.44
14:N:45:ILE:HA	14:N:48:LEU:HD12	2.00	0.44
18:R:19:LYS:H	18:R:51:ASN:ND2	2.12	0.44
24:2:15:ASP:OD1	24:2:16:ILE:N	2.51	0.44
25:3:566:GLY:H	25:3:569:ILE:HG12	1.82	0.44
26:4:515:ARG:HH22	26:4:718:SER:C	2.25	0.44
1:A:401:C:O2'	1:A:621:A:N3	2.45	0.43
1:A:673:A:O2'	1:A:674:G:H5'	2.17	0.43
1:A:1188:A:H2'	1:A:1189:U:O4'	2.17	0.43
1:A:1319:A:N7	1:A:1323:G:C5	2.86	0.43
1:A:1413:A:H61	1:A:1487:G:C1'	2.30	0.43
1:A:1486:G:H1'	1:A:1487:G:C1'	2.48	0.43
4:D:175:LEU:HD21	4:D:201:TRP:CD1	2.53	0.43
12:L:14:LYS:HG2	12:L:15:GLN:H	1.83	0.43
13:M:15:LYS:HD3	13:M:15:LYS:H	1.82	0.43
20:T:10:PHE:HE2	20:T:37:ARG:HG3	1.82	0.43
25:3:1272:GLU:HG2	25:3:1276:TRP:NE1	2.33	0.43
26:4:218:THR:HA	26:4:221:ILE:HG12	2.00	0.43
26:4:676:GLY:O	26:4:680:ASN:ND2	2.51	0.43
26:4:1175:LEU:HD22	26:4:1190:ILE:HD12	2.00	0.43
1:A:1160:G:C2	1:A:1161:C:C6	3.06	0.43
1:A:1315:U:O2	1:A:1360:A:H2	2.01	0.43
1:A:1507:A:H2'	1:A:1508:A:H8	1.83	0.43
12:L:65:VAL:HB	12:L:69:ARG:NH2	2.34	0.43
23:Z:90:MET:HB2	28:6:18:DG:H4'	2.00	0.43
25:3:297:VAL:HA	25:3:335:THR:HG22	2.00	0.43
25:3:1129:ASN:O	25:3:1133:LYS:N	2.42	0.43
1:A:266:G:H3'	18:R:69:LYS:HB2	2.00	0.43
1:A:590:U:H2'	1:A:591:U:C6	2.53	0.43
1:A:702:A:H5''	1:A:703:G:N7	2.33	0.43
1:A:737:C:C2	1:A:738:C:C5	3.06	0.43
1:A:933:G:O6	8:H:3:ARG:NH1	2.52	0.43
1:A:1188:A:O5'	1:A:1188:A:H8	2.01	0.43
1:A:1326:U:H2'	1:A:1327:C:H6	1.82	0.43
1:A:1426:G:C6	1:A:1475:G:C5	3.07	0.43
1:A:1484:C:H2'	1:A:1485:U:C6	2.54	0.43
3:C:131:LYS:HE3	3:C:131:LYS:HB3	1.80	0.43
7:G:4:TYR:CD2	7:G:71:ILE:HG21	2.53	0.43
8:H:130:ASN:OD1	8:H:130:ASN:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:1:91:ARG:HH21	24:1:122:GLU:CD	2.26	0.43
26:4:641:ILE:HD11	26:4:764:ARG:HG3	1.99	0.43
28:6:36:DA:H2'	28:6:36:DA:OP2	2.18	0.43
1:A:188:C:H2'	1:A:189:A:C8	2.54	0.43
1:A:519:C:H2'	1:A:520:A:O4'	2.19	0.43
1:A:693:G:O2'	1:A:694:A:OP1	2.33	0.43
1:A:1121:U:C2	1:A:1122:U:C5	3.06	0.43
26:4:74:LYS:NZ	26:4:87:LYS:HB2	2.33	0.43
26:4:865:HIS:CD2	26:4:867:GLN:H	2.32	0.43
1:A:269:C:N4	1:A:270:A:H62	2.17	0.43
3:C:117:LEU:HD23	3:C:117:LEU:HA	1.80	0.43
17:Q:21:VAL:O	17:Q:33:ILE:N	2.50	0.43
25:3:316:GLU:H	25:3:316:GLU:CD	2.26	0.43
25:3:615:VAL:HG22	25:3:650:VAL:HG23	2.00	0.43
26:4:196:GLN:HE21	26:4:196:GLN:HB3	1.62	0.43
26:4:985:ILE:HD11	26:4:989:GLY:HA2	2.00	0.43
1:A:1169:A:H2'	1:A:1170:A:C8	2.53	0.43
2:B:44:SER:HA	3:C:206:ALA:HA	2.00	0.43
3:C:165:ASP:OD2	3:C:168:HIS:HB2	2.18	0.43
4:D:151:VAL:HG12	4:D:200:VAL:HG22	1.99	0.43
14:N:95:LEU:HB3	14:N:96:PRO:HD2	1.99	0.43
24:1:102:LEU:O	24:1:141:SER:HA	2.19	0.43
24:2:207:THR:OG1	24:2:208:ASN:N	2.51	0.43
25:3:750:ILE:HD13	25:3:963:GLU:OE2	2.18	0.43
26:4:884:SER:OG	26:4:1254:GLU:OE1	2.29	0.43
1:A:184:G:H2'	1:A:185:U:C6	2.54	0.43
1:A:463:U:O2	1:A:463:U:O4'	2.36	0.43
1:A:636:U:H2'	1:A:637:C:C6	2.54	0.43
1:A:782:A:H62	1:A:800:G:N2	2.17	0.43
1:A:1123:U:O2'	1:A:1124:G:H5'	2.19	0.43
1:A:1475:G:OP1	1:A:1475:G:H4'	2.19	0.43
11:K:88:MET:HE3	23:Z:141:PHE:HD1	1.76	0.43
14:N:83:LEU:HD13	20:T:65:GLU:HB3	2.00	0.43
23:Z:22:VAL:HG22	23:Z:88:ARG:HB2	1.99	0.43
23:Z:165:PHE:O	23:Z:167:ARG:N	2.47	0.43
24:1:228:LEU:HD21	24:2:224:LEU:HB3	2.01	0.43
25:3:289:VAL:O	25:3:293:ALA:N	2.49	0.43
26:4:132:LEU:HA	26:4:135:ILE:HG12	2.01	0.43
28:6:14:DT:H2''	28:6:15:DA:H5'	1.99	0.43
1:A:72:A:H61	1:A:98:A:H2	1.67	0.43
1:A:806:C:H2'	1:A:807:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:997:U:H2'	1:A:998:C:O4'	2.19	0.43
1:A:1465:A:H2'	1:A:1466:C:H6	1.84	0.43
21:U:4:ILE:O	21:U:8:LYS:HG3	2.19	0.43
25:3:595:THR:OG1	25:3:600:THR:OG1	2.31	0.43
26:4:847:ASP:N	26:4:847:ASP:OD1	2.50	0.43
1:A:967:5MC:H2'	1:A:968:A:C8	2.54	0.43
1:A:1410:A:O5'	1:A:1410:A:H8	2.02	0.43
21:U:50:ALA:HA	21:U:53:GLU:HG2	2.01	0.43
24:1:231:PHE:CD1	24:2:217:ILE:HD11	2.54	0.43
25:3:540:ARG:NH1	25:3:568:ASN:OD1	2.51	0.43
1:A:1312:G:H5'	20:T:5:LEU:HD11	2.01	0.43
1:A:1489:G:OP1	1:A:1489:G:C4'	2.58	0.43
8:H:17:LYS:HE3	8:H:18:PHE:CZ	2.54	0.43
9:I:18:GLN:HG2	9:I:63:LEU:HD13	2.01	0.43
23:Z:155:LYS:HB3	23:Z:157:ARG:HB2	2.01	0.43
25:3:228:VAL:HB	25:3:245:ARG:NH1	2.34	0.43
25:3:582:ASN:OD1	25:3:583:GLU:N	2.48	0.43
26:4:786:THR:HA	26:4:789:LYS:HZ3	1.84	0.43
28:6:20:DT:O2	28:6:20:DT:H2'	2.18	0.43
1:A:6:G:H3'	1:A:6:G:N3	2.34	0.42
1:A:840:C:H2'	1:A:841:C:H5''	2.01	0.42
1:A:967:5MC:OP2	1:A:967:5MC:C6	2.60	0.42
1:A:981:U:O5'	1:A:981:U:H6	2.01	0.42
1:A:1272:G:H2'	1:A:1273:C:C6	2.54	0.42
1:A:1302:C:C6	14:N:17:ILE:HG21	2.54	0.42
1:A:1308:U:H2'	1:A:1309:G:C8	2.54	0.42
5:E:11:LEU:O	5:E:15:GLU:HG2	2.19	0.42
5:E:144:SER:HB3	5:E:179:GLU:HG3	2.00	0.42
18:R:62:ARG:HG3	18:R:74:THR:HG23	2.01	0.42
22:X:6:G:H8	22:X:6:G:C5'	2.27	0.42
25:3:93:SER:OG	25:3:126:GLU:OE1	2.32	0.42
25:3:184:LEU:HB2	25:3:389:PHE:CE1	2.54	0.42
25:3:406:ASN:HD22	25:3:414:ILE:HA	1.83	0.42
26:4:289:ASP:HA	26:4:292:VAL:HG22	2.01	0.42
26:4:399:LYS:O	26:4:403:ARG:HG2	2.19	0.42
26:4:588:PRO:O	26:4:591:ILE:HG12	2.19	0.42
1:A:83:C:H2'	1:A:85:U:C4	2.54	0.42
1:A:562:U:C4	13:M:15:LYS:HD2	2.54	0.42
1:A:706:A:C6	1:A:707:U:C4	3.08	0.42
1:A:1147:C:O2	10:J:18:ARG:NH1	2.52	0.42
1:A:1157:A:OP2	3:C:131:LYS:HE2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1389:C:OP2	1:A:1389:C:C6	2.72	0.42
1:A:1417:G:C6	1:A:1482:G:C6	3.07	0.42
7:G:90:MET:HE3	7:G:90:MET:HB2	1.92	0.42
24:1:192:VAL:HG12	24:1:193:GLU:HG3	2.00	0.42
25:3:1140:LYS:O	25:3:1143:GLU:HB3	2.18	0.42
25:3:1256:GLN:HB3	25:3:1301:ARG:NH2	2.32	0.42
26:4:981:GLU:HG2	26:4:996:LYS:HG3	2.01	0.42
1:A:1005:A:H3'	1:A:1006:G:H8	1.84	0.42
13:M:110:ARG:HB3	13:M:119:VAL:HG21	2.01	0.42
18:R:65:ARG:NH1	18:R:66:PRO:O	2.53	0.42
25:3:211:ARG:HB2	25:3:362:ALA:HB2	2.02	0.42
26:4:305:ALA:O	26:4:309:ASN:HB2	2.19	0.42
26:4:516:ASP:HB3	26:4:573:THR:HG21	2.01	0.42
27:5:25:ARG:HH21	27:5:68:GLU:CD	2.28	0.42
1:A:152:A:N6	1:A:169:C:C2	2.86	0.42
1:A:160:A:H2'	1:A:161:A:O4'	2.19	0.42
1:A:427:U:OP1	5:E:13:ARG:NH1	2.49	0.42
1:A:706:A:H2'	1:A:707:U:C6	2.54	0.42
1:A:1488:G:H2'	1:A:1489:G:O4'	2.20	0.42
4:D:138:VAL:HG22	4:D:149:ILE:CD1	2.49	0.42
5:E:10:LYS:HE3	5:E:10:LYS:HB2	1.85	0.42
11:K:65:TYR:HE1	15:O:98:LYS:HZ3	1.67	0.42
24:1:91:ARG:HD3	24:1:210:THR:O	2.19	0.42
25:3:632:ASP:N	25:3:632:ASP:OD1	2.52	0.42
26:4:460:ASP:N	26:4:460:ASP:OD1	2.49	0.42
26:4:742:GLY:O	26:4:762:ASN:ND2	2.52	0.42
1:A:62:U:H2'	1:A:63:C:C6	2.55	0.42
1:A:98:A:H2'	1:A:99:C:C6	2.54	0.42
1:A:471:U:H2'	1:A:472:U:H6	1.84	0.42
1:A:1007:U:H2'	1:A:1008:U:C6	2.54	0.42
1:A:1133:G:C2	1:A:1142:G:C2	3.08	0.42
4:D:138:VAL:HG22	4:D:149:ILE:HD12	2.00	0.42
5:E:161:LEU:HD12	5:E:161:LEU:H	1.84	0.42
7:G:10:VAL:HG13	7:G:58:HIS:HB3	2.01	0.42
15:O:46:LEU:O	15:O:50:THR:HG23	2.19	0.42
19:S:72:ASP:OD1	19:S:72:ASP:N	2.47	0.42
22:X:52:C:H2'	22:X:53:G:O4'	2.20	0.42
24:2:191:ARG:HB3	24:2:196:THR:HA	2.02	0.42
25:3:1280:ALA:HB1	26:4:431:ARG:HD2	2.02	0.42
26:4:634:ARG:HA	26:4:634:ARG:HD2	1.76	0.42
27:5:3:ARG:HA	27:5:3:ARG:HD3	1.79	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:A:H2'	1:A:132:C:H6	1.84	0.42
1:A:253:A:H2'	1:A:254:G:H8	1.83	0.42
1:A:417:G:H2'	1:A:418:C:C6	2.54	0.42
1:A:552:U:C2	1:A:553:A:N7	2.88	0.42
1:A:591:U:C2	1:A:592:G:C8	3.07	0.42
1:A:1277:C:C2'	1:A:1279:G:H8	2.31	0.42
1:A:1454:G:H8	1:A:1454:G:OP2	2.02	0.42
3:C:96:TRP:CZ2	3:C:100:MET:HB2	2.55	0.42
8:H:80:VAL:HG21	8:H:154:TYR:HB3	2.01	0.42
15:O:47:LYS:O	15:O:50:THR:OG1	2.26	0.42
25:3:1085:MET:HE2	25:3:1085:MET:HA	2.02	0.42
25:3:1164:PHE:HB2	25:3:1169:VAL:HG23	2.00	0.42
26:4:336:GLY:O	26:4:340:GLN:CB	2.68	0.42
1:A:842:U:H2'	1:A:843:U:C6	2.54	0.42
1:A:1025:U:H4'	1:A:1026:G:H5'	2.02	0.42
1:A:1315:U:H2'	1:A:1316:G:O4'	2.20	0.42
1:A:1400:C:H4'	1:A:1517:G:N2	2.35	0.42
1:A:1419:G:O6	1:A:1481:U:O4	2.38	0.42
1:A:1538:C:H2'	1:A:1539:C:H6	1.83	0.42
4:D:45:LYS:HB3	4:D:45:LYS:HE3	1.76	0.42
5:E:159:LEU:HD23	5:E:159:LEU:HA	1.91	0.42
11:K:8:ILE:HG23	11:K:98:VAL:HG23	2.01	0.42
15:O:83:LYS:HA	15:O:83:LYS:HD3	1.80	0.42
23:Z:151:VAL:HG12	23:Z:153:TYR:HB2	2.02	0.42
26:4:275:ARG:NH1	26:4:298:MET:HB3	2.24	0.42
26:4:1176:VAL:HA	26:4:1187:GLU:HA	2.01	0.42
1:A:206:C:H2'	1:A:207:C:H6	1.85	0.42
1:A:284:C:H2'	1:A:285:C:C6	2.54	0.42
1:A:441:A:H1'	1:A:497:G:N2	2.34	0.42
1:A:470:C:H2'	1:A:471:U:H6	1.85	0.42
1:A:558:G:OP2	1:A:559:A:O2'	2.30	0.42
1:A:1061:G:N7	4:D:3:GLN:NE2	2.68	0.42
5:E:50:ASP:N	5:E:50:ASP:OD1	2.52	0.42
6:F:77:ASN:HB2	6:F:82:GLN:NE2	2.35	0.42
12:L:64:GLN:HG2	12:L:95:SER:O	2.20	0.42
23:Z:87:PRO:CA	28:6:19:DA:H8	2.29	0.42
25:3:155:VAL:HA	25:3:175:ARG:O	2.20	0.42
26:4:1265:THR:HA	26:4:1279:GLN:HA	2.02	0.42
1:A:211:G:C4	1:A:212:G:H1'	2.55	0.42
1:A:470:C:H2'	1:A:471:U:C6	2.55	0.42
1:A:635:A:H2'	1:A:636:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:691:G:H2'	1:A:692:U:C6	2.54	0.42
1:A:737:C:H2'	1:A:738:C:H6	1.85	0.42
1:A:801:U:C2	1:A:802:A:C8	3.07	0.42
1:A:832:G:C6	1:A:855:U:C4	3.07	0.42
1:A:902:G:H2'	1:A:903:G:C8	2.54	0.42
1:A:1006:G:N1	1:A:1024:G:H1'	2.35	0.42
1:A:1236:A:H2'	1:A:1237:C:C6	2.54	0.42
1:A:1435:G:H2'	1:A:1436:U:H6	1.85	0.42
2:B:132:PRO:HG2	2:B:135:LEU:HD12	2.02	0.42
4:D:79:LYS:HB3	4:D:79:LYS:HE3	1.88	0.42
5:E:78:GLU:OE2	5:E:81:ARG:NH2	2.39	0.42
8:H:47:LEU:HD23	8:H:47:LEU:HA	1.82	0.42
8:H:138:ARG:HD3	8:H:142:HIS:CE1	2.54	0.42
23:Z:153:TYR:HD1	23:Z:153:TYR:HA	1.75	0.42
25:3:19:PRO:HA	25:3:1156:ARG:HD3	2.02	0.42
25:3:837:ALA:HB1	25:3:1049:ILE:HD11	2.00	0.42
25:3:1246:ARG:NE	26:4:348:ASP:OD1	2.34	0.42
26:4:257:GLY:HA3	26:4:259:ARG:NH2	2.34	0.42
26:4:1169:THR:HG23	26:4:1173:ARG:N	2.35	0.42
28:6:22:DT:OP2	28:6:22:DT:C2	2.73	0.42
29:7:8:DT:H2''	29:7:9:DC:H6	1.83	0.42
1:A:77:A:H2'	1:A:78:A:C8	2.55	0.42
1:A:158:G:C6	1:A:164:G:C5	3.08	0.42
1:A:171:A:H2'	1:A:172:A:C8	2.55	0.42
1:A:562:U:H1'	13:M:12:ARG:HD3	2.02	0.42
1:A:938:A:N3	1:A:1376:U:O2'	2.38	0.42
1:A:1166:G:O2'	1:A:1169:A:N6	2.53	0.42
2:B:101:ALA:O	2:B:105:ALA:N	2.52	0.42
3:C:188:ASP:OD1	3:C:189:THR:N	2.47	0.42
5:E:65:TYR:OH	5:E:95:GLU:OE1	2.23	0.42
15:O:46:LEU:HD13	20:T:13:LEU:HD13	2.01	0.42
21:U:34:LYS:HB2	21:U:34:LYS:HE3	1.88	0.42
23:Z:15:PHE:CD1	28:6:18:DG:C8	3.07	0.42
24:1:27:THR:HB	24:1:202:VAL:HG22	2.02	0.42
25:3:1325:VAL:HG13	26:4:249:LEU:HD13	2.01	0.42
26:4:865:HIS:CE1	26:4:868:TRP:HD1	2.38	0.42
26:4:1157:ALA:HB3	26:4:1208:ASP:HB3	2.02	0.42
26:4:1281:GLU:H	26:4:1281:GLU:CD	2.28	0.42
1:A:90:C:H1'	1:A:91:U:H5'	2.02	0.41
1:A:1000:A:H2'	1:A:1001:C:H6	1.84	0.41
1:A:1254:A:H2'	1:A:1255:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1400:C:H4'	1:A:1517:G:C2	2.55	0.41
8:H:50:LEU:HD22	8:H:124:LEU:HD13	2.02	0.41
12:L:66:ALA:O	12:L:69:ARG:HG2	2.19	0.41
24:2:196:THR:OG1	26:4:370:LYS:NZ	2.33	0.41
24:2:196:THR:HG1	26:4:370:LYS:HZ1	1.59	0.41
26:4:72:CYS:HB3	26:4:88:CYS:HB2	2.01	0.41
26:4:510:LEU:HD22	26:4:601:ILE:HD12	2.02	0.41
26:4:720:ASN:HD21	26:4:722:ILE:HB	1.84	0.41
26:4:793:SER:O	26:4:797:THR:HG23	2.19	0.41
26:4:803:VAL:HG21	26:4:1309:ILE:HG22	2.02	0.41
28:6:31:DG:H2''	28:6:32:DA:C8	2.55	0.41
29:7:2:DT:H2''	29:7:3:DC:C6	2.55	0.41
1:A:472:U:H2'	1:A:473:U:C6	2.55	0.41
1:A:1121:U:H2'	1:A:1122:U:C6	2.55	0.41
5:E:188:ARG:HH22	5:E:193:ALA:HA	1.86	0.41
25:3:593:LYS:HB2	25:3:604:HIS:HD2	1.84	0.41
26:4:47:ARG:NH1	26:4:47:ARG:HA	2.35	0.41
26:4:1075:ARG:HD2	26:4:1075:ARG:HA	1.86	0.41
26:4:1160:SER:HB2	26:4:1203:ARG:HH12	1.84	0.41
26:4:1323:ALA:O	26:4:1328:THR:OG1	2.29	0.41
1:A:377:G:H2'	1:A:378:G:C8	2.56	0.41
1:A:552:U:N3	1:A:553:A:N7	2.69	0.41
1:A:768:A:H4'	1:A:1523:G:H21	1.85	0.41
1:A:777:A:H2'	1:A:778:G:C8	2.55	0.41
1:A:1398:A:H61	1:A:1399:C:N4	2.18	0.41
2:B:73:ASP:HB2	2:B:83:LEU:O	2.20	0.41
11:K:59:LYS:HE3	11:K:62:ARG:HH22	1.85	0.41
24:1:25:LYS:HG2	24:1:204:GLU:HB3	2.01	0.41
24:1:30:PRO:HB3	24:1:198:LEU:HD23	2.02	0.41
25:3:59:ILE:HD11	25:3:476:LYS:HG3	2.02	0.41
25:3:178:PRO:HB3	25:3:395:TYR:CZ	2.55	0.41
25:3:1166:ASP:OD1	25:3:1166:ASP:N	2.52	0.41
25:3:1247:SER:HB3	26:4:375:GLU:O	2.20	0.41
26:4:816:THR:OG1	26:4:818:GLU:OE1	2.35	0.41
26:4:830:ASP:OD1	26:4:830:ASP:N	2.50	0.41
26:4:1369:ARG:HH12	26:4:1373:ARG:HD2	1.85	0.41
1:A:337:G:C2	1:A:338:A:C5	3.08	0.41
1:A:428:G:OP2	5:E:10:LYS:NZ	2.37	0.41
1:A:841:C:N4	1:A:845:A:H62	2.18	0.41
1:A:965:U:H1'	1:A:969:A:C4	2.55	0.41
1:A:1120:C:C2	1:A:1121:U:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1391:U:O2	1:A:1391:U:C2'	2.56	0.41
4:D:85:GLU:OE2	4:D:89:LYS:HE2	2.21	0.41
6:F:25:VAL:HG22	6:F:26:LYS:H	1.85	0.41
8:H:37:SER:HB3	10:J:41:ARG:NH1	2.35	0.41
24:1:84:ASN:ND2	24:1:129:VAL:O	2.54	0.41
25:3:696:ASP:O	25:3:790:ASP:HB3	2.20	0.41
25:3:1151:LEU:HD11	25:3:1197:GLU:HG2	2.03	0.41
26:4:113:HIS:HB3	26:4:116:PHE:HD2	1.86	0.41
26:4:264:ASP:OD1	26:4:264:ASP:N	2.53	0.41
26:4:591:ILE:HG13	26:4:592:VAL:HG13	2.02	0.41
1:A:57:G:H2'	1:A:58:C:C6	2.56	0.41
1:A:256:U:C2	1:A:257:G:C8	3.09	0.41
1:A:343:U:H2'	1:A:345:C:N4	2.34	0.41
1:A:592:G:H2'	1:A:593:U:C6	2.55	0.41
1:A:1007:U:H2'	1:A:1008:U:H6	1.85	0.41
1:A:1063:C:OP2	1:A:1064:G:O2'	2.29	0.41
3:C:182:PRO:HA	3:C:197:ASP:OD2	2.21	0.41
4:D:43:LEU:HD23	4:D:43:LEU:HA	1.93	0.41
7:G:37:HIS:HB3	7:G:96:VAL:O	2.21	0.41
18:R:60:GLU:HB3	18:R:76:VAL:HG12	2.02	0.41
24:1:50:SER:HB3	24:2:8:PHE:CZ	2.56	0.41
24:2:42:ALA:O	24:2:46:ILE:HG12	2.21	0.41
25:3:453:ILE:HD12	25:3:587:LEU:HD21	2.03	0.41
25:3:475:VAL:HG21	25:3:492:MET:HB3	2.01	0.41
26:4:425:ARG:HE	26:4:464:ASP:CG	2.29	0.41
26:4:701:LEU:HD23	26:4:701:LEU:HA	1.92	0.41
26:4:1266:ILE:HD13	26:4:1274:PHE:HB3	2.03	0.41
28:6:22:DT:O2	28:6:22:DT:H2'	2.20	0.41
1:A:600:A:H2'	1:A:601:G:H8	1.86	0.41
1:A:1041:G:H2'	1:A:1042:A:C8	2.55	0.41
1:A:1368:A:OP2	10:J:114:LYS:HD2	2.20	0.41
25:3:1313:HIS:HB2	27:5:31:GLN:HE22	1.85	0.41
26:4:40:LYS:O	26:4:55:GLY:HA2	2.21	0.41
26:4:122:SER:O	26:4:126:LEU:N	2.44	0.41
26:4:558:ASP:OD1	26:4:561:GLY:N	2.42	0.41
26:4:1140:ARG:HH12	26:4:1144:LEU:HD12	1.85	0.41
1:A:167:A:H2'	1:A:168:G:C8	2.54	0.41
1:A:361:G:H2'	1:A:362:G:O4'	2.21	0.41
1:A:882:C:O2	1:A:882:C:H2'	2.21	0.41
1:A:1319:A:N7	1:A:1323:G:C6	2.89	0.41
1:A:1456:A:H2'	1:A:1457:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:62:LYS:O	4:D:97:VAL:HB	2.21	0.41
4:D:142:MET:HG3	4:D:170:GLU:OE1	2.21	0.41
20:T:27:ASP:OD1	20:T:29:LYS:HG2	2.20	0.41
21:U:32:ILE:O	21:U:35:VAL:HG12	2.21	0.41
23:Z:159:LYS:HA	23:Z:172:GLU:HA	2.03	0.41
24:2:66:HIS:ND1	24:2:68:TYR:HB3	2.35	0.41
25:3:270:THR:O	25:3:274:ILE:HG13	2.20	0.41
25:3:425:ILE:O	25:3:429:MET:HG3	2.20	0.41
26:4:576:ARG:HD3	26:4:593:ASN:HA	2.03	0.41
26:4:978:ARG:HB2	26:4:1197:ASN:HD21	1.86	0.41
27:5:21:LEU:HD12	27:5:21:LEU:HA	1.84	0.41
1:A:427:U:OP2	1:A:428:G:O2'	2.24	0.41
1:A:455:G:C2	1:A:478:A:C2	3.09	0.41
1:A:677:U:O2	1:A:777:A:O2'	2.37	0.41
1:A:704:A:C5	1:A:705:G:C8	3.09	0.41
1:A:1124:G:H3'	11:K:37:ARG:HH12	1.85	0.41
18:R:31:HIS:HB3	18:R:35:GLY:H	1.85	0.41
24:1:102:LEU:HB3	24:1:142:MET:HG2	2.02	0.41
25:3:228:VAL:HG13	25:3:335:THR:OG1	2.20	0.41
25:3:555:TYR:O	25:3:557:ARG:NH1	2.54	0.41
26:4:518:VAL:HB	26:4:707:ILE:HG21	2.03	0.41
1:A:29:U:O2'	1:A:30:U:H5'	2.21	0.41
1:A:150:U:H3	1:A:171:A:H62	1.69	0.41
1:A:228:A:H4'	17:Q:63:GLN:NE2	2.36	0.41
1:A:284:C:H2'	1:A:285:C:H6	1.86	0.41
1:A:335:C:H2'	1:A:336:A:H8	1.85	0.41
1:A:415:A:C4	1:A:416:G:C8	3.08	0.41
1:A:512:U:OP1	5:E:44:ARG:NH2	2.54	0.41
1:A:551:U:H2'	1:A:552:U:H6	1.85	0.41
1:A:578:C:H2'	1:A:579:A:C8	2.56	0.41
1:A:709:U:C2	1:A:710:G:C8	3.09	0.41
1:A:757:U:OP1	1:A:822:U:O2'	2.34	0.41
1:A:795:C:H5''	12:L:128:ARG:NH1	2.36	0.41
1:A:908:A:H2'	1:A:909:A:H8	1.86	0.41
1:A:1064:G:H1'	1:A:1190:G:N2	2.36	0.41
1:A:1158:C:C4	1:A:1160:G:C8	3.09	0.41
1:A:1187:G:H2'	1:A:1188:A:C8	2.56	0.41
1:A:1307:U:H5'	14:N:108:THR:HG21	2.01	0.41
1:A:1426:G:H2'	1:A:1427:C:H6	1.84	0.41
2:B:98:LEU:HD13	2:B:166:VAL:HG21	2.03	0.41
2:B:120:PHE:CE1	2:B:136:VAL:HG21	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:6:ILE:HG13	11:K:76:ILE:HB	2.03	0.41
20:T:45:ILE:HD11	20:T:67:VAL:HG22	2.03	0.41
21:U:69:LYS:HB3	21:U:69:LYS:HE2	1.88	0.41
23:Z:15:PHE:N	28:6:18:DG:H2'	2.36	0.41
23:Z:45:PRO:O	23:Z:63:LYS:HG3	2.21	0.41
25:3:16:GLY:HA3	25:3:1156:ARG:HH21	1.85	0.41
25:3:349:GLU:O	25:3:353:VAL:HG23	2.21	0.41
26:4:709:ARG:C	26:4:711:GLY:H	2.27	0.41
26:4:960:LEU:HB3	26:4:963:VAL:HG21	2.02	0.41
26:4:1323:ALA:HB1	26:4:1328:THR:HG23	2.03	0.41
28:6:10:DG:H2''	28:6:11:DT:C5	2.56	0.41
1:A:57:G:H2'	1:A:58:C:H6	1.85	0.41
1:A:317:U:N3	1:A:318:G:N7	2.68	0.41
1:A:678:U:H2'	1:A:679:C:H6	1.86	0.41
1:A:769:G:H4'	1:A:1513:A:H4'	2.03	0.41
1:A:1478:U:C2'	1:A:1479:C:H5''	2.51	0.41
12:L:94:GLU:O	12:L:97:ILE:N	2.54	0.41
24:1:231:PHE:HD1	24:2:217:ILE:HD11	1.85	0.41
25:3:1176:LEU:HD22	25:3:1180:MET:HA	2.02	0.41
26:4:641:ILE:HD12	26:4:641:ILE:HA	1.90	0.41
26:4:958:ILE:HD12	26:4:982:LEU:HD11	2.03	0.41
26:4:1108:GLN:HE21	26:4:1108:GLN:HB2	1.64	0.41
1:A:256:U:H2'	1:A:257:G:C8	2.56	0.40
1:A:432:A:H2'	1:A:433:G:O4'	2.22	0.40
1:A:777:A:H2'	1:A:778:G:H8	1.86	0.40
1:A:830:G:H2'	1:A:831:A:C8	2.56	0.40
1:A:838:G:C6	1:A:849:G:C6	3.09	0.40
1:A:925:G:H1'	1:A:1392:G:N2	2.36	0.40
1:A:1034:G:H2'	1:A:1035:A:H8	1.85	0.40
1:A:1036:A:H2'	1:A:1037:C:O4'	2.22	0.40
1:A:1117:A:N6	1:A:1156:G:H22	2.18	0.40
10:J:18:ARG:HG3	10:J:66:THR:HB	2.03	0.40
21:U:54:MET:HB3	21:U:54:MET:HE3	1.78	0.40
23:Z:149:GLU:OE2	23:Z:159:LYS:HG2	2.21	0.40
25:3:805:MET:HE1	25:3:1221:PHE:CZ	2.56	0.40
25:3:848:GLU:HG2	25:3:889:PRO:HD3	2.02	0.40
26:4:813:ASP:OD2	26:4:897:HIS:ND1	2.54	0.40
26:4:1069:ALA:HA	26:4:1072:LYS:HB2	2.02	0.40
1:A:1070:U:H2'	1:A:1071:C:H6	1.86	0.40
1:A:1421:G:H2'	1:A:1422:G:H8	1.85	0.40
1:A:1488:G:H3'	1:A:1488:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:54:ARG:HB3	4:D:69:HIS:HB2	2.03	0.40
5:E:106:GLY:HA3	5:E:162:ALA:HB2	2.03	0.40
6:F:15:LEU:HA	6:F:37:THR:HG22	2.03	0.40
25:3:191:LYS:HD3	25:3:191:LYS:HA	1.89	0.40
25:3:757:THR:O	25:3:765:ILE:HG12	2.21	0.40
25:3:1146:GLN:NE2	25:3:1159:VAL:O	2.53	0.40
26:4:974:VAL:HA	26:4:1002:VAL:HA	2.02	0.40
1:A:71:A:O2'	1:A:72:A:H8	2.02	0.40
1:A:208:U:H2'	1:A:210:C:C5	2.56	0.40
1:A:312:C:C2	1:A:313:A:C8	3.09	0.40
1:A:453:G:C4	1:A:454:G:C8	3.09	0.40
1:A:579:A:H2'	1:A:580:C:C6	2.56	0.40
1:A:967:5MC:OP1	1:A:969:A:H5'	2.20	0.40
1:A:1277:C:H1'	1:A:1282:C:O2	2.20	0.40
3:C:73:LYS:HE2	3:C:165:ASP:OD2	2.21	0.40
3:C:107:VAL:O	3:C:111:ILE:HG12	2.21	0.40
5:E:100:ASN:ND2	5:E:111:ARG:HH21	2.19	0.40
7:G:12:PRO:HD3	7:G:57:ALA:HA	2.03	0.40
10:J:119:ARG:HH21	10:J:123:ARG:NE	2.19	0.40
12:L:25:ALA:HB1	12:L:90:GLY:HA3	2.04	0.40
12:L:78:GLY:O	12:L:80:LYS:NZ	2.34	0.40
13:M:7:LEU:HB3	18:R:34:TYR:CZ	2.57	0.40
14:N:44:LYS:H	14:N:44:LYS:HG2	1.56	0.40
24:2:11:PRO:HG2	24:2:28:LEU:HD12	2.02	0.40
25:3:719:LYS:H	25:3:751:TYR:HH	1.63	0.40
26:4:152:THR:HG22	26:4:172:PHE:CD1	2.56	0.40
29:7:23:DC:H3'	29:7:23:DC:OP2	2.22	0.40
1:A:344:A:H5''	1:A:345:C:H5	1.86	0.40
1:A:579:A:H5'	1:A:728:A:H1'	2.03	0.40
1:A:632:U:H5''	1:A:633:G:C8	2.56	0.40
1:A:662:U:H2'	1:A:663:A:C8	2.57	0.40
1:A:916:U:H2'	1:A:917:G:C8	2.56	0.40
1:A:1029:U:H2'	1:A:1031:C:N3	2.36	0.40
1:A:1524:C:C2	1:A:1525:G:C8	3.10	0.40
10:J:59:GLU:HG3	10:J:59:GLU:H	1.72	0.40
11:K:4:GLN:CD	11:K:4:GLN:H	2.29	0.40
19:S:70:TYR:HB2	19:S:74:HIS:CE1	2.56	0.40
21:U:49:LYS:HA	21:U:52:ASN:ND2	2.37	0.40
23:Z:174:ASP:OD1	23:Z:175:PHE:N	2.55	0.40
24:1:18:GLN:NE2	24:1:24:ALA:HB2	2.36	0.40
24:1:66:HIS:CE1	24:1:69:SER:HB2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:1177:ILE:HB	26:4:1186:TYR:CD2	2.52	0.40
1:A:80:A:C6	1:A:81:A:C5	3.10	0.40
1:A:100:G:C4	1:A:101:A:C8	3.10	0.40
1:A:410:G:H2'	1:A:429:U:C5	2.56	0.40
1:A:790:A:OP1	1:A:790:A:C4'	2.70	0.40
1:A:1130:A:H2'	1:A:1131:G:C8	2.53	0.40
1:A:1305:G:H22	1:A:1331:G:H1'	1.86	0.40
1:A:1488:G:H3'	1:A:1489:G:C5'	2.46	0.40
7:G:45:ARG:HH12	7:G:106:LYS:NZ	2.19	0.40
11:K:22:THR:O	11:K:26:VAL:HG12	2.22	0.40
13:M:63:VAL:HG21	13:M:95:TYR:CE1	2.57	0.40
14:N:3:ARG:HE	14:N:6:GLY:HA2	1.86	0.40
19:S:24:LYS:HE2	19:S:24:LYS:HB2	1.97	0.40
20:T:45:ILE:HD13	20:T:62:VAL:HG12	2.03	0.40
21:U:28:MET:HG3	21:U:58:VAL:HG12	2.02	0.40
23:Z:104:SER:HB2	23:Z:107:GLU:HB2	2.02	0.40
24:1:8:PHE:O	24:1:10:LYS:NZ	2.54	0.40
25:3:646:SER:O	25:3:649:GLN:HB3	2.22	0.40
25:3:1038:GLN:O	25:3:1038:GLN:NE2	2.48	0.40
26:4:156:ARG:NH2	26:4:191:SER:OG	2.55	0.40
26:4:308:ASP:OD2	26:4:311:ARG:NE	2.53	0.40
26:4:515:ARG:HH21	26:4:717:VAL:HB	1.86	0.40
26:4:597:GLY:H	26:4:600:ALA:HB3	1.87	0.40
26:4:919:ALA:HA	26:4:1252:HIS:CD2	2.56	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	171/557 (31%)	161 (94%)	10 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	222/241 (92%)	216 (97%)	6 (3%)	0	100	100
4	D	209/233 (90%)	204 (98%)	5 (2%)	0	100	100
5	E	203/206 (98%)	199 (98%)	3 (2%)	1 (0%)	24	57
6	F	155/157 (99%)	152 (98%)	3 (2%)	0	100	100
7	G	104/131 (79%)	101 (97%)	3 (3%)	0	100	100
8	H	151/156 (97%)	150 (99%)	1 (1%)	0	100	100
9	I	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
10	J	126/130 (97%)	121 (96%)	5 (4%)	0	100	100
11	K	99/103 (96%)	94 (95%)	4 (4%)	1 (1%)	12	41
12	L	115/129 (89%)	109 (95%)	4 (4%)	2 (2%)	7	30
13	M	120/124 (97%)	117 (98%)	3 (2%)	0	100	100
14	N	113/118 (96%)	111 (98%)	1 (1%)	1 (1%)	14	44
15	O	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
16	P	86/89 (97%)	86 (100%)	0	0	100	100
17	Q	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
18	R	78/84 (93%)	77 (99%)	1 (1%)	0	100	100
19	S	63/75 (84%)	62 (98%)	1 (2%)	0	100	100
20	T	81/92 (88%)	81 (100%)	0	0	100	100
21	U	84/87 (97%)	84 (100%)	0	0	100	100
23	Z	147/181 (81%)	133 (90%)	11 (8%)	3 (2%)	6	25
24	1	227/329 (69%)	223 (98%)	4 (2%)	0	100	100
24	2	215/329 (65%)	208 (97%)	7 (3%)	0	100	100
25	3	1316/1342 (98%)	1232 (94%)	84 (6%)	0	100	100
26	4	1327/1406 (94%)	1259 (95%)	66 (5%)	2 (0%)	43	73
27	5	88/91 (97%)	81 (92%)	7 (8%)	0	100	100
All	All	5805/6703 (87%)	5559 (96%)	236 (4%)	10 (0%)	44	73

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	Z	165	PHE
14	N	66	GLU
5	E	24	ASP

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Mol	Chain	Res	Type
11	K	57	VAL
12	L	119	ASN
23	Z	168	ALA
26	4	712	GLN
26	4	1159	ILE
12	L	91	PRO
23	Z	166	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	145/461 (32%)	139 (96%)	6 (4%)	27	59
3	C	186/199 (94%)	183 (98%)	3 (2%)	55	75
4	D	173/191 (91%)	168 (97%)	5 (3%)	37	66
5	E	173/174 (99%)	164 (95%)	9 (5%)	21	51
6	F	119/119 (100%)	114 (96%)	5 (4%)	26	58
7	G	92/112 (82%)	84 (91%)	8 (9%)	9	34
8	H	126/129 (98%)	121 (96%)	5 (4%)	28	60
9	I	104/105 (99%)	99 (95%)	5 (5%)	23	54
10	J	106/107 (99%)	99 (93%)	7 (7%)	15	43
11	K	88/90 (98%)	82 (93%)	6 (7%)	14	42
12	L	90/99 (91%)	74 (82%)	16 (18%)	2	9
13	M	102/103 (99%)	96 (94%)	6 (6%)	18	48
14	N	93/96 (97%)	89 (96%)	4 (4%)	26	57
15	O	83/84 (99%)	82 (99%)	1 (1%)	63	78
16	P	76/77 (99%)	76 (100%)	0	100	100
17	Q	65/65 (100%)	64 (98%)	1 (2%)	57	75
18	R	74/78 (95%)	72 (97%)	2 (3%)	39	67
19	S	56/65 (86%)	51 (91%)	5 (9%)	9	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	T	72/79 (91%)	69 (96%)	3 (4%)	26	58
21	U	65/66 (98%)	60 (92%)	5 (8%)	12	38
23	Z	135/158 (85%)	121 (90%)	14 (10%)	7	27
24	1	197/286 (69%)	187 (95%)	10 (5%)	21	52
24	2	187/286 (65%)	176 (94%)	11 (6%)	18	48
25	3	1139/1157 (98%)	1075 (94%)	64 (6%)	19	49
26	4	1118/1167 (96%)	1058 (95%)	60 (5%)	20	50
27	5	74/75 (99%)	73 (99%)	1 (1%)	59	76
All	All	4938/5628 (88%)	4676 (95%)	262 (5%)	22	51

All (262) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	19	ARG
2	B	43	LYS
2	B	69	ASP
2	B	72	LEU
2	B	155	LYS
2	B	160	ASP
3	C	5	SER
3	C	127	ASP
3	C	199	VAL
4	D	52	VAL
4	D	137	THR
4	D	149	ILE
4	D	182	ILE
4	D	192	THR
5	E	24	ASP
5	E	56	ARG
5	E	89	ASN
5	E	91	LEU
5	E	138	SER
5	E	142	VAL
5	E	145	ILE
5	E	146	ARG
5	E	194	ASP
6	F	22	SER
6	F	46	VAL
6	F	105	ILE

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Mol	Chain	Res	Type
6	F	142	ASP
6	F	151	GLU
7	G	2	ARG
7	G	18	VAL
7	G	21	MET
7	G	39	LEU
7	G	84	VAL
7	G	89	VAL
7	G	92	THR
7	G	97	THR
8	H	20	SER
8	H	75	VAL
8	H	83	SER
8	H	133	THR
8	H	153	HIS
9	I	67	GLN
9	I	72	VAL
9	I	99	LEU
9	I	101	ILE
9	I	121	LEU
10	J	29	VAL
10	J	32	GLN
10	J	58	VAL
10	J	60	LYS
10	J	63	LEU
10	J	67	VAL
10	J	94	LEU
11	K	36	VAL
11	K	52	LEU
11	K	57	VAL
11	K	89	ARG
11	K	92	LEU
11	K	98	VAL
12	L	20	VAL
12	L	31	ILE
12	L	32	VAL
12	L	33	THR
12	L	69	ARG
12	L	82	LEU
12	L	84	VAL
12	L	86	VAL
12	L	93	ARG

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Mol	Chain	Res	Type
12	L	94	GLU
12	L	95	SER
12	L	96	THR
12	L	97	ILE
12	L	108	THR
12	L	113	VAL
12	L	119	ASN
13	M	4	VAL
13	M	15	LYS
13	M	16	VAL
13	M	40	THR
13	M	63	VAL
13	M	87	VAL
14	N	28	THR
14	N	90	ARG
14	N	93	ARG
14	N	102	THR
15	O	24	ARG
17	Q	44	SER
18	R	22	VAL
18	R	76	VAL
19	S	14	THR
19	S	18	VAL
19	S	26	ILE
19	S	31	ASN
19	S	55	LEU
20	T	48	THR
20	T	51	VAL
20	T	79	THR
21	U	3	ASN
21	U	15	GLU
21	U	35	VAL
21	U	57	ILE
21	U	83	ILE
23	Z	15	PHE
23	Z	42	VAL
23	Z	103	ILE
23	Z	132	GLU
23	Z	133	MET
23	Z	143	ASP
23	Z	147	VAL
23	Z	152	ASP

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Mol	Chain	Res	Type
23	Z	153	TYR
23	Z	155	LYS
23	Z	158	LEU
23	Z	165	PHE
23	Z	167	ARG
23	Z	169	THR
24	1	7	GLU
24	1	13	LEU
24	1	26	VAL
24	1	27	THR
24	1	29	GLU
24	1	100	LEU
24	1	129	VAL
24	1	204	GLU
24	1	224	LEU
24	1	228	LEU
24	2	13	LEU
24	2	17	GLU
24	2	23	HIS
24	2	48	LEU
24	2	76	GLU
24	2	83	LEU
24	2	170	ARG
24	2	183	ILE
24	2	191	ARG
24	2	196	THR
24	2	207	THR
25	3	39	ILE
25	3	59	ILE
25	3	67	GLU
25	3	73	TYR
25	3	85	CYS
25	3	141	THR
25	3	150	HIS
25	3	173	ASN
25	3	189	ASP
25	3	196	VAL
25	3	228	VAL
25	3	235	ASN
25	3	258	ASN
25	3	261	VAL
25	3	262	TYR

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Mol	Chain	Res	Type
25	3	267	ARG
25	3	296	VAL
25	3	297	VAL
25	3	310	ILE
25	3	320	ASP
25	3	333	ILE
25	3	369	MET
25	3	412	GLU
25	3	423	ASP
25	3	468	LEU
25	3	518	ASN
25	3	565	GLU
25	3	595	THR
25	3	600	THR
25	3	615	VAL
25	3	623	LEU
25	3	633	LEU
25	3	731	ARG
25	3	733	VAL
25	3	736	VAL
25	3	748	ILE
25	3	754	THR
25	3	799	ASN
25	3	800	MET
25	3	813	GLU
25	3	822	VAL
25	3	845	LEU
25	3	854	ILE
25	3	856	ASN
25	3	888	THR
25	3	931	VAL
25	3	933	VAL
25	3	950	GLU
25	3	972	PHE
25	3	979	LEU
25	3	992	LEU
25	3	1037	THR
25	3	1038	GLN
25	3	1046	VAL
25	3	1047	LEU
25	3	1076	ILE
25	3	1085	MET

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Mol	Chain	Res	Type
25	3	1098	LEU
25	3	1159	VAL
25	3	1166	ASP
25	3	1217	THR
25	3	1254	VAL
25	3	1304	MET
25	3	1340	GLU
26	4	68	TYR
26	4	83	VAL
26	4	92	VAL
26	4	145	VAL
26	4	146	VAL
26	4	157	GLN
26	4	158	GLN
26	4	159	ILE
26	4	161	THR
26	4	188	LEU
26	4	196	GLN
26	4	213	LYS
26	4	224	LEU
26	4	227	PHE
26	4	235	GLU
26	4	260	PHE
26	4	264	ASP
26	4	281	ARG
26	4	282	LEU
26	4	290	ILE
26	4	394	ILE
26	4	418	GLU
26	4	428	THR
26	4	490	ILE
26	4	527	LEU
26	4	532	GLU
26	4	552	ILE
26	4	553	THR
26	4	554	GLU
26	4	572	THR
26	4	592	VAL
26	4	624	ILE
26	4	634	ARG
26	4	658	GLU
26	4	700	ASN

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Mol	Chain	Res	Type
26	4	736	GLN
26	4	789	LYS
26	4	800	LEU
26	4	816	THR
26	4	833	GLU
26	4	869	CYS
26	4	895	CYS
26	4	897	HIS
26	4	980	THR
26	4	985	ILE
26	4	997	VAL
26	4	1028	ILE
26	4	1035	VAL
26	4	1046	ILE
26	4	1087	ASP
26	4	1141	VAL
26	4	1155	ILE
26	4	1167	LYS
26	4	1204	VAL
26	4	1226	VAL
26	4	1258	ARG
26	4	1261	LEU
26	4	1306	LEU
26	4	1332	LEU
26	4	1365	TYR
27	5	4	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (90) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	165	ASN
3	C	18	HIS
3	C	39	HIS
3	C	122	GLN
3	C	178	ASN
4	D	8	ASN
4	D	102	ASN
4	D	140	ASN
5	E	100	ASN
5	E	136	GLN
6	F	83	HIS
6	F	135	ASN

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Mol	Chain	Res	Type
6	F	148	ASN
7	G	3	HIS
7	G	17	GLN
8	H	68	ASN
8	H	86	GLN
9	I	4	GLN
9	I	118	GLN
10	J	32	GLN
10	J	37	GLN
10	J	126	GLN
11	K	58	ASN
12	L	15	GLN
12	L	38	GLN
12	L	64	GLN
12	L	81	ASN
13	M	5	ASN
14	N	12	HIS
15	O	66	GLN
16	P	35	GLN
16	P	37	ASN
16	P	38	HIS
16	P	40	GLN
16	P	80	GLN
18	R	51	ASN
19	S	52	GLN
21	U	13	GLN
21	U	20	HIS
21	U	48	GLN
21	U	52	ASN
24	1	18	GLN
24	1	23	HIS
24	1	41	ASN
24	1	117	HIS
24	1	137	ASN
24	2	84	ASN
24	2	93	GLN
24	2	117	HIS
25	3	31	GLN
25	3	235	ASN
25	3	238	GLN
25	3	327	GLN
25	3	463	GLN

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Mol	Chain	Res	Type
25	3	494	ASN
25	3	518	ASN
25	3	580	GLN
25	3	658	GLN
25	3	686	GLN
25	3	761	GLN
25	3	767	GLN
25	3	952	GLN
25	3	955	GLN
25	3	1111	GLN
25	3	1116	HIS
25	3	1256	GLN
25	3	1313	HIS
25	3	1324	ASN
26	4	157	GLN
26	4	186	GLN
26	4	196	GLN
26	4	229	GLN
26	4	335	GLN
26	4	365	GLN
26	4	519	ASN
26	4	623	GLN
26	4	680	ASN
26	4	690	ASN
26	4	700	ASN
26	4	712	GLN
26	4	720	ASN
26	4	762	ASN
26	4	817	HIS
26	4	929	GLN
26	4	1108	GLN
26	4	1126	GLN
26	4	1259	GLN
26	4	1268	ASN
26	4	1350	ASN
27	5	31	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1523/1541 (98%)	260 (17%)	11 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	X	20/53 (37%)	6 (30%)	0
All	All	1543/1594 (96%)	266 (17%)	11 (0%)

All (266) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	6	G
1	A	9	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	71	A
1	A	72	A
1	A	74	A
1	A	75	G
1	A	76	G
1	A	80	A
1	A	81	A
1	A	84	U
1	A	85	U
1	A	86	G
1	A	87	C
1	A	88	U
1	A	89	U
1	A	90	C
1	A	91	U
1	A	95	C
1	A	120	A
1	A	121	U
1	A	122	G
1	A	130	A
1	A	131	A
1	A	141	G
1	A	146	G
1	A	164	G
1	A	166	U
1	A	183	C
1	A	184	G
1	A	189	A

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Mol	Chain	Res	Type
1	A	191	G
1	A	197	A
1	A	205	A
1	A	210	C
1	A	226	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	279	A
1	A	289	G
1	A	306	A
1	A	321	A
1	A	328	C
1	A	332	G
1	A	339	C
1	A	348	G
1	A	351	G
1	A	352	C
1	A	354	G
1	A	356	A
1	A	367	U
1	A	372	C
1	A	406	G
1	A	413	G
1	A	421	U
1	A	422	C
1	A	423	G
1	A	424	G
1	A	429	U
1	A	439	U
1	A	446	G
1	A	457	G
1	A	458	U
1	A	459	A
1	A	462	G
1	A	463	U
1	A	465	A
1	A	466	A
1	A	467	U
1	A	468	A

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Mol	Chain	Res	Type
1	A	474	G
1	A	481	G
1	A	484	G
1	A	486	U
1	A	495	A
1	A	496	A
1	A	497	G
1	A	509	A
1	A	511	C
1	A	518	C
1	A	521	G
1	A	527	G7M
1	A	528	C
1	A	547	A
1	A	559	A
1	A	562	U
1	A	563	A
1	A	564	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	C
1	A	577	G
1	A	595	A
1	A	596	A
1	A	619	U
1	A	650	G
1	A	653	U
1	A	665	A
1	A	682	G
1	A	686	U
1	A	687	A
1	A	688	G
1	A	693	G
1	A	694	A
1	A	701	U
1	A	703	G
1	A	704	A
1	A	721	G
1	A	734	G
1	A	748	G
1	A	755	G

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Mol	Chain	Res	Type
1	A	787	A
1	A	788	U
1	A	789	U
1	A	790	A
1	A	791	G
1	A	792	A
1	A	793	U
1	A	794	A
1	A	797	C
1	A	809	G
1	A	812	G
1	A	815	A
1	A	817	C
1	A	828	U
1	A	829	G
1	A	832	G
1	A	841	C
1	A	842	U
1	A	845	A
1	A	849	G
1	A	868	C
1	A	872	A
1	A	873	A
1	A	885	G
1	A	914	A
1	A	922	G
1	A	925	G
1	A	926	G
1	A	927	G
1	A	928	G
1	A	929	G
1	A	933	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	965	U
1	A	966	2MG
1	A	967	5MC
1	A	968	A
1	A	969	A
1	A	971	G
1	A	975	A

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Mol	Chain	Res	Type
1	A	976	G
1	A	977	A
1	A	979	C
1	A	981	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1009	U
1	A	1018	G
1	A	1020	G
1	A	1022	A
1	A	1024	G
1	A	1025	U
1	A	1028	C
1	A	1030	U
1	A	1031	C
1	A	1033	G
1	A	1044	A
1	A	1065	U
1	A	1085	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1104	G
1	A	1108	G
1	A	1133	G
1	A	1136	C
1	A	1137	C
1	A	1139	G
1	A	1140	C
1	A	1141	C
1	A	1151	A
1	A	1152	A
1	A	1158	C
1	A	1159	U
1	A	1184	G
1	A	1188	A
1	A	1196	A
1	A	1197	A
1	A	1213	A
1	A	1227	A

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Mol	Chain	Res	Type
1	A	1236	A
1	A	1238	A
1	A	1257	A
1	A	1260	G
1	A	1278	G
1	A	1279	G
1	A	1280	A
1	A	1286	U
1	A	1287	A
1	A	1299	A
1	A	1300	G
1	A	1302	C
1	A	1305	G
1	A	1317	C
1	A	1318	A
1	A	1320	C
1	A	1346	A
1	A	1363	A
1	A	1364	U
1	A	1370	G
1	A	1379	G
1	A	1389	C
1	A	1391	U
1	A	1392	G
1	A	1398	A
1	A	1400	C
1	A	1414	U
1	A	1415	G
1	A	1417	G
1	A	1419	G
1	A	1429	A
1	A	1430	A
1	A	1432	G
1	A	1441	A
1	A	1442	G
1	A	1452	C
1	A	1455	G
1	A	1475	G
1	A	1478	U
1	A	1479	C
1	A	1486	G
1	A	1487	G

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Mol	Chain	Res	Type
1	A	1488	G
1	A	1489	G
1	A	1492	A
1	A	1493	A
1	A	1494	G
1	A	1506	U
1	A	1509	C
1	A	1517	G
1	A	1518	MA6
1	A	1520	C
1	A	1529	G
1	A	1530	G
1	A	1531	A
1	A	1532	U
22	X	6	G
22	X	7	G
22	X	44	A
22	X	45	C
22	X	46	G
22	X	53	G

All (11) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	428	G
1	A	462	G
1	A	693	G
1	A	925	G
1	A	966	2MG
1	A	968	A
1	A	1103	C
1	A	1279	G
1	A	1391	U
1	A	1492	A
1	A	1531	A

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

9 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
13	D2T	M	89	13	8,9,10	1.77	1 (12%)	6,11,13	2.29	2 (33%)
1	2MG	A	1516	1	23,26,27	1.25	3 (13%)	33,38,41	2.45	12 (36%)
1	MA6	A	1518	1	23,26,27	1.45	5 (21%)	33,38,41	2.42	15 (45%)
1	PSU	A	516	1,30	18,21,22	1.59	5 (27%)	21,30,33	2.43	4 (19%)
1	G7M	A	527	1	23,26,27	0.71	1 (4%)	34,39,42	0.62	0
1	MA6	A	1519	1	23,26,27	1.48	5 (21%)	33,38,41	2.49	14 (42%)
1	2MG	A	1207	1	23,26,27	1.38	4 (17%)	33,38,41	2.28	8 (24%)
1	2MG	A	966	1	23,26,27	1.33	4 (17%)	33,38,41	2.26	8 (24%)
1	5MC	A	967	1	19,22,23	1.51	3 (15%)	26,32,35	1.35	2 (7%)

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
13	D2T	M	89	13	-	3/7/12/14	-
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
1	MA6	A	1518	1	-	5/11/29/30	0/3/3/3
1	PSU	A	516	1,30	-	1/7/25/26	0/2/2/2
1	G7M	A	527	1	-	3/7/25/26	0/3/3/3
1	MA6	A	1519	1	-	2/11/29/30	0/3/3/3
1	2MG	A	1207	1	-	3/9/27/28	0/3/3/3
1	2MG	A	966	1	-	1/9/27/28	0/3/3/3
1	5MC	A	967	1	-	3/7/25/26	0/2/2/2

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	967	5MC	C5-C4	4.89	1.47	1.44
1	A	1519	MA6	C5-C4	4.08	1.46	1.39
13	M	89	D2T	CB-CA	-4.06	1.53	1.54
1	A	1518	MA6	C5-C4	4.00	1.46	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	516	PSU	C4-N3	-3.60	1.32	1.38
1	A	1207	2MG	C6-N1	-3.22	1.32	1.38
1	A	1519	MA6	C5-N7	-3.10	1.33	1.39
1	A	1516	2MG	C5-C4	3.07	1.47	1.38
1	A	967	5MC	C6-N1	-3.06	1.32	1.38
1	A	966	2MG	C5-C4	2.91	1.46	1.38
1	A	966	2MG	C6-N1	-2.70	1.33	1.38
1	A	1518	MA6	C5-C6	2.62	1.48	1.41
1	A	1518	MA6	C4-N9	-2.58	1.32	1.37
1	A	516	PSU	C2-N3	-2.51	1.33	1.37
1	A	1207	2MG	C5-C4	2.49	1.45	1.38
1	A	527	G7M	C8-N7	2.48	1.37	1.33
1	A	1207	2MG	C4-N9	-2.48	1.31	1.38
1	A	516	PSU	C2'-C1'	-2.40	1.50	1.53
1	A	516	PSU	C6-C5	2.39	1.37	1.35
1	A	1207	2MG	C5-N7	-2.39	1.34	1.39
1	A	1518	MA6	C5-N7	-2.37	1.34	1.39
1	A	966	2MG	C5-N7	-2.36	1.34	1.39
1	A	1519	MA6	C5-C6	2.36	1.47	1.41
1	A	1519	MA6	C4-N9	-2.30	1.32	1.37
1	A	966	2MG	C4-N9	-2.24	1.32	1.38
1	A	967	5MC	C6-C5	2.23	1.38	1.34
1	A	1516	2MG	C6-N1	-2.18	1.34	1.38
1	A	1518	MA6	C8-N7	2.16	1.35	1.31
1	A	1516	2MG	C4-N9	-2.08	1.32	1.38
1	A	1519	MA6	C8-N9	-2.06	1.34	1.37
1	A	516	PSU	C2-N1	-2.01	1.34	1.36

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1516	2MG	C2-N3-C4	7.23	121.05	112.00
1	A	516	PSU	N1-C2-N3	7.20	122.76	115.17
1	A	1207	2MG	C2-N3-C4	7.02	120.78	112.00
1	A	966	2MG	C2-N3-C4	6.86	120.58	112.00
1	A	1516	2MG	C5-C4-N3	-5.75	119.23	128.39
1	A	966	2MG	C5-C4-N3	-5.73	119.26	128.39
1	A	1519	MA6	C5-C4-N3	-5.60	119.00	126.72
1	A	1207	2MG	C5-C4-N3	-5.55	119.56	128.39
1	A	516	PSU	C4-N3-C2	-5.18	119.23	126.37
1	A	1518	MA6	C5-C4-N3	-4.92	119.94	126.72
1	A	1519	MA6	N3-C4-N9	4.59	134.97	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1519	MA6	N1-C6-N6	4.44	122.26	116.86
1	A	1518	MA6	C9-N6-C6	-4.38	109.39	120.52
1	A	516	PSU	O2-C2-N1	-4.28	118.38	122.79
1	A	1518	MA6	C2-N1-C6	4.22	122.14	111.83
1	A	1519	MA6	C2-N1-C6	4.09	121.82	111.83
1	A	1516	2MG	N1-C2-N2	4.03	120.67	116.56
1	A	966	2MG	N9-C4-N3	4.03	134.00	125.95
1	A	1207	2MG	N9-C4-N3	3.95	133.86	125.95
13	M	89	D2T	CB1-SB-CB	3.87	109.33	102.36
1	A	1207	2MG	C6-C5-N7	3.86	137.32	130.29
1	A	1518	MA6	C4-C5-N7	-3.85	106.18	110.58
1	A	1516	2MG	C6-C5-N7	3.82	137.24	130.29
1	A	1516	2MG	N9-C4-N3	3.80	133.55	125.95
1	A	1518	MA6	N3-C4-N9	3.79	133.61	127.17
1	A	1519	MA6	C10-N6-C6	-3.72	111.05	120.52
1	A	1519	MA6	C9-N6-C6	-3.70	111.11	120.52
1	A	1518	MA6	C10-N6-C6	-3.67	111.18	120.52
1	A	1516	2MG	CM2-N2-C2	-3.57	115.97	123.65
1	A	1519	MA6	C2-N3-C4	3.53	120.46	111.83
1	A	966	2MG	C6-C5-N7	3.53	136.71	130.29
1	A	1518	MA6	C2-N3-C4	3.53	120.44	111.83
1	A	1518	MA6	C4-N9-C8	3.50	109.41	105.74
1	A	1516	2MG	N2-C2-N3	-3.47	116.09	120.51
1	A	1518	MA6	N1-C2-N3	-3.41	123.42	128.58
1	A	1519	MA6	C4-C5-N7	-3.39	106.71	110.58
1	A	967	5MC	C5-C6-N1	-3.25	119.78	123.31
1	A	1519	MA6	N1-C2-N3	-3.18	123.77	128.58
1	A	966	2MG	C2'-C1'-N9	-3.07	104.72	113.25
1	A	1519	MA6	C5-C6-N6	-3.04	120.52	125.33
1	A	516	PSU	C5-C6-N1	-2.96	118.03	122.14
13	M	89	D2T	OD2-CG-CB	2.93	119.48	113.15
1	A	1519	MA6	C4-N9-C8	2.87	108.76	105.74
1	A	1518	MA6	C5-N7-C8	2.86	107.95	103.45
1	A	1518	MA6	C2'-C1'-N9	-2.84	106.25	113.30
1	A	1516	2MG	C4-C5-N7	-2.78	106.26	110.67
1	A	1518	MA6	N9-C8-N7	-2.78	109.99	113.94
1	A	967	5MC	C5-C4-N3	-2.73	118.95	121.75
1	A	1519	MA6	C5-N7-C8	2.73	107.74	103.45
1	A	1519	MA6	C2'-C1'-N9	-2.68	106.64	113.30
1	A	1207	2MG	N1-C2-N2	2.65	119.27	116.56
1	A	1207	2MG	C4-C5-N7	-2.63	106.50	110.67
1	A	966	2MG	C4-C5-N7	-2.63	106.50	110.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1518	MA6	C6-C5-N7	2.51	137.44	133.43
1	A	1516	2MG	C2-N1-C6	-2.48	121.55	124.55
1	A	1516	2MG	C2'-C1'-N9	-2.39	106.61	113.25
1	A	1518	MA6	C10-N6-C9	-2.31	108.75	116.18
1	A	1516	2MG	O6-C6-C5	-2.27	120.53	126.53
1	A	1519	MA6	N9-C8-N7	-2.24	110.76	113.94
1	A	966	2MG	N1-C2-N2	2.24	118.84	116.56
1	A	1207	2MG	C5-C6-N1	2.10	118.60	113.25
1	A	1207	2MG	CM2-N2-C2	-2.06	119.21	123.65
1	A	966	2MG	O6-C6-C5	-2.06	121.11	126.53
1	A	1518	MA6	N1-C6-N6	2.05	119.36	116.86
1	A	1516	2MG	C5-C6-N1	2.03	118.43	113.25

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	967	5MC	O4'-C4'-C5'-O5'
1	A	1207	2MG	N1-C2-N2-CM2
1	A	1207	2MG	N3-C2-N2-CM2
1	A	1518	MA6	O4'-C4'-C5'-O5'
1	A	1518	MA6	C3'-C4'-C5'-O5'
1	A	1518	MA6	C5-C6-N6-C9
13	M	89	D2T	SB-CB-CG-OD2
1	A	967	5MC	C3'-C4'-C5'-O5'
1	A	527	G7M	O4'-C4'-C5'-O5'
1	A	527	G7M	C3'-C4'-C5'-O5'
1	A	1518	MA6	N1-C6-N6-C9
1	A	1518	MA6	C4'-C5'-O5'-P
1	A	1519	MA6	C5-C6-N6-C10
13	M	89	D2T	CG-CB-SB-CB1
1	A	967	5MC	C4'-C5'-O5'-P
1	A	1519	MA6	C3'-C4'-C5'-O5'
1	A	516	PSU	O4'-C4'-C5'-O5'
1	A	527	G7M	C4'-C5'-O5'-P
1	A	1207	2MG	O4'-C4'-C5'-O5'
13	M	89	D2T	CA-CB-SB-CB1
1	A	966	2MG	C4'-C5'-O5'-P

There are no ring outliers.

6 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	M	89	D2T	1	0
1	A	1516	2MG	6	0
1	A	1518	MA6	6	0
1	A	1519	MA6	4	0
1	A	966	2MG	3	0
1	A	967	5MC	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 121 ligands modelled in this entry, 121 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](#)

There are no chain breaks in this entry.

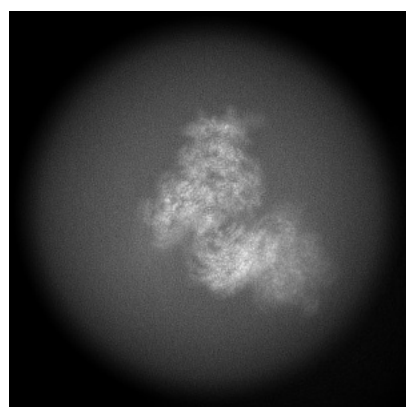
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51622. These allow visual inspection of the internal detail of the map and identification of artifacts.

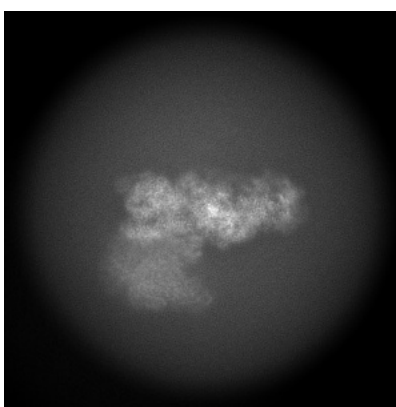
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

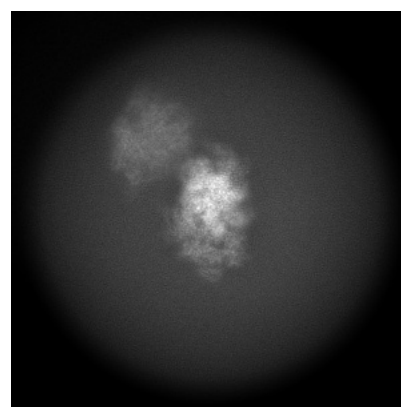
6.1.1 Primary map



X



Y

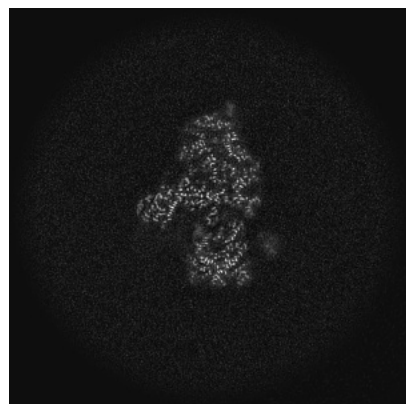


Z

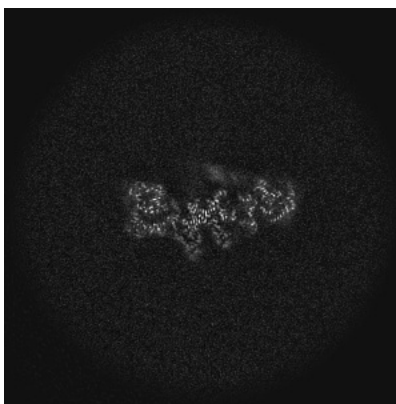
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

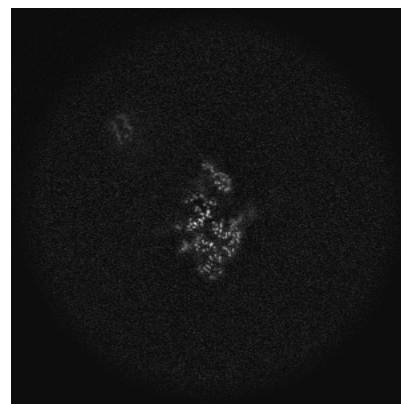
6.2.1 Primary map



X Index: 300



Y Index: 300

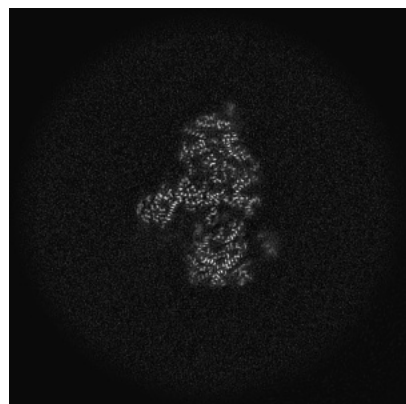


Z Index: 300

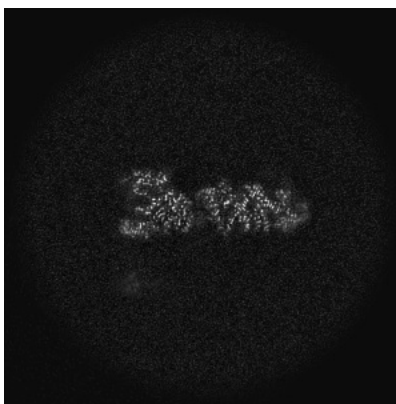
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

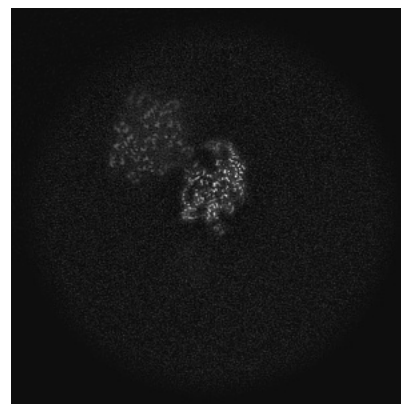
6.3.1 Primary map



X Index: 301



Y Index: 335

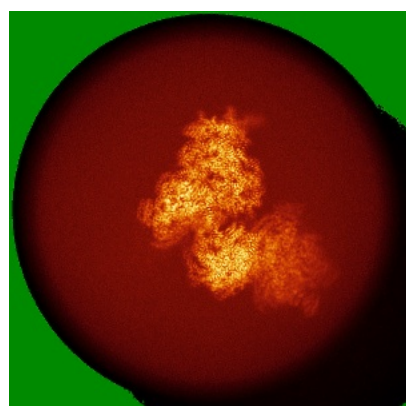


Z Index: 231

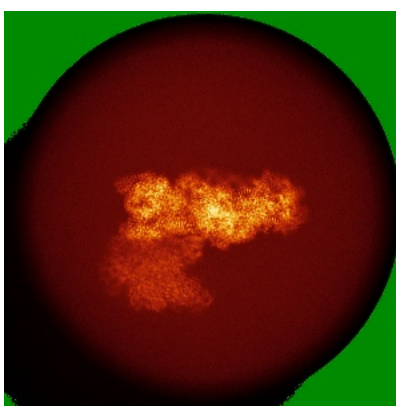
The images above show the largest variance slices of the map in three orthogonal directions.

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

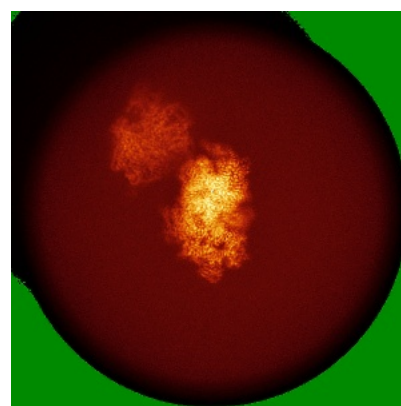
6.4.1 Primary map



X



Y

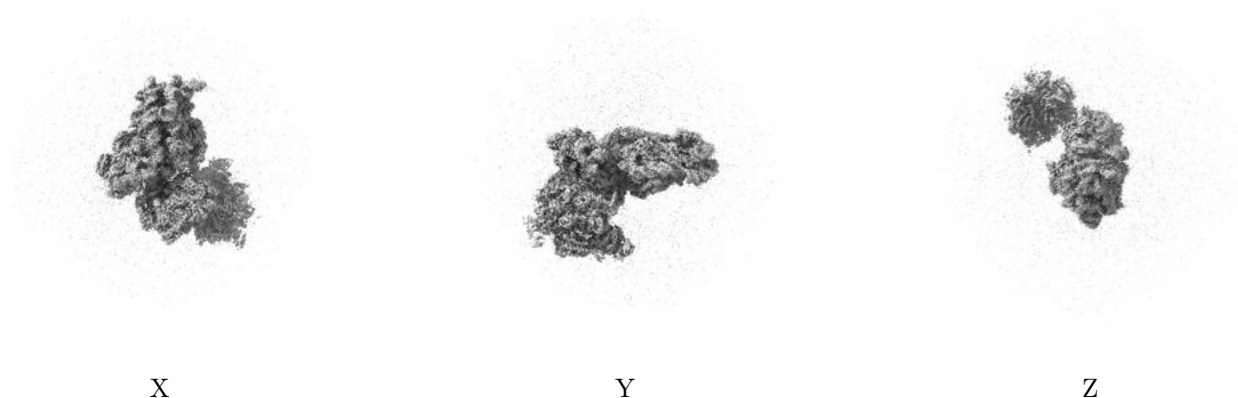


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.411. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

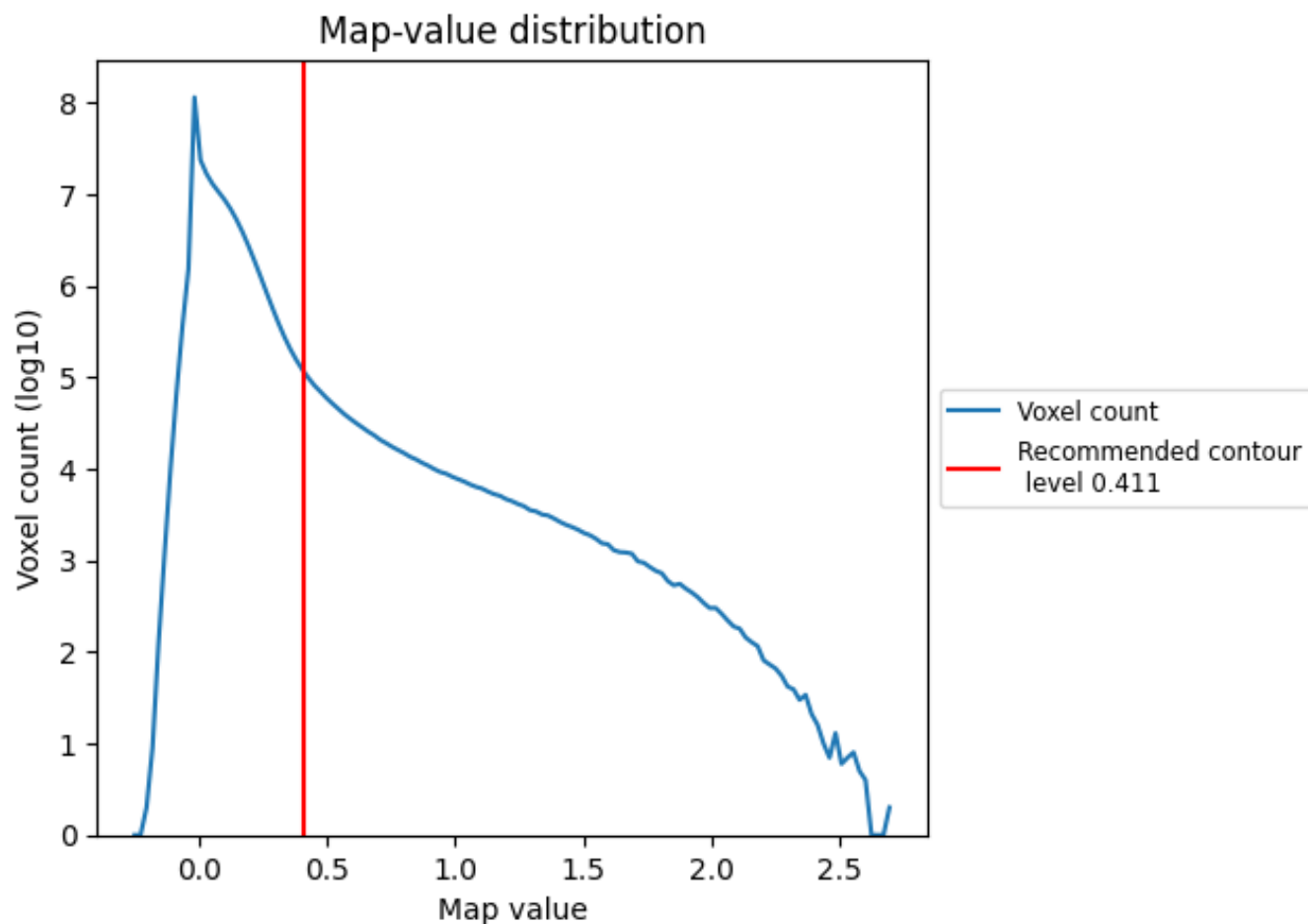
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

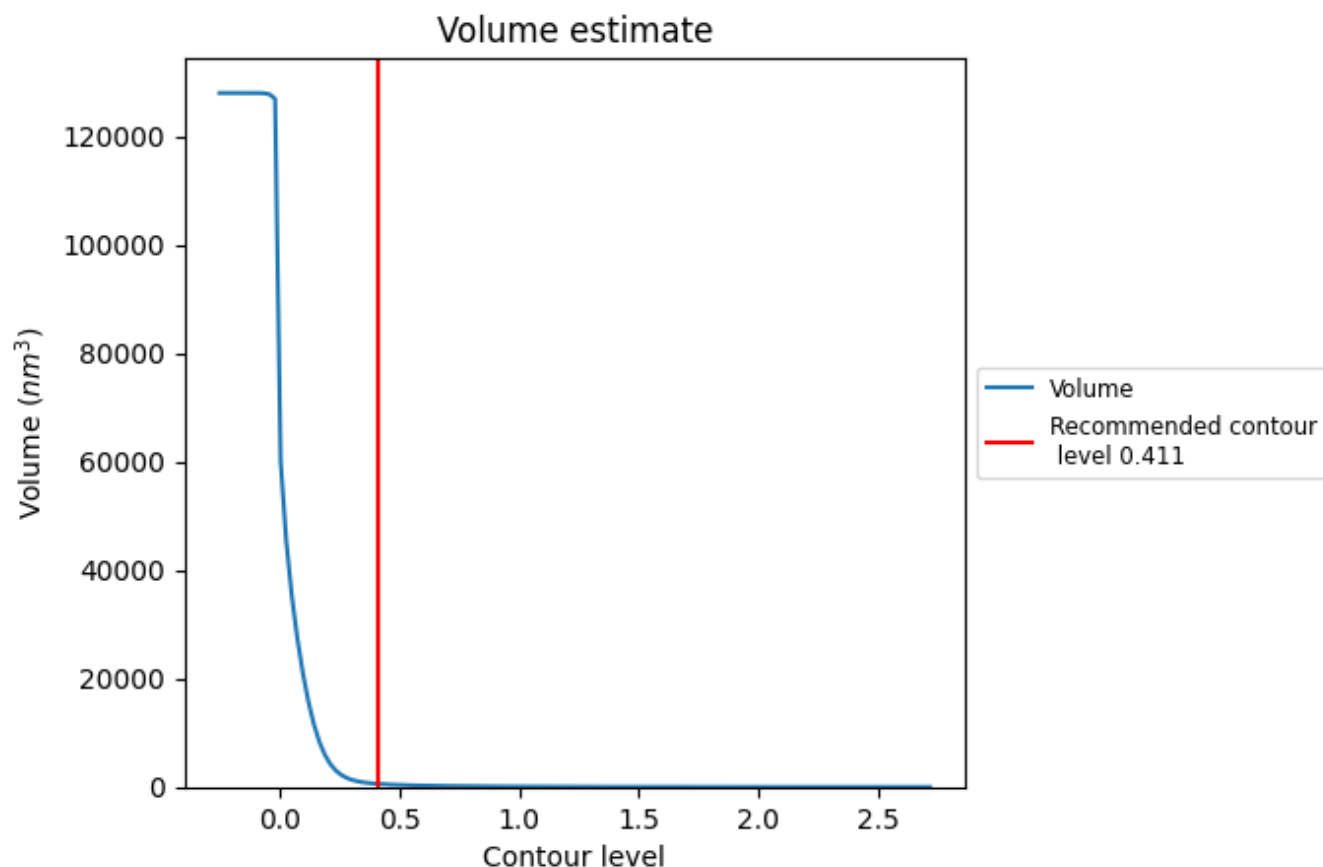
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

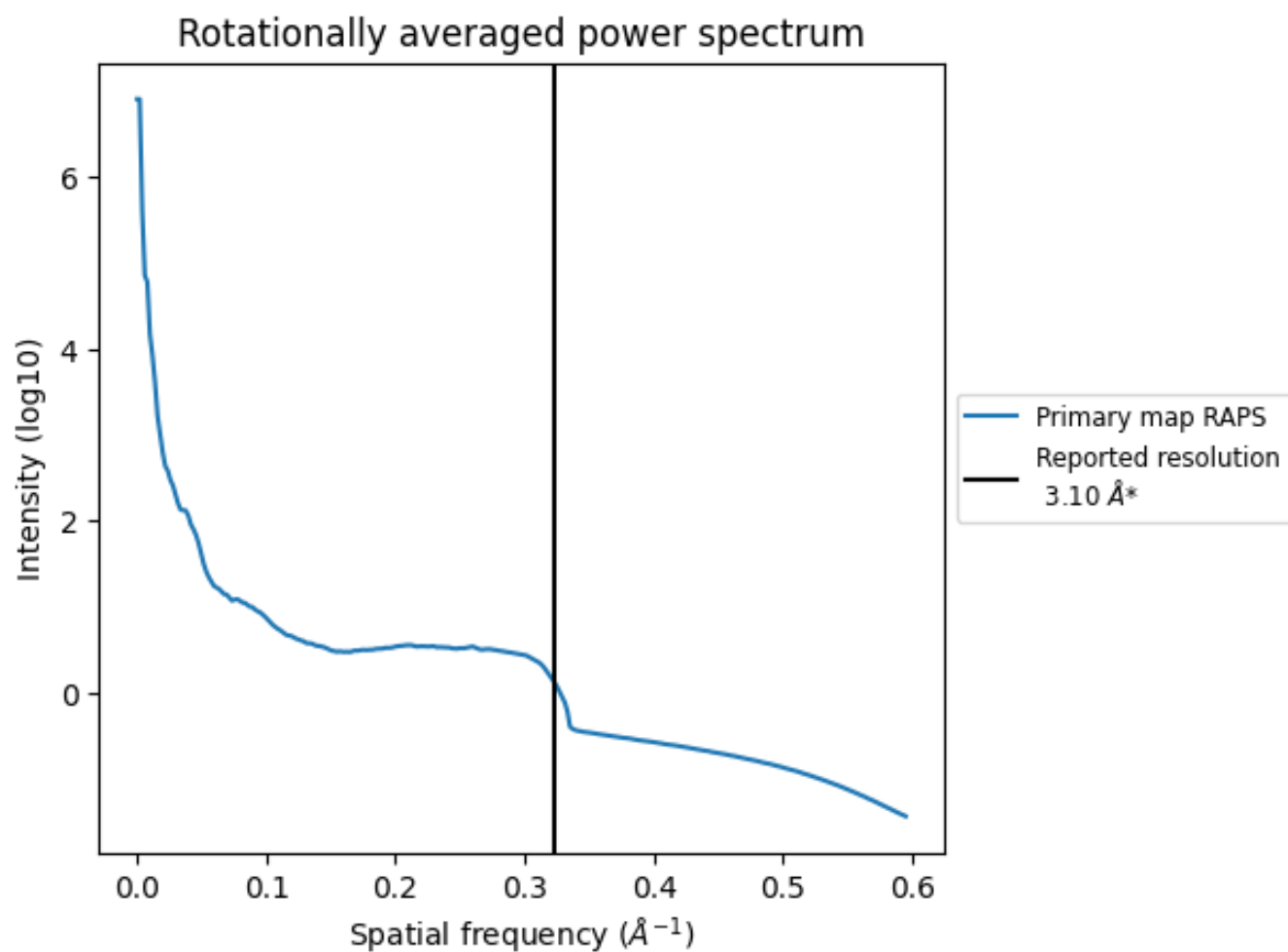
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 574 nm^3 ; this corresponds to an approximate mass of 519 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 0.323 Å⁻¹

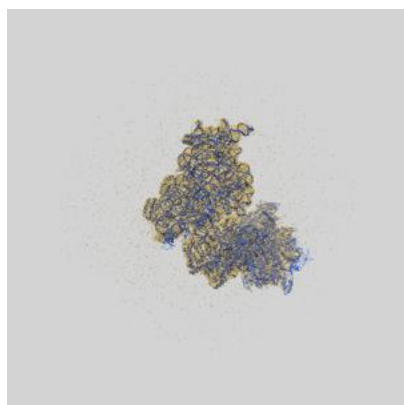
8 Fourier-Shell correlation

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

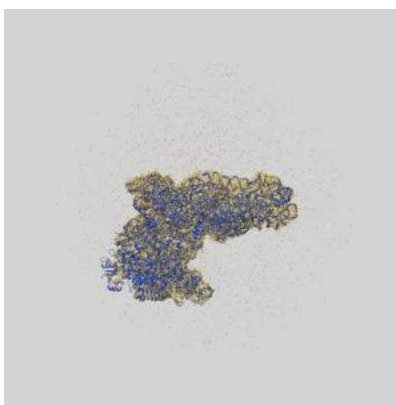
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51622 and PDB model 9GUW. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

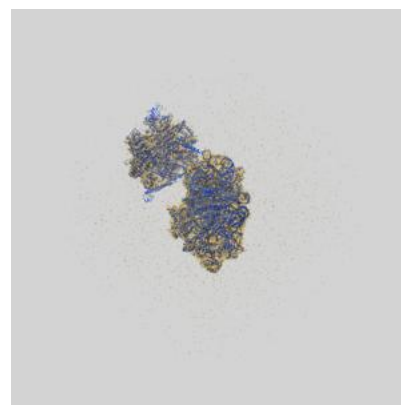
9.1 Map-model overlay [i](#)



X



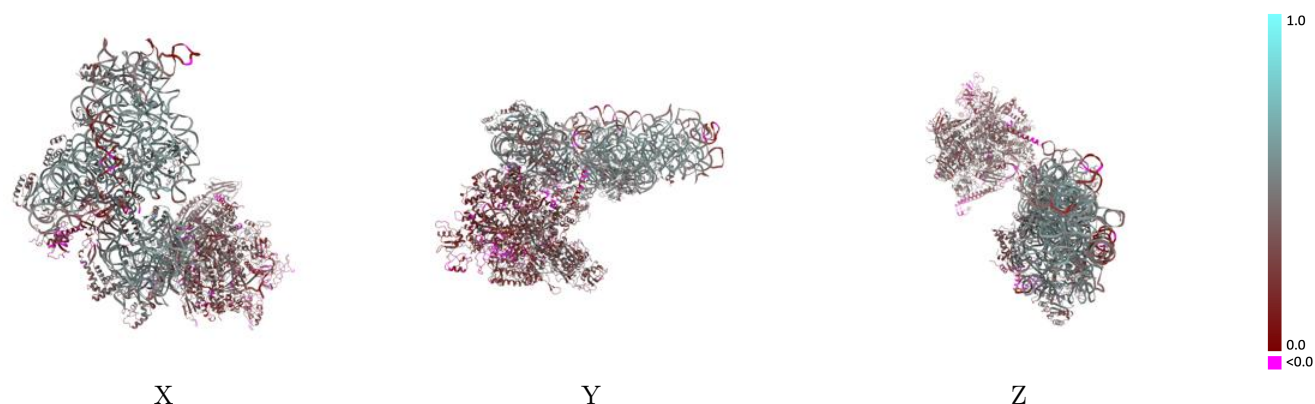
Y



Z

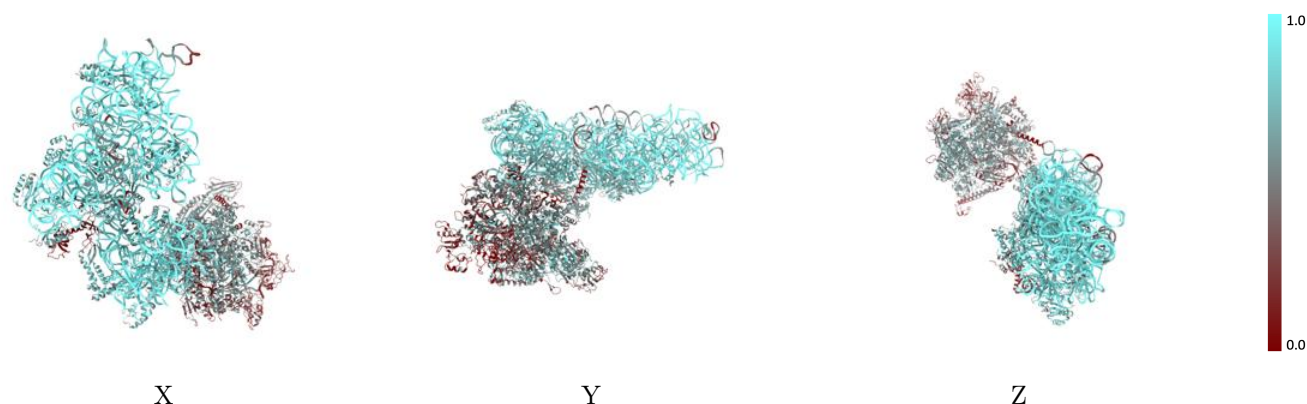
The images above show the 3D surface view of the map at the recommended contour level 0.411 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



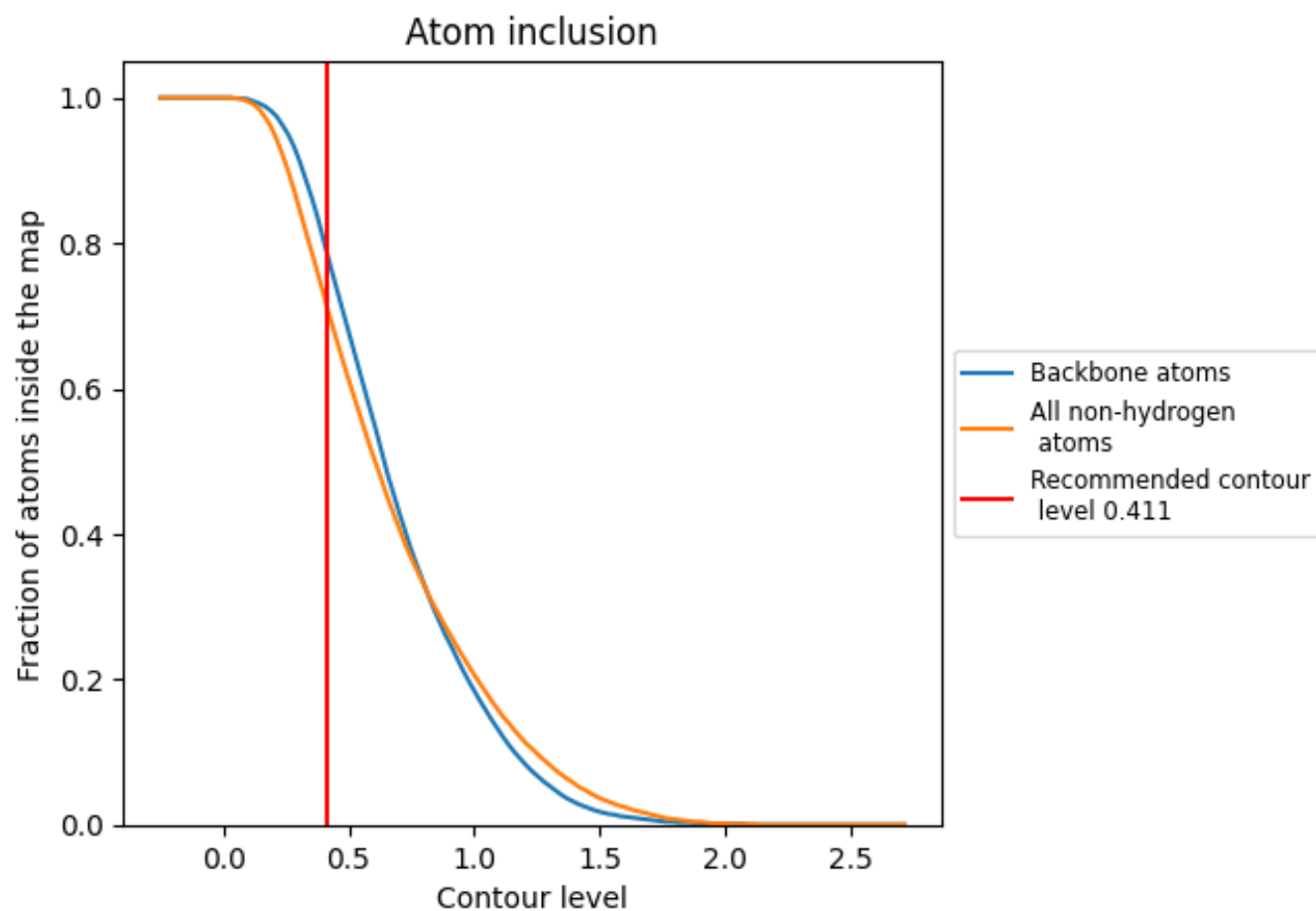
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.411).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 72% 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 (0.411) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7150	 0.3940
1	 0.5120	 0.3300
2	 0.4530	 0.3090
3	 0.4650	 0.2790
4	 0.4350	 0.2700
5	 0.3920	 0.2330
6	 0.3400	 0.2020
7	 0.5580	 0.2960
A	 0.9270	 0.4890
B	 0.0900	 0.0510
C	 0.7340	 0.3840
D	 0.7980	 0.4650
E	 0.8030	 0.4580
F	 0.8230	 0.4830
G	 0.7600	 0.3990
H	 0.6910	 0.3510
I	 0.8450	 0.4880
J	 0.8060	 0.4360
K	 0.7090	 0.4040
L	 0.6920	 0.3270
M	 0.8170	 0.4770
N	 0.7860	 0.4310
O	 0.8270	 0.4660
P	 0.8300	 0.4560
Q	 0.8290	 0.4900
R	 0.7670	 0.4400
S	 0.8070	 0.4320
T	 0.8190	 0.4630
U	 0.8180	 0.4600
X	 0.4030	 0.1470
Z	 0.3090	 0.1940

