



## Full wwPDB EM Validation Report ⓘ

Oct 12, 2024 – 04:16 PM EDT

PDB ID : 6DDG  
EMDB ID : EMD-7870  
Title : Structure of the 50S ribosomal subunit from Methicillin Resistant Staphylococcus aureus in complex with the oxazolidinone antibiotic LZD-6  
Authors : Belousoff, M.J.; Venugopal, H.; Bamert, R.S.; Lithgow, T.  
Deposited on : 2018-05-10  
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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev113  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

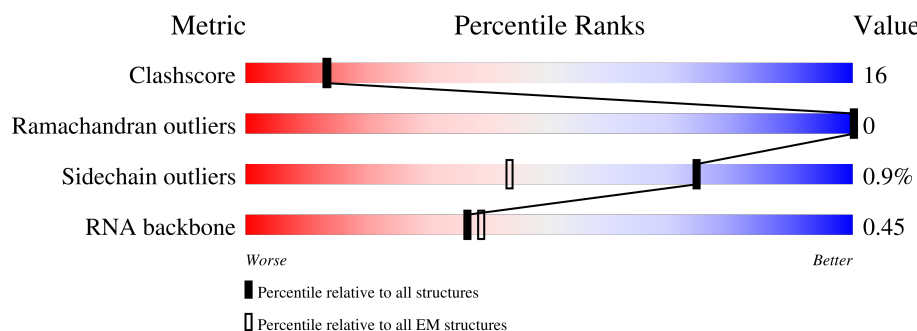
# 1 Overall quality at a glance

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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	116	
2	B	276	
3	C	118	
4	D	102	
5	E	116	
6	F	91	
7	G	105	

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Mol	Chain	Length	Quality of chain
8	H	217	
9	I	85	
10	J	62	
11	K	69	
12	L	217	
13	M	59	
14	N	57	
15	O	49	
16	P	45	
17	Q	65	
18	R	37	
19	S	207	
20	V	145	
21	W	122	
22	X	146	
23	Y	144	
24	Z	122	
25	a	119	
26	1	2923	
27	2	115	

## 2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 79603 atoms, of which 19 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	113	Total	C	N	O	0	0
			915	576	184	155		

- Molecule 2 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	270	Total	C	N	O	S	0	0
			2063	1285	410	363	5		

- Molecule 3 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	116	Total	C	N	O	S	0	0
			943	593	189	157	4		

- Molecule 4 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	100	Total	C	N	O	S	0	0
			785	499	139	146	1		

- Molecule 5 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	111	Total	C	N	O	S	0	0
			853	532	163	155	3		

- Molecule 6 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	84	Total	C	N	O	S	0	0
			684	430	125	125	4		

- Molecule 7 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	91	Total	C	N	O	S	0	0
			697	441	128	127	1		

- Molecule 8 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	93	Total	C	N	O	S	0	0
			727	465	129	132	1		

- Molecule 9 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	78	Total	C	N	O	S	0	0
			597	367	116	114			

- Molecule 10 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	57	Total	C	N	O	S	0	0
			449	278	97	73	1		

- Molecule 11 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	56	Total	C	N	O	S	0	0
			463	285	88	90			

- Molecule 12 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	215	Total	C	N	O	S	0	0
			1628	1018	299	306	5		

- Molecule 13 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	56	Total	C	N	O	S	0	0
			432	269	82	81			

- Molecule 14 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	50	Total	C	N	O	S	0	0
			397	241	83	68	5		

- Molecule 15 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	47	Total	C	N	O	S	0	0
			390	233	79	73	5		

- Molecule 16 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	44	Total	C	N	O	S	0	0
			372	228	90	53	1		

- Molecule 17 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 18 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

- Molecule 19 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	188	Total	C	N	O	S	0	0
			1441	904	267	268	2		

- Molecule 20 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	143	Total	C	N	O	S	0	0
			1138	710	209	217	2		

- Molecule 21 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	120	Total	C	N	O	S	0	0
			903	561	172	167	3		

- Molecule 22 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	144	Total	C	N	O		0	0
			1082	669	213	200			

- Molecule 23 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	135	Total	C	N	O	S	0	0
			1080	693	205	178	4		

- Molecule 24 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	121	Total	C	N	O	S	0	0
			955	586	183	185	1		

- Molecule 25 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	100	Total	C	N	O		0	0
			787	493	153	141			

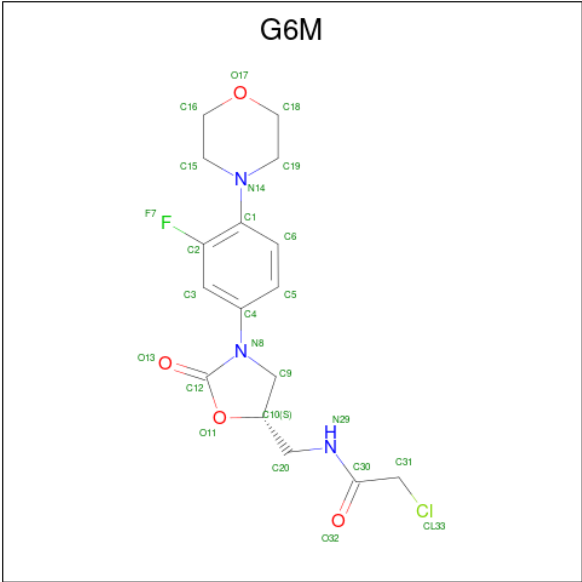
- Molecule 26 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	2646	Total	C	N	O	P	0	0
			56747	25338	10405	18361	2643		

- Molecule 27 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	104	Total	C	N	O	P	0	0
			2214	990	395	725	104		

- Molecule 28 is 2-chloro-N-((5S)-3-[3-fluoro-4-(morpholin-4-yl)phenyl]-2-oxo-1,3-oxazolidin-5-yl)methyl)acetamide (three-letter code: G6M) (formula: C<sub>16</sub>H<sub>19</sub>ClFN<sub>3</sub>O<sub>4</sub>).

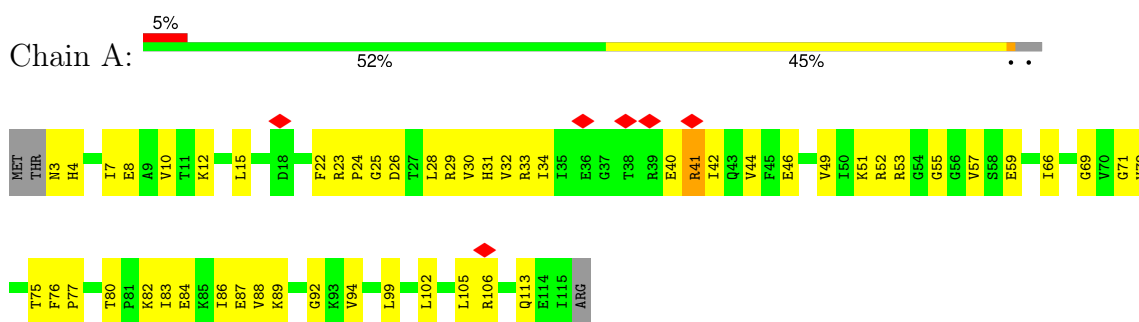


Mol	Chain	Residues	Atoms							AltConf
			Total	C	Cl	F	H	N	O	
28	1	1	44	16	1	1	19	3	4	0

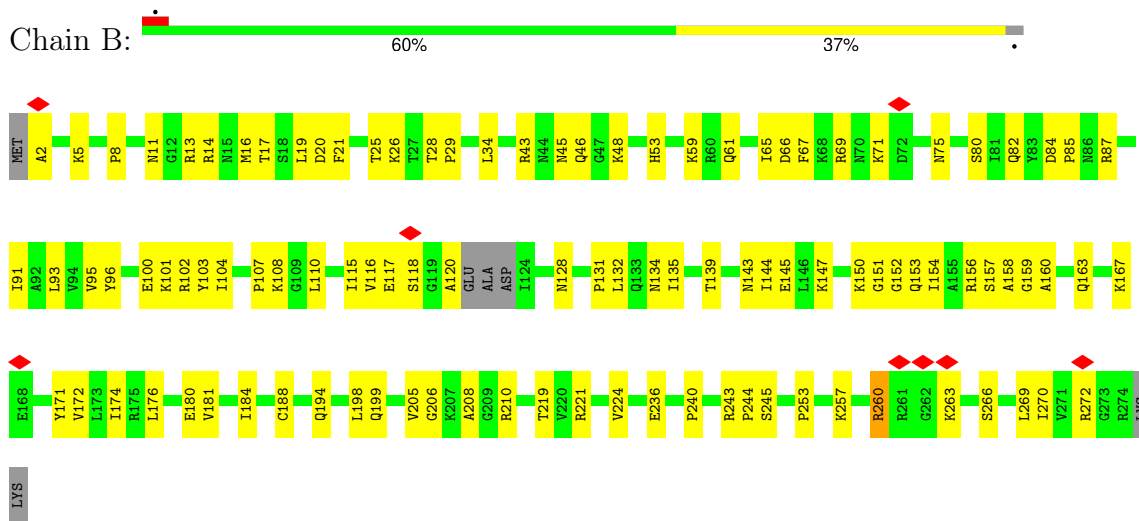
### 3 Residue-property plots

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

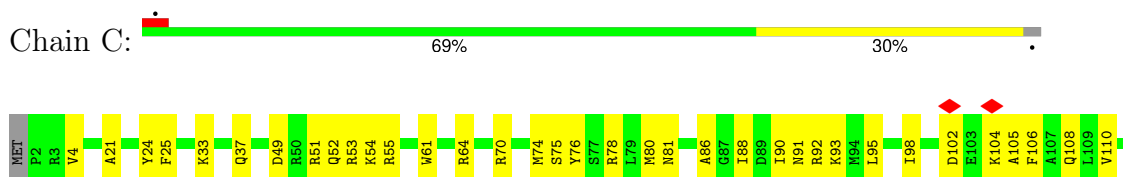
- Molecule 1: 50S ribosomal protein L19



- Molecule 2: 50S ribosomal protein L2

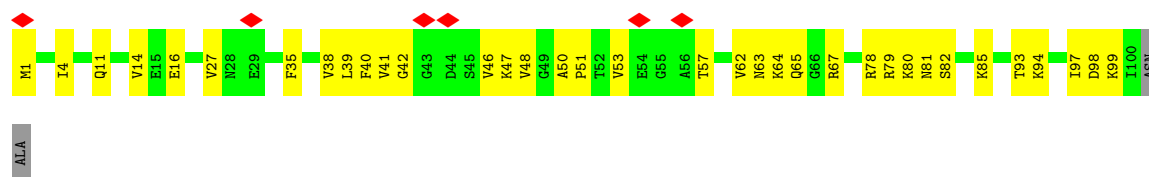


- Molecule 3: 50S ribosomal protein L20

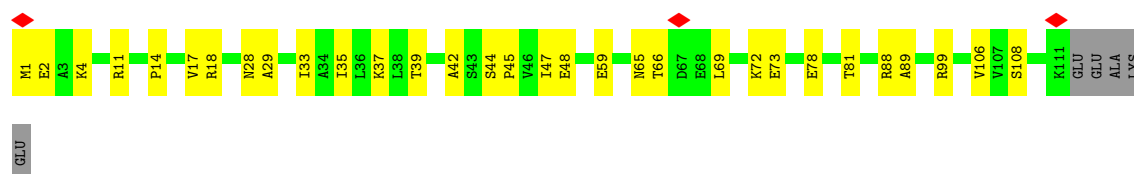




- Molecule 4: 50S ribosomal protein L21



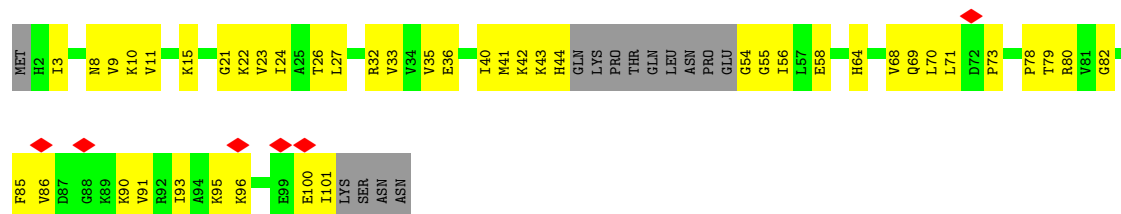
- Molecule 5: 50S ribosomal protein L22



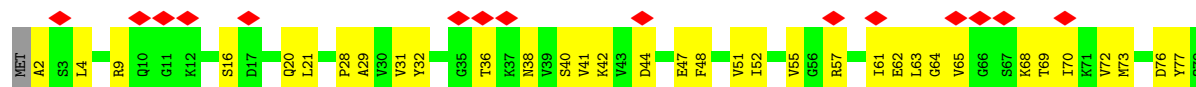
- Molecule 6: 50S ribosomal protein L23

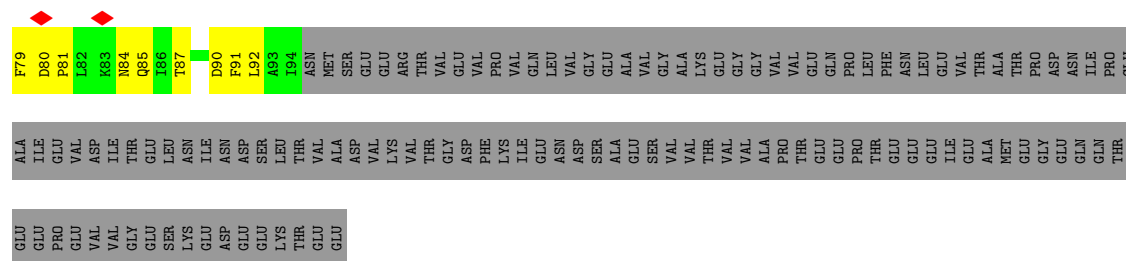


- Molecule 7: 50S ribosomal protein L24



- Molecule 8: 50S ribosomal protein L25

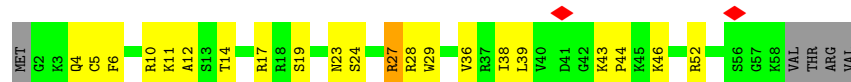




• Molecule 9: 50S ribosomal protein L27



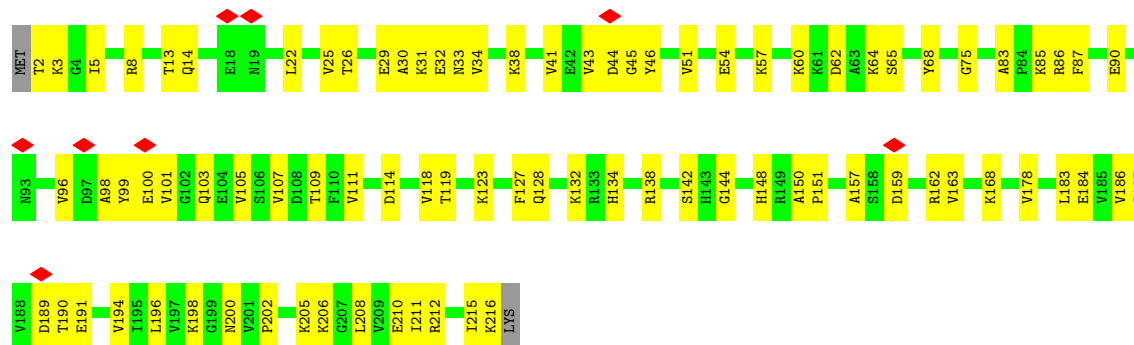
• Molecule 10: 50S ribosomal protein L28



• Molecule 11: 50S ribosomal protein L29



• Molecule 12: 50S ribosomal protein L3



• Molecule 13: 50S ribosomal protein L30





- Molecule 14: 50S ribosomal protein L32



- Molecule 15: 50S ribosomal protein L33



- Molecule 16: 50S ribosomal protein L34



- Molecule 17: 50S ribosomal protein L35

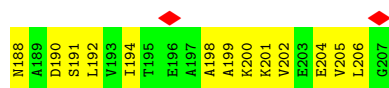


- Molecule 18: 50S ribosomal protein L36



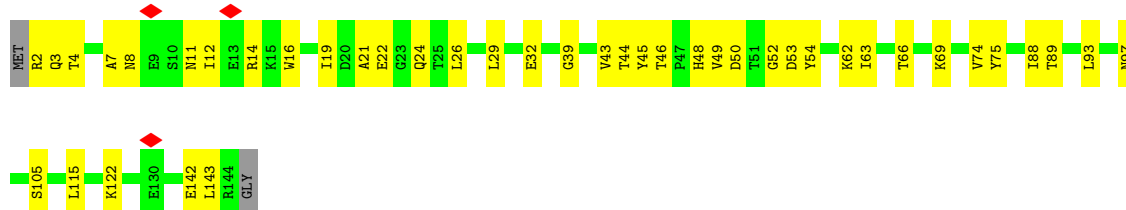
- Molecule 19: 50S ribosomal protein L4





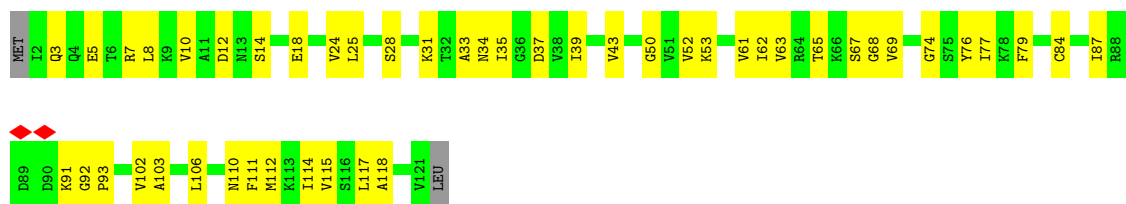
- Molecule 20: 50S ribosomal protein L13

Chain V: 70% 29%



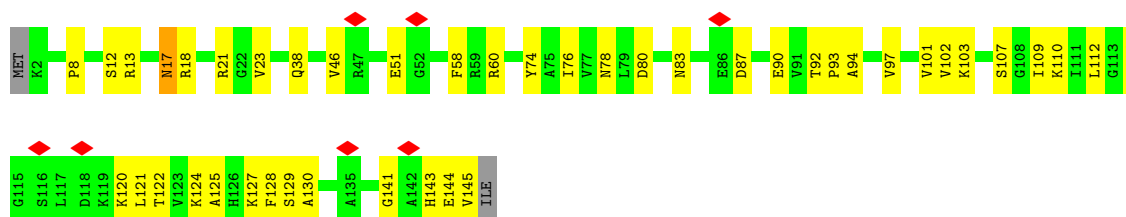
- Molecule 21: 50S ribosomal protein L14

Chain W: 60% 39%



- Molecule 22: 50S ribosomal protein L15

Chain X: 5% 68% 29%



- Molecule 23: 50S ribosomal protein L16

Chain Y: 56% 38% 6%

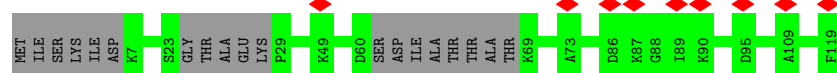


- Molecule 24: 50S ribosomal protein L17

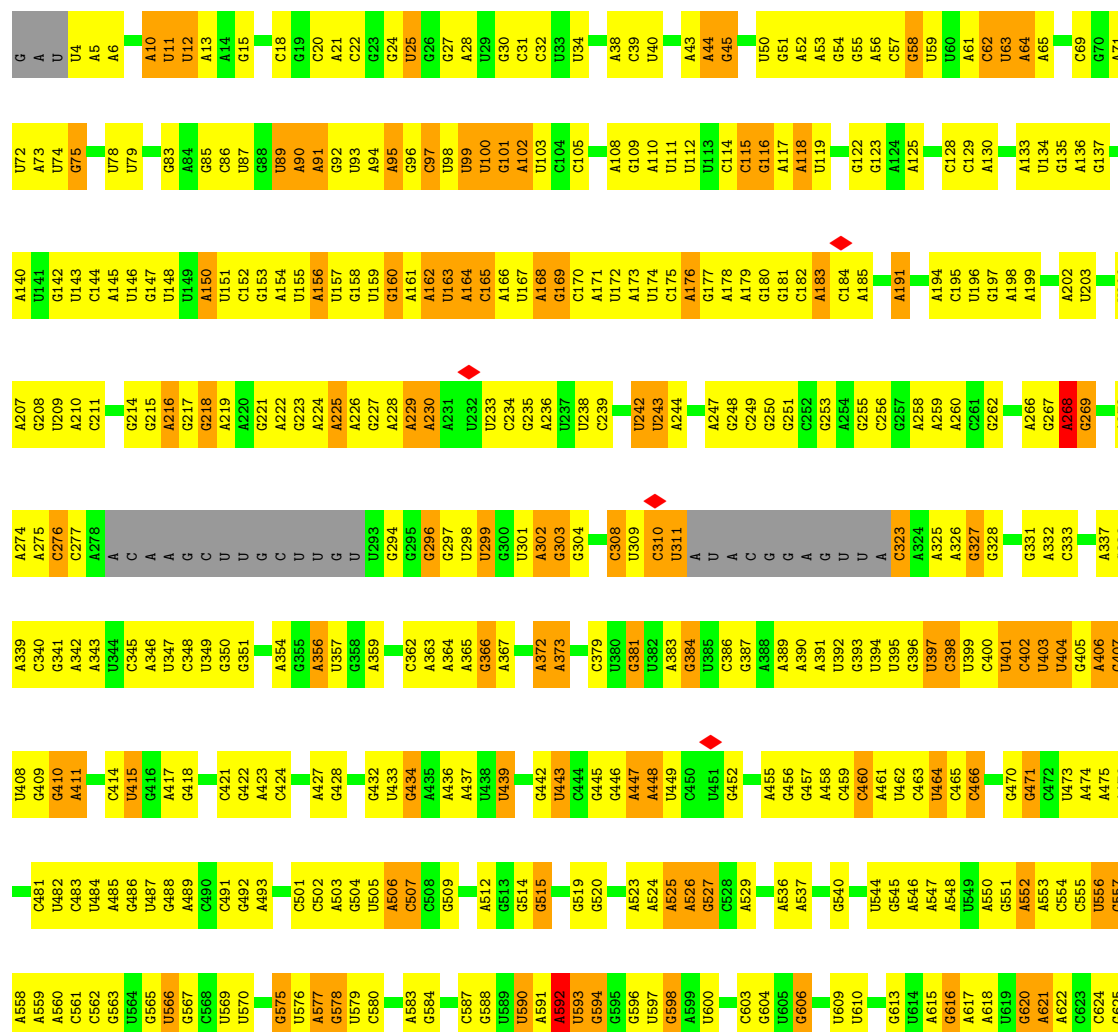
Frequency	Percentage
Daily	59%
Occasionally	40%



- Chain a:  8% 84% 16%

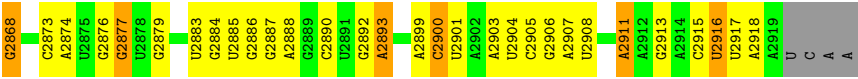
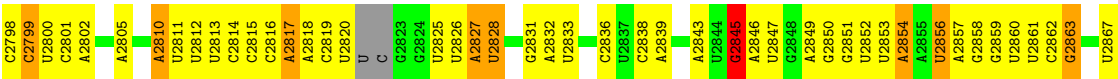


- Chain 1: 

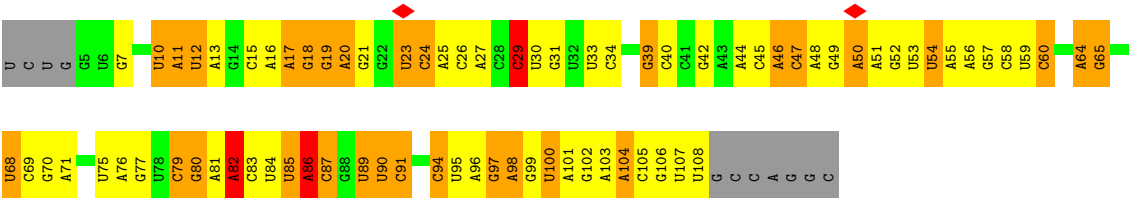
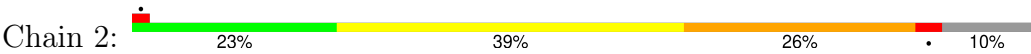








• Molecule 27: 5S rRNA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	49223	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.284	Depositor
Minimum map value	-0.180	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	385.83997, 385.83997, 385.83997	wwPDB
Map dimensions	364, 364, 364	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: G6M

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	0.39	0/927	0.54	0/1239
2	B	0.42	0/2097	0.52	0/2814
3	C	0.44	0/955	0.51	0/1265
4	D	0.40	0/795	0.54	0/1062
5	E	0.36	0/861	0.57	0/1159
6	F	0.38	0/691	0.56	0/921
7	G	0.32	0/703	0.51	0/936
8	H	0.32	0/735	0.49	0/986
9	I	0.44	0/603	0.56	0/801
10	J	0.36	0/455	0.52	0/605
11	K	0.30	0/464	0.49	0/619
12	L	0.42	0/1652	0.55	0/2216
13	M	0.36	0/434	0.57	0/585
14	N	0.39	0/404	0.55	0/537
15	O	0.33	0/393	0.53	0/523
16	P	0.43	0/376	0.52	0/491
17	Q	0.39	0/526	0.52	0/690
18	R	0.40	0/299	0.51	0/393
19	S	0.38	0/1463	0.52	0/1976
20	V	0.39	0/1160	0.49	0/1563
21	W	0.39	0/910	0.51	0/1222
22	X	0.38	0/1096	0.56	0/1461
23	Y	0.39	0/1104	0.51	0/1481
24	Z	0.37	0/959	0.53	0/1282
25	a	0.32	0/794	0.49	0/1056
26	1	0.81	0/63551	0.90	55/99100 (0.1%)
27	2	0.50	1/2475 (0.0%)	0.99	9/3854 (0.2%)
All	All	0.72	1/86882 (0.0%)	0.84	64/130837 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	2	68	U	C1'-N1	5.19	1.56	1.48

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	1	1867	G	N9-C1'-C2'	-8.39	102.77	112.00
26	1	556	U	N3-C2-O2	-7.58	116.89	122.20
26	1	1503	U	N1-C2-O2	7.44	128.01	122.80
26	1	2518	U	C2-N1-C1'	7.34	126.51	117.70
26	1	557	G	O4'-C1'-N9	7.12	113.89	108.20
26	1	1503	U	N3-C2-O2	-6.98	117.31	122.20
26	1	1503	U	C2-N1-C1'	6.74	125.79	117.70
26	1	793	G	C8-N9-C4	-6.67	103.73	106.40
26	1	2518	U	N1-C2-O2	6.62	127.44	122.80
26	1	2239	A	N7-C8-N9	6.52	117.06	113.80
26	1	2845	G	N3-C4-N9	-6.35	122.19	126.00
27	2	91	C	C1'-C2'-O2'	-6.17	92.09	110.60
26	1	2607	U	N3-C2-O2	-6.16	117.89	122.20
26	1	125	A	N7-C8-N9	6.09	116.84	113.80
26	1	1867	G	C4'-C3'-O3'	6.08	125.17	113.00
26	1	1924	G	C1'-C2'-O2'	-6.06	92.42	110.60
26	1	268	A	O4'-C1'-N9	6.05	113.04	108.20
26	1	1954	A	C1'-C2'-O2'	-6.02	92.54	110.60
27	2	82	A	N9-C1'-C2'	-5.92	105.49	112.00
26	1	592	A	N1-C6-N6	-5.90	115.06	118.60
26	1	2845	G	N3-C4-C5	5.83	131.52	128.60
26	1	323	C	C2-N1-C1'	5.82	125.20	118.80
26	1	323	C	N1-C2-O2	5.82	122.39	118.90
26	1	2518	U	N3-C2-O2	-5.80	118.14	122.20
26	1	556	U	N1-C2-O2	5.78	126.85	122.80
26	1	2417	U	N3-C2-O2	-5.77	118.16	122.20
26	1	1845	U	P-O3'-C3'	5.73	126.58	119.70
26	1	1781	C	C2-N1-C1'	5.68	125.05	118.80
26	1	2339	U	C2-N1-C1'	5.67	124.51	117.70
26	1	1593	G	N3-C4-C5	5.62	131.41	128.60
26	1	1593	G	N3-C4-N9	-5.55	122.67	126.00
27	2	86	A	O4'-C1'-N9	5.53	112.62	108.20
27	2	89	U	C4'-C3'-O3'	5.50	124.00	113.00
26	1	2239	A	C8-N9-C4	-5.49	103.60	105.80
26	1	1866	G	N9-C1'-C2'	-5.48	105.97	112.00
26	1	1781	C	N3-C2-O2	-5.46	118.07	121.90
27	2	29	C	C2-N1-C1'	5.45	124.80	118.80
26	1	793	G	N7-C8-N9	5.44	115.82	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	1	403	U	C2-N1-C1'	5.40	124.17	117.70
26	1	2056	G	C5-N7-C8	-5.34	101.63	104.30
27	2	90	U	C1'-C2'-O2'	-5.33	94.60	110.60
26	1	1215	U	N1-C2-O2	5.31	126.52	122.80
27	2	29	C	C6-N1-C2	-5.30	118.18	120.30
26	1	2639	C	C2-N1-C1'	5.27	124.59	118.80
26	1	1574	G	N3-C4-N9	-5.22	122.87	126.00
26	1	1566	G	N3-C4-N9	-5.21	122.87	126.00
26	1	125	A	C8-N9-C4	-5.21	103.72	105.80
27	2	91	C	N1-C1'-C2'	-5.21	106.27	112.00
26	1	125	A	C5-N7-C8	-5.21	101.30	103.90
26	1	439	U	C2-N1-C1'	5.19	123.92	117.70
26	1	2417	U	N1-C2-O2	5.18	126.43	122.80
26	1	515	G	C8-N9-C4	-5.17	104.33	106.40
26	1	1215	U	C2-N1-C1'	5.16	123.89	117.70
26	1	2056	G	O4'-C1'-N9	5.16	112.32	108.20
26	1	2639	C	N3-C2-O2	-5.14	118.30	121.90
26	1	1781	C	C6-N1-C2	-5.13	118.25	120.30
26	1	2845	G	C2-N3-C4	-5.11	109.35	111.90
27	2	80	G	N9-C1'-C2'	-5.09	106.41	112.00
26	1	2518	U	C6-N1-C1'	-5.07	114.10	121.20
26	1	721	A	O4'-C1'-N9	5.05	112.24	108.20
26	1	2845	G	N3-C2-N2	-5.03	116.38	119.90
26	1	1676	A	O4'-C1'-N9	5.02	112.22	108.20
26	1	515	G	N7-C8-N9	5.01	115.61	113.10
26	1	1351	C	C2-N1-C1'	5.00	124.30	118.80

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	915	0	987	48	0
2	B	2063	0	2176	90	0
3	C	943	0	1014	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	785	0	825	38	0
5	E	853	0	914	28	0
6	F	684	0	726	29	0
7	G	697	0	754	36	0
8	H	727	0	777	38	0
9	I	597	0	607	20	0
10	J	449	0	485	14	0
11	K	463	0	487	17	0
12	L	1628	0	1667	81	0
13	M	432	0	472	18	0
14	N	397	0	407	11	0
15	O	390	0	396	20	0
16	P	372	0	420	13	0
17	Q	521	0	586	27	0
18	R	296	0	340	24	0
19	S	1441	0	1487	62	0
20	V	1138	0	1130	39	0
21	W	903	0	958	40	0
22	X	1082	0	1119	41	0
23	Y	1080	0	1149	48	0
24	Z	955	0	1002	41	0
25	a	787	0	826	0	0
26	1	56747	0	28540	1238	0
27	2	2214	0	1120	69	0
28	1	25	19	0	0	0
All	All	79584	19	51371	1981	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 16.

All (1981) 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)
26:1:1489:A:H62	26:1:1509:G:N2	1.46	1.12
26:1:1489:A:N6	26:1:1509:G:H21	1.50	1.08
19:S:40:GLN:HG2	19:S:184:LEU:HB2	1.37	1.06
19:S:125:VAL:HG22	19:S:194:ILE:HD11	1.42	1.00
1:A:29:ARG:HG2	1:A:46:GLU:HG2	1.43	0.99
12:L:60:LYS:HE3	12:L:62:ASP:HB2	1.47	0.97
26:1:591:A:H4'	26:1:592:A:H5'	1.48	0.95
26:1:699:U:H4'	26:1:700:A:H5'	1.50	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:131:PHE:HB2	19:S:162:ASN:HB3	1.50	0.93
15:O:4:ASN:HA	15:O:20:THR:HG22	1.51	0.92
2:B:107:PRO:HD2	2:B:110:LEU:HD22	1.52	0.90
9:I:73:GLY:HA3	9:I:90:TYR:O	1.71	0.90
23:Y:1:MET:HB3	23:Y:48:GLU:HG3	1.52	0.90
26:1:1728:C:H2'	26:1:1729:C:H5''	1.53	0.89
26:1:2876:G:H2'	26:1:2877:G:H5''	1.53	0.88
26:1:1489:A:H62	26:1:1509:G:H21	0.89	0.88
7:G:42:LYS:HD2	26:1:544:U:H5''	1.53	0.87
12:L:41:VAL:HA	12:L:45:GLY:HA2	1.56	0.87
9:I:81:GLY:HA2	27:2:10:U:H5'	1.57	0.86
19:S:155:VAL:HB	19:S:194:ILE:HG22	1.55	0.85
2:B:95:VAL:HG12	2:B:101:LYS:HD3	1.57	0.85
12:L:38:LYS:HE3	12:L:100:GLU:HG3	1.59	0.85
3:C:91:ASN:HD21	26:1:1040:A:H4'	1.43	0.84
3:C:4:VAL:HG22	26:1:1238:U:H1'	1.57	0.83
26:1:167:U:H2'	26:1:168:A:H5''	1.60	0.83
8:H:65:VAL:HG11	8:H:70:ILE:HD13	1.60	0.83
12:L:43:VAL:HG12	26:1:2811:U:H4'	1.61	0.82
2:B:16:MET:HG3	2:B:206:GLY:HA3	1.62	0.82
8:H:44:ASP:HB2	8:H:47:GLU:HB3	1.63	0.81
24:Z:25:ILE:HD11	24:Z:66:LEU:HD11	1.62	0.81
3:C:92:ARG:NH2	3:C:95:LEU:O	2.14	0.80
16:P:25:THR:HG22	16:P:27:ASN:H	1.46	0.80
12:L:38:LYS:HB3	12:L:100:GLU:HG2	1.63	0.80
8:H:80:ASP:HB2	8:H:85:GLN:HE21	1.47	0.80
26:1:505:U:H2'	26:1:506:A:H5''	1.65	0.79
8:H:31:VAL:HG12	8:H:36:THR:HG21	1.63	0.79
26:1:1521:A:H61	26:1:1559:G:H1	1.29	0.79
2:B:84:ASP:OD2	2:B:87:ARG:NH1	2.15	0.79
26:1:1084:U:H2'	26:1:1085:U:H5''	1.65	0.79
17:Q:58:VAL:HG13	17:Q:61:LEU:HB2	1.64	0.78
7:G:10:LYS:HE3	7:G:78:PRO:HG3	1.65	0.77
26:1:1620:G:H2'	26:1:1621:C:H5'	1.65	0.77
8:H:2:ALA:HB3	8:H:51:VAL:HG23	1.67	0.77
26:1:1946:A:H2'	26:1:1947:C:H5'	1.65	0.77
14:N:9:SER:HB2	26:1:2047:A:H5'	1.65	0.77
1:A:3:ASN:HD22	26:1:2863:G:H21	1.32	0.77
4:D:27:VAL:HG21	4:D:62:VAL:HG21	1.67	0.77
22:X:76:ILE:HG23	22:X:112:LEU:HD12	1.67	0.77
26:1:793:G:H22	26:1:796:A:H5'	1.49	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:118:SER:O	2:B:134:ASN:ND2	2.17	0.76
23:Y:57:TYR:OH	23:Y:116:GLU:OE1	2.04	0.76
26:1:1510:U:O2'	26:1:1511:C:O4'	2.04	0.76
26:1:1770:C:H2'	26:1:1771:A:H5''	1.68	0.76
26:1:2429:U:H2'	26:1:2430:C:H5'	1.68	0.76
3:C:78:ARG:HH12	26:1:1195:A:H1'	1.51	0.76
12:L:25:VAL:HG21	12:L:196:LEU:HB3	1.67	0.76
12:L:54:GLU:O	12:L:86:ARG:N	2.13	0.76
19:S:110:LEU:HD22	19:S:206:LEU:HD21	1.68	0.76
26:1:1320:G:N2	26:1:1323:A:OP2	2.15	0.76
7:G:91:VAL:HG11	7:G:100:GLU:HG2	1.66	0.75
13:M:15:ARG:HD2	13:M:53:LEU:HD21	1.68	0.75
21:W:65:THR:HG22	21:W:67:SER:H	1.50	0.75
26:1:1085:U:N3	26:1:1158:G:N1	2.34	0.75
12:L:128:GLN:HE21	12:L:132:LYS:HG2	1.51	0.75
22:X:125:ALA:HB3	22:X:128:PHE:HE1	1.51	0.75
26:1:1063:U:OP1	26:1:1079:U:O2'	2.04	0.75
26:1:527:G:O2'	26:1:552:A:N6	2.20	0.74
3:C:37:GLN:HE22	26:1:606:G:H21	1.33	0.74
17:Q:40:GLN:NE2	26:1:2389:G:OP1	2.21	0.74
27:2:18:G:H2'	27:2:19:G:H5'	1.70	0.74
26:1:645:A:O2'	26:1:647:G:O2'	2.04	0.74
15:O:31:GLU:HG2	15:O:46:ARG:HD2	1.70	0.74
26:1:142:G:H2'	26:1:143:U:H5'	1.70	0.74
26:1:326:A:H2'	26:1:327:G:H5''	1.69	0.73
27:2:31:G:N2	27:2:33:U:O4	2.21	0.73
9:I:57:GLU:HG2	9:I:88:SER:HB2	1.69	0.73
24:Z:31:GLU:HG2	24:Z:118:ILE:HG12	1.71	0.73
27:2:59:U:H2'	27:2:60:C:H5'	1.71	0.73
26:1:2740:A:O2'	26:1:2742:C:OP2	2.05	0.72
2:B:108:LYS:HD2	2:B:198:LEU:HD11	1.70	0.72
24:Z:102:ARG:HH21	24:Z:122:VAL:HG23	1.52	0.72
26:1:308:C:O2	26:1:407:G:N2	2.19	0.72
23:Y:42:ILE:HA	23:Y:46:GLN:HE21	1.53	0.72
26:1:1780:G:N2	26:1:1783:G:OP2	2.22	0.72
2:B:5:LYS:HD2	2:B:17:THR:HG22	1.72	0.72
16:P:2:VAL:N	26:1:1663:G:HO2'	1.85	0.72
7:G:80:ARG:HB2	7:G:95:LYS:HG3	1.70	0.72
8:H:4:LEU:HD12	8:H:61:ILE:HG21	1.71	0.72
17:Q:35:ASN:ND2	26:1:2417:U:OP2	2.22	0.72
26:1:403:U:H2'	26:1:404:U:H5''	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1337:A:H4'	26:1:1338:U:H5''	1.72	0.72
26:1:1901:C:H2'	26:1:1902:G:H5'	1.71	0.72
5:E:78:GLU:OE2	26:1:562:C:O2'	2.05	0.71
26:1:629:A:H62	26:1:1289:A:H2	1.38	0.71
4:D:64:LYS:HB3	4:D:94:LYS:HG2	1.71	0.71
23:Y:14:ARG:HD2	23:Y:41:TRP:HH2	1.55	0.71
26:1:373:A:H2	26:1:1248:U:H2'	1.55	0.71
3:C:98:ILE:HD11	4:D:4:ILE:HD11	1.73	0.71
26:1:1482:U:H3	26:1:1600:A:H2	1.37	0.71
11:K:37:LEU:HD21	11:K:42:ARG:HH11	1.56	0.71
18:R:7:VAL:HG22	18:R:37:GLY:HA2	1.71	0.71
26:1:367:A:N6	26:1:381:G:O2'	2.24	0.71
26:1:2608:G:N2	26:1:2608:G:OP2	2.23	0.71
1:A:77:PRO:HB2	1:A:80:THR:HG23	1.71	0.71
4:D:50:ALA:HB1	4:D:51:PRO:HD2	1.73	0.71
26:1:85:G:O2'	26:1:102:A:N6	2.24	0.71
26:1:1711:G:O2'	26:1:2018:U:O4	2.09	0.71
13:M:44:ARG:HD3	13:M:47:ILE:HD11	1.72	0.70
27:2:29:C:O2'	27:2:51:A:N6	2.23	0.70
18:R:23:VAL:HB	18:R:37:GLY:HA3	1.73	0.70
21:W:12:ASP:OD2	21:W:14:SER:OG	2.08	0.70
21:W:28:SER:HG	26:1:2590:U:HO2'	1.36	0.70
26:1:2343:U:H2'	26:1:2344:C:C6	2.26	0.70
26:1:2680:U:OP2	26:1:2681:A:O2'	2.07	0.70
1:A:75:THR:HB	21:W:76:TYR:HB2	1.72	0.70
9:I:55:PRO:HG3	9:I:61:ARG:HB2	1.73	0.70
26:1:1862:G:H1	26:1:1932:C:H5	1.40	0.70
26:1:758:G:H1'	26:1:763:A:H61	1.56	0.70
19:S:148:GLN:NE2	19:S:191:SER:OG	2.24	0.70
26:1:514:G:H2'	26:1:515:G:H5'	1.73	0.70
1:A:69:GLY:O	1:A:106:ARG:NH2	2.24	0.69
26:1:1515:G:H1	26:1:1565:U:H3	1.38	0.69
26:1:1633:A:OP2	26:1:1634:A:N6	2.25	0.69
26:1:1931:G:H21	26:1:1955:A:H8	1.39	0.69
19:S:82:GLN:HB2	26:1:1294:G:H21	1.57	0.69
26:1:342:A:N3	26:1:362:C:O2'	2.25	0.69
10:J:14:THR:HG22	10:J:28:ARG:HG2	1.74	0.69
26:1:1395:G:O2'	26:1:1410:A:N6	2.25	0.69
26:1:2355:A:H2'	26:1:2356:A:C8	2.27	0.69
12:L:38:LYS:HE3	12:L:100:GLU:CG	2.23	0.69
12:L:57:LYS:HB2	12:L:68:TYR:HD1	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:29:ASN:HD22	19:S:108:LEU:HD21	1.57	0.69
26:1:1512:U:H2'	26:1:1513:A:C8	2.28	0.69
2:B:174:ILE:HG13	2:B:184:ILE:HD12	1.72	0.69
26:1:1063:U:H3	26:1:1186:A:H62	1.41	0.69
26:1:1520:A:H2'	26:1:1521:A:O4'	1.93	0.69
26:1:721:A:H8	26:1:2096:G:H21	1.40	0.68
26:1:2272:U:H5''	26:1:2273:G:H5'	1.76	0.68
23:Y:32:PHE:CZ	23:Y:111:GLU:HG2	2.28	0.68
26:1:350:G:H1'	26:1:373:A:H61	1.57	0.68
26:1:897:A:H61	26:1:971:U:H3	1.42	0.68
27:2:96:A:C2'	27:2:97:G:H5'	2.23	0.68
26:1:161:A:H2'	26:1:162:A:H5''	1.73	0.68
12:L:46:TYR:OH	26:1:2663:U:O2'	2.11	0.68
26:1:116:G:OP2	26:1:118:A:O2'	2.07	0.68
9:I:40:THR:HG22	9:I:41:GLY:H	1.58	0.68
13:M:52:HIS:CD2	13:M:52:HIS:H	2.10	0.68
4:D:46:VAL:O	4:D:47:LYS:HD2	1.94	0.67
26:1:753:U:H2'	26:1:754:U:C6	2.30	0.67
26:1:1017:A:H5'	26:1:1227:U:H1'	1.75	0.67
26:1:173:A:H2'	26:1:174:U:C6	2.30	0.67
26:1:1901:C:C2'	26:1:1902:G:H5'	2.24	0.67
26:1:2580:G:H8	26:1:2609:G:H21	1.42	0.67
2:B:245:SER:OG	26:1:1869:G:O2'	2.11	0.67
7:G:27:LEU:HD12	7:G:32:ARG:HB2	1.75	0.67
26:1:10:A:O2'	26:1:11:U:OP1	2.11	0.67
26:1:2858:G:H1	26:1:2900:C:H5	1.41	0.67
27:2:104:A:H2'	27:2:105:C:C6	2.29	0.67
11:K:6:ILE:HG12	11:K:53:LEU:HD23	1.74	0.67
26:1:1943:A:H5''	26:1:1944:U:H5	1.60	0.67
7:G:43:LYS:O	7:G:56:ILE:HA	1.93	0.67
26:1:181:G:H2'	26:1:182:C:O4'	1.94	0.67
26:1:273:A:OP2	26:1:297:G:N1	2.22	0.67
26:1:1248:U:OP1	26:1:1249:U:O2'	2.10	0.67
2:B:29:PRO:HB2	2:B:34:LEU:HD11	1.77	0.67
2:B:65:ILE:HD11	2:B:91:ILE:HG21	1.76	0.67
12:L:86:ARG:NH1	26:1:2850:G:OP2	2.28	0.67
26:1:2309:G:H4'	26:1:2416:G:O2'	1.95	0.67
26:1:2560:U:H2'	26:1:2561:C:H5'	1.77	0.67
23:Y:14:ARG:HD2	23:Y:41:TRP:CH2	2.29	0.67
26:1:1385:G:H2'	26:1:1386:U:H5'	1.77	0.67
26:1:1077:U:O2'	26:1:2777:A:N6	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2340:C:H2'	26:1:2341:A:C8	2.30	0.66
12:L:3:LYS:NZ	12:L:98:ALA:HB2	2.10	0.66
26:1:2307:G:C2'	26:1:2308:C:H5'	2.25	0.66
9:I:54:TYR:OH	26:1:2359:C:OP1	2.13	0.66
26:1:2123:A:H2'	26:1:2124:U:C6	2.30	0.66
26:1:89:U:H3'	26:1:90:A:H3'	1.76	0.66
26:1:340:C:H2'	26:1:341:G:O4'	1.95	0.66
26:1:1431:U:C2'	26:1:1432:A:H5'	2.26	0.66
26:1:2817:A:O2'	26:1:2818:A:H5''	1.95	0.66
26:1:788:A:O2'	26:1:1703:U:OP1	2.12	0.66
26:1:2649:U:O3'	26:1:2845:G:N2	2.21	0.66
22:X:18:ARG:NH2	26:1:1288:G:N7	2.44	0.66
26:1:1728:C:C2'	26:1:1729:C:H5''	2.26	0.66
26:1:2342:U:H2'	26:1:2343:U:C6	2.31	0.66
26:1:1880:A:H2'	26:1:1881:A:C8	2.30	0.66
26:1:2314:A:H62	26:1:2371:U:H3	1.44	0.66
17:Q:58:VAL:HG13	17:Q:61:LEU:HD12	1.77	0.66
18:R:30:PRO:HB2	26:1:2554:C:H5''	1.77	0.65
21:W:63:VAL:HG11	21:W:102:VAL:HG12	1.78	0.65
23:Y:51:ARG:HD3	23:Y:66:ILE:HD11	1.77	0.65
26:1:1588:U:H2'	26:1:1589:U:H6	1.60	0.65
26:1:901:G:H2'	26:1:902:A:C8	2.31	0.65
2:B:240:PRO:HB2	26:1:1930:G:OP1	1.95	0.65
26:1:105:C:O2'	26:1:337:A:O2'	2.14	0.65
26:1:793:G:N2	26:1:795:A:H3'	2.11	0.65
26:1:1070:A:OP2	26:1:1178:C:O2'	2.13	0.65
26:1:1212:U:H2'	26:1:1213:C:C6	2.30	0.65
26:1:1463:A:H2'	26:1:1464:U:H5''	1.79	0.65
26:1:1556:G:O2'	26:1:1557:C:OP2	2.12	0.65
4:D:81:ASN:HB3	22:X:23:VAL:HG11	1.77	0.65
15:O:9:CYS:HB3	15:O:13:GLY:O	1.96	0.65
23:Y:54:MET:CG	23:Y:121:ALA:HB2	2.27	0.65
26:1:575:G:N2	26:1:2050:A:OP1	2.29	0.65
26:1:1588:U:H2'	26:1:1589:U:C6	2.32	0.65
26:1:805:G:H2'	26:1:806:A:O4'	1.97	0.65
1:A:102:LEU:HD23	1:A:105:LEU:HD12	1.78	0.65
26:1:786:U:H2'	26:1:787:U:C6	2.32	0.65
26:1:1966:U:OP1	26:1:2631:U:O2'	2.14	0.65
6:F:13:THR:H	6:F:16:SER:HB3	1.61	0.65
26:1:1769:C:H2'	26:1:1770:C:C6	2.32	0.65
26:1:2507:C:H2'	26:1:2508:G:H5'	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:95:LEU:HD13	4:D:4:ILE:HD13	1.80	0.64
26:1:1185:U:H4'	26:1:1186:A:O4'	1.97	0.64
8:H:29:ALA:HB3	8:H:41:VAL:HG23	1.78	0.64
24:Z:74:GLU:HB3	24:Z:77:THR:HB	1.79	0.64
3:C:98:ILE:HD11	4:D:4:ILE:CD1	2.28	0.64
26:1:889:U:H3'	26:1:890:G:C8	2.32	0.64
10:J:39:LEU:HD23	10:J:44:PRO:HB3	1.79	0.64
26:1:1481:A:H2'	26:1:1482:U:C6	2.33	0.64
2:B:167:LYS:HG2	2:B:172:VAL:HG12	1.79	0.64
17:Q:8:ARG:NH2	26:1:247:A:OP2	2.28	0.64
26:1:1563:U:H2'	26:1:1564:G:H8	1.62	0.64
16:P:12:LYS:O	16:P:16:VAL:HG12	1.97	0.64
26:1:2038:U:H2'	26:1:2039:G:O4'	1.98	0.64
26:1:2885:U:OP2	26:1:2886:G:O2'	2.14	0.64
5:E:89:ALA:HB2	26:1:793:G:H5'	1.77	0.64
26:1:1162:C:H3'	26:1:1163:U:H5''	1.80	0.64
26:1:1519:U:O2'	26:1:1520:A:H5'	1.97	0.64
26:1:1943:A:H3'	26:1:1944:U:C6	2.33	0.64
23:Y:36:ALA:HB2	23:Y:103:LEU:HD21	1.80	0.64
26:1:2006:C:C2'	26:1:2007:G:H5'	2.28	0.64
26:1:403:U:C2'	26:1:404:U:H5''	2.28	0.63
26:1:2532:G:O2'	26:1:2533:U:H5''	1.98	0.63
1:A:10:VAL:HG11	12:L:196:LEU:HD11	1.80	0.63
23:Y:45:ARG:HD3	26:1:2511:G:OP1	1.98	0.63
26:1:748:U:H2'	26:1:749:G:O4'	1.97	0.63
26:1:1066:G:N2	26:1:1067:U:O4	2.30	0.63
26:1:2599:A:O2'	26:1:2602:C:OP1	2.09	0.63
23:Y:36:ALA:HB2	23:Y:103:LEU:CD2	2.28	0.63
26:1:156:A:H62	26:1:172:U:H3	1.46	0.63
20:V:7:ALA:H	20:V:46:THR:HG21	1.63	0.63
26:1:629:A:N1	26:1:854:G:O2'	2.27	0.63
26:1:2876:G:C2'	26:1:2877:G:H5''	2.25	0.63
9:I:79:ARG:HA	9:I:85:LYS:HA	1.79	0.63
21:W:61:VAL:HG11	21:W:111:PHE:CE1	2.33	0.63
26:1:963:A:H62	26:1:2295:A:H2	1.47	0.63
7:G:42:LYS:HB3	7:G:58:GLU:HG2	1.81	0.63
26:1:162:A:H8	26:1:2244:G:H21	1.46	0.63
26:1:183:A:H3'	26:1:183:A:OP2	1.99	0.63
26:1:1218:G:H2'	26:1:1219:G:C8	2.33	0.63
24:Z:13:ARG:NH2	26:1:2717:A:OP2	2.32	0.63
27:2:83:C:H42	27:2:86:A:H61	1.45	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:13:ARG:HD2	26:1:773:G:H4'	1.80	0.63
26:1:1072:A:N3	26:1:2513:G:O2'	2.30	0.63
26:1:89:U:H3'	26:1:90:A:C3'	2.28	0.63
26:1:1085:U:O4	26:1:1158:G:O6	2.16	0.63
12:L:157:ALA:HB3	26:1:2602:C:H5'	1.81	0.62
17:Q:31:HIS:CD2	17:Q:32:LEU:HG	2.34	0.62
7:G:24:ILE:HD11	7:G:36:GLU:HA	1.80	0.62
26:1:1797:G:H1	26:1:2009:U:H3	1.47	0.62
14:N:3:VAL:HG12	26:1:2042:A:C2	2.34	0.62
19:S:115:SER:O	19:S:119:GLN:HG2	1.99	0.62
26:1:758:G:H1'	26:1:763:A:N6	2.14	0.62
26:1:1387:C:H2'	26:1:1388:C:H5'	1.81	0.62
15:O:18:ILE:HG21	26:1:2446:U:H4'	1.80	0.62
22:X:124:LYS:HE2	22:X:144:GLU:HB2	1.79	0.62
24:Z:48:ILE:HD12	24:Z:89:ILE:HG22	1.81	0.62
26:1:1022:G:H2'	26:1:1023:A:H5'	1.80	0.62
26:1:1387:C:C2'	26:1:1388:C:H5'	2.28	0.62
27:2:45:C:H2'	27:2:46:A:H5'	1.80	0.62
27:2:59:U:C2'	27:2:60:C:H5'	2.30	0.62
4:D:41:VAL:HG22	4:D:48:VAL:CG2	2.29	0.62
8:H:9:ARG:HE	8:H:40:SER:HB3	1.63	0.62
21:W:50:GLY:O	21:W:53:LYS:NZ	2.25	0.62
24:Z:74:GLU:CB	24:Z:77:THR:HB	2.29	0.62
3:C:70:ARG:HE	3:C:75:SER:HA	1.64	0.62
7:G:44:HIS:O	7:G:54:GLY:N	2.33	0.62
26:1:613:G:H2'	26:1:2057:A:N7	2.15	0.62
26:1:785:C:O2'	26:1:786:U:H5'	1.99	0.62
26:1:2331:G:H22	26:1:2339:U:H5	1.47	0.62
12:L:65:SER:OG	26:1:2851:G:OP2	2.06	0.62
21:W:43:VAL:HG21	21:W:52:VAL:CG1	2.30	0.62
21:W:69:VAL:HG22	21:W:77:ILE:HG22	1.82	0.62
26:1:1169:G:OP2	26:1:1170:A:O2'	2.13	0.62
17:Q:14:VAL:CG2	17:Q:22:LEU:HB3	2.30	0.62
26:1:363:A:O2'	26:1:365:A:OP2	2.17	0.62
26:1:1962:G:H1	26:1:1989:C:HO2'	1.48	0.62
27:2:105:C:H2'	27:2:106:G:O4'	2.00	0.62
2:B:69:ARG:HD3	2:B:104:ILE:HD12	1.81	0.62
26:1:460:C:H2'	26:1:461:A:C8	2.35	0.62
1:A:34:ILE:O	1:A:40:GLU:HA	1.99	0.61
8:H:4:LEU:HD11	8:H:51:VAL:HG11	1.82	0.61
23:Y:77:LYS:HE2	26:1:1000:G:H5''	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:69:C:H4'	26:1:75:G:N7	2.15	0.61
1:A:53:ARG:NH2	26:1:2710:C:OP1	2.23	0.61
22:X:103:LYS:HE2	26:1:648:G:O6	2.00	0.61
26:1:434:G:H2'	26:1:436:A:C2	2.35	0.61
26:1:2584:G:H2'	26:1:2585:C:C6	2.35	0.61
26:1:2102:U:OP2	26:1:2265:G:O2'	2.13	0.61
26:1:514:G:C2'	26:1:515:G:H5'	2.30	0.61
26:1:556:U:C2'	26:1:557:G:H5'	2.30	0.61
26:1:1268:C:H2'	26:1:1269:A:C8	2.35	0.61
26:1:1771:A:H2'	26:1:1772:G:O4'	1.99	0.61
19:S:48:THR:O	26:1:488:G:N2	2.29	0.61
24:Z:74:GLU:HB2	24:Z:77:THR:O	2.00	0.61
26:1:195:C:H2'	26:1:196:U:H5'	1.82	0.61
26:1:1981:G:O2'	26:1:1983:U:O4	2.08	0.61
26:1:2915:C:H2'	26:1:2916:U:C6	2.34	0.61
1:A:29:ARG:HD2	1:A:89:LYS:HE2	1.81	0.61
26:1:632:U:H2'	26:1:633:A:H8	1.66	0.61
26:1:1085:U:O2	26:1:1158:G:N2	2.33	0.61
26:1:2676:U:H2'	26:1:2677:C:C6	2.35	0.61
26:1:631:U:H2'	26:1:632:U:C6	2.36	0.61
26:1:1988:C:O2'	26:1:1989:C:OP1	2.13	0.61
3:C:91:ASN:HB2	4:D:11:GLN:CD	2.21	0.61
26:1:89:U:H3'	26:1:90:A:H2'	1.81	0.61
26:1:414:C:C2'	26:1:415:U:H5'	2.31	0.61
26:1:632:U:H2'	26:1:633:A:C8	2.35	0.61
26:1:1632:A:H4'	26:1:1633:A:C4	2.34	0.61
19:S:26:ILE:HG13	19:S:111:ARG:NH1	2.15	0.61
26:1:1766:C:H2'	26:1:1767:G:H5'	1.81	0.61
26:1:2429:U:C2'	26:1:2430:C:H5'	2.30	0.61
2:B:117:GLU:OE2	2:B:120:ALA:HA	2.01	0.61
26:1:774:G:H5'	26:1:775:A:H5''	1.83	0.61
26:1:2594:G:H2'	26:1:2595:C:C6	2.36	0.61
8:H:65:VAL:HG21	8:H:70:ILE:HD11	1.83	0.60
17:Q:18:ALA:CB	26:1:673:G:H5''	2.31	0.60
19:S:164:GLU:HG3	19:S:165:LEU:HG	1.83	0.60
1:A:29:ARG:HB2	1:A:87:GLU:HG2	1.83	0.60
3:C:53:ARG:NH1	26:1:580:C:O3'	2.33	0.60
24:Z:45:GLU:HB3	26:1:2859:G:H4'	1.84	0.60
26:1:1176:U:O2'	26:1:1177:A:H5'	2.01	0.60
26:1:889:U:H3'	26:1:890:G:H8	1.66	0.60
26:1:1220:A:H2'	26:1:1221:C:C6	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1329:G:H2'	26:1:1330:U:C6	2.36	0.60
26:1:1409:U:HO2'	26:1:2239:A:H8	1.48	0.60
26:1:1450:A:H3'	26:1:1451:U:C5	2.37	0.60
26:1:2317:G:O2'	26:1:2318:U:H5'	2.01	0.60
26:1:2341:A:H2'	26:1:2342:U:C6	2.36	0.60
26:1:92:G:H2'	26:1:93:U:C6	2.36	0.60
26:1:1565:U:H2'	26:1:1566:G:C8	2.35	0.60
27:2:47:C:H2'	27:2:48:A:C8	2.35	0.60
23:Y:24:GLY:N	26:1:952:A:OP1	2.32	0.60
26:1:59:U:O2'	26:1:74:U:OP2	2.20	0.60
4:D:14:VAL:CG2	4:D:97:ILE:HG13	2.31	0.60
26:1:348:C:H2'	26:1:349:U:C6	2.36	0.60
26:1:651:A:H2'	26:1:652:A:C8	2.37	0.60
26:1:2288:C:C2'	26:1:2289:U:H5'	2.32	0.60
12:L:57:LYS:HB2	12:L:68:TYR:CD1	2.36	0.60
16:P:38:LYS:NZ	26:1:514:G:OP2	2.34	0.60
20:V:54:TYR:CE1	20:V:122:LYS:HG2	2.37	0.60
26:1:2224:U:H1'	26:1:2225:A:C2	2.36	0.60
4:D:65:GLN:HG3	4:D:93:THR:HG22	1.84	0.60
9:I:76:LYS:HD3	9:I:90:TYR:CE2	2.37	0.60
26:1:1563:U:H2'	26:1:1564:G:C8	2.36	0.60
9:I:17:SER:HB3	26:1:2282:G:H21	1.65	0.60
11:K:8:ASP:O	11:K:60:ARG:NH1	2.24	0.60
15:O:31:GLU:HG2	15:O:46:ARG:CD	2.32	0.60
22:X:125:ALA:HB3	22:X:128:PHE:CE1	2.34	0.60
26:1:238:U:H2'	26:1:239:C:C6	2.37	0.60
26:1:2222:U:O2'	26:1:2223:C:H5'	2.02	0.60
19:S:91:GLY:HA2	26:1:1286:G:H5'	1.84	0.60
26:1:100:U:H5'	26:1:101:G:C8	2.37	0.60
26:1:394:U:H2'	26:1:395:U:C6	2.37	0.60
26:1:505:U:C2'	26:1:506:A:H5''	2.32	0.60
26:1:597:U:O2'	26:1:598:G:H5'	2.02	0.60
26:1:1577:G:H22	26:1:1588:U:H3	1.48	0.60
26:1:2318:U:H2'	26:1:2319:U:C6	2.37	0.60
2:B:174:ILE:CG1	2:B:184:ILE:HD12	2.32	0.59
26:1:1745:A:H2'	26:1:1746:G:H5'	1.84	0.59
6:F:25:TYR:HH	6:F:86:SER:HG	1.47	0.59
21:W:39:ILE:HD13	21:W:62:ILE:HD11	1.84	0.59
22:X:128:PHE:CE2	22:X:143:HIS:HB2	2.37	0.59
26:1:64:A:H62	26:1:90:A:H61	1.50	0.59
26:1:2273:G:H2'	26:1:2274:A:C8	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:99:TYR:HB3	12:L:101:VAL:HG22	1.84	0.59
17:Q:14:VAL:HG21	17:Q:22:LEU:HB3	1.84	0.59
23:Y:42:ILE:HA	23:Y:46:GLN:NE2	2.17	0.59
26:1:902:A:C2'	26:1:903:G:H5'	2.32	0.59
4:D:41:VAL:HG22	4:D:48:VAL:HG22	1.85	0.59
4:D:79:ARG:NH2	26:1:615:A:OP2	2.34	0.59
26:1:1352:C:O2'	26:1:1429:G:N3	2.34	0.59
26:1:1410:A:H5'	26:1:2239:A:H1'	1.84	0.59
2:B:26:LYS:HE2	2:B:28:THR:O	2.03	0.59
24:Z:45:GLU:CB	26:1:2859:G:H4'	2.32	0.59
26:1:1494:G:H2'	26:1:1495:C:H5'	1.84	0.59
26:1:1884:G:H21	26:1:1912:A:H62	1.50	0.59
26:1:2383:C:H2'	26:1:2384:U:O4'	2.03	0.59
7:G:32:ARG:HD3	7:G:64:HIS:HA	1.84	0.59
15:O:18:ILE:HD13	26:1:2446:U:H5'	1.83	0.59
20:V:29:LEU:HD13	20:V:143:LEU:HD11	1.83	0.59
20:V:53:ASP:O	20:V:122:LYS:HD3	2.02	0.59
26:1:100:U:H3'	26:1:101:G:H5'	1.83	0.59
26:1:448:A:H2'	26:1:449:U:H5'	1.83	0.59
27:2:69:C:H2'	27:2:70:G:O4'	2.03	0.59
12:L:2:THR:HB	12:L:109:THR:HB	1.85	0.59
20:V:29:LEU:CD1	20:V:143:LEU:HD11	2.32	0.59
26:1:339:A:H2'	26:1:340:C:C6	2.38	0.59
26:1:1897:U:H3	26:1:1899:U:H5'	1.66	0.59
26:1:2688:G:H2'	26:1:2689:A:O4'	2.03	0.59
1:A:30:VAL:HG13	1:A:83:ILE:HG23	1.85	0.59
5:E:1:MET:HG2	5:E:2:GLU:H	1.68	0.59
16:P:41:LYS:HG3	26:1:505:U:H5''	1.84	0.59
18:R:24:MET:HG2	18:R:35:ARG:CB	2.32	0.59
6:F:10:PRO:HD3	11:K:30:PHE:CD1	2.38	0.59
8:H:16:SER:HB3	27:2:89:U:H5''	1.85	0.59
12:L:134:HIS:CD2	12:L:168:LYS:HD2	2.37	0.59
21:W:5:GLU:HG3	26:1:1713:A:C8	2.38	0.59
26:1:396:G:H2'	26:1:397:U:C6	2.37	0.59
26:1:1726:A:H2'	26:1:1727:C:C6	2.37	0.59
26:1:2221:U:H2'	26:1:2222:U:H6	1.68	0.59
26:1:2308:C:O2'	26:1:2309:G:H5'	2.03	0.59
1:A:76:PHE:HB3	1:A:83:ILE:HD11	1.84	0.59
2:B:208:ALA:HB2	26:1:1817:C:O2'	2.03	0.59
24:Z:41:ARG:O	24:Z:45:GLU:HG2	2.03	0.59
26:1:259:A:H2'	26:1:260:A:C8	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2340:C:O2'	26:1:2341:A:H5'	2.03	0.59
26:1:2917:U:H2'	26:1:2918:A:C8	2.37	0.59
26:1:247:A:H2'	26:1:248:G:O4'	2.02	0.58
26:1:447:A:H2'	26:1:448:A:H8	1.68	0.58
26:1:858:U:H2'	26:1:859:C:C6	2.38	0.58
26:1:1442:C:H2'	26:1:1443:A:C8	2.38	0.58
26:1:1911:A:H2'	26:1:1912:A:C8	2.38	0.58
26:1:2746:G:O2'	26:1:2747:U:H5'	2.03	0.58
8:H:4:LEU:HD21	8:H:51:VAL:HG11	1.85	0.58
26:1:637:U:H2'	26:1:638:U:C6	2.37	0.58
26:1:642:U:O2'	26:1:643:G:H5'	2.03	0.58
26:1:1312:A:H4'	26:1:1313:G:OP1	2.02	0.58
26:1:1514:A:O2'	26:1:1515:G:H5'	2.03	0.58
26:1:1943:A:H3'	26:1:1944:U:H6	1.67	0.58
26:1:2041:A:H2'	26:1:2042:A:C8	2.38	0.58
27:2:51:A:H2'	27:2:52:G:H5'	1.84	0.58
5:E:42:ALA:HB2	26:1:2037:G:H5''	1.85	0.58
19:S:152:VAL:HG12	19:S:191:SER:HB3	1.86	0.58
26:1:397:U:H2'	26:1:398:C:C6	2.39	0.58
26:1:2224:U:H1'	26:1:2225:A:H2	1.67	0.58
2:B:118:SER:HA	2:B:131:PRO:CD	2.33	0.58
7:G:91:VAL:HG11	7:G:100:GLU:CG	2.33	0.58
22:X:46:VAL:HG13	22:X:51:GLU:HA	1.84	0.58
26:1:1219:G:O2'	26:1:1220:A:O4'	2.21	0.58
26:1:2516:G:O2'	26:1:2517:G:H5'	2.03	0.58
22:X:76:ILE:CG2	22:X:112:LEU:HD12	2.32	0.58
26:1:242:U:O2'	26:1:243:U:H5'	2.02	0.58
26:1:1031:C:O2'	26:1:1044:A:N3	2.34	0.58
26:1:2123:A:O2'	26:1:2124:U:O4'	2.15	0.58
26:1:2270:U:H2'	26:1:2271:U:C6	2.38	0.58
27:2:33:U:H2'	27:2:34:C:C6	2.38	0.58
18:R:17:ILE:HG21	18:R:26:ILE:HD11	1.85	0.58
24:Z:16:MET:CE	26:1:1314:A:H4'	2.34	0.58
26:1:133:A:H2'	26:1:134:U:C6	2.39	0.58
26:1:1390:A:H2'	26:1:1391:A:C8	2.38	0.58
26:1:2058:A:N3	26:1:2482:G:O2'	2.30	0.58
6:F:4:ARG:HG2	6:F:5:ASP:H	1.69	0.58
26:1:991:A:H2'	26:1:992:A:C8	2.39	0.58
26:1:1492:G:O2'	26:1:1575:A:O2'	2.16	0.58
26:1:2300:A:H2'	26:1:2301:A:C8	2.38	0.58
15:O:12:CYS:SG	15:O:39:GLU:HG3	2.44	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:328:G:O6	26:1:399:U:O2	2.21	0.58
13:M:4:LEU:HB3	13:M:6:ILE:HD11	1.85	0.58
19:S:67:GLN:NE2	26:1:720:A:H4'	2.19	0.58
15:O:7:LEU:HA	15:O:46:ARG:O	2.03	0.58
23:Y:66:ILE:HG12	23:Y:104:PHE:CE1	2.39	0.58
26:1:1355:A:H2'	26:1:1356:G:H5'	1.86	0.58
27:2:12:U:O2'	27:2:102:G:H1'	2.04	0.58
7:G:8:ASN:HA	7:G:21:GLY:O	2.03	0.57
7:G:15:LYS:NZ	26:1:546:A:OP1	2.33	0.57
19:S:22:ALA:O	19:S:111:ARG:NH1	2.36	0.57
26:1:221:G:H22	26:1:238:U:H4'	1.69	0.57
26:1:1512:U:H2'	26:1:1513:A:H8	1.66	0.57
26:1:2658:G:H4'	26:1:2911:A:H5''	1.86	0.57
27:2:47:C:H2'	27:2:48:A:H8	1.69	0.57
26:1:160:G:H21	26:1:168:A:H2	1.53	0.57
26:1:373:A:C2	26:1:1248:U:H2'	2.39	0.57
26:1:962:A:H5''	26:1:2295:A:N6	2.19	0.57
26:1:1083:G:H2'	26:1:1084:U:C6	2.39	0.57
13:M:4:LEU:O	13:M:6:ILE:HD12	2.05	0.57
26:1:1943:A:H5''	26:1:1944:U:C5	2.39	0.57
26:1:2006:C:H2'	26:1:2007:G:H5'	1.86	0.57
11:K:21:SER:HA	11:K:50:ILE:CD1	2.34	0.57
23:Y:77:LYS:HB3	23:Y:78:PRO:HD2	1.87	0.57
26:1:24:G:H2'	26:1:25:U:H6	1.69	0.57
26:1:2061:U:O2'	26:1:2062:G:H5'	2.03	0.57
26:1:2676:U:H2'	26:1:2677:C:H6	1.69	0.57
7:G:11:VAL:HA	7:G:68:VAL:HG12	1.86	0.57
26:1:402:C:H2'	26:1:403:U:O2	2.04	0.57
26:1:561:C:O2'	26:1:562:C:H5'	2.05	0.57
26:1:1562:C:H2'	26:1:1563:U:C6	2.40	0.57
26:1:1982:U:O4	26:1:2583:C:N4	2.37	0.57
26:1:2221:U:H2'	26:1:2222:U:C6	2.40	0.57
26:1:2543:G:O2'	26:1:2544:C:H5'	2.04	0.57
26:1:2604:A:H2'	26:1:2641:A:N6	2.20	0.57
2:B:67:PHE:HB3	2:B:152:GLY:H	1.67	0.57
6:F:58:TYR:OH	26:1:1377:U:OP2	2.23	0.57
19:S:46:GLN:NE2	26:1:487:U:O2'	2.37	0.57
21:W:91:LYS:CD	21:W:110:ASN:HB2	2.33	0.57
26:1:1385:G:C2'	26:1:1386:U:H5'	2.34	0.57
26:1:145:A:H2'	26:1:146:U:C6	2.38	0.57
26:1:481:C:H2'	26:1:482:U:H5'	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1081:G:H2'	26:1:1082:C:C6	2.40	0.57
6:F:10:PRO:HD3	11:K:30:PHE:CE1	2.39	0.57
12:L:64:LYS:HE2	26:1:2851:G:C5	2.40	0.57
23:Y:34:LEU:HD11	23:Y:129:THR:OG1	2.05	0.57
26:1:1160:C:H2'	26:1:1161:A:C8	2.40	0.57
26:1:1514:A:H2	26:1:1566:G:H22	1.53	0.57
2:B:205:VAL:HG23	26:1:1818:A:H4'	1.87	0.57
19:S:153:LEU:HB3	19:S:192:LEU:HD23	1.87	0.57
26:1:38:A:H2'	26:1:39:C:O4'	2.05	0.57
26:1:1558:U:H2'	26:1:1559:G:C8	2.39	0.57
2:B:67:PHE:CE1	2:B:156:ARG:HD2	2.40	0.57
2:B:180:GLU:OE2	2:B:270:ILE:HG23	2.05	0.57
26:1:1828:U:O4	26:1:2229:C:H4'	2.05	0.57
26:1:2541:U:H2'	26:1:2542:C:C6	2.39	0.57
4:D:35:PHE:O	4:D:57:THR:HB	2.05	0.56
8:H:57:ARG:HH22	8:H:77:TYR:HE1	1.53	0.56
26:1:89:U:H3'	26:1:90:A:C2'	2.34	0.56
7:G:22:LYS:O	7:G:35:VAL:HG13	2.04	0.56
26:1:1770:C:C2'	26:1:1771:A:H5''	2.35	0.56
26:1:1959:A:H2'	26:1:1960:G:O4'	2.05	0.56
1:A:22:PHE:CE2	1:A:52:ARG:HD2	2.40	0.56
1:A:28:LEU:CD2	1:A:88:VAL:HG22	2.35	0.56
1:A:92:GLY:HA2	1:A:113:GLN:O	2.05	0.56
2:B:147:LYS:HE3	26:1:2231:C:H1'	1.86	0.56
26:1:916:U:O2'	26:1:917:U:H5'	2.05	0.56
26:1:1988:C:O2'	26:1:1989:C:H5'	2.06	0.56
26:1:2904:U:H2'	26:1:2905:C:O4'	2.04	0.56
2:B:176:LEU:HB2	2:B:180:GLU:HB3	1.87	0.56
11:K:50:ILE:O	11:K:54:LYS:HG2	2.06	0.56
17:Q:10:ALA:O	17:Q:14:VAL:HG12	2.06	0.56
23:Y:17:THR:O	23:Y:39:THR:HG21	2.04	0.56
26:1:753:U:H2'	26:1:754:U:H6	1.69	0.56
26:1:2496:A:H2'	26:1:2497:G:O4'	2.05	0.56
26:1:2610:G:C2'	26:1:2611:U:H5'	2.35	0.56
6:F:7:LEU:HD12	6:F:45:ILE:HD12	1.88	0.56
26:1:1881:A:H62	26:1:1915:G:H8	1.52	0.56
26:1:2419:A:H2	26:1:2451:C:H42	1.52	0.56
22:X:124:LYS:CD	22:X:144:GLU:HB2	2.36	0.56
23:Y:35:GLN:HB2	23:Y:132:VAL:HG21	1.88	0.56
26:1:1900:G:H2'	26:1:1901:C:C6	2.40	0.56
26:1:615:A:H61	26:1:2056:G:H8	1.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1161:A:H2'	26:1:1162:C:C6	2.41	0.56
26:1:2761:C:H2'	26:1:2762:G:O4'	2.05	0.56
1:A:10:VAL:CG2	12:L:194:VAL:HG21	2.36	0.56
2:B:236:GLU:HG3	26:1:2627:A:H2	1.71	0.56
6:F:16:SER:O	6:F:20:MET:HG2	2.05	0.56
12:L:118:VAL:HG22	12:L:211:ILE:HD13	1.88	0.56
18:R:14:CYS:SG	18:R:32:HIS:ND1	2.78	0.56
26:1:242:U:C2'	26:1:243:U:H5'	2.36	0.56
26:1:1084:U:C2'	26:1:1085:U:H5''	2.34	0.56
26:1:1464:U:H5'	26:1:1465:G:OP2	2.06	0.56
26:1:1897:U:H2'	26:1:1898:C:H4'	1.88	0.56
2:B:16:MET:CG	2:B:206:GLY:HA3	2.35	0.56
19:S:149:PRO:HG2	19:S:191:SER:HB2	1.88	0.56
26:1:2101:U:H2'	26:1:2102:U:C6	2.41	0.56
2:B:26:LYS:HD3	2:B:82:GLN:HE21	1.70	0.56
2:B:176:LEU:HD12	2:B:180:GLU:HG2	1.87	0.56
8:H:31:VAL:O	8:H:38:ASN:HA	2.05	0.56
12:L:189:ASP:HB3	12:L:194:VAL:CG2	2.36	0.56
12:L:189:ASP:HB3	12:L:194:VAL:HG23	1.87	0.56
15:O:34:LYS:HB2	15:O:45:HIS:CD2	2.41	0.56
26:1:178:A:O2'	26:1:179:A:H5'	2.06	0.56
26:1:753:U:O2'	26:1:754:U:H5'	2.06	0.56
26:1:1895:C:H2'	26:1:1896:U:O4'	2.06	0.56
2:B:159:GLY:HA2	2:B:198:LEU:CD2	2.36	0.55
7:G:10:LYS:CE	7:G:78:PRO:HG3	2.36	0.55
14:N:5:LYS:NZ	26:1:2081:A:H2'	2.21	0.55
26:1:830:U:H4'	26:1:1806:U:H4'	1.88	0.55
26:1:878:C:H2'	26:1:879:U:C6	2.41	0.55
26:1:2083:G:H1	26:1:2639:C:H5	1.54	0.55
26:1:2360:A:H5'	26:1:2362:A:H1'	1.88	0.55
26:1:2560:U:C2'	26:1:2561:C:H5'	2.35	0.55
2:B:260:ARG:HB2	26:1:1825:U:OP1	2.05	0.55
4:D:85:LYS:HD2	26:1:1263:A:H4'	1.89	0.55
6:F:62:LYS:HB3	6:F:71:TYR:CE1	2.41	0.55
12:L:138:ARG:HG2	26:1:2024:A:OP2	2.07	0.55
26:1:1472:C:C5	26:1:1616:A:H5''	2.41	0.55
27:2:19:G:H2'	27:2:20:A:C8	2.41	0.55
8:H:73:MET:O	8:H:91:PHE:HA	2.06	0.55
9:I:61:ARG:O	9:I:61:ARG:HD3	2.05	0.55
24:Z:4:ARG:NH1	26:1:1696:C:OP1	2.39	0.55
27:2:30:U:H1'	27:2:50:A:H61	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1352:C:H2'	26:1:1353:A:H8	1.71	0.55
2:B:145:GLU:HG2	2:B:151:GLY:O	2.06	0.55
12:L:118:VAL:HG22	12:L:211:ILE:CD1	2.36	0.55
21:W:25:LEU:CD2	26:1:2589:U:H4'	2.36	0.55
26:1:446:G:C2'	26:1:447:A:H5''	2.37	0.55
26:1:699:U:C4'	26:1:700:A:H5'	2.30	0.55
26:1:1075:G:C2'	26:1:1076:A:H5'	2.37	0.55
26:1:1515:G:H22	26:1:1565:U:H3	1.54	0.55
12:L:43:VAL:CG1	26:1:2811:U:H4'	2.33	0.55
20:V:14:ARG:NH1	20:V:50:ASP:O	2.40	0.55
26:1:24:G:H2'	26:1:25:U:C6	2.42	0.55
26:1:275:A:H2'	26:1:276:C:H5'	1.88	0.55
26:1:1897:U:O2	26:1:1899:U:H5'	2.06	0.55
26:1:2495:A:N1	26:1:2508:G:O2'	2.32	0.55
2:B:205:VAL:O	2:B:210:ARG:HD3	2.06	0.55
3:C:4:VAL:HG22	26:1:1238:U:C1'	2.35	0.55
4:D:81:ASN:HB3	22:X:23:VAL:CG1	2.36	0.55
18:R:32:HIS:O	18:R:34:GLN:HG3	2.07	0.55
2:B:150:LYS:HE3	2:B:153:GLN:NE2	2.22	0.55
8:H:21:LEU:CD1	8:H:42:LYS:HD3	2.37	0.55
26:1:268:A:H2'	26:1:269:G:O4'	2.07	0.55
26:1:393:G:O2'	26:1:394:U:H5'	2.06	0.55
26:1:1829:A:H2'	26:1:1830:A:C8	2.42	0.55
2:B:71:LYS:HG3	2:B:96:TYR:CE1	2.42	0.55
26:1:1603:U:H2'	26:1:1604:C:C6	2.42	0.55
26:1:2770:U:H2'	26:1:2771:G:O4'	2.07	0.55
8:H:48:PHE:HA	8:H:51:VAL:HG12	1.88	0.54
16:P:38:LYS:HZ1	26:1:515:G:H22	1.54	0.54
26:1:748:U:O2'	26:1:749:G:H5'	2.07	0.54
26:1:2696:G:H3'	26:1:2697:G:H5''	1.89	0.54
27:2:39:G:H2'	27:2:39:G:N3	2.22	0.54
3:C:64:ARG:HD2	20:V:43:VAL:O	2.08	0.54
16:P:25:THR:HB	16:P:28:GLY:H	1.72	0.54
26:1:1916:A:H2'	26:1:1917:A:C8	2.42	0.54
23:Y:54:MET:HG3	23:Y:121:ALA:HB2	1.90	0.54
26:1:150:A:H61	26:1:179:A:H2	1.55	0.54
26:1:583:A:H2'	26:1:584:G:O4'	2.08	0.54
5:E:44:SER:O	5:E:48:GLU:HG3	2.07	0.54
15:O:29:ARG:HD3	15:O:46:ARG:HH21	1.71	0.54
26:1:1906:C:H2'	26:1:1907:U:O4'	2.08	0.54
6:F:35:LYS:HB2	6:F:53:VAL:HG13	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:169:ASN:ND2	26:1:366:G:H2'	2.21	0.54
20:V:8:ASN:OD1	26:1:583:A:H4'	2.07	0.54
24:Z:22:THR:O	24:Z:26:ILE:HG12	2.08	0.54
26:1:2326:G:H2'	26:1:2327:A:C8	2.43	0.54
27:2:12:U:HO2'	27:2:102:G:H1'	1.71	0.54
5:E:29:ALA:O	5:E:33:ILE:HD12	2.08	0.54
9:I:77:PHE:CD1	9:I:87:VAL:HG22	2.42	0.54
26:1:1326:C:OP1	26:1:1691:G:N2	2.34	0.54
26:1:1710:G:C2'	26:1:1711:G:H5'	2.37	0.54
26:1:2664:U:O2'	26:1:2665:G:H5'	2.08	0.54
1:A:41:ARG:O	1:A:42:ILE:HD13	2.06	0.54
13:M:21:LYS:O	13:M:24:GLU:HG3	2.08	0.54
17:Q:28:PHE:CD1	26:1:2419:A:H4'	2.43	0.54
26:1:12:U:H5''	26:1:13:A:OP2	2.07	0.54
26:1:801:A:H2'	26:1:802:G:O4'	2.08	0.54
26:1:2307:G:H2'	26:1:2308:C:H5'	1.88	0.54
27:2:79:C:H2'	27:2:80:G:C8	2.43	0.54
5:E:81:THR:HG22	5:E:99:ARG:HG2	1.89	0.54
12:L:13:THR:HG22	12:L:14:GLN:H	1.72	0.54
26:1:1504:U:O4	26:1:1505:G:N1	2.41	0.54
26:1:1897:U:C2	26:1:1899:U:H5'	2.43	0.54
20:V:48:HIS:CD2	20:V:49:VAL:HG13	2.43	0.54
23:Y:32:PHE:CE2	23:Y:111:GLU:HA	2.42	0.54
24:Z:49:THR:OG1	26:1:2860:U:OP1	2.16	0.54
24:Z:51:GLY:HA2	24:Z:86:PHE:CE1	2.43	0.54
26:1:2326:G:H2'	26:1:2327:A:H8	1.73	0.54
26:1:2354:A:H2'	26:1:2355:A:C8	2.42	0.54
2:B:67:PHE:HD1	2:B:143:ASN:HD21	1.56	0.54
2:B:69:ARG:O	2:B:116:VAL:HG11	2.08	0.54
19:S:134:PRO:HB3	19:S:165:LEU:HB2	1.89	0.54
23:Y:48:GLU:O	23:Y:52:ILE:HG12	2.08	0.54
26:1:556:U:H4'	26:1:1273:G:H4'	1.89	0.54
26:1:1501:G:H22	26:1:2729:G:H22	1.56	0.54
26:1:1821:U:H2'	26:1:1822:C:C6	2.43	0.54
26:1:2457:A:HO2'	26:1:2458:U:H6	1.56	0.54
3:C:76:TYR:OH	3:C:93:LYS:HD2	2.08	0.53
26:1:165:C:H3'	26:1:166:A:H8	1.72	0.53
26:1:414:C:H2'	26:1:415:U:H5'	1.90	0.53
26:1:1669:C:H2'	26:1:1670:A:O4'	2.09	0.53
26:1:2262:G:H2'	26:1:2263:C:C6	2.44	0.53
26:1:2867:U:H2'	26:1:2868:G:O4'	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:123:LYS:HE3	26:1:2708:C:OP2	2.08	0.53
16:P:33:ALA:O	16:P:37:ARG:HG2	2.09	0.53
22:X:121:LEU:O	22:X:141:GLY:HA3	2.08	0.53
26:1:308:C:H2'	26:1:309:U:C6	2.43	0.53
26:1:390:A:H2'	26:1:391:A:C8	2.43	0.53
26:1:447:A:H2'	26:1:448:A:C8	2.43	0.53
26:1:920:A:H2'	26:1:921:C:O4'	2.08	0.53
26:1:1075:G:O2'	26:1:1076:A:H5'	2.08	0.53
26:1:1931:G:O2'	26:1:1932:C:H5'	2.08	0.53
27:2:54:U:O2'	27:2:55:A:OP2	2.23	0.53
2:B:91:ILE:HD12	2:B:103:TYR:CD1	2.42	0.53
4:D:78:ARG:NH2	26:1:606:G:OP2	2.40	0.53
26:1:75:G:H22	26:1:110:A:H2	1.56	0.53
26:1:506:A:H2'	26:1:507:C:H5'	1.89	0.53
26:1:2494:C:H2'	26:1:2495:A:O4'	2.07	0.53
26:1:2856:U:H2'	26:1:2857:A:C8	2.44	0.53
1:A:29:ARG:HD2	1:A:89:LYS:NZ	2.23	0.53
26:1:342:A:H2'	26:1:343:A:C8	2.44	0.53
26:1:1643:C:C2'	26:1:1644:C:H5'	2.39	0.53
26:1:2818:A:H2'	26:1:2819:C:C6	2.43	0.53
14:N:44:LYS:HA	14:N:44:LYS:HE2	1.90	0.53
21:W:43:VAL:HG21	21:W:52:VAL:HG12	1.90	0.53
26:1:404:U:H3'	26:1:404:U:OP1	2.08	0.53
26:1:421:C:H2'	26:1:422:G:H8	1.73	0.53
26:1:1446:U:H2'	26:1:1447:A:C8	2.43	0.53
26:1:2394:G:O2'	26:1:2395:C:H5'	2.08	0.53
1:A:29:ARG:HD2	1:A:89:LYS:CE	2.38	0.53
5:E:42:ALA:O	5:E:45:PRO:HD2	2.09	0.53
8:H:63:LEU:HG	8:H:64:GLY:H	1.73	0.53
26:1:403:U:C3'	26:1:404:U:H5''	2.39	0.53
26:1:770:G:O2'	26:1:771:G:H5'	2.08	0.53
26:1:969:A:H3'	26:1:970:U:C4'	2.38	0.53
26:1:2702:A:H2'	26:1:2703:C:O4'	2.09	0.53
26:1:2831:G:O2'	26:1:2832:A:H5'	2.08	0.53
27:2:58:C:H2'	27:2:59:U:C5	2.44	0.53
7:G:86:VAL:HG21	7:G:100:GLU:OE2	2.08	0.53
9:I:77:PHE:CD2	26:1:902:A:H5'	2.44	0.53
26:1:872:U:O2'	26:1:2095:U:N3	2.42	0.53
26:1:1249:U:OP1	26:1:1249:U:H2'	2.08	0.53
26:1:2810:A:H2'	26:1:2811:U:C6	2.44	0.53
3:C:106:PHE:O	3:C:110:VAL:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:45:LEU:HD11	9:I:69:ALA:HB2	1.91	0.53
26:1:27:G:O2'	26:1:28:A:OP2	2.27	0.53
26:1:445:G:H2'	26:1:446:G:O4'	2.09	0.53
26:1:519:G:O2'	26:1:520:G:H5'	2.09	0.53
26:1:597:U:C2'	26:1:598:G:H5'	2.39	0.53
26:1:1326:C:H2'	26:1:1327:C:C6	2.44	0.53
26:1:2533:U:H3	26:1:2610:G:H1	1.56	0.53
2:B:266:SER:O	2:B:269:LEU:N	2.40	0.53
10:J:36:VAL:O	10:J:46:LYS:HA	2.09	0.53
26:1:575:G:O2'	26:1:577:A:N7	2.41	0.53
26:1:597:U:H2'	26:1:598:G:O4'	2.08	0.53
26:1:1450:A:H3'	26:1:1451:U:C6	2.43	0.53
26:1:2826:U:H2'	26:1:2827:A:N9	2.24	0.53
23:Y:30:GLY:O	23:Y:134:ARG:NH2	2.42	0.53
26:1:30:G:H2'	26:1:31:C:C6	2.43	0.53
26:1:161:A:O2'	26:1:2235:A:H4'	2.08	0.53
26:1:1372:C:O2'	26:1:1373:U:H5'	2.08	0.53
26:1:1773:A:H2'	26:1:1774:A:O4'	2.09	0.53
26:1:2340:C:H2'	26:1:2341:A:H8	1.71	0.53
2:B:11:ASN:O	26:1:774:G:N2	2.41	0.52
23:Y:39:THR:OG1	23:Y:99:PRO:HD3	2.08	0.52
26:1:1462:G:H8	26:1:1626:A:H62	1.57	0.52
3:C:49:ASP:OD2	26:1:579:U:O2'	2.15	0.52
26:1:4:U:H2'	26:1:5:A:C8	2.44	0.52
26:1:544:U:H2'	26:1:545:G:O4'	2.08	0.52
26:1:1356:G:O2'	26:1:1357:G:H5'	2.08	0.52
26:1:1452:C:H3'	26:1:1453:G:H5''	1.91	0.52
26:1:1454:U:O4	26:1:1629:U:H2'	2.10	0.52
26:1:2377:C:H2'	26:1:2378:G:O4'	2.09	0.52
26:1:2619:G:H2'	26:1:2620:U:O4'	2.08	0.52
27:2:58:C:H2'	27:2:59:U:C6	2.44	0.52
2:B:263:LYS:HZ3	2:B:266:SER:HB3	1.74	0.52
3:C:105:ALA:O	3:C:108:GLN:HB2	2.08	0.52
5:E:81:THR:CG2	5:E:99:ARG:HG2	2.39	0.52
13:M:40:ASN:HB2	13:M:43:ILE:H	1.74	0.52
26:1:720:A:O2'	26:1:721:A:H5'	2.10	0.52
26:1:1459:A:N6	26:1:1630:A:O4'	2.43	0.52
26:1:1501:G:H22	26:1:2729:G:H1	1.56	0.52
26:1:2774:G:O6	26:1:2782:C:H5''	2.08	0.52
26:1:2883:U:H2'	26:1:2884:G:C8	2.44	0.52
1:A:29:ARG:HD3	1:A:87:GLU:OE2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:159:GLY:HA2	2:B:198:LEU:HD23	1.91	0.52
6:F:37:GLN:HE21	26:1:144:C:H4'	1.74	0.52
17:Q:55:MET:O	17:Q:59:LYS:HB3	2.10	0.52
26:1:620:G:H2'	26:1:621:A:C8	2.45	0.52
26:1:908:A:H2'	26:1:909:G:C8	2.44	0.52
26:1:1593:G:H5''	26:1:1594:U:OP1	2.09	0.52
26:1:2240:U:H3'	26:1:2241:C:H5'	1.92	0.52
26:1:2794:C:C2'	26:1:2795:C:H5'	2.39	0.52
26:1:2818:A:H2'	26:1:2819:C:H6	1.75	0.52
4:D:4:ILE:HB	4:D:40:PHE:HB3	1.90	0.52
20:V:32:GLU:HG2	20:V:143:LEU:HD22	1.91	0.52
26:1:100:U:H3'	26:1:101:G:C5'	2.40	0.52
26:1:970:U:OP1	26:1:971:U:H5'	2.10	0.52
26:1:1880:A:H2'	26:1:1881:A:H8	1.72	0.52
27:2:23:U:H5'	27:2:24:C:H5	1.74	0.52
7:G:95:LYS:HA	7:G:95:LYS:HE2	1.90	0.52
26:1:389:A:H2'	26:1:390:A:H5'	1.91	0.52
26:1:448:A:C2'	26:1:449:U:H5'	2.40	0.52
26:1:712:U:H2'	26:1:713:A:O4'	2.10	0.52
26:1:749:G:H1'	26:1:772:A:N6	2.24	0.52
26:1:1753:U:O2'	26:1:1754:C:H5'	2.10	0.52
26:1:1914:C:C2'	26:1:1915:G:H5'	2.39	0.52
26:1:2098:A:H2'	26:1:2099:G:C8	2.44	0.52
26:1:2260:A:H2'	26:1:2261:G:C8	2.45	0.52
27:2:81:A:H2'	27:2:82:A:C8	2.45	0.52
20:V:54:TYR:HE1	20:V:122:LYS:HG2	1.74	0.52
26:1:194:A:H2'	26:1:195:C:C6	2.44	0.52
2:B:132:LEU:HG	2:B:188:CYS:O	2.10	0.52
10:J:36:VAL:HG13	10:J:38:ILE:HG23	1.91	0.52
12:L:159:ASP:HB2	26:1:2598:U:O3'	2.10	0.52
26:1:2313:A:H4'	26:1:2314:A:O4'	2.09	0.52
27:2:81:A:H2'	27:2:82:A:H8	1.75	0.52
2:B:243:ARG:HB3	2:B:244:PRO:HD2	1.92	0.52
11:K:10:THR:O	11:K:13:GLU:HB3	2.10	0.52
12:L:3:LYS:HZ3	12:L:98:ALA:HB2	1.74	0.52
26:1:238:U:H2'	26:1:239:C:H6	1.75	0.52
26:1:1939:A:H62	26:1:1944:U:H3	1.56	0.52
5:E:59:GLU:HG3	5:E:66:THR:CG2	2.40	0.52
8:H:2:ALA:O	8:H:61:ILE:HG23	2.10	0.52
12:L:210:GLU:HG3	12:L:212:ARG:HH12	1.74	0.52
16:P:38:LYS:NZ	26:1:515:G:H22	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:109:ILE:HD11	22:X:125:ALA:HB2	1.92	0.52
24:Z:5:LYS:HD2	26:1:2029:G:OP1	2.09	0.52
26:1:487:U:O2'	26:1:488:G:H5'	2.10	0.52
26:1:1517:A:C2'	26:1:1518:G:H5'	2.40	0.52
26:1:2236:C:H5''	26:1:2237:U:H2'	1.92	0.52
4:D:80:LYS:O	4:D:82:SER:N	2.43	0.51
23:Y:32:PHE:HZ	23:Y:111:GLU:HG2	1.73	0.51
26:1:167:U:C2'	26:1:168:A:H5''	2.34	0.51
26:1:556:U:H2'	26:1:557:G:H5'	1.91	0.51
26:1:1022:G:C2'	26:1:1023:A:H5'	2.40	0.51
26:1:1353:A:H2'	26:1:1354:G:C8	2.44	0.51
26:1:1886:A:H2'	26:1:1887:G:O4'	2.10	0.51
26:1:625:G:H2'	26:1:626:G:C8	2.45	0.51
26:1:1388:C:H2'	26:1:1389:U:C6	2.45	0.51
26:1:1865:C:O2	26:1:1865:C:H2'	2.09	0.51
12:L:127:PHE:HB2	26:1:2843:A:OP1	2.10	0.51
26:1:155:U:C2'	26:1:156:A:H5'	2.40	0.51
26:1:992:A:H2'	26:1:993:C:C6	2.45	0.51
26:1:1763:U:H2'	26:1:1765:A:OP2	2.11	0.51
26:1:1816:A:O2'	26:1:1817:C:H5'	2.10	0.51
26:1:1897:U:N3	26:1:1899:U:H5'	2.25	0.51
26:1:2391:C:H2'	26:1:2392:G:O4'	2.11	0.51
26:1:2801:C:H2'	26:1:2802:A:O4'	2.11	0.51
27:2:11:A:H2'	27:2:12:U:H5''	1.91	0.51
3:C:52:GLN:HG2	3:C:55:ARG:NH2	2.26	0.51
12:L:38:LYS:HD2	12:L:96:VAL:HB	1.91	0.51
21:W:68:GLY:HA3	21:W:77:ILE:O	2.10	0.51
22:X:110:LYS:HA	22:X:127:LYS:O	2.10	0.51
26:1:78:U:H2'	26:1:79:U:C6	2.45	0.51
26:1:593:U:O2'	26:1:594:G:OP1	2.23	0.51
26:1:1767:G:H2'	26:1:1768:C:C6	2.45	0.51
26:1:1918:G:H2'	26:1:1919:C:C6	2.45	0.51
26:1:2488:C:H2'	26:1:2489:U:C6	2.46	0.51
5:E:35:ILE:O	5:E:39:THR:HG23	2.10	0.51
7:G:80:ARG:HG3	26:1:379:C:OP1	2.10	0.51
22:X:122:THR:HG22	22:X:141:GLY:HA2	1.93	0.51
24:Z:109:ARG:HG2	24:Z:110:ARG:O	2.10	0.51
26:1:21:A:H2'	26:1:22:C:O4'	2.11	0.51
26:1:266:A:H2'	26:1:267:G:O4'	2.11	0.51
26:1:309:U:O2'	26:1:310:C:H2'	2.11	0.51
26:1:1308:C:H5''	26:1:1309:G:O5'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1848:A:H2'	26:1:1849:G:C8	2.45	0.51
26:1:2231:C:H2'	26:1:2232:A:C8	2.46	0.51
26:1:2489:U:H1'	26:1:2518:U:O4	2.11	0.51
26:1:2494:C:O2'	26:1:2495:A:H5'	2.10	0.51
1:A:8:GLU:O	1:A:12:LYS:HG2	2.11	0.51
12:L:60:LYS:HD3	12:L:68:TYR:CE2	2.46	0.51
17:Q:28:PHE:CE1	26:1:2419:A:H4'	2.46	0.51
21:W:91:LYS:HD2	21:W:110:ASN:HB2	1.93	0.51
26:1:955:A:H2'	26:1:956:A:C8	2.46	0.51
7:G:79:THR:HG21	7:G:96:LYS:HG3	1.93	0.51
17:Q:23:LYS:HE2	17:Q:47:ALA:HB3	1.93	0.51
21:W:7:ARG:HB3	21:W:18:GLU:OE2	2.10	0.51
26:1:1020:G:HO2'	26:1:1199:A:HO2'	1.57	0.51
26:1:1310:A:H3'	26:1:1311:A:C8	2.46	0.51
26:1:1598:U:H2'	26:1:1599:G:O4'	2.11	0.51
26:1:1804:U:O2'	26:1:1805:U:H5'	2.11	0.51
26:1:1978:U:H2'	26:1:1980:A:OP2	2.10	0.51
26:1:2679:U:H2'	26:1:2680:U:C6	2.46	0.51
27:2:19:G:H2'	27:2:20:A:H8	1.74	0.51
10:J:19:SER:HB3	26:1:2107:G:OP1	2.09	0.51
11:K:17:GLN:HG2	11:K:53:LEU:HB3	1.93	0.51
22:X:90:GLU:HA	22:X:122:THR:OG1	2.10	0.51
26:1:128:C:O2'	26:1:129:C:H5'	2.11	0.51
26:1:175:C:H5''	26:1:176:A:OP1	2.11	0.51
26:1:687:G:N2	26:1:689:A:H3'	2.26	0.51
26:1:1820:G:H2'	26:1:1821:U:O4'	2.09	0.51
26:1:1996:A:H5'	26:1:1997:A:OP1	2.11	0.51
26:1:2404:A:H2'	26:1:2405:A:H8	1.75	0.51
27:2:75:U:H3	27:2:94:C:H5	1.58	0.51
19:S:133:ALA:HB1	19:S:134:PRO:HD2	1.93	0.51
26:1:133:A:H2'	26:1:134:U:H6	1.76	0.51
26:1:383:A:C2'	26:1:384:G:H5'	2.41	0.51
26:1:633:A:H2'	26:1:634:C:C6	2.46	0.51
27:2:15:C:H41	27:2:103:A:H2	1.58	0.51
27:2:52:G:O2'	27:2:53:U:H5'	2.11	0.51
27:2:107:U:H2'	27:2:108:U:C6	2.45	0.51
1:A:28:LEU:HD23	1:A:88:VAL:HG22	1.93	0.51
2:B:5:LYS:HD2	2:B:17:THR:CG2	2.41	0.51
2:B:66:ASP:OD2	2:B:102:ARG:HD3	2.11	0.51
22:X:80:ASP:HA	22:X:83:ASN:ND2	2.25	0.51
26:1:2329:U:H2'	26:1:2330:G:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2350:G:O2'	26:1:2351:U:H5'	2.11	0.51
27:2:76:A:H2'	27:2:77:G:H5'	1.92	0.51
1:A:25:GLY:HA3	1:A:94:VAL:HG11	1.93	0.50
2:B:145:GLU:HB2	2:B:188:CYS:HB3	1.93	0.50
12:L:87:PHE:CD1	12:L:208:LEU:HD22	2.46	0.50
14:N:16:ARG:NH2	26:1:1302:G:OP1	2.34	0.50
19:S:39:LEU:HD11	19:S:99:TYR:O	2.11	0.50
22:X:93:PRO:O	22:X:97:VAL:HG23	2.11	0.50
23:Y:68:ILE:HD12	23:Y:68:ILE:O	2.10	0.50
26:1:1463:A:C2'	26:1:1464:U:H5''	2.41	0.50
26:1:1572:G:H22	26:1:1593:G:H1	1.57	0.50
26:1:1634:A:H2'	26:1:1635:A:O4'	2.10	0.50
26:1:1975:G:O2'	26:1:1976:G:H5'	2.11	0.50
2:B:75:ASN:HA	2:B:115:ILE:HG22	1.94	0.50
2:B:253:PRO:HG2	2:B:257:LYS:HE3	1.94	0.50
9:I:23:ASP:OD1	26:1:2290:C:N4	2.44	0.50
19:S:110:LEU:O	19:S:110:LEU:HD23	2.10	0.50
26:1:225:A:N6	26:1:235:G:H1'	2.26	0.50
26:1:1471:A:H4'	26:1:1472:C:O5'	2.09	0.50
26:1:2299:U:H5''	26:1:2300:A:OP1	2.11	0.50
26:1:2883:U:H2'	26:1:2884:G:H8	1.75	0.50
4:D:27:VAL:CG2	4:D:62:VAL:HG21	2.39	0.50
6:F:7:LEU:HD11	6:F:42:VAL:HG12	1.92	0.50
19:S:165:LEU:HB3	26:1:364:A:O4'	2.11	0.50
26:1:63:U:H1'	26:1:64:A:C2	2.47	0.50
26:1:145:A:H2'	26:1:146:U:H6	1.77	0.50
26:1:206:U:OP2	26:1:207:A:O2'	2.16	0.50
26:1:858:U:H2'	26:1:859:C:H6	1.75	0.50
26:1:1491:C:H2'	26:1:1492:G:H5'	1.92	0.50
26:1:2317:G:C2'	26:1:2318:U:H5'	2.41	0.50
26:1:2341:A:O2'	26:1:2342:U:H5'	2.12	0.50
26:1:2404:A:H2'	26:1:2405:A:C8	2.46	0.50
2:B:139:THR:O	2:B:163:GLN:HA	2.12	0.50
3:C:81:ASN:ND2	26:1:1195:A:H4'	2.27	0.50
6:F:12:ILE:O	6:F:12:ILE:HG13	2.12	0.50
19:S:88:ILE:HG22	19:S:90:PHE:O	2.12	0.50
22:X:87:ASP:OD1	22:X:120:LYS:N	2.38	0.50
23:Y:39:THR:HA	23:Y:97:VAL:O	2.11	0.50
26:1:155:U:H2'	26:1:156:A:H5'	1.93	0.50
26:1:747:U:O2'	26:1:748:U:H5'	2.12	0.50
8:H:70:ILE:HG13	8:H:72:VAL:HG13	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:74:TYR:CD1	22:X:107:SER:HB3	2.47	0.50
24:Z:25:ILE:CD1	24:Z:85:LEU:HD12	2.42	0.50
26:1:525:A:H4'	26:1:526:A:OP1	2.11	0.50
26:1:900:G:H2'	26:1:901:G:O4'	2.11	0.50
26:1:1567:A:OP2	26:1:1568:U:O2'	2.19	0.50
2:B:132:LEU:HD23	2:B:135:ILE:HD12	1.93	0.50
8:H:65:VAL:HG21	8:H:70:ILE:CD1	2.42	0.50
23:Y:42:ILE:HD11	23:Y:68:ILE:HD13	1.92	0.50
26:1:44:A:O2'	26:1:45:G:OP1	2.24	0.50
26:1:884:U:O2'	26:1:885:C:H5'	2.11	0.50
26:1:1045:A:H2'	26:1:1046:G:O4'	2.11	0.50
26:1:1207:G:O2'	26:1:1208:A:H5'	2.12	0.50
26:1:1210:U:H5'	26:1:1211:G:OP2	2.12	0.50
26:1:1319:U:H2'	26:1:1320:G:O4'	2.12	0.50
26:1:1624:C:H2'	26:1:1625:U:C1'	2.42	0.50
26:1:1700:C:H2'	26:1:1701:U:C6	2.47	0.50
26:1:2092:C:H2'	26:1:2093:C:C6	2.46	0.50
27:2:64:A:H4'	27:2:65:G:OP1	2.10	0.50
8:H:61:ILE:O	8:H:72:VAL:N	2.40	0.50
13:M:40:ASN:H	13:M:43:ILE:HG22	1.77	0.50
14:N:3:VAL:HG12	26:1:2042:A:N3	2.26	0.50
19:S:139:PHE:CE2	19:S:143:LEU:HD11	2.47	0.50
26:1:741:G:O2'	26:1:742:U:H5'	2.12	0.50
26:1:1368:C:O2'	26:1:1369:G:H5'	2.11	0.50
26:1:1865:C:H4'	26:1:1866:G:H5''	1.92	0.50
7:G:69:GLN:CB	7:G:78:PRO:HB2	2.42	0.50
23:Y:66:ILE:HG12	23:Y:104:PHE:HE1	1.75	0.50
26:1:99:U:OP1	26:1:100:U:H2'	2.12	0.50
26:1:154:A:H2'	26:1:155:U:O4'	2.11	0.50
26:1:446:G:O2'	26:1:447:A:H5''	2.12	0.50
26:1:969:A:H3'	26:1:970:U:O4'	2.12	0.50
26:1:1780:G:H2'	26:1:1782:A:OP2	2.12	0.50
3:C:91:ASN:HB2	4:D:11:GLN:OE1	2.11	0.50
19:S:67:GLN:HE21	26:1:720:A:H4'	1.77	0.50
20:V:14:ARG:NH1	20:V:50:ASP:OD1	2.45	0.50
24:Z:103:ILE:HG23	24:Z:117:VAL:HB	1.93	0.50
26:1:158:G:H2'	26:1:159:U:O4'	2.12	0.50
26:1:1431:U:H2'	26:1:1432:A:H5'	1.92	0.50
26:1:1501:G:N2	26:1:2729:G:H22	2.09	0.50
26:1:1644:C:O2'	26:1:1645:G:H5'	2.11	0.50
26:1:1724:U:N3	26:1:1791:G:OP2	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:33:ILE:O	5:E:37:LYS:HG3	2.12	0.49
19:S:157:GLU:HA	19:S:198:ALA:HB2	1.94	0.49
23:Y:83:MET:HE1	26:1:1000:G:H1'	1.94	0.49
26:1:877:G:H2'	26:1:878:C:C6	2.47	0.49
26:1:1891:U:OP1	26:1:2437:G:O2'	2.29	0.49
26:1:2222:U:C2'	26:1:2223:C:H5'	2.41	0.49
3:C:37:GLN:HE21	26:1:1290:G:H1	1.59	0.49
21:W:24:VAL:HG13	21:W:33:ALA:HB2	1.94	0.49
26:1:143:U:H2'	26:1:144:C:O4'	2.13	0.49
26:1:346:A:H2'	26:1:347:U:C6	2.47	0.49
26:1:523:A:H2'	26:1:524:A:C8	2.47	0.49
26:1:1727:C:H2'	26:1:1728:C:C6	2.46	0.49
26:1:2082:C:H5'	26:1:2083:G:O5'	2.12	0.49
26:1:2310:C:C6	26:1:2416:G:H2'	2.47	0.49
26:1:2400:U:H2'	26:1:2401:C:C6	2.47	0.49
2:B:176:LEU:HD12	2:B:180:GLU:CG	2.42	0.49
9:I:73:GLY:CA	9:I:90:TYR:O	2.52	0.49
12:L:30:ALA:HB3	12:L:107:VAL:CG1	2.43	0.49
23:Y:118:LEU:HD12	23:Y:131:PHE:CE1	2.47	0.49
26:1:1211:G:H5''	26:1:1212:U:OP2	2.13	0.49
26:1:1241:A:H2'	26:1:1242:A:C8	2.46	0.49
26:1:1522:G:O2'	26:1:1523:G:H5'	2.12	0.49
26:1:2420:U:H2'	26:1:2421:C:O4'	2.12	0.49
26:1:2580:G:C8	26:1:2610:G:H1'	2.47	0.49
26:1:2690:G:H2'	26:1:2691:G:C8	2.48	0.49
26:1:267:G:O2'	26:1:268:A:H5''	2.12	0.49
26:1:1734:A:H2'	26:1:1735:C:O4'	2.12	0.49
26:1:2007:G:O2'	26:1:2009:U:OP2	2.26	0.49
26:1:2484:U:O2'	26:1:2485:U:H5'	2.13	0.49
2:B:65:ILE:HD11	2:B:91:ILE:CG2	2.43	0.49
2:B:150:LYS:HD3	26:1:2231:C:H4'	1.94	0.49
10:J:43:LYS:HD2	10:J:44:PRO:HD2	1.94	0.49
11:K:9:LEU:O	11:K:13:GLU:HB2	2.12	0.49
12:L:142:SER:OG	26:1:2020:U:H4'	2.11	0.49
14:N:9:SER:CB	26:1:2047:A:H5'	2.40	0.49
26:1:61:A:H2'	26:1:62:C:C6	2.48	0.49
26:1:799:U:O2'	26:1:800:G:H5'	2.12	0.49
26:1:1575:A:O2'	26:1:1576:A:H5'	2.12	0.49
26:1:2418:G:C6	26:1:2454:C:H1'	2.47	0.49
26:1:2444:C:O2'	26:1:2445:A:H5'	2.12	0.49
26:1:2611:U:H2'	26:1:2612:U:H5''	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:399:U:H2'	26:1:400:C:C6	2.47	0.49
26:1:504:G:O2'	26:1:515:G:O6	2.25	0.49
26:1:1065:A:H8	26:1:1066:G:H5''	1.76	0.49
26:1:1217:U:H1'	26:1:1218:G:C2	2.47	0.49
26:1:1481:A:O4'	26:1:1561:G:N2	2.46	0.49
26:1:1710:G:O2'	26:1:1711:G:H5'	2.13	0.49
12:L:178:VAL:HG23	12:L:202:PRO:CG	2.43	0.49
19:S:139:PHE:HE2	19:S:173:VAL:HG11	1.77	0.49
26:1:45:G:H2'	26:1:218:G:C8	2.48	0.49
26:1:793:G:N2	26:1:796:A:OP2	2.46	0.49
26:1:1215:U:H5'	26:1:1216:U:C2	2.47	0.49
26:1:1326:C:H2'	26:1:1327:C:H6	1.77	0.49
26:1:2117:A:O2'	26:1:2118:U:H5'	2.12	0.49
26:1:2322:C:O2'	26:1:2323:U:H5'	2.13	0.49
1:A:77:PRO:HB2	1:A:80:THR:CG2	2.42	0.49
2:B:263:LYS:NZ	2:B:266:SER:HB3	2.28	0.49
7:G:69:GLN:HB2	7:G:78:PRO:HB2	1.94	0.49
26:1:248:G:O2'	26:1:249:C:H5'	2.12	0.49
26:1:785:C:C2'	26:1:786:U:H5'	2.43	0.49
4:D:1:MET:HA	4:D:42:GLY:O	2.13	0.49
18:R:30:PRO:HG2	26:1:2555:U:OP1	2.13	0.49
22:X:124:LYS:CE	22:X:144:GLU:HB2	2.41	0.49
26:1:274:A:O2'	26:1:275:A:H5'	2.13	0.49
26:1:862:C:O2'	26:1:884:U:OP1	2.28	0.49
26:1:1352:C:H2'	26:1:1353:A:C8	2.47	0.49
26:1:2356:A:H2'	26:1:2357:G:C8	2.47	0.49
20:V:19:ILE:HD13	20:V:142:GLU:HA	1.94	0.49
1:A:31:HIS:ND1	1:A:44:VAL:HG12	2.28	0.48
4:D:11:GLN:HG3	4:D:39:LEU:HD12	1.93	0.48
8:H:21:LEU:HD11	8:H:42:LYS:HD3	1.95	0.48
10:J:17:ARG:HB2	10:J:27:ARG:HG2	1.95	0.48
21:W:5:GLU:HG3	26:1:1713:A:H8	1.78	0.48
24:Z:25:ILE:HD13	24:Z:85:LEU:HD12	1.95	0.48
24:Z:26:ILE:CD1	24:Z:71:ILE:HD11	2.42	0.48
26:1:1043:U:O2'	26:1:1044:A:H5'	2.13	0.48
26:1:2267:C:O2'	26:1:2268:A:H5'	2.12	0.48
26:1:173:A:H2'	26:1:174:U:H6	1.75	0.48
26:1:391:A:H2'	26:1:392:U:C6	2.49	0.48
26:1:1219:G:O2'	26:1:1220:A:O5'	2.30	0.48
26:1:1407:C:H2'	26:1:1408:G:O4'	2.13	0.48
26:1:1491:C:O2	26:1:1574:G:N2	2.25	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2051:C:H2'	26:1:2052:C:C6	2.48	0.48
26:1:326:A:C2'	26:1:327:G:H5''	2.40	0.48
26:1:702:U:H2'	26:1:703:A:C8	2.49	0.48
26:1:1013:U:H2'	26:1:1014:U:C6	2.49	0.48
26:1:1298:G:H2'	26:1:1299:U:O4'	2.13	0.48
26:1:2860:U:H2'	26:1:2861:U:C6	2.48	0.48
11:K:31:GLN:HB3	11:K:37:LEU:HB2	1.95	0.48
17:Q:18:ALA:HB2	26:1:673:G:H5''	1.95	0.48
22:X:124:LYS:HE2	22:X:144:GLU:OE1	2.13	0.48
23:Y:67:LYS:NZ	23:Y:105:GLU:OE2	2.40	0.48
26:1:64:A:H5'	26:1:64:A:N3	2.28	0.48
26:1:226:A:O2'	26:1:466:C:O2	2.31	0.48
26:1:509:G:N2	26:1:512:A:OP2	2.42	0.48
26:1:992:A:H2'	26:1:993:C:H6	1.78	0.48
26:1:1365:G:H2'	26:1:1367:C:C5	2.48	0.48
26:1:1918:G:H2'	26:1:1919:C:H6	1.77	0.48
26:1:2270:U:O2'	26:1:2461:A:N1	2.34	0.48
26:1:2563:G:C2'	26:1:2564:U:H5'	2.42	0.48
26:1:2618:C:H2'	26:1:2619:G:C8	2.48	0.48
19:S:110:LEU:HD22	19:S:206:LEU:CD2	2.39	0.48
23:Y:51:ARG:HA	23:Y:54:MET:HE3	1.96	0.48
26:1:61:A:H2'	26:1:62:C:H6	1.78	0.48
26:1:168:A:C5	26:1:169:G:H1'	2.49	0.48
26:1:1914:C:H2'	26:1:1915:G:H5'	1.95	0.48
26:1:2715:G:N1	26:1:2747:U:OP2	2.35	0.48
27:2:82:A:H61	27:2:87:C:H42	1.61	0.48
2:B:45:ASN:OD1	2:B:46:GLN:HG3	2.13	0.48
12:L:186:VAL:HG12	12:L:187:GLN:HG3	1.94	0.48
19:S:198:ALA:O	19:S:201:LYS:HB2	2.13	0.48
22:X:21:ARG:HA	26:1:856:U:H2'	1.95	0.48
26:1:122:G:H2'	26:1:123:G:O4'	2.13	0.48
26:1:400:C:H3'	26:1:401:U:H5''	1.95	0.48
26:1:408:U:H2'	26:1:409:G:H5'	1.96	0.48
26:1:948:U:H2'	26:1:949:C:C6	2.49	0.48
26:1:2293:A:H4'	26:1:2294:A:O5'	2.13	0.48
26:1:2329:U:H2'	26:1:2330:G:O4'	2.13	0.48
2:B:65:ILE:HD12	2:B:87:ARG:CZ	2.44	0.48
3:C:91:ASN:HB2	4:D:11:GLN:CG	2.43	0.48
10:J:12:ALA:HA	10:J:29:TRP:O	2.13	0.48
16:P:5:THR:HG22	26:1:732:C:H1'	1.95	0.48
18:R:18:LYS:NZ	18:R:21:GLY:O	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:34:PHE:CE2	22:X:8:PRO:HB3	2.49	0.48
20:V:24:GLN:NE2	20:V:143:LEU:HD12	2.28	0.48
26:1:147:G:H2'	26:1:148:U:O4'	2.14	0.48
26:1:164:A:H5'	26:1:165:C:OP2	2.13	0.48
26:1:170:C:O2'	26:1:171:A:H5'	2.14	0.48
26:1:1078:G:H2'	26:1:1079:U:C6	2.49	0.48
26:1:1080:G:O2'	26:1:1081:G:H5'	2.14	0.48
26:1:1516:C:H2'	26:1:1517:A:O4'	2.14	0.48
26:1:1712:A:H4'	26:1:1713:A:O5'	2.13	0.48
27:2:56:A:O2'	27:2:57:G:H5'	2.14	0.48
3:C:21:ALA:HB1	3:C:24:TYR:CD2	2.48	0.48
7:G:73:PRO:HG2	7:G:101:ILE:HG22	1.95	0.48
20:V:3:GLN:O	20:V:3:GLN:HG2	2.14	0.48
21:W:114:ILE:O	21:W:118:ALA:N	2.46	0.48
26:1:273:A:O2'	26:1:274:A:H5'	2.14	0.48
26:1:770:G:H2'	26:1:771:G:O4'	2.13	0.48
26:1:1707:U:O2'	26:1:2713:G:H4'	2.14	0.48
26:1:1900:G:H2'	26:1:1901:C:H6	1.79	0.48
26:1:1988:C:H2'	26:1:1989:C:O4'	2.14	0.48
26:1:2810:A:H2'	26:1:2811:U:H6	1.78	0.48
7:G:27:LEU:HD12	7:G:32:ARG:CB	2.42	0.48
12:L:142:SER:O	12:L:144:GLY:N	2.45	0.48
12:L:144:GLY:O	26:1:2607:U:H5'	2.14	0.48
24:Z:40:VAL:O	24:Z:44:VAL:HG12	2.13	0.48
26:1:686:U:H2'	26:1:687:G:O4'	2.13	0.48
26:1:1085:U:C4	26:1:1158:G:O6	2.67	0.48
2:B:8:PRO:HB3	2:B:14:ARG:HG3	1.96	0.48
8:H:51:VAL:O	8:H:55:VAL:HG22	2.14	0.48
9:I:53:ILE:O	9:I:67:LEU:HD11	2.14	0.48
17:Q:57:ARG:HG3	26:1:879:U:H5'	1.95	0.48
19:S:26:ILE:HG13	19:S:111:ARG:HH12	1.78	0.48
21:W:111:PHE:HB3	21:W:114:ILE:HD12	1.95	0.48
26:1:902:A:O2'	26:1:903:G:H5'	2.13	0.48
26:1:1766:C:H2'	26:1:1767:G:C5'	2.43	0.48
26:1:1864:C:H2'	26:1:1926:A:N6	2.29	0.48
27:2:23:U:O2	27:2:27:A:N6	2.46	0.48
27:2:29:C:O2	27:2:29:C:H2'	2.13	0.48
27:2:96:A:H2'	27:2:97:G:H5'	1.96	0.48
5:E:69:LEU:HA	5:E:108:SER:O	2.13	0.47
12:L:22:LEU:HD13	21:W:74:GLY:HA3	1.94	0.47
17:Q:5:LYS:NZ	26:1:256:C:OP2	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:35:ILE:HG21	21:W:103:ALA:HB3	1.95	0.47
23:Y:109:VAL:CG1	23:Y:113:VAL:HB	2.44	0.47
26:1:615:A:H5''	26:1:616:G:OP2	2.14	0.47
26:1:917:U:O2'	26:1:918:G:H5'	2.14	0.47
26:1:1353:A:H2'	26:1:1354:G:H8	1.77	0.47
26:1:1489:A:N6	26:1:1509:G:N2	2.25	0.47
26:1:2293:A:H4'	26:1:2294:A:N3	2.29	0.47
27:2:79:C:H42	27:2:90:U:H3	1.61	0.47
1:A:51:LYS:HE2	1:A:53:ARG:HB2	1.95	0.47
5:E:4:LYS:HB3	5:E:106:VAL:HG22	1.95	0.47
12:L:99:TYR:CB	12:L:101:VAL:HG22	2.44	0.47
13:M:12:VAL:HA	13:M:15:ARG:HG3	1.97	0.47
16:P:16:VAL:HG13	16:P:17:HIS:ND1	2.29	0.47
17:Q:23:LYS:HE2	17:Q:47:ALA:CB	2.44	0.47
20:V:2:ARG:NH2	20:V:3:GLN:OE1	2.47	0.47
26:1:234:C:H2'	26:1:235:G:O4'	2.15	0.47
26:1:390:A:H2'	26:1:391:A:H8	1.79	0.47
26:1:1961:C:C2'	26:1:1962:G:H5'	2.45	0.47
27:2:50:A:H3'	27:2:50:A:N3	2.30	0.47
26:1:102:A:H5''	26:1:103:U:H5	1.79	0.47
26:1:859:C:O2'	26:1:860:U:H5'	2.14	0.47
26:1:1845:U:O2'	26:1:1846:A:OP2	2.23	0.47
26:1:2322:C:H2'	26:1:2323:U:O4'	2.14	0.47
2:B:96:TYR:HE2	2:B:102:ARG:HD2	1.78	0.47
4:D:16:GLU:HG2	4:D:16:GLU:O	2.13	0.47
26:1:54:G:H2'	26:1:55:G:O4'	2.14	0.47
26:1:750:A:H2'	26:1:751:A:C8	2.50	0.47
26:1:1170:A:H4'	26:1:1171:A:O5'	2.14	0.47
26:1:1343:U:O2'	26:1:1344:A:H5'	2.14	0.47
26:1:1349:U:H4'	26:1:1350:U:O5'	2.14	0.47
26:1:1884:G:H2'	26:1:1885:G:O4'	2.14	0.47
26:1:2397:G:O2'	26:1:2398:G:H5'	2.15	0.47
27:2:97:G:H2'	27:2:98:A:C8	2.50	0.47
2:B:43:ARG:HA	2:B:48:LYS:O	2.14	0.47
12:L:98:ALA:HB1	12:L:103:GLN:HE22	1.80	0.47
12:L:215:ILE:HD12	12:L:216:LYS:HG3	1.95	0.47
18:R:17:ILE:HG13	18:R:18:LYS:H	1.80	0.47
26:1:159:U:H2'	26:1:160:G:H5'	1.96	0.47
26:1:408:U:C2'	26:1:409:G:H5'	2.45	0.47
26:1:1878:U:H2'	26:1:1879:U:O4'	2.14	0.47
26:1:2016:A:H2'	26:1:2017:C:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2561:C:H2'	26:1:2562:G:O4'	2.15	0.47
26:1:2873:C:H2'	26:1:2874:A:C8	2.50	0.47
27:2:76:A:C2'	27:2:77:G:H5'	2.44	0.47
1:A:33:ARG:O	1:A:34:ILE:HD13	2.15	0.47
20:V:48:HIS:O	26:1:600:U:O2'	2.30	0.47
22:X:38:GLN:OE1	26:1:876:G:O2'	2.30	0.47
26:1:114:C:H2'	26:1:115:C:C6	2.49	0.47
26:1:464:U:H2'	26:1:465:C:C6	2.50	0.47
26:1:685:C:H2'	26:1:686:U:C6	2.50	0.47
2:B:167:LYS:CG	2:B:172:VAL:HG12	2.44	0.47
12:L:190:THR:HG22	12:L:191:GLU:H	1.77	0.47
12:L:190:THR:O	12:L:191:GLU:HB2	2.15	0.47
19:S:78:ILE:HG13	19:S:79:ARG:HG2	1.95	0.47
26:1:296:G:O2'	26:1:297:G:H5'	2.15	0.47
26:1:590:U:OP1	26:1:1257:G:O2'	2.23	0.47
26:1:651:A:H2'	26:1:652:A:H8	1.78	0.47
26:1:769:U:O2'	26:1:770:G:H5'	2.13	0.47
26:1:889:U:H2'	26:1:890:G:O4'	2.14	0.47
26:1:1053:A:N3	26:1:1197:C:O2'	2.43	0.47
26:1:1325:U:O2'	26:1:1326:C:OP1	2.32	0.47
26:1:1483:A:H2'	26:1:1484:G:O4'	2.14	0.47
26:1:1867:G:H2'	26:1:1868:U:C6	2.50	0.47
26:1:1959:A:H61	26:1:1995:G:H1'	1.79	0.47
26:1:2092:C:H2'	26:1:2093:C:H6	1.80	0.47
26:1:2124:U:H2'	26:1:2125:U:O4'	2.14	0.47
26:1:2325:A:N6	26:1:2345:A:H1'	2.29	0.47
26:1:2540:A:H2'	26:1:2541:U:C6	2.50	0.47
7:G:26:THR:HG23	7:G:33:VAL:HG12	1.97	0.47
7:G:40:ILE:CG2	7:G:58:GLU:HB3	2.45	0.47
8:H:16:SER:O	8:H:20:GLN:HG2	2.14	0.47
13:M:44:ARG:CD	13:M:47:ILE:HD11	2.42	0.47
19:S:64:PRO:HB2	19:S:65:TRP:CE3	2.49	0.47
19:S:74:ARG:NH2	26:1:2472:G:OP1	2.42	0.47
19:S:183:VAL:O	19:S:187:THR:HG22	2.15	0.47
26:1:298:U:H4'	26:1:299:U:H5'	1.97	0.47
26:1:1238:U:H2'	26:1:1239:C:C6	2.50	0.47
26:1:1497:A:H3'	26:1:1497:A:N3	2.30	0.47
26:1:1611:C:H2'	26:1:1612:C:C6	2.50	0.47
26:1:2360:A:C5'	26:1:2362:A:H1'	2.44	0.47
1:A:31:HIS:HB3	1:A:42:ILE:CG2	2.45	0.47
3:C:78:ARG:NH1	26:1:1195:A:H1'	2.24	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:75:VAL:HG12	9:I:89:VAL:HG22	1.96	0.47
26:1:43:A:H62	26:1:482:U:H3	1.63	0.47
26:1:341:G:H5''	26:1:342:A:OP1	2.15	0.47
26:1:417:A:H4'	26:1:418:G:OP1	2.14	0.47
26:1:625:G:H2'	26:1:626:G:H8	1.78	0.47
26:1:872:U:H5'	26:1:873:U:C5	2.49	0.47
26:1:908:A:O2'	26:1:909:G:H5'	2.15	0.47
26:1:1437:U:O2'	26:1:1438:G:H5'	2.15	0.47
26:1:1733:A:H2'	26:1:1734:A:C8	2.49	0.47
26:1:2505:A:H1'	26:1:2555:U:O2'	2.14	0.47
26:1:2826:U:H2'	26:1:2827:A:C8	2.49	0.47
1:A:30:VAL:HG12	1:A:32:VAL:HG13	1.97	0.47
9:I:53:ILE:CG2	9:I:87:VAL:HG23	2.45	0.47
13:M:17:GLU:OE2	13:M:21:LYS:HE2	2.15	0.47
20:V:69:LYS:HE2	26:1:1066:G:N7	2.30	0.47
26:1:64:A:H2'	26:1:65:A:O4'	2.15	0.47
26:1:422:G:H2'	26:1:423:A:C8	2.50	0.47
26:1:455:A:O2'	26:1:456:G:H5'	2.15	0.47
26:1:1727:C:H2'	26:1:1728:C:H6	1.78	0.47
26:1:1806:U:H5	26:1:1811:A:N7	2.12	0.47
26:1:2356:A:H2'	26:1:2357:G:H8	1.80	0.47
27:2:15:C:H2'	27:2:16:A:O4'	2.15	0.47
27:2:90:U:H2'	27:2:91:C:C6	2.50	0.47
3:C:53:ARG:HD3	26:1:580:C:O2'	2.15	0.46
5:E:42:ALA:CB	26:1:2037:G:H5''	2.44	0.46
5:E:88:ARG:HD3	26:1:793:G:OP2	2.15	0.46
6:F:17:SER:HA	6:F:20:MET:CG	2.45	0.46
7:G:71:LEU:HA	7:G:78:PRO:HA	1.97	0.46
26:1:481:C:C2'	26:1:482:U:H5'	2.45	0.46
26:1:578:G:H2'	26:1:579:U:C6	2.50	0.46
26:1:1334:C:OP1	26:1:2737:C:H4'	2.15	0.46
26:1:2626:G:O2'	26:1:2627:A:H5'	2.15	0.46
26:1:2812:U:H2'	26:1:2813:U:C6	2.51	0.46
26:1:163:U:H6	26:1:165:C:H41	1.63	0.46
26:1:268:A:H2'	26:1:269:G:C4'	2.45	0.46
26:1:899:U:O2'	26:1:900:G:H5'	2.14	0.46
26:1:1081:G:N2	26:1:1163:U:H1'	2.30	0.46
26:1:1617:A:H2'	26:1:1618:A:C8	2.50	0.46
26:1:2262:G:O2'	26:1:2263:C:H5'	2.15	0.46
26:1:2622:G:N2	26:1:2625:A:OP2	2.39	0.46
26:1:2748:A:H1'	26:1:2893:A:O2'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:23:ASN:ND2	26:1:203:U:OP1	2.46	0.46
19:S:125:VAL:CG2	19:S:194:ILE:HD11	2.30	0.46
26:1:349:U:C2'	26:1:350:G:H5'	2.45	0.46
26:1:536:A:H2'	26:1:537:A:C8	2.50	0.46
26:1:551:G:H4'	26:1:552:A:H5''	1.97	0.46
26:1:596:G:H2'	26:1:597:U:C6	2.51	0.46
26:1:907:G:H2'	26:1:908:A:O4'	2.15	0.46
26:1:1350:U:O2'	26:1:1351:C:OP1	2.20	0.46
26:1:1517:A:H2'	26:1:1518:G:H5'	1.97	0.46
26:1:2308:C:C2'	26:1:2309:G:H5'	2.45	0.46
3:C:51:ARG:NH1	26:1:1200:A:O4'	2.48	0.46
17:Q:58:VAL:CG1	17:Q:61:LEU:HD12	2.43	0.46
26:1:486:G:O2'	26:1:487:U:H5'	2.15	0.46
26:1:646:A:H4'	26:1:647:G:OP1	2.16	0.46
26:1:1459:A:H61	26:1:1630:A:C4'	2.29	0.46
26:1:2482:G:H2'	26:1:2483:C:C6	2.50	0.46
26:1:2696:G:H5''	26:1:2697:G:OP2	2.16	0.46
26:1:2852:U:H1'	26:1:2854:A:C4	2.50	0.46
27:2:45:C:H2'	27:2:46:A:C5'	2.44	0.46
1:A:15:LEU:CD2	1:A:57:VAL:HG22	2.46	0.46
13:M:17:GLU:CD	13:M:21:LYS:HE2	2.36	0.46
26:1:86:C:O2'	26:1:87:U:H5'	2.16	0.46
26:1:422:G:H2'	26:1:423:A:H8	1.81	0.46
26:1:1640:U:O2'	26:1:1641:G:H5'	2.15	0.46
26:1:2091:C:H2'	26:1:2092:C:C6	2.50	0.46
6:F:10:PRO:HD2	11:K:33:ALA:CB	2.46	0.46
6:F:26:THR:HG23	6:F:79:ILE:HG12	1.97	0.46
19:S:149:PRO:CG	19:S:191:SER:HB2	2.45	0.46
23:Y:7:VAL:HG11	23:Y:93:TRP:CH2	2.50	0.46
26:1:663:U:H2'	26:1:664:G:O4'	2.16	0.46
26:1:1003:A:H2'	26:1:1004:A:C8	2.50	0.46
26:1:1758:A:H3'	26:1:1758:A:N3	2.30	0.46
26:1:2836:C:O2	26:1:2903:A:O2'	2.28	0.46
7:G:32:ARG:HH22	26:1:524:A:H5'	1.80	0.46
12:L:41:VAL:HG12	12:L:45:GLY:HA2	1.97	0.46
20:V:66:THR:HG21	26:1:1185:U:P	2.55	0.46
24:Z:61:ASN:O	24:Z:64:LYS:HG2	2.16	0.46
26:1:142:G:C2'	26:1:143:U:H5'	2.42	0.46
26:1:1315:C:H2'	26:1:1316:G:C8	2.50	0.46
26:1:1869:G:H2'	26:1:1870:C:C6	2.51	0.46
26:1:2396:A:O2'	26:1:2397:G:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:2:103:A:H3'	27:2:104:A:H5'	1.96	0.46
27:2:104:A:H2'	27:2:105:C:H6	1.78	0.46
1:A:26:ASP:O	1:A:49:VAL:HG23	2.15	0.46
2:B:19:LEU:HD11	2:B:199:GLN:HB2	1.97	0.46
7:G:55:GLY:N	26:1:529:A:O2'	2.40	0.46
14:N:38:LEU:O	14:N:41:ARG:HB2	2.15	0.46
21:W:63:VAL:CG1	21:W:102:VAL:HG12	2.44	0.46
2:B:2:ALA:HA	2:B:199:GLN:HG3	1.97	0.46
11:K:17:GLN:NE2	11:K:53:LEU:O	2.49	0.46
13:M:17:GLU:OE1	13:M:21:LYS:HE2	2.16	0.46
15:O:34:LYS:NZ	26:1:2374:C:OP1	2.30	0.46
21:W:28:SER:OG	26:1:2590:U:O2'	2.12	0.46
24:Z:107:GLY:N	24:Z:115:GLU:OE2	2.47	0.46
26:1:178:A:H2'	26:1:179:A:O4'	2.16	0.46
26:1:214:G:O2'	26:1:215:G:H5'	2.16	0.46
26:1:718:C:C2'	26:1:719:G:H5'	2.45	0.46
26:1:983:G:C2'	26:1:984:G:H5'	2.46	0.46
18:R:10:ILE:HG23	26:1:2504:C:N4	2.31	0.46
20:V:46:THR:OG1	20:V:49:VAL:HG22	2.15	0.46
20:V:88:ILE:HG13	20:V:89:THR:H	1.81	0.46
24:Z:74:GLU:HB2	24:Z:77:THR:HB	1.97	0.46
26:1:215:G:H2'	26:1:216:A:O4'	2.16	0.46
26:1:1452:C:C3'	26:1:1453:G:H5''	2.46	0.46
26:1:1461:C:H5''	26:1:1462:G:OP2	2.16	0.46
26:1:2317:G:H2'	26:1:2318:U:C6	2.51	0.46
18:R:19:ARG:NE	26:1:2783:U:OP2	2.49	0.45
19:S:125:VAL:HG13	19:S:194:ILE:CD1	2.46	0.45
21:W:91:LYS:HD2	21:W:110:ASN:HD22	1.80	0.45
26:1:20:C:O2'	26:1:21:A:H5'	2.16	0.45
26:1:97:C:O2'	26:1:98:U:H5'	2.16	0.45
26:1:135:G:H2'	26:1:136:A:C8	2.51	0.45
26:1:663:U:O2'	26:1:664:G:H5'	2.16	0.45
26:1:811:C:H2'	26:1:812:U:O4'	2.16	0.45
26:1:888:G:H2'	26:1:889:U:H6	1.80	0.45
26:1:1498:U:O2	26:1:1498:U:H2'	2.16	0.45
26:1:1645:G:O2'	26:1:1646:U:H5'	2.16	0.45
26:1:1863:C:H2'	26:1:1864:C:C6	2.51	0.45
26:1:1883:A:O2'	26:1:1884:G:H5'	2.16	0.45
26:1:2570:G:H2'	26:1:2571:G:C8	2.51	0.45
2:B:61:GLN:NE2	26:1:1616:A:H4'	2.30	0.45
6:F:6:ILE:HD11	6:F:38:VAL:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:1:MET:HG2	26:1:2311:U:OP1	2.17	0.45
19:S:157:GLU:CA	19:S:198:ALA:HB2	2.46	0.45
20:V:21:ALA:HB1	20:V:63:ILE:CG2	2.46	0.45
26:1:207:A:H4'	26:1:208:G:OP1	2.17	0.45
26:1:461:A:O2'	26:1:462:U:H5'	2.16	0.45
26:1:2321:C:O2'	26:1:2322:C:H5'	2.16	0.45
26:1:2416:G:H5'	26:1:2417:U:C5'	2.46	0.45
26:1:2664:U:H2'	26:1:2665:G:O4'	2.16	0.45
26:1:2693:C:H3'	26:1:2694:C:C6	2.51	0.45
3:C:102:ASP:OD2	4:D:47:LYS:HE2	2.17	0.45
5:E:59:GLU:HG3	5:E:66:THR:HG23	1.97	0.45
6:F:17:SER:O	6:F:20:MET:HB2	2.16	0.45
8:H:4:LEU:HD12	8:H:61:ILE:CG2	2.43	0.45
8:H:65:VAL:O	8:H:68:LYS:HG2	2.16	0.45
13:M:4:LEU:HB3	13:M:6:ILE:CD1	2.45	0.45
21:W:91:LYS:HD3	21:W:110:ASN:HB2	1.98	0.45
22:X:109:ILE:HG13	22:X:125:ALA:HB1	1.98	0.45
23:Y:83:MET:HE2	26:1:1006:G:N2	2.31	0.45
26:1:156:A:H2'	26:1:157:U:O4'	2.16	0.45
26:1:181:G:O2'	26:1:182:C:H5'	2.16	0.45
26:1:372:A:H4'	26:1:373:A:OP2	2.16	0.45
26:1:383:A:H2'	26:1:384:G:H5'	1.98	0.45
26:1:427:A:H2'	26:1:428:G:O4'	2.15	0.45
26:1:1322:G:N2	26:1:1366:U:OP1	2.35	0.45
26:1:1517:A:H61	26:1:1563:U:H3	1.65	0.45
26:1:1745:A:C2'	26:1:1746:G:H5'	2.45	0.45
26:1:1781:C:C5	26:1:2744:G:H5'	2.51	0.45
26:1:1884:G:O2'	26:1:1885:G:H5'	2.16	0.45
26:1:1988:C:HO2'	26:1:1989:C:P	2.36	0.45
26:1:2509:A:H2'	26:1:2510:C:H5'	1.97	0.45
26:1:2846:A:H2'	26:1:2847:U:H5'	1.99	0.45
26:1:2873:C:H2'	26:1:2874:A:H8	1.81	0.45
12:L:75:GLY:HA3	26:1:2813:U:O2'	2.17	0.45
26:1:183:A:H3'	26:1:183:A:P	2.56	0.45
26:1:1070:A:H2'	26:1:1071:A:H5'	1.99	0.45
26:1:1869:G:H2'	26:1:1870:C:H6	1.81	0.45
26:1:2275:C:C2'	26:1:2276:U:H5'	2.46	0.45
6:F:11:VAL:HB	6:F:26:THR:HB	1.97	0.45
8:H:85:GLN:NE2	8:H:87:THR:OG1	2.48	0.45
9:I:78:GLU:O	9:I:85:LYS:HB2	2.16	0.45
19:S:57:VAL:HG21	19:S:87:GLY:HA2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:V:50:ASP:HB3	20:V:115:LEU:HD11	1.98	0.45
26:1:91:A:H5''	26:1:92:G:OP2	2.17	0.45
26:1:1268:C:H2'	26:1:1269:A:H8	1.81	0.45
26:1:1426:G:H2'	26:1:1427:U:O4'	2.17	0.45
26:1:1479:G:O2'	26:1:1480:G:H5'	2.15	0.45
26:1:1560:A:H5''	26:1:1561:G:OP1	2.16	0.45
26:1:1955:A:H2'	26:1:1956:G:O4'	2.16	0.45
1:A:76:PHE:CB	1:A:83:ILE:HD11	2.47	0.45
2:B:171:TYR:OH	26:1:2250:A:OP1	2.31	0.45
7:G:3:ILE:HG22	7:G:23:VAL:HG21	1.99	0.45
8:H:32:TYR:HB3	8:H:38:ASN:ND2	2.31	0.45
15:O:26:ASN:HD21	26:1:2313:A:H2'	1.82	0.45
18:R:17:ILE:HG21	18:R:26:ILE:CD1	2.45	0.45
18:R:24:MET:HG2	18:R:35:ARG:HB3	1.97	0.45
20:V:22:GLU:HG2	20:V:62:LYS:CB	2.47	0.45
26:1:136:A:H2'	26:1:137:G:C8	2.50	0.45
26:1:153:G:O2'	26:1:154:A:H5'	2.16	0.45
26:1:268:A:N6	26:1:473:U:O2'	2.50	0.45
26:1:356:A:O2'	26:1:357:U:H5'	2.17	0.45
26:1:483:C:O2'	26:1:484:U:H5'	2.16	0.45
26:1:2084:G:O2'	26:1:2085:A:H5'	2.16	0.45
27:2:16:A:H2'	27:2:17:A:O4'	2.17	0.45
1:A:32:VAL:O	1:A:42:ILE:HA	2.17	0.45
24:Z:9:THR:HG22	24:Z:10:SER:H	1.79	0.45
26:1:161:A:H1'	26:1:2235:A:O2'	2.17	0.45
26:1:341:G:O6	26:1:381:G:H5''	2.17	0.45
26:1:872:U:H5'	26:1:873:U:C4	2.52	0.45
26:1:1426:G:O2'	26:1:1427:U:H5'	2.16	0.45
26:1:2268:A:H2'	26:1:2269:G:C8	2.51	0.45
26:1:2786:G:O2'	26:1:2787:C:H5'	2.17	0.45
27:2:57:G:H3'	27:2:58:C:H6	1.80	0.45
5:E:66:THR:HG22	5:E:69:LEU:HD11	1.98	0.45
12:L:13:THR:HG22	12:L:14:GLN:N	2.32	0.45
19:S:157:GLU:N	19:S:198:ALA:HB2	2.32	0.45
21:W:87:ILE:HG13	21:W:92:GLY:O	2.17	0.45
26:1:159:U:H2'	26:1:160:G:C5'	2.47	0.45
26:1:221:G:N2	26:1:238:U:H4'	2.31	0.45
26:1:222:A:H2'	26:1:223:G:O4'	2.17	0.45
26:1:747:U:H2'	26:1:748:U:C6	2.52	0.45
26:1:747:U:H2'	26:1:748:U:H6	1.82	0.45
26:1:1085:U:N3	26:1:1158:G:C6	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1355:A:C2'	26:1:1356:G:H5'	2.46	0.45
1:A:77:PRO:HD3	21:W:74:GLY:O	2.16	0.45
2:B:118:SER:HA	2:B:131:PRO:HD3	1.99	0.45
12:L:83:ALA:O	12:L:85:LYS:HE3	2.17	0.45
26:1:310:C:H3'	26:1:310:C:OP2	2.17	0.45
26:1:461:A:H2'	26:1:462:U:C6	2.52	0.45
26:1:464:U:H2'	26:1:465:C:H6	1.81	0.45
26:1:864:A:H5''	26:1:1017:A:N1	2.32	0.45
26:1:1315:C:H2'	26:1:1316:G:H8	1.81	0.45
26:1:1325:U:HO2'	26:1:1326:C:P	2.40	0.45
3:C:54:LYS:NZ	26:1:1038:C:OP2	2.43	0.45
8:H:9:ARG:NH1	8:H:28:PRO:HB3	2.32	0.45
15:O:5:VAL:HG11	15:O:21:LYS:HD3	1.98	0.45
17:Q:31:HIS:HD2	17:Q:32:LEU:HG	1.79	0.45
24:Z:37:ALA:CB	24:Z:117:VAL:HG21	2.47	0.45
26:1:405:G:H2'	26:1:406:A:C4'	2.46	0.45
26:1:1592:A:H3'	26:1:1593:G:C8	2.52	0.45
26:1:1767:G:H2'	26:1:1768:C:H6	1.82	0.45
26:1:1823:U:H2'	26:1:1824:C:C6	2.51	0.45
26:1:1994:C:C2'	26:1:1995:G:H5'	2.47	0.45
26:1:2777:A:H1'	26:1:2779:C:N4	2.32	0.45
2:B:53:HIS:CD2	2:B:219:THR:HA	2.51	0.44
2:B:154:ILE:HG21	2:B:176:LEU:HD22	1.99	0.44
10:J:10:ARG:HH21	10:J:52:ARG:HG2	1.82	0.44
12:L:163:VAL:O	26:1:2646:U:H5'	2.17	0.44
14:N:5:LYS:HZ3	26:1:2081:A:H2'	1.82	0.44
19:S:47:GLY:HA2	19:S:49:HIS:CD2	2.52	0.44
19:S:74:ARG:O	19:S:74:ARG:HG2	2.17	0.44
19:S:152:VAL:HA	19:S:191:SER:O	2.17	0.44
21:W:106:LEU:HG	21:W:111:PHE:HB2	1.99	0.44
26:1:720:A:C2'	26:1:721:A:H5'	2.46	0.44
26:1:2713:G:H2'	26:1:2714:U:C6	2.51	0.44
12:L:25:VAL:CG2	12:L:196:LEU:HB3	2.45	0.44
12:L:41:VAL:HA	12:L:45:GLY:CA	2.39	0.44
16:P:41:LYS:CG	26:1:505:U:H5''	2.46	0.44
18:R:24:MET:HG2	18:R:35:ARG:HB2	1.98	0.44
21:W:35:ILE:HD12	21:W:69:VAL:HG13	1.98	0.44
26:1:91:A:H3'	26:1:92:G:C8	2.53	0.44
26:1:191:A:H2	26:1:211:C:H42	1.63	0.44
26:1:325:A:O2'	26:1:326:A:H5'	2.17	0.44
26:1:362:C:O2'	26:1:363:A:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:793:G:H2'	26:1:793:G:N3	2.33	0.44
26:1:1637:A:H2'	26:1:1638:G:C8	2.52	0.44
26:1:1683:U:H2'	26:1:1684:A:H5'	1.99	0.44
26:1:1771:A:N3	26:1:1771:A:H5'	2.32	0.44
26:1:2342:U:O2'	26:1:2343:U:H5'	2.18	0.44
19:S:125:VAL:HG13	19:S:194:ILE:HD12	1.98	0.44
24:Z:28:GLU:OE2	24:Z:84:LYS:NZ	2.39	0.44
26:1:135:G:H2'	26:1:136:A:H8	1.82	0.44
26:1:1794:C:H2'	26:1:1795:A:O4'	2.17	0.44
26:1:2543:G:C2'	26:1:2544:C:H5'	2.47	0.44
27:2:85:U:H6	27:2:85:U:H5''	1.82	0.44
14:N:30:CYS:HB3	14:N:33:CYS:HB2	1.99	0.44
16:P:16:VAL:HG13	16:P:17:HIS:CE1	2.52	0.44
20:V:26:LEU:HD21	20:V:105:SER:OG	2.16	0.44
26:1:210:A:H2'	26:1:211:C:O4'	2.17	0.44
26:1:698:U:H2'	26:1:699:U:H5'	2.00	0.44
26:1:898:U:O2'	26:1:899:U:H5'	2.17	0.44
26:1:1161:A:H2'	26:1:1162:C:H6	1.81	0.44
26:1:1700:C:H2'	26:1:1701:U:H6	1.82	0.44
26:1:2521:G:C2'	26:1:2522:G:H5'	2.48	0.44
8:H:31:VAL:CG1	8:H:36:THR:HG21	2.41	0.44
15:O:3:VAL:HG23	15:O:23:LYS:HB2	1.99	0.44
19:S:49:HIS:ND1	19:S:92:PRO:HB3	2.33	0.44
22:X:125:ALA:O	22:X:145:VAL:HA	2.17	0.44
26:1:569:U:H2'	26:1:570:U:C6	2.53	0.44
26:1:841:C:H2'	26:1:842:U:C6	2.53	0.44
26:1:1218:G:H2'	26:1:1219:G:O4'	2.17	0.44
26:1:1450:A:H2'	26:1:1450:A:N3	2.33	0.44
26:1:1710:G:H2'	26:1:1711:G:O4'	2.18	0.44
26:1:2262:G:H2'	26:1:2263:C:H6	1.82	0.44
27:2:79:C:N4	27:2:91:C:N3	2.66	0.44
3:C:33:LYS:HE2	26:1:624:C:OP2	2.16	0.44
19:S:135:LYS:O	19:S:166:SER:HB2	2.18	0.44
21:W:35:ILE:HG21	21:W:103:ALA:CB	2.47	0.44
22:X:74:TYR:CE2	22:X:127:LYS:HD3	2.52	0.44
24:Z:34:GLU:O	24:Z:38:LYS:HG2	2.17	0.44
24:Z:48:ILE:CD1	24:Z:89:ILE:HG22	2.47	0.44
26:1:5:A:O2'	26:1:6:A:H5'	2.17	0.44
26:1:2045:A:O2'	26:1:2046:U:H5'	2.18	0.44
26:1:2350:G:H2'	26:1:2351:U:O4'	2.18	0.44
26:1:2455:G:H5''	26:1:2456:G:O5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2501:U:H3'	26:1:2502:C:C6	2.52	0.44
26:1:2516:G:C2'	26:1:2517:G:H5'	2.48	0.44
11:K:21:SER:HA	11:K:50:ILE:HD13	1.99	0.44
20:V:32:GLU:CG	20:V:143:LEU:HD22	2.47	0.44
22:X:128:PHE:HE2	22:X:143:HIS:HB2	1.81	0.44
24:Z:7:GLY:C	24:Z:8:ARG:HD2	2.38	0.44
26:1:1390:A:H2'	26:1:1391:A:H8	1.80	0.44
26:1:2439:A:H2'	26:1:2440:G:H5'	1.99	0.44
5:E:72:LYS:HG2	5:E:73:GLU:HG3	2.00	0.44
7:G:82:GLY:O	7:G:93:ILE:HG22	2.17	0.44
12:L:31:LYS:HG3	12:L:32:GLU:OE1	2.17	0.44
23:Y:59:LYS:HE2	23:Y:59:LYS:HA	1.99	0.44
24:Z:36:ARG:O	24:Z:40:VAL:HG23	2.18	0.44
26:1:421:C:H2'	26:1:422:G:C8	2.53	0.44
26:1:1283:G:C2'	26:1:1284:A:H5'	2.47	0.44
26:1:1631:G:O2'	26:1:1632:A:O5'	2.20	0.44
26:1:1877:G:H2'	26:1:1878:U:C6	2.53	0.44
26:1:2109:A:H2'	26:1:2110:G:O4'	2.17	0.44
26:1:2347:A:H5'	26:1:2348:G:C5	2.53	0.44
27:2:89:U:H2'	27:2:90:U:H6	1.83	0.44
2:B:95:VAL:HA	2:B:100:GLU:O	2.17	0.44
10:J:17:ARG:O	10:J:24:SER:HA	2.17	0.44
11:K:27:ASN:O	11:K:31:GLN:HG3	2.18	0.44
12:L:3:LYS:HZ1	12:L:98:ALA:HB2	1.83	0.44
12:L:215:ILE:HD11	26:1:2798:C:H4'	2.00	0.44
26:1:52:A:H2'	26:1:53:A:C8	2.53	0.44
26:1:140:A:H1'	26:1:1445:C:O2'	2.18	0.44
26:1:153:G:H2'	26:1:154:A:H8	1.83	0.44
26:1:302:A:O2'	26:1:303:G:OP2	2.30	0.44
26:1:474:A:O2'	26:1:475:A:H5'	2.18	0.44
26:1:763:A:H2'	26:1:764:C:O4'	2.17	0.44
26:1:1388:C:O2'	26:1:1618:A:H1'	2.18	0.44
26:1:1651:C:H4'	26:1:1652:A:C5'	2.48	0.44
26:1:2098:A:H2'	26:1:2099:G:H8	1.82	0.44
26:1:2289:U:H4'	26:1:2355:A:H2	1.83	0.44
26:1:2662:U:H2'	26:1:2663:U:O4'	2.18	0.44
5:E:14:PRO:O	5:E:18:ARG:HG3	2.18	0.43
12:L:138:ARG:HB2	12:L:148:HIS:O	2.18	0.43
19:S:199:ALA:O	19:S:202:VAL:HG22	2.19	0.43
26:1:108:A:H2'	26:1:109:G:O4'	2.18	0.43
26:1:174:U:O2'	26:1:175:C:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:268:A:O2'	26:1:269:G:H4'	2.17	0.43
26:1:609:U:O2'	26:1:610:U:H5'	2.17	0.43
26:1:1297:G:O2'	26:1:1298:G:H5'	2.17	0.43
26:1:1572:G:C2'	26:1:1573:A:H5'	2.48	0.43
26:1:2814:C:H2'	26:1:2815:C:C6	2.53	0.43
2:B:25:THR:HB	2:B:80:SER:HB3	1.99	0.43
3:C:61:TRP:HB3	3:C:93:LYS:O	2.17	0.43
3:C:104:LYS:HB2	4:D:47:LYS:NZ	2.32	0.43
6:F:62:LYS:HA	6:F:71:TYR:HA	2.00	0.43
20:V:75:TYR:HB2	20:V:88:ILE:HG22	2.00	0.43
22:X:60:ARG:NH1	26:1:2455:G:H21	2.16	0.43
22:X:78:ASN:CG	22:X:114:ASN:HB3	2.39	0.43
22:X:80:ASP:HA	22:X:83:ASN:HD22	1.83	0.43
26:1:44:A:HO2'	26:1:45:G:P	2.40	0.43
26:1:98:U:C2'	26:1:99:U:H5''	2.47	0.43
26:1:303:G:H2'	26:1:304:G:O4'	2.17	0.43
26:1:640:G:O2'	26:1:641:A:H5'	2.18	0.43
26:1:1356:G:H2'	26:1:1357:G:N3	2.34	0.43
27:2:99:G:C5	27:2:100:U:H1'	2.53	0.43
2:B:145:GLU:HG2	2:B:151:GLY:C	2.39	0.43
3:C:90:ILE:HD11	3:C:92:ARG:NE	2.33	0.43
7:G:80:ARG:HH22	26:1:343:A:H3'	1.83	0.43
8:H:79:PHE:CZ	8:H:84:ASN:HA	2.54	0.43
12:L:43:VAL:HG23	12:L:43:VAL:O	2.18	0.43
12:L:111:VAL:N	12:L:114:ASP:OD2	2.28	0.43
18:R:1:MET:CE	26:1:2769:G:H5'	2.47	0.43
19:S:58:SER:O	19:S:79:ARG:NE	2.43	0.43
23:Y:55:THR:CG2	23:Y:60:ARG:HG3	2.48	0.43
26:1:78:U:O2'	26:1:79:U:H5'	2.18	0.43
26:1:1028:G:H2'	26:1:1028:G:N3	2.33	0.43
26:1:1816:A:H2'	26:1:1817:C:O4'	2.18	0.43
26:1:2500:U:H2'	26:1:2501:U:O2	2.18	0.43
26:1:2597:G:H2'	26:1:2598:U:O4'	2.18	0.43
26:1:2714:U:H2'	26:1:2715:G:O4'	2.18	0.43
26:1:2907:A:H2'	26:1:2908:U:C6	2.54	0.43
2:B:115:ILE:H	2:B:128:ASN:ND2	2.16	0.43
18:R:2:LYS:HE2	18:R:31:LYS:O	2.18	0.43
26:1:4:U:H2'	26:1:5:A:H8	1.83	0.43
26:1:74:U:H4'	26:1:75:G:O5'	2.19	0.43
26:1:442:G:C2'	26:1:443:U:H5'	2.48	0.43
26:1:908:A:H2'	26:1:909:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1651:C:H4'	26:1:1652:A:H5'	2.01	0.43
26:1:1865:C:H4'	26:1:1866:G:C5'	2.48	0.43
26:1:1950:U:H2'	26:1:1951:C:C6	2.53	0.43
26:1:2052:C:H2'	26:1:2053:U:C6	2.54	0.43
26:1:2827:A:H2'	26:1:2828:U:C6	2.53	0.43
2:B:93:LEU:HD12	2:B:102:ARG:O	2.18	0.43
22:X:92:THR:HG22	22:X:94:ALA:H	1.83	0.43
23:Y:55:THR:HG22	23:Y:60:ARG:HG3	1.99	0.43
23:Y:80:GLU:HG3	23:Y:80:GLU:O	2.19	0.43
26:1:674:C:O2	26:1:684:U:O2'	2.37	0.43
26:1:700:A:H4'	26:1:701:G:OP1	2.18	0.43
26:1:862:C:C2'	26:1:863:G:H5'	2.49	0.43
26:1:1350:U:HO2'	26:1:1351:C:P	2.37	0.43
26:1:2764:G:O2'	26:1:2765:A:H5'	2.19	0.43
4:D:38:VAL:HG13	4:D:53:VAL:HB	2.00	0.43
5:E:14:PRO:HG3	5:E:78:GLU:HG3	2.00	0.43
13:M:11:SER:HG	26:1:1033:G:P	2.40	0.43
18:R:29:ASN:HD22	18:R:32:HIS:CE1	2.36	0.43
19:S:200:LYS:O	19:S:204:GLU:HG3	2.17	0.43
23:Y:101:ARG:NH2	26:1:953:C:OP1	2.50	0.43
26:1:216:A:H4'	26:1:216:A:OP1	2.17	0.43
26:1:310:C:H1'	26:1:311:U:C6	2.54	0.43
26:1:565:G:H2'	26:1:566:U:O4'	2.18	0.43
26:1:702:U:H2'	26:1:703:A:H8	1.83	0.43
26:1:766:G:O2'	26:1:767:A:H5'	2.18	0.43
26:1:1240:U:H2'	26:1:1241:A:C8	2.53	0.43
26:1:2011:U:H2'	26:1:2012:G:C8	2.53	0.43
26:1:2690:G:H2'	26:1:2691:G:H8	1.82	0.43
2:B:132:LEU:HD13	2:B:172:VAL:HG21	2.01	0.43
15:O:29:ARG:HG3	15:O:47:GLU:HA	2.01	0.43
21:W:112:MET:HA	21:W:115:VAL:HG22	2.00	0.43
22:X:17:ASN:HD22	22:X:18:ARG:H	1.67	0.43
22:X:124:LYS:HD3	22:X:144:GLU:HB2	2.01	0.43
23:Y:74:TYR:CE2	23:Y:91:GLU:HB3	2.53	0.43
26:1:114:C:H2'	26:1:115:C:H6	1.84	0.43
26:1:577:A:H4'	26:1:578:G:C8	2.54	0.43
26:1:587:C:O2'	26:1:588:G:H5'	2.18	0.43
26:1:899:U:H2'	26:1:900:G:H8	1.83	0.43
26:1:901:G:H2'	26:1:902:A:H8	1.78	0.43
26:1:1182:G:H2'	26:1:1183:G:O4'	2.18	0.43
26:1:1225:G:H2'	26:1:1226:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1757:U:O2'	26:1:1758:A:H5'	2.19	0.43
26:1:1904:A:H2'	26:1:1905:G:C8	2.53	0.43
27:2:96:A:O2'	27:2:97:G:H5'	2.18	0.43
2:B:205:VAL:CG2	26:1:1818:A:H5''	2.48	0.43
3:C:86:ALA:HB3	3:C:88:ILE:HG22	2.01	0.43
3:C:90:ILE:HD11	3:C:92:ARG:HE	1.84	0.43
5:E:37:LYS:HA	5:E:48:GLU:OE2	2.19	0.43
6:F:60:PRO:HB2	6:F:71:TYR:HB3	2.01	0.43
8:H:62:GLU:HB3	8:H:69:THR:HB	2.01	0.43
9:I:27:LYS:O	9:I:29:LEU:HB2	2.19	0.43
11:K:13:GLU:O	11:K:17:GLN:HG3	2.19	0.43
12:L:99:TYR:H	12:L:103:GLN:HE22	1.67	0.43
12:L:150:ALA:HB1	12:L:151:PRO:HD2	2.00	0.43
17:Q:58:VAL:CG1	17:Q:61:LEU:HB2	2.40	0.43
22:X:101:VAL:HG12	22:X:102:VAL:HG23	2.01	0.43
26:1:2055:U:O2'	26:1:2056:G:H5'	2.19	0.43
26:1:2263:C:H2'	26:1:2264:G:O4'	2.19	0.43
26:1:2431:C:H2'	26:1:2432:G:O4'	2.18	0.43
2:B:263:LYS:NZ	26:1:1827:C:OP2	2.52	0.43
5:E:2:GLU:CD	5:E:72:LYS:HE2	2.39	0.43
19:S:164:GLU:HG3	19:S:165:LEU:N	2.34	0.43
20:V:74:VAL:HG13	20:V:88:ILE:O	2.19	0.43
22:X:12:SER:O	22:X:13:ARG:HD3	2.18	0.43
24:Z:100:TYR:O	24:Z:122:VAL:HG12	2.18	0.43
26:1:40:U:H3	26:1:485:A:H61	1.67	0.43
26:1:176:A:OP2	26:1:176:A:H4'	2.18	0.43
26:1:181:G:C2'	26:1:182:C:H5'	2.49	0.43
26:1:725:A:H2'	26:1:726:G:C8	2.54	0.43
26:1:887:A:H2'	26:1:888:G:O4'	2.18	0.43
26:1:1749:G:O2'	26:1:1750:U:H5'	2.19	0.43
26:1:2406:G:H2'	26:1:2407:A:C8	2.53	0.43
26:1:2495:A:O2'	26:1:2508:G:N2	2.52	0.43
26:1:2772:C:H2'	26:1:2773:U:C6	2.54	0.43
27:2:57:G:C2	27:2:58:C:H1'	2.54	0.43
12:L:34:VAL:O	12:L:51:VAL:HA	2.18	0.43
26:1:57:C:H2'	26:1:58:G:O4'	2.19	0.43
26:1:717:C:O2'	26:1:718:C:H5'	2.19	0.43
26:1:1443:A:H2'	26:1:1444:C:C6	2.54	0.43
26:1:1669:C:O2'	26:1:1670:A:H5'	2.19	0.43
26:1:1817:C:H2'	26:1:1818:A:C8	2.53	0.43
26:1:1904:A:H2'	26:1:1905:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2767:A:H2'	26:1:2768:A:C8	2.54	0.43
26:1:391:A:H2'	26:1:392:U:O4'	2.19	0.42
26:1:768:A:H2'	26:1:769:U:C6	2.53	0.42
26:1:909:G:H2'	26:1:910:C:C6	2.54	0.42
26:1:1215:U:H5'	26:1:1216:U:N3	2.34	0.42
26:1:2388:A:C2'	26:1:2389:G:H5'	2.49	0.42
1:A:10:VAL:HG22	12:L:194:VAL:HG21	2.00	0.42
2:B:176:LEU:HD12	2:B:180:GLU:HB3	1.99	0.42
3:C:105:ALA:HB1	4:D:40:PHE:HZ	1.84	0.42
13:M:2:ALA:HA	13:M:38:GLU:HG2	2.01	0.42
18:R:19:ARG:HG2	26:1:2783:U:OP2	2.19	0.42
20:V:19:ILE:CD1	20:V:142:GLU:HA	2.49	0.42
26:1:825:G:H2'	26:1:827:A:N7	2.34	0.42
26:1:1487:G:H1	26:1:1595:C:H42	1.67	0.42
1:A:33:ARG:NH2	1:A:82:LYS:HA	2.34	0.42
3:C:91:ASN:HB2	4:D:11:GLN:HB2	2.00	0.42
5:E:4:LYS:CB	5:E:106:VAL:HG22	2.49	0.42
11:K:42:ARG:O	11:K:46:VAL:HG23	2.19	0.42
12:L:157:ALA:HB2	26:1:2602:C:H4'	2.00	0.42
20:V:8:ASN:O	20:V:12:ILE:HG13	2.20	0.42
23:Y:118:LEU:HD12	23:Y:131:PHE:HE1	1.84	0.42
26:1:89:U:H2'	26:1:90:A:H2'	2.01	0.42
26:1:793:G:H1	26:1:796:A:H5'	1.84	0.42
26:1:896:U:H2'	26:1:897:A:H8	1.83	0.42
26:1:1724:U:H2'	26:1:1725:G:O4'	2.19	0.42
26:1:1776:A:H2'	26:1:1777:G:O4'	2.19	0.42
26:1:1832:C:O2'	26:1:1833:C:H5'	2.18	0.42
26:1:1924:G:H2'	26:1:1925:U:C6	2.55	0.42
1:A:23:ARG:HA	1:A:24:PRO:HD3	1.91	0.42
1:A:29:ARG:CG	1:A:89:LYS:HE2	2.49	0.42
1:A:72:VAL:HG12	21:W:79:PHE:CD1	2.54	0.42
2:B:20:ASP:OD1	2:B:21:PHE:N	2.52	0.42
4:D:67:ARG:NH2	26:1:1261:G:OP1	2.52	0.42
8:H:48:PHE:O	8:H:52:ILE:HG22	2.19	0.42
8:H:79:PHE:O	8:H:81:PRO:HD3	2.19	0.42
18:R:7:VAL:CG2	18:R:37:GLY:HA2	2.45	0.42
20:V:4:THR:OG1	26:1:1039:C:O2	2.18	0.42
26:1:269:G:H21	26:1:323:C:H6	1.66	0.42
26:1:1044:A:H2'	26:1:1045:A:C8	2.55	0.42
26:1:1445:C:O2'	26:1:1446:U:H5'	2.20	0.42
26:1:1863:C:H2'	26:1:1864:C:H6	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:55:ILE:HD12	6:F:76:ARG:HH11	1.84	0.42
12:L:8:ARG:HB3	12:L:29:GLU:HG2	2.01	0.42
24:Z:20:LEU:HD13	24:Z:40:VAL:HG21	2.01	0.42
26:1:197:G:H2'	26:1:198:A:O4'	2.20	0.42
26:1:752:G:C2'	26:1:753:U:H5'	2.49	0.42
26:1:2051:C:H2'	26:1:2052:C:H6	1.83	0.42
26:1:2388:A:H2'	26:1:2389:G:H5'	2.01	0.42
2:B:53:HIS:NE2	2:B:219:THR:HA	2.35	0.42
2:B:59:LYS:HB2	26:1:1615:G:H4'	2.01	0.42
3:C:64:ARG:HD3	20:V:45:TYR:O	2.19	0.42
4:D:63:ASN:HB3	4:D:94:LYS:HG3	2.01	0.42
6:F:4:ARG:HH21	6:F:6:ILE:HG22	1.83	0.42
21:W:8:LEU:HD13	21:W:84:CYS:HB3	2.01	0.42
21:W:34:ASN:N	21:W:37:ASP:OD2	2.33	0.42
26:1:101:G:O2'	26:1:102:A:OP2	2.32	0.42
26:1:437:A:N3	26:1:437:A:H2'	2.33	0.42
26:1:565:G:H2'	26:1:566:U:C6	2.54	0.42
26:1:575:G:N3	26:1:575:G:H2'	2.33	0.42
26:1:750:A:H2'	26:1:751:A:O4'	2.19	0.42
27:2:56:A:H2'	27:2:57:G:H8	1.84	0.42
27:2:90:U:H2'	27:2:91:C:H6	1.84	0.42
5:E:17:VAL:HG13	5:E:47:ILE:HD11	2.02	0.42
13:M:23:VAL:HG23	13:M:28:LEU:HD12	2.01	0.42
26:1:94:A:H2'	26:1:95:A:O4'	2.20	0.42
26:1:389:A:H2'	26:1:390:A:C5'	2.49	0.42
26:1:525:A:HO2'	26:1:527:G:H8	1.66	0.42
26:1:559:A:H2'	26:1:560:A:O4'	2.19	0.42
26:1:561:C:C2'	26:1:562:C:H5'	2.49	0.42
26:1:1034:A:O2'	26:1:1036:C:OP2	2.32	0.42
26:1:1428:U:H2'	26:1:1430:A:OP2	2.20	0.42
26:1:2618:C:H2'	26:1:2619:G:H8	1.84	0.42
7:G:85:PHE:HD1	7:G:90:LYS:HD2	1.85	0.42
12:L:5:ILE:HG22	12:L:105:VAL:HG12	2.01	0.42
12:L:119:THR:HB	12:L:210:GLU:HG2	2.02	0.42
17:Q:57:ARG:HD3	26:1:878:C:O2'	2.20	0.42
18:R:36:GLN:NE2	26:1:1169:G:H5'	2.34	0.42
20:V:39:GLY:HA3	20:V:52:GLY:HA2	2.01	0.42
24:Z:59:ARG:HG3	24:Z:86:PHE:CE2	2.55	0.42
26:1:89:U:C2'	26:1:90:A:H2'	2.50	0.42
26:1:491:C:O2'	26:1:492:G:H5'	2.20	0.42
26:1:1215:U:H3'	26:1:1216:U:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1425:G:O2'	26:1:1426:G:H5'	2.20	0.42
26:1:1463:A:H5'	26:1:1463:A:N3	2.35	0.42
26:1:1499:U:H2'	26:1:1500:G:O4'	2.20	0.42
26:1:1696:C:H2'	26:1:1697:G:O4'	2.20	0.42
26:1:2620:U:H2'	26:1:2621:C:C6	2.55	0.42
1:A:66:ILE:HA	1:A:71:GLY:HA2	2.01	0.42
6:F:35:LYS:HB3	6:F:55:ILE:HD13	2.02	0.42
10:J:5:CYS:SG	10:J:6:PHE:N	2.93	0.42
13:M:2:ALA:N	13:M:38:GLU:HG2	2.35	0.42
17:Q:58:VAL:HG11	22:X:58:PHE:CE2	2.55	0.42
22:X:129:SER:OG	22:X:130:ALA:N	2.53	0.42
26:1:726:G:H2'	26:1:727:G:O4'	2.20	0.42
26:1:1269:A:H2'	26:1:1270:U:C6	2.55	0.42
26:1:1459:A:N3	26:1:1459:A:H2'	2.34	0.42
26:1:1822:C:H2'	26:1:1823:U:O4'	2.19	0.42
26:1:1917:A:H2'	26:1:1918:G:H5'	2.02	0.42
26:1:2605:G:OP2	26:1:2605:G:H4'	2.19	0.42
27:2:68:U:O2'	27:2:69:C:H5'	2.20	0.42
4:D:11:GLN:OE1	4:D:11:GLN:N	2.53	0.42
8:H:76:ASP:H	8:H:90:ASP:HB2	1.84	0.42
12:L:90:GLU:OE1	26:1:2662:U:O2'	2.30	0.42
17:Q:35:ASN:HB3	26:1:2417:U:H5''	2.02	0.42
19:S:123:LEU:HA	19:S:192:LEU:HB2	2.02	0.42
24:Z:16:MET:HE2	24:Z:20:LEU:HD11	2.02	0.42
26:1:32:C:N4	26:1:493:A:OP2	2.53	0.42
26:1:69:C:H4'	26:1:75:G:C8	2.55	0.42
26:1:217:G:H2'	26:1:218:G:O4'	2.20	0.42
26:1:410:G:HO2'	26:1:411:A:H2	1.67	0.42
26:1:630:G:N3	26:1:630:G:H5'	2.34	0.42
26:1:1217:U:H1'	26:1:1218:G:N1	2.35	0.42
26:1:1491:C:C2'	26:1:1492:G:H5'	2.50	0.42
26:1:2231:C:H2'	26:1:2232:A:H8	1.84	0.42
26:1:2348:G:H5''	26:1:2349:A:OP2	2.19	0.42
26:1:2825:U:H2'	26:1:2826:U:C6	2.54	0.42
1:A:99:LEU:HD23	1:A:102:LEU:CD1	2.50	0.41
6:F:62:LYS:HB3	6:F:71:TYR:HE1	1.83	0.41
7:G:9:VAL:HG12	7:G:70:LEU:HD13	2.01	0.41
17:Q:58:VAL:HG22	17:Q:61:LEU:HD12	2.02	0.41
18:R:17:ILE:HG13	18:R:18:LYS:N	2.34	0.41
19:S:57:VAL:CG1	19:S:79:ARG:HD2	2.50	0.41
21:W:93:PRO:HG3	21:W:117:LEU:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1314:A:H2'	26:1:1315:C:C6	2.56	0.41
26:1:1465:G:H5'	26:1:2238:U:H6	1.84	0.41
26:1:1562:C:H2'	26:1:1563:U:H6	1.85	0.41
26:1:1571:G:H2'	26:1:1572:G:H8	1.85	0.41
26:1:1632:A:H4'	26:1:1633:A:N3	2.35	0.41
26:1:1651:C:H5''	26:1:1652:A:H5'	2.01	0.41
26:1:1752:C:O2'	26:1:1753:U:H5'	2.20	0.41
26:1:1893:A:C6	26:1:1894:G:H1'	2.55	0.41
26:1:2725:U:H2'	26:1:2726:C:C6	2.55	0.41
27:2:39:G:O2'	27:2:40:C:OP1	2.36	0.41
6:F:7:LEU:HD23	6:F:29:VAL:HG12	2.02	0.41
12:L:60:LYS:NZ	12:L:62:ASP:OD2	2.26	0.41
26:1:151:U:H2'	26:1:152:C:C6	2.54	0.41
26:1:161:A:C2'	26:1:162:A:H5''	2.44	0.41
26:1:905:U:H1'	26:1:2295:A:H5'	2.01	0.41
26:1:1520:A:C2'	26:1:1521:A:H5'	2.50	0.41
26:1:2422:C:H2'	26:1:2423:G:C8	2.54	0.41
26:1:2626:G:C2'	26:1:2627:A:H5'	2.50	0.41
26:1:2860:U:H2'	26:1:2861:U:H6	1.85	0.41
1:A:33:ARG:HD3	1:A:84:GLU:OE2	2.20	0.41
2:B:84:ASP:OD1	2:B:85:PRO:HD2	2.20	0.41
2:B:160:ALA:O	2:B:194:GLN:HG3	2.20	0.41
5:E:78:GLU:O	26:1:24:G:O2'	2.39	0.41
5:E:89:ALA:HB1	26:1:793:G:N2	2.35	0.41
12:L:184:GLU:HB2	12:L:198:LYS:HD2	2.02	0.41
14:N:9:SER:HB2	26:1:2047:A:C5'	2.42	0.41
19:S:201:LYS:O	19:S:205:VAL:HG23	2.20	0.41
20:V:44:THR:O	20:V:44:THR:HG22	2.20	0.41
26:1:56:A:H2'	26:1:57:C:O4'	2.20	0.41
26:1:111:U:H2'	26:1:112:U:H5'	2.02	0.41
26:1:207:A:H5'	26:1:209:U:O4'	2.20	0.41
26:1:830:U:H2'	26:1:831:C:C6	2.55	0.41
26:1:970:U:H4'	26:1:971:U:O5'	2.20	0.41
26:1:1283:G:O2'	26:1:1284:A:H5'	2.21	0.41
26:1:1621:C:H2'	26:1:1622:C:C6	2.55	0.41
26:1:1976:G:H2'	26:1:1977:G:O4'	2.19	0.41
26:1:2223:C:H2'	26:1:2224:U:C6	2.56	0.41
26:1:2288:C:O2'	26:1:2289:U:H5'	2.21	0.41
26:1:2794:C:H2'	26:1:2795:C:H5'	2.02	0.41
26:1:2799:C:H2'	26:1:2800:U:C6	2.55	0.41
1:A:4:HIS:HB3	1:A:7:ILE:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:GLY:HA2	1:A:59:GLU:HG2	2.00	0.41
2:B:144:ILE:HG22	2:B:145:GLU:O	2.21	0.41
6:F:82:LEU:HD23	6:F:82:LEU:HA	1.84	0.41
12:L:215:ILE:HD13	26:1:2798:C:H5'	2.02	0.41
19:S:182:ASN:O	19:S:186:ILE:HG13	2.19	0.41
20:V:39:GLY:CA	20:V:52:GLY:HA2	2.50	0.41
26:1:266:A:H1'	26:1:476:A:N3	2.36	0.41
26:1:1041:G:O2'	26:1:1042:C:H5'	2.20	0.41
26:1:1409:U:O2'	26:1:2239:A:H8	2.04	0.41
26:1:2541:U:H2'	26:1:2542:C:H6	1.84	0.41
1:A:33:ARG:HH21	1:A:82:LYS:HA	1.86	0.41
2:B:65:ILE:HD12	2:B:87:ARG:NH1	2.35	0.41
12:L:26:THR:OG1	12:L:200:ASN:HA	2.21	0.41
15:O:7:LEU:HB3	15:O:45:HIS:HB3	2.03	0.41
17:Q:7:HIS:HD2	17:Q:10:ALA:HB2	1.85	0.41
23:Y:32:PHE:HE2	23:Y:111:GLU:HA	1.82	0.41
24:Z:102:ARG:NH2	24:Z:122:VAL:HG23	2.25	0.41
26:1:402:C:H2'	26:1:403:U:C2	2.55	0.41
26:1:730:A:H5'	26:1:819:A:N6	2.35	0.41
26:1:1059:A:O2'	26:1:1060:U:H5'	2.20	0.41
26:1:1081:G:H22	26:1:1163:U:H1'	1.84	0.41
26:1:1266:G:H2'	26:1:1267:A:O4'	2.21	0.41
26:1:1903:A:H2'	26:1:1904:A:C8	2.55	0.41
26:1:2027:G:O2'	26:1:2028:A:H5'	2.21	0.41
26:1:2519:U:H2'	26:1:2520:U:C6	2.55	0.41
26:1:2799:C:H2'	26:1:2800:U:H6	1.85	0.41
26:1:2815:C:C2'	26:1:2816:C:H5'	2.51	0.41
26:1:2838:C:O2'	26:1:2839:A:H5'	2.20	0.41
1:A:28:LEU:HD22	1:A:86:ILE:CG2	2.51	0.41
4:D:11:GLN:HE21	4:D:39:LEU:CD1	2.33	0.41
6:F:35:LYS:O	6:F:53:VAL:HG11	2.20	0.41
15:O:9:CYS:HB2	15:O:45:HIS:CE1	2.55	0.41
26:1:92:G:H2'	26:1:93:U:H6	1.81	0.41
26:1:349:U:H2'	26:1:350:G:H5'	2.03	0.41
26:1:888:G:H2'	26:1:889:U:C6	2.54	0.41
26:1:969:A:HO2'	26:1:971:U:H6	1.67	0.41
26:1:1737:U:H4'	26:1:1738:C:OP2	2.20	0.41
26:1:2271:U:H2'	26:1:2272:U:O4'	2.21	0.41
26:1:2427:G:H2'	26:1:2428:U:C6	2.56	0.41
26:1:2555:U:H2'	26:1:2557:U:O5'	2.21	0.41
26:1:2617:A:H2'	26:1:2618:C:H6	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:17:SER:HA	6:F:20:MET:HG3	2.02	0.41
20:V:75:TYR:HB2	20:V:88:ILE:CG2	2.51	0.41
20:V:88:ILE:HG13	20:V:89:THR:N	2.36	0.41
23:Y:43:THR:H	23:Y:46:GLN:NE2	2.18	0.41
24:Z:84:LYS:HA	24:Z:88:GLU:OE1	2.21	0.41
24:Z:112:ASP:O	26:1:2036:G:H1'	2.21	0.41
26:1:356:A:H2'	26:1:357:U:C6	2.56	0.41
26:1:679:G:H2'	26:1:680:C:C6	2.56	0.41
26:1:691:A:H2'	26:1:692:G:O4'	2.20	0.41
26:1:894:A:H2'	26:1:895:U:O2	2.20	0.41
26:1:1238:U:H2'	26:1:1239:C:H6	1.84	0.41
26:1:1350:U:H5	26:1:1647:A:N1	2.19	0.41
26:1:1411:G:O2'	26:1:1412:G:H5'	2.20	0.41
26:1:1916:A:H2'	26:1:1917:A:O4'	2.19	0.41
26:1:1951:C:O2'	26:1:1952:C:H5'	2.21	0.41
26:1:1994:C:H2'	26:1:1995:G:H5'	2.03	0.41
2:B:221:ARG:O	2:B:224:VAL:HG22	2.21	0.41
7:G:69:GLN:OE1	7:G:78:PRO:HB2	2.21	0.41
8:H:2:ALA:HB3	8:H:51:VAL:CG2	2.44	0.41
19:S:54:ARG:HD2	26:1:718:C:OP1	2.21	0.41
21:W:3:GLN:O	21:W:3:GLN:HG3	2.21	0.41
21:W:69:VAL:HG22	21:W:77:ILE:CG2	2.50	0.41
26:1:1203:U:O2'	26:1:1204:G:H5'	2.20	0.41
26:1:1772:G:C2'	26:1:1773:A:H5'	2.51	0.41
26:1:2250:A:H2'	26:1:2251:G:O4'	2.21	0.41
26:1:2581:U:H2'	26:1:2582:U:C6	2.56	0.41
2:B:205:VAL:HG21	26:1:1818:A:H5''	2.02	0.41
2:B:260:ARG:HD3	2:B:260:ARG:O	2.21	0.41
4:D:11:GLN:HE21	4:D:39:LEU:HD11	1.86	0.41
4:D:98:ASP:O	4:D:99:LYS:HD2	2.21	0.41
7:G:41:MET:HE1	26:1:526:A:O5'	2.20	0.41
15:O:7:LEU:HD21	15:O:32:MET:HG3	2.01	0.41
26:1:165:C:H5'	26:1:166:A:OP2	2.21	0.41
26:1:470:G:H2'	26:1:471:G:O4'	2.21	0.41
26:1:526:A:H3'	26:1:527:G:H5''	2.03	0.41
26:1:1316:G:C2'	26:1:1317:G:H5'	2.50	0.41
26:1:1347:G:H2'	26:1:1348:U:H5'	2.03	0.41
26:1:1514:A:C2'	26:1:1515:G:H5'	2.51	0.41
26:1:1576:A:H2'	26:1:1577:G:O4'	2.21	0.41
26:1:1605:A:H4'	26:1:1606:C:OP1	2.21	0.41
26:1:1756:U:O2	26:1:1756:U:H2'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1875:A:H61	26:1:1921:C:H1'	1.85	0.41
26:1:1904:A:O2'	26:1:1905:G:H5'	2.20	0.41
26:1:1939:A:N7	26:1:1944:U:O4	2.54	0.41
26:1:2529:G:H5''	26:1:2530:A:H5''	2.03	0.41
26:1:2793:G:H2'	26:1:2793:G:N3	2.36	0.41
27:2:46:A:O2'	27:2:47:C:OP2	2.32	0.41
3:C:25:PHE:N	26:1:578:G:OP1	2.42	0.41
3:C:70:ARG:HD3	3:C:74:MET:O	2.20	0.41
3:C:76:TYR:CZ	3:C:80:MET:HG3	2.56	0.41
8:H:92:LEU:HD13	27:2:99:G:H4'	2.03	0.41
19:S:40:GLN:NE2	26:1:660:A:O2'	2.54	0.41
19:S:169:ASN:HB2	26:1:365:A:OP2	2.20	0.41
19:S:190:ASP:N	19:S:190:ASP:OD1	2.54	0.41
22:X:109:ILE:CG1	22:X:125:ALA:HB1	2.50	0.41
24:Z:79:GLN:NE2	24:Z:88:GLU:OE2	2.34	0.41
26:1:89:U:C3'	26:1:90:A:H2'	2.47	0.41
26:1:229:A:H4'	26:1:230:A:OP1	2.20	0.41
26:1:262:G:H1'	26:1:666:A:O2'	2.21	0.41
26:1:525:A:H1'	26:1:526:A:H5''	2.03	0.41
26:1:1513:A:H3'	26:1:1514:A:H8	1.85	0.41
26:1:1781:C:H5	26:1:2743:U:O2'	2.04	0.41
26:1:2260:A:H2'	26:1:2261:G:H8	1.85	0.41
1:A:15:LEU:HD21	1:A:57:VAL:HG22	2.03	0.40
3:C:54:LYS:HE2	26:1:1038:C:C5	2.56	0.40
4:D:42:GLY:HA2	4:D:46:VAL:O	2.21	0.40
12:L:33:ASN:HB3	12:L:105:VAL:HB	2.03	0.40
12:L:57:LYS:HG3	12:L:68:TYR:HE1	1.85	0.40
23:Y:64:VAL:HG22	23:Y:106:VAL:HG12	2.03	0.40
23:Y:109:VAL:HG12	23:Y:110:SER:O	2.21	0.40
26:1:523:A:O2'	26:1:524:A:H5'	2.20	0.40
26:1:603:C:H2'	26:1:604:G:O4'	2.21	0.40
26:1:793:G:N2	26:1:796:A:H5'	2.27	0.40
26:1:2288:C:H2'	26:1:2289:U:H5'	2.03	0.40
26:1:2367:A:H2'	26:1:2368:G:C8	2.56	0.40
27:2:23:U:H4'	27:2:24:C:C5	2.56	0.40
27:2:44:A:H2'	27:2:45:C:C6	2.56	0.40
5:E:11:ARG:HG3	5:E:11:ARG:O	2.21	0.40
18:R:1:MET:N	26:1:2553:G:O2'	2.45	0.40
26:1:2610:G:H2'	26:1:2611:U:H5'	2.02	0.40
26:1:2686:G:C3'	26:1:2687:A:H5''	2.51	0.40
2:B:181:VAL:HB	2:B:272:ARG:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:36:CYS:HB2	15:O:43:THR:CG2	2.51	0.40
17:Q:39:LYS:O	17:Q:43:GLN:HB2	2.21	0.40
20:V:93:LEU:CD1	20:V:97:ASN:HB3	2.51	0.40
26:1:442:G:O2'	26:1:443:U:H5'	2.21	0.40
26:1:895:U:H5	26:1:973:A:N1	2.19	0.40
26:1:1478:A:O2'	26:1:1479:G:H5'	2.20	0.40
26:1:2105:C:H2'	26:1:2106:U:C6	2.56	0.40
26:1:2400:U:H2'	26:1:2401:C:H6	1.86	0.40
26:1:2507:C:C2'	26:1:2508:G:H5'	2.50	0.40
26:1:2559:G:N2	26:1:2690:G:O2'	2.54	0.40
26:1:2610:G:O2'	26:1:2611:U:H5'	2.21	0.40
26:1:2683:U:O2	26:1:2692:A:N7	2.55	0.40
26:1:2832:A:H2'	26:1:2833:U:O4'	2.22	0.40
27:2:33:U:H3	27:2:48:A:H1'	1.85	0.40
2:B:157:SER:OG	2:B:158:ALA:N	2.55	0.40
12:L:44:ASP:HB3	12:L:46:TYR:CE1	2.57	0.40
12:L:64:LYS:HE2	26:1:2851:G:C6	2.56	0.40
12:L:205:LYS:O	12:L:206:LYS:HB2	2.20	0.40
26:1:18:C:O2'	26:1:597:U:OP1	2.29	0.40
26:1:50:U:H4'	26:1:51:G:OP2	2.22	0.40
26:1:386:C:O2'	26:1:387:G:H5'	2.22	0.40
26:1:683:G:H2'	26:1:684:U:O4'	2.22	0.40
26:1:1085:U:C2	26:1:1158:G:N1	2.88	0.40
26:1:1423:C:H2'	26:1:1424:A:H8	1.86	0.40
26:1:1759:G:H3'	26:1:1760:G:H5'	2.03	0.40
26:1:1772:G:H2'	26:1:1773:A:H5'	2.02	0.40
26:1:2563:G:O2'	26:1:2564:U:H5'	2.21	0.40
10:J:4:GLN:OE1	10:J:11:LYS:HE2	2.22	0.40
10:J:4:GLN:HG3	10:J:5:CYS:O	2.21	0.40
12:L:183:LEU:HD22	12:L:198:LYS:O	2.22	0.40
18:R:24:MET:HA	18:R:35:ARG:HA	2.02	0.40
20:V:16:TRP:HA	20:V:54:TYR:O	2.22	0.40
21:W:10:VAL:HG22	21:W:84:CYS:SG	2.62	0.40
23:Y:42:ILE:CD1	23:Y:68:ILE:HD13	2.51	0.40
26:1:155:U:O2'	26:1:156:A:H5'	2.21	0.40
26:1:162:A:H5'	26:1:163:U:H2'	2.04	0.40
26:1:262:G:H21	26:1:666:A:H8	1.68	0.40
26:1:423:A:H2'	26:1:424:C:C6	2.56	0.40
26:1:1301:U:H2'	26:1:1302:G:C8	2.56	0.40
26:1:1394:U:H2'	26:1:1395:G:O4'	2.22	0.40
26:1:1479:G:H2'	26:1:1480:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1494:G:C2'	26:1:1495:C:H5'	2.50	0.40
26:1:1756:U:H3	26:1:1773:A:H62	1.69	0.40
26:1:1873:G:O2'	26:1:1874:A:H5'	2.22	0.40
26:1:2439:A:C2'	26:1:2440:G:H5'	2.52	0.40
27:2:15:C:N4	27:2:103:A:H2	2.18	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	
1	A	111/116 (96%)	98 (88%)	13 (12%)	0	100	100
2	B	266/276 (96%)	237 (89%)	29 (11%)	0	100	100
3	C	114/118 (97%)	106 (93%)	8 (7%)	0	100	100
4	D	98/102 (96%)	91 (93%)	7 (7%)	0	100	100
5	E	109/116 (94%)	102 (94%)	7 (6%)	0	100	100
6	F	82/91 (90%)	75 (92%)	7 (8%)	0	100	100
7	G	87/105 (83%)	76 (87%)	11 (13%)	0	100	100
8	H	91/217 (42%)	81 (89%)	10 (11%)	0	100	100
9	I	76/85 (89%)	67 (88%)	9 (12%)	0	100	100
10	J	55/62 (89%)	47 (86%)	8 (14%)	0	100	100
11	K	54/69 (78%)	50 (93%)	4 (7%)	0	100	100
12	L	213/217 (98%)	188 (88%)	25 (12%)	0	100	100
13	M	54/59 (92%)	47 (87%)	7 (13%)	0	100	100
14	N	48/57 (84%)	45 (94%)	3 (6%)	0	100	100
15	O	45/49 (92%)	41 (91%)	4 (9%)	0	100	100
16	P	42/45 (93%)	42 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Q	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
18	R	35/37 (95%)	30 (86%)	5 (14%)	0	100	100
19	S	186/207 (90%)	173 (93%)	13 (7%)	0	100	100
20	V	141/145 (97%)	131 (93%)	10 (7%)	0	100	100
21	W	118/122 (97%)	108 (92%)	10 (8%)	0	100	100
22	X	142/146 (97%)	121 (85%)	21 (15%)	0	100	100
23	Y	133/144 (92%)	127 (96%)	6 (4%)	0	100	100
24	Z	119/122 (98%)	107 (90%)	12 (10%)	0	100	100
25	a	94/119 (79%)	85 (90%)	9 (10%)	0	100	100
All	All	2575/2891 (89%)	2334 (91%)	241 (9%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	99/102 (97%)	98 (99%)	1 (1%)	73	86
2	B	218/223 (98%)	217 (100%)	1 (0%)	86	92
3	C	96/98 (98%)	96 (100%)	0	100	100
4	D	85/86 (99%)	85 (100%)	0	100	100
5	E	90/94 (96%)	88 (98%)	2 (2%)	47	71
6	F	76/82 (93%)	75 (99%)	1 (1%)	65	82
7	G	76/90 (84%)	76 (100%)	0	100	100
8	H	81/190 (43%)	81 (100%)	0	100	100
9	I	61/66 (92%)	60 (98%)	1 (2%)	58	79
10	J	47/52 (90%)	46 (98%)	1 (2%)	48	72
11	K	51/62 (82%)	51 (100%)	0	100	100
12	L	173/175 (99%)	172 (99%)	1 (1%)	84	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	M	50/53 (94%)	50 (100%)	0	100	100
14	N	45/50 (90%)	45 (100%)	0	100	100
15	O	45/47 (96%)	45 (100%)	0	100	100
16	P	39/40 (98%)	38 (97%)	1 (3%)	41	68
17	Q	55/56 (98%)	55 (100%)	0	100	100
18	R	35/35 (100%)	35 (100%)	0	100	100
19	S	154/170 (91%)	148 (96%)	6 (4%)	27	58
20	V	122/123 (99%)	121 (99%)	1 (1%)	79	89
21	W	98/100 (98%)	97 (99%)	1 (1%)	73	86
22	X	110/112 (98%)	109 (99%)	1 (1%)	75	88
23	Y	112/119 (94%)	111 (99%)	1 (1%)	75	88
24	Z	101/102 (99%)	101 (100%)	0	100	100
25	a	80/95 (84%)	80 (100%)	0	100	100
All	All	2199/2422 (91%)	2180 (99%)	19 (1%)	74	88

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ARG
2	B	260	ARG
5	E	28	ASN
5	E	65	ASN
6	F	75	ARG
9	I	61	ARG
10	J	27	ARG
12	L	162	ARG
16	P	9	ASN
19	S	38	ASN
19	S	74	ARG
19	S	84	ARG
19	S	168	ARG
19	S	169	ASN
19	S	188	ASN
20	V	11	ASN
21	W	31	LYS
22	X	17	ASN
23	Y	133	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	4	HIS
2	B	82	GLN
2	B	128	ASN
3	C	37	GLN
3	C	38	GLN
3	C	91	ASN
5	E	28	ASN
5	E	65	ASN
6	F	37	GLN
6	F	54	ASN
6	F	57	ASN
8	H	38	ASN
8	H	85	GLN
8	H	88	HIS
11	K	27	ASN
12	L	128	GLN
12	L	134	HIS
12	L	146	HIS
13	M	52	HIS
14	N	45	ASN
15	O	25	ASN
15	O	26	ASN
16	P	7	GLN
16	P	9	ASN
16	P	17	HIS
17	Q	7	HIS
17	Q	31	HIS
18	R	29	ASN
19	S	29	ASN
19	S	40	GLN
19	S	46	GLN
19	S	67	GLN
19	S	141	ASN
19	S	148	GLN
19	S	188	ASN
20	V	24	GLN
20	V	48	HIS
20	V	119	GLN
21	W	110	ASN
22	X	4	HIS

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Mol	Chain	Res	Type
22	X	17	ASN
23	Y	46	GLN
23	Y	71	HIS
25	a	37	ASN
25	a	39	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	1	2634/2923 (90%)	648 (24%)	18 (0%)
27	2	103/115 (89%)	38 (36%)	1 (0%)
All	All	2737/3038 (90%)	686 (25%)	19 (0%)

All (686) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
26	1	10	A
26	1	11	U
26	1	12	U
26	1	15	G
26	1	25	U
26	1	34	U
26	1	44	A
26	1	45	G
26	1	58	G
26	1	62	C
26	1	63	U
26	1	64	A
26	1	71	A
26	1	72	U
26	1	73	A
26	1	75	G
26	1	83	G
26	1	89	U
26	1	90	A
26	1	91	A
26	1	95	A
26	1	96	G
26	1	97	C
26	1	99	U
26	1	100	U

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Mol	Chain	Res	Type
26	1	101	G
26	1	102	A
26	1	115	C
26	1	116	G
26	1	117	A
26	1	118	A
26	1	119	U
26	1	130	A
26	1	150	A
26	1	156	A
26	1	160	G
26	1	162	A
26	1	163	U
26	1	164	A
26	1	165	C
26	1	168	A
26	1	169	G
26	1	176	A
26	1	177	G
26	1	180	G
26	1	183	A
26	1	184	C
26	1	185	A
26	1	191	A
26	1	199	A
26	1	202	A
26	1	216	A
26	1	218	G
26	1	219	A
26	1	224	A
26	1	225	A
26	1	227	G
26	1	228	A
26	1	230	A
26	1	233	U
26	1	236	A
26	1	242	U
26	1	243	U
26	1	244	A
26	1	250	G
26	1	251	G
26	1	253	G

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Mol	Chain	Res	Type
26	1	255	G
26	1	258	A
26	1	268	A
26	1	269	G
26	1	277	C
26	1	294	G
26	1	296	G
26	1	299	U
26	1	301	U
26	1	302	A
26	1	303	G
26	1	308	C
26	1	310	C
26	1	311	U
26	1	327	G
26	1	331	G
26	1	332	A
26	1	333	C
26	1	338	G
26	1	345	C
26	1	351	G
26	1	354	A
26	1	356	A
26	1	359	A
26	1	366	G
26	1	372	A
26	1	373	A
26	1	381	G
26	1	384	G
26	1	397	U
26	1	398	C
26	1	401	U
26	1	402	C
26	1	404	U
26	1	406	A
26	1	407	G
26	1	410	G
26	1	411	A
26	1	415	U
26	1	432	G
26	1	434	G
26	1	439	U

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Mol	Chain	Res	Type
26	1	443	U
26	1	447	A
26	1	448	A
26	1	452	G
26	1	457	G
26	1	458	A
26	1	459	C
26	1	460	C
26	1	463	C
26	1	464	U
26	1	466	C
26	1	471	G
26	1	489	A
26	1	501	C
26	1	502	C
26	1	503	A
26	1	506	A
26	1	507	C
26	1	526	A
26	1	527	G
26	1	540	G
26	1	547	A
26	1	548	A
26	1	550	A
26	1	552	A
26	1	553	A
26	1	554	C
26	1	555	C
26	1	558	A
26	1	563	G
26	1	566	U
26	1	567	G
26	1	575	G
26	1	576	U
26	1	577	A
26	1	578	G
26	1	590	U
26	1	592	A
26	1	593	U
26	1	594	G
26	1	598	G
26	1	606	G

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Mol	Chain	Res	Type
26	1	616	G
26	1	617	A
26	1	618	A
26	1	620	G
26	1	621	A
26	1	622	A
26	1	630	G
26	1	646	A
26	1	647	G
26	1	650	U
26	1	657	U
26	1	658	A
26	1	659	A
26	1	660	A
26	1	665	G
26	1	667	G
26	1	679	G
26	1	680	C
26	1	682	A
26	1	683	G
26	1	689	A
26	1	690	U
26	1	691	A
26	1	698	U
26	1	699	U
26	1	700	A
26	1	723	C
26	1	727	G
26	1	730	A
26	1	731	U
26	1	735	C
26	1	740	G
26	1	744	A
26	1	754	U
26	1	756	A
26	1	757	G
26	1	765	U
26	1	771	G
26	1	775	A
26	1	785	C
26	1	786	U
26	1	792	U

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Mol	Chain	Res	Type
26	1	793	G
26	1	796	A
26	1	802	G
26	1	809	A
26	1	810	A
26	1	819	A
26	1	820	G
26	1	821	C
26	1	822	G
26	1	823	G
26	1	827	A
26	1	829	U
26	1	830	U
26	1	834	A
26	1	837	G
26	1	838	A
26	1	850	G
26	1	857	C
26	1	891	A
26	1	903	G
26	1	904	G
26	1	911	A
26	1	912	C
26	1	914	G
26	1	917	U
26	1	920	A
26	1	921	C
26	1	954	A
26	1	955	A
26	1	960	C
26	1	969	A
26	1	970	U
26	1	971	U
26	1	972	A
26	1	977	A
26	1	982	G
26	1	985	A
26	1	989	A
26	1	990	G
26	1	997	G
26	1	1002	U
26	1	1005	G

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Mol	Chain	Res	Type
26	1	1018	A
26	1	1020	G
26	1	1027	A
26	1	1040	A
26	1	1045	A
26	1	1049	C
26	1	1054	A
26	1	1055	A
26	1	1056	U
26	1	1057	A
26	1	1065	A
26	1	1066	G
26	1	1070	A
26	1	1072	A
26	1	1076	A
26	1	1077	U
26	1	1085	U
26	1	1158	G
26	1	1161	A
26	1	1162	C
26	1	1163	U
26	1	1173	A
26	1	1174	U
26	1	1176	U
26	1	1177	A
26	1	1179	C
26	1	1183	G
26	1	1186	A
26	1	1187	A
26	1	1190	A
26	1	1193	U
26	1	1195	A
26	1	1210	U
26	1	1211	G
26	1	1213	C
26	1	1214	C
26	1	1215	U
26	1	1216	U
26	1	1217	U
26	1	1218	G
26	1	1220	A
26	1	1248	U

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Mol	Chain	Res	Type
26	1	1249	U
26	1	1258	A
26	1	1267	A
26	1	1271	G
26	1	1276	G
26	1	1278	G
26	1	1284	A
26	1	1288	G
26	1	1291	A
26	1	1293	U
26	1	1294	G
26	1	1309	G
26	1	1310	A
26	1	1311	A
26	1	1312	A
26	1	1313	G
26	1	1317	G
26	1	1321	A
26	1	1323	A
26	1	1326	C
26	1	1337	A
26	1	1338	U
26	1	1339	U
26	1	1340	G
26	1	1344	A
26	1	1345	A
26	1	1349	U
26	1	1351	C
26	1	1358	A
26	1	1366	U
26	1	1375	G
26	1	1378	U
26	1	1382	C
26	1	1386	U
26	1	1388	C
26	1	1389	U
26	1	1396	A
26	1	1402	A
26	1	1405	G
26	1	1415	A
26	1	1416	U
26	1	1421	A

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Mol	Chain	Res	Type
26	1	1423	C
26	1	1430	A
26	1	1432	A
26	1	1433	U
26	1	1436	C
26	1	1447	A
26	1	1448	U
26	1	1449	A
26	1	1450	A
26	1	1451	U
26	1	1452	C
26	1	1453	G
26	1	1454	U
26	1	1462	G
26	1	1463	A
26	1	1464	U
26	1	1465	G
26	1	1471	A
26	1	1472	C
26	1	1473	G
26	1	1477	U
26	1	1496	G
26	1	1497	A
26	1	1499	U
26	1	1502	A
26	1	1503	U
26	1	1504	U
26	1	1509	G
26	1	1510	U
26	1	1511	C
26	1	1512	U
26	1	1516	C
26	1	1517	A
26	1	1519	U
26	1	1520	A
26	1	1557	C
26	1	1561	G
26	1	1563	U
26	1	1566	G
26	1	1570	G
26	1	1572	G
26	1	1575	A

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Mol	Chain	Res	Type
26	1	1590	C
26	1	1591	G
26	1	1592	A
26	1	1594	U
26	1	1595	C
26	1	1600	A
26	1	1606	C
26	1	1607	A
26	1	1613	G
26	1	1616	A
26	1	1623	U
26	1	1625	U
26	1	1627	G
26	1	1628	A
26	1	1629	U
26	1	1631	G
26	1	1632	A
26	1	1634	A
26	1	1636	U
26	1	1644	C
26	1	1652	A
26	1	1653	A
26	1	1654	A
26	1	1662	A
26	1	1663	G
26	1	1676	A
26	1	1683	U
26	1	1690	A
26	1	1691	G
26	1	1692	C
26	1	1693	G
26	1	1698	A
26	1	1708	A
26	1	1711	G
26	1	1716	C
26	1	1718	G
26	1	1720	A
26	1	1722	A
26	1	1729	C
26	1	1739	G
26	1	1740	G
26	1	1747	G

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Mol	Chain	Res	Type
26	1	1756	U
26	1	1758	A
26	1	1759	G
26	1	1760	G
26	1	1761	G
26	1	1765	A
26	1	1767	G
26	1	1771	A
26	1	1772	G
26	1	1790	G
26	1	1791	G
26	1	1795	A
26	1	1800	A
26	1	1809	C
26	1	1811	A
26	1	1815	C
26	1	1826	G
26	1	1827	C
26	1	1828	U
26	1	1836	A
26	1	1839	G
26	1	1841	G
26	1	1842	A
26	1	1843	U
26	1	1846	A
26	1	1856	A
26	1	1865	C
26	1	1866	G
26	1	1875	A
26	1	1881	A
26	1	1886	A
26	1	1887	G
26	1	1893	A
26	1	1894	G
26	1	1898	C
26	1	1900	G
26	1	1901	C
26	1	1902	G
26	1	1910	G
26	1	1911	A
26	1	1913	U
26	1	1924	G

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Mol	Chain	Res	Type
26	1	1927	A
26	1	1933	G
26	1	1939	A
26	1	1940	A
26	1	1941	C
26	1	1942	U
26	1	1943	A
26	1	1944	U
26	1	1946	A
26	1	1949	G
26	1	1954	A
26	1	1956	G
26	1	1957	G
26	1	1959	A
26	1	1962	G
26	1	1963	A
26	1	1965	A
26	1	1967	U
26	1	1970	U
26	1	1974	C
26	1	1982	U
26	1	1989	C
26	1	1990	C
26	1	1993	A
26	1	1994	C
26	1	1997	A
26	1	1998	A
26	1	1999	G
26	1	2003	U
26	1	2007	G
26	1	2008	A
26	1	2009	U
26	1	2018	U
26	1	2023	C
26	1	2046	U
26	1	2049	U
26	1	2050	A
26	1	2058	A
26	1	2059	G
26	1	2060	A
26	1	2063	C
26	1	2070	C

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Mol	Chain	Res	Type
26	1	2073	G
26	1	2079	G
26	1	2082	C
26	1	2083	G
26	1	2087	A
26	1	2088	G
26	1	2091	C
26	1	2093	C
26	1	2095	U
26	1	2096	G
26	1	2107	G
26	1	2108	U
26	1	2120	G
26	1	2122	A
26	1	2223	C
26	1	2226	A
26	1	2231	C
26	1	2235	A
26	1	2237	U
26	1	2238	U
26	1	2239	A
26	1	2241	C
26	1	2252	A
26	1	2265	G
26	1	2266	G
26	1	2289	U
26	1	2295	A
26	1	2300	A
26	1	2307	G
26	1	2308	C
26	1	2310	C
26	1	2313	A
26	1	2314	A
26	1	2315	A
26	1	2318	U
26	1	2329	U
26	1	2330	G
26	1	2331	G
26	1	2341	A
26	1	2346	U
26	1	2347	A
26	1	2349	A

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Mol	Chain	Res	Type
26	1	2362	A
26	1	2374	C
26	1	2377	C
26	1	2410	G
26	1	2412	C
26	1	2416	G
26	1	2417	U
26	1	2429	U
26	1	2432	G
26	1	2433	C
26	1	2450	U
26	1	2452	A
26	1	2453	A
26	1	2456	G
26	1	2468	C
26	1	2474	G
26	1	2475	A
26	1	2479	C
26	1	2480	A
26	1	2486	A
26	1	2499	G
26	1	2500	U
26	1	2501	U
26	1	2502	C
26	1	2505	A
26	1	2514	G
26	1	2521	G
26	1	2523	C
26	1	2525	C
26	1	2529	G
26	1	2532	G
26	1	2533	U
26	1	2540	A
26	1	2544	C
26	1	2545	A
26	1	2546	U
26	1	2556	G
26	1	2560	U
26	1	2562	G
26	1	2564	U
26	1	2581	U
26	1	2585	C

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Mol	Chain	Res	Type
26	1	2593	A
26	1	2594	G
26	1	2600	C
26	1	2609	G
26	1	2611	U
26	1	2612	U
26	1	2629	A
26	1	2630	G
26	1	2636	U
26	1	2637	C
26	1	2640	U
26	1	2642	U
26	1	2650	G
26	1	2657	G
26	1	2663	U
26	1	2673	C
26	1	2675	G
26	1	2677	C
26	1	2683	U
26	1	2687	A
26	1	2688	G
26	1	2693	C
26	1	2694	C
26	1	2696	G
26	1	2697	G
26	1	2700	G
26	1	2712	G
26	1	2716	U
26	1	2717	A
26	1	2718	C
26	1	2727	G
26	1	2741	G
26	1	2747	U
26	1	2753	U
26	1	2759	G
26	1	2760	A
26	1	2762	G
26	1	2769	G
26	1	2771	G
26	1	2772	C
26	1	2775	A
26	1	2777	A

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Mol	Chain	Res	Type
26	1	2778	G
26	1	2784	A
26	1	2791	A
26	1	2792	A
26	1	2793	G
26	1	2795	C
26	1	2799	C
26	1	2805	A
26	1	2810	A
26	1	2817	A
26	1	2820	U
26	1	2827	A
26	1	2828	U
26	1	2845	G
26	1	2849	A
26	1	2853	U
26	1	2854	A
26	1	2856	U
26	1	2862	C
26	1	2863	G
26	1	2868	G
26	1	2877	G
26	1	2879	G
26	1	2887	G
26	1	2888	A
26	1	2890	C
26	1	2892	G
26	1	2893	A
26	1	2899	A
26	1	2900	C
26	1	2901	U
26	1	2906	G
26	1	2911	A
26	1	2913	G
26	1	2916	U
27	2	7	G
27	2	10	U
27	2	11	A
27	2	12	U
27	2	13	A
27	2	17	A
27	2	18	G

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Mol	Chain	Res	Type
27	2	19	G
27	2	20	A
27	2	21	G
27	2	23	U
27	2	24	C
27	2	25	A
27	2	26	C
27	2	29	C
27	2	39	G
27	2	42	G
27	2	46	A
27	2	47	C
27	2	49	G
27	2	50	A
27	2	54	U
27	2	60	C
27	2	64	A
27	2	65	G
27	2	71	A
27	2	79	C
27	2	82	A
27	2	85	U
27	2	86	A
27	2	87	C
27	2	94	C
27	2	95	U
27	2	97	G
27	2	98	A
27	2	100	U
27	2	101	A
27	2	104	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	1	10	A
26	1	44	A
26	1	90	A
26	1	229	A
26	1	276	C
26	1	433	U
26	1	525	A

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Mol	Chain	Res	Type
26	1	1350	U
26	1	1510	U
26	1	1631	G
26	1	1845	U
26	1	1865	C
26	1	1926	A
26	1	1988	C
26	1	2330	G
26	1	2783	U
26	1	2827	A
26	1	2887	G
27	2	84	U

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
28	G6M	1	3001	-	27,27,27	1.81	2 (7%)	37,37,37	1.96	9 (24%)

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
28	G6M	1	3001	-	-	8/15/35/35	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	1	3001	G6M	O11-C12	6.97	1.45	1.35
28	1	3001	G6M	C12-N8	-4.76	1.31	1.36

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	3001	G6M	C10-O11-C12	-5.56	105.66	110.10
28	1	3001	G6M	C19-N14-C15	4.70	122.14	111.57
28	1	3001	G6M	C9-N8-C12	3.96	114.10	111.17
28	1	3001	G6M	C3-C2-C1	-3.93	119.88	123.35
28	1	3001	G6M	C18-C19-N14	-2.99	104.27	109.93
28	1	3001	G6M	O11-C10-C9	2.91	107.32	104.50
28	1	3001	G6M	C10-C9-N8	-2.31	99.67	101.85
28	1	3001	G6M	C4-N8-C12	-2.11	123.77	125.98
28	1	3001	G6M	C10-C20-N29	2.05	116.06	111.98

There are no chirality outliers.

All (8) torsion outliers are listed below:

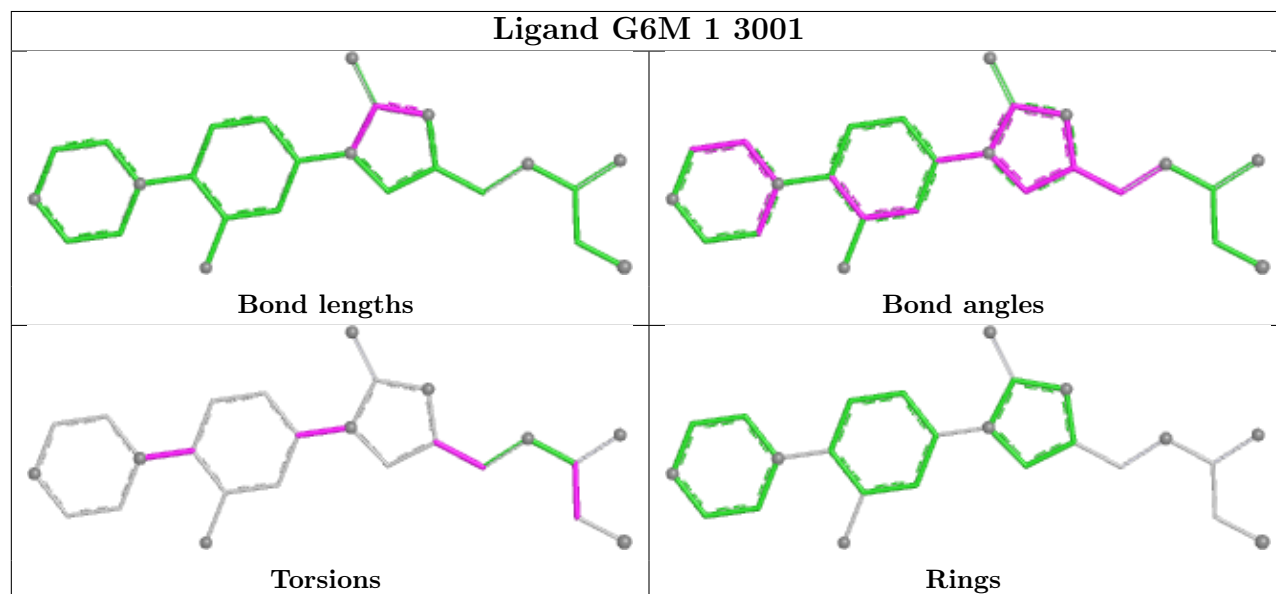
Mol	Chain	Res	Type	Atoms
28	1	3001	G6M	C2-C1-N14-C15
28	1	3001	G6M	N29-C30-C31-CL33
28	1	3001	G6M	O32-C30-C31-CL33
28	1	3001	G6M	C3-C4-N8-C12
28	1	3001	G6M	C6-C1-N14-C15
28	1	3001	G6M	C5-C4-N8-C12
28	1	3001	G6M	C9-C10-C20-N29
28	1	3001	G6M	C2-C1-N14-C19

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

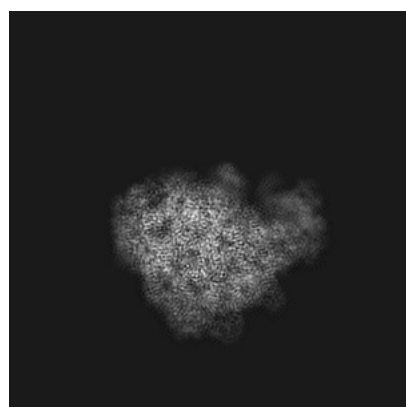
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7870. These allow visual inspection of the internal detail of the map and identification of artifacts.

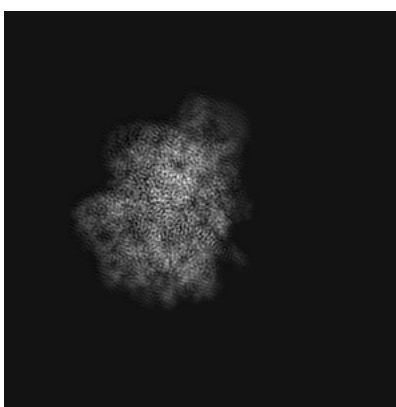
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

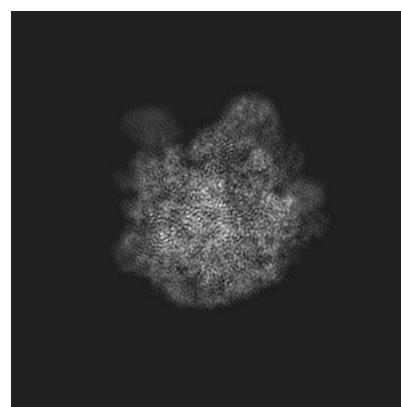
#### 6.1.1 Primary map



X



Y



Z

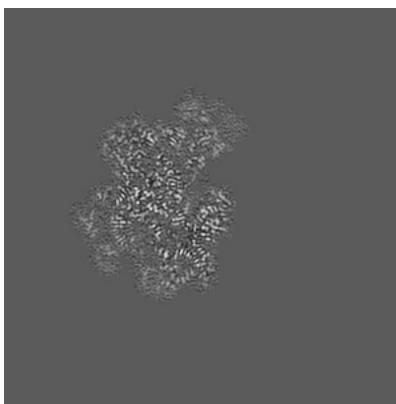
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

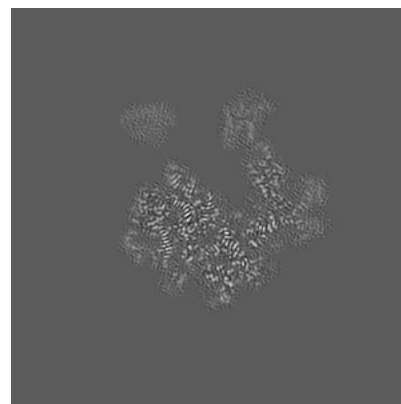
#### 6.2.1 Primary map



X Index: 182



Y Index: 182



Z Index: 182

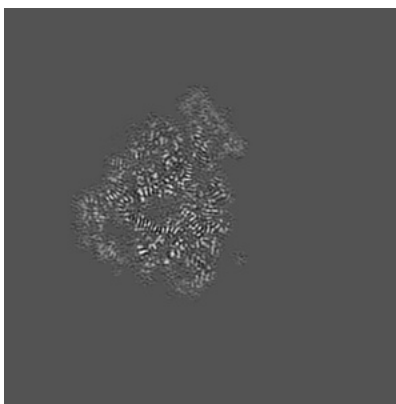
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

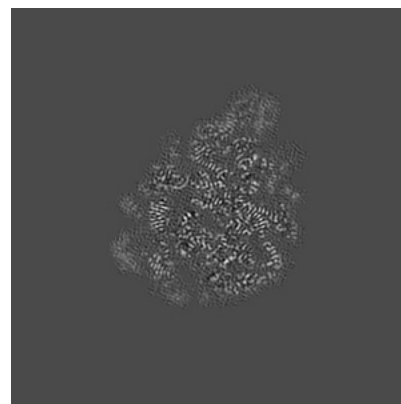
### 6.3.1 Primary map



X Index: 190



Y Index: 165

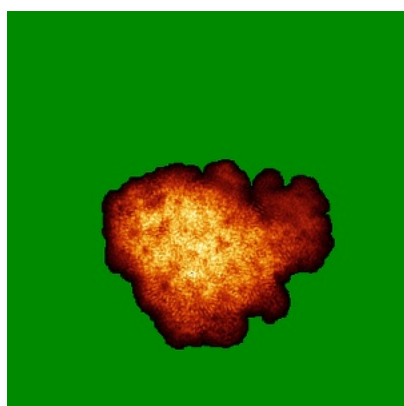


Z Index: 147

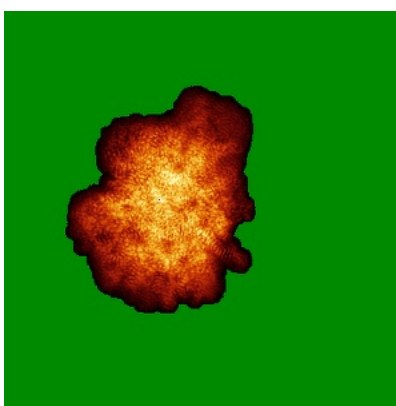
The images above show the largest variance slices of the map in three orthogonal directions.

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

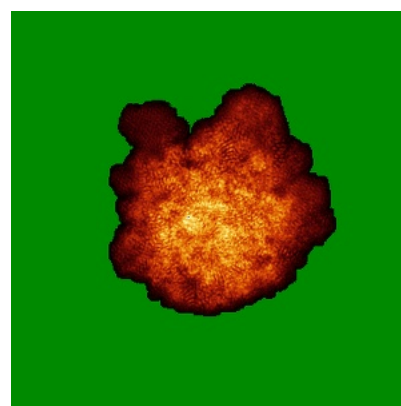
### 6.4.1 Primary map



X



Y

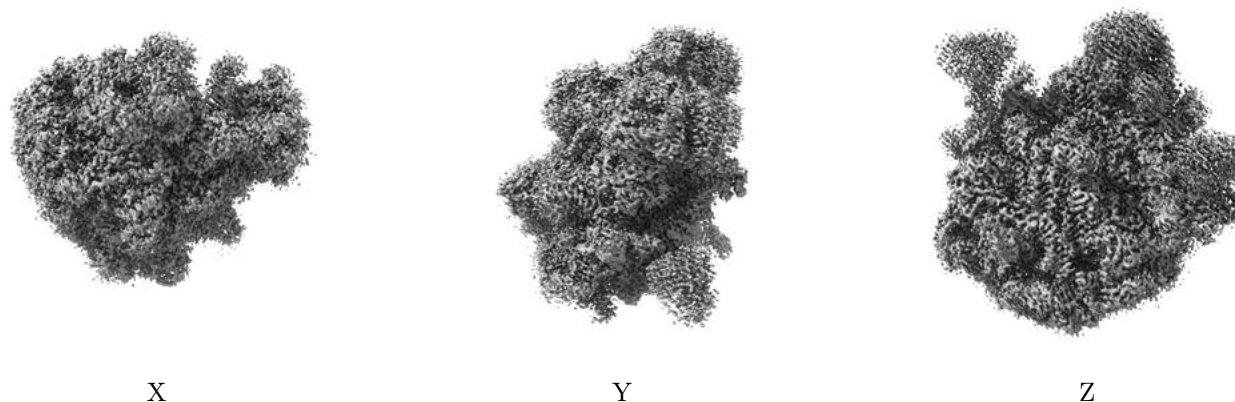


Z

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

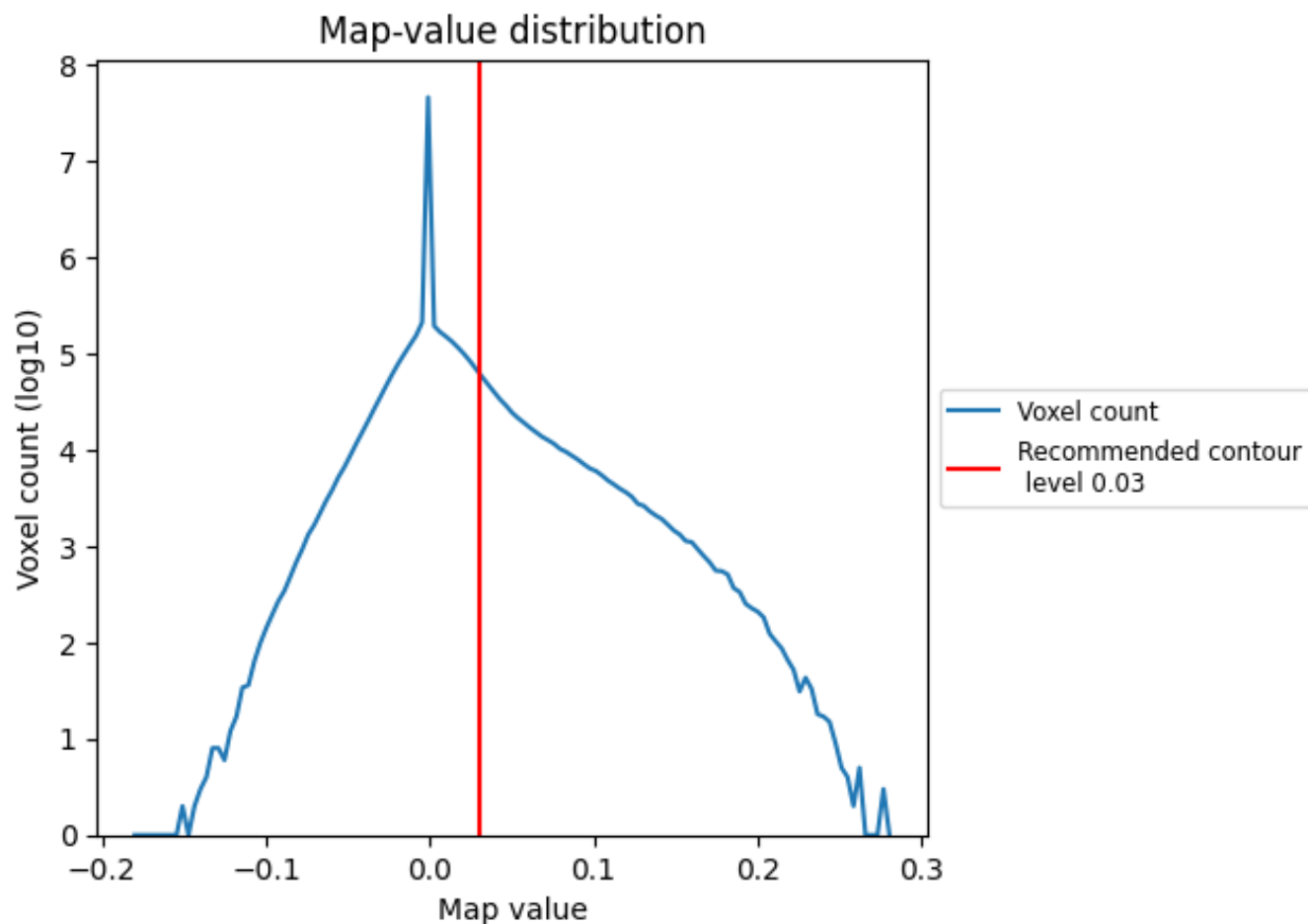
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

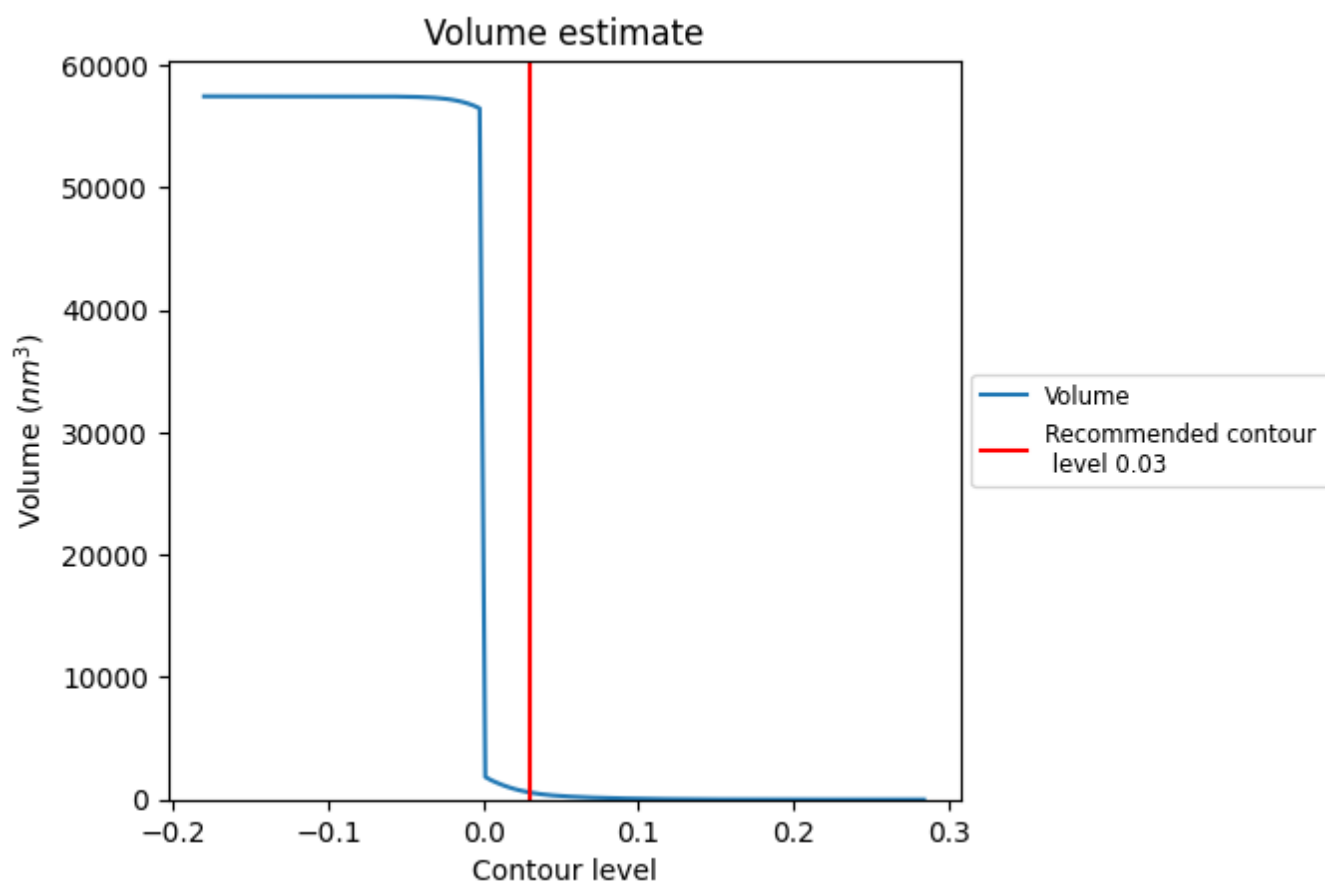
This section contains the results of statistical analysis of the map.

### 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.

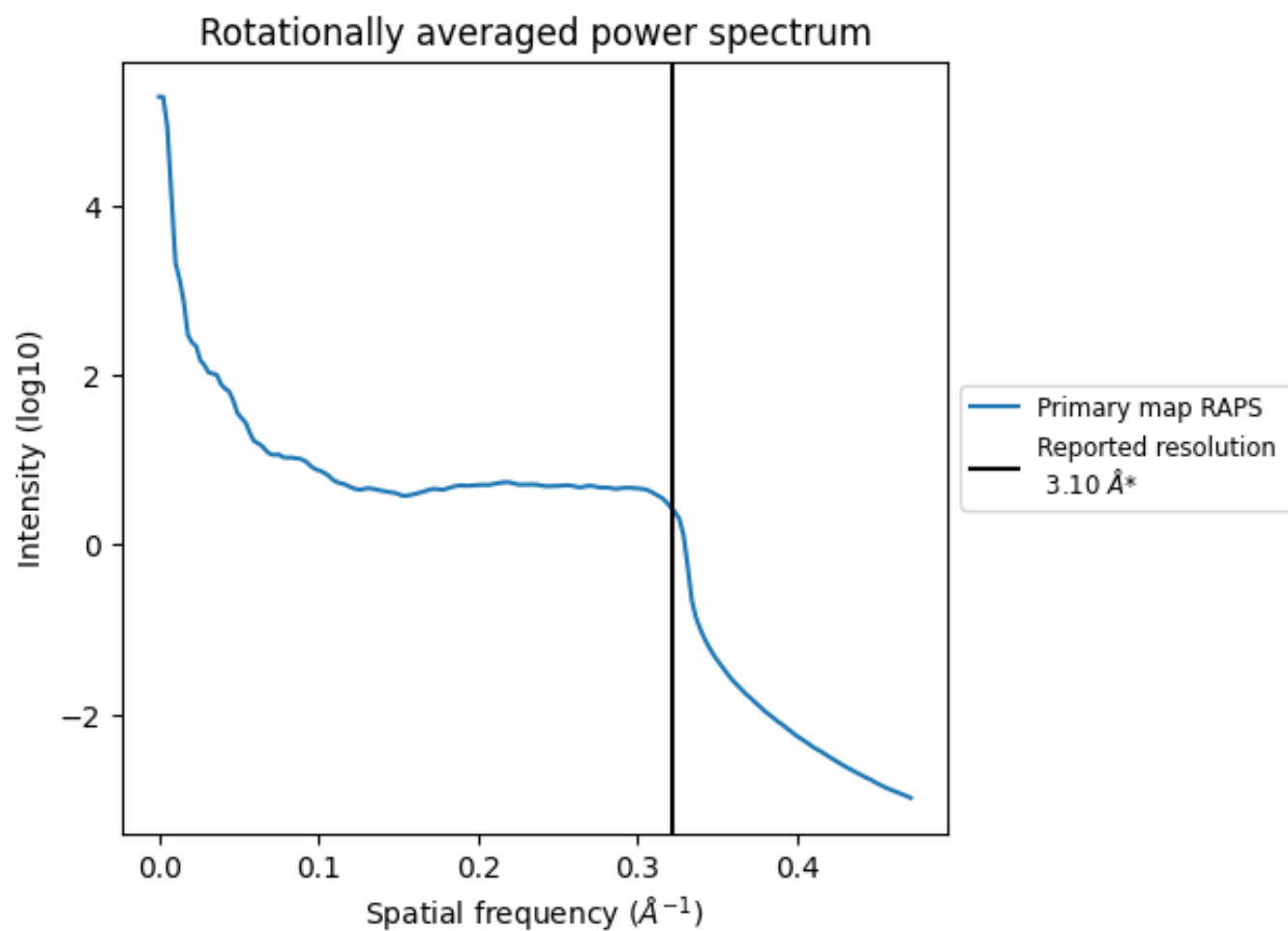
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 573 nm<sup>3</sup>; this corresponds to an approximate mass of 518 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<sup>-1</sup>

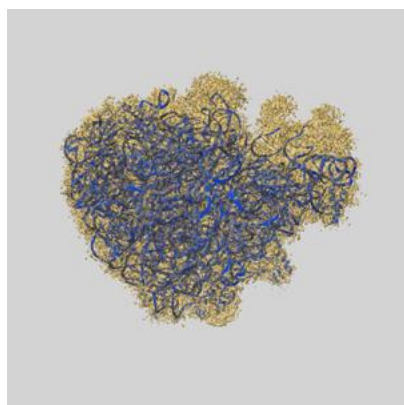
## 8 Fourier-Shell correlation ⓘ

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

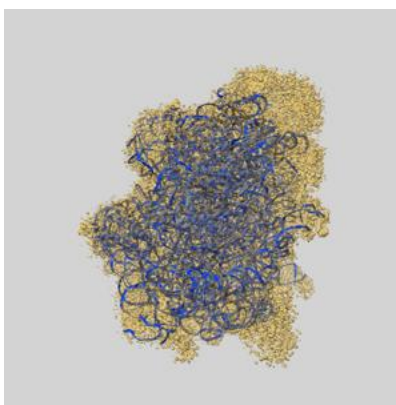
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7870 and PDB model 6DDG. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

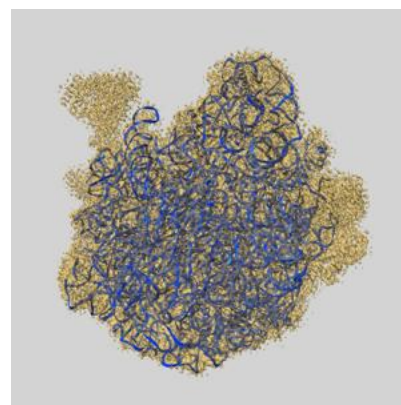
### 9.1 Map-model overlay [i](#)



X



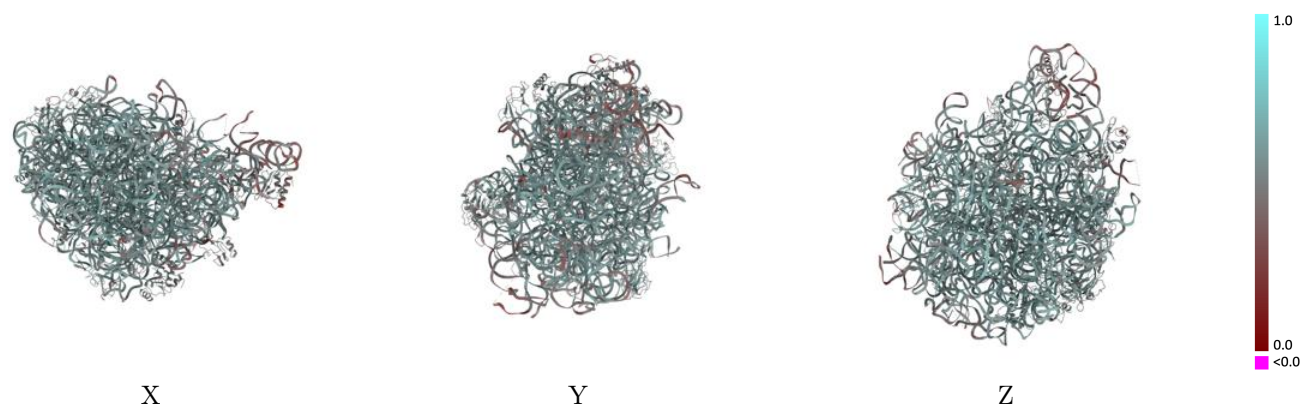
Y



Z

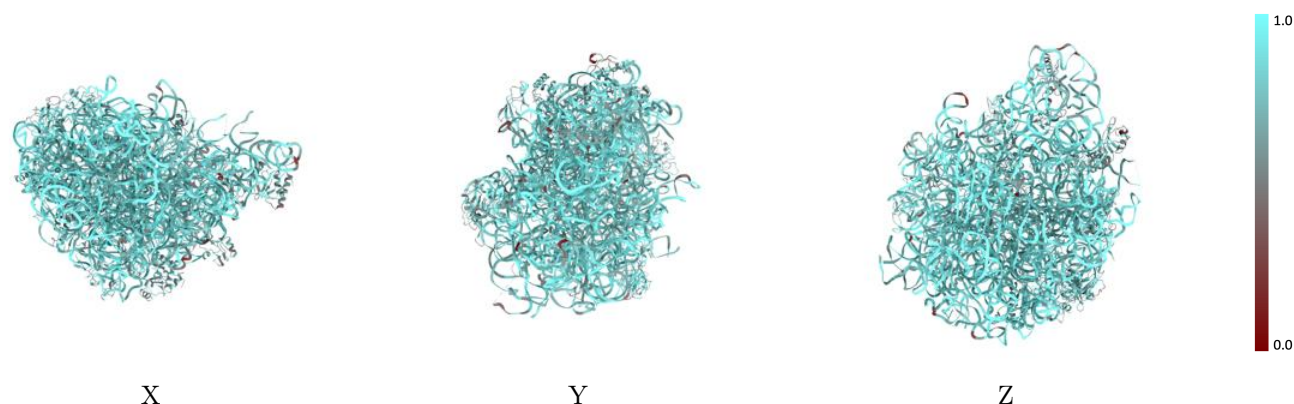
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



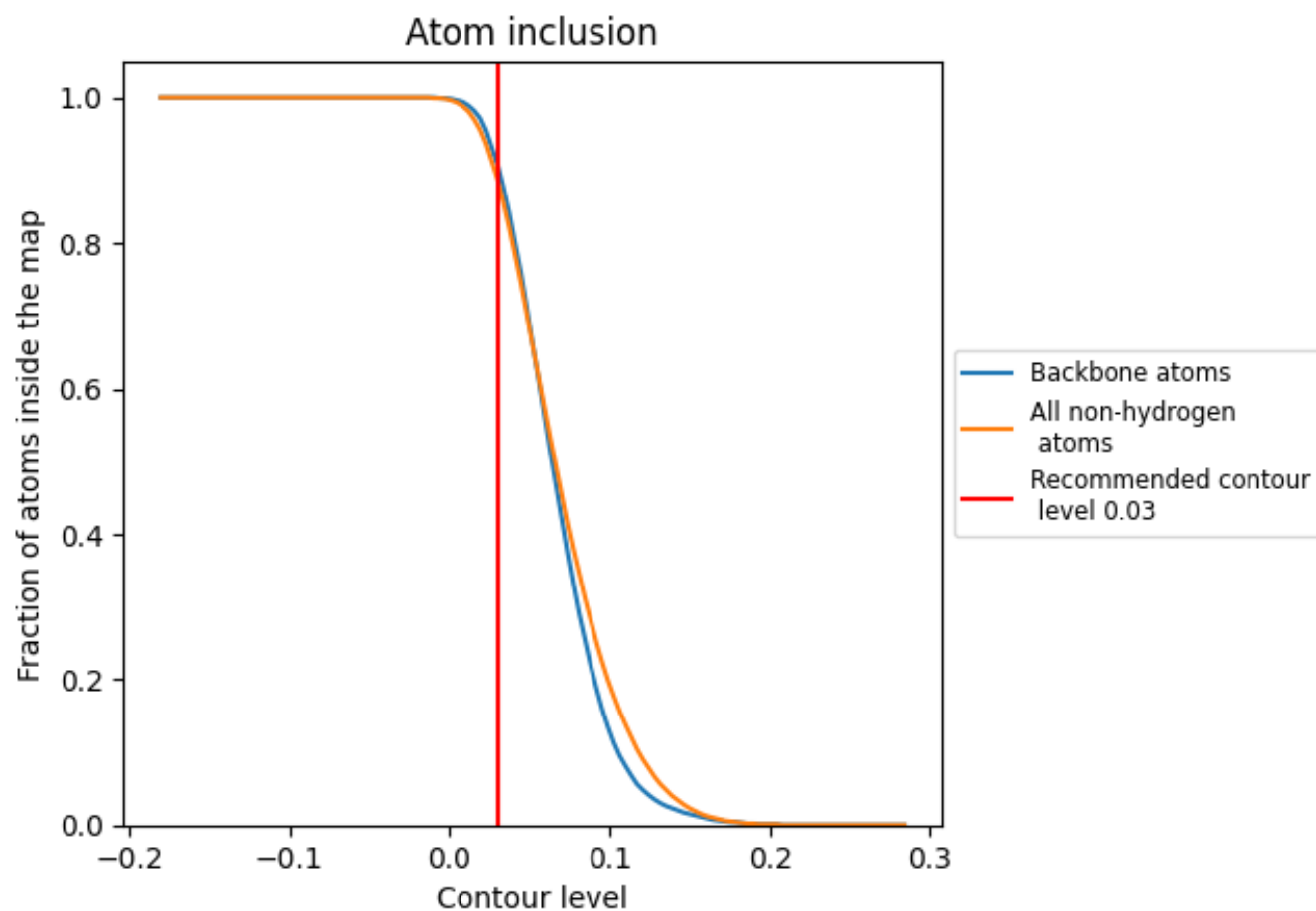
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

























































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 89% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8890	 0.5620
1	 0.9260	 0.5750
2	 0.7980	 0.4590
A	 0.7610	 0.5240
B	 0.8470	 0.5660
C	 0.8500	 0.5520
D	 0.7850	 0.5340
E	 0.8290	 0.5570
F	 0.7810	 0.5300
G	 0.6840	 0.4880
H	 0.6180	 0.4720
I	 0.8220	 0.5510
J	 0.7690	 0.5420
K	 0.7290	 0.4980
L	 0.8300	 0.5530
M	 0.8280	 0.5520
N	 0.8560	 0.5690
O	 0.7530	 0.5010
P	 0.8830	 0.6010
Q	 0.8800	 0.5810
R	 0.8280	 0.5470
S	 0.7750	 0.5310
V	 0.8390	 0.5560
W	 0.7950	 0.5410
X	 0.7900	 0.5270
Y	 0.8120	 0.5460
Z	 0.8070	 0.5440
a	 0.6630	 0.4430

