



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 03:34 AM UTC

PDB ID : 2OM7 / pdb_00002om7
EMDB ID : EMD-1315
Title : Structural Basis for Interaction of the Ribosome with the Switch Regions of GTP-bound Elongation Factors
Authors : Connell, S.R.; Wilson, D.N.; Rost, M.; Schueler, M.; Giesebrecht, J.; Dabrowski, M.; Mielke, T.; Fucini, P.; Spahn, C.M.T.
Deposited on : 2007-01-21
Resolution : 7.30 Å (reported)
Based on initial models : 1GIX, 1YL3, 1FNM, 2J00, 2J01

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

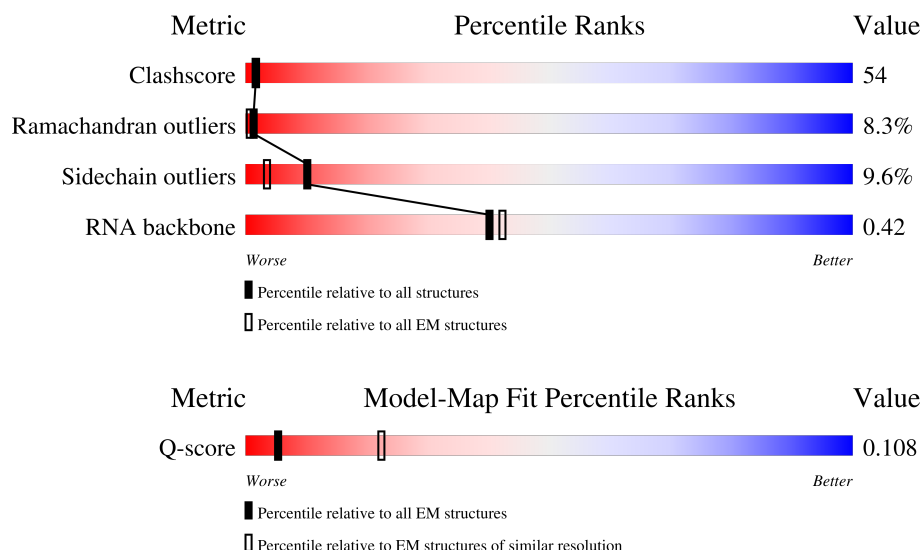
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 7.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



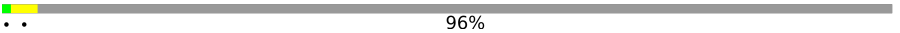
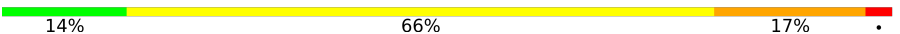
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	436 (6.80 - 7.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	12	
2	B	28	
3	C	96	

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Mol	Chain	Length	Quality of chain
4	D	303	 96%
5	F	29	 14% 66% 17%
6	G	54	 35% 43% 22%
7	H	42	 43% 38% 19%
8	I	58	 34% 45% 19%
9	J	102	 16% 29% 25% 28%
10	M	74	 11% 36% 32% 20%
11	E	135	 31% 43% 17% 7%
12	K	229	 40% 33% 13% 17%
13	L	691	 17% 44% 44% 6% 5%
14	N	256	 27% 54% 18% 8%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	4SU	M	8	-	-	X	-

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 19031 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called Fragment of 16S rRNA (h14).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	12	Total	C	N	O	P	0	0
			256	114	46	84	12		

- Molecule 2 is a RNA chain called Fragment of 16S rRNA (h15).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	10	Total	C	N	O	P	0	0
			214	95	38	71	10		

- Molecule 3 is a RNA chain called Fragment of 16S rRNA (h44).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	96	Total	C	N	O	P	0	0
			2069	919	387	667	96		

- Molecule 4 is a RNA chain called 16S ribosomal RNA (H5).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	13	Total	C	N	O	P	0	0
			278	124	50	91	13		

- Molecule 5 is a RNA chain called Fragment of 23S rRNA (H95).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	29	Total	C	N	O	P	0	0
			624	278	116	201	29		

- Molecule 6 is a RNA chain called Fragment of 23S rRNA (H68).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	54	Total	C	N	O	P	0	0
			1172	521	228	369	54		

- Molecule 7 is a RNA chain called Fragment of23S rRNA (H89).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	42	Total	C	N	O	P	0	0
			898	399	161	296	42		

- Molecule 8 is a RNA chain called Fragment of23S rRNA (H42-44).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	58	Total	C	N	O	P	0	0
			1241	554	224	405	58		

- Molecule 9 is a RNA chain called Fragment of23S rRNA (H76).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	73	Total	C	N	O	P	0	0
			1569	696	284	516	73		

- Molecule 10 is a RNA chain called p/E-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	M	74	Total	C	N	O	P	S	0	0
			1570	702	269	524	74	1		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	125	Total	C	N	O	S	0	1
			971	611	196	163	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	2	VAL	-	insertion	UNP P17293
E	3	ALA	-	insertion	UNP P17293
E	4	LEU	-	insertion	UNP P17293

- Molecule 12 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	K	191	Total	C	N	O	0	1
			1142	691	221	230		

- Molecule 13 is a protein called Elongation factor G.

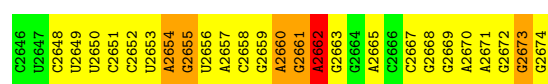
Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	655	Total	C	N	O	S	0	0
			5126	3259	874	975	18		

- Molecule 14 is a protein called 30S ribosomal protein S2.

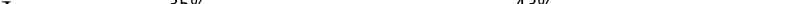
Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	235	Total	C	N	O	S	0	1
			1901	1213	342	341	5		

- Molecule 5: Fragment of 23S rRNA (H95)

Chain F: 14% 66% 17% .

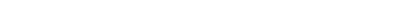


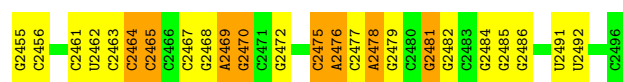
- Molecule 6: Fragment of 23S rRNA (H68)

Chain G: 

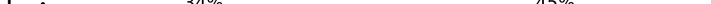


- Molecule 7: Fragment of 23S rRNA (H89)

Chain H:  43% 38% 19%

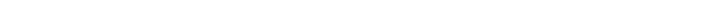


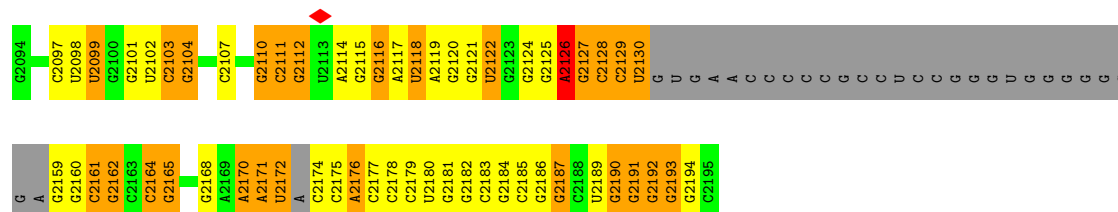
- Molecule 8: Fragment of 23S rRNA (H42-44)

Chain I:  34% 45% 19%

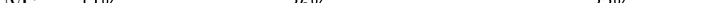


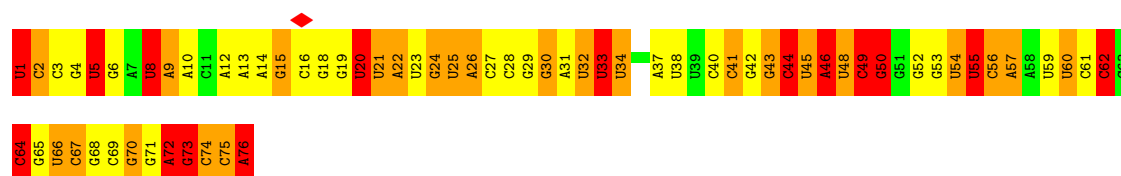
- Molecule 9: Fragment of 23S rRNA (H76)

Chain J: 



- Molecule 10: p/E-tRNA

Chain M:  11% 36% 32% 20%



• Molecule 11: 30S ribosomal protein S12

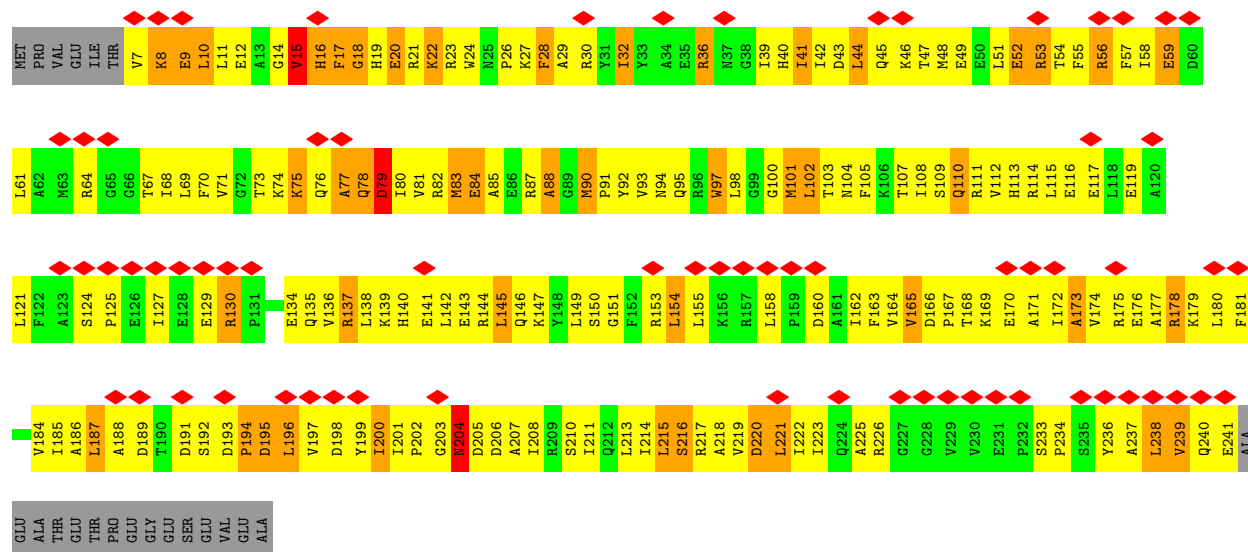


• Molecule 12: 50S ribosomal protein L1



• Molecule 13: Elongation factor G





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	77038	Depositor
Resolution determination method	Not provided	
CTF correction method	defocus groups	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	19	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	11069.200	Depositor
Minimum map value	-4968.550	Depositor
Average map value	-29.848	Depositor
Map value standard deviation	976.693	Depositor
Recommended contour level	1820	Depositor
Map size ($\text{\AA}$)	378, 378, 378	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	1.26, 1.26, 1.26	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 4SU, PSU, 5MC, 5MU, H2U

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	0.55	0/285	0.63	0/442
2	B	0.56	0/237	0.65	0/365
3	C	0.60	0/2315	0.71	3/3613 (0.1%)
4	D	0.61	0/309	0.65	0/477
5	F	0.56	0/698	0.74	1/1087 (0.1%)
6	G	0.61	0/1314	0.74	1/2051 (0.0%)
7	H	0.57	0/1002	0.70	1/1561 (0.1%)
8	I	0.76	2/1388 (0.1%)	1.12	10/2162 (0.5%)
9	J	0.50	0/1753	0.70	2/2735 (0.1%)
10	M	1.55	15/1616 (0.9%)	2.26	64/2512 (2.5%)
11	E	0.68	1/987 (0.1%)	1.09	5/1322 (0.4%)
12	K	0.65	1/1145 (0.1%)	1.07	12/1556 (0.8%)
13	L	0.70	1/5219 (0.0%)	1.18	33/7063 (0.5%)
14	N	0.60	1/1936 (0.1%)	0.93	5/2611 (0.2%)
All	All	0.75	21/20204 (0.1%)	1.12	137/29557 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
3	C	0	7
5	F	1	0
7	H	0	1
8	I	0	5
9	J	1	0
All	All	2	14

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	M	33	U	O3'-P	24.81	1.98	1.61
10	M	15	G	O3'-P	18.83	1.89	1.61
10	M	26	A	O3'-P	-18.60	1.33	1.61
10	M	24	G	O3'-P	15.21	1.83	1.61
10	M	56	C	O3'-P	14.12	1.82	1.61
10	M	25	U	O3'-P	13.32	1.81	1.61
10	M	21	H2U	O3'-P	-10.95	1.44	1.61
10	M	46	A	O3'-P	10.75	1.77	1.61
10	M	8	4SU	O3'-P	-9.31	1.50	1.61
10	M	72	A	O3'-P	8.53	1.74	1.61
10	M	45	U	O3'-P	-8.37	1.48	1.61
8	I	1083	U	C3'-O3'	7.09	1.52	1.42
10	M	75	C	O3'-P	-6.72	1.51	1.61
10	M	1	U	OP3-P	6.59	1.61	1.48
10	M	73	G	O3'-P	-6.47	1.51	1.61
8	I	1083	U	O3'-P	6.20	1.70	1.61
13	L	139	MET	SD-CE	-6.11	1.64	1.79
11	E	128	ALA	C-N	-5.51	1.25	1.33
10	M	55	PSU	O3'-P	5.48	1.69	1.61
12	K	223	ARG	C-N	-5.46	1.25	1.33
14	N	240	GLN	C-N	-5.10	1.26	1.33

All (137) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	L	600	VAL	O-C-N	-27.72	92.28	123.05
10	M	15	G	O3'-P-O5'	27.12	144.68	104.00
10	M	8	4SU	O3'-P-O5'	-27.02	52.65	104.00
10	M	25	U	P-O3'-C3'	24.67	157.21	120.20
10	M	31	A	O3'-P-O5'	-24.23	67.66	104.00
10	M	75	C	P-O3'-C3'	-24.03	84.16	120.20
10	M	40	C	O3'-P-O5'	-22.50	70.24	104.00
10	M	44	C	O3'-P-O5'	22.50	137.75	104.00
10	M	24	G	P-O3'-C3'	-20.13	90.00	120.20
10	M	15	G	P-O3'-C3'	19.20	149.00	120.20
13	L	600	VAL	CA-C-N	17.83	154.06	121.97
13	L	600	VAL	C-N-CA	17.83	154.06	121.97
13	L	530	VAL	N-CA-C	17.32	126.67	112.12
10	M	31	A	OP2-P-O3'	16.24	156.73	108.00
10	M	8	4SU	OP1-P-O3'	15.56	139.43	105.20
10	M	75	C	O3'-P-O5'	14.99	126.49	104.00
10	M	40	C	OP2-P-O3'	14.82	152.47	108.00
10	M	8	4SU	P-O3'-C3'	-13.09	104.00	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	M	72	A	P-O3'-C3'	12.60	139.09	120.20
3	C	1498	U	C2'-C3'-O3'	12.52	128.28	109.50
10	M	16	C	P-O3'-C3'	12.15	138.42	120.20
10	M	29	G	O3'-P-O5'	11.43	121.14	104.00
10	M	32	U	O3'-P-O5'	11.23	120.85	104.00
10	M	29	G	OP1-P-O3'	-11.10	74.70	108.00
10	M	32	U	OP1-P-O3'	-10.72	75.84	108.00
10	M	33	U	P-O3'-C3'	10.36	135.74	120.20
8	I	1084	A	O5'-P-OP2	-9.83	78.50	108.00
10	M	44	C	P-O3'-C3'	-9.46	106.01	120.20
13	L	532	GLY	N-CA-C	-9.44	100.37	114.90
10	M	21	H2U	O3'-P-O5'	8.98	117.46	104.00
10	M	31	A	OP1-P-O3'	-8.81	81.56	108.00
10	M	56	C	P-O3'-C3'	-8.77	107.05	120.20
10	M	1	U	P-O3'-C3'	8.69	133.23	120.20
10	M	26	A	O3'-P-O5'	8.46	116.70	104.00
9	J	2191	G	C2'-C3'-O3'	8.45	126.37	113.70
10	M	75	C	P-O5'-C5'	-8.38	108.32	120.90
10	M	40	C	OP1-P-O3'	-8.24	83.29	108.00
8	I	1084	A	C5'-C4'-C3'	-8.00	104.00	116.00
5	F	2662	A	N9-C1'-C2'	7.88	123.82	112.00
10	M	75	C	OP1-P-O3'	-7.88	84.38	108.00
10	M	42	G	O3'-P-O5'	7.82	115.72	104.00
10	M	25	U	O3'-P-O5'	-7.78	92.33	104.00
10	M	42	G	OP1-P-O3'	-7.67	84.99	108.00
13	L	169	GLY	N-CA-C	-7.65	103.72	112.29
14	N	160	ASP	N-CA-C	-7.56	104.08	113.38
8	I	1083	U	O3'-P-O5'	7.54	115.30	104.00
10	M	74	C	P-O3'-C3'	-7.53	108.91	120.20
10	M	27	C	OP1-P-O3'	-7.51	85.47	108.00
11	E	119	LYS	N-CA-C	-7.50	98.36	110.20
13	L	591	LYS	N-CA-C	-7.45	103.16	111.28
10	M	28	C	O3'-P-O5'	7.41	115.11	104.00
13	L	280	LEU	CA-C-N	7.40	127.40	119.78
13	L	280	LEU	C-N-CA	7.40	127.40	119.78
10	M	46	A	OP2-P-O3'	-7.16	86.51	108.00
12	K	174	PRO	N-CA-CB	7.11	110.71	103.25
10	M	46	A	OP1-P-O3'	7.08	129.24	108.00
10	M	21	H2U	P-O3'-C3'	7.02	130.74	120.20
10	M	46	A	P-O3'-C3'	-6.90	109.85	120.20
10	M	28	C	OP1-P-O3'	-6.89	87.34	108.00
12	K	39	GLU	N-CA-C	-6.88	104.91	113.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	200	ILE	N-CA-C	6.88	118.75	108.23
13	L	529	ILE	CA-C-N	-6.81	115.62	122.77
13	L	529	ILE	C-N-CA	-6.81	115.62	122.77
13	L	419	ALA	N-CA-C	-6.79	103.97	111.36
11	E	118	SER	N-CA-C	-6.78	103.13	111.33
10	M	29	G	C5'-C4'-C3'	-6.73	105.91	116.00
10	M	44	C	OP1-P-O3'	-6.66	88.01	108.00
10	M	15	G	OP2-P-O3'	-6.65	88.06	108.00
9	J	2126	A	C2'-C3'-O3'	6.64	119.45	109.50
10	M	15	G	OP1-P-O3'	-6.54	88.39	108.00
8	I	1105	U	N1-C1'-C2'	6.49	121.73	112.00
10	M	33	U	OP2-P-O3'	-6.48	88.57	108.00
11	E	26	ALA	N-CA-C	-6.47	105.25	112.57
13	L	109	ASP	N-CA-C	-6.42	98.71	108.67
12	K	133	PRO	N-CA-CB	6.38	109.95	103.25
11	E	58	VAL	N-CA-C	6.28	117.34	108.17
12	K	181	PRO	N-CA-CB	6.24	109.13	103.08
10	M	50	G	O5'-C5'-C4'	-6.23	102.15	111.50
10	M	33	U	OP1-P-O3'	6.21	126.62	108.00
13	L	608	VAL	N-CA-C	6.19	116.78	108.11
13	L	156	ARG	N-CA-C	6.16	117.66	111.07
14	N	173	ALA	N-CA-C	-6.16	104.26	110.97
12	K	220	PRO	N-CA-CB	6.15	109.71	103.25
13	L	530	VAL	CB-CA-C	-6.15	104.88	110.91
13	L	645	ALA	N-CA-C	6.13	117.56	108.60
12	K	201	PRO	N-CA-CB	6.08	109.64	103.25
13	L	281	PRO	N-CA-C	6.06	120.85	111.21
13	L	282	SER	N-CA-C	-6.04	101.16	110.58
8	I	1103	A	C2'-C3'-O3'	-6.01	104.69	113.70
8	I	1085	A	N9-C1'-C2'	5.98	122.97	114.00
12	K	182	PRO	N-CA-CB	5.97	109.51	103.25
10	M	32	U	O4'-C1'-N1	5.95	117.42	108.50
12	K	102	LYS	N-CA-C	-5.93	105.71	113.12
6	G	1899	G	C4'-C3'-O3'	-5.85	104.23	113.00
10	M	41	C	P-O5'-C5'	5.83	129.65	120.90
8	I	1083	U	C4'-C3'-O3'	5.81	121.72	113.00
13	L	205	TYR	N-CA-C	-5.78	104.94	113.61
12	K	50	ASP	N-CA-C	5.77	117.26	109.24
8	I	1104	C	C5'-C4'-C3'	5.76	124.64	116.00
12	K	140	PRO	N-CA-CB	5.69	109.22	103.25
13	L	289	ILE	N-CA-C	-5.68	103.79	110.21
10	M	66	U	O5'-C5'-C4'	-5.67	103.00	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	L	179	ASP	N-CA-C	-5.64	100.62	109.25
13	L	214	GLU	N-CA-C	-5.64	105.03	111.07
10	M	57	A	P-O3'-C3'	5.60	128.60	120.20
8	I	1059	G	N9-C1'-C2'	-5.57	103.65	112.00
13	L	357	ARG	N-CA-C	-5.54	100.15	109.07
10	M	67	C	O5'-C5'-C4'	-5.50	103.25	111.50
10	M	76	A	C3'-C2'-O2'	-5.45	106.42	114.60
10	M	64	C	P-O3'-C3'	-5.45	112.03	120.20
14	N	56	ARG	N-CA-C	-5.44	104.38	111.02
10	M	24	G	O3'-P-O5'	5.42	112.13	104.00
8	I	1070	A	N9-C1'-C2'	5.41	120.11	112.00
13	L	148	LEU	N-CA-C	-5.37	105.59	111.82
10	M	43	G	O3'-P-O5'	5.34	112.01	104.00
10	M	60	U	P-O3'-C3'	-5.33	112.20	120.20
13	L	679	VAL	CA-C-N	5.33	125.32	119.89
13	L	679	VAL	C-N-CA	5.33	125.32	119.89
10	M	30	G	C1'-O4'-C4'	-5.32	104.58	109.90
10	M	61	C	O5'-C5'-C4'	-5.32	103.53	111.50
13	L	416	LYS	N-CA-C	5.24	119.67	113.28
12	K	129	ARG	N-CA-C	-5.21	106.76	113.01
12	K	197	GLU	N-CA-C	-5.20	106.63	112.87
3	C	1492	A	N9-C1'-C2'	5.19	119.78	112.00
13	L	393	ASP	N-CA-C	-5.14	104.47	111.56
14	N	220	ASP	N-CA-C	-5.10	104.80	111.02
7	H	2475	C	N1-C1'-C2'	5.08	119.62	112.00
11	E	7	ILE	N-CA-C	-5.08	105.37	110.30
10	M	29	G	OP2-P-O3'	5.07	123.21	108.00
3	C	1473	A	C3'-C2'-O2'	5.05	118.28	110.70
10	M	5	U	P-O3'-C3'	5.03	127.74	120.20
10	M	42	G	C1'-O4'-C4'	-5.03	104.87	109.90
13	L	663	THR	N-CA-C	-5.03	106.46	112.59
13	L	552	SER	N-CA-C	5.02	115.73	107.20
13	L	293	THR	CA-C-N	-5.01	114.44	119.56
13	L	293	THR	C-N-CA	-5.01	114.44	119.56
10	M	62	C	N1-C1'-C2'	-5.00	104.50	112.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	F	2662	A	C1'
9	J	2191	G	C3'

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	371	G	Sidechain
3	C	1407	C	Sidechain
3	C	1417	G	Sidechain
3	C	1418	A	Sidechain
3	C	1434	A	Sidechain
3	C	1463	C	Sidechain
3	C	1474	G	Sidechain
3	C	1485	U	Sidechain
7	H	2464	C	Sidechain
8	I	1059	G	Sidechain
8	I	1091	G	Sidechain
8	I	1092	C	Sidechain
8	I	1093	G	Sidechain
8	I	1101	U	Sidechain

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	256	0	131	5	0
2	B	214	0	110	24	0
3	C	2069	0	1046	86	0
4	D	278	0	141	28	0
5	F	624	0	314	86	0
6	G	1172	0	591	47	0
7	H	898	0	456	20	0
8	I	1241	0	625	316	0
9	J	1569	0	790	79	0
10	M	1570	0	800	109	0
11	E	971	0	1057	113	0
12	K	1142	0	865	117	0
13	L	5126	0	5164	647	0
14	N	1901	0	1951	261	0
All	All	19031	0	14041	1771	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 54.

All (1771) 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)
4:D:55:A:C2	13:L:322:VAL:HG12	1.22	1.75
13:L:556:ILE:CD1	13:L:601:ILE:HD13	1.28	1.64
13:L:408:VAL:CG1	13:L:669:PHE:HE1	1.12	1.57
5:F:2661:G:N1	13:L:20:HIS:CE1	1.72	1.54
2:B:368:U:C5	13:L:354:ARG:CD	1.92	1.52
2:B:368:U:C5	13:L:354:ARG:HD2	1.00	1.51
5:F:2662:A:H61	13:L:21:ILE:CD1	1.22	1.49
13:L:594:VAL:CG1	13:L:599:PRO:HB3	1.38	1.49
13:L:484:ARG:HB3	13:L:606:MET:CG	1.41	1.48
13:L:484:ARG:NE	13:L:649:LEU:CD1	1.73	1.47
13:L:484:ARG:NH2	13:L:671:MET:HE1	1.20	1.47
13:L:408:VAL:CG1	13:L:669:PHE:CE1	1.95	1.47
4:D:55:A:H2	13:L:322:VAL:CG1	1.24	1.45
13:L:484:ARG:HH21	13:L:671:MET:CE	1.26	1.45
9:J:2168:G:N2	10:M:56:C:N3	1.63	1.41
13:L:484:ARG:CA	13:L:649:LEU:HA	1.48	1.41
8:I:1095:A:C5'	13:L:617:MET:HB3	1.45	1.40
13:L:408:VAL:HG12	13:L:669:PHE:CE1	1.54	1.39
13:L:484:ARG:HB3	13:L:606:MET:CB	1.49	1.39
5:F:2662:A:C6	13:L:21:ILE:HG12	1.57	1.39
5:F:2660:A:C2'	13:L:660:ARG:HG3	1.52	1.39
5:F:2662:A:N1	13:L:21:ILE:HG12	1.31	1.39
4:D:55:A:C2	13:L:322:VAL:CG1	1.97	1.37
13:L:484:ARG:HA	13:L:649:LEU:CA	1.53	1.34
5:F:2662:A:N6	13:L:21:ILE:HD11	1.36	1.33
5:F:2661:G:N1	13:L:20:HIS:HE1	0.86	1.32
13:L:406:GLU:HG3	13:L:669:PHE:O	1.24	1.31
13:L:484:ARG:NE	13:L:649:LEU:HD12	0.98	1.31
13:L:484:ARG:C	13:L:648:PRO:C	1.84	1.31
5:F:2662:A:N6	13:L:21:ILE:CG1	1.94	1.30
8:I:1067:A:O2'	13:L:634:MET:N	1.61	1.29
13:L:406:GLU:OE2	13:L:671:MET:N	1.61	1.29
10:M:75:C:C2'	10:M:76:A:H5'	1.59	1.28
13:L:486:THR:HG22	13:L:600:VAL:CG1	1.62	1.28
4:D:55:A:H1'	13:L:321:TYR:CA	1.36	1.28
13:L:485:GLU:N	13:L:649:LEU:N	1.61	1.28
10:M:75:C:H2'	10:M:76:A:C5'	1.62	1.28
5:F:2660:A:H2'	13:L:660:ARG:CG	1.62	1.27
5:F:2662:A:N6	13:L:21:ILE:CD1	1.92	1.27
13:L:406:GLU:OE2	13:L:670:VAL:CA	1.82	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:485:GLU:CA	13:L:647:VAL:O	1.83	1.25
13:L:556:ILE:CG1	13:L:601:ILE:HD13	1.66	1.25
13:L:556:ILE:HG12	13:L:601:ILE:CD1	1.66	1.24
8:I:1095:A:H5'	13:L:617:MET:CB	1.45	1.24
13:L:127:LYS:NZ	13:L:402:ILE:HG13	1.47	1.24
5:F:2662:A:H61	13:L:21:ILE:CG1	1.50	1.24
13:L:484:ARG:O	13:L:647:VAL:HG22	1.22	1.24
13:L:556:ILE:HD11	13:L:601:ILE:CG2	1.66	1.23
13:L:594:VAL:CG1	13:L:599:PRO:CB	2.14	1.23
5:F:2662:A:C6	13:L:21:ILE:CG1	2.21	1.23
13:L:485:GLU:HB2	13:L:604:PRO:O	1.38	1.22
5:F:2661:G:C2	13:L:20:HIS:HE1	1.59	1.21
10:M:33:U:O3'	10:M:34:U:P	1.98	1.21
13:L:485:GLU:HB3	13:L:605:ILE:CD1	1.69	1.20
13:L:127:LYS:CE	13:L:402:ILE:HG13	1.68	1.20
13:L:406:GLU:CD	13:L:670:VAL:HA	1.67	1.20
8:I:1095:A:C2	13:L:614:GLU:OE1	1.94	1.20
13:L:406:GLU:CG	13:L:670:VAL:HA	1.72	1.19
13:L:406:GLU:OE2	13:L:670:VAL:C	1.83	1.19
8:I:1095:A:N1	13:L:614:GLU:OE1	1.75	1.18
13:L:594:VAL:HG13	13:L:599:PRO:CB	1.72	1.18
5:F:2662:A:N1	13:L:21:ILE:CG1	2.05	1.18
13:L:484:ARG:O	13:L:647:VAL:C	1.86	1.18
13:L:486:THR:N	13:L:600:VAL:O	1.76	1.17
13:L:124:GLN:HE22	13:L:401:SER:CB	1.57	1.17
13:L:556:ILE:CG1	13:L:601:ILE:CD1	2.21	1.17
13:L:485:GLU:HB3	13:L:605:ILE:HD13	1.16	1.16
13:L:556:ILE:CD1	13:L:601:ILE:CD1	2.24	1.16
13:L:408:VAL:HG12	13:L:669:PHE:CZ	1.78	1.16
13:L:484:ARG:CD	13:L:606:MET:HG3	1.75	1.16
2:B:368:U:H5	13:L:354:ARG:CD	1.39	1.16
13:L:555:LEU:O	13:L:688:ILE:HG23	1.47	1.15
8:I:1095:A:OP1	13:L:617:MET:CB	1.95	1.15
9:J:2175:C:H2'	9:J:2176:A:H5''	1.28	1.14
8:I:1054:A:N6	8:I:1105:U:H3	1.46	1.14
8:I:1085:A:H1'	8:I:1086:A:C4'	1.78	1.13
13:L:484:ARG:CB	13:L:606:MET:HB2	1.79	1.13
8:I:1085:A:H1'	8:I:1086:A:H4'	1.13	1.13
8:I:1095:A:P	13:L:617:MET:HB3	1.88	1.13
13:L:484:ARG:O	13:L:647:VAL:CG2	1.95	1.13
13:L:485:GLU:N	13:L:647:VAL:O	1.81	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:92:ILE:HG21	13:L:436:PRO:HD2	1.28	1.13
13:L:408:VAL:HG11	13:L:669:PHE:HE1	1.00	1.13
13:L:556:ILE:HG22	13:L:688:ILE:CA	1.77	1.13
13:L:484:ARG:HE	13:L:649:LEU:CD1	1.46	1.12
13:L:556:ILE:HG22	13:L:688:ILE:HA	1.18	1.12
5:F:2660:A:C1'	13:L:660:ARG:HG3	1.79	1.11
13:L:406:GLU:CG	13:L:669:PHE:O	1.96	1.11
2:B:368:U:C4	13:L:354:ARG:HD2	1.85	1.11
8:I:1095:A:OP1	13:L:617:MET:HB2	1.49	1.11
13:L:484:ARG:CB	13:L:606:MET:CG	2.28	1.11
3:C:1441:G:H5''	3:C:1442:G:H5''	1.24	1.10
13:L:485:GLU:CB	13:L:605:ILE:HD13	1.82	1.09
3:C:1494:G:O4'	13:L:502:GLY:HA2	1.46	1.09
13:L:484:ARG:HB3	13:L:606:MET:HG3	1.34	1.08
13:L:484:ARG:C	13:L:647:VAL:O	1.96	1.08
13:L:555:LEU:O	13:L:688:ILE:HG12	1.51	1.08
5:F:2660:A:C2'	13:L:660:ARG:CG	2.22	1.08
9:J:2128:C:H2'	9:J:2129:C:H5''	1.29	1.08
5:F:2660:A:H2'	13:L:660:ARG:CD	1.74	1.08
5:F:2660:A:C1'	13:L:665:GLY:N	2.17	1.08
8:I:1061:U:H4'	8:I:1070:A:C1'	1.83	1.08
9:J:2168:G:N2	10:M:56:C:C4	2.22	1.08
13:L:484:ARG:HB3	13:L:606:MET:HB2	1.21	1.08
13:L:406:GLU:OE2	13:L:670:VAL:HA	1.45	1.07
10:M:64:C:H5'	12:K:53:ARG:HH21	0.91	1.06
12:K:58:VAL:HG21	12:K:166:ASP:H	0.97	1.06
14:N:22:LYS:HA	14:N:22:LYS:NZ	1.69	1.06
10:M:64:C:H5'	12:K:53:ARG:NH2	1.70	1.06
13:L:484:ARG:HD3	13:L:606:MET:HG3	1.10	1.05
8:I:1095:A:C5'	13:L:617:MET:CB	2.18	1.05
14:N:22:LYS:HA	14:N:22:LYS:HZ3	1.03	1.05
10:M:73:G:O2'	10:M:74:C:H5'	1.57	1.04
6:G:1884:A:H2'	6:G:1885:A:H5''	1.40	1.04
8:I:1095:A:O5'	13:L:617:MET:HB3	1.55	1.04
13:L:484:ARG:CB	13:L:606:MET:CB	2.34	1.04
13:L:127:LYS:NZ	13:L:402:ILE:CG1	2.14	1.03
13:L:484:ARG:HG2	13:L:652:MET:HG3	1.40	1.03
5:F:2661:G:C2	13:L:20:HIS:CE1	2.40	1.02
13:L:485:GLU:C	13:L:605:ILE:HG23	1.84	1.02
4:D:55:A:C1'	13:L:321:TYR:CA	2.29	1.02
13:L:556:ILE:HD13	13:L:601:ILE:CD1	1.88	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1494:G:O4'	13:L:502:GLY:CA	2.04	1.02
5:F:2660:A:H1'	13:L:665:GLY:CA	1.90	1.02
8:I:1067:A:N7	13:L:631:ILE:O	1.93	1.02
10:M:64:C:C5'	12:K:53:ARG:HH21	1.72	1.02
13:L:484:ARG:C	13:L:649:LEU:N	2.05	1.01
13:L:484:ARG:CB	13:L:606:MET:HG3	1.87	1.01
13:L:556:ILE:CD1	13:L:601:ILE:HG21	1.89	1.01
13:L:486:THR:HG22	13:L:600:VAL:HG12	1.38	1.01
13:L:486:THR:CG2	13:L:600:VAL:HG12	1.90	1.01
7:H:2464:C:HO2'	7:H:2465:C:H6	1.08	1.01
5:F:2660:A:H1'	13:L:665:GLY:N	1.76	1.00
8:I:1061:U:H4'	8:I:1070:A:H1'	1.38	1.00
11:E:46:LYS:HG2	11:E:47:LYS:H	1.19	1.00
4:D:55:A:H1'	13:L:321:TYR:HA	1.04	1.00
9:J:2129:C:H2'	9:J:2130:U:H4'	1.38	1.00
5:F:2660:A:H2'	13:L:660:ARG:HG3	1.12	0.99
10:M:8:4SU:C4'	10:M:49:5MC:H5'	1.92	0.99
13:L:484:ARG:HD3	13:L:606:MET:CG	1.92	0.99
13:L:556:ILE:HD13	13:L:601:ILE:HD13	1.01	0.99
6:G:1879:C:H2'	6:G:1880:C:H5''	1.41	0.99
8:I:1063:G:N2	8:I:1075:C:N3	2.11	0.99
13:L:406:GLU:HG3	13:L:670:VAL:HA	1.34	0.99
5:F:2660:A:C1'	13:L:665:GLY:CA	2.41	0.98
9:J:2103:C:H3'	9:J:2104:G:H5''	1.41	0.98
13:L:556:ILE:HD11	13:L:601:ILE:HG21	1.02	0.98
12:K:58:VAL:HG21	12:K:166:ASP:N	1.78	0.98
13:L:486:THR:O	13:L:600:VAL:N	1.95	0.98
8:I:1065:U:C3'	8:I:1066:U:H5''	1.93	0.98
13:L:482:ALA:HA	13:L:653:PHE:HA	1.45	0.98
5:F:2660:A:O4'	13:L:665:GLY:N	1.97	0.97
14:N:185:ILE:HG22	14:N:199:TYR:HB2	1.45	0.97
13:L:482:ALA:N	13:L:655:TYR:H	1.51	0.97
13:L:594:VAL:HG12	13:L:599:PRO:CB	1.85	0.97
5:F:2662:A:C6	13:L:21:ILE:CD1	2.45	0.97
8:I:1085:A:O2'	8:I:1086:A:O4'	1.81	0.97
13:L:594:VAL:HG12	13:L:599:PRO:HB3	1.34	0.97
8:I:1061:U:C4'	8:I:1070:A:H1'	1.94	0.97
13:L:486:THR:CG2	13:L:600:VAL:CG1	2.41	0.97
12:K:168:THR:HA	12:K:173:ALA:HB2	1.45	0.97
13:L:124:GLN:NE2	13:L:401:SER:OG	1.98	0.97
13:L:484:ARG:CZ	13:L:671:MET:HE1	1.86	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:46:LYS:HE2	12:K:46:LYS:HA	1.46	0.96
9:J:2175:C:C2'	9:J:2176:A:H5''	1.95	0.96
13:L:482:ALA:H	13:L:655:TYR:H	1.10	0.96
13:L:410:ASP:OD1	13:L:653:PHE:HD1	1.47	0.95
8:I:1061:U:H3'	8:I:1061:U:OP2	1.66	0.95
11:E:59:ARG:HH21	13:L:418:LYS:HE3	1.31	0.95
8:I:1067:A:N3	13:L:634:MET:HE1	1.82	0.95
13:L:556:ILE:HG12	13:L:601:ILE:CG1	1.96	0.94
8:I:1087:G:H21	8:I:1103:A:H2'	1.32	0.94
13:L:484:ARG:CZ	13:L:649:LEU:CD1	2.46	0.94
13:L:409:ILE:HD13	13:L:654:GLY:HA2	1.50	0.94
13:L:142:THR:HA	13:L:171:GLU:HG2	1.50	0.94
11:E:47:LYS:HB3	11:E:48:PRO:HD3	1.48	0.94
8:I:1057:A:H61	8:I:1081:U:H3	1.11	0.94
13:L:406:GLU:HG3	13:L:669:PHE:C	1.92	0.94
8:I:1102:C:H1'	8:I:1103:A:C8	2.04	0.93
13:L:485:GLU:C	13:L:647:VAL:O	2.11	0.93
9:J:2128:C:C2'	9:J:2129:C:H5''	1.99	0.93
13:L:484:ARG:CD	13:L:649:LEU:HD12	1.97	0.93
5:F:2662:A:N1	13:L:21:ILE:CD1	2.32	0.92
8:I:1069:A:H4'	8:I:1070:A:C5'	1.98	0.92
10:M:8:4SU:C5'	10:M:49:5MC:H5'	1.98	0.92
13:L:555:LEU:O	13:L:688:ILE:CG2	2.16	0.92
14:N:18:GLY:H	14:N:42:ILE:HG22	1.32	0.92
13:L:594:VAL:HG13	13:L:599:PRO:HB3	0.95	0.92
8:I:1065:U:H3'	8:I:1066:U:H5''	1.49	0.92
5:F:2662:A:N6	13:L:21:ILE:HG13	1.82	0.92
9:J:2168:G:N2	10:M:56:C:C2	2.38	0.92
11:E:6:THR:H	11:E:9:GLN:HE21	1.12	0.92
10:M:37:A:O3'	10:M:38:U:P	2.27	0.92
11:E:32:PHE:HB3	11:E:84:LEU:HD21	1.50	0.92
4:D:55:A:C1'	13:L:321:TYR:HA	1.91	0.91
13:L:556:ILE:HG22	13:L:688:ILE:N	1.85	0.91
13:L:486:THR:HG22	13:L:600:VAL:HG11	1.53	0.91
13:L:486:THR:HG21	13:L:678:GLU:CD	1.94	0.91
13:L:409:ILE:HA	13:L:654:GLY:HA2	1.50	0.91
5:F:2656:U:H4'	13:L:141:LYS:HZ2	1.35	0.91
8:I:1064:C:H2'	8:I:1065:U:H6	1.36	0.90
8:I:1081:U:H2'	8:I:1082:U:C5	2.06	0.90
3:C:1442:G:H5'	3:C:1442:G:C8	2.06	0.90
8:I:1095:A:P	13:L:617:MET:CB	2.55	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:2660:A:H1'	13:L:665:GLY:HA2	1.50	0.90
8:I:1054:A:N1	8:I:1105:U:O2	2.05	0.90
13:L:127:LYS:HZ3	13:L:402:ILE:CG1	1.81	0.90
13:L:410:ASP:OD1	13:L:653:PHE:CD1	2.23	0.90
13:L:555:LEU:C	13:L:688:ILE:HG12	1.96	0.90
13:L:484:ARG:CG	13:L:606:MET:HG3	2.02	0.90
8:I:1087:G:H21	8:I:1103:A:C2'	1.85	0.89
13:L:484:ARG:CD	13:L:649:LEU:CD1	2.50	0.89
10:M:8:4SU:O2'	10:M:46:A:H1'	1.71	0.89
10:M:66:U:H2'	10:M:67:C:C6	2.08	0.89
13:L:406:GLU:HG3	13:L:670:VAL:CA	2.03	0.89
8:I:1058:G:O2'	8:I:1059:G:H5'	1.73	0.89
8:I:1064:C:H2'	8:I:1065:U:C6	2.08	0.89
13:L:519:ARG:HG2	13:L:677:GLN:HE22	1.35	0.88
2:B:368:U:C4	13:L:354:ARG:NH1	2.41	0.88
9:J:2175:C:H1'	12:K:215:THR:HA	1.52	0.88
13:L:89:ASP:HB3	13:L:454:MET:SD	2.14	0.88
5:F:2662:A:C6	13:L:21:ILE:HD11	2.07	0.88
8:I:1063:G:N1	8:I:1075:C:N4	2.22	0.88
13:L:137:ASN:HD21	13:L:263:ALA:H	1.19	0.88
13:L:484:ARG:O	13:L:648:PRO:C	2.15	0.88
8:I:1069:A:C4'	8:I:1070:A:H5''	2.03	0.87
8:I:1069:A:H4'	8:I:1070:A:H5''	1.54	0.87
10:M:8:4SU:H5''	10:M:49:5MC:H5'	1.55	0.87
6:G:1879:C:C2'	6:G:1880:C:H5''	2.03	0.87
13:L:555:LEU:O	13:L:688:ILE:CG1	2.21	0.87
13:L:484:ARG:CZ	13:L:649:LEU:HD12	2.02	0.87
14:N:67:THR:HA	14:N:90:MET:HE1	1.56	0.87
10:M:73:G:C2'	10:M:74:C:H5'	2.04	0.87
13:L:127:LYS:HD2	13:L:401:SER:HA	1.53	0.87
13:L:556:ILE:HG23	13:L:601:ILE:HD11	1.55	0.87
5:F:2662:A:H61	13:L:21:ILE:HD11	0.94	0.87
14:N:48:MET:HA	14:N:51:LEU:HD12	1.56	0.87
6:G:1884:A:C2'	6:G:1885:A:H5''	2.05	0.87
13:L:484:ARG:C	13:L:647:VAL:C	2.40	0.87
14:N:137:ARG:HA	14:N:137:ARG:HH11	1.38	0.87
12:K:49:ILE:H	12:K:49:ILE:HD12	1.39	0.86
13:L:484:ARG:O	13:L:648:PRO:N	2.07	0.86
8:I:1054:A:H2'	8:I:1055:G:C8	2.09	0.86
13:L:483:TYR:O	13:L:649:LEU:O	1.94	0.86
5:F:2660:A:C2'	13:L:660:ARG:CD	2.46	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:1067:A:O2'	13:L:633:GLY:C	2.07	0.86
4:D:55:A:C2	13:L:322:VAL:HG13	2.08	0.86
11:E:18:VAL:HG23	11:E:19:ARG:H	1.41	0.86
13:L:486:THR:CG2	13:L:678:GLU:CD	2.48	0.86
10:M:19:G:H4'	10:M:20:H2U:OP1	1.74	0.85
10:M:69:C:H2'	10:M:70:G:C8	2.11	0.85
13:L:556:ILE:CG2	13:L:688:ILE:N	2.39	0.85
5:F:2659:G:O3'	13:L:664:GLN:OE1	1.89	0.85
13:L:482:ALA:N	13:L:655:TYR:N	2.25	0.84
14:N:187:LEU:HD23	14:N:201:ILE:HG22	1.57	0.84
11:E:41:ARG:HB3	11:E:41:ARG:HH11	1.40	0.84
6:G:1840:G:H1	6:G:1902:C:H42	1.24	0.84
13:L:92:ILE:HG21	13:L:436:PRO:CD	2.07	0.84
14:N:51:LEU:HD23	14:N:201:ILE:HD12	1.58	0.84
5:F:2660:A:H1'	13:L:665:GLY:H	1.40	0.84
11:E:60:LEU:HD21	11:E:66:VAL:HG22	1.57	0.84
13:L:484:ARG:C	13:L:648:PRO:O	2.19	0.84
5:F:2661:G:N2	13:L:20:HIS:CE1	2.46	0.84
8:I:1067:A:HO2'	13:L:634:MET:N	1.72	0.84
10:M:14:A:H2'	10:M:15:G:C8	2.13	0.84
13:L:409:ILE:HD13	13:L:654:GLY:CA	2.06	0.84
13:L:415:PRO:HG3	13:L:421:GLN:HG2	1.60	0.84
10:M:1:U:H2'	10:M:2:C:H6	1.43	0.84
13:L:556:ILE:HG12	13:L:601:ILE:HG12	1.60	0.84
5:F:2656:U:H4'	13:L:141:LYS:NZ	1.91	0.84
9:J:2189:U:H3'	9:J:2190:G:H5''	1.60	0.83
10:M:52:G:H1	10:M:62:C:H42	1.25	0.83
13:L:485:GLU:C	13:L:605:ILE:CG2	2.42	0.83
6:G:1846:G:H5'	6:G:1847:A:OP2	1.78	0.83
12:K:49:ILE:HG22	12:K:50:ASP:H	1.43	0.83
12:K:44:HIS:CD2	12:K:175:VAL:HA	2.14	0.83
9:J:2189:U:C3'	9:J:2190:G:H5''	2.09	0.83
10:M:64:C:C5'	12:K:53:ARG:NH2	2.34	0.82
13:L:556:ILE:CG2	13:L:688:ILE:HA	2.07	0.82
13:L:165:GLN:HE21	13:L:260:LEU:H	1.24	0.82
8:I:1063:G:C2	8:I:1075:C:N3	2.47	0.82
13:L:484:ARG:HH21	13:L:671:MET:HE1	0.69	0.82
13:L:484:ARG:CZ	13:L:649:LEU:HD11	2.09	0.82
8:I:1061:U:C5'	8:I:1070:A:H4'	2.09	0.82
13:L:124:GLN:NE2	13:L:401:SER:CB	2.41	0.82
4:D:55:A:N3	13:L:322:VAL:CG1	2.42	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:238:THR:HG22	13:L:241:GLU:H	1.45	0.82
13:L:481:VAL:HG11	13:L:658:ASP:OD1	1.79	0.82
5:F:2660:A:O2'	13:L:660:ARG:HD2	1.80	0.81
8:I:1063:G:O6	8:I:1069:A:O3'	1.96	0.81
13:L:482:ALA:HA	13:L:653:PHE:CA	2.07	0.81
13:L:556:ILE:HG12	13:L:601:ILE:HD11	1.61	0.81
12:K:18:LYS:HD2	12:K:19:VAL:HG23	1.62	0.81
10:M:8:4SU:H4'	10:M:49:5MC:H5'	1.61	0.81
10:M:66:U:H2'	10:M:67:C:H6	1.43	0.81
10:M:69:C:H2'	10:M:70:G:H8	1.44	0.81
14:N:67:THR:HG21	14:N:155:LEU:HG	1.62	0.81
12:K:58:VAL:CG2	12:K:166:ASP:H	1.87	0.81
13:L:413:ILE:HD13	13:L:451:ILE:HD11	1.63	0.81
13:L:406:GLU:CB	13:L:669:PHE:O	2.28	0.80
13:L:408:VAL:O	13:L:655:TYR:N	2.14	0.80
3:C:1468:A:H2'	3:C:1469:G:O4'	1.80	0.80
14:N:44:LEU:H	14:N:44:LEU:HD12	1.46	0.80
11:E:24:VAL:HG13	11:E:98:TYR:CE2	2.16	0.80
13:L:484:ARG:CG	13:L:652:MET:HG3	2.03	0.80
2:B:368:U:H5	13:L:354:ARG:CG	1.94	0.79
3:C:1497:G:O2'	3:C:1498:U:H5'	1.82	0.79
10:M:1:U:H2'	10:M:2:C:C6	2.16	0.79
13:L:316:ILE:HD12	13:L:324:ARG:HH21	1.46	0.79
13:L:531:GLY:H	13:L:533:VAL:HG23	1.48	0.79
8:I:1066:U:O2'	8:I:1067:A:H3'	1.82	0.79
13:L:165:GLN:HE21	13:L:260:LEU:HD13	1.46	0.79
2:B:368:U:OP1	13:L:351:ARG:NE	2.16	0.79
8:I:1057:A:N6	8:I:1081:U:H3	1.80	0.78
3:C:1442:G:H2'	3:C:1442(A):G:H5''	1.65	0.78
14:N:36:ARG:HB2	14:N:41:ILE:HD11	1.64	0.78
4:D:55:A:N3	13:L:322:VAL:HG13	1.99	0.78
3:C:1490:C:O2'	3:C:1491:G:H5'	1.83	0.78
13:L:165:GLN:NE2	13:L:260:LEU:H	1.82	0.78
14:N:84:GLU:HB3	14:N:219:VAL:HG21	1.66	0.78
13:L:486:THR:O	13:L:600:VAL:HG12	1.84	0.77
8:I:1067:A:N3	13:L:634:MET:CE	2.47	0.77
11:E:46:LYS:CG	11:E:47:LYS:H	1.97	0.77
13:L:127:LYS:CD	13:L:401:SER:HA	2.14	0.77
8:I:1089:G:H8	8:I:1089:G:O5'	1.67	0.77
11:E:89:ARG:NH1	11:E:89:ARG:HB2	2.00	0.77
14:N:67:THR:C	14:N:68:ILE:HD12	2.09	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:2468:G:H22	7:H:2481:G:H2'	1.48	0.77
12:K:64:LEU:HD13	12:K:65:PRO:HD2	1.64	0.77
14:N:20:GLU:HG3	14:N:191:ASP:HB2	1.65	0.77
13:L:408:VAL:HG13	13:L:669:PHE:CE1	2.17	0.76
13:L:556:ILE:CG2	13:L:601:ILE:HD11	2.15	0.76
6:G:1887:C:C3'	6:G:1888:G:H5''	2.16	0.76
5:F:2660:A:N9	13:L:660:ARG:HG3	2.00	0.76
10:M:3:C:O2'	10:M:4:G:H5'	1.84	0.76
11:E:59:ARG:NH2	13:L:418:LYS:HE3	2.00	0.76
14:N:201:ILE:HG21	14:N:214:ILE:HG21	1.67	0.76
9:J:2180:U:H2'	9:J:2181:G:C8	2.20	0.76
14:N:178:ARG:HH22	14:N:196:LEU:C	1.93	0.76
10:M:24:G:C6	10:M:25:U:C4	2.73	0.76
13:L:484:ARG:HB2	13:L:606:MET:HB2	1.67	0.76
14:N:19:HIS:O	14:N:39:ILE:HG23	1.84	0.76
3:C:1422:G:H2'	3:C:1423:G:H8	1.51	0.75
14:N:158:LEU:H	14:N:158:LEU:HD12	1.51	0.75
8:I:1069:A:H4'	8:I:1070:A:O5'	1.83	0.75
8:I:1067:A:C5	13:L:631:ILE:C	2.61	0.75
3:C:1458:G:H2'	3:C:1459:C:H6	1.51	0.75
3:C:1443:G:N2	3:C:1460:A:H1'	2.02	0.75
8:I:1061:U:H3'	8:I:1061:U:P	2.26	0.75
8:I:1085:A:C1'	8:I:1086:A:H4'	2.07	0.75
13:L:519:ARG:HG2	13:L:677:GLN:NE2	2.00	0.75
5:F:2661:G:H22	13:L:20:HIS:CE1	2.05	0.75
7:H:2468:G:N2	7:H:2481:G:H2'	2.00	0.75
9:J:2110:G:H1	9:J:2179:C:H42	1.32	0.75
12:K:44:HIS:HD2	12:K:175:VAL:HA	1.49	0.75
13:L:556:ILE:CG2	13:L:688:ILE:CA	2.61	0.75
8:I:1056:G:O6	8:I:1101:U:H3'	1.86	0.74
13:L:127:LYS:HZ1	13:L:402:ILE:HG13	1.44	0.74
1:A:349:A:O2'	1:A:350:G:H5'	1.87	0.74
8:I:1068:G:H4'	8:I:1096:A:H1'	1.69	0.74
13:L:545:GLY:HA2	13:L:583:LYS:HE3	1.69	0.74
8:I:1061:U:H4'	8:I:1070:A:O4'	1.86	0.74
14:N:36:ARG:H	14:N:41:ILE:HD13	1.52	0.74
14:N:204:ASN:HD21	14:N:207:ALA:N	1.85	0.74
10:M:8:4SU:H5''	10:M:49:5MC:C5'	2.17	0.74
13:L:408:VAL:HG11	13:L:669:PHE:CE1	1.90	0.74
14:N:97:TRP:CH2	14:N:173:ALA:HA	2.23	0.74
13:L:321:TYR:O	13:L:322:VAL:HG13	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:178:ARG:HB2	14:N:178:ARG:HH11	1.53	0.74
6:G:1879:C:C3'	6:G:1880:C:H5''	2.18	0.74
8:I:1086:A:OP1	8:I:1104:C:H4'	1.86	0.74
5:F:2660:A:O4'	13:L:664:GLN:C	2.30	0.73
9:J:2168:G:C2	10:M:56:C:N3	2.55	0.73
13:L:406:GLU:HB2	13:L:669:PHE:O	1.87	0.73
6:G:1899:G:N2	6:G:1902:C:H41	1.86	0.73
13:L:621:ILE:HD11	13:L:643:ILE:HD13	1.69	0.73
13:L:484:ARG:C	13:L:647:VAL:HG22	2.12	0.73
14:N:10:LEU:H	14:N:10:LEU:HD23	1.53	0.73
8:I:1095:A:P	13:L:618:GLY:H	2.12	0.73
13:L:13:ARG:HH11	13:L:277:VAL:HA	1.53	0.73
3:C:1494:G:O3'	13:L:503:GLY:HA2	1.87	0.73
6:G:1899:G:H22	6:G:1902:C:H41	1.35	0.73
8:I:1084:A:N1	8:I:1085:A:N1	2.36	0.73
13:L:321:TYR:O	13:L:322:VAL:HG22	1.89	0.73
14:N:88:ALA:HB2	14:N:219:VAL:HG13	1.71	0.73
13:L:166:LEU:HD22	13:L:180:VAL:HG11	1.70	0.73
13:L:484:ARG:HB3	13:L:606:MET:HG2	1.60	0.73
13:L:536:LYS:HD2	13:L:537:GLU:N	2.04	0.73
8:I:1095:A:OP1	13:L:617:MET:N	2.22	0.72
10:M:68:G:O2'	10:M:69:C:H5'	1.89	0.72
13:L:484:ARG:O	13:L:648:PRO:O	2.07	0.72
8:I:1083:U:OP2	8:I:1083:U:H6	1.72	0.72
12:K:45:ALA:CB	12:K:210:ARG:HA	2.19	0.72
14:N:7:VAL:O	14:N:11:LEU:HG	1.88	0.72
13:L:169:GLY:HA3	13:L:173:THR:O	1.90	0.72
14:N:69:LEU:HB3	14:N:162:ILE:HG22	1.70	0.72
14:N:77:ALA:HB2	14:N:211:ILE:HD13	1.69	0.72
13:L:484:ARG:CA	13:L:649:LEU:CA	2.30	0.72
8:I:1073:A:N7	8:I:1074:G:C5	2.57	0.72
8:I:1086:A:H3'	8:I:1087:G:H5'	1.72	0.72
13:L:486:THR:HG21	13:L:678:GLU:OE1	1.88	0.72
13:L:556:ILE:CG2	13:L:687:LEU:C	2.63	0.72
14:N:204:ASN:HD21	14:N:207:ALA:H	1.36	0.72
8:I:1095:A:H5''	13:L:618:GLY:N	2.04	0.71
11:E:115:LYS:O	11:E:117:ARG:HG3	1.90	0.71
13:L:110:SER:HB3	13:L:139:MET:HE3	1.71	0.71
14:N:74:LYS:NZ	14:N:76:GLN:HB2	2.06	0.71
8:I:1087:G:N2	8:I:1103:A:H2'	2.04	0.71
11:E:47:LYS:CB	11:E:48:PRO:HD3	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1435:G:H2'	3:C:1436:U:C6	2.26	0.71
8:I:1066:U:O2	8:I:1068:G:H3'	1.90	0.71
8:I:1087:G:H2'	8:I:1103:A:H2	1.55	0.71
10:M:24:G:C5	10:M:25:U:C5	2.79	0.71
3:C:1428:A:H2'	3:C:1429:C:C6	2.26	0.70
13:L:467:LYS:O	13:L:471:LYS:HA	1.91	0.70
12:K:49:ILE:HG22	12:K:50:ASP:N	2.06	0.70
5:F:2660:A:C1'	13:L:665:GLY:H	1.96	0.70
6:G:1887:C:H3'	6:G:1888:G:H5''	1.73	0.70
10:M:67:C:H2'	10:M:68:G:H8	1.55	0.70
13:L:536:LYS:HD2	13:L:537:GLU:H	1.56	0.70
5:F:2661:G:C6	13:L:20:HIS:CE1	2.77	0.70
13:L:405:PRO:HB2	13:L:454:MET:HG2	1.72	0.70
6:G:1899:G:H22	6:G:1902:C:N4	1.89	0.70
7:H:2461:C:H2'	7:H:2462:U:C6	2.27	0.70
10:M:22:A:H5'	10:M:22:A:H8	1.54	0.70
13:L:424:LEU:HD13	13:L:472:VAL:HG11	1.74	0.70
3:C:1442(A):G:H3'	3:C:1442(B):A:H5''	1.71	0.70
8:I:1087:G:H21	8:I:1103:A:C3'	2.04	0.70
13:L:114:VAL:HG12	13:L:152:THR:OG1	1.91	0.70
14:N:233:SER:HB2	14:N:234:PRO:HD2	1.74	0.70
5:F:2672:G:H2'	5:F:2673:G:H5''	1.73	0.70
8:I:1080:C:H2'	8:I:1081:U:O4'	1.90	0.70
10:M:22:A:H2'	10:M:23:U:H5'	1.74	0.70
14:N:18:GLY:H	14:N:42:ILE:CG2	2.02	0.70
8:I:1065:U:C2'	8:I:1066:U:H5''	2.21	0.70
8:I:1067:A:C5	13:L:631:ILE:O	2.45	0.70
14:N:30:ARG:HH21	14:N:194:PRO:CG	2.04	0.70
8:I:1063:G:C6	8:I:1075:C:N4	2.59	0.69
9:J:2178:C:H4'	12:K:46:LYS:NZ	2.07	0.69
13:L:485:GLU:HB3	13:L:605:ILE:HD12	1.73	0.69
2:B:368:U:OP2	13:L:351:ARG:HG3	1.92	0.69
10:M:25:U:H2'	10:M:26:A:C8	2.27	0.69
11:E:28:LYS:O	11:E:29:GLY:C	2.34	0.69
14:N:218:ALA:O	14:N:222:ILE:HG13	1.93	0.69
2:B:368:U:P	13:L:351:ARG:HE	2.13	0.69
13:L:482:ALA:CA	13:L:653:PHE:HA	2.18	0.69
8:I:1058:G:O2'	8:I:1059:G:C5'	2.40	0.69
8:I:1086:A:C3'	8:I:1087:G:H5'	2.23	0.69
14:N:21:ARG:HB3	14:N:39:ILE:HA	1.75	0.69
2:B:368:U:OP2	13:L:351:ARG:CG	2.41	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:6:THR:OG1	11:E:9:GLN:HG3	1.93	0.69
11:E:24:VAL:HG13	11:E:98:TYR:HE2	1.54	0.69
11:E:24:VAL:O	11:E:24:VAL:HG12	1.91	0.69
13:L:555:LEU:HB3	13:L:688:ILE:HD11	1.74	0.69
14:N:121:LEU:HD23	14:N:121:LEU:O	1.92	0.69
11:E:58:VAL:O	11:E:65:GLU:HA	1.93	0.69
12:K:82:LYS:NZ	12:K:151:GLU:HA	2.08	0.69
13:L:556:ILE:HG21	13:L:687:LEU:CB	2.22	0.69
8:I:1053:C:O2'	8:I:1054:A:H5'	1.92	0.68
10:M:37:A:C3'	10:M:38:U:P	2.80	0.68
9:J:2180:U:H2'	9:J:2181:G:H8	1.55	0.68
8:I:1092:C:C6	8:I:1092:C:H3'	2.28	0.68
13:L:556:ILE:HD11	13:L:601:ILE:HG23	1.73	0.68
8:I:1087:G:N2	8:I:1103:A:C2'	2.55	0.68
8:I:1091:G:N1	8:I:1101:U:C4	2.62	0.68
11:E:92:ASP:O	11:E:93:LEU:HD23	1.93	0.68
13:L:481:VAL:HG23	13:L:655:TYR:HB2	1.74	0.68
13:L:482:ALA:H	13:L:655:TYR:N	1.89	0.68
13:L:484:ARG:NH2	13:L:671:MET:CE	2.04	0.68
13:L:556:ILE:HG21	13:L:687:LEU:HB2	1.75	0.68
8:I:1102:C:O2'	8:I:1103:A:O5'	2.12	0.68
14:N:36:ARG:H	14:N:41:ILE:CD1	2.06	0.68
9:J:2121:G:H2'	9:J:2122:U:C6	2.28	0.68
11:E:41:ARG:HH11	11:E:41:ARG:CB	2.06	0.68
13:L:607:ARG:HH22	13:L:644:ARG:HE	1.40	0.68
8:I:1102:C:C1'	8:I:1103:A:C8	2.78	0.67
9:J:2168:G:N2	10:M:19:G:H1	1.91	0.67
13:L:92:ILE:CG2	13:L:436:PRO:HD2	2.16	0.67
8:I:1067:A:C4	13:L:634:MET:HE1	2.29	0.67
11:E:41:ARG:CG	11:E:42:THR:H	2.05	0.67
9:J:2127:G:H2'	9:J:2128:C:C6	2.29	0.67
13:L:539:ILE:O	13:L:542:VAL:HG12	1.94	0.67
8:I:1061:U:H5''	8:I:1070:A:H4'	1.75	0.67
14:N:163:PHE:HA	14:N:185:ILE:HG13	1.76	0.67
8:I:1060:U:H5''	8:I:1061:U:O4	1.93	0.67
8:I:1102:C:C2'	8:I:1103:A:H8	2.08	0.67
13:L:594:VAL:CG1	13:L:599:PRO:HB2	2.18	0.67
14:N:102:LEU:CD1	14:N:102:LEU:H	2.07	0.67
13:L:238:THR:HG23	13:L:240:GLU:OE2	1.94	0.67
13:L:627:ARG:HH21	13:L:655:TYR:HD1	1.43	0.67
3:C:1460:A:H2'	3:C:1461:G:O4'	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:1087:G:H2'	8:I:1089:G:H4'	1.77	0.67
12:K:50:ASP:CG	12:K:55:ASP:HA	2.20	0.67
8:I:1057:A:C8	8:I:1085:A:N1	2.63	0.67
8:I:1063:G:H2'	8:I:1064:C:C6	2.30	0.67
10:M:37:A:H3'	10:M:38:U:P	2.35	0.67
11:E:119:LYS:C	11:E:120:TYR:HD1	2.02	0.67
12:K:51:PRO:HG3	12:K:204:ALA:HB3	1.77	0.67
9:J:2182:G:H2'	9:J:2183:C:H6	1.60	0.67
14:N:18:GLY:N	14:N:42:ILE:HG22	2.08	0.67
8:I:1071:G:C8	8:I:1089:G:C6	2.82	0.66
10:M:52:G:H1	10:M:62:C:N4	1.93	0.66
13:L:142:THR:HA	13:L:171:GLU:CG	2.22	0.66
13:L:484:ARG:HD3	13:L:606:MET:HE2	1.78	0.66
13:L:556:ILE:HG22	13:L:687:LEU:C	2.20	0.66
11:E:46:LYS:HG2	11:E:47:LYS:N	2.03	0.66
12:K:191:ALA:O	12:K:195:ALA:HB3	1.95	0.66
13:L:485:GLU:CB	13:L:605:ILE:CD1	2.54	0.66
13:L:637:ARG:HG3	13:L:637:ARG:HH11	1.60	0.66
3:C:1458:G:H2'	3:C:1459:C:C6	2.31	0.66
13:L:91:THR:HG21	13:L:403:GLU:O	1.95	0.66
13:L:555:LEU:O	13:L:688:ILE:CB	2.43	0.66
3:C:1441:G:C5'	3:C:1442:G:H5''	2.16	0.66
13:L:519:ARG:NE	13:L:678:GLU:HG3	2.10	0.66
13:L:546:ILE:O	13:L:550:MET:HG3	1.95	0.66
1:A:340:U:O2'	1:A:341:C:H5'	1.96	0.66
3:C:1442(A):G:C3'	3:C:1442(B):A:H5''	2.26	0.66
5:F:2660:A:O2'	13:L:665:GLY:HA2	1.96	0.66
2:B:368:U:C5	13:L:354:ARG:NE	2.64	0.66
8:I:1068:G:N1	8:I:1073:A:C2	2.64	0.66
5:F:2660:A:C4'	13:L:665:GLY:HA3	2.26	0.66
8:I:1074:G:O2'	8:I:1075:C:H5'	1.96	0.66
8:I:1102:C:H1'	8:I:1103:A:N7	2.11	0.66
13:L:13:ARG:NH1	13:L:277:VAL:O	2.29	0.66
5:F:2660:A:O4'	13:L:665:GLY:CA	2.43	0.65
7:H:2455:G:H2'	7:H:2456:C:C6	2.30	0.65
9:J:2177:C:O2'	12:K:46:LYS:HE3	1.96	0.65
12:K:47:LEU:HD21	12:K:172:HIS:CB	2.26	0.65
13:L:408:VAL:O	13:L:654:GLY:C	2.38	0.65
13:L:608:VAL:HG21	13:L:652:MET:HE2	1.78	0.65
8:I:1062:G:N3	8:I:1062:G:H2'	2.11	0.65
9:J:2178:C:H4'	12:K:46:LYS:HZ3	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:2181:G:H2'	9:J:2182:G:H8	1.61	0.65
11:E:27:LEU:O	11:E:29:GLY:N	2.29	0.65
13:L:484:ARG:CA	13:L:649:LEU:N	2.57	0.65
10:M:54:5MU:C2'	10:M:55:PSU:H5''	2.25	0.65
13:L:423:LYS:HG3	13:L:472:VAL:HG22	1.76	0.65
4:D:55:A:C2	13:L:322:VAL:HA	2.32	0.65
8:I:1062:G:O6	8:I:1077:A:C5	2.50	0.65
8:I:1071:G:H8	8:I:1071:G:OP2	1.79	0.65
12:K:41:VAL:HB	12:K:178:ALA:HB3	1.79	0.65
14:N:135:GLN:O	14:N:139:LYS:HB2	1.95	0.65
3:C:1426:C:O2'	3:C:1427:U:H5'	1.95	0.65
13:L:345:THR:O	13:L:346:LYS:HG3	1.97	0.65
9:J:2129:C:H2'	9:J:2130:U:C4'	2.21	0.65
14:N:75:LYS:HG2	14:N:78:GLN:NE2	2.12	0.65
5:F:2653:U:C5'	5:F:2654:A:H5''	2.26	0.65
9:J:2175:C:C3'	9:J:2176:A:H5''	2.27	0.65
13:L:110:SER:HB3	13:L:139:MET:CE	2.26	0.65
13:L:517:LEU:HD13	13:L:564:LYS:HB2	1.79	0.65
14:N:23:ARG:HG3	14:N:23:ARG:HH11	1.62	0.65
8:I:1071:G:H2'	8:I:1072:C:C5'	2.27	0.64
8:I:1085:A:O2'	8:I:1086:A:C4'	2.46	0.64
8:I:1095:A:O4'	13:L:617:MET:HG3	1.97	0.64
13:L:556:ILE:HG23	13:L:688:ILE:HG12	1.79	0.64
3:C:1435:G:H2'	3:C:1436:U:H6	1.61	0.64
8:I:1091:G:H1	8:I:1100:C:N4	1.96	0.64
12:K:77:ILE:HG21	12:K:122:ALA:C	2.22	0.64
12:K:76:ALA:HB3	12:K:94:VAL:CG1	2.27	0.64
13:L:9:LEU:HD13	13:L:284:LEU:HD13	1.80	0.64
5:F:2672:G:C2'	5:F:2673:G:H5''	2.28	0.64
8:I:1054:A:N6	8:I:1104:C:N4	2.45	0.64
8:I:1063:G:N2	8:I:1076:C:C6	2.66	0.64
8:I:1107:G:O2'	8:I:1108:U:H5'	1.98	0.64
11:E:75:HIS:CD2	11:E:77:LEU:H	2.15	0.64
14:N:21:ARG:CB	14:N:39:ILE:HA	2.27	0.64
8:I:1061:U:C4'	8:I:1070:A:C1'	2.63	0.64
8:I:1069:A:C2	8:I:1096:A:H5'	2.33	0.64
8:I:1071:G:H2'	8:I:1072:C:H5'	1.80	0.64
11:E:6:THR:N	11:E:9:GLN:HE21	1.92	0.64
8:I:1052:C:O2'	8:I:1053:C:H5'	1.97	0.64
8:I:1095:A:C1'	13:L:617:MET:HE2	1.82	0.64
11:E:102:ARG:HG2	11:E:102:ARG:HH11	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:422:GLU:O	13:L:426:GLN:HG2	1.98	0.64
6:G:1844:C:O2'	6:G:1845:G:H5'	1.97	0.64
8:I:1067:A:C6	8:I:1068:G:O6	2.50	0.64
8:I:1087:G:N2	8:I:1103:A:H3'	2.13	0.64
12:K:56:GLN:O	12:K:57:ASN:HB2	1.96	0.64
8:I:1070:A:N6	8:I:1096:A:C2	2.66	0.64
12:K:191:ALA:C	12:K:193:ILE:H	2.06	0.64
13:L:519:ARG:CZ	13:L:678:GLU:HG3	2.28	0.64
1:A:341:C:O2'	1:A:342:C:H5'	1.97	0.64
4:D:55:A:H1'	13:L:321:TYR:C	2.19	0.64
8:I:1063:G:N7	8:I:1070:A:P	2.71	0.64
14:N:144:ARG:HG3	14:N:145:LEU:N	2.13	0.64
8:I:1091:G:N2	8:I:1101:U:C6	2.66	0.64
14:N:165:VAL:HG23	14:N:166:ASP:H	1.61	0.64
8:I:1063:G:H2'	8:I:1064:C:H6	1.62	0.63
13:L:481:VAL:HG11	13:L:658:ASP:CG	2.22	0.63
13:L:486:THR:CG2	13:L:600:VAL:HG11	2.21	0.63
14:N:97:TRP:HZ2	14:N:102:LEU:HD13	1.62	0.63
14:N:114:ARG:HA	14:N:117:GLU:HG3	1.81	0.63
6:G:1842:G:H2'	6:G:1843:C:C6	2.33	0.63
8:I:1092:C:N4	8:I:1093:G:C4	2.67	0.63
14:N:101:MET:HA	14:N:108:ILE:HG13	1.81	0.63
14:N:115:LEU:HD23	14:N:153:ARG:CZ	2.29	0.63
6:G:1887:C:H2'	6:G:1888:G:H5''	1.80	0.63
8:I:1081:U:H2'	8:I:1082:U:C4	2.33	0.63
8:I:1060:U:H5''	8:I:1061:U:C4	2.32	0.63
10:M:1:U:O2'	10:M:2:C:H5'	1.98	0.63
13:L:139:MET:HE2	13:L:144:ALA:HB1	1.81	0.63
8:I:1064:C:C2'	8:I:1065:U:H6	2.12	0.63
9:J:2116:G:H5'	9:J:2117:A:OP2	1.98	0.63
13:L:114:VAL:HG12	13:L:152:THR:CB	2.27	0.63
13:L:513:LYS:HG3	13:L:568:TYR:CE1	2.33	0.63
5:F:2662:A:H61	13:L:21:ILE:HG13	1.46	0.63
8:I:1091:G:N2	8:I:1100:C:N3	2.45	0.63
13:L:288:PRO:HG2	13:L:300:GLU:HG2	1.81	0.63
13:L:600:VAL:CG2	13:L:684:GLN:OE1	2.47	0.63
3:C:1431:C:H2'	3:C:1432:G:H5'	1.81	0.63
13:L:166:LEU:HD22	13:L:180:VAL:CG1	2.29	0.63
13:L:556:ILE:CG2	13:L:601:ILE:CD1	2.77	0.63
14:N:44:LEU:HA	14:N:47:THR:OG1	1.99	0.63
14:N:42:ILE:HD11	14:N:202:PRO:HB2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:1057:A:N1	8:I:1082:U:O4	2.32	0.62
8:I:1057:A:N3	8:I:1058:G:C8	2.67	0.62
13:L:92:ILE:HG23	13:L:93:GLU:N	2.13	0.62
13:L:316:ILE:HD13	13:L:326:THR:HB	1.80	0.62
13:L:484:ARG:HG2	13:L:652:MET:CG	2.23	0.62
3:C:1401:G:H2'	3:C:1402:C:O4'	1.98	0.62
6:G:1847:A:H3'	6:G:1848:A:H5'	1.81	0.62
11:E:91:LYS:O	11:E:92:ASP:HB2	1.97	0.62
12:K:18:LYS:HB3	12:K:22:ILE:HD11	1.81	0.62
12:K:82:LYS:HZ2	12:K:151:GLU:HA	1.62	0.62
12:K:85:GLU:HB3	12:K:153:ILE:CB	2.28	0.62
13:L:95:GLU:HB3	13:L:128:TYR:OH	1.99	0.62
13:L:484:ARG:HD3	13:L:649:LEU:HD13	1.79	0.62
14:N:169:LYS:HD2	14:N:170:GLU:OE2	1.99	0.62
5:F:2658:C:O2	5:F:2658:C:H2'	1.99	0.62
6:G:1899:G:O2'	6:G:1900:A:H5''	1.99	0.62
12:K:18:LYS:O	12:K:20:TYR:N	2.32	0.62
12:K:45:ALA:HB2	12:K:210:ARG:HA	1.80	0.62
9:J:2162:G:H5'	9:J:2171:A:H5''	1.81	0.62
12:K:74:VAL:HA	12:K:119:VAL:CB	2.30	0.62
8:I:1087:G:N2	8:I:1103:A:C3'	2.63	0.62
10:M:67:C:H2'	10:M:68:G:C8	2.34	0.62
10:M:73:G:N2	10:M:74:C:H1'	2.14	0.62
14:N:41:ILE:HD12	14:N:41:ILE:N	2.14	0.62
11:E:88:GLY:H	11:E:98:TYR:HA	1.65	0.62
13:L:408:VAL:O	13:L:656:ALA:N	2.32	0.62
13:L:413:ILE:HD13	13:L:451:ILE:CD1	2.29	0.62
13:L:607:ARG:NH2	13:L:644:ARG:HE	1.97	0.62
14:N:167:PRO:HG2	14:N:168:THR:H	1.65	0.62
2:B:392:G:H2'	2:B:393:A:H8	1.65	0.62
8:I:1064:C:C2'	8:I:1065:U:C6	2.82	0.62
9:J:2168:G:N1	10:M:19:G:N1	2.47	0.62
11:E:119:LYS:C	11:E:120:TYR:CD1	2.78	0.62
12:K:21:THR:O	12:K:22:ILE:HD13	2.00	0.62
8:I:1061:U:O4'	8:I:1070:A:H1'	1.99	0.62
8:I:1066:U:H2'	8:I:1067:A:H5''	1.81	0.62
13:L:139:MET:HE2	13:L:139:MET:HA	1.81	0.62
13:L:455:GLY:HA2	13:L:657:THR:HG22	1.82	0.62
12:K:76:ALA:HB3	12:K:94:VAL:HG13	1.82	0.61
13:L:20:HIS:HD2	13:L:117:GLN:H	1.46	0.61
13:L:556:ILE:HG21	13:L:687:LEU:C	2.24	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:2660:A:C1'	13:L:660:ARG:CG	2.68	0.61
13:L:137:ASN:ND2	13:L:263:ALA:H	1.95	0.61
13:L:462:ILE:O	13:L:466:LEU:HD13	2.00	0.61
13:L:484:ARG:HD3	13:L:606:MET:CE	2.30	0.61
14:N:92:TYR:CE2	14:N:151:GLY:HA3	2.35	0.61
12:K:34:THR:O	12:K:35:ALA:CB	2.48	0.61
3:C:1431:C:C2'	3:C:1432:G:H5'	2.30	0.61
13:L:19:ALA:HB2	13:L:107:VAL:HB	1.82	0.61
5:F:2672:G:C3'	5:F:2673:G:H5''	2.31	0.61
8:I:1078:U:H5''	8:I:1079:C:OP1	2.00	0.61
8:I:1092:C:C6	8:I:1092:C:C3'	2.84	0.61
13:L:105:ILE:HG12	13:L:133:ILE:HD11	1.82	0.61
13:L:129:LYS:HB3	13:L:253:LEU:HD21	1.83	0.61
8:I:1069:A:N6	8:I:1073:A:C4	2.69	0.61
8:I:1095:A:OP1	13:L:617:MET:CA	2.48	0.61
8:I:1106:G:C6	8:I:1107:G:C6	2.89	0.61
12:K:22:ILE:CG2	12:K:25:ALA:HB2	2.30	0.61
3:C:1412:C:H2'	3:C:1413:A:C8	2.36	0.61
11:E:82:VAL:HB	11:E:106:ASP:OD1	2.01	0.61
13:L:445:GLU:HG3	13:L:446:THR:H	1.66	0.61
8:I:1091:G:C2	8:I:1101:U:C2	2.89	0.61
10:M:22:A:C2'	10:M:23:U:H5'	2.31	0.61
14:N:36:ARG:HB2	14:N:41:ILE:CD1	2.30	0.61
7:H:2464:C:O2'	7:H:2465:C:H6	1.80	0.60
11:E:47:LYS:HB3	11:E:48:PRO:CD	2.25	0.60
13:L:181:LEU:HD12	13:L:181:LEU:O	2.01	0.60
13:L:481:VAL:CG2	13:L:655:TYR:CA	2.78	0.60
13:L:481:VAL:CG2	13:L:655:TYR:HA	2.26	0.60
12:K:191:ALA:O	12:K:193:ILE:N	2.34	0.60
13:L:556:ILE:HG23	13:L:688:ILE:CG1	2.30	0.60
13:L:127:LYS:HE2	13:L:402:ILE:HG13	1.76	0.60
14:N:142:LEU:HD23	14:N:142:LEU:C	2.26	0.60
3:C:1456:G:H2'	3:C:1457:G:O4'	2.00	0.60
8:I:1059:G:OP2	8:I:1061:U:O4	2.19	0.60
8:I:1095:A:O5'	13:L:617:MET:CB	2.36	0.60
10:M:64:C:C4'	12:K:53:ARG:NH2	2.64	0.60
11:E:45:PRO:HD3	11:E:51:ALA:O	2.01	0.60
11:E:89:ARG:HB2	11:E:89:ARG:HH11	1.65	0.60
2:B:368:U:C5	13:L:354:ARG:CG	2.74	0.60
10:M:8:4SU:O2'	10:M:46:A:C1'	2.48	0.60
12:K:47:LEU:HD23	12:K:47:LEU:N	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:49:ILE:H	12:K:49:ILE:CD1	2.12	0.60
3:C:1442(A):G:H3'	3:C:1442(B):A:C5'	2.30	0.60
8:I:1077:A:H2'	8:I:1078:U:O4'	2.02	0.60
13:L:621:ILE:CD1	13:L:643:ILE:HD13	2.31	0.60
8:I:1056:G:C2	8:I:1102:C:N4	2.70	0.60
9:J:2186:G:H2'	9:J:2187:G:H5''	1.84	0.60
14:N:219:VAL:HA	14:N:222:ILE:HD12	1.83	0.60
13:L:213:HIS:O	13:L:217:VAL:HG23	2.02	0.60
13:L:409:ILE:HD13	13:L:654:GLY:C	2.27	0.60
9:J:2182:G:H2'	9:J:2183:C:C6	2.35	0.60
13:L:682:GLN:HG3	13:L:686:LYS:HE3	1.84	0.60
12:K:89:ALA:HB2	12:K:153:ILE:HA	1.83	0.59
5:F:2653:U:H5'	5:F:2654:A:H5''	1.81	0.59
13:L:427:ALA:HB1	13:L:470:PHE:CD2	2.37	0.59
13:L:486:THR:HG21	13:L:678:GLU:CG	2.32	0.59
14:N:115:LEU:HD13	14:N:145:LEU:HD12	1.83	0.59
14:N:187:LEU:HA	14:N:201:ILE:HB	1.84	0.59
8:I:1102:C:HO2'	8:I:1103:A:H8	1.50	0.59
10:M:73:G:N2	10:M:74:C:C1'	2.64	0.59
11:E:23:LYS:O	11:E:24:VAL:HG23	2.02	0.59
13:L:600:VAL:HG22	13:L:684:GLN:OE1	2.03	0.59
14:N:103:THR:HA	14:N:180:LEU:HD11	1.84	0.59
14:N:141:GLU:O	14:N:145:LEU:HB2	2.02	0.59
10:M:73:G:C2'	10:M:74:C:C5'	2.79	0.59
13:L:190:ASN:C	13:L:190:ASN:HD22	2.09	0.59
14:N:197:VAL:CG1	14:N:200:ILE:HG12	2.33	0.59
2:B:368:U:O2	4:D:356:A:H2	1.86	0.59
8:I:1087:G:H2'	8:I:1103:A:C2	2.36	0.59
9:J:2168:G:H22	10:M:56:C:N4	2.00	0.59
13:L:294:PRO:HD3	13:L:396:ARG:O	2.02	0.59
3:C:1437:C:O2'	3:C:1438:G:H5'	2.03	0.59
5:F:2657:A:H1'	5:F:2665:A:N6	2.18	0.59
8:I:1065:U:H3'	8:I:1066:U:C5'	2.28	0.59
13:L:20:HIS:CD2	13:L:117:GLN:HB2	2.38	0.59
13:L:486:THR:O	13:L:600:VAL:CG1	2.51	0.59
14:N:194:PRO:HG2	14:N:195:ASP:H	1.68	0.59
4:D:55:A:N3	13:L:322:VAL:N	2.50	0.59
5:F:2660:A:O2'	13:L:660:ARG:CD	2.45	0.59
11:E:60:LEU:HD22	11:E:60:LEU:N	2.18	0.59
12:K:46:LYS:HA	12:K:46:LYS:CE	2.27	0.59
13:L:110:SER:CB	13:L:139:MET:HE3	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:171:ALA:O	14:N:174:VAL:HB	2.03	0.59
6:G:1887:C:C2'	6:G:1888:G:H5''	2.33	0.59
8:I:1063:G:N2	8:I:1075:C:C2	2.71	0.59
11:E:45:PRO:HB3	11:E:49:ASN:HB2	1.84	0.59
12:K:77:ILE:O	12:K:77:ILE:HD13	2.02	0.59
6:G:1840:G:H1	6:G:1902:C:N4	1.97	0.58
9:J:2175:C:H2'	9:J:2176:A:C5'	2.19	0.58
12:K:77:ILE:HD12	12:K:123:VAL:N	2.18	0.58
14:N:59:GLU:HB2	14:N:221:LEU:HD11	1.85	0.58
14:N:97:TRP:HH2	14:N:176:GLU:CD	2.11	0.58
3:C:1484:C:H2'	3:C:1485:U:H6	1.69	0.58
6:G:1884:A:C3'	6:G:1885:A:H5''	2.34	0.58
10:M:55:PSU:H2'	10:M:57:A:OP2	2.03	0.58
11:E:53:ARG:HG2	11:E:53:ARG:HH11	1.67	0.58
7:H:2463:C:O2'	7:H:2464:C:H5'	2.02	0.58
8:I:1054:A:C2'	8:I:1055:G:C8	2.83	0.58
8:I:1063:G:N2	8:I:1076:C:N1	2.51	0.58
3:C:1410:G:H2'	3:C:1411:C:C6	2.39	0.58
9:J:2098:U:H2'	9:J:2099:U:C6	2.39	0.58
13:L:35:TYR:OH	13:L:193:GLY:HA3	2.03	0.58
13:L:405:PRO:HG3	13:L:437:THR:HB	1.83	0.58
13:L:483:TYR:C	13:L:649:LEU:O	2.45	0.58
14:N:167:PRO:O	14:N:171:ALA:N	2.37	0.58
8:I:1083:U:OP2	8:I:1083:U:C6	2.53	0.58
14:N:24:TRP:CD1	14:N:24:TRP:H	2.21	0.58
14:N:236:TYR:HA	14:N:239:VAL:HG23	1.86	0.58
8:I:1067:A:HO2'	13:L:633:GLY:C	1.99	0.58
12:K:49:ILE:CG2	12:K:50:ASP:H	2.16	0.58
13:L:484:ARG:HD3	13:L:649:LEU:CD1	2.31	0.58
10:M:75:C:H2'	10:M:76:A:H5'	0.70	0.58
11:E:84:LEU:HD23	11:E:85:ILE:N	2.19	0.58
14:N:22:LYS:HZ3	14:N:22:LYS:CA	1.96	0.58
14:N:32:ILE:HA	14:N:42:ILE:HA	1.85	0.58
14:N:43:ASP:OD2	14:N:46:LYS:HB2	2.03	0.58
8:I:1095:A:C5'	13:L:618:GLY:N	2.67	0.58
13:L:417:THR:C	13:L:419:ALA:H	2.10	0.58
13:L:619:ASP:OD2	13:L:619:ASP:N	2.36	0.58
8:I:1054:A:H2'	8:I:1055:G:N7	2.18	0.58
8:I:1065:U:H2'	8:I:1066:U:H5''	1.85	0.58
8:I:1066:U:C2	8:I:1069:A:OP2	2.57	0.58
8:I:1068:G:N1	8:I:1073:A:H2	2.01	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:M:25:U:O4	10:M:26:A:N6	2.36	0.58
10:M:73:G:H2'	10:M:74:C:H5'	1.82	0.58
11:E:32:PHE:HB3	11:E:84:LEU:CD2	2.28	0.58
11:E:120:TYR:HD1	11:E:120:TYR:N	2.02	0.58
13:L:542:VAL:O	13:L:546:ILE:HG13	2.04	0.58
3:C:1404:C:H2'	3:C:1405:G:C8	2.39	0.58
6:G:1899:G:N2	6:G:1902:C:N4	2.49	0.58
8:I:1071:G:C8	8:I:1071:G:OP2	2.57	0.58
10:M:19:G:C4'	10:M:20:H2U:OP1	2.42	0.58
13:L:238:THR:HG22	13:L:241:GLU:N	2.17	0.58
14:N:213:LEU:C	14:N:213:LEU:HD23	2.29	0.58
4:D:358:U:OP1	13:L:381:LYS:HE3	2.04	0.57
9:J:2098:U:H2'	9:J:2099:U:H6	1.68	0.57
9:J:2103:C:H3'	9:J:2104:G:C5'	2.25	0.57
9:J:2103:C:C3'	9:J:2104:G:H5''	2.25	0.57
9:J:2181:G:H2'	9:J:2182:G:C8	2.38	0.57
12:K:40:THR:HG21	12:K:215:THR:CB	2.34	0.57
13:L:409:ILE:HG13	13:L:455:GLY:HA2	1.85	0.57
14:N:194:PRO:O	14:N:195:ASP:C	2.47	0.57
7:H:2491:U:O2'	7:H:2492:U:H5'	2.04	0.57
10:M:25:U:H2'	10:M:26:A:H8	1.70	0.57
11:E:18:VAL:HG23	11:E:19:ARG:N	2.15	0.57
14:N:47:THR:HG23	14:N:202:PRO:HG2	1.85	0.57
11:E:102:ARG:HH11	11:E:102:ARG:CG	2.16	0.57
12:K:97:GLU:HA	12:K:100:ILE:HG12	1.85	0.57
14:N:165:VAL:HG23	14:N:166:ASP:N	2.19	0.57
5:F:2662:A:H2'	13:L:457:LEU:HD13	1.87	0.57
8:I:1097:U:H2'	8:I:1098:A:O5'	2.04	0.57
10:M:10:A:C6	10:M:26:A:C2	2.93	0.57
14:N:91:PRO:HG3	14:N:154:LEU:HD12	1.85	0.57
14:N:113:HIS:O	14:N:117:GLU:HG2	2.05	0.57
3:C:1497:G:C2'	3:C:1498:U:H5'	2.33	0.57
11:E:32:PHE:CB	11:E:84:LEU:HD21	2.29	0.57
11:E:89:ARG:NE	11:E:91:LYS:HE2	2.19	0.57
13:L:101:LEU:C	13:L:101:LEU:HD12	2.28	0.57
13:L:445:GLU:HG3	13:L:446:THR:N	2.18	0.57
14:N:185:ILE:HG22	14:N:199:TYR:CB	2.26	0.57
4:D:55:A:N3	13:L:321:TYR:C	2.62	0.57
12:K:39:GLU:HG2	12:K:180:PHE:CB	2.35	0.57
12:K:49:ILE:HD12	12:K:49:ILE:N	2.13	0.57
13:L:17:ILE:N	13:L:17:ILE:HD12	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:408:VAL:CG1	13:L:669:PHE:CZ	2.58	0.57
8:I:1058:G:N1	8:I:1081:U:C2	2.72	0.57
8:I:1073:A:N7	8:I:1074:G:C6	2.72	0.57
8:I:1102:C:O2'	8:I:1103:A:H8	1.88	0.57
9:J:2186:G:C2'	9:J:2187:G:H5''	2.35	0.57
2:B:390:C:H2'	2:B:391:G:C8	2.40	0.57
8:I:1082:U:H3'	8:I:1083:U:C6	2.39	0.57
12:K:50:ASP:OD1	12:K:55:ASP:HA	2.05	0.57
12:K:89:ALA:HB2	12:K:153:ILE:CB	2.34	0.57
13:L:114:VAL:HG12	13:L:152:THR:HB	1.87	0.57
13:L:506:GLN:NE2	13:L:578:SER:OG	2.38	0.57
14:N:100:GLY:O	14:N:104:ASN:N	2.38	0.57
8:I:1078:U:C2	8:I:1088:A:H1'	2.40	0.57
8:I:1082:U:O5'	8:I:1082:U:H6	1.88	0.57
11:E:18:VAL:O	11:E:19:ARG:HB3	2.03	0.57
13:L:484:ARG:CD	13:L:606:MET:HE2	2.34	0.57
14:N:134:GLU:HA	14:N:137:ARG:HB2	1.86	0.57
8:I:1066:U:C2'	8:I:1067:A:H5''	2.35	0.57
8:I:1086:A:H3'	8:I:1087:G:C5'	2.35	0.57
13:L:600:VAL:HA	13:L:684:GLN:NE2	2.20	0.57
8:I:1102:C:O2	8:I:1102:C:H2'	2.03	0.56
14:N:158:LEU:HD12	14:N:158:LEU:N	2.20	0.56
14:N:193:ASP:OD2	14:N:196:LEU:HD11	2.04	0.56
6:G:1847:A:H3'	6:G:1848:A:C5'	2.34	0.56
8:I:1052:C:C2	8:I:1053:C:C5	2.92	0.56
13:L:391:GLY:C	13:L:393:ASP:H	2.13	0.56
13:L:554:PRO:HG3	13:L:599:PRO:HG3	1.86	0.56
13:L:684:GLN:O	13:L:688:ILE:HG13	2.04	0.56
14:N:70:PHE:CE2	14:N:163:PHE:HD1	2.23	0.56
14:N:236:TYR:HA	14:N:239:VAL:CG2	2.36	0.56
8:I:1056:G:N2	8:I:1104:C:N4	2.53	0.56
8:I:1065:U:N3	8:I:1066:U:C6	2.73	0.56
10:M:62:C:H2'	10:M:62:C:O2	2.05	0.56
11:E:39:VAL:HG12	11:E:40:VAL:N	2.20	0.56
11:E:70:ILE:HD12	11:E:70:ILE:N	2.20	0.56
13:L:486:THR:O	13:L:600:VAL:CB	2.52	0.56
13:L:486:THR:C	13:L:600:VAL:HG12	2.30	0.56
14:N:75:LYS:HA	14:N:78:GLN:HG3	1.87	0.56
8:I:1087:G:C2	8:I:1103:A:C4	2.93	0.56
9:J:2189:U:C2'	9:J:2190:G:H5''	2.36	0.56
14:N:32:ILE:HD13	14:N:40:HIS:HB3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:41:VAL:HB	12:K:178:ALA:CB	2.36	0.56
14:N:112:VAL:HG22	14:N:149:LEU:HD13	1.88	0.56
5:F:2660:A:H4'	13:L:665:GLY:HA3	1.88	0.56
5:F:2662:A:N1	13:L:21:ILE:HD13	2.17	0.56
8:I:1068:G:C6	8:I:1073:A:C2	2.93	0.56
13:L:404:VAL:HG13	13:L:405:PRO:HD2	1.86	0.56
10:M:22:A:H2'	10:M:23:U:C5'	2.36	0.56
14:N:144:ARG:HA	14:N:147:LYS:HB3	1.86	0.56
2:B:390:C:H2'	2:B:391:G:H8	1.70	0.56
8:I:1057:A:C2	8:I:1058:G:C8	2.93	0.56
11:E:60:LEU:N	11:E:64:TYR:O	2.34	0.56
11:E:120:TYR:CD1	11:E:120:TYR:N	2.73	0.56
12:K:75:LEU:HD23	12:K:76:ALA:N	2.21	0.56
13:L:391:GLY:O	13:L:392:GLU:HB3	2.05	0.56
14:N:14:GLY:O	14:N:15:VAL:HG13	2.04	0.56
14:N:69:LEU:HD13	14:N:91:PRO:HB2	1.87	0.56
11:E:22:SER:C	11:E:24:VAL:H	2.13	0.56
13:L:647:VAL:HG21	13:L:652:MET:SD	2.46	0.56
14:N:87:ARG:HD2	14:N:87:ARG:O	2.06	0.56
11:E:21:LYS:HD2	11:E:21:LYS:N	2.21	0.56
13:L:329:ARG:HH21	13:L:372:GLY:HA2	1.71	0.56
14:N:23:ARG:HG2	14:N:23:ARG:O	2.06	0.56
3:C:1410:G:H2'	3:C:1411:C:H6	1.70	0.55
3:C:1422:G:H2'	3:C:1423:G:C8	2.38	0.55
8:I:1092:C:N4	8:I:1093:G:N3	2.53	0.55
10:M:14:A:N6	10:M:46:A:C2	2.74	0.55
14:N:24:TRP:H	14:N:24:TRP:HD1	1.54	0.55
13:L:188:TYR:CE1	13:L:196:ILE:HG12	2.41	0.55
8:I:1082:U:H3'	8:I:1082:U:C6	2.41	0.55
8:I:1087:G:C5	8:I:1103:A:C6	2.95	0.55
11:E:69:TYR:C	11:E:70:ILE:HD12	2.30	0.55
13:L:316:ILE:CD1	13:L:326:THR:HB	2.37	0.55
8:I:1058:G:C6	8:I:1081:U:C2	2.94	0.55
8:I:1074:G:C5	8:I:1075:C:H5	2.25	0.55
9:J:2102:U:C5	9:J:2187:G:O6	2.59	0.55
10:M:50:G:O6	10:M:65:G:C6	2.59	0.55
10:M:70:G:H2'	10:M:71:G:H8	1.70	0.55
11:E:27:LEU:HD22	11:E:27:LEU:N	2.22	0.55
13:L:414:GLU:C	13:L:474:ALA:HB1	2.30	0.55
3:C:1441:G:H5''	3:C:1442:G:C5'	2.17	0.55
4:D:55:A:C2	13:L:322:VAL:CA	2.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:1067:A:N7	13:L:631:ILE:C	2.65	0.55
8:I:1085:A:O2'	8:I:1086:A:C5'	2.54	0.55
9:J:2175:C:H1'	12:K:215:THR:CA	2.33	0.55
11:E:119:LYS:O	11:E:120:TYR:HB2	2.07	0.55
14:N:114:ARG:O	14:N:117:GLU:HB2	2.07	0.55
14:N:142:LEU:HD23	14:N:142:LEU:O	2.07	0.55
11:E:82:VAL:O	11:E:106:ASP:HB2	2.07	0.55
12:K:75:LEU:HD23	12:K:75:LEU:C	2.32	0.55
8:I:1077:A:N7	8:I:1078:U:N3	2.55	0.55
9:J:2184:G:H2'	9:J:2185:C:C6	2.42	0.55
10:M:69:C:C2	10:M:70:G:N7	2.74	0.55
8:I:1068:G:C2	8:I:1069:A:N6	2.72	0.55
8:I:1070:A:N6	8:I:1096:A:H2	2.04	0.55
8:I:1107:G:C2'	8:I:1108:U:H5'	2.37	0.55
11:E:41:ARG:HG2	11:E:42:THR:H	1.72	0.55
11:E:90:VAL:O	11:E:90:VAL:HG12	2.07	0.55
13:L:486:THR:CA	13:L:600:VAL:HG12	2.36	0.55
13:L:594:VAL:HG12	13:L:599:PRO:CG	2.37	0.55
4:D:55:A:C2	13:L:322:VAL:CB	2.87	0.55
8:I:1054:A:H61	8:I:1105:U:H3	0.68	0.55
8:I:1084:A:C2	8:I:1085:A:C2	2.94	0.55
12:K:46:LYS:HB2	12:K:209:LEU:CB	2.37	0.55
12:K:89:ALA:HB2	12:K:153:ILE:CA	2.36	0.55
3:C:1442:G:C2'	3:C:1442(A):G:H5''	2.36	0.54
8:I:1064:C:H3'	8:I:1065:U:C5	2.42	0.54
13:L:602:LEU:HD23	13:L:678:GLU:HA	1.88	0.54
14:N:19:HIS:CE1	14:N:206:ASP:HB2	2.42	0.54
8:I:1070:A:C8	8:I:1097:U:O5'	2.59	0.54
11:E:126:LYS:HE2	11:E:128:ALA:H	1.72	0.54
13:L:124:GLN:HE22	13:L:401:SER:HB3	1.61	0.54
13:L:449:THR:O	13:L:450:ILE:HD13	2.07	0.54
8:I:1072:C:H2'	8:I:1093:G:O6	2.08	0.54
12:K:212:VAL:O	12:K:213:TYR:CB	2.55	0.54
13:L:415:PRO:CG	13:L:421:GLN:HG2	2.35	0.54
13:L:519:ARG:HD2	13:L:677:GLN:HA	1.89	0.54
14:N:194:PRO:O	14:N:196:LEU:N	2.39	0.54
8:I:1070:A:H8	8:I:1097:U:O5'	1.90	0.54
9:J:2111:C:H1'	9:J:2118:U:H1'	1.89	0.54
12:K:39:GLU:HA	12:K:180:PHE:HA	1.89	0.54
13:L:449:THR:C	13:L:450:ILE:HD13	2.33	0.54
13:L:648:PRO:HG2	13:L:651:GLU:CG	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:98:LEU:HB2	14:N:101:MET:HE3	1.89	0.54
13:L:363:ARG:HH11	13:L:363:ARG:HG3	1.71	0.54
14:N:216:SER:C	14:N:218:ALA:H	2.16	0.54
5:F:2662:A:O2'	13:L:457:LEU:CD1	2.56	0.54
8:I:1077:A:C8	8:I:1078:U:C4	2.96	0.54
10:M:53:G:H2'	10:M:53:G:N3	2.23	0.54
13:L:137:ASN:ND2	13:L:138:LYS:H	2.06	0.54
14:N:188:ALA:O	14:N:202:PRO:HA	2.07	0.54
7:H:2469:A:H2	7:H:2481:G:H21	1.55	0.54
8:I:1061:U:H5'	8:I:1070:A:H4'	1.86	0.54
13:L:481:VAL:HG23	13:L:655:TYR:CA	2.37	0.54
14:N:158:LEU:H	14:N:158:LEU:CD1	2.20	0.54
9:J:2101:G:C6	9:J:2102:U:C5	2.96	0.54
9:J:2168:G:C2	10:M:56:C:C2	2.94	0.54
11:E:34:ARG:HG2	11:E:35:GLY:N	2.23	0.54
13:L:406:GLU:HG3	13:L:670:VAL:N	2.22	0.54
14:N:75:LYS:C	14:N:77:ALA:H	2.16	0.54
14:N:102:LEU:HD12	14:N:102:LEU:N	2.23	0.54
9:J:2189:U:H2'	9:J:2190:G:H5''	1.90	0.54
4:D:55:A:C4'	13:L:321:TYR:HB3	2.27	0.54
8:I:1052:C:C2	8:I:1053:C:H5	2.26	0.54
8:I:1063:G:N2	8:I:1076:C:C2	2.76	0.54
11:E:50:SER:O	11:E:51:ALA:HB2	2.08	0.54
13:L:115:GLU:HB3	13:L:116:PRO:HD2	1.90	0.54
13:L:238:THR:HB	13:L:241:GLU:OE1	2.08	0.54
13:L:481:VAL:HG23	13:L:655:TYR:CB	2.37	0.54
13:L:625:ASN:HD21	13:L:631:ILE:HD13	1.73	0.54
14:N:74:LYS:HZ1	14:N:76:GLN:HB2	1.73	0.54
7:H:2485:G:O2'	7:H:2486:G:H5'	2.08	0.53
8:I:1053:C:C2'	8:I:1054:A:H5'	2.37	0.53
8:I:1080:C:O2'	8:I:1081:U:H5'	2.08	0.53
14:N:70:PHE:O	14:N:92:TYR:HA	2.08	0.53
14:N:163:PHE:HA	14:N:185:ILE:O	2.07	0.53
4:D:358:U:H2'	4:D:359:U:C6	2.43	0.53
7:H:2461:C:H2'	7:H:2462:U:H6	1.69	0.53
8:I:1061:U:O2	8:I:1061:U:H2'	2.08	0.53
13:L:555:LEU:HB3	13:L:688:ILE:CD1	2.39	0.53
11:E:89:ARG:HE	11:E:91:LYS:HE2	1.74	0.53
12:K:18:LYS:HD3	12:K:19:VAL:H	1.74	0.53
8:I:1099:G:H2'	8:I:1100:C:H6	1.74	0.53
13:L:127:LYS:HZ3	13:L:402:ILE:HG12	1.69	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:417:THR:O	13:L:419:ALA:N	2.39	0.53
13:L:519:ARG:CG	13:L:677:GLN:NE2	2.69	0.53
14:N:102:LEU:CD1	14:N:102:LEU:N	2.69	0.53
3:C:1431:C:H2'	3:C:1432:G:C5'	2.38	0.53
5:F:2660:A:C1'	13:L:665:GLY:HA2	2.19	0.53
13:L:165:GLN:NE2	13:L:260:LEU:HD13	2.21	0.53
14:N:121:LEU:O	14:N:127:ILE:HD11	2.08	0.53
10:M:75:C:C2	10:M:76:A:H4'	2.44	0.53
11:E:71:PRO:HD2	11:E:102:ARG:NH1	2.23	0.53
13:L:408:VAL:HG12	13:L:669:PHE:HZ	1.63	0.53
2:B:368:U:OP2	13:L:351:ARG:HG2	2.09	0.53
11:E:41:ARG:CB	11:E:41:ARG:NH1	2.72	0.53
13:L:486:THR:N	13:L:600:VAL:HG12	2.24	0.53
14:N:54:THR:HG23	14:N:199:TYR:HB3	1.91	0.53
5:F:2668:G:O2'	5:F:2669:G:H5'	2.09	0.53
8:I:1059:G:N7	8:I:1060:U:O4'	2.42	0.53
9:J:2178:C:O5'	12:K:46:LYS:HD2	2.09	0.53
13:L:484:ARG:O	13:L:648:PRO:CA	2.54	0.53
14:N:8:LYS:O	14:N:9:GLU:C	2.51	0.53
5:F:2649:U:H2'	5:F:2650:U:C6	2.43	0.53
6:G:1876:A:H2'	6:G:1877:A:C8	2.44	0.53
11:E:34:ARG:HG2	11:E:35:GLY:H	1.72	0.53
13:L:32:ILE:HG23	13:L:273:LEU:HD11	1.89	0.53
14:N:130:ARG:HA	14:N:130:ARG:HE	1.74	0.53
3:C:1405:G:O2'	3:C:1406:U:H5'	2.08	0.52
3:C:1458:G:O2'	3:C:1459:C:H5'	2.08	0.52
8:I:1057:A:C2	8:I:1058:G:C5	2.98	0.52
13:L:182:ARG:HB2	13:L:184:LYS:HD2	1.91	0.52
13:L:425:SER:HA	13:L:428:LEU:HD12	1.90	0.52
14:N:68:ILE:HD12	14:N:68:ILE:N	2.24	0.52
14:N:216:SER:O	14:N:218:ALA:N	2.43	0.52
5:F:2673:G:O2'	5:F:2674:G:H5'	2.08	0.52
12:K:22:ILE:HG22	12:K:25:ALA:HB2	1.90	0.52
13:L:308:PRO:HB2	13:L:394:ALA:HB1	1.91	0.52
4:D:356:A:H2'	4:D:357:G:H8	1.74	0.52
4:D:357:G:C2	4:D:358:U:C5	2.98	0.52
5:F:2660:A:O2'	13:L:660:ARG:CG	2.57	0.52
8:I:1095:A:C8	8:I:1096:A:H8	2.28	0.52
11:E:41:ARG:CG	11:E:42:THR:N	2.72	0.52
12:K:89:ALA:CB	12:K:153:ILE:HA	2.39	0.52
13:L:118:SER:O	13:L:121:VAL:HG22	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:170:ARG:HG2	13:L:170:ARG:HH11	1.74	0.52
14:N:30:ARG:HH21	14:N:194:PRO:HG2	1.74	0.52
2:B:392:G:H2'	2:B:393:A:C8	2.44	0.52
8:I:1057:A:C4	8:I:1058:G:C8	2.97	0.52
10:M:69:C:N3	10:M:70:G:N7	2.57	0.52
13:L:550:MET:SD	13:L:563:ILE:HD11	2.49	0.52
14:N:112:VAL:O	14:N:115:LEU:HB3	2.09	0.52
8:I:1095:A:C8	8:I:1096:A:C8	2.97	0.52
8:I:1106:G:C6	8:I:1107:G:O6	2.63	0.52
10:M:65:G:O2'	10:M:66:U:H5'	2.08	0.52
12:K:168:THR:CA	12:K:173:ALA:HB2	2.31	0.52
13:L:483:TYR:OH	13:L:627:ARG:CZ	2.56	0.52
13:L:546:ILE:HG23	13:L:590:ILE:HG12	1.92	0.52
4:D:52:G:O2'	4:D:53:A:H5'	2.10	0.52
8:I:1072:C:H2'	8:I:1093:G:C6	2.44	0.52
11:E:86:ARG:HB2	11:E:101:VAL:HG22	1.91	0.52
12:K:64:LEU:HD13	12:K:65:PRO:CD	2.37	0.52
13:L:344:THR:C	13:L:346:LYS:H	2.18	0.52
8:I:1102:C:C2'	8:I:1103:A:O5'	2.57	0.52
13:L:114:VAL:CG1	13:L:152:THR:HB	2.39	0.52
13:L:160:ARG:HD3	13:L:255:ILE:HG22	1.92	0.52
13:L:636:PRO:HD3	13:L:641:GLN:HE22	1.75	0.52
14:N:109:SER:O	14:N:112:VAL:N	2.43	0.52
14:N:204:ASN:C	14:N:204:ASN:ND2	2.68	0.52
6:G:1865:G:H5'	6:G:1866:C:OP2	2.10	0.52
8:I:1091:G:N1	8:I:1100:C:N4	2.57	0.52
8:I:1094:U:C5	8:I:1096:A:OP2	2.63	0.52
12:K:62:VAL:O	12:K:63:SER:C	2.53	0.52
13:L:181:LEU:HD12	13:L:181:LEU:C	2.35	0.52
14:N:124:SER:OG	14:N:125:PRO:HD2	2.09	0.52
14:N:162:ILE:O	14:N:185:ILE:HG12	2.09	0.52
14:N:178:ARG:HH22	14:N:196:LEU:CA	2.22	0.52
10:M:71:G:H2'	10:M:72:A:H8	1.75	0.52
13:L:115:GLU:HB3	13:L:116:PRO:CD	2.39	0.52
14:N:15:VAL:H	14:N:16:HIS:CE1	2.27	0.52
3:C:1457:G:C2	3:C:1458:G:C8	2.98	0.52
8:I:1084:A:H2'	8:I:1084:A:N3	2.24	0.52
9:J:2193:G:H5'	9:J:2193:G:H8	1.74	0.52
10:M:22:A:H5'	10:M:22:A:C8	2.42	0.52
6:G:1880:C:H6	6:G:1880:C:H5'	1.74	0.51
8:I:1089:G:O5'	8:I:1089:G:C8	2.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:2127:G:N1	9:J:2161:C:H1'	2.25	0.51
13:L:127:LYS:CE	13:L:402:ILE:CG1	2.63	0.51
14:N:215:LEU:O	14:N:218:ALA:HB3	2.10	0.51
9:J:2168:G:C2	10:M:19:G:N1	2.77	0.51
11:E:83:VAL:HG13	11:E:84:LEU:N	2.24	0.51
13:L:486:THR:HG21	13:L:678:GLU:HG2	1.91	0.51
14:N:90:MET:HE2	14:N:90:MET:HA	1.92	0.51
8:I:1091:G:N1	8:I:1101:U:N3	2.58	0.51
14:N:88:ALA:HB2	14:N:219:VAL:CG1	2.39	0.51
14:N:144:ARG:HG3	14:N:145:LEU:H	1.75	0.51
14:N:166:ASP:HB2	14:N:205:ASP:OD2	2.10	0.51
9:J:2115:G:H5'	9:J:2116:G:OP2	2.11	0.51
11:E:113:ARG:HG2	11:E:113:ARG:HH11	1.75	0.51
14:N:27:LYS:C	14:N:29:ALA:H	2.19	0.51
10:M:25:U:C2	10:M:26:A:C8	2.98	0.51
13:L:8:ASP:OD1	13:L:10:LYS:HE2	2.10	0.51
7:H:2467:C:H2'	7:H:2468:G:O4'	2.09	0.51
9:J:2186:G:C3'	9:J:2187:G:H5''	2.41	0.51
11:E:41:ARG:HG2	11:E:42:THR:N	2.26	0.51
3:C:1443:G:H22	3:C:1460:A:H1'	1.75	0.51
8:I:1086:A:C2'	8:I:1087:G:H5'	2.41	0.51
10:M:25:U:N3	10:M:26:A:C5	2.79	0.51
13:L:85:PRO:HG2	13:L:94:VAL:CG2	2.40	0.51
13:L:519:ARG:HA	13:L:519:ARG:HH11	1.75	0.51
14:N:168:THR:HG21	14:N:192:SER:HA	1.92	0.51
14:N:216:SER:C	14:N:218:ALA:N	2.68	0.51
1:A:348:G:O2'	1:A:349:A:H5'	2.10	0.51
8:I:1063:G:C4	8:I:1064:C:C5	2.99	0.51
10:M:53:G:C2	10:M:62:C:C2	2.99	0.51
10:M:69:C:C2	10:M:70:G:C8	2.99	0.51
11:E:52:LEU:O	11:E:54:LYS:HD2	2.11	0.51
8:I:1068:G:C4	8:I:1069:A:N6	2.79	0.51
13:L:90:PHE:O	13:L:94:VAL:HG23	2.11	0.51
14:N:208:ILE:HA	14:N:211:ILE:HD12	1.93	0.51
2:B:390:C:O5'	2:B:390:C:H6	1.93	0.50
8:I:1087:G:N3	8:I:1103:A:C4	2.80	0.50
11:E:62:SER:O	11:E:64:TYR:HD1	1.93	0.50
13:L:95:GLU:CD	13:L:402:ILE:HA	2.36	0.50
13:L:127:LYS:CD	13:L:401:SER:CA	2.88	0.50
13:L:519:ARG:CZ	13:L:678:GLU:CG	2.89	0.50
14:N:184:VAL:O	14:N:198:ASP:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:1061:U:H4'	8:I:1070:A:C4'	2.41	0.50
8:I:1087:G:C4	8:I:1103:A:C2	2.99	0.50
12:K:191:ALA:C	12:K:193:ILE:N	2.69	0.50
14:N:153:ARG:O	14:N:154:LEU:C	2.54	0.50
14:N:175:ARG:O	14:N:176:GLU:C	2.55	0.50
5:F:2660:A:O2'	13:L:665:GLY:CA	2.58	0.50
8:I:1062:G:C6	8:I:1077:A:C4	2.99	0.50
11:E:61:THR:OG1	11:E:62:SER:N	2.45	0.50
12:K:51:PRO:HB3	12:K:203:GLY:C	2.37	0.50
13:L:335:LEU:HD11	13:L:341:VAL:HG11	1.94	0.50
14:N:144:ARG:O	14:N:147:LYS:HB3	2.11	0.50
5:F:2656:U:C4	5:F:2657:A:H2	2.30	0.50
8:I:1071:G:C2'	8:I:1072:C:H5'	2.41	0.50
8:I:1085:A:HO2'	8:I:1086:A:C4'	2.09	0.50
8:I:1097:U:H2'	8:I:1098:A:C5'	2.41	0.50
8:I:1102:C:C1'	8:I:1103:A:H8	2.22	0.50
9:J:2111:C:H5'	9:J:2112:G:OP1	2.11	0.50
13:L:87:HIS:HB3	13:L:90:PHE:CE1	2.47	0.50
14:N:204:ASN:C	14:N:204:ASN:HD22	2.19	0.50
3:C:1436:U:O2'	3:C:1437:C:H5'	2.10	0.50
13:L:34:TYR:CZ	13:L:38:ARG:HD3	2.47	0.50
14:N:97:TRP:CH2	14:N:176:GLU:OE2	2.65	0.50
8:I:1086:A:H2'	8:I:1087:G:H5'	1.94	0.50
9:J:2107:C:H42	9:J:2182:G:H1	1.60	0.50
13:L:85:PRO:HG2	13:L:94:VAL:N	2.27	0.50
13:L:519:ARG:HD3	13:L:562:ASP:OD1	2.12	0.50
14:N:19:HIS:HD2	14:N:189:ASP:OD2	1.95	0.50
14:N:19:HIS:HE1	14:N:206:ASP:HB2	1.76	0.50
14:N:59:GLU:C	14:N:61:LEU:H	2.20	0.50
3:C:1433:A:C6	3:C:1468:A:C4	3.00	0.50
3:C:1459:C:O2'	3:C:1460:A:H5'	2.11	0.50
8:I:1063:G:N7	8:I:1070:A:OP2	2.45	0.50
8:I:1082:U:C6	8:I:1082:U:C3'	2.94	0.50
11:E:90:VAL:O	11:E:92:ASP:N	2.45	0.50
13:L:431:LEU:HD11	13:L:465:ARG:HD3	1.93	0.50
8:I:1053:C:O2	8:I:1053:C:H2'	2.11	0.50
8:I:1057:A:N1	8:I:1058:G:C5	2.80	0.50
9:J:2164:C:H5''	9:J:2165:G:N7	2.27	0.50
11:E:89:ARG:HA	11:E:97:ARG:HA	1.93	0.50
12:K:46:LYS:HB2	12:K:208:PHE:O	2.12	0.50
14:N:73:THR:HG22	14:N:95:GLN:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:84:GLU:OE1	14:N:216:SER:HA	2.12	0.50
14:N:98:LEU:O	14:N:101:MET:HG3	2.11	0.50
5:F:2662:A:O2'	13:L:457:LEU:HD11	2.11	0.49
13:L:484:ARG:C	13:L:649:LEU:CA	2.69	0.49
13:L:606:MET:HE3	13:L:671:MET:HG2	1.92	0.49
14:N:178:ARG:NH2	14:N:196:LEU:HA	2.27	0.49
14:N:213:LEU:HD22	14:N:214:ILE:HD13	1.94	0.49
2:B:368:U:C6	13:L:354:ARG:CD	2.80	0.49
8:I:1054:A:N1	8:I:1105:U:C2	2.77	0.49
13:L:534:ILE:HD12	13:L:567:LEU:HD11	1.94	0.49
14:N:194:PRO:O	14:N:197:VAL:N	2.45	0.49
3:C:1436:U:H2'	3:C:1437:C:H6	1.77	0.49
8:I:1095:A:O4'	13:L:617:MET:CG	2.60	0.49
9:J:2162:G:H5'	9:J:2171:A:C5'	2.42	0.49
11:E:55:VAL:HG12	11:E:56:ALA:N	2.27	0.49
13:L:13:ARG:HH11	13:L:277:VAL:CA	2.24	0.49
14:N:164:VAL:CG1	14:N:165:VAL:N	2.75	0.49
12:K:20:TYR:CG	12:K:21:THR:N	2.80	0.49
13:L:485:GLU:C	13:L:605:ILE:CD1	2.85	0.49
14:N:28:PHE:CD1	14:N:28:PHE:O	2.66	0.49
14:N:55:PHE:HE1	14:N:218:ALA:HA	1.78	0.49
13:L:122:TRP:CD2	13:L:157:LEU:HD13	2.48	0.49
13:L:607:ARG:NH2	13:L:644:ARG:HH21	2.11	0.49
14:N:12:GLU:C	14:N:14:GLY:N	2.67	0.49
14:N:84:GLU:HB3	14:N:219:VAL:CG2	2.39	0.49
14:N:149:LEU:O	14:N:153:ARG:HG3	2.13	0.49
8:I:1071:G:H2'	8:I:1072:C:H5''	1.94	0.49
10:M:73:G:H2'	10:M:73:G:N3	2.27	0.49
13:L:658:ASP:O	13:L:661:SER:HB3	2.12	0.49
8:I:1064:C:H3'	8:I:1065:U:H5	1.75	0.49
8:I:1065:U:C3'	8:I:1066:U:C5'	2.80	0.49
11:E:53:ARG:HG2	11:E:53:ARG:NH1	2.27	0.49
12:K:49:ILE:CG2	12:K:50:ASP:N	2.75	0.49
13:L:536:LYS:HD2	13:L:537:GLU:HG3	1.95	0.49
14:N:185:ILE:HG22	14:N:199:TYR:CD1	2.48	0.49
14:N:187:LEU:O	14:N:187:LEU:HD13	2.12	0.49
7:H:2469:A:H3'	7:H:2470:G:O4'	2.12	0.49
8:I:1083:U:C6	8:I:1083:U:H5''	2.48	0.49
8:I:1087:G:O6	8:I:1102:C:N3	2.46	0.49
14:N:178:ARG:HH11	14:N:178:ARG:CB	2.23	0.49
3:C:1478:C:O2'	3:C:1479:C:H5'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:1064:C:C4	8:I:1075:C:N4	2.80	0.49
8:I:1069:A:O2'	8:I:1070:A:H5''	2.13	0.49
9:J:2184:G:H2'	9:J:2185:C:H6	1.76	0.49
12:K:99:ILE:HG22	12:K:99:ILE:O	2.13	0.49
13:L:328:ILE:O	13:L:328:ILE:HD13	2.12	0.49
13:L:417:THR:O	13:L:418:LYS:HB2	2.13	0.49
13:L:454:MET:H	13:L:458:HIS:HD2	1.59	0.49
14:N:24:TRP:CZ3	14:N:26:PRO:HA	2.48	0.49
14:N:107:THR:HG23	14:N:110:GLN:OE1	2.12	0.49
5:F:2660:A:H3'	5:F:2661:G:O4'	2.12	0.49
11:E:45:PRO:HG2	11:E:51:ALA:N	2.28	0.49
13:L:409:ILE:HD11	13:L:657:THR:H	1.77	0.49
13:L:485:GLU:HB2	13:L:605:ILE:HD13	1.83	0.49
14:N:80:ILE:HG13	14:N:81:VAL:H	1.78	0.49
2:B:368:U:H5	13:L:354:ARG:HD2	0.68	0.48
3:C:1404:C:O5'	3:C:1404:C:H6	1.95	0.48
8:I:1054:A:N6	8:I:1104:C:H42	2.11	0.48
8:I:1054:A:C5	8:I:1055:G:O6	2.66	0.48
13:L:484:ARG:HD3	13:L:606:MET:SD	2.53	0.48
3:C:1473:A:H2'	3:C:1474:G:C8	2.47	0.48
10:M:1:U:O2'	10:M:2:C:C5'	2.61	0.48
10:M:73:G:H2'	10:M:74:C:C5'	2.42	0.48
11:E:20:LYS:H	11:E:20:LYS:HD3	1.77	0.48
13:L:484:ARG:CD	13:L:649:LEU:HD13	2.33	0.48
13:L:507:TYR:CD1	13:L:507:TYR:C	2.91	0.48
14:N:97:TRP:CH2	14:N:176:GLU:CD	2.91	0.48
8:I:1057:A:N1	8:I:1081:U:O2	2.46	0.48
8:I:1085:A:C1'	8:I:1086:A:C4'	2.72	0.48
10:M:50:G:C6	10:M:65:G:C6	3.01	0.48
13:L:85:PRO:HG2	13:L:94:VAL:CA	2.43	0.48
13:L:486:THR:C	13:L:600:VAL:H	2.21	0.48
14:N:83:MET:O	14:N:85:ALA:N	2.47	0.48
3:C:1442:G:H5'	3:C:1442:G:N9	2.27	0.48
3:C:1470:G:O2'	3:C:1471:G:H5'	2.13	0.48
13:L:312:LEU:HD23	13:L:399:LEU:HB2	1.96	0.48
14:N:162:ILE:O	14:N:162:ILE:HG13	2.13	0.48
3:C:1495:U:H2'	3:C:1496:C:H6	1.78	0.48
6:G:1848:A:C4	6:G:1849:G:C8	3.01	0.48
6:G:1866:C:H2'	6:G:1876:A:O4'	2.12	0.48
10:M:50:G:C6	10:M:65:G:N1	2.81	0.48
10:M:59:U:C5	10:M:60:U:C4	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:146:LEU:O	13:L:150:ILE:HG12	2.14	0.48
13:L:291:GLY:O	13:L:299:VAL:N	2.45	0.48
13:L:443:HIS:HB3	13:L:446:THR:OG1	2.13	0.48
13:L:587:SER:O	13:L:591:LYS:HG2	2.14	0.48
9:J:2127:G:H2'	9:J:2128:C:N1	2.28	0.48
13:L:127:LYS:HE3	13:L:402:ILE:HG13	1.80	0.48
13:L:417:THR:C	13:L:419:ALA:N	2.72	0.48
13:L:481:VAL:HG21	13:L:627:ARG:HH21	1.77	0.48
13:L:486:THR:CG2	13:L:678:GLU:CG	2.91	0.48
6:G:1842:G:H2'	6:G:1843:C:H6	1.79	0.48
8:I:1082:U:C5	8:I:1083:U:C5	3.02	0.48
9:J:2160:G:H3'	9:J:2161:C:H5''	1.95	0.48
14:N:197:VAL:HG12	14:N:200:ILE:HG12	1.95	0.48
13:L:345:THR:C	13:L:346:LYS:HG3	2.39	0.48
13:L:607:ARG:HH21	13:L:644:ARG:HH21	1.60	0.48
3:C:1484:C:H2'	3:C:1485:U:C6	2.48	0.48
8:I:1057:A:C8	8:I:1085:A:C6	3.01	0.48
13:L:485:GLU:C	13:L:647:VAL:C	2.63	0.48
14:N:46:LYS:O	14:N:47:THR:C	2.55	0.48
14:N:129:GLU:O	14:N:130:ARG:HB2	2.14	0.48
3:C:1431:C:H42	3:C:1469:G:H1	1.60	0.48
10:M:24:G:C6	10:M:25:U:C5	3.02	0.48
14:N:41:ILE:CD1	14:N:41:ILE:N	2.77	0.48
14:N:52:GLU:O	14:N:53:ARG:C	2.57	0.48
14:N:124:SER:O	14:N:127:ILE:HG12	2.14	0.48
5:F:2651:C:O2'	5:F:2652:C:H5'	2.13	0.47
8:I:1071:G:C2'	8:I:1072:C:C5'	2.91	0.47
11:E:58:VAL:O	11:E:60:LEU:HD22	2.13	0.47
12:K:208:PHE:O	12:K:209:LEU:CB	2.62	0.47
13:L:486:THR:CG2	13:L:678:GLU:HG2	2.44	0.47
13:L:510:VAL:HG11	13:L:542:VAL:HG21	1.96	0.47
14:N:49:GLU:O	14:N:52:GLU:HB3	2.14	0.47
3:C:1411:C:O2'	3:C:1412:C:H5'	2.14	0.47
5:F:2656:U:C4'	13:L:141:LYS:HZ2	2.15	0.47
6:G:1899:G:N2	6:G:1902:C:C5	2.82	0.47
8:I:1091:G:N2	8:I:1101:U:N1	2.61	0.47
11:E:102:ARG:CG	11:E:102:ARG:NH1	2.74	0.47
12:K:77:ILE:HG21	12:K:122:ALA:CA	2.43	0.47
13:L:8:ASP:O	13:L:9:LEU:C	2.57	0.47
13:L:85:PRO:HG3	13:L:93:GLU:HB3	1.95	0.47
13:L:92:ILE:CG2	13:L:93:GLU:N	2.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:22:LYS:H	14:N:40:HIS:CE1	2.32	0.47
14:N:172:ILE:HD12	14:N:172:ILE:N	2.30	0.47
3:C:1466:C:H2'	3:C:1467:G:H5'	1.95	0.47
5:F:2648:C:O2'	5:F:2649:U:H5'	2.14	0.47
5:F:2671:A:H2'	5:F:2672:G:H8	1.79	0.47
6:G:1854:A:H3'	6:G:1855:G:H8	1.80	0.47
8:I:1058:G:C2'	8:I:1059:G:O5'	2.62	0.47
8:I:1071:G:C5	8:I:1089:G:C2	3.02	0.47
14:N:100:GLY:O	14:N:104:ASN:HB3	2.15	0.47
6:G:1848:A:C5	6:G:1849:G:C8	3.02	0.47
8:I:1054:A:C6	8:I:1055:G:O6	2.66	0.47
13:L:122:TRP:CE3	13:L:157:LEU:HD13	2.49	0.47
8:I:1059:G:N7	8:I:1060:U:C1'	2.78	0.47
14:N:23:ARG:HG3	14:N:23:ARG:NH1	2.27	0.47
14:N:102:LEU:H	14:N:102:LEU:HD13	1.76	0.47
14:N:238:LEU:N	14:N:238:LEU:HD23	2.29	0.47
14:N:43:ASP:OD1	14:N:45:GLN:HB3	2.15	0.47
14:N:239:VAL:O	14:N:239:VAL:HG12	2.15	0.47
3:C:1402:C:H2'	3:C:1403:C:H6	1.79	0.47
3:C:1436:U:H2'	3:C:1437:C:C6	2.49	0.47
3:C:1466:C:C2'	3:C:1467:G:H5'	2.44	0.47
9:J:2192:G:C2	9:J:2193:G:C8	3.02	0.47
10:M:12:A:O2'	10:M:13:A:H5'	2.15	0.47
11:E:60:LEU:HD22	11:E:60:LEU:H	1.79	0.47
13:L:483:TYR:HB2	13:L:651:GLU:N	2.03	0.47
13:L:631:ILE:HD12	13:L:631:ILE:N	2.30	0.47
14:N:61:LEU:HA	14:N:64:ARG:HG2	1.95	0.47
2:B:394:G:HO2'	13:L:340:TYR:HH	1.63	0.47
5:F:2662:A:C2'	13:L:457:LEU:HD13	2.44	0.47
8:I:1092:C:H3'	8:I:1092:C:H6	1.80	0.47
13:L:318:ALA:HA	13:L:324:ARG:HA	1.96	0.47
13:L:361:ASN:O	13:L:362:HIS:HB3	2.15	0.47
13:L:363:ARG:HG3	13:L:363:ARG:NH1	2.30	0.47
13:L:519:ARG:CG	13:L:677:GLN:HE22	2.15	0.47
13:L:556:ILE:CG1	13:L:601:ILE:CG1	2.77	0.47
3:C:1423:G:O2'	3:C:1424:C:H5'	2.15	0.47
8:I:1066:U:N3	8:I:1069:A:OP1	2.48	0.47
12:K:40:THR:HG23	12:K:40:THR:O	2.15	0.47
13:L:166:LEU:CD2	13:L:180:VAL:HG11	2.41	0.47
13:L:487:ILE:HG22	13:L:599:PRO:N	2.30	0.47
14:N:92:TYR:CE2	14:N:151:GLY:CA	2.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:1063:G:C2	8:I:1075:C:C4	3.02	0.47
9:J:2162:G:H3'	9:J:2162:G:OP2	2.14	0.47
10:M:43:G:H2'	10:M:44:C:O4'	2.15	0.47
11:E:71:PRO:HD2	11:E:102:ARG:HH11	1.78	0.47
13:L:9:LEU:O	13:L:11:ARG:N	2.48	0.47
13:L:556:ILE:CD1	13:L:601:ILE:CG2	2.60	0.47
14:N:19:HIS:CD2	14:N:205:ASP:OD1	2.68	0.46
5:F:2656:U:C5'	13:L:141:LYS:HZ1	2.28	0.46
6:G:1878:G:H2'	6:G:1879:C:C6	2.49	0.46
8:I:1069:A:C3'	8:I:1070:A:H5''	2.46	0.46
9:J:2114:A:H2'	9:J:2114:A:N3	2.30	0.46
11:E:22:SER:C	11:E:24:VAL:N	2.70	0.46
13:L:114:VAL:HG13	13:L:114:VAL:O	2.16	0.46
13:L:408:VAL:O	13:L:654:GLY:CA	2.62	0.46
13:L:89:ASP:O	13:L:91:THR:N	2.42	0.46
5:F:2658:C:O2	5:F:2658:C:C2'	2.63	0.46
8:I:1097:U:C2'	8:I:1098:A:O5'	2.64	0.46
12:K:68:LEU:CD2	12:K:179:SER:HA	2.46	0.46
13:L:264:LEU:O	13:L:264:LEU:HD23	2.15	0.46
13:L:415:PRO:HA	13:L:474:ALA:HB2	1.98	0.46
14:N:187:LEU:HA	14:N:201:ILE:O	2.15	0.46
3:C:1496:C:H2'	3:C:1497:G:C8	2.51	0.46
8:I:1057:A:C2	8:I:1058:G:N7	2.83	0.46
9:J:2124:G:C2'	9:J:2125:G:H5'	2.45	0.46
12:K:92:ASP:CG	12:K:93:TYR:N	2.73	0.46
12:K:183:GLU:CB	12:K:186:ALA:HB3	2.45	0.46
13:L:319:ASP:HB2	13:L:325:LEU:HD12	1.98	0.46
13:L:600:VAL:HG11	13:L:678:GLU:OE2	2.16	0.46
13:L:627:ARG:NH2	13:L:655:TYR:HD1	2.13	0.46
3:C:1416:G:H2'	3:C:1417:G:O4'	2.15	0.46
8:I:1071:G:C3'	8:I:1072:C:H5'	2.44	0.46
11:E:7:ILE:O	11:E:10:LEU:N	2.49	0.46
12:K:18:LYS:CD	12:K:19:VAL:HG23	2.41	0.46
13:L:196:ILE:HD13	13:L:197:ARG:N	2.31	0.46
13:L:555:LEU:HD13	13:L:684:GLN:HG2	1.26	0.46
13:L:636:PRO:HD3	13:L:641:GLN:NE2	2.30	0.46
14:N:223:ILE:C	14:N:225:ALA:N	2.70	0.46
3:C:1430:C:O2'	3:C:1431:C:H5'	2.16	0.46
3:C:1469:G:H2'	3:C:1470:G:H8	1.81	0.46
8:I:1078:U:C5'	8:I:1079:C:OP1	2.63	0.46
8:I:1095:A:C2'	13:L:617:MET:HE2	2.12	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:60:LEU:HD23	11:E:64:TYR:HB3	1.98	0.46
8:I:1053:C:C2	8:I:1106:G:N2	2.77	0.46
8:I:1077:A:H3'	8:I:1078:U:C6	2.50	0.46
8:I:1105:U:HO2'	8:I:1106:G:P	2.38	0.46
11:E:62:SER:C	11:E:64:TYR:H	2.23	0.46
11:E:86:ARG:HB2	11:E:101:VAL:CG2	2.45	0.46
4:D:55:A:H2	13:L:322:VAL:HG12	0.42	0.46
5:F:2660:A:O4'	13:L:665:GLY:HA3	2.09	0.46
6:G:1860:G:H2'	6:G:1861:G:H8	1.81	0.46
10:M:70:G:H2'	10:M:71:G:C8	2.50	0.46
11:E:42:THR:HG23	11:E:42:THR:O	2.15	0.46
11:E:48:PRO:C	11:E:49:ASN:HD22	2.24	0.46
14:N:178:ARG:HH22	14:N:196:LEU:HA	1.81	0.46
5:F:2653:U:C3'	5:F:2654:A:H5''	2.46	0.46
7:H:2464:C:O2'	7:H:2465:C:P	2.74	0.46
13:L:403:GLU:HG2	13:L:404:VAL:N	2.31	0.46
14:N:80:ILE:HG13	14:N:81:VAL:N	2.30	0.46
14:N:155:LEU:N	14:N:155:LEU:HD22	2.31	0.46
3:C:1488:G:O2'	3:C:1489:G:H5'	2.16	0.45
8:I:1097:U:C2	8:I:1098:A:O4'	2.69	0.45
10:M:4:G:C2'	10:M:5:U:O5'	2.64	0.45
12:K:41:VAL:O	12:K:178:ALA:HB3	2.16	0.45
13:L:110:SER:OG	13:L:136:ALA:HB1	2.16	0.45
13:L:609:GLU:HB2	13:L:670:VAL:CG2	2.46	0.45
14:N:239:VAL:O	14:N:241:GLU:N	2.49	0.45
8:I:1074:G:C4	8:I:1075:C:H5	2.34	0.45
9:J:2176:A:H2'	9:J:2177:C:C6	2.52	0.45
11:E:119:LYS:O	11:E:120:TYR:CB	2.64	0.45
14:N:189:ASP:OD1	14:N:205:ASP:HB3	2.16	0.45
2:B:393:A:C2	2:B:394:G:C8	3.04	0.45
4:D:358:U:H2'	4:D:359:U:H6	1.80	0.45
8:I:1057:A:H2	8:I:1082:U:H3	1.63	0.45
8:I:1087:G:N9	8:I:1103:A:C2	2.84	0.45
11:E:88:GLY:O	11:E:99:HIS:ND1	2.48	0.45
12:K:77:ILE:HD12	12:K:123:VAL:H	1.80	0.45
12:K:196:LEU:C	12:K:198:ALA:N	2.71	0.45
13:L:288:PRO:HB2	13:L:301:ILE:O	2.16	0.45
13:L:345:THR:O	13:L:345:THR:HG22	2.17	0.45
13:L:484:ARG:HA	13:L:649:LEU:HA	0.62	0.45
13:L:583:LYS:C	13:L:583:LYS:HE2	2.42	0.45
14:N:78:GLN:HB3	14:N:94:ASN:HD21	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:91:PRO:CG	14:N:154:LEU:HD12	2.46	0.45
14:N:97:TRP:CZ3	14:N:173:ALA:HA	2.51	0.45
14:N:220:ASP:O	14:N:223:ILE:N	2.49	0.45
6:G:1843:C:O2'	6:G:1844:C:H5'	2.17	0.45
9:J:2170:A:O2'	9:J:2171:A:C8	2.66	0.45
10:M:46:A:H2'	10:M:48:U:C4'	2.47	0.45
12:K:67:GLY:O	12:K:68:LEU:HB2	2.17	0.45
13:L:487:ILE:CG2	13:L:594:VAL:HA	2.46	0.45
13:L:595:GLN:HA	13:L:599:PRO:HG3	1.99	0.45
8:I:1056:G:H21	8:I:1104:C:N4	2.15	0.45
8:I:1063:G:C2	8:I:1075:C:N4	2.85	0.45
8:I:1096:A:N7	8:I:1097:U:C6	2.85	0.45
3:C:1484:C:O2'	3:C:1485:U:H5'	2.17	0.45
5:F:2656:U:C4'	13:L:141:LYS:NZ	2.73	0.45
5:F:2656:U:C5'	13:L:141:LYS:NZ	2.80	0.45
7:H:2464:C:O2'	7:H:2465:C:O5'	2.35	0.45
8:I:1075:C:O2	8:I:1075:C:H2'	2.15	0.45
10:M:22:A:H2'	10:M:23:U:O4'	2.16	0.45
10:M:24:G:C4	10:M:25:U:C5	3.05	0.45
12:K:47:LEU:HD21	12:K:172:HIS:CA	2.46	0.45
14:N:16:HIS:HB3	14:N:210:SER:CB	2.46	0.45
3:C:1437:C:H2'	3:C:1438:G:H8	1.80	0.45
10:M:75:C:C2'	10:M:76:A:C5'	2.41	0.45
12:K:34:THR:O	12:K:35:ALA:HB2	2.17	0.45
13:L:458:HIS:CE1	13:L:462:ILE:HD11	2.51	0.45
13:L:606:MET:HE2	13:L:671:MET:HE3	1.99	0.45
4:D:55:A:N3	13:L:322:VAL:CA	2.79	0.45
4:D:57:G:O2'	4:D:58:C:H5'	2.17	0.45
8:I:1068:G:C2	8:I:1073:A:C2	3.05	0.45
8:I:1072:C:H42	8:I:1100:C:H41	1.65	0.45
13:L:146:LEU:C	13:L:146:LEU:HD13	2.42	0.45
13:L:413:ILE:CD1	13:L:451:ILE:HD11	2.40	0.45
14:N:19:HIS:CG	14:N:20:GLU:H	2.34	0.45
14:N:39:ILE:CG2	14:N:40:HIS:N	2.79	0.45
14:N:52:GLU:O	14:N:54:THR:N	2.50	0.45
14:N:219:VAL:O	14:N:222:ILE:HB	2.16	0.45
10:M:50:G:C6	10:M:65:G:C2	3.05	0.45
13:L:92:ILE:HG23	13:L:93:GLU:H	1.79	0.45
13:L:418:LYS:HA	13:L:421:GLN:CB	2.47	0.45
13:L:616:TYR:HA	13:L:619:ASP:OD1	2.17	0.45
3:C:1431:C:O2'	3:C:1432:G:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:51:PRO:HB2	12:K:202:GLU:CB	2.46	0.45
13:L:461:ILE:O	13:L:465:ARG:HB2	2.17	0.45
13:L:493:VAL:HG11	13:L:592:GLU:HG3	1.99	0.45
14:N:198:ASP:OD2	14:N:198:ASP:N	2.47	0.45
3:C:1471:G:O2'	3:C:1472:U:H5'	2.17	0.44
8:I:1063:G:N7	8:I:1070:A:OP1	2.50	0.44
8:I:1064:C:N4	8:I:1075:C:N4	2.65	0.44
8:I:1069:A:H2	8:I:1096:A:H5'	1.78	0.44
11:E:89:ARG:NH2	11:E:91:LYS:HD3	2.32	0.44
12:K:64:LEU:HD12	12:K:66:HIS:HB2	1.98	0.44
13:L:483:TYR:HB3	13:L:651:GLU:HB2	1.97	0.44
8:I:1062:G:O6	8:I:1077:A:C4	2.70	0.44
8:I:1078:U:N3	8:I:1088:A:O2'	2.45	0.44
11:E:21:LYS:HD2	11:E:21:LYS:H	1.83	0.44
11:E:30:ALA:O	11:E:31:PRO:C	2.59	0.44
13:L:485:GLU:CB	13:L:605:ILE:HA	2.37	0.44
13:L:485:GLU:OE2	13:L:650:ALA:HB3	2.17	0.44
13:L:680:PRO:HD2	13:L:683:VAL:HG21	2.00	0.44
14:N:74:LYS:HG3	14:N:77:ALA:HB3	1.99	0.44
8:I:1057:A:C8	8:I:1085:A:C2	3.05	0.44
13:L:28:THR:O	13:L:32:ILE:HG13	2.17	0.44
13:L:481:VAL:HB	13:L:655:TYR:HA	1.37	0.44
13:L:530:VAL:O	13:L:530:VAL:CG1	2.62	0.44
14:N:211:ILE:O	14:N:215:LEU:HB2	2.17	0.44
7:H:2476:A:H3'	7:H:2476:A:N3	2.32	0.44
9:J:2192:G:H2'	9:J:2193:G:H5''	1.99	0.44
13:L:82:ILE:HG12	13:L:100:VAL:HG12	1.99	0.44
13:L:280:LEU:HD12	13:L:280:LEU:HA	1.75	0.44
13:L:481:VAL:HG21	13:L:627:ARG:NH2	2.31	0.44
14:N:68:ILE:H	14:N:90:MET:CE	2.29	0.44
14:N:101:MET:O	14:N:105:PHE:N	2.50	0.44
6:G:1851:U:C2'	6:G:1852:C:H5'	2.48	0.44
8:I:1061:U:O2'	8:I:1070:A:N3	2.45	0.44
8:I:1106:G:O6	8:I:1107:G:O6	2.35	0.44
9:J:2103:C:H5'	9:J:2104:G:OP2	2.17	0.44
11:E:5:PRO:HA	11:E:9:GLN:NE2	2.33	0.44
11:E:58:VAL:N	11:E:66:VAL:O	2.49	0.44
11:E:117:ARG:O	11:E:118:SER:C	2.60	0.44
13:L:238:THR:HG22	13:L:241:GLU:HG3	1.98	0.44
14:N:19:HIS:O	14:N:20:GLU:C	2.60	0.44
14:N:203:GLY:O	14:N:204:ASN:C	2.59	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:55:A:C6	4:D:56:U:C2	3.06	0.44
10:M:62:C:O2	10:M:62:C:C2'	2.63	0.44
13:L:600:VAL:HG11	13:L:678:GLU:HB3	1.99	0.44
14:N:77:ALA:HB2	14:N:211:ILE:CD1	2.45	0.44
3:C:1423:G:H2'	3:C:1424:C:H6	1.83	0.44
3:C:1472:U:O2'	3:C:1473:A:H5'	2.18	0.44
8:I:1063:G:N1	8:I:1075:C:C4	2.84	0.44
12:K:41:VAL:C	12:K:178:ALA:HB3	2.43	0.44
12:K:180:PHE:O	12:K:182:PRO:N	2.51	0.44
13:L:406:GLU:O	13:L:408:VAL:HG13	2.17	0.44
14:N:114:ARG:HA	14:N:117:GLU:CG	2.46	0.44
3:C:1401:G:C2	3:C:1402:C:H1'	2.53	0.44
3:C:1412:C:H2'	3:C:1413:A:H8	1.79	0.44
8:I:1067:A:N6	13:L:631:ILE:H	2.16	0.44
9:J:2175:C:C1'	12:K:215:THR:HA	2.37	0.44
10:M:54:5MU:H2'	10:M:55:PSU:H5''	1.98	0.44
12:K:97:GLU:CA	12:K:100:ILE:HG12	2.46	0.44
13:L:20:HIS:CD2	13:L:117:GLN:H	2.31	0.44
13:L:114:VAL:O	13:L:114:VAL:HG22	2.17	0.44
13:L:438:PHE:HB2	13:L:452:SER:O	2.17	0.44
3:C:1452:C:H4'	3:C:1456:G:C5'	2.47	0.44
8:I:1071:G:O5'	8:I:1089:G:O6	2.36	0.44
8:I:1090:U:OP2	8:I:1090:U:H6	2.01	0.44
10:M:73:G:N2	10:M:74:C:O4'	2.51	0.44
13:L:409:ILE:O	13:L:452:SER:HA	2.18	0.44
13:L:487:ILE:HA	13:L:599:PRO:HA	2.00	0.44
14:N:44:LEU:O	14:N:45:GLN:C	2.61	0.44
14:N:189:ASP:OD1	14:N:189:ASP:N	2.49	0.44
6:G:1844:C:C2'	6:G:1845:G:H5'	2.47	0.43
9:J:2124:G:O2'	9:J:2125:G:H5'	2.18	0.43
13:L:269:VAL:O	13:L:273:LEU:HD22	2.18	0.43
14:N:17:PHE:CD2	14:N:17:PHE:N	2.85	0.43
14:N:71:VAL:HG13	14:N:93:VAL:HB	1.99	0.43
14:N:116:GLU:HA	14:N:119:GLU:CB	2.48	0.43
3:C:1488:G:H2'	3:C:1489:G:H8	1.83	0.43
5:F:2653:U:H5'	5:F:2654:A:C5'	2.45	0.43
8:I:1059:G:O6	8:I:1060:U:H1'	2.17	0.43
13:L:348:ARG:HH21	13:L:350:GLU:HA	1.83	0.43
13:L:608:VAL:HG12	13:L:610:VAL:HG23	2.01	0.43
3:C:1446:U:O2'	3:C:1447:A:H3'	2.19	0.43
7:H:2472:G:H2'	7:H:2475:C:H42	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:2193:G:C4	9:J:2194:G:C8	3.06	0.43
12:K:68:LEU:HD22	12:K:179:SER:HA	1.99	0.43
13:L:240:GLU:H	13:L:240:GLU:CD	2.26	0.43
13:L:260:LEU:C	13:L:260:LEU:HD22	2.43	0.43
13:L:637:ARG:HG3	13:L:637:ARG:NH1	2.29	0.43
14:N:68:ILE:N	14:N:68:ILE:CD1	2.81	0.43
8:I:1053:C:H2'	8:I:1054:A:O4'	2.18	0.43
8:I:1082:U:H3'	8:I:1083:U:H6	1.82	0.43
8:I:1095:A:OP2	13:L:618:GLY:N	2.43	0.43
11:E:62:SER:C	11:E:64:TYR:N	2.76	0.43
13:L:20:HIS:O	13:L:21:ILE:C	2.60	0.43
13:L:409:ILE:CD1	13:L:657:THR:H	2.32	0.43
13:L:606:MET:HB3	13:L:671:MET:HG3	1.99	0.43
14:N:42:ILE:CD1	14:N:202:PRO:HB2	2.47	0.43
11:E:84:LEU:CD2	11:E:84:LEU:C	2.92	0.43
13:L:109:ASP:CG	13:L:138:LYS:HD2	2.42	0.43
13:L:409:ILE:HD11	13:L:657:THR:N	2.29	0.43
14:N:12:GLU:O	14:N:14:GLY:N	2.52	0.43
14:N:21:ARG:HB2	14:N:39:ILE:HA	1.99	0.43
3:C:1415:G:H2'	3:C:1416:G:H8	1.84	0.43
8:I:1085:A:C2'	8:I:1086:A:O4'	2.66	0.43
8:I:1095:A:P	13:L:617:MET:HB2	2.44	0.43
9:J:2126:A:O2'	9:J:2127:G:P	2.76	0.43
13:L:186:TYR:HB3	13:L:196:ILE:HD11	2.00	0.43
13:L:348:ARG:HH11	13:L:382:GLU:HG3	1.84	0.43
14:N:19:HIS:CD2	14:N:20:GLU:HG2	2.53	0.43
14:N:79:ASP:O	14:N:82:ARG:HB3	2.19	0.43
6:G:1863:G:H2'	6:G:1864:U:O4'	2.19	0.43
8:I:1073:A:OP2	8:I:1094:U:O4	2.36	0.43
11:E:27:LEU:O	11:E:28:LYS:C	2.61	0.43
11:E:75:HIS:CG	11:E:76:ASN:N	2.81	0.43
13:L:85:PRO:HG2	13:L:94:VAL:HA	2.00	0.43
13:L:164:MET:C	13:L:180:VAL:HG22	2.43	0.43
14:N:46:LYS:HA	14:N:49:GLU:OE1	2.18	0.43
6:G:1885:A:H5'	6:G:1885:A:C8	2.54	0.43
6:G:1899:G:H21	6:G:1902:C:H5	1.64	0.43
8:I:1077:A:C5	8:I:1078:U:C2	3.06	0.43
9:J:2189:U:H3'	9:J:2190:G:C5'	2.39	0.43
12:K:38:ASP:O	12:K:180:PHE:HA	2.19	0.43
14:N:54:THR:O	14:N:57:PHE:HB3	2.18	0.43
3:C:1446:U:H4'	3:C:1447:A:N7	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:308:PRO:HB2	13:L:394:ALA:CB	2.49	0.43
13:L:519:ARG:HA	13:L:519:ARG:NH1	2.33	0.43
14:N:30:ARG:H	14:N:30:ARG:HG2	1.67	0.43
3:C:1495:U:H2'	3:C:1496:C:C6	2.53	0.43
3:C:1499:A:C4	3:C:1500:A:C8	3.07	0.43
8:I:1078:U:O2	8:I:1088:A:H4'	2.18	0.43
10:M:9:A:N6	10:M:46:A:C2	2.87	0.43
12:K:18:LYS:HD3	12:K:19:VAL:N	2.32	0.43
13:L:252:ASP:O	13:L:253:LEU:HB2	2.18	0.43
13:L:324:ARG:NH2	13:L:383:THR:O	2.51	0.43
13:L:355:LEU:HD13	13:L:369:LEU:HD22	2.00	0.43
6:G:1854:A:H3'	6:G:1855:G:C8	2.54	0.42
13:L:546:ILE:HD13	13:L:565:VAL:HG11	2.01	0.42
14:N:55:PHE:O	14:N:56:ARG:C	2.60	0.42
14:N:111:ARG:HG2	14:N:111:ARG:HH11	1.84	0.42
14:N:144:ARG:O	14:N:147:LYS:N	2.52	0.42
5:F:2662:A:O2'	13:L:457:LEU:HD13	2.19	0.42
8:I:1052:C:O2	8:I:1053:C:C6	2.72	0.42
8:I:1068:G:C6	8:I:1073:A:H2	2.34	0.42
8:I:1082:U:C5	8:I:1083:U:C4	3.07	0.42
8:I:1084:A:N1	8:I:1085:A:C2	2.87	0.42
12:K:49:ILE:O	12:K:51:PRO:HD3	2.19	0.42
13:L:539:ILE:N	13:L:540:PRO:HD2	2.34	0.42
14:N:15:VAL:C	14:N:16:HIS:CG	2.97	0.42
14:N:71:VAL:HB	14:N:164:VAL:HG22	2.01	0.42
14:N:221:LEU:O	14:N:221:LEU:HD13	2.19	0.42
8:I:1067:A:C8	13:L:632:LEU:C	2.98	0.42
8:I:1094:U:N3	8:I:1096:A:H5''	2.34	0.42
9:J:2124:G:H2'	9:J:2125:G:O4'	2.19	0.42
9:J:2178:C:C5'	12:K:46:LYS:HD2	2.50	0.42
10:M:65:G:H2'	10:M:66:U:C6	2.54	0.42
12:K:20:TYR:N	12:K:20:TYR:CD1	2.88	0.42
8:I:1106:G:H2'	8:I:1107:G:C8	2.54	0.42
11:E:7:ILE:O	11:E:10:LEU:HB2	2.19	0.42
12:K:19:VAL:HB	12:K:20:TYR:HD1	1.85	0.42
13:L:276:VAL:O	13:L:280:LEU:HB2	2.19	0.42
13:L:317:MET:O	13:L:325:LEU:N	2.52	0.42
13:L:409:ILE:HG12	13:L:656:ALA:HB3	2.01	0.42
13:L:680:PRO:O	13:L:681:LYS:C	2.62	0.42
14:N:17:PHE:N	14:N:17:PHE:HD2	2.16	0.42
14:N:174:VAL:O	14:N:177:ALA:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1499:A:C2	3:C:1500:A:C8	3.08	0.42
7:H:2462:U:O2'	7:H:2463:C:H5'	2.20	0.42
10:M:46:A:H2'	10:M:48:U:O5'	2.20	0.42
13:L:682:GLN:HG3	13:L:686:LYS:CE	2.48	0.42
7:H:2463:C:C2'	7:H:2464:C:H5'	2.49	0.42
11:E:89:ARG:HB2	11:E:89:ARG:CZ	2.47	0.42
13:L:427:ALA:HB1	13:L:470:PHE:CG	2.55	0.42
13:L:535:PRO:HD3	13:L:572:TYR:CD1	2.55	0.42
13:L:556:ILE:CG1	13:L:601:ILE:HD11	2.22	0.42
13:L:611:THR:OG1	13:L:642:VAL:HG22	2.20	0.42
13:L:627:ARG:O	13:L:651:GLU:HG3	2.20	0.42
11:E:7:ILE:HD13	11:E:7:ILE:HA	1.81	0.42
2:B:370:C:O2'	2:B:371:G:H5'	2.20	0.42
10:M:73:G:O2'	10:M:74:C:C5'	2.47	0.42
13:L:185:ALA:HB3	13:L:199:ILE:O	2.19	0.42
13:L:324:ARG:O	13:L:324:ARG:HG3	2.20	0.42
13:L:414:GLU:O	13:L:474:ALA:HB1	2.19	0.42
14:N:47:THR:O	14:N:48:MET:C	2.63	0.42
14:N:138:LEU:O	14:N:139:LYS:C	2.61	0.42
14:N:165:VAL:O	14:N:187:LEU:O	2.38	0.42
8:I:1067:A:O2'	13:L:634:MET:CG	2.68	0.42
8:I:1107:G:C8	8:I:1108:U:C5	3.07	0.42
10:M:75:C:C2	10:M:76:A:H5'	2.55	0.42
13:L:600:VAL:HG23	13:L:684:GLN:OE1	2.16	0.42
1:A:339:C:H2'	1:A:340:U:C6	2.55	0.42
8:I:1075:C:O2	8:I:1075:C:C2'	2.68	0.42
8:I:1099:G:C4	8:I:1100:C:C5	3.08	0.42
8:I:1102:C:C2	8:I:1103:A:N7	2.88	0.42
12:K:169:GLY:O	12:K:170:ALA:HB3	2.19	0.42
13:L:110:SER:CB	13:L:139:MET:CE	2.95	0.42
13:L:573:HIS:O	13:L:574:GLU:C	2.62	0.42
8:I:1061:U:P	8:I:1061:U:C3'	3.03	0.41
8:I:1077:A:C8	8:I:1078:U:N3	2.88	0.41
8:I:1080:C:C2'	8:I:1081:U:H5'	2.49	0.41
11:E:45:PRO:HG2	11:E:50:SER:C	2.45	0.41
11:E:113:ARG:NH1	11:E:120:TYR:CD2	2.88	0.41
12:K:86:ALA:HB1	12:K:94:VAL:HG11	2.02	0.41
13:L:9:LEU:HD22	13:L:283:PRO:HB2	2.02	0.41
13:L:302:HIS:O	13:L:332:SER:HB3	2.20	0.41
14:N:58:ILE:HD11	14:N:185:ILE:HD12	2.02	0.41
14:N:108:ILE:O	14:N:109:SER:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:163:PHE:O	14:N:164:VAL:HG23	2.20	0.41
3:C:1422:G:C2	3:C:1423:G:C5	3.08	0.41
8:I:1072:C:OP2	8:I:1073:A:OP1	2.39	0.41
8:I:1086:A:C3'	8:I:1087:G:C5'	2.95	0.41
10:M:50:G:C5	10:M:65:G:C2	3.09	0.41
10:M:66:U:C4	10:M:67:C:N4	2.88	0.41
12:K:196:LEU:C	12:K:198:ALA:H	2.28	0.41
13:L:88:VAL:HG12	13:L:121:VAL:HG12	2.01	0.41
13:L:321:TYR:O	13:L:322:VAL:CG1	2.63	0.41
14:N:80:ILE:HD13	14:N:208:ILE:HG23	2.02	0.41
14:N:102:LEU:H	14:N:102:LEU:HD12	1.81	0.41
14:N:109:SER:O	14:N:111:ARG:N	2.54	0.41
14:N:191:ASP:OD1	14:N:191:ASP:O	2.39	0.41
10:M:24:G:C4	10:M:25:U:C6	3.08	0.41
10:M:74:C:H2'	10:M:75:C:O4'	2.20	0.41
12:K:92:ASP:CG	12:K:93:TYR:H	2.28	0.41
13:L:203:GLU:HA	13:L:206:LEU:HB2	2.01	0.41
13:L:282:SER:C	13:L:284:LEU:H	2.27	0.41
14:N:17:PHE:CD1	14:N:44:LEU:HD21	2.55	0.41
14:N:163:PHE:CD2	14:N:186:ALA:HA	2.55	0.41
6:G:1899:G:HO2'	6:G:1900:A:H5''	1.85	0.41
8:I:1083:U:O2	8:I:1083:U:H2'	2.19	0.41
8:I:1094:U:H3	8:I:1096:A:H5''	1.85	0.41
10:M:4:G:H2'	10:M:5:U:O5'	2.21	0.41
13:L:435:ASP:C	13:L:435:ASP:OD1	2.62	0.41
14:N:136:VAL:O	14:N:140:HIS:HB2	2.21	0.41
6:G:1862:G:O2'	6:G:1863:G:H5'	2.19	0.41
6:G:1885:A:H5'	6:G:1885:A:H8	1.86	0.41
11:E:7:ILE:O	11:E:8:ASN:C	2.63	0.41
12:K:79:LYS:O	12:K:96:GLY:HA3	2.20	0.41
13:L:9:LEU:C	13:L:11:ARG:N	2.78	0.41
13:L:20:HIS:CE1	13:L:21:ILE:HG22	2.54	0.41
13:L:95:GLU:OE1	13:L:402:ILE:HA	2.19	0.41
13:L:108:PHE:HE2	13:L:134:ALA:HB1	1.85	0.41
13:L:416:LYS:HG2	13:L:474:ALA:HA	2.01	0.41
14:N:9:GLU:HB2	14:N:10:LEU:H	1.73	0.41
14:N:168:THR:HG23	14:N:192:SER:OG	2.19	0.41
5:F:2655:G:H2'	5:F:2655:G:N3	2.35	0.41
8:I:1087:G:O3'	8:I:1089:G:H5'	2.21	0.41
8:I:1087:G:C2'	8:I:1103:A:H2	2.31	0.41
9:J:2097:C:O2'	9:J:2098:U:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:189:ILE:C	12:K:191:ALA:N	2.76	0.41
13:L:13:ARG:HD3	13:L:276:VAL:O	2.21	0.41
13:L:459:LEU:O	13:L:463:VAL:HG23	2.20	0.41
3:C:1419:G:C2	3:C:1420:C:C2	3.08	0.41
8:I:1081:U:O4	8:I:1086:A:C4	2.74	0.41
8:I:1085:A:O2'	8:I:1086:A:O5'	2.39	0.41
9:J:2097:C:H2'	9:J:2098:U:O4'	2.20	0.41
11:E:32:PHE:HD1	11:E:86:ARG:HA	1.85	0.41
12:K:76:ALA:HB3	12:K:94:VAL:HG11	1.99	0.41
13:L:87:HIS:HB3	13:L:90:PHE:HE1	1.86	0.41
13:L:442:THR:HG23	13:L:447:GLY:O	2.20	0.41
13:L:484:ARG:O	13:L:647:VAL:HG23	2.06	0.41
14:N:80:ILE:O	14:N:83:MET:HB2	2.20	0.41
14:N:97:TRP:CZ2	14:N:102:LEU:HD13	2.49	0.41
14:N:142:LEU:CD2	14:N:146:GLN:NE2	2.83	0.41
14:N:143:GLU:O	14:N:147:LYS:HB2	2.20	0.41
8:I:1063:G:C6	8:I:1064:C:N4	2.89	0.41
8:I:1066:U:C2	8:I:1069:A:P	3.13	0.41
10:M:69:C:C4	10:M:70:G:N7	2.88	0.41
12:K:42:GLU:HG2	12:K:176:GLY:O	2.21	0.41
13:L:88:VAL:CG1	13:L:121:VAL:HG12	2.51	0.41
14:N:75:LYS:HG2	14:N:78:GLN:HE21	1.83	0.41
8:I:1056:G:H21	8:I:1104:C:H42	1.69	0.41
8:I:1071:G:N2	8:I:1089:G:H2'	2.36	0.41
8:I:1095:A:C6	13:L:614:GLU:OE1	2.62	0.41
9:J:2172:U:H2'	9:J:2174:C:O4'	2.21	0.41
10:M:14:A:N6	10:M:46:A:H2	2.19	0.41
10:M:25:U:C4	10:M:26:A:C5	3.09	0.41
13:L:85:PRO:HG2	13:L:94:VAL:HG22	2.02	0.41
13:L:116:PRO:HB3	13:L:666:ARG:HG2	2.02	0.41
13:L:202:PRO:O	13:L:203:GLU:C	2.63	0.41
13:L:327:PHE:CE1	13:L:376:ALA:HB2	2.56	0.41
13:L:486:THR:O	13:L:600:VAL:CA	2.67	0.41
13:L:579:GLU:O	13:L:583:LYS:HB2	2.21	0.41
14:N:69:LEU:HD12	14:N:92:TYR:HA	2.03	0.41
14:N:142:LEU:CD2	14:N:146:GLN:HE21	2.34	0.41
3:C:1495:U:C2	3:C:1496:C:C5	3.08	0.41
8:I:1095:A:H5''	13:L:618:GLY:H	1.84	0.41
8:I:1097:U:C2	8:I:1098:A:C8	3.09	0.41
12:K:51:PRO:HB3	12:K:204:ALA:HB2	2.02	0.41
13:L:344:THR:HG21	13:L:396:ARG:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:561:VAL:HG13	13:L:602:LEU:HD12	1.98	0.41
13:L:648:PRO:HG2	13:L:651:GLU:HG3	2.03	0.41
3:C:1446:U:O3'	3:C:1447:A:H8	2.04	0.40
5:F:2669:G:C2	5:F:2670:A:C8	3.08	0.40
8:I:1097:U:O2	8:I:1098:A:O4'	2.38	0.40
8:I:1105:U:O2'	8:I:1106:G:P	2.79	0.40
12:K:41:VAL:C	12:K:42:GLU:HG3	2.45	0.40
12:K:46:LYS:NZ	12:K:172:HIS:CB	2.84	0.40
12:K:51:PRO:O	12:K:52:ARG:HB2	2.22	0.40
12:K:124:GLY:O	12:K:125:SER:CB	2.68	0.40
13:L:409:ILE:HA	13:L:480:GLN:O	2.20	0.40
13:L:627:ARG:HB3	13:L:651:GLU:HB3	2.02	0.40
13:L:635:GLU:HA	13:L:636:PRO:HD2	1.95	0.40
14:N:39:ILE:HG22	14:N:40:HIS:N	2.34	0.40
14:N:75:LYS:HA	14:N:78:GLN:HE21	1.86	0.40
14:N:213:LEU:CD2	14:N:214:ILE:HD13	2.50	0.40
6:G:1847:A:N3	6:G:1847:A:H2'	2.36	0.40
6:G:1860:G:H2'	6:G:1861:G:C8	2.56	0.40
7:H:2478:A:H3'	7:H:2479:G:H8	1.87	0.40
9:J:2128:C:C3'	9:J:2129:C:H5''	2.50	0.40
11:E:126:LYS:HD2	11:E:127:GLU:H	1.87	0.40
13:L:177:ILE:HD12	13:L:271:LEU:HD12	2.03	0.40
3:C:1452:C:H4'	3:C:1456:G:O5'	2.22	0.40
3:C:1469:G:H2'	3:C:1470:G:C8	2.55	0.40
5:F:2660:A:O2'	13:L:660:ARG:HB2	2.21	0.40
8:I:1085:A:C1'	8:I:1086:A:O5'	2.70	0.40
8:I:1097:U:C6	8:I:1098:A:C8	3.09	0.40
11:E:30:ALA:HA	11:E:31:PRO:HD3	1.96	0.40
13:L:17:ILE:N	13:L:17:ILE:CD1	2.84	0.40
13:L:345:THR:HG21	13:L:387:ASP:OD1	2.21	0.40
14:N:113:HIS:O	14:N:116:GLU:HG2	2.21	0.40
14:N:115:LEU:HD23	14:N:153:ARG:NE	2.35	0.40
14:N:116:GLU:HA	14:N:119:GLU:HB2	2.02	0.40
14:N:164:VAL:HG13	14:N:165:VAL:N	2.36	0.40
5:F:2655:G:HO2'	5:F:2656:U:H5	1.67	0.40
5:F:2667:C:C5	5:F:2668:G:N7	2.90	0.40
6:G:1882:C:O2	6:G:1882:C:H2'	2.20	0.40
6:G:1886:C:H2'	6:G:1887:C:H6	1.86	0.40
8:I:1069:A:N7	8:I:1073:A:C5	2.89	0.40
8:I:1091:G:C2	8:I:1101:U:N3	2.90	0.40
12:K:64:LEU:HD22	12:K:193:ILE:CB	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:92:ILE:CG2	13:L:93:GLU:H	2.35	0.40
13:L:301:ILE:HD12	13:L:399:LEU:HD11	2.02	0.40
14:N:142:LEU:C	14:N:142:LEU:CD2	2.94	0.40
8:I:1095:A:O4'	13:L:617:MET:SD	2.60	0.40
11:E:46:LYS:HB2	11:E:92:ASP:O	2.21	0.40
13:L:100:VAL:HG21	13:L:314:PHE:CD2	2.56	0.40
14:N:9:GLU:O	14:N:10:LEU:C	2.64	0.40
14:N:98:LEU:CB	14:N:101:MET:HE3	2.51	0.40
14:N:169:LYS:HB3	14:N:170:GLU:OE2	2.22	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	
11	E	123/135 (91%)	83 (68%)	24 (20%)	16 (13%)	0	4
12	K	183/229 (80%)	90 (49%)	50 (27%)	43 (24%)	0	1
13	L	645/691 (93%)	583 (90%)	55 (8%)	7 (1%)	11	46
14	N	233/256 (91%)	150 (64%)	51 (22%)	32 (14%)	0	3
All	All	1184/1311 (90%)	906 (76%)	180 (15%)	98 (8%)	1	9

All (98) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	E	28	LYS
11	E	47	LYS
11	E	91	LYS
11	E	92	ASP
12	K	19	VAL
12	K	35	ALA

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Mol	Chain	Res	Type
12	K	46	LYS
12	K	57	ASN
12	K	63	SER
12	K	160	ARG
12	K	161	ILE
12	K	166	ASP
12	K	172	HIS
12	K	173	ALA
12	K	174	PRO
12	K	179	SER
12	K	182	PRO
12	K	191	ALA
12	K	192	PHE
12	K	201	PRO
12	K	205	LYS
12	K	209	LEU
12	K	213	TYR
12	K	216	THR
12	K	220	PRO
13	L	322	VAL
14	N	15	VAL
14	N	52	GLU
14	N	77	ALA
14	N	84	GLU
14	N	154	LEU
14	N	165	VAL
14	N	195	ASP
14	N	226	ARG
11	E	12	ARG
11	E	29	GLY
11	E	72	GLY
12	K	62	VAL
12	K	125	SER
12	K	133	PRO
12	K	148	ASN
12	K	211	SER
12	K	214	VAL
13	L	10	LYS
14	N	8	LYS
14	N	9	GLU
14	N	32	ILE
14	N	78	GLN

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Mol	Chain	Res	Type
14	N	88	ALA
14	N	110	GLN
14	N	194	PRO
14	N	204	ASN
14	N	217	ARG
14	N	238	LEU
11	E	45	PRO
11	E	62	SER
11	E	96	VAL
11	E	115	LYS
12	K	49	ILE
12	K	140	PRO
12	K	198	ALA
12	K	204	ALA
12	K	210	ARG
12	K	217	THR
13	L	403	GLU
13	L	444	PRO
14	N	28	PHE
14	N	53	ARG
14	N	79	ASP
14	N	83	MET
14	N	101	MET
14	N	150	SER
14	N	237	ALA
11	E	51	ALA
11	E	79	GLU
12	K	55	ASP
12	K	64	LEU
12	K	77	ILE
12	K	183	GLU
12	K	202	GLU
14	N	18	GLY
14	N	20	GLU
14	N	97	TRP
14	N	130	ARG
14	N	216	SER
14	N	239	VAL
12	K	159	GLY
13	L	69	VAL
13	L	203	GLU
14	N	181	PHE

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Mol	Chain	Res	Type
11	E	18	VAL
12	K	130	ILE
12	K	149	ILE
12	K	175	VAL
11	E	43	VAL
13	L	554	PRO
11	E	48	PRO
12	K	103	ILE

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	
11	E	104/111 (94%)	93 (89%)	11 (11%)	6	21
12	K	61/181 (34%)	55 (90%)	6 (10%)	7	24
13	L	553/582 (95%)	504 (91%)	49 (9%)	9	28
14	N	202/220 (92%)	180 (89%)	22 (11%)	6	20
All	All	920/1094 (84%)	832 (90%)	88 (10%)	10	25

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	E	7	ILE
11	E	41	ARG
11	E	53	ARG
11	E	62	SER
11	E	83	VAL
11	E	84	LEU
11	E	85	ILE
11	E	86	ARG
11	E	89	ARG
11	E	102	ARG
11	E	120	TYR
12	K	41	VAL
12	K	49	ILE

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Mol	Chain	Res	Type
12	K	58	VAL
12	K	64	LEU
12	K	77	ILE
12	K	101	GLN
13	L	33	LEU
13	L	69	VAL
13	L	100	VAL
13	L	130	VAL
13	L	132	ARG
13	L	162	VAL
13	L	165	GLN
13	L	166	LEU
13	L	167	PRO
13	L	170	ARG
13	L	171	GLU
13	L	181	LEU
13	L	190	ASN
13	L	196	ILE
13	L	203	GLU
13	L	204	GLU
13	L	232	LEU
13	L	238	THR
13	L	253	LEU
13	L	260	LEU
13	L	273	LEU
13	L	280	LEU
13	L	284	LEU
13	L	295	GLU
13	L	315	LYS
13	L	321	TYR
13	L	326	THR
13	L	328	ILE
13	L	336	THR
13	L	352	VAL
13	L	369	LEU
13	L	377	VAL
13	L	385	THR
13	L	389	LEU
13	L	403	GLU
13	L	420	ASP
13	L	461	ILE
13	L	473	ASP

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Mol	Chain	Res	Type
13	L	481	VAL
13	L	536	LYS
13	L	583	LYS
13	L	590	ILE
13	L	614	GLU
13	L	616	TYR
13	L	619	ASP
13	L	634	MET
13	L	647	VAL
13	L	659	LEU
13	L	660	ARG
14	N	10	LEU
14	N	15	VAL
14	N	16	HIS
14	N	17	PHE
14	N	22	LYS
14	N	36	ARG
14	N	41	ILE
14	N	44	LEU
14	N	59	GLU
14	N	75	LYS
14	N	79	ASP
14	N	90	MET
14	N	102	LEU
14	N	137	ARG
14	N	145	LEU
14	N	178	ARG
14	N	179	LYS
14	N	187	LEU
14	N	196	LEU
14	N	204	ASN
14	N	215	LEU
14	N	221	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
11	E	8	ASN
11	E	9	GLN
11	E	49	ASN
11	E	75	HIS
13	L	20	HIS

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Mol	Chain	Res	Type
13	L	80	ASN
13	L	124	GLN
13	L	137	ASN
13	L	154	GLN
13	L	165	GLN
13	L	208	GLN
13	L	226	ASN
13	L	426	GLN
13	L	448	GLN
13	L	458	HIS
13	L	475	ASN
13	L	480	GLN
13	L	500	GLN
13	L	506	GLN
13	L	543	GLN
13	L	551	GLN
13	L	625	ASN
13	L	641	GLN
13	L	677	GLN
14	N	37	ASN
14	N	40	HIS
14	N	78	GLN
14	N	94	ASN
14	N	146	GLN
14	N	204	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	11/12 (91%)	1 (9%)	0
10	M	74/74 (100%)	26 (35%)	2 (2%)
2	B	8/28 (28%)	0	0
3	C	95/96 (98%)	11 (11%)	2 (2%)
4	D	11/303 (3%)	0	0
5	F	28/29 (96%)	7 (25%)	1 (3%)
6	G	53/54 (98%)	12 (22%)	1 (1%)
7	H	41/42 (97%)	8 (19%)	1 (2%)
8	I	57/58 (98%)	35 (61%)	5 (8%)
9	J	72/102 (70%)	29 (40%)	2 (2%)
All	All	450/798 (56%)	129 (28%)	14 (3%)

All (129) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	345	C
3	C	1419	G
3	C	1442	G
3	C	1442(A)	G
3	C	1442(B)	A
3	C	1443	G
3	C	1447	A
3	C	1452	C
3	C	1487	G
3	C	1492	A
3	C	1498	U
3	C	1499	A
5	F	2654	A
5	F	2655	G
5	F	2660	A
5	F	2661	G
5	F	2662	A
5	F	2663	G
5	F	2673	G
6	G	1847	A
6	G	1858	G
6	G	1865	G
6	G	1866	C
6	G	1877	A
6	G	1878	G
6	G	1880	C
6	G	1882	C
6	G	1885	A
6	G	1886	C
6	G	1888	G
6	G	1900	A
7	H	2465	C
7	H	2469	A
7	H	2470	G
7	H	2476	A
7	H	2477	C
7	H	2478	A
7	H	2482	G
7	H	2484	G
8	I	1056	G
8	I	1059	G
8	I	1060	U
8	I	1061	U

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Mol	Chain	Res	Type
8	I	1062	G
8	I	1063	G
8	I	1066	U
8	I	1067	A
8	I	1068	G
8	I	1069	A
8	I	1070	A
8	I	1071	G
8	I	1072	C
8	I	1073	A
8	I	1074	G
8	I	1077	A
8	I	1083	U
8	I	1084	A
8	I	1085	A
8	I	1086	A
8	I	1087	G
8	I	1088	A
8	I	1089	G
8	I	1090	U
8	I	1091	G
8	I	1093	G
8	I	1096	A
8	I	1097	U
8	I	1098	A
8	I	1099	G
8	I	1101	U
8	I	1103	A
8	I	1104	C
8	I	1105	U
8	I	1106	G
9	J	2099	U
9	J	2103	C
9	J	2104	G
9	J	2110	G
9	J	2111	C
9	J	2112	G
9	J	2116	G
9	J	2118	U
9	J	2119	A
9	J	2120	G
9	J	2122	U

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Mol	Chain	Res	Type
9	J	2127	G
9	J	2128	C
9	J	2129	C
9	J	2130	U
9	J	2159	G
9	J	2161	C
9	J	2162	G
9	J	2164	C
9	J	2165	G
9	J	2170	A
9	J	2171	A
9	J	2172	U
9	J	2176	A
9	J	2187	G
9	J	2190	G
9	J	2191	G
9	J	2192	G
9	J	2193	G
10	M	2	C
10	M	5	U
10	M	6	G
10	M	8	4SU
10	M	9	A
10	M	18	G
10	M	20	H2U
10	M	21	H2U
10	M	22	A
10	M	30	G
10	M	32	U
10	M	34	U
10	M	41	C
10	M	44	C
10	M	45	U
10	M	46	A
10	M	48	U
10	M	49	5MC
10	M	50	G
10	M	55	PSU
10	M	62	C
10	M	64	C
10	M	70	G
10	M	72	A

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Mol	Chain	Res	Type
10	M	73	G
10	M	76	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	C	1442	G
3	C	1498	U
5	F	2662	A
6	G	1885	A
7	H	2481	G
8	I	1069	A
8	I	1083	U
8	I	1085	A
8	I	1097	U
8	I	1100	C
9	J	2126	A
9	J	2191	G
10	M	1	U
10	M	33	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
10	H2U	M	21	10	18,21,22	0.58	0	19,30,33	0.92	1 (5%)
10	H2U	M	20	10	18,21,22	0.50	0	19,30,33	0.70	1 (5%)
10	PSU	M	55	10	18,21,22	0.68	0	21,30,33	0.83	1 (4%)
10	5MC	M	49	10	19,22,23	0.67	0	26,32,35	0.99	1 (3%)
10	4SU	M	8	10	18,21,22	0.66	0	25,30,33	0.54	0
10	5MU	M	54	10	19,22,23	0.74	0	27,32,35	1.39	3 (11%)

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
10	H2U	M	21	10	-	2/7/38/39	0/2/2/2
10	H2U	M	20	10	-	0/7/38/39	0/2/2/2
10	PSU	M	55	10	-	4/7/25/26	0/2/2/2
10	5MC	M	49	10	-	2/7/25/26	0/2/2/2
10	4SU	M	8	10	-	0/7/25/26	0/2/2/2
10	5MU	M	54	10	-	2/7/25/26	0/2/2/2

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	M	54	5MU	C5-C4-N3	3.94	118.75	115.32
10	M	54	5MU	C4-N3-C2	-3.09	123.28	127.34
10	M	49	5MC	C5-C4-N3	-2.57	119.12	121.75
10	M	21	H2U	N3-C2-N1	-2.27	114.36	116.65
10	M	20	H2U	N3-C2-N1	-2.19	114.44	116.65
10	M	55	PSU	O4'-C1'-C2'	2.18	108.17	105.15
10	M	54	5MU	O2'-C2'-C3'	-2.01	105.38	111.82

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	M	49	5MC	O4'-C4'-C5'-O5'
10	M	55	PSU	C3'-C4'-C5'-O5'
10	M	55	PSU	O4'-C4'-C5'-O5'
10	M	49	5MC	C3'-C4'-C5'-O5'
10	M	21	H2U	O4'-C4'-C5'-O5'
10	M	21	H2U	C4'-C5'-O5'-P
10	M	55	PSU	O4'-C1'-C5'-C4
10	M	54	5MU	C3'-C4'-C5'-O5'
10	M	55	PSU	O4'-C1'-C5'-C6
10	M	54	5MU	O4'-C4'-C5'-O5'

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	M	20	H2U	2	0
10	M	55	PSU	3	0
10	M	49	5MC	5	0
10	M	8	4SU	7	0
10	M	54	5MU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
10	M	10
13	L	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L	485:GLU	C	486:THR	N	15.61
1	L	400:GLU	C	401:SER	N	15.51
1	L	598:ASP	C	599:PRO	N	2.97
1	M	37:A	O3'	38:U	P	2.27
1	M	48:U	O3'	49:5MC	P	1.99
1	M	33:U	O3'	34:U	P	1.98
1	M	7:A	O3'	8:4SU	P	1.93
1	M	15:G	O3'	16:C	P	1.89
1	M	24:G	O3'	25:U	P	1.84
1	M	56:C	O3'	57:A	P	1.82
1	M	25:U	O3'	26:A	P	1.81

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	46:A	O3'	48:U	P	1.77
1	M	26:A	O3'	27:C	P	1.33

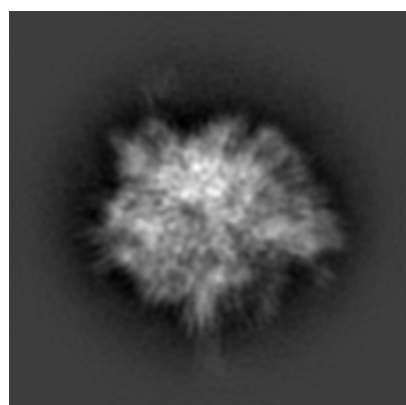
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1315. These allow visual inspection of the internal detail of the map and identification of artifacts.

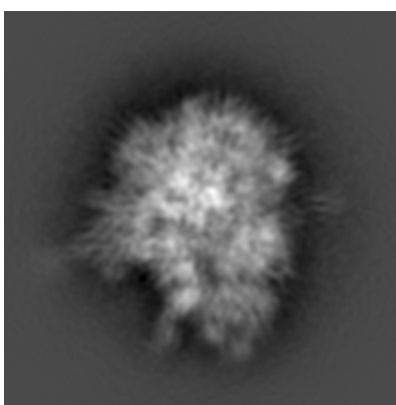
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

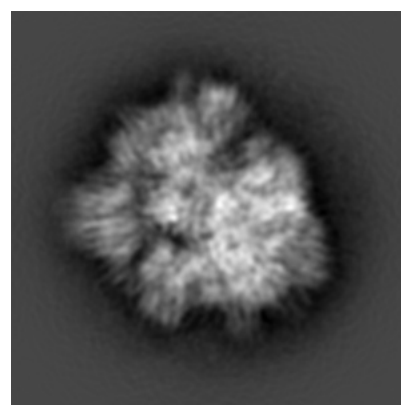
6.1.1 Primary map



X



Y

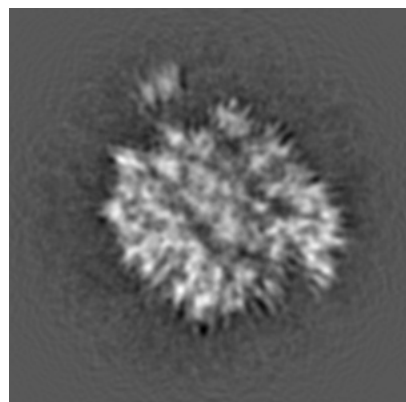


Z

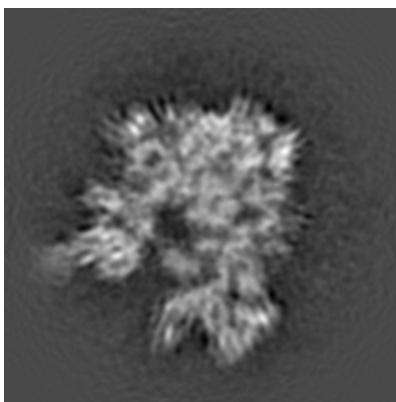
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

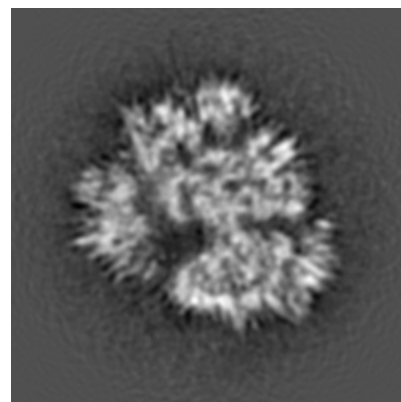
6.2.1 Primary map



X Index: 150



Y Index: 150

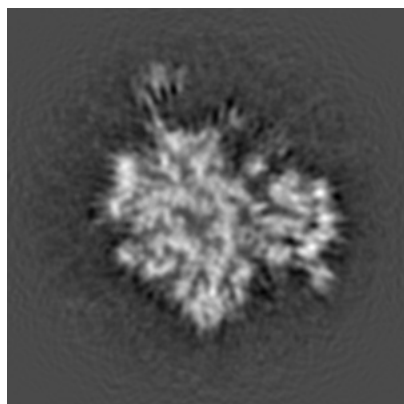


Z Index: 150

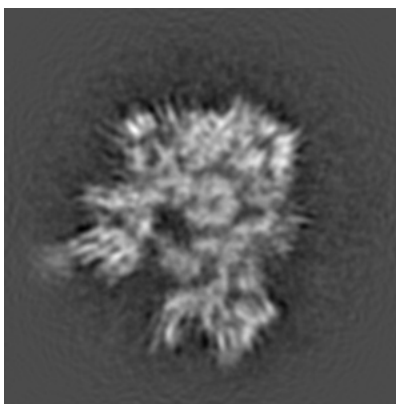
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

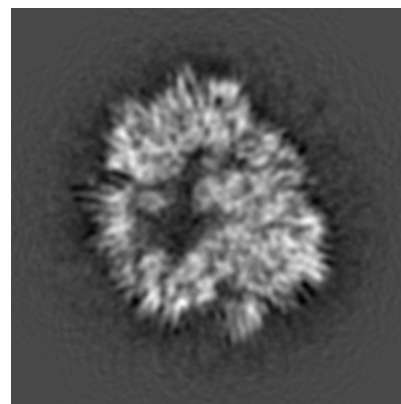
6.3.1 Primary map



X Index: 155



Y Index: 152

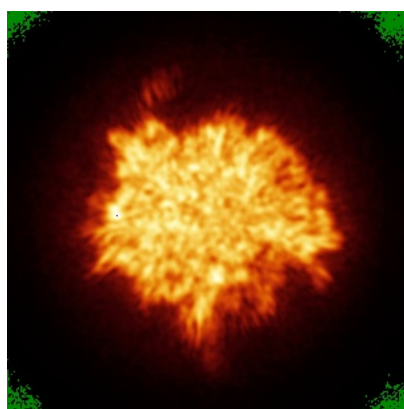


Z Index: 137

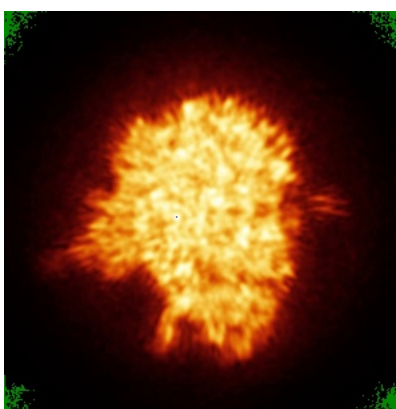
The images above show the largest variance slices of the map in three orthogonal directions.

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

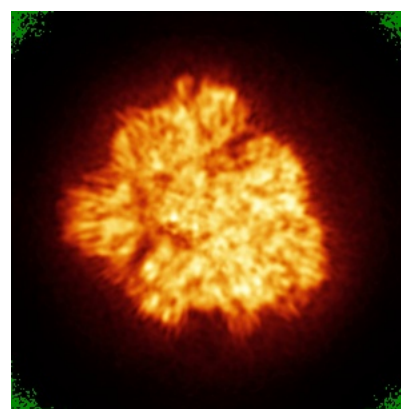
6.4.1 Primary map



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 1820.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

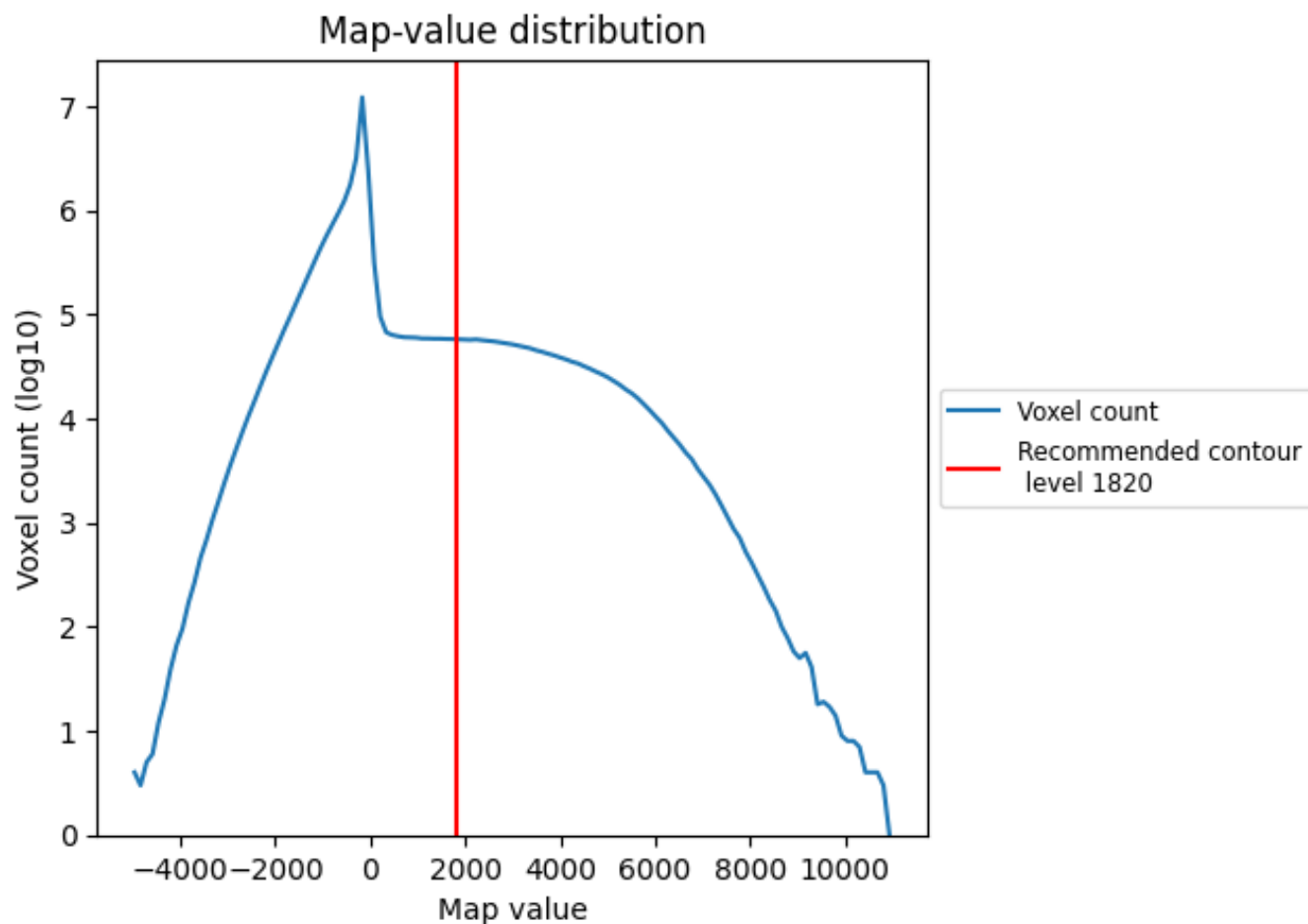
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

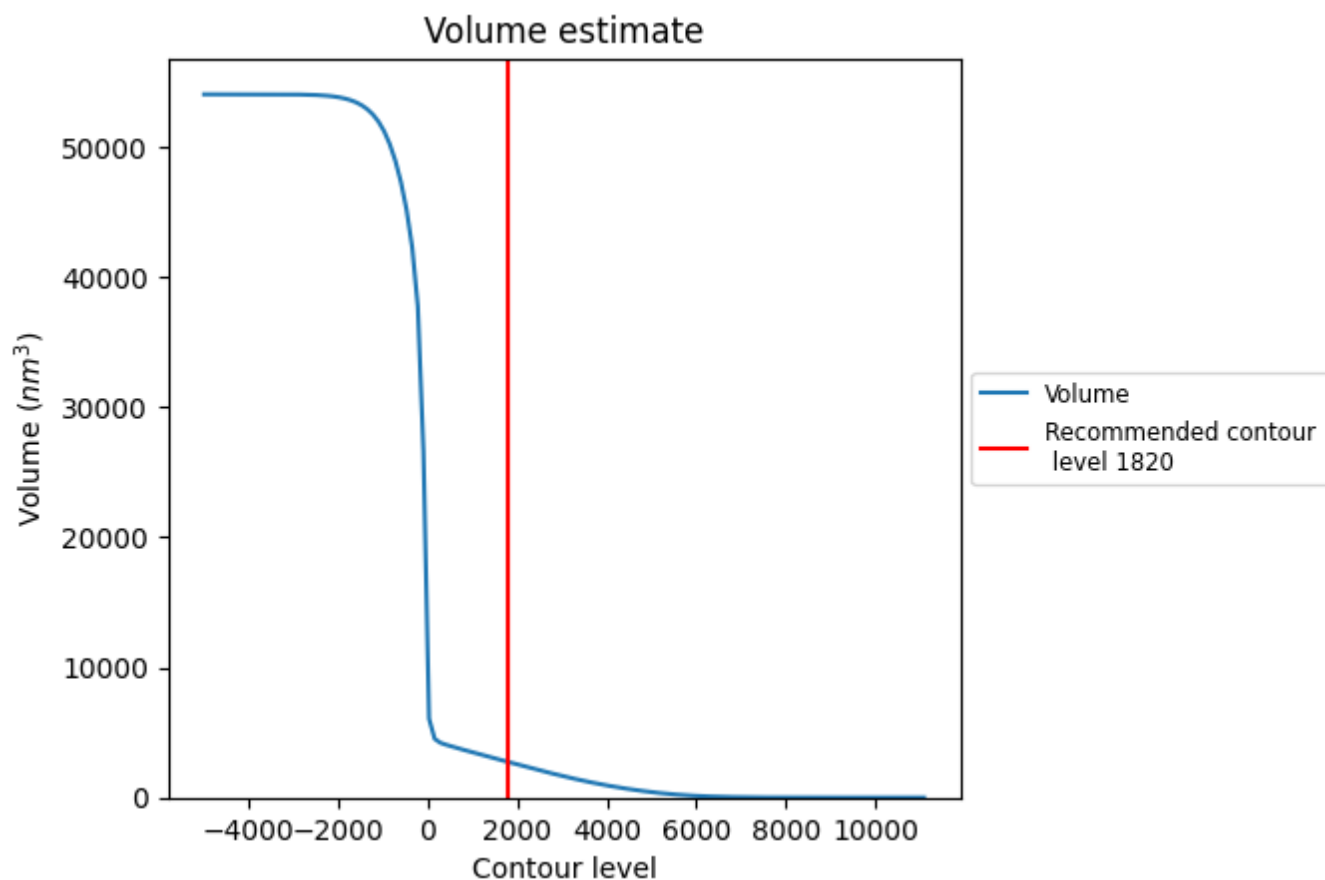
This section contains the results of statistical analysis of the map.

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.

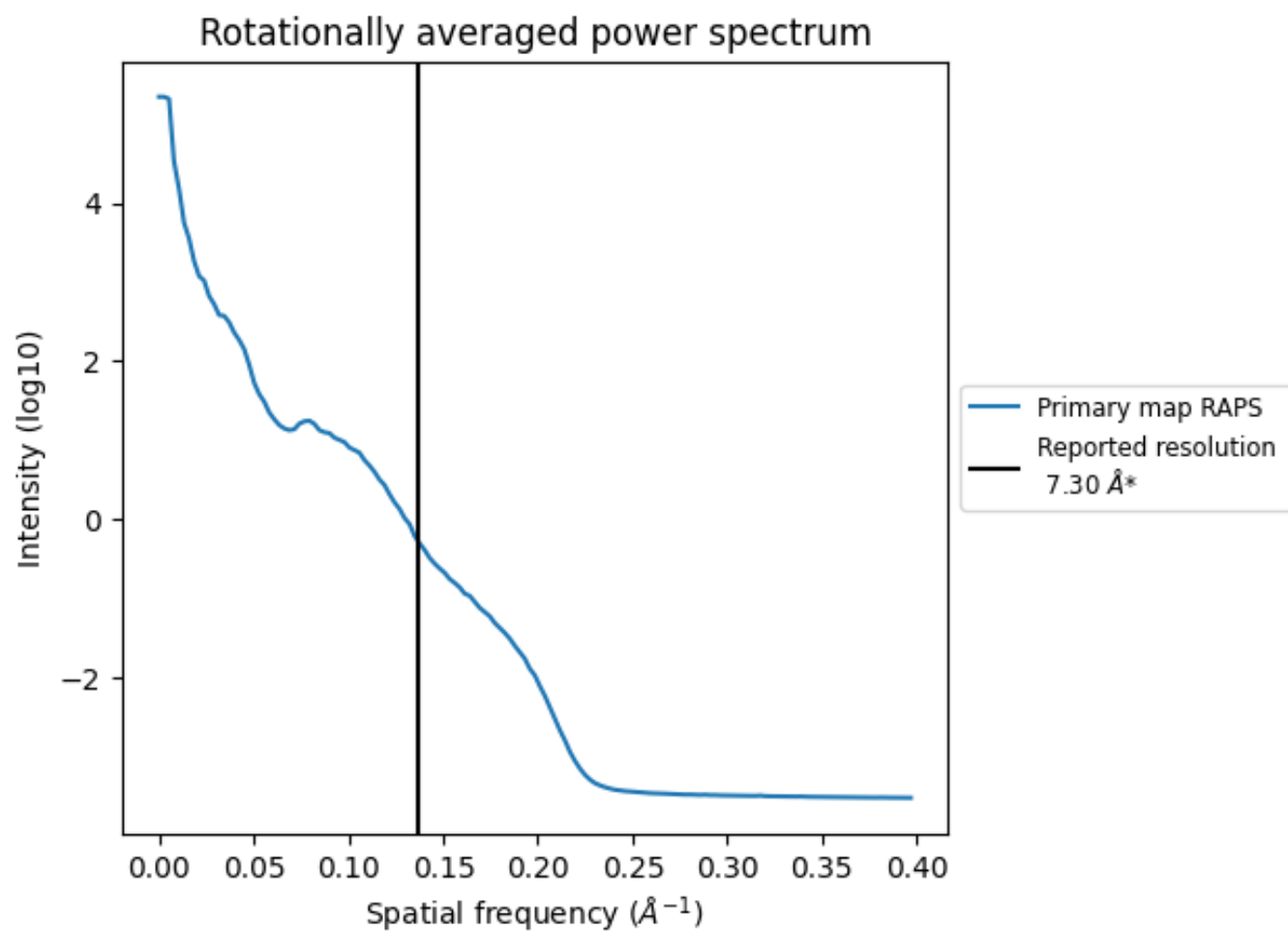
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2722 nm³; this corresponds to an approximate mass of 2458 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 0.137 Å⁻¹

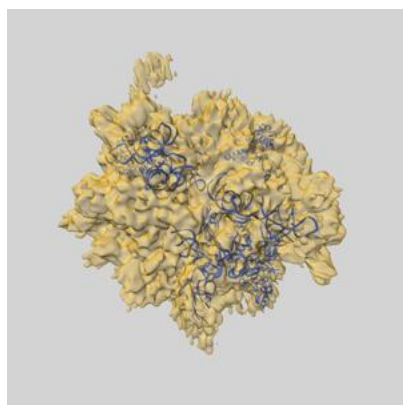
8 Fourier-Shell correlation

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

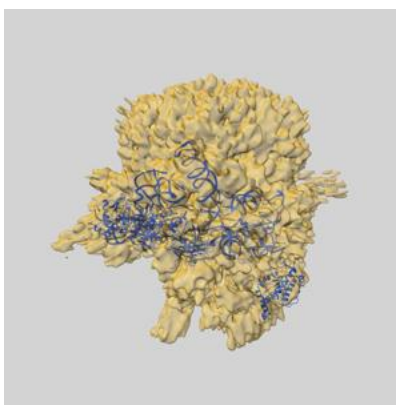
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1315 and PDB model 2OM7. Per-residue inclusion information can be found in section [3](#) on page [7](#).

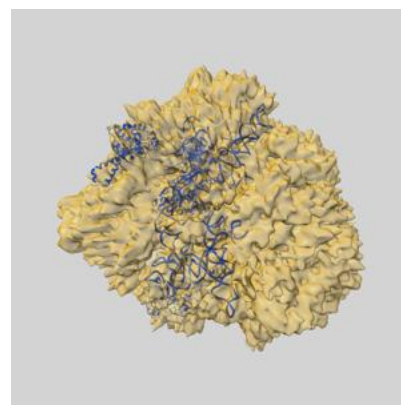
9.1 Map-model overlay [i](#)



X



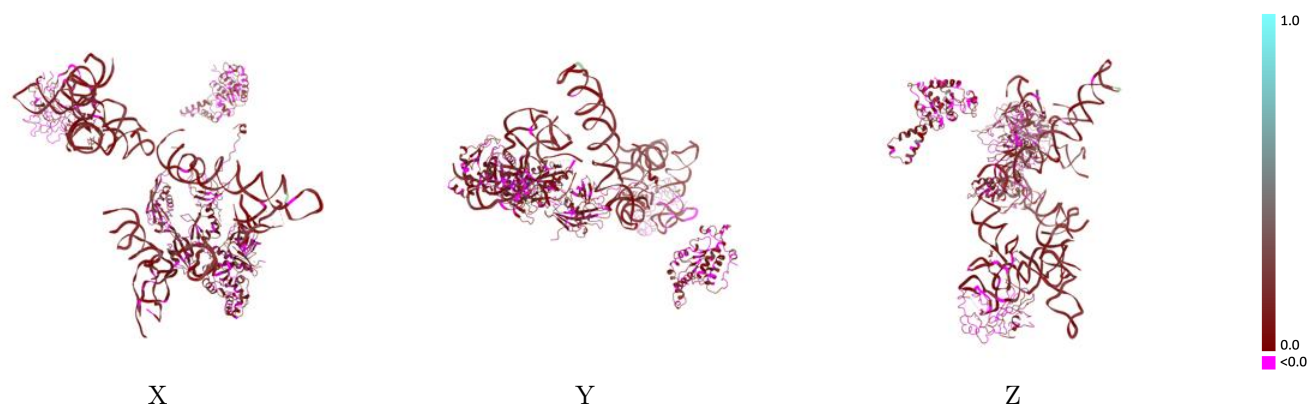
Y



Z

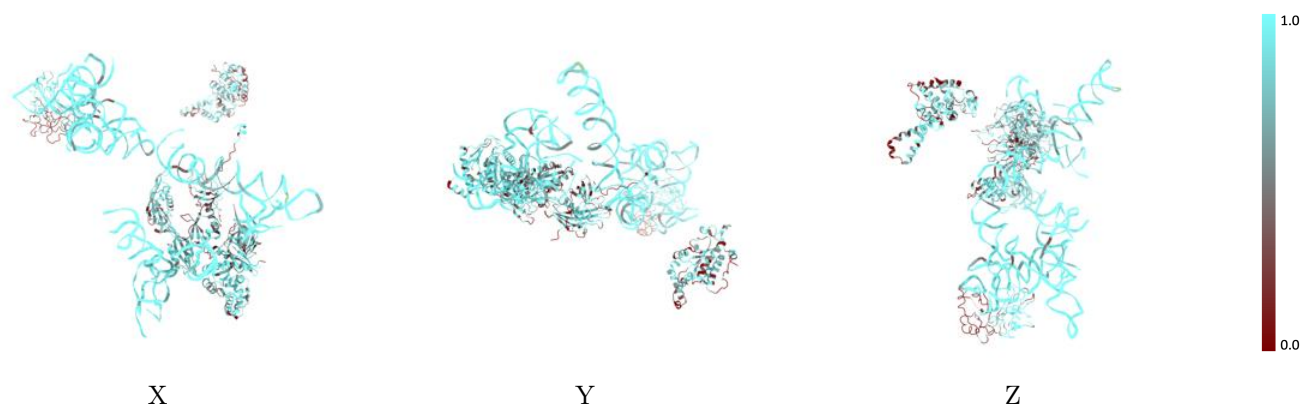
The images above show the 3D surface view of the map at the recommended contour level 1820.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



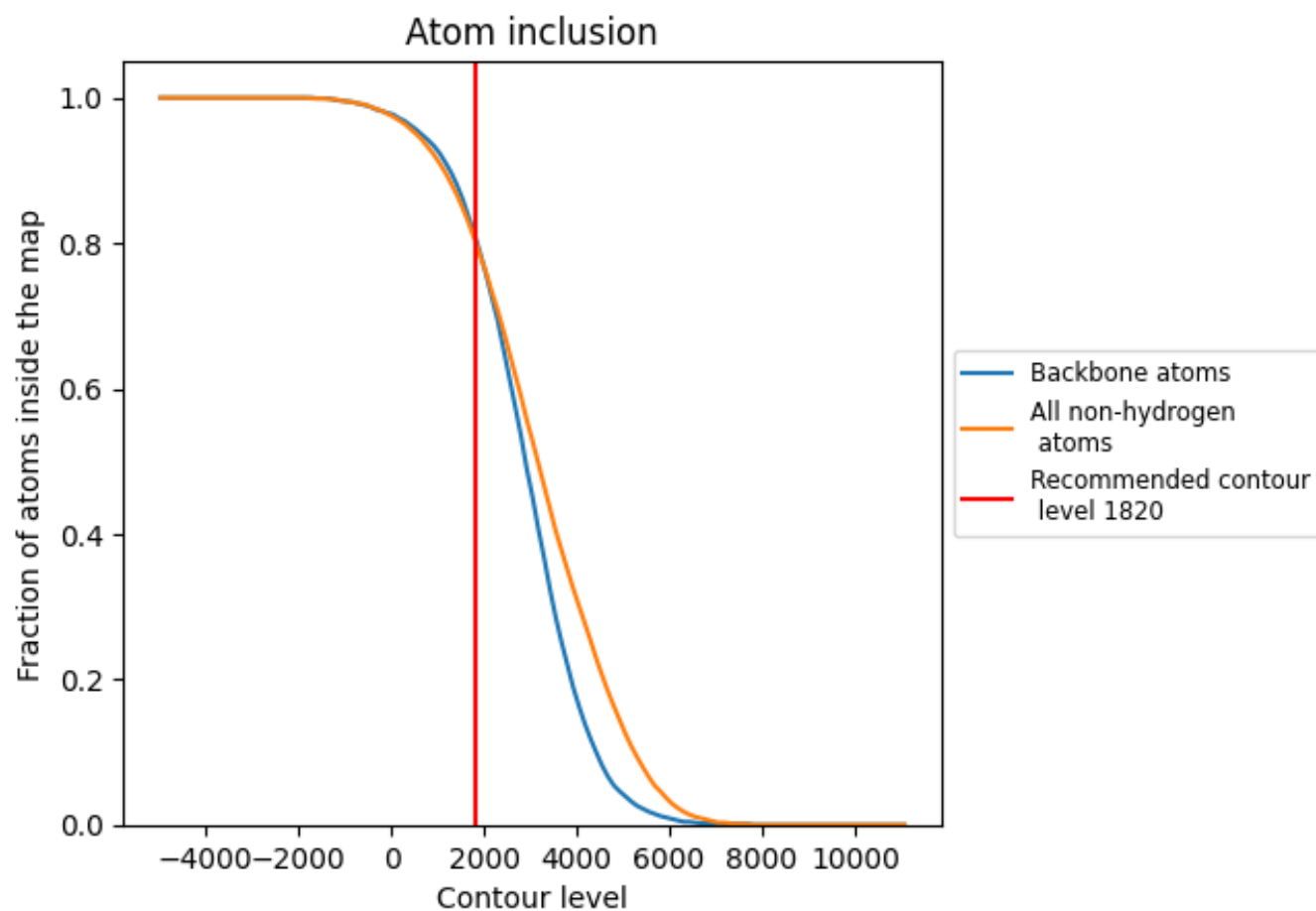
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1820).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 80% 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 (1820) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8020	 0.1080
A	 0.7580	 0.1270
B	 0.9530	 0.1210
C	 0.8840	 0.1420
D	 0.9570	 0.1070
E	 0.5810	 0.0790
F	 0.9620	 0.1450
G	 0.9510	 0.1700
H	 0.9640	 0.1480
I	 0.9500	 0.1170
J	 0.9110	 0.0980
K	 0.5030	 0.0150
L	 0.7330	 0.1000
M	 0.9340	 0.1240
N	 0.6220	 0.0820

