



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 10:50 AM UTC

PDB ID : 3J7Z / pdb_00003j7z
EMDB ID : EMD-6057
Title : Structure of the E. coli 50S subunit with ErmCL nascent chain
Authors : Arenz, S.; Meydan, S.; Starosta, A.L.; Berninghausen, O.; Beckmann, R.;
Vazquez-Laslop, N.; Wilson, D.N.
Deposited on : 2014-08-27
Resolution : 3.90 Å(reported)
Based on initial model : 4KIX

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:

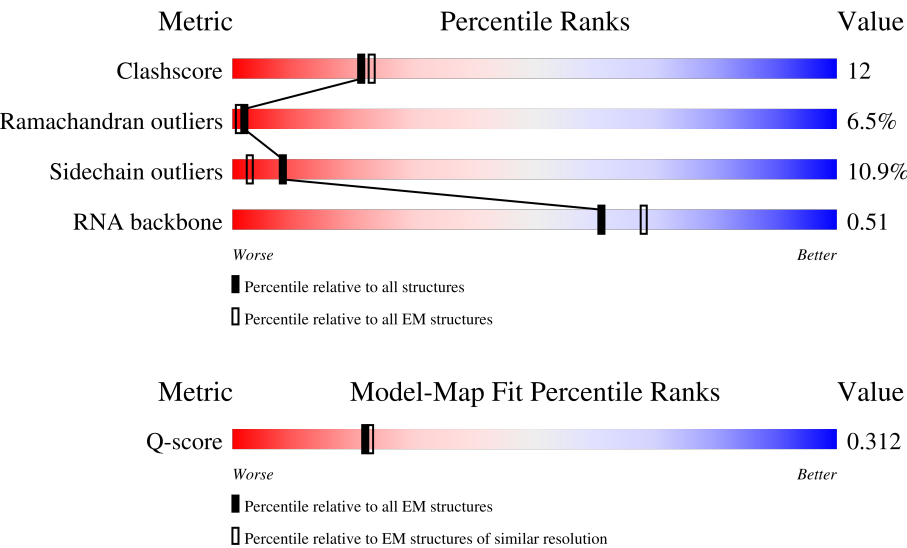
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.90 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.



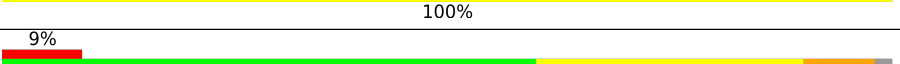
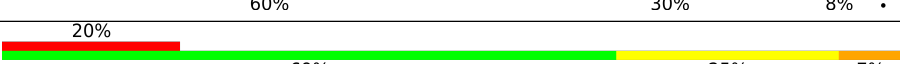
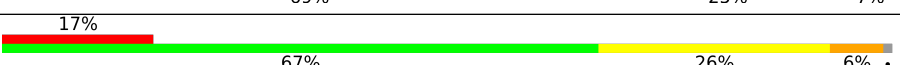
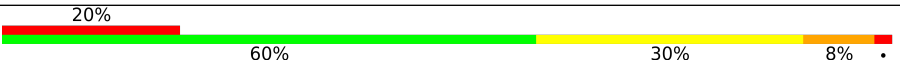
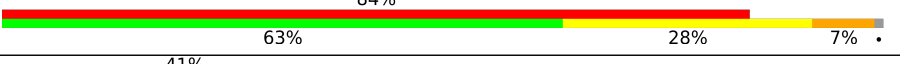
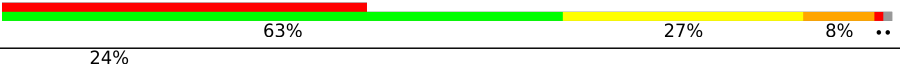
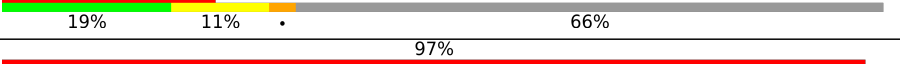
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	0	57	
2	1	55	
3	2	46	

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Mol	Chain	Length	Quality of chain
4	3	65	
5	4	38	
6	5	165	
7	6	121	
8	7	3	
9	A	2903	
10	B	118	
11	C	273	
12	D	209	
13	E	201	
14	F	179	
15	G	177	
16	H	149	
17	I	142	
18	J	142	
19	K	123	
20	L	144	
21	M	136	
22	N	127	
23	O	117	
24	P	115	
25	Q	118	
26	R	103	
27	S	110	
28	T	100	

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Mol	Chain	Length	Quality of chain
29	U	104	46%60%31%7%••
30	V	94	27%71%26%•
31	W	85	22%33%32%25%•7%
32	X	78	17%68%23%8%•
33	Y	63	43%56%41%•
34	Z	59	14%51%37%10%•
35	a	19	5%26%5%63%

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 90700 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 protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

- Molecule 7 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 8 is a RNA chain called P-tRNA CCA-end.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	3	Total	C	N	O	P	0	0
			58	28	11	17	2		

- Molecule 9 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	2854	Total	C	N	O	P	0	0
			61274	27334	11279	19807	2854		

- Molecule 10 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 11 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 13 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 14 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 15 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	50	Total	C	N	O	S	0	0
			384	247	68	68	1		

- Molecule 17 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 18 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 19 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 20 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 21 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 22 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 23 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 24 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 25 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 26 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 27 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 28 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 29 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 30 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 31 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 32 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 33 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

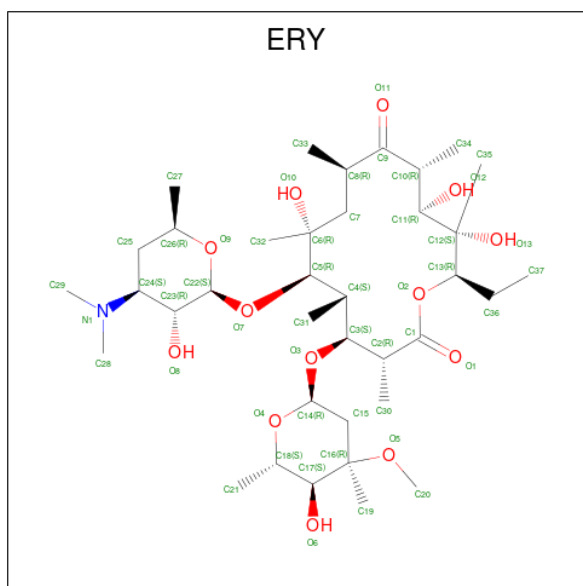
- Molecule 34 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 35 is a protein called ErmCL nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	a	7	Total	C	N	O	0	3
			36	27	4	5		

- Molecule 36 is ERYTHROMYCIN A (CCD ID: ERY) (formula: $C_{37}H_{67}NO_{13}$).

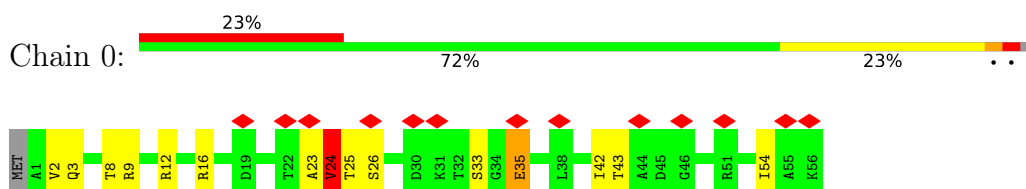


Mol	Chain	Residues	Atoms				AltConf
36	A	1	Total	C	N	O	0
			51	37	1	13	

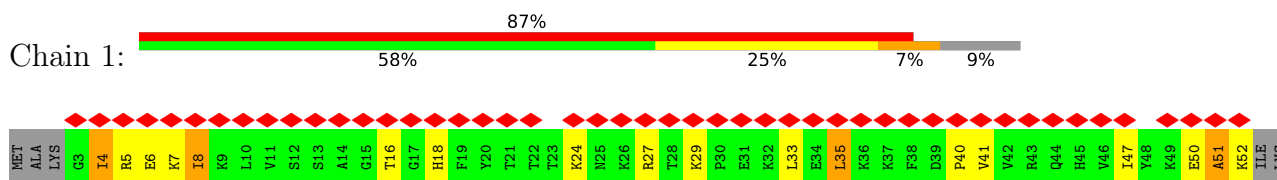
3 Residue-property plots [i](#)

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

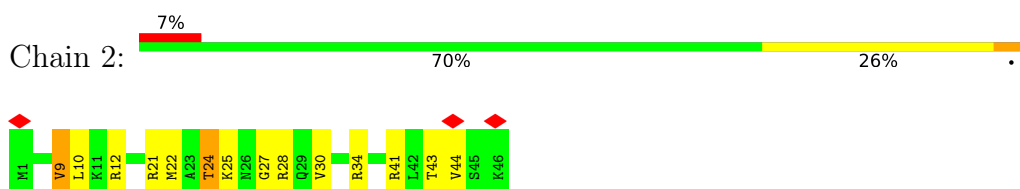
- Molecule 1: 50S ribosomal protein L32



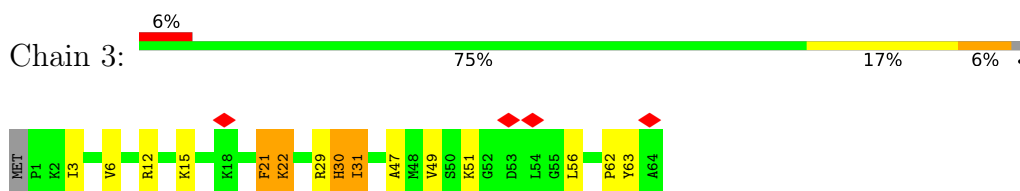
- Molecule 2: 50S ribosomal protein L33



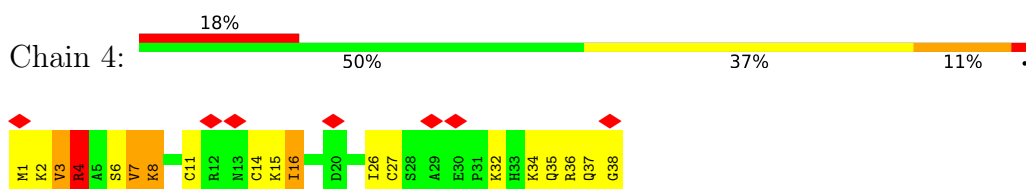
- Molecule 3: 50S ribosomal protein L34



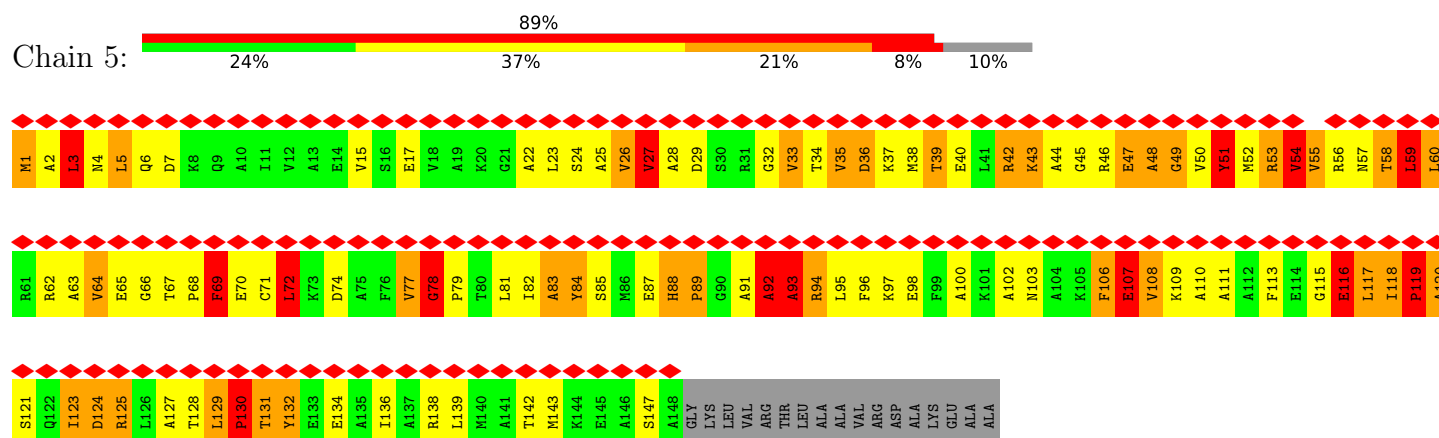
- Molecule 4: 50S ribosomal protein L35



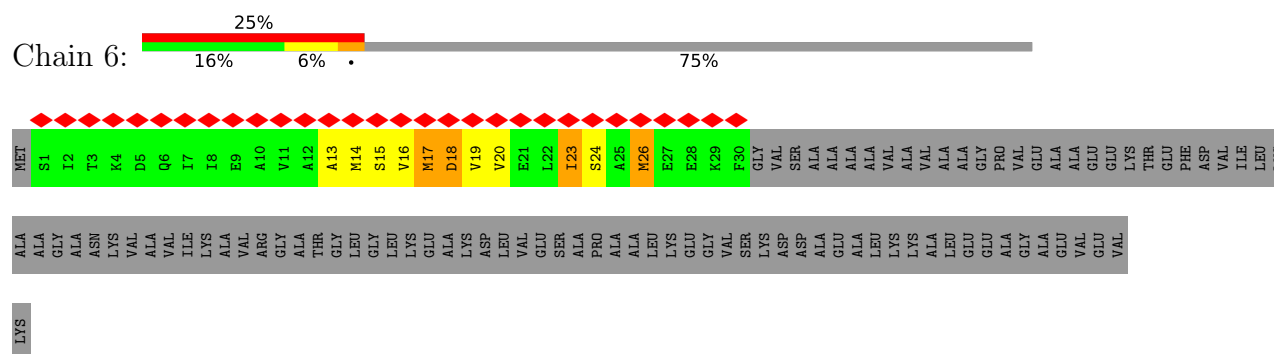
- Molecule 5: 50S ribosomal protein L36



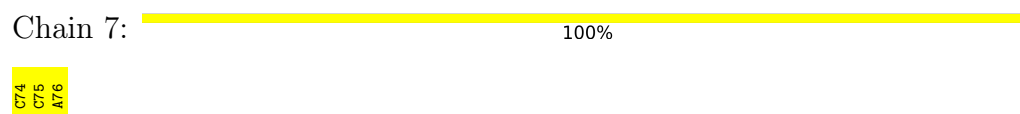
- Molecule 6: 50S ribosomal protein L10



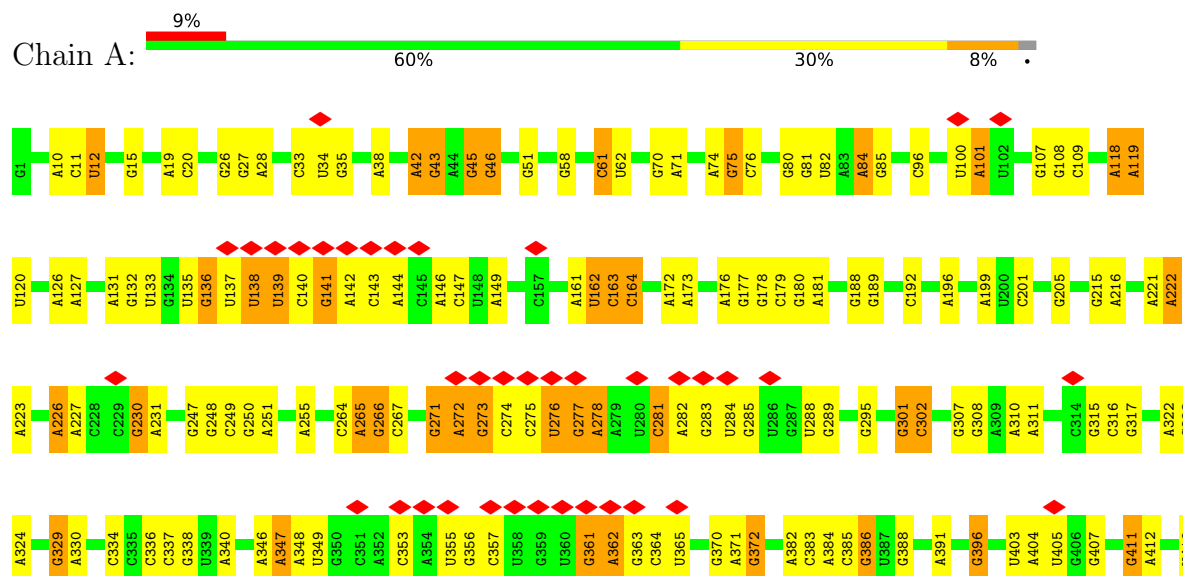
- Molecule 7: 50S ribosomal protein L7/L12

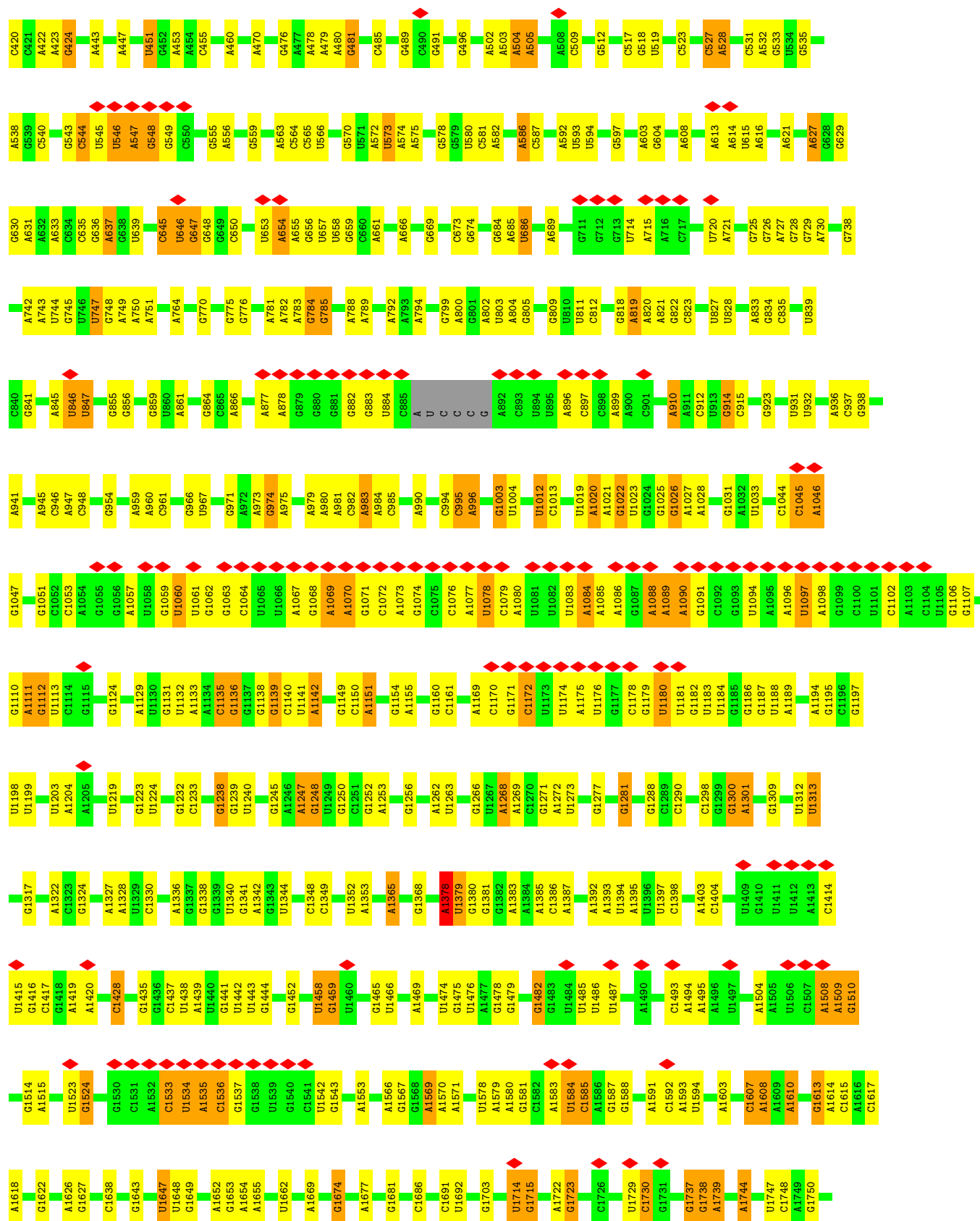


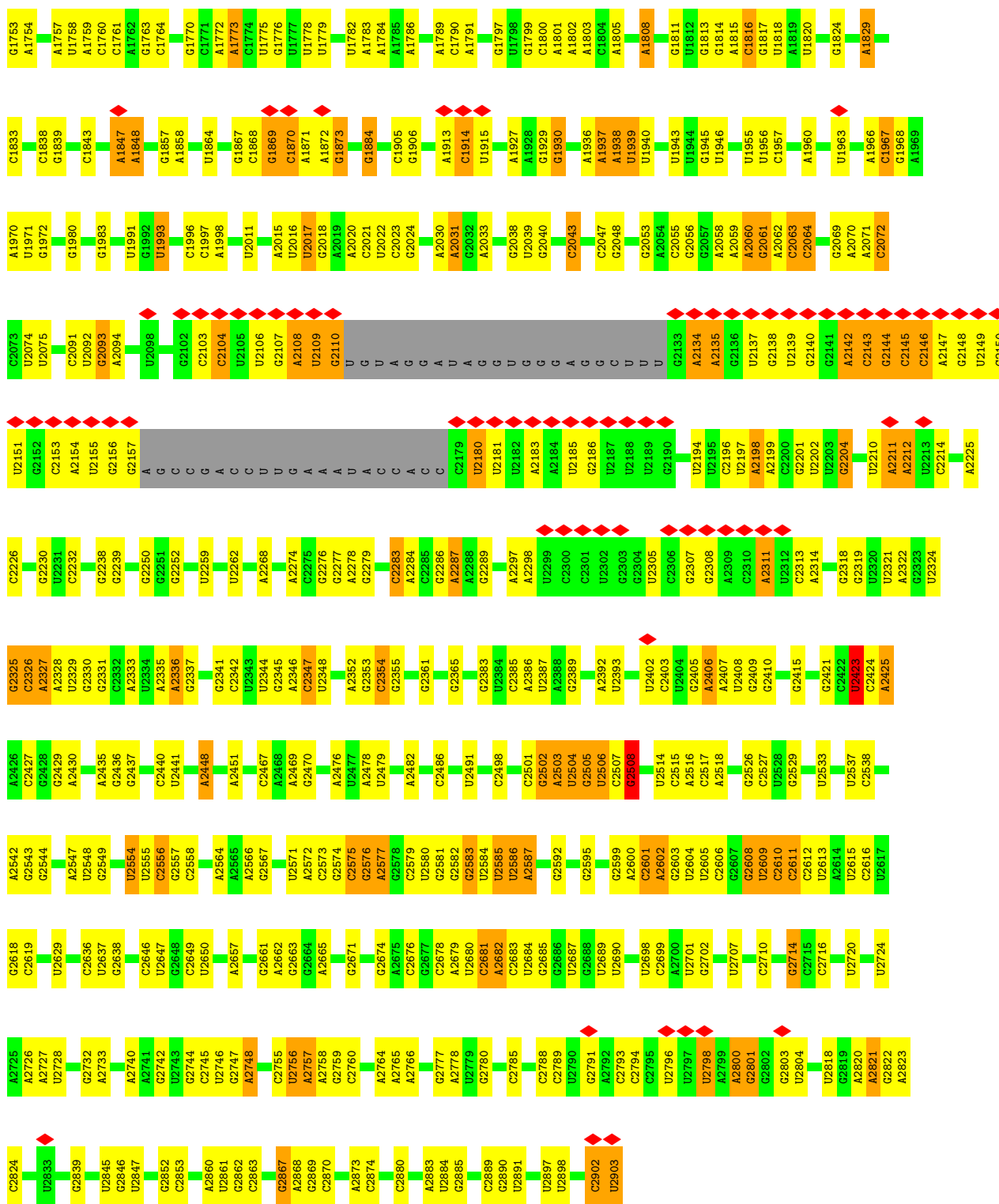
- Molecule 8: P-tRNA CCA-end

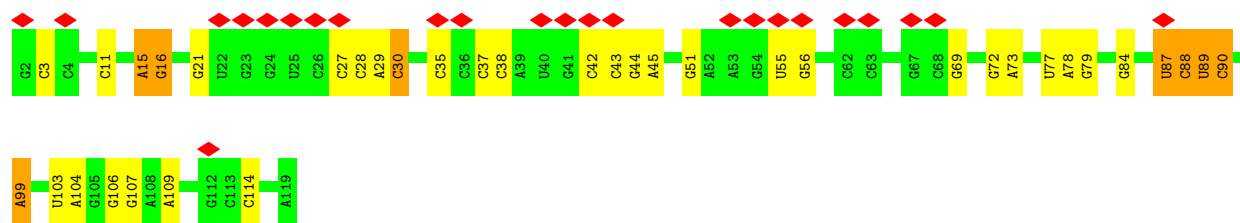


- Molecule 9: 23S rRNA

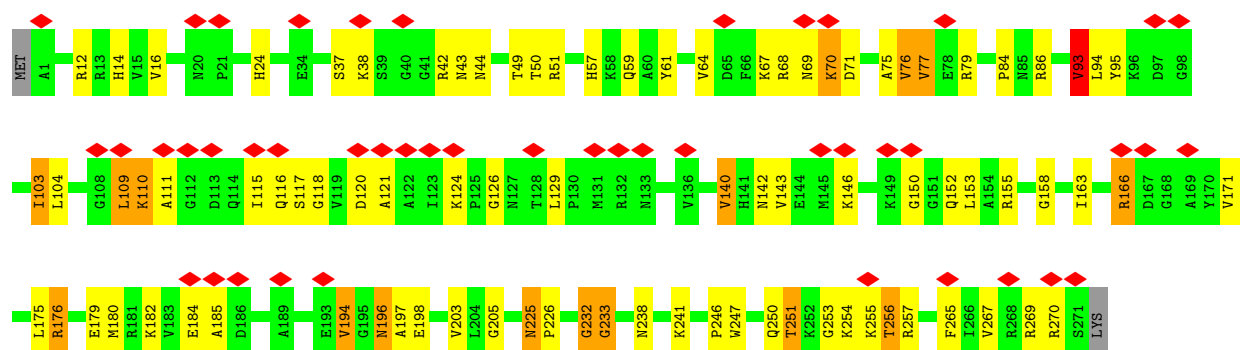




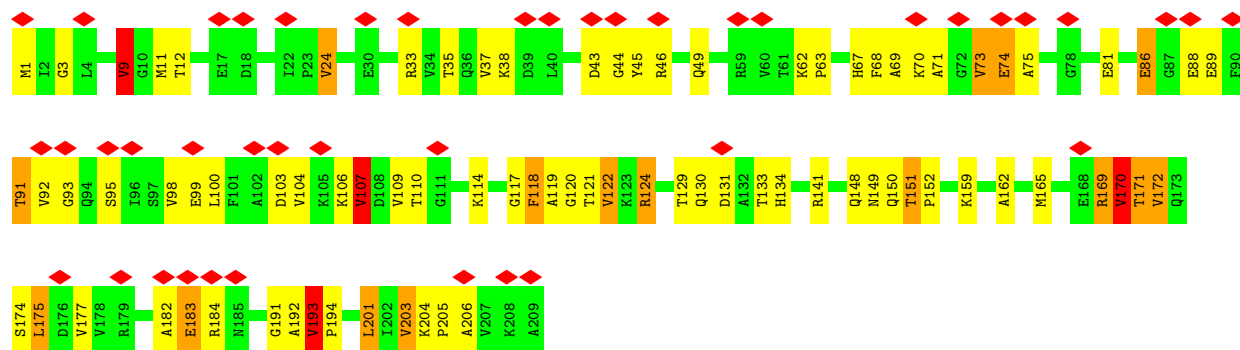




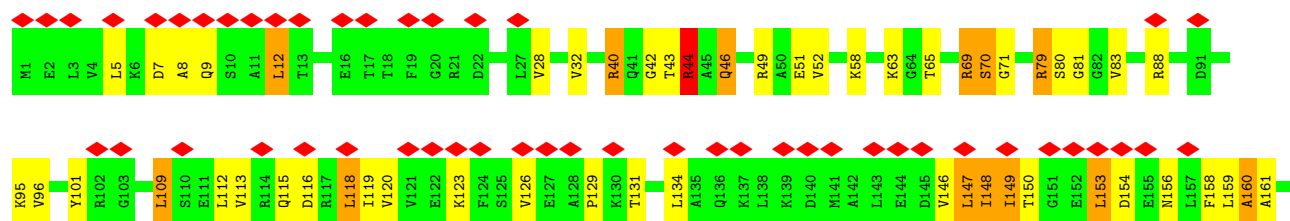
• Molecule 11: 50S ribosomal protein L2

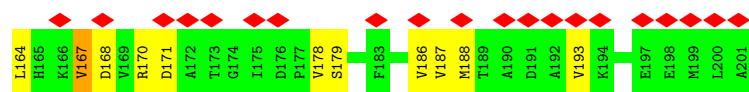


• Molecule 12: 50S ribosomal protein L3

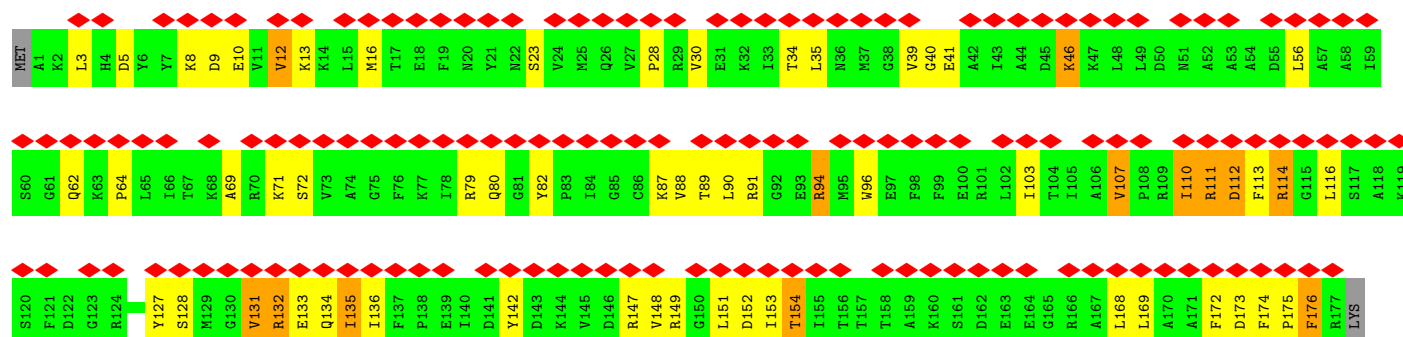
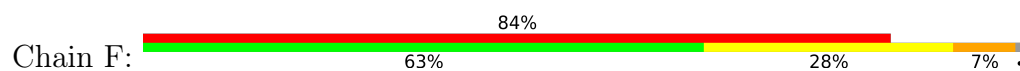


• Molecule 13: 50S ribosomal protein L4

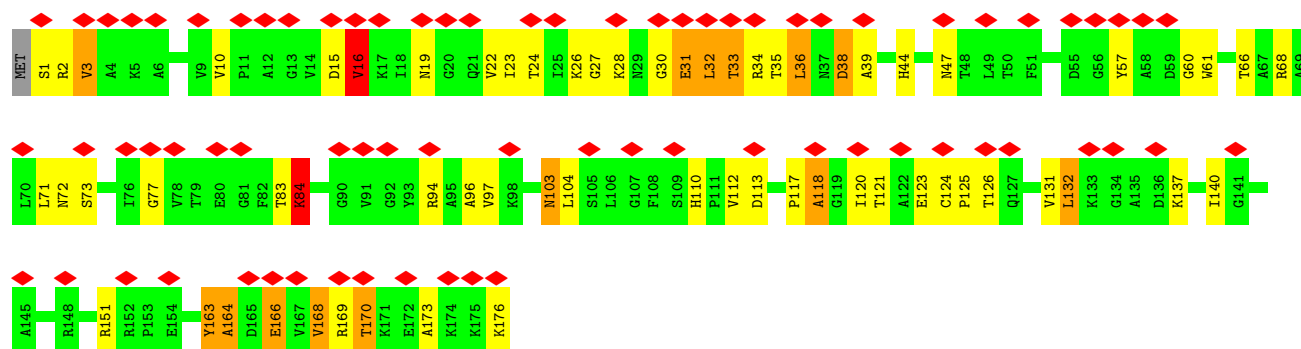
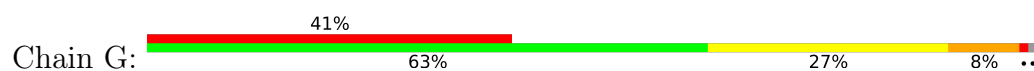




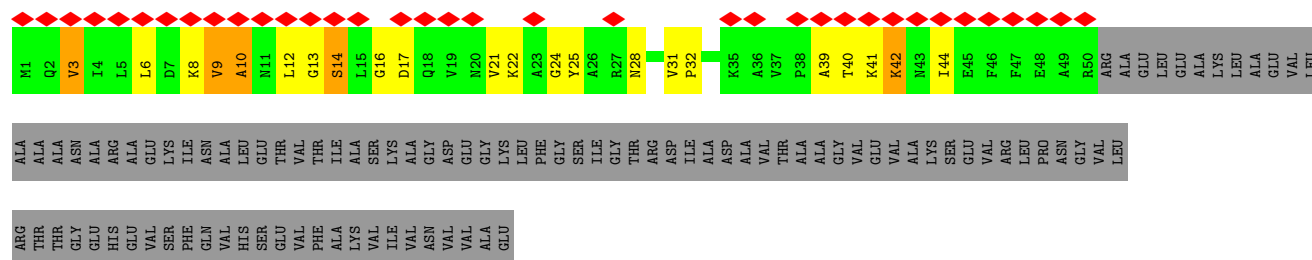
• Molecule 14: 50S ribosomal protein L5



• Molecule 15: 50S ribosomal protein L6

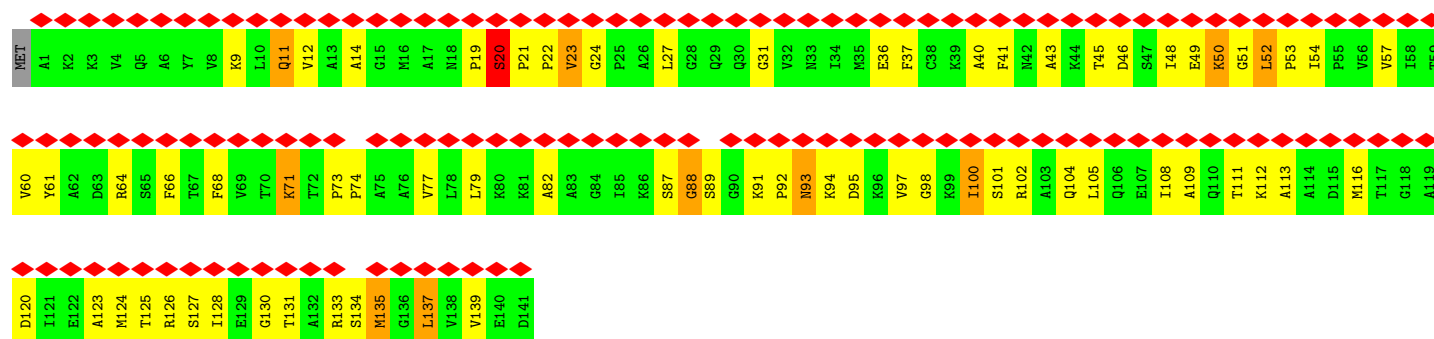


• Molecule 16: 50S ribosomal protein L9

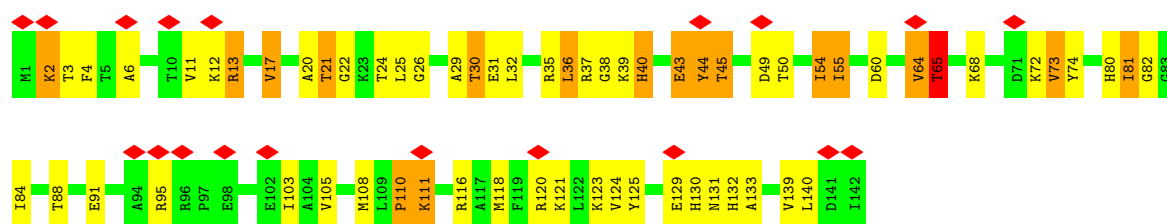


• Molecule 17: 50S ribosomal protein L11

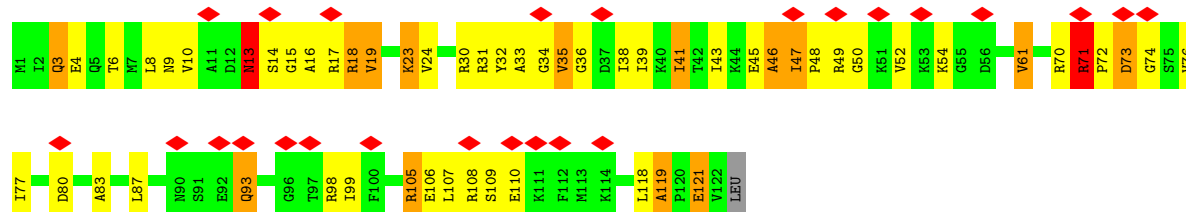




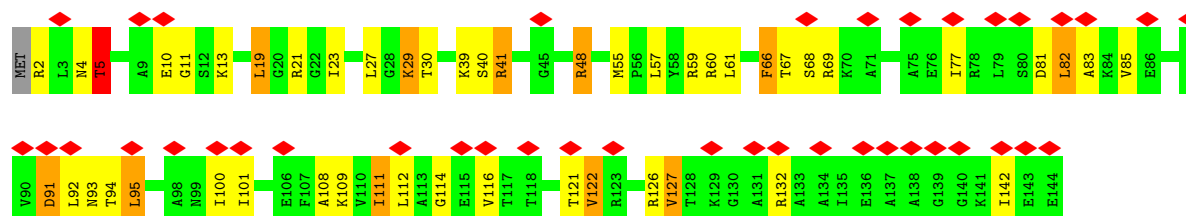
• Molecule 18: 50S ribosomal protein L13



• Molecule 19: 50S ribosomal protein L14

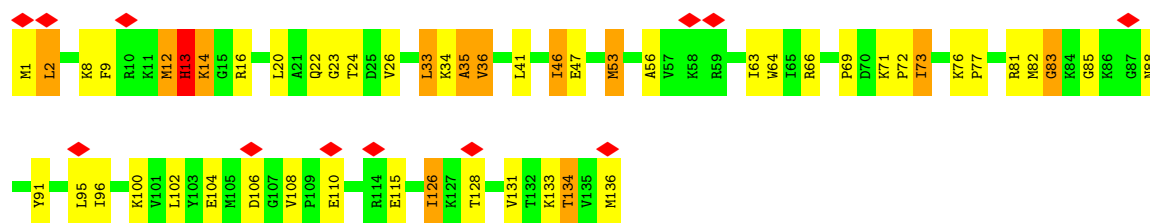


• Molecule 20: 50S ribosomal protein L15

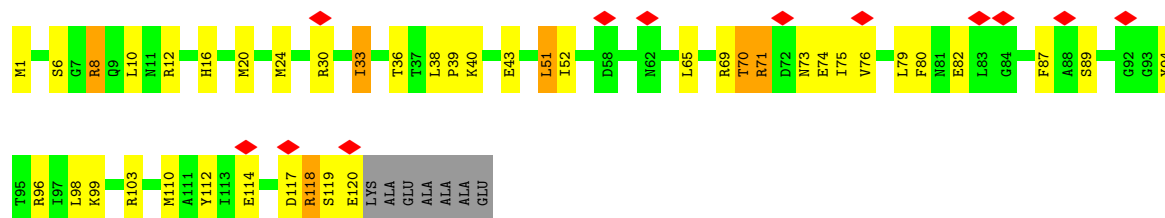


• Molecule 21: 50S ribosomal protein L16

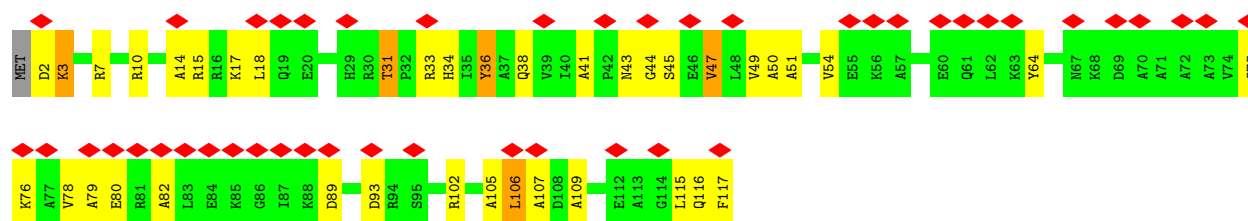
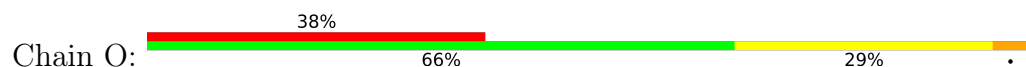




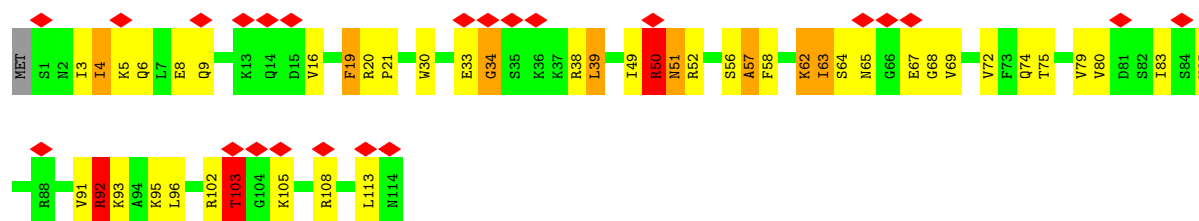
• Molecule 22: 50S ribosomal protein L17



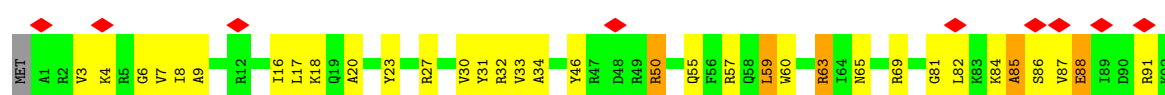
• Molecule 23: 50S ribosomal protein L18

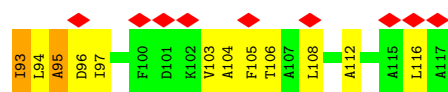


• Molecule 24: 50S ribosomal protein L19

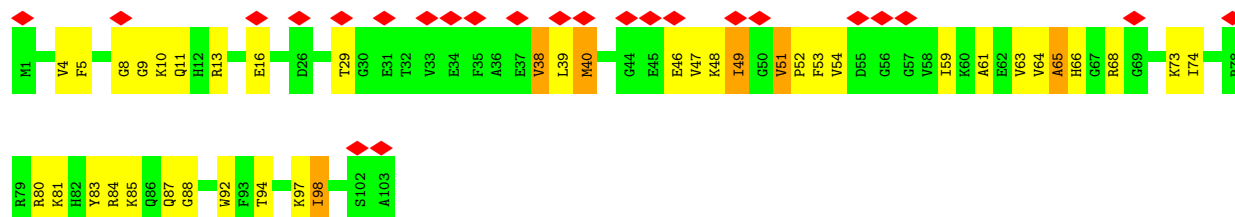


• Molecule 25: 50S ribosomal protein L20

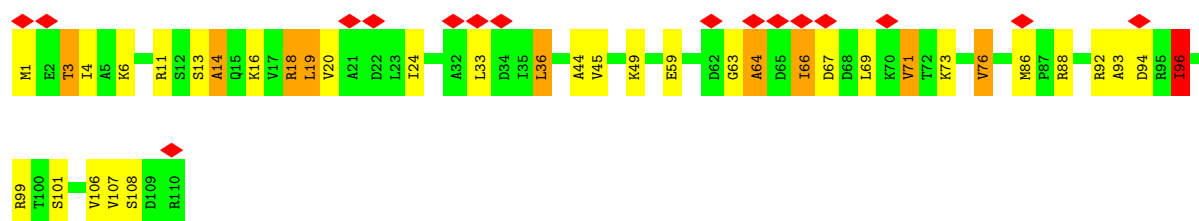




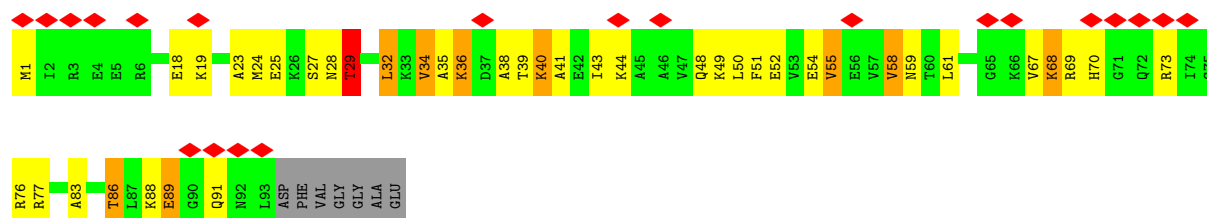
• Molecule 26: 50S ribosomal protein L21



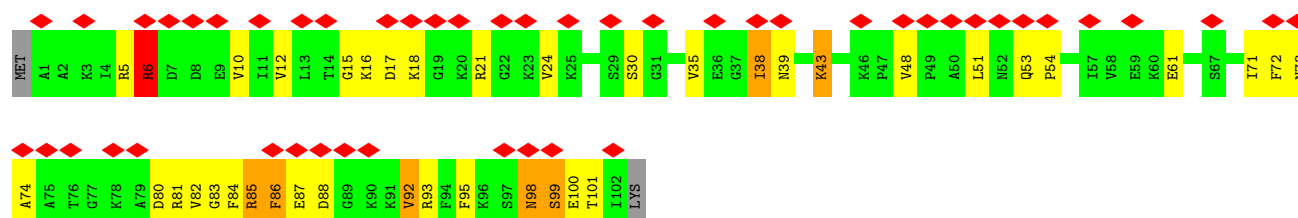
• Molecule 27: 50S ribosomal protein L22



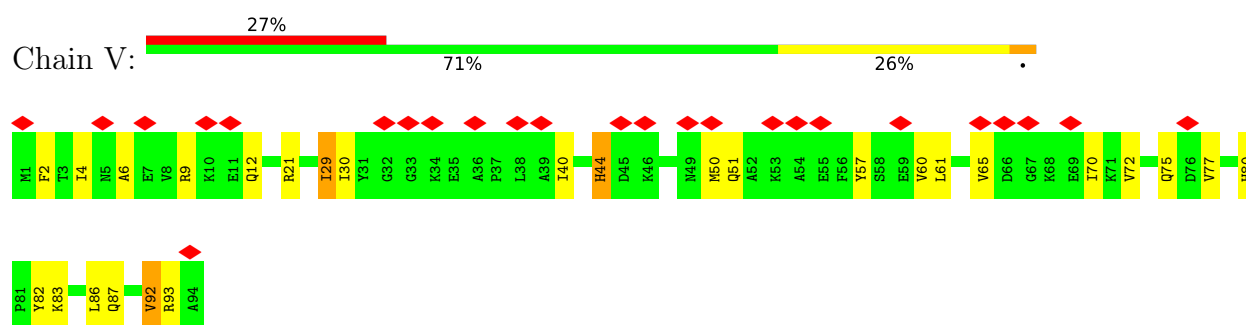
• Molecule 28: 50S ribosomal protein L23



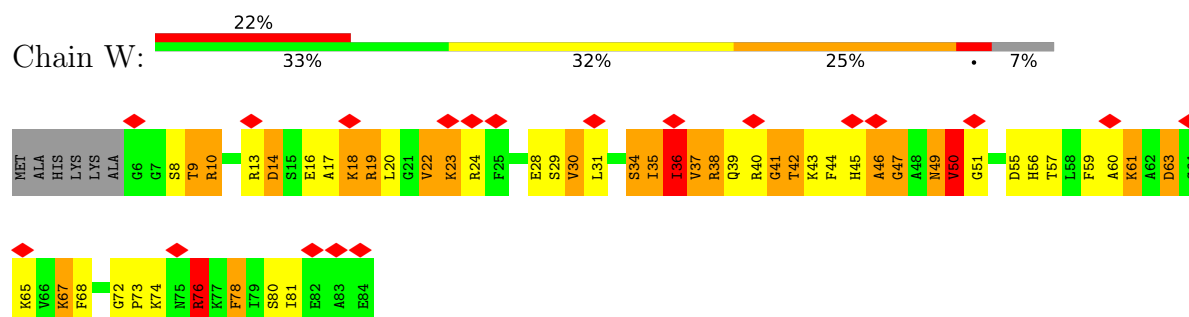
• Molecule 29: 50S ribosomal protein L24



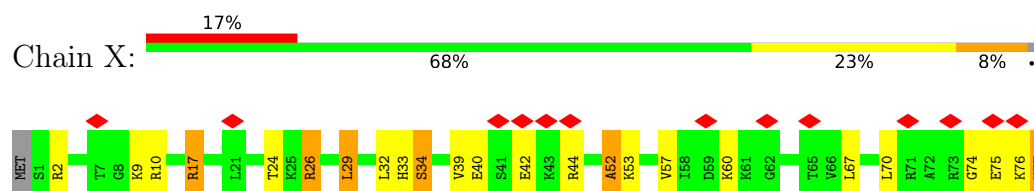
• Molecule 30: 50S ribosomal protein L25



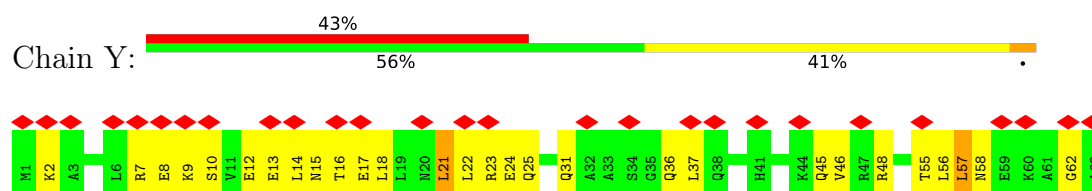
• Molecule 31: 50S ribosomal protein L27



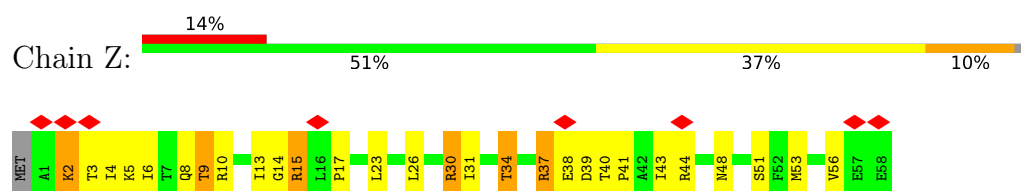
• Molecule 32: 50S ribosomal protein L28



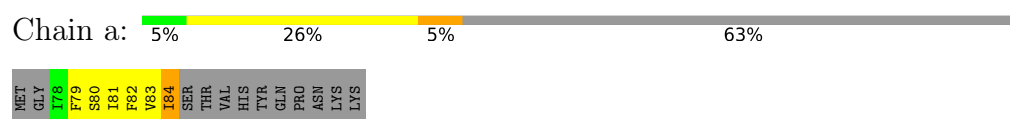
• Molecule 33: 50S ribosomal protein L29



• Molecule 34: 50S ribosomal protein L30



• Molecule 35: ErmCL nascent chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	269163	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	defocus groups	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	125085	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.019	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	Depositor
Map size ($\text{\AA}$)	196.11601, 202.764, 255.94801	wwPDB
Map dimensions	177, 183, 231	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.108, 1.108, 1.108	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0	0.69	0/450	0.91	0/599
2	1	0.68	0/416	1.01	2/554 (0.4%)
3	2	0.72	0/380	1.00	0/498
4	3	0.72	0/513	0.99	1/676 (0.1%)
5	4	0.85	1/303 (0.3%)	1.19	1/397 (0.3%)
6	5	0.90	1/1131 (0.1%)	2.04	51/1524 (3.3%)
7	6	0.78	0/227	0.98	1/304 (0.3%)
8	7	0.34	0/64	0.66	0/97
9	A	0.44	0/68626	0.60	8/107056 (0.0%)
10	B	0.37	0/2828	0.55	0/4410
11	C	0.71	0/2121	1.10	10/2852 (0.4%)
12	D	0.74	0/1586	1.12	7/2134 (0.3%)
13	E	0.69	0/1571	1.02	4/2113 (0.2%)
14	F	0.60	0/1434	0.99	5/1926 (0.3%)
15	G	0.69	0/1343	0.99	1/1816 (0.1%)
16	H	0.68	0/389	1.05	1/523 (0.2%)
17	I	0.83	0/1046	1.23	13/1410 (0.9%)
18	J	0.81	1/1152 (0.1%)	1.07	3/1551 (0.2%)
19	K	0.83	0/947	1.02	1/1268 (0.1%)
20	L	0.74	0/1054	1.01	0/1403
21	M	0.79	0/1093	1.05	3/1460 (0.2%)
22	N	0.68	0/973	0.91	0/1301
23	O	0.59	0/902	0.98	1/1209 (0.1%)
24	P	0.67	0/929	1.03	3/1242 (0.2%)
25	Q	0.79	0/960	0.96	1/1278 (0.1%)
26	R	0.71	0/829	1.04	3/1107 (0.3%)
27	S	0.77	1/864 (0.1%)	0.99	2/1156 (0.2%)
28	T	0.73	0/744	1.11	3/994 (0.3%)
29	U	0.69	0/787	1.08	0/1051
30	V	0.61	0/766	0.92	3/1025 (0.3%)
31	W	0.94	2/603 (0.3%)	1.30	5/797 (0.6%)
32	X	0.66	0/635	1.00	1/848 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.55	0/510	0.98	0/677
34	Z	0.74	0/453	1.08	0/605
35	a	0.87	0/32	1.55	1/40 (2.5%)
All	All	0.53	6/98661 (0.0%)	0.76	135/147901 (0.1%)

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
6	5	0	1
11	C	0	1
12	D	0	1
18	J	0	1
19	K	0	1
All	All	0	5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	W	35	ILE	CA-CB	6.45	1.62	1.54
5	4	3	VAL	CA-CB	-5.95	1.49	1.55
31	W	50	VAL	CA-CB	5.58	1.62	1.54
18	J	43	GLU	CA-C	-5.34	1.45	1.52
27	S	96	ILE	CA-CB	5.22	1.61	1.54
6	5	50	VAL	CA-CB	5.07	1.61	1.54

All (135) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	D	151	THR	CA-C-N	-14.35	103.98	119.19
12	D	151	THR	C-N-CA	-14.35	103.98	119.19
6	5	131	THR	N-CA-C	-13.41	96.67	111.28
6	5	92	ALA	CA-C-N	12.65	145.71	121.54
6	5	92	ALA	C-N-CA	12.65	145.71	121.54
6	5	93	ALA	CA-C-N	11.94	144.35	121.54
6	5	93	ALA	C-N-CA	11.94	144.35	121.54
6	5	72	LEU	CA-C-N	11.56	140.14	121.18
6	5	72	LEU	C-N-CA	11.56	140.14	121.18
6	5	59	LEU	CA-C-N	10.66	136.81	120.82
6	5	59	LEU	C-N-CA	10.66	136.81	120.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	5	84	TYR	CA-C-N	10.54	137.86	123.00
6	5	84	TYR	C-N-CA	10.54	137.86	123.00
6	5	49	GLY	CA-C-N	10.47	140.81	121.97
6	5	49	GLY	C-N-CA	10.47	140.81	121.97
6	5	51	TYR	CA-C-N	10.01	140.95	122.74
6	5	51	TYR	C-N-CA	10.01	140.95	122.74
6	5	119	PRO	CA-C-N	10.00	140.64	121.54
6	5	119	PRO	C-N-CA	10.00	140.64	121.54
6	5	83	ALA	N-CA-C	9.97	122.60	108.54
6	5	28	ALA	CA-C-N	9.40	139.50	121.54
6	5	28	ALA	C-N-CA	9.40	139.50	121.54
6	5	47	GLU	CA-C-N	9.27	139.25	121.54
6	5	47	GLU	C-N-CA	9.27	139.25	121.54
6	5	147	SER	CA-C-N	8.99	137.88	121.70
6	5	147	SER	C-N-CA	8.99	137.88	121.70
6	5	50	VAL	CA-C-N	8.77	137.65	121.52
6	5	50	VAL	C-N-CA	8.77	137.65	121.52
6	5	40	GLU	CA-C-N	8.77	137.78	122.09
6	5	40	GLU	C-N-CA	8.77	137.78	122.09
6	5	39	THR	CA-C-N	8.74	137.24	120.99
6	5	39	THR	C-N-CA	8.74	137.24	120.99
31	W	42	THR	N-CA-C	-8.66	101.75	111.71
19	K	121	GLU	N-CA-C	8.42	119.01	107.73
16	H	42	LYS	N-CA-C	-8.33	103.63	113.88
9	A	2508	G	O3'-P-O5'	8.31	116.47	104.00
6	5	53	ARG	CA-C-N	8.13	136.60	121.97
6	5	53	ARG	C-N-CA	8.13	136.60	121.97
17	I	97	VAL	N-CA-C	8.12	119.00	111.45
6	5	60	LEU	N-CA-C	-8.07	98.05	111.37
6	5	64	VAL	N-CA-C	-8.06	104.90	112.96
26	R	51	VAL	CA-C-N	-7.98	112.13	120.03
26	R	51	VAL	C-N-CA	-7.98	112.13	120.03
11	C	93	VAL	N-CA-C	7.92	118.92	111.48
12	D	9	VAL	N-CA-C	-7.77	105.13	111.81
13	E	146	VAL	N-CA-C	7.63	118.42	108.35
35	a	84	ILE	CB-CA-C	-7.52	96.55	111.60
6	5	117	LEU	CA-C-N	7.51	136.02	122.13
6	5	117	LEU	C-N-CA	7.51	136.02	122.13
17	I	133	ARG	N-CA-C	-7.49	102.38	112.26
14	F	110	ILE	N-CA-C	7.29	117.89	108.12
11	C	166	ARG	N-CA-C	6.99	118.65	110.41
11	C	233	GLY	N-CA-C	-6.99	96.62	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	R	9	GLY	N-CA-C	-6.85	103.11	114.48
18	J	124	VAL	N-CA-C	6.82	119.45	112.90
7	6	23	ILE	N-CA-C	-6.81	105.85	111.91
30	V	44	HIS	N-CA-C	6.80	118.38	110.97
9	A	1378	A	C4'-C3'-O3'	6.79	119.58	109.40
32	X	52	ALA	N-CA-C	-6.76	101.16	110.35
28	T	68	LYS	N-CA-C	6.64	117.34	108.38
6	5	28	ALA	N-CA-C	6.62	120.67	107.62
12	D	172	VAL	N-CA-C	6.62	117.68	112.12
28	T	29	THR	N-CA-C	6.45	124.54	110.80
23	O	54	VAL	N-CA-C	-6.41	105.34	113.22
18	J	73	VAL	N-CA-C	6.34	116.51	110.74
9	A	2508	G	P-O3'-C3'	-6.28	110.78	120.20
6	5	129	LEU	CA-C-N	6.25	127.65	119.84
6	5	129	LEU	C-N-CA	6.25	127.65	119.84
2	1	29	LYS	CA-C-N	6.25	125.87	119.56
2	1	29	LYS	C-N-CA	6.25	125.87	119.56
31	W	35	ILE	N-CA-C	-6.23	107.17	113.47
9	A	2423	U	C2'-C3'-O3'	6.11	118.67	109.50
27	S	6	LYS	N-CA-C	6.04	118.04	108.79
14	F	110	ILE	CB-CA-C	-6.03	104.78	111.35
6	5	27	VAL	CG1-CB-CG2	6.01	124.02	110.80
5	4	7	VAL	N-CA-C	6.00	117.12	111.48
11	C	118	GLY	N-CA-C	5.90	117.55	111.95
6	5	77	VAL	CA-C-N	5.90	131.13	121.87
6	5	77	VAL	C-N-CA	5.90	131.13	121.87
17	I	31	GLY	N-CA-C	-5.87	106.89	115.63
6	5	123	ILE	CG1-CB-CG2	5.81	128.13	110.70
12	D	91	THR	N-CA-C	5.76	119.57	112.54
17	I	20	SER	CA-C-N	-5.76	114.45	120.38
17	I	20	SER	C-N-CA	-5.76	114.45	120.38
12	D	193	VAL	CA-C-N	5.73	125.70	120.03
12	D	193	VAL	C-N-CA	5.73	125.70	120.03
13	E	44	ARG	N-CA-C	5.69	117.93	108.99
27	S	18	ARG	N-CA-C	-5.65	102.89	110.24
11	C	76	VAL	N-CA-C	5.64	118.61	113.20
6	5	78	GLY	CA-C-N	-5.60	114.20	119.85
6	5	78	GLY	C-N-CA	-5.60	114.20	119.85
13	E	160	ALA	N-CA-C	-5.54	102.70	110.50
9	A	2508	G	P-O5'-C5'	-5.52	112.62	120.90
6	5	130	PRO	CA-N-CD	-5.52	104.28	112.00
30	V	70	ILE	N-CA-C	-5.46	107.11	111.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	5	117	LEU	N-CA-C	5.45	118.34	108.69
17	I	54	ILE	CA-C-N	-5.45	114.08	119.92
17	I	54	ILE	C-N-CA	-5.45	114.08	119.92
14	F	12	VAL	N-CA-C	-5.45	104.24	111.05
6	5	39	THR	N-CA-C	5.42	116.88	110.97
24	P	57	ALA	N-CA-C	5.41	117.48	109.69
31	W	76	ARG	NE-CZ-NH2	5.41	124.07	119.20
15	G	168	VAL	N-CA-C	5.41	120.59	109.34
28	T	25	GLU	N-CA-C	-5.40	103.30	111.56
14	F	112	ASP	N-CA-C	-5.40	106.00	113.18
24	P	50	ARG	CB-CG-CD	5.38	123.67	111.30
13	E	44	ARG	NE-CZ-NH2	5.31	123.98	119.20
31	W	38	ARG	N-CA-C	-5.29	104.60	111.74
9	A	1247	A	C2'-C3'-O3'	5.28	117.42	109.50
9	A	2423	U	P-O3'-C3'	5.26	128.09	120.20
6	5	35	VAL	N-CA-C	-5.25	104.48	111.05
30	V	60	VAL	N-CA-C	-5.25	102.82	109.80
17	I	52	LEU	CA-C-N	5.24	125.54	119.93
17	I	52	LEU	C-N-CA	5.24	125.54	119.93
14	F	107	VAL	CB-CA-C	-5.24	108.80	114.35
21	M	83	GLY	CA-C-N	-5.16	114.71	122.24
21	M	83	GLY	C-N-CA	-5.16	114.71	122.24
17	I	100	ILE	N-CA-C	5.16	117.03	108.99
25	Q	3	VAL	N-CA-C	5.14	114.15	106.85
6	5	54	VAL	CG1-CB-CG2	5.13	122.09	110.80
18	J	64	VAL	N-CA-C	5.13	120.01	109.34
9	A	1378	A	P-O3'-C3'	5.12	127.88	120.20
11	C	42	ARG	N-CA-C	5.11	117.81	109.59
11	C	140	VAL	N-CA-C	5.11	119.96	109.34
4	3	21	PHE	N-CA-C	5.08	121.01	114.56
17	I	50	LYS	N-CA-C	5.07	117.67	109.06
11	C	86	ARG	N-CA-C	5.06	115.98	108.60
6	5	93	ALA	N-CA-C	5.05	121.56	110.80
17	I	100	ILE	CB-CA-C	-5.05	103.63	110.90
21	M	85	GLY	CA-C-O	-5.04	118.76	122.23
31	W	67	LYS	N-CA-C	5.03	118.83	111.34
24	P	74	GLN	N-CA-C	-5.02	101.57	109.25
11	C	225	ASN	CA-C-N	5.02	125.04	119.32
11	C	225	ASN	C-N-CA	5.02	125.04	119.32
17	I	135	MET	N-CA-C	-5.00	107.12	113.43

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	5	130	PRO	Peptide
11	C	233	GLY	Peptide
12	D	9	VAL	Peptide
18	J	110	PRO	Peptide
19	K	71	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	18	0
2	1	409	0	440	15	0
3	2	377	0	418	9	0
4	3	504	0	574	10	0
5	4	302	0	340	16	0
6	5	1117	0	1155	132	0
7	6	227	0	237	6	0
8	7	58	0	33	12	0
9	A	61274	0	30817	823	0
10	B	2529	0	1281	20	0
11	C	2082	0	2157	54	0
12	D	1565	0	1616	58	0
13	E	1552	0	1619	44	0
14	F	1410	0	1447	46	0
15	G	1323	0	1374	41	0
16	H	384	0	405	14	0
17	I	1032	0	1088	60	0
18	J	1129	0	1162	58	0
19	K	938	0	1012	43	0
20	L	1045	0	1117	41	0
21	M	1074	0	1157	30	0
22	N	960	0	1000	30	0
23	O	892	0	923	23	0
24	P	917	0	965	40	0
25	Q	947	0	1022	54	0
26	R	816	0	839	35	0
27	S	857	0	922	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	T	738	0	807	38	0
29	U	779	0	834	28	0
30	V	753	0	780	16	0
31	W	596	0	610	84	0
32	X	625	0	655	17	0
33	Y	509	0	543	16	0
34	Z	449	0	491	17	0
35	a	36	0	34	10	0
36	A	51	0	67	12	0
All	All	90700	0	60402	1745	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (1745) 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)
9:A:912:C:OP1	21:M:8:LYS:NZ	1.79	1.15
9:A:2062:A:N6	36:A:9000:ERY:H273	1.64	1.13
9:A:2061:G:OP2	13:E:63:LYS:NZ	1.88	1.06
6:5:71:CYS:HB3	6:5:117:LEU:HD12	1.33	1.04
9:A:2579:C:H2'	9:A:2580:U:H5'	1.40	1.03
36:A:9000:ERY:C21	35:a:81:ILE:O	2.06	1.03
9:A:2579:C:C2'	9:A:2580:U:H5'	1.88	1.02
9:A:2574:G:C2'	9:A:2575:C:H5'	1.90	1.01
6:5:3:LEU:O	6:5:7:ASP:OD1	1.79	1.00
6:5:26:VAL:HG21	6:5:115:GLY:H	1.23	1.00
9:A:2063:C:C5	9:A:2064:C:C5	2.50	1.00
9:A:2574:G:H2'	9:A:2575:C:H5'	1.46	0.98
8:7:74:C:O2	9:A:2252:G:N2	1.97	0.97
36:A:9000:ERY:H213	35:a:81:ILE:O	1.66	0.96
9:A:2063:C:H2'	9:A:2064:C:H5'	1.48	0.95
9:A:2582:G:C2	9:A:2583:G:C8	2.55	0.94
6:5:117:LEU:CD2	6:5:120:ALA:HA	1.97	0.94
9:A:2600:A:H2'	9:A:2601:C:H5'	1.48	0.94
6:5:71:CYS:HB3	6:5:117:LEU:CD1	1.98	0.92
9:A:1154:G:OP2	25:Q:57:ARG:NH1	2.03	0.92
9:A:2580:U:H2'	9:A:2581:G:H5'	1.52	0.91
6:5:71:CYS:CB	6:5:117:LEU:HD12	2.00	0.91
9:A:1248:G:OP2	13:E:44:ARG:NH1	2.03	0.91
35:a:82:PHE:C	35:a:83:VAL:CA	2.44	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:43:C:O2	14:F:91:ARG:NH2	2.04	0.90
9:A:2279:G:N7	31:W:10:ARG:NH2	2.20	0.90
29:U:98:ASN:O	29:U:100:GLU:N	2.06	0.89
9:A:1336:A:OP2	28:T:68:LYS:NZ	2.06	0.88
9:A:2582:G:N3	9:A:2583:G:C8	2.41	0.88
9:A:2600:A:C2'	9:A:2601:C:H5'	2.04	0.88
6:5:71:CYS:CB	6:5:117:LEU:CD1	2.50	0.88
9:A:996:A:OP2	25:Q:91:ARG:NH2	2.07	0.88
6:5:24:SER:HB2	6:5:116:GLU:HG2	1.54	0.87
9:A:2505:G:O2'	9:A:2506:U:H5''	1.75	0.87
9:A:2599:G:O2'	9:A:2600:A:H5'	1.74	0.87
9:A:2062:A:H62	36:A:9000:ERY:H273	1.33	0.86
28:T:39:THR:O	28:T:41:ALA:N	2.09	0.86
6:5:77:VAL:C	6:5:79:PRO:HD2	2.00	0.85
9:A:1723:G:O6	9:A:1737:G:O2'	1.94	0.85
36:A:9000:ERY:H212	35:a:81:ILE:O	1.76	0.84
9:A:2061:G:OP2	13:E:63:LYS:CE	2.24	0.84
6:5:71:CYS:HA	6:5:117:LEU:HD13	1.60	0.84
9:A:2053:G:N2	9:A:2616:C:N3	2.24	0.84
9:A:1069:A:N3	9:A:1073:A:N6	2.26	0.84
6:5:91:ALA:C	6:5:93:ALA:H	1.87	0.83
6:5:33:VAL:N	6:5:36:ASP:OD2	2.12	0.82
6:5:71:CYS:HA	6:5:117:LEU:CD1	2.09	0.82
9:A:2603:G:O2'	9:A:2604:U:H5'	1.80	0.82
9:A:504:A:O2'	9:A:505:A:OP1	1.98	0.81
24:P:50:ARG:HB3	24:P:57:ALA:H	1.43	0.81
23:O:34:HIS:O	23:O:102:ARG:NH1	2.14	0.81
6:5:103:ASN:ND2	6:5:107:GLU:O	2.13	0.81
11:C:196:ASN:O	11:C:198:GLU:N	2.12	0.81
35:a:79:PHE:CA	35:a:80:SER:N	2.44	0.81
9:A:1782:U:O2	9:A:2608:G:O2'	1.97	0.80
9:A:2576:G:O2'	9:A:2577:A:O5'	1.98	0.80
9:A:1012:U:OP2	25:Q:69:ARG:NH1	2.14	0.80
35:a:83:VAL:CA	35:a:84:ILE:N	2.43	0.80
9:A:2576:G:N3	9:A:2576:G:H5'	1.97	0.79
9:A:2720:U:OP1	24:P:52:ARG:NH2	2.15	0.79
6:5:33:VAL:HG12	6:5:34:THR:H	1.48	0.79
6:5:43:LYS:NZ	6:5:98:GLU:OE1	2.16	0.79
9:A:2579:C:O2'	9:A:2580:U:H5'	1.82	0.79
9:A:2576:G:H4'	9:A:2577:A:OP1	1.80	0.78
9:A:2585:U:H5'	9:A:2586:U:OP2	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:76:A:C6	9:A:2451:A:H4'	2.18	0.78
9:A:2581:G:O2'	9:A:2610:C:N4	2.15	0.78
19:K:105:ARG:NH1	19:K:106:GLU:OE2	2.16	0.78
33:Y:18:LEU:O	33:Y:22:LEU:N	2.17	0.78
6:5:71:CYS:CA	6:5:117:LEU:CD1	2.62	0.77
9:A:1799:G:OP2	11:C:269:ARG:NH2	2.16	0.77
9:A:1509:A:O2'	9:A:1510:G:OP2	2.01	0.77
6:5:117:LEU:HD23	6:5:120:ALA:HA	1.65	0.77
9:A:2063:C:H2'	9:A:2064:C:C5'	2.15	0.77
6:5:35:VAL:HA	6:5:38:MET:SD	2.24	0.77
9:A:2611:C:H2'	9:A:2612:C:H6	1.47	0.77
12:D:184:ARG:NH1	24:P:6:GLN:OE1	2.17	0.77
9:A:2581:G:H2'	9:A:2581:G:N3	2.00	0.77
11:C:68:ARG:NH2	11:C:126:GLY:O	2.18	0.76
11:C:69:ASN:O	11:C:71:ASP:N	2.18	0.76
9:A:2580:U:C2'	9:A:2581:G:H5'	2.15	0.76
9:A:1187:G:OP1	26:R:85:LYS:NZ	2.19	0.75
6:5:131:THR:O	6:5:134:GLU:N	2.20	0.75
9:A:1342:A:O2'	9:A:1344:U:OP2	2.04	0.75
9:A:2331:G:O2'	31:W:39:GLN:O	2.04	0.74
9:A:572:A:OP2	26:R:80:ARG:NH2	2.21	0.74
6:5:57:ASN:O	6:5:59:LEU:N	2.21	0.74
9:A:2592:G:N1	9:A:2603:G:C6	2.55	0.74
12:D:91:THR:O	12:D:93:GLY:N	2.21	0.74
5:4:11:CYS:SG	5:4:14:CYS:N	2.60	0.74
9:A:2707:U:O2	22:N:71:ARG:NH1	2.20	0.73
9:A:1998:A:OP2	12:D:141:ARG:NH2	2.21	0.73
9:A:2611:C:H2'	9:A:2612:C:C6	2.24	0.73
17:I:113:ALA:HA	17:I:124:MET:HE1	1.70	0.73
18:J:43:GLU:O	18:J:45:THR:N	2.22	0.73
9:A:2586:U:C4	35:a:81:ILE:HG12	2.24	0.72
9:A:1799:G:O2'	11:C:179:GLU:OE2	2.07	0.72
15:G:22:VAL:HG12	15:G:36:LEU:CD1	2.19	0.72
9:A:2061:G:H4'	9:A:2061:G:OP1	1.89	0.72
9:A:2579:C:H2'	9:A:2580:U:C5'	2.17	0.72
6:5:106:PHE:O	6:5:108:VAL:N	2.23	0.71
9:A:2060:A:O2'	9:A:2061:G:OP2	2.08	0.71
24:P:5:LYS:NZ	24:P:9:GLN:OE1	2.23	0.71
6:5:1:MET:SD	6:5:2:ALA:N	2.58	0.71
9:A:2063:C:C6	9:A:2064:C:C5	2.78	0.71
9:A:2599:G:C2'	9:A:2600:A:H5'	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1993:U:H4'	12:D:133:THR:HG21	1.73	0.70
5:4:2:LYS:NZ	9:A:2478:A:OP2	2.23	0.70
9:A:1805:A:N3	11:C:49:THR:OG1	2.24	0.70
8:7:76:A:C6	9:A:2451:A:C4'	2.74	0.70
9:A:161:A:H3'	9:A:162:U:H5''	1.72	0.70
9:A:2353:G:H1'	31:W:30:VAL:HG12	1.72	0.70
9:A:2580:U:H2'	9:A:2581:G:C5'	2.20	0.70
9:A:971:G:OP2	9:A:974:G:N2	2.25	0.70
9:A:2063:C:O4'	35:a:84:ILE:HD11	1.92	0.70
14:F:116:LEU:N	14:F:176:PHE:O	2.24	0.69
9:A:587:C:OP2	20:L:21:ARG:NH1	2.25	0.69
9:A:1783:A:N1	9:A:2587:A:H2'	2.07	0.69
9:A:2503:A:H3'	9:A:2503:A:OP2	1.92	0.69
9:A:2502:G:C5'	9:A:2503:A:H5''	2.22	0.69
21:M:66:ARG:NH1	21:M:104:GLU:OE1	2.26	0.69
34:Z:8:GLN:O	34:Z:10:ARG:N	2.25	0.69
9:A:2324:U:H3'	9:A:2325:G:H5''	1.74	0.68
6:5:25:ALA:O	6:5:26:VAL:HG13	1.94	0.68
6:5:129:LEU:O	6:5:131:THR:N	2.26	0.68
9:A:2061:G:N7	9:A:2501:C:H1'	2.09	0.68
9:A:2582:G:H2'	9:A:2583:G:H5'	1.75	0.68
9:A:2592:G:C2	9:A:2603:G:C6	2.82	0.68
9:A:1820:U:OP1	11:C:176:ARG:NH2	2.27	0.68
9:A:1936:A:N6	9:A:1963:U:O2	2.26	0.68
17:I:100:ILE:HB	17:I:139:VAL:HA	1.75	0.68
9:A:2091:C:O2	32:X:33:HIS:NE2	2.26	0.68
6:5:24:SER:CB	6:5:116:GLU:HG2	2.24	0.68
9:A:301:G:OP2	29:U:81:ARG:NH1	2.26	0.68
12:D:149:ASN:OD1	12:D:150:GLN:N	2.26	0.68
20:L:93:ASN:O	20:L:95:LEU:N	2.27	0.67
6:5:26:VAL:O	6:5:27:VAL:HB	1.93	0.67
10:B:73:A:C4	10:B:104:A:C2	2.82	0.67
9:A:2062:A:H62	36:A:9000:ERY:C27	2.05	0.67
18:J:4:PHE:N	18:J:44:TYR:OH	2.28	0.67
6:5:117:LEU:HD22	6:5:120:ALA:HA	1.76	0.67
9:A:948:C:O2	9:A:984:A:O2'	2.12	0.67
19:K:76:VAL:HB	24:P:72:VAL:HG22	1.76	0.66
9:A:324:A:N6	9:A:338:G:O2'	2.27	0.66
19:K:18:ARG:HB2	19:K:45:GLU:HB2	1.77	0.66
20:L:93:ASN:OD1	20:L:94:THR:N	2.28	0.66
31:W:30:VAL:HG13	31:W:30:VAL:O	1.92	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:7:76:A:N6	9:A:2451:A:H4'	2.10	0.66
9:A:42:A:C2'	9:A:43:G:H5'	2.25	0.66
9:A:2142:A:H4'	9:A:2143:C:OP2	1.96	0.66
9:A:2063:C:C5	9:A:2064:C:C4	2.84	0.66
19:K:71:ARG:HB3	19:K:72:PRO:HD3	1.78	0.65
31:W:37:VAL:HG12	31:W:38:ARG:H	1.61	0.65
9:A:2582:G:C2'	9:A:2583:G:H5'	2.26	0.65
22:N:118:ARG:O	22:N:120:GLU:N	2.30	0.65
6:5:39:THR:HA	6:5:42:ARG:HD2	1.78	0.65
9:A:363:G:H2'	9:A:364:C:C6	2.32	0.65
8:7:76:A:N3	9:A:2451:A:H1'	2.12	0.65
9:A:2061:G:C2	9:A:2063:C:C4	2.84	0.65
9:A:2576:G:N3	9:A:2576:G:H3'	2.11	0.65
9:A:2503:A:H4'	9:A:2504:U:OP1	1.96	0.65
23:O:76:LYS:NZ	23:O:80:GLU:OE1	2.29	0.64
9:A:2604:U:O5'	9:A:2604:U:H6	1.80	0.64
11:C:43:ASN:OD1	11:C:44:ASN:N	2.30	0.64
9:A:1199:U:H5'	25:Q:4:LYS:HE3	1.79	0.64
13:E:58:LYS:NZ	13:E:70:SER:O	2.31	0.64
24:P:50:ARG:HG3	24:P:57:ALA:O	1.97	0.64
9:A:819:A:OP2	9:A:1187:G:N2	2.23	0.64
15:G:38:ASP:N	15:G:38:ASP:OD1	2.29	0.64
9:A:2063:C:C5	9:A:2064:C:H5	2.08	0.64
24:P:4:ILE:O	24:P:6:GLN:N	2.31	0.64
27:S:18:ARG:O	27:S:19:LEU:HB2	1.98	0.64
8:7:76:A:N1	9:A:2451:A:O4'	2.31	0.64
9:A:1482:G:H1'	9:A:1509:A:H61	1.62	0.63
10:B:87:U:H3'	10:B:88:C:H5'	1.80	0.63
29:U:73:ASN:ND2	29:U:80:ASP:OD2	2.31	0.63
8:7:75:C:O5'	8:7:75:C:H6	1.81	0.63
9:A:1417:C:HO2'	9:A:1587:G:HO2'	1.45	0.63
9:A:2011:U:OP2	27:S:16:LYS:NZ	2.31	0.63
15:G:1:SER:O	15:G:3:VAL:N	2.31	0.63
18:J:44:TYR:HB2	25:Q:63:ARG:HB3	1.79	0.63
9:A:2502:G:C5'	9:A:2503:A:C5'	2.76	0.63
18:J:6:ALA:HB3	18:J:45:THR:HG21	1.78	0.63
1:0:42:ILE:HD11	22:N:98:LEU:HB3	1.79	0.63
9:A:861:A:N3	10:B:79:G:O2'	2.27	0.63
9:A:1813:G:H1'	11:C:49:THR:HG21	1.81	0.63
9:A:2608:G:O5'	9:A:2608:G:H8	1.82	0.63
9:A:2346:A:H3'	9:A:2347:C:C5'	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:W:35:ILE:O	31:W:37:VAL:N	2.31	0.63
9:A:1378:A:O2'	9:A:1380:G:N7	2.27	0.63
17:I:108:ILE:O	17:I:111:THR:OG1	2.17	0.63
9:A:1385:A:H1'	9:A:1386:C:C6	2.34	0.63
9:A:2062:A:O2'	9:A:2063:C:O5'	2.17	0.62
17:I:131:THR:O	17:I:134:SER:OG	2.16	0.62
9:A:923:G:H1'	31:W:23:LYS:HD3	1.81	0.62
17:I:73:PRO:O	17:I:112:LYS:NZ	2.31	0.62
29:U:15:GLY:O	29:U:17:ASP:N	2.32	0.62
9:A:42:A:H2'	9:A:43:G:H5'	1.80	0.62
9:A:163:C:O2'	9:A:164:C:O5'	2.17	0.62
25:Q:63:ARG:HH22	25:Q:95:ALA:C	2.08	0.62
24:P:50:ARG:CB	24:P:57:ALA:H	2.11	0.62
9:A:546:U:O2'	9:A:547:A:H4'	1.99	0.62
9:A:2063:C:C6	9:A:2064:C:H5	2.17	0.62
22:N:73:ASN:HA	22:N:76:VAL:HG12	1.81	0.61
9:A:856:G:H21	31:W:19:ARG:NH1	1.97	0.61
9:A:1248:G:N7	13:E:46:GLN:NE2	2.48	0.61
9:A:2599:G:HO2'	9:A:2600:A:H5'	1.66	0.61
9:A:2603:G:C2	9:A:2604:U:C2	2.88	0.61
28:T:32:LEU:H	28:T:83:ALA:HB3	1.63	0.61
9:A:2060:A:O2'	13:E:63:LYS:NZ	2.32	0.61
6:5:29:ASP:HA	6:5:108:VAL:HG11	1.82	0.61
9:A:1567:G:H5'	11:C:57:HIS:CD2	2.35	0.61
22:N:98:LEU:O	22:N:112:TYR:N	2.34	0.61
6:5:26:VAL:HG21	6:5:115:GLY:N	2.06	0.61
5:4:36:ARG:HG2	5:4:37:GLN:H	1.66	0.61
9:A:76:C:O2'	33:Y:55:THR:OG1	2.16	0.61
12:D:38:LYS:NZ	12:D:81:GLU:OE1	2.26	0.61
6:5:27:VAL:HG13	6:5:83:ALA:HB3	1.83	0.61
9:A:616:A:H4'	13:E:101:TYR:CE2	2.36	0.61
12:D:118:PHE:HD1	12:D:119:ALA:H	1.49	0.60
9:A:2502:G:H5''	9:A:2503:A:H5''	1.81	0.60
17:I:100:ILE:HG22	17:I:101:SER:N	2.15	0.60
9:A:2502:G:H5'	9:A:2503:A:C5'	2.31	0.60
9:A:276:U:O2'	9:A:278:A:N7	2.34	0.60
23:O:105:ALA:O	23:O:107:ALA:N	2.34	0.60
9:A:480:A:OP2	29:U:43:LYS:NZ	2.34	0.60
9:A:2581:G:HO2'	9:A:2610:C:H41	1.49	0.60
6:5:129:LEU:C	6:5:131:THR:H	2.10	0.60
7:6:18:ASP:OD1	7:6:18:ASP:N	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:983:A:C6	9:A:984:A:C2	2.90	0.60
9:A:2579:C:C2'	9:A:2580:U:C5'	2.72	0.60
9:A:2595:G:N1	9:A:2599:G:C6	2.70	0.60
18:J:6:ALA:CB	18:J:45:THR:HG21	2.31	0.60
9:A:27:G:O2'	9:A:28:A:OP2	2.19	0.60
6:5:15:VAL:HG22	6:5:66:GLY:HA3	1.84	0.60
9:A:1262:A:OP2	27:S:99:ARG:NH2	2.35	0.60
9:A:2353:G:N3	31:W:30:VAL:CG1	2.65	0.60
31:W:55:ASP:O	31:W:57:THR:N	2.34	0.60
9:A:635:C:OP2	20:L:126:ARG:NH1	2.35	0.59
9:A:2502:G:H5'	9:A:2503:A:H5''	1.82	0.59
11:C:16:VAL:N	11:C:203:VAL:HG12	2.18	0.59
23:O:89:ASP:HA	23:O:116:GLN:HB3	1.84	0.59
9:A:1803:A:O3'	11:C:256:THR:OG1	2.19	0.59
9:A:2592:G:N2	9:A:2603:G:C5	2.70	0.59
9:A:2800:A:H3'	9:A:2801:G:C5'	2.32	0.59
29:U:38:ILE:CG2	29:U:39:ASN:N	2.64	0.59
31:W:51:GLY:HA3	31:W:59:PHE:CE1	2.38	0.59
8:7:76:A:C4	9:A:2451:A:H1'	2.38	0.59
17:I:92:PRO:O	17:I:94:LYS:N	2.36	0.59
17:I:93:ASN:ND2	17:I:135:MET:O	2.36	0.59
24:P:63:ILE:HA	24:P:68:GLY:HA2	1.85	0.59
9:A:370:G:O2'	9:A:424:G:OP1	2.15	0.58
9:A:1076:C:H2'	9:A:1077:A:O4'	2.03	0.58
9:A:2063:C:C2'	9:A:2064:C:H5'	2.26	0.58
9:A:2780:G:OP2	18:J:120:ARG:NE	2.33	0.58
28:T:35:ALA:HB3	28:T:38:ALA:HB2	1.85	0.58
28:T:50:LEU:C	28:T:52:GLU:H	2.11	0.58
9:A:2581:G:HO2'	9:A:2610:C:H5	1.50	0.58
28:T:19:LYS:O	28:T:23:ALA:N	2.35	0.58
9:A:1131:G:OP1	18:J:82:GLY:HA2	2.02	0.58
25:Q:63:ARG:NH1	25:Q:95:ALA:O	2.35	0.58
6:5:62:ARG:NH2	9:A:1106:G:OP1	2.35	0.58
31:W:76:ARG:HH21	31:W:76:ARG:CG	2.16	0.58
9:A:784:G:O2'	9:A:785:G:OP2	2.15	0.58
25:Q:84:LYS:O	25:Q:86:SER:N	2.36	0.58
13:E:168:ASP:OD2	13:E:170:ARG:NH2	2.36	0.58
9:A:1076:C:H1'	17:I:93:ASN:HB3	1.86	0.58
28:T:54:GLU:HG3	28:T:88:LYS:HB2	1.86	0.58
31:W:51:GLY:HA3	31:W:59:PHE:CZ	2.38	0.58
9:A:2582:G:C2	9:A:2583:G:N7	2.71	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:45:GLY:HA2	6:5:49:GLY:HA2	1.85	0.57
9:A:2574:G:O2'	9:A:2575:C:H5'	2.04	0.57
35:a:81:ILE:O	35:a:82:PHE:HB2	2.02	0.57
9:A:1386:C:H2'	9:A:1387:A:C8	2.39	0.57
9:A:2517:C:C6	9:A:2542:A:N7	2.72	0.57
19:K:121:GLU:OE1	24:P:62:LYS:NZ	2.37	0.57
21:M:41:LEU:HD11	21:M:126:ILE:HD13	1.85	0.57
9:A:2061:G:C2	9:A:2063:C:N3	2.72	0.57
9:A:422:A:C2	9:A:423:A:C4	2.92	0.57
9:A:1936:A:H2	9:A:1943:U:C5	2.23	0.57
11:C:77:VAL:HG23	11:C:111:ALA:HA	1.86	0.57
25:Q:81:GLY:O	25:Q:85:ALA:N	2.37	0.57
9:A:2331:G:O2'	9:A:2336:A:N1	2.38	0.57
17:I:37:PHE:O	17:I:41:PHE:HB3	2.04	0.57
24:P:33:GLU:CD	24:P:34:GLY:N	2.63	0.57
31:W:28:GLU:HB3	31:W:31:LEU:HD21	1.86	0.57
31:W:37:VAL:HG13	31:W:55:ASP:C	2.29	0.57
8:7:76:A:C2	9:A:2451:A:O4'	2.57	0.57
9:A:673:C:OP1	13:E:49:ARG:NH2	2.36	0.57
9:A:1654:A:O2'	12:D:118:PHE:CG	2.55	0.57
9:A:2063:C:C5	9:A:2064:C:N4	2.73	0.57
13:E:150:THR:HG21	13:E:153:LEU:HA	1.87	0.57
3:2:22:MET:HE3	3:2:28:ARG:HD3	1.86	0.56
6:5:3:LEU:CD1	6:5:5:LEU:HG	2.35	0.56
9:A:1324:G:C4	9:A:1328:A:N6	2.73	0.56
9:A:1509:A:HO2'	9:A:1510:G:P	2.26	0.56
9:A:2583:G:N2	9:A:2584:U:C2	2.73	0.56
11:C:14:HIS:O	11:C:203:VAL:HG11	2.05	0.56
24:P:58:PHE:CD1	24:P:75:THR:HG22	2.40	0.56
31:W:39:GLN:HG2	31:W:41:GLY:H	1.69	0.56
9:A:2548:U:O2	19:K:23:LYS:NZ	2.37	0.56
17:I:100:ILE:HD11	17:I:137:LEU:HG	1.87	0.56
25:Q:105:PHE:O	25:Q:108:LEU:N	2.38	0.56
2:1:8:ILE:HD11	2:1:24:LYS:N	2.21	0.56
9:A:2574:G:H2'	9:A:2575:C:C5'	2.30	0.56
9:A:1773:A:N7	9:A:1829:A:H1'	2.20	0.56
32:X:32:LEU:O	32:X:33:HIS:ND1	2.39	0.56
9:A:2680:U:H5'	12:D:194:PRO:HA	1.88	0.56
25:Q:94:LEU:C	25:Q:96:ASP:H	2.14	0.56
33:Y:56:LEU:O	33:Y:58:ASN:N	2.39	0.56
6:5:58:THR:CG2	9:A:1107:G:H5''	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:132:TYR:CZ	7:6:23:ILE:HD11	2.40	0.56
9:A:2061:G:OP2	13:E:63:LYS:HE2	2.06	0.56
9:A:85:G:OP2	29:U:6:ARG:HG3	2.06	0.56
9:A:443:A:N7	13:E:40:ARG:HD3	2.21	0.56
9:A:1353:A:C8	9:A:1378:A:N6	2.73	0.56
18:J:81:ILE:HG13	18:J:82:GLY:N	2.21	0.56
24:P:50:ARG:HB3	24:P:57:ALA:N	2.17	0.56
9:A:100:U:H4'	9:A:101:A:O5'	2.06	0.55
9:A:2502:G:H5''	9:A:2503:A:C5'	2.36	0.55
9:A:2585:U:C4	9:A:2608:G:O6	2.59	0.55
9:A:2603:G:H2'	9:A:2604:U:C6	2.41	0.55
17:I:135:MET:HB3	17:I:137:LEU:HD22	1.88	0.55
25:Q:94:LEU:C	25:Q:96:ASP:N	2.64	0.55
28:T:59:ASN:O	28:T:83:ALA:O	2.24	0.55
6:5:64:VAL:O	6:5:68:PRO:HD2	2.06	0.55
9:A:1750:G:O2'	9:A:2860:A:N1	2.37	0.55
14:F:151:LEU:HD12	14:F:152:ASP:N	2.21	0.55
20:L:85:VAL:CG2	20:L:94:THR:HG22	2.36	0.55
31:W:18:LYS:HG3	31:W:19:ARG:N	2.21	0.55
9:A:811:U:C4	20:L:21:ARG:NH2	2.74	0.55
6:5:43:LYS:HZ3	6:5:98:GLU:HB2	1.72	0.55
23:O:2:ASP:OD1	23:O:3:LYS:N	2.39	0.55
6:5:56:ARG:O	6:5:57:ASN:ND2	2.39	0.55
18:J:17:VAL:HG23	18:J:139:VAL:HA	1.88	0.55
26:R:39:LEU:O	26:R:49:ILE:HG23	2.07	0.55
28:T:32:LEU:N	28:T:83:ALA:HB3	2.21	0.55
9:A:1019:U:H3	9:A:1142:A:H62	1.53	0.55
9:A:1397:U:OP2	9:A:1398:C:N4	2.34	0.55
12:D:118:PHE:O	12:D:120:GLY:N	2.36	0.55
9:A:201:C:O2'	9:A:251:A:N1	2.38	0.55
9:A:1482:G:C6	9:A:1508:A:C2	2.94	0.55
9:A:2061:G:C4	9:A:2063:C:N4	2.75	0.55
9:A:2582:G:N2	9:A:2583:G:N9	2.55	0.55
9:A:283:G:C2	9:A:284:U:H1'	2.41	0.55
9:A:1338:G:O2'	28:T:18:GLU:OE1	2.20	0.55
1:0:2:VAL:HG22	9:A:2015:A:C2	2.41	0.55
5:4:36:ARG:NH1	9:A:2742:G:OP1	2.38	0.55
9:A:2355:G:H4'	31:W:20:LEU:HD13	1.88	0.55
9:A:2636:C:O2'	12:D:45:TYR:OH	2.25	0.55
22:N:30:ARG:NH1	22:N:74:GLU:OE1	2.40	0.55
9:A:834:G:C6	9:A:835:C:C4	2.95	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2506:U:H6	9:A:2506:U:H3'	1.72	0.54
9:A:2757:A:N1	15:G:66:THR:HG21	2.21	0.54
12:D:107:VAL:CG2	12:D:203:VAL:HG23	2.38	0.54
6:5:81:LEU:HA	9:A:1107:G:H4'	1.88	0.54
9:A:1458:U:H4'	9:A:1459:G:O5'	2.07	0.54
9:A:2698:U:H2'	9:A:2699:C:H6	1.72	0.54
11:C:68:ARG:CD	11:C:103:ILE:HD11	2.37	0.54
25:Q:91:ARG:NH1	26:R:10:LYS:HB3	2.23	0.54
6:5:44:ALA:O	6:5:49:GLY:N	2.40	0.54
9:A:1715:G:N2	9:A:1744:A:OP2	2.36	0.54
9:A:1754:A:H4'	24:P:102:ARG:NH2	2.22	0.54
9:A:2576:G:HO2'	9:A:2577:A:P	2.30	0.54
19:K:107:LEU:O	19:K:109:SER:N	2.38	0.54
1:0:2:VAL:HG11	9:A:2016:U:H1'	1.89	0.54
6:5:129:LEU:HB3	6:5:130:PRO:HD2	1.89	0.54
9:A:396:G:OP2	32:X:9:LYS:NZ	2.40	0.54
9:A:674:G:H1'	13:E:69:ARG:HE	1.72	0.54
9:A:1786:A:H1'	9:A:1938:A:N6	2.22	0.54
9:A:2415:G:H4'	20:L:66:PHE:HB2	1.90	0.54
9:A:686:U:H2'	9:A:788:A:N1	2.21	0.54
9:A:877:A:C2	9:A:899:A:C2	2.95	0.54
9:A:1936:A:N6	9:A:1963:U:H3	2.05	0.54
9:A:2335:A:C6	9:A:2337:G:H1'	2.42	0.54
9:A:2533:U:OP1	9:A:2665:A:O2'	2.20	0.54
21:M:33:LEU:HD22	21:M:128:THR:HB	1.90	0.54
24:P:33:GLU:HB2	24:P:38:ARG:HH11	1.71	0.54
29:U:38:ILE:HG22	29:U:39:ASN:H	1.73	0.54
30:V:80:HIS:HD2	30:V:83:LYS:N	2.05	0.54
31:W:9:THR:OG1	31:W:10:ARG:N	2.31	0.54
9:A:1824:G:N3	11:C:251:THR:HG21	2.21	0.54
15:G:84:LYS:HG3	15:G:132:LEU:H	1.73	0.54
24:P:50:ARG:CG	24:P:57:ALA:O	2.55	0.54
6:5:60:LEU:O	6:5:64:VAL:HB	2.08	0.54
9:A:163:C:O2'	9:A:164:C:P	2.65	0.54
12:D:12:THR:OG1	24:P:8:GLU:OE2	2.21	0.54
19:K:80:ASP:HB2	24:P:67:GLU:HG3	1.90	0.54
34:Z:5:LYS:H	34:Z:5:LYS:HD2	1.72	0.54
6:5:23:LEU:HG	6:5:24:SER:N	2.22	0.54
6:5:54:VAL:HA	6:5:84:TYR:O	2.07	0.54
6:5:58:THR:HB	6:5:82:ILE:HB	1.89	0.54
9:A:910:A:N6	9:A:2277:G:O2'	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1779:U:H5	9:A:1784:A:N7	2.06	0.54
9:A:2197:U:O2	9:A:2198:A:O2'	2.21	0.54
9:A:2580:U:O2'	9:A:2581:G:H5'	2.08	0.54
20:L:77:ILE:CD1	20:L:108:ALA:HB1	2.38	0.54
24:P:4:ILE:HG22	24:P:5:LYS:H	1.72	0.54
25:Q:81:GLY:HA2	25:Q:116:LEU:CD1	2.38	0.54
5:4:1:MET:HE2	5:4:35:GLN:C	2.33	0.54
9:A:84:A:P	29:U:5:ARG:NH2	2.81	0.54
9:A:411:G:OP2	9:A:2406:A:O2'	2.25	0.54
9:A:1772:A:N1	9:A:1980:G:C6	2.75	0.54
12:D:106:LYS:HB3	12:D:206:ALA:HB3	1.89	0.54
14:F:103:ILE:HG23	14:F:175:PRO:HD3	1.90	0.54
18:J:32:LEU:HD22	18:J:54:ILE:HD12	1.90	0.54
19:K:43:ILE:CD1	19:K:52:VAL:HB	2.37	0.54
25:Q:93:ILE:O	25:Q:96:ASP:N	2.39	0.54
26:R:49:ILE:HB	26:R:51:VAL:O	2.08	0.54
9:A:855:G:H1'	31:W:23:LYS:HE3	1.89	0.54
29:U:21:ARG:CZ	29:U:72:PHE:CE2	2.90	0.53
9:A:384:A:H2'	9:A:385:C:H5'	1.91	0.53
9:A:1187:G:H5''	26:R:83:TYR:CE2	2.44	0.53
31:W:46:ALA:HB3	31:W:80:SER:HB3	1.91	0.53
5:4:1:MET:N	9:A:2526:G:N3	2.57	0.53
6:5:4:ASN:C	6:5:6:GLN:H	2.16	0.53
9:A:2505:G:C2'	9:A:2506:U:H5''	2.38	0.53
9:A:189:G:O6	9:A:205:G:O2'	2.19	0.53
9:A:265:A:H4'	9:A:266:G:OP1	2.07	0.53
9:A:2586:U:O2	9:A:2586:U:H2'	2.07	0.53
12:D:120:GLY:HA2	12:D:162:ALA:CB	2.38	0.53
19:K:10:VAL:HG11	19:K:16:ALA:HB3	1.90	0.53
27:S:73:LYS:HB3	27:S:106:VAL:HB	1.90	0.53
9:A:1930:G:O2'	9:A:1968:G:O6	2.17	0.53
17:I:98:GLY:HA3	17:I:137:LEU:HB3	1.90	0.53
25:Q:65:ASN:OD1	25:Q:69:ARG:NH2	2.42	0.53
26:R:49:ILE:HG22	26:R:54:VAL:HG13	1.89	0.53
9:A:954:G:OP2	21:M:16:ARG:NH2	2.42	0.53
9:A:1759:A:HO2'	9:A:2714:G:HO2'	1.51	0.53
15:G:84:LYS:HB3	15:G:132:LEU:O	2.09	0.53
18:J:39:LYS:HA	18:J:43:GLU:HG3	1.91	0.53
1:0:12:ARG:NH1	9:A:1263:U:OP1	2.41	0.53
6:5:4:ASN:O	6:5:6:GLN:N	2.41	0.53
6:5:25:ALA:HB3	6:5:85:SER:OG	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:630:G:N2	9:A:633:A:OP2	2.37	0.53
9:A:2425:A:H5''	9:A:2427:C:O4'	2.09	0.53
9:A:2505:G:HO2'	9:A:2506:U:H5''	1.70	0.53
12:D:68:PHE:C	12:D:73:VAL:HG12	2.33	0.53
28:T:50:LEU:HD12	28:T:50:LEU:H	1.74	0.53
9:A:273:G:N2	9:A:365:U:C2	2.77	0.53
9:A:1069:A:C4	9:A:1073:A:N7	2.77	0.53
9:A:1080:A:H1'	17:I:127:SER:HA	1.91	0.53
9:A:2053:G:H1	9:A:2616:C:H42	1.57	0.53
9:A:2547:A:H2'	9:A:2548:U:C6	2.43	0.53
24:P:50:ARG:CD	24:P:51:ASN:N	2.72	0.53
25:Q:63:ARG:HH12	25:Q:96:ASP:CA	2.22	0.53
9:A:1535:A:H4'	9:A:1536:C:OP2	2.08	0.53
9:A:2297:A:N1	9:A:2321:U:H5	2.07	0.53
23:O:31:THR:HG22	23:O:34:HIS:H	1.74	0.53
28:T:50:LEU:O	28:T:52:GLU:N	2.42	0.53
31:W:49:ASN:ND2	31:W:49:ASN:C	2.66	0.53
34:Z:48:ASN:O	34:Z:51:SER:OG	2.27	0.53
6:5:81:LEU:HD23	6:5:82:ILE:N	2.24	0.52
9:A:2092:U:H4'	9:A:2093:G:O5'	2.09	0.52
23:O:36:TYR:N	23:O:36:TYR:CD1	2.78	0.52
31:W:13:ARG:HG2	31:W:14:ASP:H	1.73	0.52
9:A:1069:A:C5	9:A:1073:A:N7	2.77	0.52
9:A:1738:G:O2'	9:A:1739:A:O5'	2.25	0.52
9:A:2582:G:H2'	9:A:2583:G:H8	1.74	0.52
22:N:103:ARG:HD3	22:N:110:MET:HE3	1.91	0.52
25:Q:31:TYR:O	25:Q:34:ALA:N	2.42	0.52
28:T:89:GLU:O	28:T:91:GLN:N	2.41	0.52
31:W:37:VAL:HB	31:W:38:ARG:HH11	1.74	0.52
1:0:2:VAL:CG1	9:A:2016:U:H1'	2.40	0.52
8:7:76:A:C2	9:A:2451:A:C1'	2.92	0.52
8:7:76:A:C2	9:A:2451:A:H1'	2.45	0.52
9:A:2232:C:P	32:X:26:ARG:HH22	2.32	0.52
22:N:73:ASN:HA	22:N:76:VAL:CG1	2.39	0.52
9:A:1288:G:C4	9:A:1327:A:C2	2.98	0.52
19:K:70:ARG:HD3	19:K:76:VAL:HG22	1.90	0.52
6:5:43:LYS:NZ	6:5:98:GLU:HB2	2.24	0.52
6:5:51:TYR:C	6:5:51:TYR:CD1	2.86	0.52
6:5:118:ILE:HB	6:5:119:PRO:CD	2.40	0.52
9:A:1328:A:H2'	9:A:1330:C:C5	2.45	0.52
2:1:33:LEU:N	2:1:51:ALA:HB3	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2211:A:O2'	9:A:2212:A:OP1	2.25	0.52
26:R:61:ALA:HB2	26:R:98:ILE:HA	1.92	0.52
28:T:44:LYS:HG3	28:T:55:VAL:HG11	1.90	0.52
29:U:35:VAL:HB	29:U:38:ILE:HG21	1.90	0.52
29:U:82:VAL:HG12	29:U:83:GLY:N	2.25	0.52
34:Z:6:ILE:O	34:Z:34:THR:HA	2.10	0.52
5:4:7:VAL:O	5:4:35:GLN:NE2	2.42	0.52
6:5:36:ASP:O	6:5:39:THR:OG1	2.26	0.52
9:A:2504:U:O5'	9:A:2504:U:H6	1.93	0.52
9:A:2507:C:O2	9:A:2507:C:H2'	2.08	0.52
18:J:39:LYS:HA	18:J:43:GLU:HB2	1.91	0.52
18:J:55:ILE:HD11	18:J:130:HIS:CG	2.44	0.52
28:T:61:LEU:C	28:T:61:LEU:HD12	2.35	0.52
9:A:38:A:O2'	13:E:43:THR:HA	2.09	0.52
9:A:974:G:H8	9:A:990:A:H62	1.58	0.52
9:A:2354:C:H4'	31:W:31:LEU:HD22	1.92	0.52
11:C:256:THR:OG1	11:C:256:THR:O	2.28	0.52
9:A:729:G:H2'	9:A:1775:U:H1'	1.91	0.51
9:A:1338:G:O2'	9:A:1393:A:N1	2.44	0.51
9:A:2039:U:H2'	9:A:2040:G:C8	2.45	0.51
9:A:2313:C:H5''	14:F:87:LYS:HD3	1.92	0.51
11:C:255:LYS:O	11:C:257:ARG:N	2.43	0.51
12:D:151:THR:HG22	12:D:152:PRO:HD3	1.92	0.51
15:G:83:THR:HA	15:G:84:LYS:CE	2.39	0.51
19:K:13:ASN:O	19:K:15:GLY:N	2.43	0.51
31:W:8:SER:O	31:W:9:THR:HG22	2.10	0.51
6:5:3:LEU:HD12	6:5:5:LEU:H	1.76	0.51
9:A:994:C:O2'	9:A:996:A:OP1	2.25	0.51
9:A:1759:A:O2'	9:A:2714:G:O2'	2.25	0.51
9:A:2061:G:C2	9:A:2063:C:N4	2.78	0.51
9:A:2604:U:H2'	9:A:2605:U:C6	2.45	0.51
17:I:116:MET:HB2	17:I:124:MET:HE3	1.91	0.51
9:A:2387:U:O2'	31:W:38:ARG:NH2	2.43	0.51
9:A:2803:G:H2'	9:A:2804:U:C6	2.45	0.51
11:C:38:LYS:NZ	11:C:57:HIS:O	2.39	0.51
20:L:91:ASP:OD1	20:L:92:LEU:N	2.43	0.51
21:M:73:ILE:HG21	21:M:91:TYR:CZ	2.45	0.51
15:G:96:ALA:HB3	15:G:103:ASN:HB2	1.92	0.51
30:V:44:HIS:HE1	30:V:86:LEU:H	1.59	0.51
30:V:51:GLN:OE1	30:V:57:TYR:OH	2.28	0.51
6:5:94:ARG:O	6:5:97:LYS:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1300:G:H4'	9:A:1301:A:H5'	1.92	0.51
9:A:1797:G:O2'	11:C:256:THR:CG2	2.59	0.51
9:A:2062:A:N6	36:A:9000:ERY:C27	2.54	0.51
13:E:148:ILE:HA	13:E:187:VAL:HB	1.93	0.51
14:F:132:ARG:O	14:F:133:GLU:HB3	2.10	0.51
16:H:41:LYS:HA	16:H:44:ILE:HG12	1.93	0.51
17:I:36:GLU:HB3	17:I:66:PHE:CE1	2.46	0.51
9:A:1816:C:C5	11:C:61:TYR:CE2	2.98	0.51
9:A:2330:G:O2'	31:W:38:ARG:O	2.25	0.51
31:W:16:GLU:O	31:W:17:ALA:HB3	2.10	0.51
3:2:27:GLY:O	3:2:30:VAL:HB	2.11	0.51
6:5:4:ASN:C	6:5:6:GLN:N	2.66	0.51
6:5:25:ALA:O	6:5:116:GLU:OE1	2.28	0.51
12:D:91:THR:O	12:D:91:THR:OG1	2.28	0.51
18:J:49:ASP:OD1	18:J:121:LYS:NZ	2.32	0.51
26:R:49:ILE:HG22	26:R:53:PHE:C	2.36	0.51
28:T:69:ARG:CG	28:T:70:HIS:H	2.23	0.51
30:V:9:ARG:NH2	30:V:12:GLN:HA	2.26	0.51
9:A:26:G:C6	9:A:27:G:N1	2.79	0.51
9:A:2063:C:C2'	9:A:2064:C:C5'	2.88	0.51
20:L:19:LEU:HD23	20:L:19:LEU:C	2.35	0.51
9:A:460:A:C2	9:A:470:A:C4	2.99	0.51
9:A:565:C:H2'	9:A:566:U:O4'	2.11	0.51
21:M:8:LYS:HE3	21:M:9:PHE:CE2	2.45	0.51
34:Z:41:PRO:HA	34:Z:44:ARG:HB3	1.93	0.51
9:A:27:G:N2	9:A:512:G:H1'	2.26	0.51
9:A:489:G:N7	27:S:49:LYS:NZ	2.58	0.51
9:A:748:G:P	27:S:88:ARG:NH2	2.83	0.51
9:A:1322:A:OP1	27:S:11:ARG:NE	2.38	0.51
9:A:2058:A:N1	36:A:9000:ERY:O8	2.43	0.51
18:J:81:ILE:CG1	18:J:82:GLY:N	2.74	0.51
5:4:3:VAL:HG23	5:4:4:ARG:H	1.74	0.50
9:A:636:G:OP2	20:L:109:LYS:NZ	2.45	0.50
9:A:1028:A:N3	9:A:2486:C:O2'	2.42	0.50
9:A:1394:U:H4'	9:A:1603:A:H4'	1.92	0.50
9:A:1533:C:C2	9:A:1534:U:C4	2.99	0.50
9:A:2314:A:OP1	14:F:87:LYS:NZ	2.44	0.50
9:A:2681:C:OP2	12:D:114:LYS:NZ	2.33	0.50
13:E:188:MET:HE2	13:E:193:VAL:HA	1.93	0.50
15:G:16:VAL:HG21	15:G:44:HIS:CD2	2.46	0.50
19:K:9:ASN:O	19:K:83:ALA:HA	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:L:81:ASP:O	20:L:83:ALA:N	2.41	0.50
25:Q:91:ARG:HE	25:Q:93:ILE:CG2	2.25	0.50
9:A:391:A:C6	9:A:411:G:C2	3.00	0.50
9:A:1533:C:H2'	9:A:1534:U:C6	2.46	0.50
15:G:30:GLY:O	15:G:32:LEU:N	2.38	0.50
27:S:86:MET:HB2	27:S:96:ILE:HG21	1.92	0.50
28:T:29:THR:OG1	28:T:86:THR:N	2.43	0.50
31:W:76:ARG:HH21	31:W:76:ARG:HG2	1.76	0.50
9:A:945:A:C5	9:A:2448:A:C2	2.98	0.50
9:A:1778:U:H2'	9:A:1784:A:N6	2.27	0.50
9:A:2508:G:O2'	9:A:2554:U:O2'	2.22	0.50
14:F:71:LYS:HD3	14:F:72:SER:N	2.26	0.50
3:2:34:ARG:NH1	3:2:41:ARG:O	2.45	0.50
9:A:277:G:O2'	9:A:278:A:OP2	2.25	0.50
9:A:1179:G:H2'	9:A:1180:U:O4'	2.12	0.50
9:A:2074:U:H2'	9:A:2075:U:C6	2.46	0.50
12:D:148:GLN:OE1	12:D:148:GLN:N	2.45	0.50
9:A:139:U:O2'	28:T:1:MET:HA	2.12	0.50
9:A:322:A:H5'	9:A:340:A:H1'	1.94	0.50
26:R:39:LEU:HA	26:R:49:ILE:HG21	1.92	0.50
9:A:1203:U:O2'	20:L:4:ASN:OD1	2.28	0.50
9:A:1654:A:H2'	9:A:1655:A:H8	1.76	0.50
9:A:1753:G:OP1	24:P:92:ARG:NE	2.38	0.50
9:A:2094:A:C2	9:A:2196:C:C2	2.99	0.50
9:A:2329:U:H2'	9:A:2330:G:C8	2.47	0.50
9:A:2352:A:C6	31:W:30:VAL:HG11	2.47	0.50
22:N:52:ILE:HB	22:N:94:TYR:CD2	2.46	0.50
5:4:36:ARG:O	5:4:37:GLN:C	2.55	0.50
9:A:2576:G:N3	9:A:2576:G:C3'	2.75	0.50
19:K:19:VAL:CG1	19:K:41:ILE:HG12	2.40	0.50
33:Y:8:GLU:O	33:Y:12:GLU:HB2	2.12	0.50
34:Z:26:LEU:O	34:Z:37:ARG:NH1	2.44	0.50
1:0:24:VAL:O	1:0:25:THR:OG1	2.30	0.50
9:A:118:A:N3	9:A:178:G:H1'	2.27	0.50
9:A:504:A:HO2'	9:A:505:A:P	2.28	0.50
9:A:654:A:H3'	9:A:654:A:N3	2.26	0.50
9:A:1437:C:H2'	9:A:1438:U:C6	2.46	0.50
9:A:1475:G:O2'	9:A:1514:G:O6	2.30	0.50
9:A:2601:C:O2'	9:A:2602:A:O5'	2.26	0.50
12:D:62:LYS:HB2	12:D:63:PRO:HD3	1.93	0.50
12:D:193:VAL:HG21	12:D:201:LEU:HD21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:H:14:SER:OG	16:H:17:ASP:CG	2.55	0.50
34:Z:30:ARG:HB3	34:Z:30:ARG:HH11	1.76	0.50
9:A:221:A:N1	9:A:265:A:O2'	2.45	0.50
9:A:1808:A:O2'	32:X:2:ARG:NH1	2.45	0.50
9:A:747:U:O2'	27:S:88:ARG:NH2	2.45	0.49
9:A:2061:G:O6	9:A:2501:C:O2	2.30	0.49
15:G:166:GLU:CD	15:G:166:GLU:C	2.80	0.49
16:H:40:THR:C	16:H:42:LYS:H	2.19	0.49
21:M:20:LEU:HD22	21:M:20:LEU:N	2.26	0.49
21:M:35:ALA:O	21:M:36:VAL:HB	2.11	0.49
2:1:4:ILE:HG23	2:1:5:ARG:H	1.76	0.49
4:3:30:HIS:HD2	9:A:2421:G:N7	2.10	0.49
9:A:1277:G:C5'	22:N:20:MET:HE2	2.43	0.49
9:A:1869:G:H3'	9:A:1870:C:H5''	1.94	0.49
12:D:86:GLU:CD	12:D:86:GLU:N	2.69	0.49
17:I:109:ALA:HB2	17:I:128:ILE:HG13	1.93	0.49
6:5:138:ARG:NH2	7:6:26:MET:HA	2.27	0.49
9:A:748:G:OP1	27:S:88:ARG:NH2	2.45	0.49
9:A:2571:U:O2'	12:D:151:THR:CG2	2.60	0.49
9:A:2604:U:H2'	9:A:2605:U:H6	1.75	0.49
12:D:151:THR:CG2	12:D:152:PRO:HD3	2.43	0.49
22:N:96:ARG:NH2	22:N:114:GLU:OE1	2.44	0.49
23:O:51:ALA:HB3	23:O:78:VAL:HG13	1.94	0.49
31:W:9:THR:HG23	31:W:10:ARG:HD3	1.94	0.49
6:5:95:LEU:HD22	6:5:95:LEU:H	1.77	0.49
9:A:1614:A:N1	27:S:93:ALA:HB2	2.27	0.49
18:J:21:THR:HG22	18:J:22:GLY:N	2.27	0.49
18:J:44:TYR:O	18:J:45:THR:HB	2.11	0.49
28:T:54:GLU:CG	28:T:88:LYS:HB2	2.42	0.49
32:X:70:LEU:O	32:X:75:GLU:N	2.45	0.49
9:A:2330:G:C2	9:A:2386:A:C2	3.01	0.49
17:I:123:ALA:HA	17:I:126:ARG:CZ	2.43	0.49
6:5:34:THR:C	6:5:38:MET:HE3	2.37	0.49
9:A:250:G:C6	9:A:251:A:C6	3.01	0.49
9:A:443:A:C5	13:E:40:ARG:HD3	2.47	0.49
9:A:1199:U:H5'	25:Q:4:LYS:CE	2.42	0.49
9:A:2109:U:H2'	9:A:2110:G:H5'	1.94	0.49
17:I:48:ILE:HG13	17:I:49:GLU:H	1.77	0.49
27:S:20:VAL:HG11	27:S:44:ALA:HA	1.93	0.49
31:W:42:THR:HG22	31:W:43:LYS:HZ2	1.78	0.49
15:G:32:LEU:O	15:G:33:THR:OG1	2.31	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:83:THR:C	15:G:84:LYS:HD3	2.37	0.49
17:I:87:SER:OG	17:I:88:GLY:N	2.43	0.49
25:Q:63:ARG:NH1	25:Q:96:ASP:HA	2.27	0.49
6:5:68:PRO:HA	6:5:72:LEU:HD11	1.94	0.49
9:A:107:G:H2'	9:A:108:G:H8	1.78	0.49
9:A:564:C:O2	9:A:578:G:N2	2.46	0.49
9:A:1567:G:H2'	11:C:84:PRO:HG3	1.95	0.49
9:A:2609:U:H3'	9:A:2610:C:H5'	1.95	0.49
9:A:2867:G:O2'	9:A:2868:A:OP2	2.28	0.49
13:E:112:LEU:HD13	13:E:186:VAL:HG11	1.94	0.49
14:F:5:ASP:OD1	14:F:8:LYS:NZ	2.46	0.49
6:5:55:VAL:HG13	9:A:1084:A:H5'	1.93	0.49
9:A:223:A:C5	9:A:422:A:C8	3.00	0.49
9:A:2580:U:C2'	9:A:2581:G:C5'	2.86	0.49
15:G:84:LYS:HG3	15:G:132:LEU:N	2.28	0.49
28:T:34:VAL:O	28:T:34:VAL:CG2	2.61	0.49
31:W:19:ARG:C	31:W:19:ARG:CD	2.85	0.49
4:3:51:LYS:NZ	9:A:938:G:OP2	2.33	0.49
9:A:308:G:O2'	9:A:329:G:N2	2.46	0.49
9:A:1022:G:C5	9:A:1140:C:C4	3.00	0.49
9:A:1474:U:H2'	9:A:1475:G:H5'	1.95	0.49
9:A:1730:C:OP1	9:A:1730:C:H4'	2.12	0.49
9:A:1778:U:H2'	9:A:1784:A:H62	1.78	0.49
9:A:2211:A:O2'	9:A:2212:A:P	2.70	0.49
9:A:2701:U:H3'	9:A:2702:G:C5'	2.42	0.49
21:M:106:ASP:O	21:M:108:VAL:N	2.44	0.49
27:S:13:SER:O	27:S:14:ALA:CB	2.60	0.49
9:A:1327:A:N6	9:A:1328:A:C2	2.81	0.48
9:A:1485:U:H2'	9:A:1486:U:C6	2.48	0.48
9:A:1607:C:H4'	9:A:1608:A:O5'	2.13	0.48
9:A:2063:C:C4	9:A:2064:C:C4	3.01	0.48
9:A:2393:U:H5'	20:L:60:ARG:O	2.13	0.48
12:D:174:SER:OG	12:D:175:LEU:N	2.46	0.48
16:H:9:VAL:O	16:H:13:GLY:N	2.46	0.48
21:M:136:MET:HE3	30:V:77:VAL:HG23	1.95	0.48
27:S:24:ILE:HG22	27:S:71:VAL:HG11	1.95	0.48
1:0:2:VAL:CG2	9:A:2015:A:C2	2.96	0.48
6:5:38:MET:HE2	9:A:1057:A:O2'	2.12	0.48
9:A:960:A:H61	21:M:82:MET:HE3	1.78	0.48
9:A:2016:U:H2'	9:A:2017:U:C6	2.48	0.48
9:A:2508:G:HO2'	9:A:2554:U:HO2'	1.54	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:73:SER:O	15:G:77:GLY:N	2.45	0.48
6:5:71:CYS:CA	6:5:117:LEU:HD13	2.31	0.48
9:A:2600:A:C2'	9:A:2601:C:C5'	2.86	0.48
14:F:79:ARG:HB3	14:F:82:TYR:CE1	2.48	0.48
17:I:14:ALA:HB3	17:I:51:GLY:H	1.79	0.48
18:J:43:GLU:O	18:J:45:THR:HG22	2.13	0.48
20:L:19:LEU:HB2	20:L:27:LEU:HB3	1.94	0.48
21:M:12:MET:HE3	21:M:71:LYS:HG3	1.95	0.48
24:P:91:VAL:O	24:P:92:ARG:HG2	2.12	0.48
29:U:85:ARG:HD3	29:U:86:PHE:N	2.28	0.48
11:C:265:PHE:N	11:C:265:PHE:CD1	2.82	0.48
12:D:149:ASN:CG	12:D:150:GLN:H	2.21	0.48
14:F:79:ARG:HB3	14:F:82:TYR:CZ	2.48	0.48
21:M:34:LYS:HD2	21:M:131:VAL:HG11	1.95	0.48
9:A:580:U:H2'	9:A:581:C:H6	1.79	0.48
9:A:856:G:H21	31:W:19:ARG:HH12	1.58	0.48
9:A:856:G:O2'	31:W:22:VAL:HG23	2.14	0.48
9:A:1348:C:H2'	9:A:1349:C:H5'	1.96	0.48
9:A:2580:U:H6	9:A:2580:U:O5'	1.96	0.48
9:A:2747:G:O2'	15:G:66:THR:HG22	2.14	0.48
32:X:39:VAL:HG22	32:X:44:ARG:O	2.14	0.48
9:A:391:A:C5	9:A:411:G:C2	3.02	0.48
9:A:923:G:H1'	31:W:23:LYS:CD	2.43	0.48
9:A:1022:G:C6	9:A:1140:C:C4	3.01	0.48
9:A:1135:C:N4	9:A:1139:G:C6	2.82	0.48
9:A:1760:C:H2'	9:A:1761:C:O4'	2.14	0.48
9:A:2800:A:H3'	9:A:2801:G:H5''	1.96	0.48
11:C:225:ASN:HB3	11:C:226:PRO:HD2	1.96	0.48
13:E:164:LEU:HB3	13:E:167:VAL:CG1	2.44	0.48
21:M:1:MET:O	21:M:2:LEU:CB	2.62	0.48
31:W:18:LYS:HA	31:W:36:ILE:HG13	1.95	0.48
32:X:70:LEU:O	32:X:74:GLY:N	2.46	0.48
34:Z:38:GLU:O	34:Z:43:ILE:HG12	2.13	0.48
6:5:58:THR:HG23	9:A:1107:G:H5''	1.94	0.48
9:A:301:G:H1'	9:A:302:C:C6	2.48	0.48
9:A:528:A:C2	9:A:2043:C:H4'	2.49	0.48
9:A:597:G:O2'	20:L:11:GLY:O	2.27	0.48
9:A:995:C:O2	18:J:3:THR:HG23	2.13	0.48
9:A:1996:C:OP1	19:K:31:ARG:NE	2.46	0.48
9:A:2230:G:O3'	32:X:29:LEU:HD23	2.14	0.48
9:A:2678:C:H2'	9:A:2679:A:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:F:110:ILE:O	14:F:112:ASP:N	2.46	0.48
32:X:67:LEU:HD23	32:X:70:LEU:HD12	1.96	0.48
3:2:10:LEU:HD23	9:A:770:G:H5''	1.96	0.48
6:5:54:VAL:O	6:5:55:VAL:C	2.57	0.48
9:A:11:C:C3'	9:A:12:U:H5'	2.44	0.48
9:A:586:A:N1	9:A:809:G:O2'	2.39	0.48
9:A:1738:G:HO2'	9:A:1739:A:P	2.37	0.48
9:A:2355:G:H4'	31:W:20:LEU:CD1	2.44	0.48
13:E:32:VAL:HG23	13:E:178:VAL:HG12	1.95	0.48
18:J:32:LEU:CD2	18:J:54:ILE:HD12	2.44	0.48
24:P:19:PHE:N	24:P:19:PHE:CD1	2.82	0.48
9:A:996:A:H4'	25:Q:91:ARG:NE	2.29	0.48
9:A:1069:A:C1'	9:A:1073:A:H62	2.26	0.48
9:A:1327:A:H2'	9:A:1328:A:O4'	2.14	0.48
14:F:10:GLU:O	14:F:12:VAL:N	2.44	0.48
15:G:22:VAL:HG23	15:G:22:VAL:O	2.14	0.48
15:G:23:ILE:HG21	15:G:71:LEU:HD11	1.95	0.48
26:R:49:ILE:HD12	26:R:52:PRO:HA	1.95	0.48
31:W:18:LYS:CG	31:W:19:ARG:N	2.77	0.48
9:A:749:A:C6	9:A:1618:A:C2	3.01	0.48
9:A:973:A:P	26:R:81:LYS:HZ3	2.36	0.48
9:A:995:C:N4	18:J:2:LYS:HB3	2.29	0.48
9:A:1799:G:C5	11:C:175:LEU:HD23	2.49	0.48
12:D:148:GLN:HB2	12:D:152:PRO:HG2	1.96	0.48
15:G:15:ASP:O	15:G:16:VAL:HG13	2.12	0.48
15:G:104:LEU:HB2	15:G:112:VAL:HG21	1.96	0.48
18:J:44:TYR:CD1	25:Q:63:ARG:HG2	2.49	0.48
31:W:44:PHE:HD1	31:W:45:HIS:CE1	2.31	0.48
6:5:110:ALA:HB1	6:5:113:PHE:CZ	2.49	0.47
9:A:479:A:C2	9:A:480:A:C4	3.01	0.47
9:A:983:A:N6	9:A:984:A:C2	2.82	0.47
9:A:1417:C:N3	9:A:1581:G:N2	2.60	0.47
9:A:2062:A:H61	36:A:9000:ERY:H273	1.70	0.47
9:A:2592:G:C6	9:A:2603:G:O6	2.67	0.47
15:G:118:ALA:O	15:G:120:ILE:N	2.41	0.47
17:I:60:VAL:HG22	17:I:66:PHE:HB3	1.95	0.47
22:N:117:ASP:O	22:N:118:ARG:C	2.57	0.47
24:P:105:LYS:HA	24:P:108:ARG:HD2	1.95	0.47
9:A:1814:G:C6	9:A:1815:A:N6	2.82	0.47
11:C:232:GLY:H	11:C:241:LYS:HE3	1.79	0.47
14:F:134:GLN:O	14:F:136:ILE:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:S:24:ILE:HD11	27:S:36:LEU:HD13	1.96	0.47
27:S:63:GLY:O	27:S:64:ALA:CB	2.62	0.47
31:W:23:LYS:HE2	31:W:24:ARG:H	1.78	0.47
14:F:64:PRO:HA	14:F:88:VAL:HG22	1.95	0.47
17:I:100:ILE:HD13	17:I:137:LEU:HD12	1.96	0.47
18:J:84:ILE:HG23	18:J:84:ILE:O	2.15	0.47
19:K:72:PRO:O	19:K:74:GLY:N	2.43	0.47
26:R:68:ARG:HD3	26:R:92:TRP:CZ2	2.49	0.47
31:W:47:GLY:H	31:W:80:SER:HB3	1.80	0.47
6:5:23:LEU:H	6:5:87:GLU:HB2	1.79	0.47
6:5:110:ALA:HB1	6:5:113:PHE:CE1	2.49	0.47
9:A:983:A:N6	9:A:984:A:N1	2.62	0.47
9:A:2406:A:C2	20:L:69:ARG:NH2	2.82	0.47
9:A:2862:G:C5	9:A:2863:C:C5	3.02	0.47
14:F:69:ALA:N	14:F:82:TYR:O	2.47	0.47
31:W:63:ASP:OD1	31:W:63:ASP:N	2.35	0.47
32:X:39:VAL:HG21	32:X:42:GLU:HB2	1.96	0.47
2:1:16:THR:HG21	2:1:41:VAL:HG13	1.97	0.47
9:A:587:C:P	20:L:21:ARG:NH1	2.88	0.47
25:Q:91:ARG:HH21	25:Q:93:ILE:HD13	1.80	0.47
31:W:49:ASN:HA	31:W:61:LYS:HB2	1.94	0.47
5:4:6:SER:HB2	9:A:1031:G:H4'	1.95	0.47
6:5:15:VAL:HG21	6:5:66:GLY:HA2	1.96	0.47
6:5:123:ILE:HG12	6:5:124:ASP:N	2.30	0.47
6:5:127:ALA:O	6:5:129:LEU:N	2.48	0.47
9:A:451:U:C2	9:A:453:A:N7	2.83	0.47
9:A:478:A:C6	9:A:480:A:C6	3.03	0.47
9:A:2346:A:H3'	9:A:2347:C:H5''	1.95	0.47
19:K:24:VAL:HG13	19:K:33:ALA:HB2	1.95	0.47
20:L:82:LEU:CD1	20:L:116:VAL:HG23	2.44	0.47
33:Y:56:LEU:O	33:Y:57:LEU:HB3	2.14	0.47
6:5:39:THR:HA	6:5:42:ARG:CD	2.43	0.47
6:5:60:LEU:HD23	6:5:78:GLY:HA3	1.97	0.47
6:5:88:HIS:CB	6:5:89:PRO:HD3	2.44	0.47
6:5:100:ALA:HB2	6:5:125:ARG:HE	1.79	0.47
9:A:419:U:H2'	9:A:420:C:C6	2.50	0.47
9:A:725:G:C6	9:A:726:G:N1	2.82	0.47
9:A:1090:A:C2	9:A:1102:C:H1'	2.50	0.47
9:A:1417:C:O2'	9:A:1587:G:O2'	2.19	0.47
9:A:1474:U:C2'	9:A:1475:G:H5'	2.44	0.47
9:A:2061:G:N2	9:A:2063:C:N3	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2425:A:C5'	9:A:2427:C:O4'	2.62	0.47
11:C:246:PRO:HG2	11:C:247:TRP:CZ3	2.50	0.47
17:I:89:SER:OG	17:I:135:MET:SD	2.68	0.47
17:I:135:MET:HB3	17:I:137:LEU:CD2	2.43	0.47
26:R:64:VAL:HG21	26:R:97:LYS:HB2	1.97	0.47
31:W:39:GLN:HG2	31:W:40:ARG:N	2.28	0.47
6:5:15:VAL:HG22	6:5:66:GLY:CA	2.44	0.47
9:A:523:C:H5''	9:A:540:C:O2'	2.15	0.47
9:A:947:A:O2'	9:A:984:A:H2	1.98	0.47
9:A:1478:G:C2	9:A:1479:G:N7	2.83	0.47
9:A:1614:A:N6	27:S:92:ARG:O	2.43	0.47
9:A:2210:U:H4'	9:A:2211:A:H5'	1.97	0.47
9:A:2902:C:C2'	9:A:2903:U:O5'	2.63	0.47
36:A:9000:ERY:H8	36:A:9000:ERY:H321	1.58	0.47
10:B:55:U:O3'	14:F:23:SER:OG	2.21	0.47
17:I:40:ALA:O	17:I:43:ALA:HB3	2.14	0.47
18:J:36:LEU:O	18:J:121:LYS:NZ	2.39	0.47
18:J:43:GLU:O	18:J:44:TYR:C	2.58	0.47
24:P:50:ARG:HG2	24:P:57:ALA:N	2.30	0.47
31:W:9:THR:HG23	31:W:10:ARG:N	2.30	0.47
31:W:60:ALA:HA	31:W:81:ILE:HD12	1.97	0.47
1:0:9:ARG:NH2	9:A:517:C:OP2	2.48	0.47
6:5:51:TYR:HD1	6:5:52:MET:N	2.12	0.47
9:A:846:U:HO2'	9:A:847:U:P	2.37	0.47
9:A:1161:C:H1'	26:R:8:GLY:O	2.15	0.47
9:A:1198:U:O3'	25:Q:4:LYS:HE3	2.15	0.47
9:A:2063:C:H5	9:A:2064:C:H41	1.63	0.47
9:A:2609:U:C3'	9:A:2610:C:H5'	2.44	0.47
9:A:2839:G:N2	9:A:2880:C:C4	2.82	0.47
14:F:131:VAL:HG22	14:F:151:LEU:H	1.80	0.47
17:I:116:MET:SD	17:I:124:MET:HE3	2.55	0.47
22:N:20:MET:HE1	22:N:40:LYS:HE2	1.97	0.47
31:W:28:GLU:O	31:W:30:VAL:N	2.48	0.47
31:W:30:VAL:HG23	31:W:60:ALA:O	2.15	0.47
34:Z:39:ASP:CG	34:Z:44:ARG:HH11	2.23	0.47
6:5:54:VAL:HG22	6:5:83:ALA:HB1	1.97	0.47
9:A:479:A:H4'	9:A:480:A:OP1	2.15	0.47
9:A:1079:C:O2	17:I:130:GLY:HA3	2.15	0.47
9:A:1088:A:HO2'	9:A:1089:A:P	2.37	0.47
21:M:46:ILE:HD13	21:M:47:GLU:N	2.30	0.47
9:A:657:U:H2'	9:A:658:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1817:G:H2'	9:A:1818:U:H5'	1.97	0.46
12:D:169:ARG:O	12:D:170:VAL:HG13	2.15	0.46
15:G:112:VAL:HG23	15:G:113:ASP:N	2.28	0.46
17:I:14:ALA:HB1	17:I:45:THR:HG23	1.97	0.46
20:L:23:ILE:HD12	26:R:84:ARG:CZ	2.45	0.46
25:Q:4:LYS:HZ3	25:Q:7:VAL:HG11	1.79	0.46
26:R:68:ARG:HD3	26:R:92:TRP:CE2	2.50	0.46
28:T:69:ARG:CD	28:T:70:HIS:H	2.28	0.46
6:5:67:THR:C	6:5:69:PHE:N	2.73	0.46
9:A:747:U:C2'	27:S:88:ARG:NH2	2.78	0.46
9:A:1219:U:OP2	25:Q:18:LYS:NZ	2.46	0.46
9:A:1392:A:N6	9:A:1393:A:N6	2.63	0.46
9:A:1509:A:C4	9:A:1510:G:C8	3.04	0.46
9:A:2134:A:HO2'	9:A:2135:A:H8	1.64	0.46
13:E:44:ARG:HH21	13:E:44:ARG:HG3	1.80	0.46
16:H:8:LYS:O	16:H:9:VAL:HB	2.15	0.46
19:K:24:VAL:CG1	19:K:30:ARG:HD3	2.45	0.46
20:L:68:SER:O	20:L:69:ARG:HB3	2.15	0.46
22:N:12:ARG:CZ	22:N:20:MET:HE1	2.46	0.46
25:Q:63:ARG:HH22	25:Q:96:ASP:N	2.12	0.46
9:A:2318:G:C6	9:A:2319:G:C6	3.03	0.46
9:A:2365:G:H4'	31:W:59:PHE:CZ	2.51	0.46
9:A:2889:C:N4	9:A:2890:G:C6	2.83	0.46
14:F:39:VAL:HG13	14:F:40:GLY:N	2.31	0.46
15:G:123:GLU:HG2	15:G:124:CYS:N	2.30	0.46
16:H:21:VAL:CG2	16:H:25:TYR:CD2	2.98	0.46
18:J:37:ARG:HA	18:J:118:MET:CE	2.45	0.46
19:K:98:ARG:HA	19:K:118:LEU:HD23	1.97	0.46
21:M:22:GLN:O	21:M:24:THR:N	2.48	0.46
28:T:54:GLU:N	28:T:54:GLU:OE1	2.48	0.46
31:W:72:GLY:N	31:W:73:PRO:CD	2.78	0.46
6:5:68:PRO:HA	6:5:72:LEU:CG	2.46	0.46
9:A:2335:A:C5	9:A:2337:G:C4	3.02	0.46
9:A:2583:G:N2	9:A:2584:U:O2	2.48	0.46
15:G:23:ILE:HD12	15:G:23:ILE:H	1.81	0.46
15:G:30:GLY:C	15:G:32:LEU:H	2.24	0.46
17:I:19:PRO:CG	17:I:23:VAL:HG23	2.45	0.46
19:K:30:ARG:NH1	19:K:32:TYR:O	2.45	0.46
20:L:85:VAL:HG22	20:L:94:THR:HG22	1.97	0.46
25:Q:4:LYS:NZ	25:Q:7:VAL:CG1	2.79	0.46
1:0:42:ILE:H	1:0:42:ILE:HD12	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2436:G:C2	9:A:2437:G:C8	3.04	0.46
9:A:2698:U:H2'	9:A:2699:C:C6	2.51	0.46
11:C:67:LYS:HG2	11:C:150:GLY:HA2	1.97	0.46
16:H:31:VAL:HB	16:H:32:PRO:CD	2.46	0.46
17:I:120:ASP:O	17:I:123:ALA:N	2.46	0.46
25:Q:91:ARG:HH21	25:Q:93:ILE:HG21	1.81	0.46
6:5:136:ILE:HG13	6:5:139:LEU:HD12	1.98	0.46
9:A:747:U:H2'	27:S:88:ARG:NH2	2.30	0.46
9:A:1313:U:H2'	9:A:1610:A:C2	2.51	0.46
9:A:1341:G:H1	28:T:24:MET:HE2	1.80	0.46
9:A:1567:G:C2'	11:C:84:PRO:HG3	2.46	0.46
9:A:1569:A:N6	9:A:1570:A:C6	2.84	0.46
9:A:1838:C:H4'	9:A:1839:G:C8	2.51	0.46
9:A:2581:G:H4'	9:A:2582:G:C8	2.51	0.46
10:B:29:A:H2'	10:B:30:C:C6	2.50	0.46
10:B:37:C:C5	10:B:38:C:C4	3.04	0.46
11:C:75:ALA:HB2	11:C:95:TYR:HA	1.97	0.46
12:D:1:MET:HG2	12:D:205:PRO:HG3	1.98	0.46
14:F:30:VAL:CG1	14:F:96:TRP:CH2	2.99	0.46
9:A:1939:U:O2	9:A:1967:C:H4'	2.15	0.46
9:A:2701:U:H3'	9:A:2702:G:H5''	1.96	0.46
9:A:2897:U:H2'	9:A:2898:U:C6	2.51	0.46
17:I:57:VAL:HG23	17:I:71:LYS:CE	2.46	0.46
23:O:79:ALA:O	23:O:82:ALA:N	2.49	0.46
26:R:66:HIS:CG	26:R:94:THR:HG22	2.49	0.46
29:U:73:ASN:HA	29:U:95:PHE:CE2	2.51	0.46
31:W:9:THR:CG2	31:W:10:ARG:HD3	2.44	0.46
9:A:2024:G:C4	9:A:2040:G:N2	2.84	0.46
9:A:2793:C:H2'	9:A:2794:C:C6	2.50	0.46
11:C:93:VAL:HG12	11:C:94:LEU:N	2.31	0.46
14:F:147:ARG:HG3	14:F:148:VAL:N	2.30	0.46
17:I:24:GLY:O	17:I:27:LEU:HG	2.16	0.46
17:I:61:TYR:N	17:I:61:TYR:CD1	2.82	0.46
24:P:50:ARG:CB	24:P:57:ALA:N	2.78	0.46
28:T:29:THR:HB	28:T:86:THR:HG22	1.98	0.46
28:T:29:THR:CB	28:T:86:THR:H	2.29	0.46
2:1:4:ILE:HD11	2:1:27:ARG:HB2	1.97	0.46
9:A:247:G:H4'	9:A:386:G:C5	2.51	0.46
9:A:593:U:H2'	9:A:594:U:C6	2.51	0.46
9:A:751:A:C6	9:A:789:A:C5	3.04	0.46
9:A:959:A:H62	21:M:82:MET:CE	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:F:62:GLN:NE2	14:F:89:THR:O	2.47	0.46
15:G:163:TYR:O	15:G:164:ALA:HB2	2.16	0.46
17:I:100:ILE:CG2	17:I:101:SER:N	2.79	0.46
19:K:61:VAL:HG22	19:K:87:LEU:HD11	1.98	0.46
20:L:132:ARG:HG3	20:L:142:ILE:HD12	1.98	0.46
24:P:58:PHE:CE1	24:P:75:THR:HG22	2.51	0.46
24:P:72:VAL:HG23	24:P:72:VAL:O	2.15	0.46
31:W:19:ARG:CZ	31:W:22:VAL:HB	2.46	0.46
12:D:193:VAL:HB	12:D:194:PRO:HD2	1.98	0.46
14:F:113:PHE:HE1	14:F:116:LEU:HD13	1.81	0.46
6:5:63:ALA:HB3	6:5:84:TYR:CE2	2.52	0.45
6:5:71:CYS:CA	6:5:117:LEU:HD11	2.43	0.45
8:7:76:A:C6	9:A:2451:A:O4'	2.69	0.45
9:A:281:C:H2'	9:A:282:A:C8	2.51	0.45
9:A:1057:A:C6	9:A:1086:A:C2	3.04	0.45
9:A:1060:U:H3	9:A:1088:A:H2	1.64	0.45
9:A:1936:A:N6	9:A:1963:U:C2	2.84	0.45
18:J:12:LYS:O	18:J:13:ARG:HB2	2.15	0.45
18:J:44:TYR:O	18:J:45:THR:CB	2.64	0.45
19:K:13:ASN:O	19:K:14:SER:OG	2.29	0.45
1:0:3:GLN:HA	9:A:2615:U:C2	2.51	0.45
9:A:11:C:H2'	9:A:12:U:H5'	1.98	0.45
9:A:33:C:O2	9:A:447:A:N6	2.50	0.45
9:A:118:A:C8	9:A:119:A:C8	3.04	0.45
9:A:597:G:C2	9:A:661:A:C2	3.04	0.45
9:A:923:G:N3	31:W:23:LYS:HD2	2.31	0.45
9:A:1171:G:C6	9:A:1172:C:C4	3.04	0.45
9:A:1248:G:C5	13:E:46:GLN:NE2	2.84	0.45
9:A:1593:A:H2'	9:A:1594:U:O4'	2.17	0.45
9:A:1662:U:O2	9:A:2687:U:H4'	2.17	0.45
11:C:24:HIS:NE2	11:C:79:ARG:NH2	2.65	0.45
17:I:137:LEU:HD23	17:I:137:LEU:H	1.81	0.45
29:U:98:ASN:O	29:U:99:SER:C	2.59	0.45
4:3:21:PHE:O	4:3:22:LYS:O	2.33	0.45
6:5:57:ASN:C	6:5:59:LEU:N	2.74	0.45
9:A:141:G:N1	28:T:1:MET:O	2.44	0.45
9:A:271:G:H4'	9:A:272:A:OP1	2.17	0.45
9:A:1783:A:N1	9:A:2587:A:C4	2.85	0.45
10:B:51:G:OP2	23:O:64:TYR:HD2	1.98	0.45
19:K:80:ASP:CB	24:P:67:GLU:HG3	2.47	0.45
19:K:98:ARG:HA	19:K:118:LEU:CD2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:N:70:THR:HB	22:N:75:ILE:CD1	2.46	0.45
23:O:15:ARG:NE	23:O:93:ASP:OD2	2.44	0.45
27:S:1:MET:O	27:S:108:SER:HB2	2.16	0.45
30:V:80:HIS:HD2	30:V:83:LYS:H	1.62	0.45
31:W:39:GLN:HG3	31:W:42:THR:H	1.81	0.45
1:O:8:THR:HG21	9:A:2021:C:P	2.56	0.45
4:3:3:ILE:HG21	4:3:62:PRO:HG3	1.98	0.45
4:3:12:ARG:HD3	20:L:61:LEU:O	2.16	0.45
9:A:1150:C:H2'	9:A:1151:A:O5'	2.17	0.45
9:A:2144:G:H3'	9:A:2144:G:N3	2.31	0.45
9:A:2262:U:H4'	9:A:2328:A:C2	2.52	0.45
9:A:2822:G:O2'	9:A:2824:C:OP2	2.33	0.45
9:A:2852:G:C6	9:A:2853:C:N3	2.84	0.45
9:A:2862:G:C6	9:A:2863:C:C4	3.04	0.45
12:D:70:LYS:O	12:D:71:ALA:HB3	2.17	0.45
18:J:12:LYS:O	18:J:13:ARG:CB	2.64	0.45
19:K:99:ILE:HG21	19:K:119:ALA:HB2	1.98	0.45
30:V:80:HIS:CD2	30:V:83:LYS:HB2	2.52	0.45
2:1:33:LEU:N	2:1:51:ALA:CB	2.80	0.45
5:4:8:LYS:NZ	9:A:2467:C:OP1	2.48	0.45
9:A:85:G:OP1	29:U:6:ARG:N	2.49	0.45
9:A:799:G:C6	9:A:800:A:C6	3.05	0.45
9:A:2108:A:C2'	9:A:2109:U:O5'	2.65	0.45
9:A:2326:C:C6	9:A:2326:C:H3'	2.52	0.45
9:A:2326:C:H4'	9:A:2327:A:OP1	2.16	0.45
9:A:2581:G:N3	9:A:2581:G:C2'	2.75	0.45
9:A:2649:C:H2'	9:A:2650:U:C6	2.50	0.45
9:A:2758:A:H2'	9:A:2759:G:H5'	1.99	0.45
10:B:11:C:O2'	10:B:15:A:N6	2.50	0.45
13:E:119:ILE:HG13	13:E:119:ILE:O	2.16	0.45
15:G:10:VAL:HG22	15:G:47:ASN:C	2.41	0.45
18:J:55:ILE:HD11	18:J:130:HIS:CD2	2.51	0.45
25:Q:91:ARG:HH12	26:R:10:LYS:HB3	1.82	0.45
27:S:18:ARG:HG3	27:S:76:VAL:HG13	1.98	0.45
1:O:42:ILE:HD11	22:N:98:LEU:CB	2.46	0.45
2:1:4:ILE:HG23	2:1:5:ARG:N	2.32	0.45
6:5:48:ALA:HB3	6:5:51:TYR:HB3	1.98	0.45
6:5:71:CYS:HA	6:5:117:LEU:HD11	1.96	0.45
6:5:77:VAL:O	6:5:79:PRO:HD2	2.13	0.45
9:A:2478:A:H2'	9:A:2479:U:H5'	1.98	0.45
9:A:2592:G:C2	9:A:2603:G:C5	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2740:A:C6	9:A:2764:A:C8	3.04	0.45
24:P:21:PRO:HD3	24:P:49:ILE:HD12	1.98	0.45
2:1:6:GLU:OE1	2:1:52:LYS:CE	2.64	0.45
6:5:110:ALA:O	6:5:113:PHE:N	2.46	0.45
9:A:855:G:H21	31:W:23:LYS:HG2	1.82	0.45
9:A:1141:U:H4'	9:A:1142:A:O4'	2.17	0.45
9:A:1428:C:C5	9:A:1569:A:H5''	2.52	0.45
9:A:2058:A:C5	9:A:2059:A:N6	2.85	0.45
13:E:187:VAL:O	13:E:188:MET:HB3	2.16	0.45
17:I:124:MET:HE2	17:I:124:MET:HB3	1.88	0.45
17:I:125:THR:O	17:I:128:ILE:N	2.48	0.45
22:N:33:ILE:CD1	22:N:118:ARG:NE	2.80	0.45
24:P:91:VAL:HG11	24:P:96:LEU:HD21	1.98	0.45
30:V:80:HIS:CD2	30:V:82:TYR:H	2.35	0.45
34:Z:3:THR:HA	34:Z:37:ARG:O	2.16	0.45
9:A:728:G:H4'	11:C:12:ARG:HD3	1.98	0.45
9:A:996:A:H4'	25:Q:91:ARG:CD	2.47	0.45
14:F:127:TYR:O	14:F:128:SER:CB	2.65	0.45
2:1:8:ILE:HG21	2:1:51:ALA:HA	1.98	0.45
5:4:2:LYS:HZ1	9:A:2478:A:P	2.40	0.45
6:5:125:ARG:CZ	6:5:125:ARG:HA	2.46	0.45
9:A:2405:G:O2'	9:A:2406:A:OP1	2.26	0.45
9:A:2407:A:C2	9:A:2408:U:C2	3.05	0.45
11:C:163:ILE:HG23	11:C:171:VAL:CG1	2.47	0.45
22:N:103:ARG:CZ	22:N:110:MET:CE	2.95	0.45
23:O:43:ASN:O	23:O:45:SER:N	2.50	0.45
24:P:102:ARG:O	24:P:103:THR:HG22	2.17	0.45
25:Q:91:ARG:HH11	26:R:11:GLN:H	1.64	0.45
5:4:6:SER:HB2	9:A:1031:G:C4'	2.47	0.45
6:5:129:LEU:CB	6:5:130:PRO:HD2	2.47	0.45
9:A:192:C:O2'	9:A:802:A:N3	2.50	0.45
9:A:2564:A:C2	9:A:2647:U:H4'	2.52	0.45
12:D:73:VAL:HG23	12:D:74:GLU:H	1.82	0.45
14:F:107:VAL:HG11	14:F:116:LEU:HD21	1.99	0.45
14:F:128:SER:HA	14:F:154:THR:HA	1.99	0.45
18:J:30:THR:HG22	18:J:31:GLU:N	2.32	0.45
25:Q:4:LYS:NZ	25:Q:7:VAL:HG11	2.31	0.45
25:Q:7:VAL:HG13	25:Q:8:ILE:N	2.32	0.45
31:W:17:ALA:O	31:W:18:LYS:CB	2.64	0.45
9:A:627:A:C6	9:A:637:A:C8	3.04	0.44
9:A:973:A:O4'	9:A:1188:U:C6	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:980:A:C4	9:A:1136:G:O4'	2.70	0.44
9:A:2043:C:OP1	9:A:2777:G:O2'	2.24	0.44
9:A:2283:C:H5''	9:A:2389:G:O2'	2.18	0.44
10:B:51:G:H5''	23:O:64:TYR:CD2	2.52	0.44
12:D:121:THR:O	12:D:122:VAL:HB	2.17	0.44
16:H:8:LYS:O	16:H:13:GLY:HA2	2.16	0.44
19:K:118:LEU:O	19:K:119:ALA:HB3	2.17	0.44
21:M:102:LEU:N	21:M:102:LEU:HD12	2.32	0.44
9:A:646:U:H3'	9:A:647:G:H5''	1.99	0.44
9:A:1181:U:H2'	9:A:1182:G:C8	2.53	0.44
9:A:1387:A:H5'	9:A:1469:A:H1'	2.00	0.44
9:A:2307:G:N2	9:A:2311:A:C8	2.85	0.44
12:D:44:GLY:HA3	12:D:45:TYR:HD1	1.82	0.44
17:I:109:ALA:CB	17:I:128:ILE:HG13	2.48	0.44
21:M:53:MET:HE3	21:M:63:ILE:HG21	1.97	0.44
28:T:40:LYS:HG2	28:T:58:VAL:HG22	1.99	0.44
29:U:53:GLN:N	29:U:54:PRO:CD	2.80	0.44
31:W:37:VAL:HG11	31:W:55:ASP:HB2	1.99	0.44
34:Z:15:ARG:HG2	34:Z:15:ARG:HH11	1.82	0.44
6:5:15:VAL:CG2	6:5:66:GLY:HA2	2.47	0.44
9:A:81:G:O2'	9:A:295:G:O2'	2.26	0.44
9:A:315:G:H2'	9:A:316:C:C6	2.52	0.44
9:A:750:A:OP1	9:A:1615:C:N4	2.40	0.44
9:A:792:A:C6	9:A:2440:C:C6	3.05	0.44
9:A:819:A:C4	9:A:1189:A:C2	3.05	0.44
9:A:1443:U:H2'	9:A:1444:G:C8	2.53	0.44
9:A:1686:C:C2	9:A:1703:G:C2	3.05	0.44
9:A:1936:A:C2	9:A:1943:U:C5	3.03	0.44
12:D:3:GLY:HA3	12:D:204:LYS:HG2	1.99	0.44
14:F:72:SER:HB2	14:F:80:GLN:HB2	2.00	0.44
18:J:80:HIS:O	18:J:82:GLY:N	2.50	0.44
29:U:6:ARG:O	29:U:24:VAL:HB	2.17	0.44
3:2:24:THR:O	3:2:25:LYS:C	2.61	0.44
6:5:2:ALA:CB	6:5:6:GLN:CD	2.91	0.44
6:5:100:ALA:HB3	6:5:125:ARG:HD2	1.98	0.44
9:A:277:G:H2'	9:A:361:G:O6	2.17	0.44
9:A:818:G:H5'	9:A:839:U:OP1	2.18	0.44
9:A:1867:G:C5	9:A:1868:C:C5	3.06	0.44
9:A:2344:U:H4'	9:A:2345:G:OP1	2.17	0.44
9:A:2586:U:O4	35:a:81:ILE:HG12	2.17	0.44
9:A:2683:C:O2	19:K:70:ARG:NH2	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:G:24:THR:HG23	15:G:34:ARG:HG2	1.99	0.44
15:G:60:GLY:O	15:G:61:TRP:HB2	2.17	0.44
17:I:100:ILE:HD11	17:I:137:LEU:CG	2.48	0.44
25:Q:103:VAL:HG23	25:Q:104:ALA:N	2.32	0.44
31:W:19:ARG:NH1	31:W:22:VAL:HG21	2.33	0.44
31:W:19:ARG:C	31:W:19:ARG:HD2	2.43	0.44
1:O:3:GLN:NE2	9:A:2016:U:O2	2.46	0.44
9:A:666:A:H4'	20:L:48:ARG:HD2	1.99	0.44
9:A:994:C:H1'	26:R:10:LYS:CE	2.47	0.44
9:A:1045:C:C3'	9:A:1046:A:H5'	2.48	0.44
9:A:1482:G:H1'	9:A:1509:A:N6	2.30	0.44
9:A:1523:U:O2'	9:A:1524:G:H5'	2.18	0.44
9:A:2108:A:H2'	9:A:2109:U:O5'	2.17	0.44
9:A:2276:G:P	21:M:83:GLY:O	2.76	0.44
9:A:2283:C:C2	9:A:2389:G:C2	3.06	0.44
9:A:2582:G:C2	9:A:2583:G:N9	2.86	0.44
9:A:2584:U:H5''	9:A:2584:U:H6	1.82	0.44
9:A:2745:C:C4	9:A:2746:U:C4	3.05	0.44
9:A:2747:G:O6	9:A:2755:C:H5''	2.18	0.44
9:A:2846:G:H2'	9:A:2847:U:O4'	2.17	0.44
13:E:147:LEU:HB3	13:E:186:VAL:HG23	1.99	0.44
15:G:104:LEU:HB2	15:G:112:VAL:CG2	2.47	0.44
18:J:54:ILE:HD13	18:J:54:ILE:C	2.42	0.44
27:S:96:ILE:C	27:S:96:ILE:HD12	2.43	0.44
34:Z:5:LYS:HD2	34:Z:5:LYS:N	2.32	0.44
6:5:51:TYR:CE1	6:5:52:MET:HG2	2.53	0.44
9:A:336:C:N3	9:A:337:C:C5	2.86	0.44
9:A:820:A:H2'	9:A:821:A:O4'	2.16	0.44
9:A:1197:G:H2'	9:A:1198:U:H6	1.83	0.44
9:A:2577:A:H8	9:A:2577:A:OP2	1.99	0.44
9:A:2582:G:C2	9:A:2583:G:C5	3.06	0.44
9:A:2788:C:H2'	9:A:2789:C:C6	2.53	0.44
9:A:2902:C:H2'	9:A:2903:U:O5'	2.18	0.44
14:F:94:ARG:HH11	14:F:94:ARG:CG	2.31	0.44
17:I:46:ASP:HA	17:I:50:LYS:HD2	2.00	0.44
19:K:10:VAL:HG21	19:K:17:ARG:H	1.81	0.44
27:S:66:ILE:HD13	27:S:67:ASP:N	2.33	0.44
3:2:12:ARG:HH11	3:2:44:VAL:HG11	1.82	0.44
4:3:31:ILE:O	4:3:31:ILE:HG13	2.17	0.44
9:A:61:C:H2'	9:A:62:U:H5'	2.00	0.44
9:A:278:A:N1	9:A:362:A:C8	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:855:G:H21	31:W:23:LYS:CG	2.31	0.44
9:A:979:A:H2'	9:A:982:C:H42	1.82	0.44
9:A:1340:U:H4'	9:A:1341:G:OP2	2.17	0.44
9:A:1542:U:H2'	9:A:1543:G:O4'	2.16	0.44
9:A:1737:G:H5''	9:A:1738:G:OP2	2.17	0.44
9:A:1779:U:C5	9:A:1784:A:N7	2.86	0.44
9:A:2577:A:OP2	9:A:2577:A:C8	2.70	0.44
10:B:78:A:H2'	10:B:79:G:O4'	2.18	0.44
11:C:24:HIS:CE1	11:C:79:ARG:HH21	2.36	0.44
17:I:40:ALA:O	17:I:68:PHE:CZ	2.71	0.44
17:I:92:PRO:C	17:I:94:LYS:H	2.25	0.44
18:J:44:TYR:HA	25:Q:59:LEU:CD2	2.48	0.44
28:T:48:GLN:O	28:T:52:GLU:HA	2.17	0.44
9:A:132:G:C2'	9:A:133:U:H5'	2.48	0.44
9:A:201:C:OP1	32:X:17:ARG:NH1	2.51	0.44
9:A:222:A:N6	9:A:231:A:C2	2.86	0.44
9:A:948:C:H1'	9:A:984:A:O2'	2.18	0.44
9:A:1232:G:C5	9:A:1233:C:C5	3.06	0.44
9:A:2103:C:H2'	9:A:2104:C:C5'	2.47	0.44
12:D:69:ALA:HA	12:D:73:VAL:CG1	2.47	0.44
21:M:13:HIS:O	21:M:14:LYS:CB	2.66	0.44
22:N:38:LEU:HB3	22:N:39:PRO:CD	2.48	0.44
2:1:8:ILE:CD1	2:1:24:LYS:HG2	2.48	0.44
2:1:24:LYS:NZ	2:1:51:ALA:O	2.51	0.44
6:5:131:THR:O	6:5:132:TYR:C	2.61	0.44
9:A:288:U:H2'	9:A:289:G:C8	2.52	0.44
9:A:555:G:O2'	9:A:556:A:OP2	2.31	0.44
9:A:2661:G:C6	9:A:2662:A:C2	3.06	0.44
10:B:78:A:C2	10:B:99:A:C4	3.06	0.44
13:E:44:ARG:HH21	13:E:44:ARG:CG	2.31	0.44
15:G:35:THR:HG22	15:G:36:LEU:N	2.33	0.44
18:J:44:TYR:O	18:J:44:TYR:CD2	2.71	0.44
28:T:69:ARG:CG	28:T:70:HIS:N	2.81	0.44
30:V:29:ILE:HD13	30:V:30:ILE:N	2.33	0.44
31:W:18:LYS:N	31:W:36:ILE:HG13	2.33	0.44
9:A:223:A:N1	9:A:407:G:O2'	2.46	0.43
9:A:720:U:H2'	9:A:721:A:C8	2.53	0.43
9:A:980:A:C6	9:A:981:A:N1	2.86	0.43
9:A:1071:G:H1'	9:A:1089:A:C5	2.53	0.43
9:A:2335:A:N6	9:A:2337:G:H1'	2.33	0.43
9:A:2423:U:H5'	9:A:2423:U:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2603:G:C2'	9:A:2604:U:H5'	2.47	0.43
9:A:2657:A:C2	9:A:2665:A:C4	3.06	0.43
11:C:76:VAL:HG22	11:C:76:VAL:O	2.17	0.43
18:J:44:TYR:HD1	25:Q:63:ARG:HG2	1.81	0.43
20:L:112:LEU:HD23	20:L:114:GLY:H	1.83	0.43
31:W:19:ARG:HA	31:W:34:SER:HA	2.00	0.43
33:Y:45:GLN:O	33:Y:46:VAL:HB	2.17	0.43
6:5:3:LEU:HB2	6:5:4:ASN:H	1.68	0.43
9:A:1439:A:C2	9:A:1553:A:C4	3.06	0.43
9:A:1584:U:H2'	9:A:1585:C:H5'	2.00	0.43
9:A:1786:A:N6	9:A:2606:C:O4'	2.46	0.43
9:A:1857:G:C2	9:A:1884:G:N3	2.86	0.43
11:C:265:PHE:N	11:C:265:PHE:HD1	2.15	0.43
18:J:4:PHE:O	18:J:44:TYR:OH	2.34	0.43
18:J:110:PRO:HB2	18:J:111:LYS:HG3	2.00	0.43
20:L:2:ARG:HA	20:L:5:THR:CG2	2.48	0.43
25:Q:91:ARG:HH11	26:R:11:GLN:N	2.16	0.43
4:3:31:ILE:O	4:3:31:ILE:CG1	2.66	0.43
6:5:17:GLU:OE1	6:5:53:ARG:NH1	2.51	0.43
6:5:71:CYS:HB3	6:5:74:ASP:OD2	2.18	0.43
6:5:77:VAL:C	6:5:79:PRO:CD	2.83	0.43
7:6:13:ALA:HB1	7:6:17:MET:CE	2.49	0.43
9:A:545:U:H6	9:A:545:U:O5'	2.02	0.43
9:A:581:C:H2'	9:A:582:A:C8	2.53	0.43
9:A:936:A:H2'	9:A:937:C:C6	2.54	0.43
9:A:1252:G:C2	25:Q:32:ARG:HG2	2.52	0.43
9:A:2031:A:C6	9:A:2498:C:H1'	2.53	0.43
9:A:2180:U:C2	9:A:2181:U:C5	3.06	0.43
9:A:2517:C:C5	9:A:2542:A:C5	3.06	0.43
9:A:2595:G:C6	9:A:2599:G:O6	2.72	0.43
11:C:109:LEU:HD23	11:C:110:LYS:H	1.83	0.43
12:D:45:TYR:N	12:D:45:TYR:CD1	2.86	0.43
15:G:36:LEU:N	15:G:36:LEU:HD22	2.33	0.43
19:K:47:ILE:HG13	19:K:48:PRO:HD2	2.00	0.43
20:L:111:ILE:N	20:L:111:ILE:HD12	2.33	0.43
31:W:24:ARG:HD3	31:W:65:LYS:CD	2.48	0.43
6:5:17:GLU:HA	6:5:88:HIS:CE1	2.54	0.43
9:A:172:A:H2'	9:A:173:A:C8	2.53	0.43
9:A:684:G:C2	9:A:794:A:C2	3.06	0.43
9:A:822:G:H2'	9:A:823:C:H6	1.83	0.43
9:A:1914:C:H2'	9:A:1915:U:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2134:A:O2'	9:A:2135:A:O4'	2.36	0.43
10:B:27:C:C5	10:B:28:C:C5	3.06	0.43
11:C:44:ASN:C	11:C:44:ASN:OD1	2.60	0.43
12:D:133:THR:HG23	12:D:134:HIS:N	2.33	0.43
13:E:158:PHE:HD2	13:E:159:LEU:HD12	1.83	0.43
13:E:160:ALA:O	13:E:161:ALA:HB3	2.18	0.43
14:F:134:GLN:OE1	14:F:149:ARG:HB3	2.18	0.43
15:G:123:GLU:HG2	15:G:125:PRO:HD3	2.00	0.43
17:I:82:ALA:HB1	17:I:108:ILE:HG21	2.00	0.43
26:R:64:VAL:O	26:R:65:ALA:HB3	2.18	0.43
26:R:74:ILE:HB	26:R:87:GLN:O	2.18	0.43
6:5:71:CYS:SG	6:5:117:LEU:HD12	2.58	0.43
6:5:129:LEU:C	6:5:131:THR:N	2.73	0.43
9:A:1138:G:N3	18:J:108:MET:HE2	2.32	0.43
9:A:1171:G:N2	9:A:1179:G:C4	2.86	0.43
12:D:124:ARG:HA	12:D:165:MET:SD	2.58	0.43
22:N:70:THR:HB	22:N:75:ILE:HD11	2.01	0.43
25:Q:63:ARG:HH12	25:Q:95:ALA:C	2.26	0.43
31:W:49:ASN:ND2	31:W:50:VAL:N	2.67	0.43
2:1:5:ARG:CZ	2:1:24:LYS:HA	2.49	0.43
9:A:247:G:N7	9:A:249:C:C2	2.86	0.43
9:A:2582:G:N3	9:A:2582:G:H2'	2.34	0.43
14:F:142:TYR:CD1	14:F:142:TYR:C	2.96	0.43
18:J:11:VAL:HG11	18:J:50:THR:HA	2.01	0.43
19:K:35:VAL:HG12	19:K:36:GLY:N	2.34	0.43
20:L:2:ARG:HA	20:L:5:THR:HG21	2.01	0.43
20:L:91:ASP:CG	20:L:92:LEU:N	2.77	0.43
25:Q:94:LEU:CD1	26:R:13:ARG:HB2	2.49	0.43
29:U:73:ASN:O	29:U:74:ALA:HB3	2.17	0.43
31:W:24:ARG:HD3	31:W:65:LYS:HG2	2.00	0.43
33:Y:21:LEU:HA	33:Y:25:GLN:HB3	2.01	0.43
2:1:7:LYS:NZ	9:A:2421:G:P	2.92	0.43
6:5:87:GLU:OE2	6:5:95:LEU:HD23	2.18	0.43
9:A:323:C:OP1	9:A:338:G:N2	2.51	0.43
9:A:545:U:H2'	9:A:546:U:O3'	2.18	0.43
9:A:580:U:O3'	25:Q:30:VAL:HG13	2.18	0.43
9:A:744:U:H2'	9:A:745:G:O4'	2.19	0.43
9:A:1485:U:H2'	9:A:1486:U:H6	1.82	0.43
9:A:1536:C:H1'	9:A:1537:G:N2	2.34	0.43
9:A:1956:U:H2'	9:A:1957:C:H5'	2.01	0.43
9:A:2204:G:OP2	11:C:146:LYS:NZ	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:90:C:H6	10:B:90:C:H5''	1.83	0.43
14:F:103:ILE:HG21	14:F:173:ASP:HB2	2.01	0.43
19:K:3:GLN:HG3	19:K:4:GLU:N	2.34	0.43
20:L:122:VAL:CG1	20:L:142:ILE:HG12	2.47	0.43
21:M:26:VAL:HB	21:M:133:LYS:HA	2.00	0.43
25:Q:60:TRP:CE2	25:Q:93:ILE:HB	2.54	0.43
28:T:29:THR:HB	28:T:86:THR:HA	2.01	0.43
34:Z:15:ARG:HD3	34:Z:53:MET:SD	2.59	0.43
4:3:22:LYS:HA	4:3:47:ALA:O	2.19	0.43
9:A:139:U:C5	28:T:1:MET:HE2	2.53	0.43
9:A:274:C:H2'	9:A:275:C:O4'	2.19	0.43
9:A:479:A:N3	9:A:481:G:H5''	2.34	0.43
9:A:645:C:O2	9:A:645:C:O2'	2.35	0.43
9:A:975:A:C5	9:A:990:A:N7	2.86	0.43
9:A:1003:G:N2	9:A:1004:U:C2	2.86	0.43
9:A:1188:U:H4'	26:R:81:LYS:O	2.19	0.43
9:A:1378:A:C4	9:A:1380:G:N7	2.87	0.43
9:A:1441:G:H2'	9:A:1442:U:C6	2.53	0.43
9:A:1494:A:C2	9:A:1495:A:C4	3.06	0.43
9:A:2094:A:P	16:H:22:LYS:HD2	2.59	0.43
9:A:2353:G:N3	31:W:30:VAL:HG12	2.32	0.43
9:A:2576:G:N3	9:A:2576:G:C5'	2.76	0.43
9:A:2601:C:HO2'	9:A:2602:A:P	2.41	0.43
13:E:187:VAL:O	13:E:188:MET:CB	2.67	0.43
16:H:8:LYS:O	16:H:9:VAL:CB	2.66	0.43
17:I:45:THR:O	17:I:48:ILE:HG13	2.18	0.43
31:W:17:ALA:O	31:W:18:LYS:HB2	2.18	0.43
32:X:67:LEU:HD22	32:X:77:TYR:CE1	2.53	0.43
33:Y:13:GLU:C	33:Y:15:ASN:N	2.76	0.43
33:Y:31:GLN:HG2	33:Y:36:GLN:HB2	2.01	0.43
4:3:63:TYR:HH	9:A:592:A:HO2'	1.62	0.43
9:A:570:G:C4	9:A:2030:A:N7	2.87	0.43
9:A:764:A:C6	9:A:781:A:C2	3.06	0.43
9:A:1509:A:O2'	9:A:1510:G:P	2.76	0.43
9:A:2682:A:C8	12:D:11:MET:HG3	2.53	0.43
18:J:60:ASP:N	18:J:60:ASP:OD1	2.52	0.43
19:K:13:ASN:C	19:K:15:GLY:N	2.77	0.43
19:K:34:GLY:O	19:K:35:VAL:C	2.61	0.43
25:Q:4:LYS:HZ3	25:Q:7:VAL:CG1	2.32	0.43
25:Q:20:ALA:HA	25:Q:23:TYR:CE2	2.54	0.43
29:U:35:VAL:O	29:U:38:ILE:HB	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:W:36:ILE:O	31:W:36:ILE:HG22	2.18	0.43
31:W:44:PHE:O	31:W:78:PHE:HA	2.19	0.43
33:Y:56:LEU:HD22	33:Y:56:LEU:H	1.84	0.43
3:2:43:THR:O	3:2:44:VAL:C	2.62	0.43
9:A:476:G:H4'	9:A:502:A:N1	2.33	0.43
9:A:528:A:P	18:J:116:ARG:HH21	2.42	0.43
9:A:742:A:H2'	9:A:743:A:C8	2.53	0.43
9:A:1096:A:H2'	9:A:1097:U:H5''	2.01	0.43
9:A:1223:G:P	26:R:68:ARG:HH11	2.41	0.43
9:A:1476:U:C5	9:A:1514:G:C2	3.07	0.43
9:A:2070:A:H2'	9:A:2071:A:O4'	2.19	0.43
9:A:2507:C:C2	9:A:2508:G:C8	3.07	0.43
13:E:154:ASP:OD1	13:E:154:ASP:N	2.50	0.43
14:F:172:PHE:C	14:F:174:PHE:H	2.27	0.43
17:I:93:ASN:HA	17:I:135:MET:HE1	2.00	0.43
33:Y:23:ARG:O	33:Y:24:GLU:C	2.61	0.43
1:0:42:ILE:HG22	1:0:43:THR:O	2.19	0.42
9:A:1281:G:C2	9:A:1290:C:C2	3.07	0.42
9:A:2516:A:N6	9:A:2517:C:N4	2.67	0.42
9:A:2611:C:C3'	9:A:2611:C:C6	3.02	0.42
10:B:72:G:N2	10:B:103:U:C5	2.87	0.42
11:C:180:MET:O	11:C:267:VAL:N	2.42	0.42
12:D:110:THR:HG23	12:D:171:THR:HG22	2.00	0.42
18:J:88:THR:HG22	18:J:91:GLU:CG	2.49	0.42
19:K:13:ASN:O	19:K:14:SER:CB	2.67	0.42
22:N:8:ARG:HB3	22:N:10:LEU:CD2	2.48	0.42
23:O:41:ALA:O	23:O:44:GLY:N	2.41	0.42
28:T:50:LEU:C	28:T:52:GLU:N	2.77	0.42
28:T:69:ARG:HG3	28:T:70:HIS:H	1.83	0.42
28:T:76:ARG:HG3	28:T:77:ARG:N	2.34	0.42
29:U:17:ASP:O	29:U:18:LYS:C	2.62	0.42
30:V:12:GLN:C	30:V:12:GLN:CD	2.87	0.42
30:V:72:VAL:HG12	30:V:93:ARG:HA	2.01	0.42
9:A:226:A:C6	9:A:227:A:C6	3.07	0.42
9:A:348:A:C5	9:A:349:U:C5	3.07	0.42
9:A:580:U:H2'	9:A:581:C:C6	2.54	0.42
9:A:833:A:OP1	20:L:39:LYS:HE3	2.19	0.42
9:A:1747:U:H2'	9:A:1748:C:C6	2.55	0.42
9:A:2823:A:C5	9:A:2824:C:C5	3.07	0.42
12:D:118:PHE:HZ	22:N:1:MET:HB2	1.85	0.42
13:E:115:GLN:O	13:E:116:ASP:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:I:93:ASN:HB2	17:I:135:MET:SD	2.59	0.42
25:Q:86:SER:O	26:R:51:VAL:HA	2.18	0.42
26:R:5:PHE:HB3	26:R:59:ILE:HD12	2.01	0.42
27:S:59:GLU:HA	27:S:64:ALA:CB	2.50	0.42
33:Y:14:LEU:HA	33:Y:17:GLU:HB3	2.01	0.42
5:4:34:LYS:C	5:4:35:GLN:HG3	2.44	0.42
6:5:67:THR:CG2	6:5:72:LEU:HA	2.49	0.42
6:5:142:THR:OG1	6:5:143:MET:N	2.52	0.42
9:A:864:G:OP2	21:M:22:GLN:NE2	2.52	0.42
9:A:1094:U:N3	9:A:1097:U:OP2	2.51	0.42
9:A:1224:U:H4'	26:R:88:GLY:O	2.18	0.42
9:A:2047:C:O2'	9:A:2048:G:H5'	2.19	0.42
9:A:2748:A:H1'	15:G:66:THR:CG2	2.49	0.42
10:B:89:U:H3'	10:B:90:C:C5'	2.49	0.42
13:E:8:ALA:O	13:E:9:GLN:C	2.63	0.42
13:E:52:VAL:HG11	13:E:81:GLY:HA3	2.01	0.42
15:G:39:ALA:HB2	15:G:57:TYR:CD2	2.54	0.42
25:Q:27:ARG:HA	25:Q:33:VAL:HG12	2.00	0.42
30:V:75:GLN:HB2	30:V:92:VAL:CG2	2.48	0.42
9:A:959:A:N6	21:M:82:MET:CE	2.82	0.42
9:A:1112:G:C5	9:A:1113:U:C5	3.07	0.42
9:A:1312:U:H4'	9:A:1313:U:O5'	2.20	0.42
9:A:1681:G:N2	9:A:1763:G:OP2	2.45	0.42
9:A:2287:A:C8	9:A:2289:G:C8	3.08	0.42
14:F:111:ARG:NE	14:F:111:ARG:HA	2.34	0.42
22:N:79:LEU:O	22:N:80:PHE:HB2	2.19	0.42
6:5:108:VAL:CG1	6:5:109:LYS:N	2.82	0.42
7:6:15:SER:OG	7:6:16:VAL:N	2.53	0.42
9:A:146:A:H2'	9:A:147:C:C6	2.54	0.42
9:A:479:A:C2	9:A:480:A:C5	3.08	0.42
9:A:573:U:O2'	9:A:574:A:H3'	2.19	0.42
9:A:966:G:C6	9:A:967:U:C4	3.07	0.42
9:A:1204:A:C2	9:A:1240:U:N3	2.87	0.42
9:A:1239:G:H2'	9:A:1240:U:O4'	2.19	0.42
9:A:1814:G:C6	9:A:1815:A:C6	3.08	0.42
9:A:1937:A:N7	9:A:1939:U:H2'	2.35	0.42
9:A:2526:G:C5	9:A:2527:C:C5	3.08	0.42
14:F:134:GLN:HG2	14:F:135:ILE:N	2.34	0.42
17:I:91:LYS:HB2	17:I:95:ASP:HB2	2.00	0.42
29:U:10:VAL:HG12	29:U:71:ILE:HA	2.01	0.42
31:W:37:VAL:HB	31:W:38:ARG:NH1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:18:HIS:CE1	2:1:40:PRO:HD3	2.54	0.42
6:5:47:GLU:HG2	6:5:95:LEU:HD21	2.00	0.42
9:A:945:A:C4	9:A:2448:A:C2	3.07	0.42
9:A:1638:C:H4'	9:A:2710:C:O2	2.18	0.42
9:A:2039:U:H2'	9:A:2040:G:H8	1.82	0.42
9:A:2274:A:C5	9:A:2276:G:C8	3.07	0.42
9:A:2557:G:H2'	9:A:2558:C:C6	2.54	0.42
9:A:2582:G:C4	9:A:2583:G:N7	2.88	0.42
9:A:2637:U:C2'	9:A:2638:G:H5'	2.50	0.42
9:A:2727:A:C6	9:A:2728:U:O4	2.73	0.42
12:D:120:GLY:HA2	12:D:162:ALA:HA	2.00	0.42
14:F:94:ARG:HH11	14:F:94:ARG:HB2	1.84	0.42
18:J:64:VAL:HG13	18:J:65:THR:N	2.35	0.42
19:K:73:ASP:OD1	19:K:73:ASP:C	2.62	0.42
21:M:8:LYS:CE	21:M:9:PHE:CE2	3.02	0.42
24:P:92:ARG:O	24:P:92:ARG:CG	2.68	0.42
25:Q:6:GLY:HA2	25:Q:9:ALA:HB3	2.02	0.42
26:R:16:GLU:HA	26:R:98:ILE:HG22	2.01	0.42
26:R:74:ILE:HD12	26:R:74:ILE:N	2.34	0.42
29:U:38:ILE:HG23	29:U:39:ASN:N	2.33	0.42
9:A:19:A:H2'	9:A:20:C:O4'	2.20	0.42
9:A:126:A:C6	9:A:127:A:N1	2.88	0.42
9:A:356:G:C6	9:A:357:C:C4	3.07	0.42
9:A:372:G:C4	32:X:60:LYS:HE2	2.54	0.42
9:A:635:C:O2'	9:A:639:U:OP1	2.34	0.42
9:A:996:A:C5	9:A:1160:G:C2	3.08	0.42
9:A:1179:G:C6	9:A:1180:U:C4	3.08	0.42
9:A:2062:A:O2'	9:A:2063:C:C6	2.70	0.42
9:A:2661:G:H2'	9:A:2662:A:O4'	2.20	0.42
9:A:2821:A:C2	9:A:2822:G:C4	3.08	0.42
10:B:106:G:H2'	10:B:107:G:O4'	2.19	0.42
11:C:16:VAL:N	11:C:203:VAL:CG1	2.82	0.42
16:H:10:ALA:C	16:H:12:LEU:H	2.28	0.42
17:I:20:SER:HB3	17:I:21:PRO:HD3	2.02	0.42
25:Q:91:ARG:HE	25:Q:93:ILE:HG23	1.85	0.42
27:S:96:ILE:O	27:S:96:ILE:HG13	2.20	0.42
30:V:4:ILE:CG1	30:V:50:MET:HE1	2.49	0.42
6:5:3:LEU:HD12	6:5:5:LEU:N	2.35	0.42
9:A:1084:A:C6	9:A:1085:A:C6	3.08	0.42
9:A:1171:G:H1	9:A:1178:C:H42	1.66	0.42
9:A:1183:U:H2'	9:A:1184:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1238:G:O2'	9:A:1239:G:H5'	2.19	0.42
9:A:1465:G:H2'	9:A:1466:U:O4'	2.19	0.42
9:A:2071:A:H2'	9:A:2072:C:C6	2.54	0.42
9:A:2543:G:C6	9:A:2544:G:C6	3.08	0.42
9:A:2585:U:C5	9:A:2608:G:O6	2.73	0.42
9:A:2611:C:H5'	36:A:9000:ERY:H301	2.01	0.42
10:B:16:G:C5	10:B:69:G:C2	3.07	0.42
11:C:203:VAL:O	11:C:205:GLY:N	2.53	0.42
12:D:24:VAL:HA	12:D:191:GLY:H	1.85	0.42
12:D:117:GLY:C	12:D:118:PHE:CD2	2.98	0.42
13:E:42:GLY:O	13:E:43:THR:OG1	2.35	0.42
20:L:77:ILE:HD13	20:L:108:ALA:HB1	2.02	0.42
23:O:14:ALA:O	23:O:17:LYS:N	2.52	0.42
6:5:22:ALA:N	6:5:87:GLU:O	2.53	0.42
6:5:88:HIS:CB	6:5:89:PRO:CD	2.97	0.42
9:A:803:U:C4	9:A:804:A:N7	2.88	0.42
9:A:1026:G:H2'	9:A:1027:A:C8	2.55	0.42
9:A:1268:A:H2'	9:A:1269:A:O4'	2.20	0.42
9:A:1789:A:H2'	9:A:1790:C:O4'	2.20	0.42
9:A:2506:U:C3'	9:A:2506:U:C6	3.02	0.42
9:A:2803:G:H2'	9:A:2804:U:H6	1.84	0.42
17:I:9:LYS:HB3	17:I:71:LYS:NZ	2.34	0.42
18:J:4:PHE:C	18:J:44:TYR:HE2	2.28	0.42
18:J:4:PHE:CD2	18:J:44:TYR:CE2	3.08	0.42
18:J:38:GLY:O	18:J:43:GLU:HB2	2.19	0.42
18:J:88:THR:HG22	18:J:91:GLU:CD	2.45	0.42
21:M:53:MET:CE	21:M:63:ILE:HG21	2.50	0.42
23:O:31:THR:HG22	23:O:34:HIS:N	2.33	0.42
23:O:117:PHE:CD1	23:O:117:PHE:C	2.98	0.42
24:P:58:PHE:HD1	24:P:75:THR:HG22	1.83	0.42
28:T:39:THR:O	28:T:40:LYS:C	2.63	0.42
9:A:653:U:H5	9:A:654:A:C2	2.38	0.42
9:A:2352:A:N1	31:W:30:VAL:HG21	2.35	0.42
9:A:2796:U:C4	9:A:2798:U:C5	3.08	0.42
12:D:35:THR:N	12:D:49:GLN:O	2.41	0.42
12:D:130:GLN:O	12:D:131:ASP:C	2.62	0.42
12:D:182:ALA:C	12:D:184:ARG:N	2.76	0.42
13:E:118:LEU:C	13:E:118:LEU:CD2	2.92	0.42
14:F:107:VAL:HG13	14:F:110:ILE:HD12	2.02	0.42
18:J:81:ILE:CG1	18:J:82:GLY:H	2.33	0.42
19:K:71:ARG:HB3	19:K:72:PRO:CD	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:L:40:SER:O	20:L:41:ARG:CB	2.67	0.42
23:O:75:GLY:HA3	23:O:109:ALA:HB3	2.00	0.42
29:U:84:PHE:O	29:U:85:ARG:HB3	2.19	0.42
31:W:39:GLN:HG2	31:W:41:GLY:N	2.34	0.42
32:X:52:ALA:O	32:X:53:LYS:CB	2.67	0.42
6:5:33:VAL:HB	6:5:36:ASP:OD1	2.20	0.41
6:5:46:ARG:C	6:5:48:ALA:H	2.26	0.41
9:A:75:G:H4'	33:Y:48:ARG:NH2	2.35	0.41
9:A:528:A:H2	9:A:2043:C:H5'	1.85	0.41
9:A:1194:A:C2'	9:A:1195:G:O5'	2.68	0.41
9:A:1298:C:C2	9:A:1643:G:N2	2.88	0.41
9:A:1414:C:O2	9:A:1588:G:N2	2.44	0.41
9:A:1486:U:H2'	9:A:1487:U:C6	2.55	0.41
9:A:1607:C:H42	9:A:1622:G:P	2.43	0.41
9:A:1770:G:C6	9:A:1983:G:C6	3.07	0.41
9:A:2755:C:O2'	9:A:2756:U:H2'	2.19	0.41
9:A:2869:G:C6	9:A:2870:C:C4	3.09	0.41
11:C:16:VAL:HB	11:C:203:VAL:HG12	2.02	0.41
14:F:28:PRO:HB2	14:F:168:LEU:HD22	2.02	0.41
16:H:14:SER:HG	16:H:17:ASP:CG	2.27	0.41
29:U:98:ASN:ND2	29:U:100:GLU:OE1	2.53	0.41
34:Z:2:LYS:C	34:Z:3:THR:HG23	2.45	0.41
34:Z:4:ILE:HD13	34:Z:44:ARG:NH1	2.34	0.41
9:A:45:G:H5'	9:A:46:G:H5'	2.02	0.41
9:A:485:C:C2	9:A:496:G:N2	2.88	0.41
9:A:518:G:H2'	9:A:519:U:C6	2.54	0.41
9:A:866:A:N7	9:A:914:G:C6	2.89	0.41
9:A:1591:A:H2'	9:A:1592:C:C6	2.55	0.41
9:A:1936:A:C2	9:A:1943:U:H5	2.38	0.41
9:A:1945:G:C6	9:A:1946:U:C4	3.09	0.41
9:A:2609:U:C3'	9:A:2610:C:C5'	2.98	0.41
9:A:2676:C:P	19:K:31:ARG:HH12	2.44	0.41
13:E:12:LEU:HD12	13:E:193:VAL:HG11	2.01	0.41
13:E:79:ARG:O	13:E:80:SER:C	2.63	0.41
13:E:129:PRO:HG3	13:E:156:ASN:OD1	2.21	0.41
13:E:134:LEU:CD2	13:E:161:ALA:HB2	2.50	0.41
15:G:166:GLU:C	15:G:166:GLU:OE2	2.63	0.41
31:W:60:ALA:CB	31:W:81:ILE:CD1	2.98	0.41
34:Z:13:ILE:HG22	34:Z:14:GLY:N	2.34	0.41
6:5:131:THR:HA	6:5:134:GLU:CG	2.50	0.41
9:A:685:A:C2	9:A:689:A:C6	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:1019:U:H3	9:A:1142:A:N6	2.17	0.41
9:A:1669:A:O2'	9:A:2549:G:OP1	2.36	0.41
9:A:1817:G:C2'	9:A:1818:U:H5'	2.51	0.41
9:A:2058:A:C6	9:A:2059:A:N6	2.88	0.41
9:A:2341:G:H2'	9:A:2342:C:C6	2.55	0.41
11:C:16:VAL:H	11:C:203:VAL:HG12	1.84	0.41
12:D:182:ALA:C	12:D:184:ARG:H	2.29	0.41
15:G:26:LYS:CG	15:G:27:GLY:N	2.83	0.41
28:T:34:VAL:O	28:T:34:VAL:HG22	2.20	0.41
28:T:70:HIS:HB3	28:T:73:ARG:O	2.19	0.41
31:W:24:ARG:HH11	31:W:65:LYS:HG2	1.85	0.41
6:5:51:TYR:CD1	6:5:52:MET:HG2	2.55	0.41
9:A:109:C:H4'	9:A:348:A:H4'	2.02	0.41
9:A:527:C:H4'	9:A:528:A:O5'	2.21	0.41
9:A:1747:U:H2'	9:A:1748:C:H6	1.85	0.41
9:A:1843:C:O2'	11:C:253:GLY:O	2.29	0.41
9:A:2201:G:C6	9:A:2202:U:C4	3.08	0.41
9:A:2259:U:H1'	9:A:2427:C:C2	2.56	0.41
9:A:2478:A:C2'	9:A:2479:U:H5'	2.51	0.41
9:A:2685:G:H1	9:A:2724:U:H3	1.68	0.41
11:C:77:VAL:HG23	11:C:77:VAL:O	2.20	0.41
15:G:31:GLU:O	15:G:33:THR:N	2.52	0.41
22:N:8:ARG:HB3	22:N:10:LEU:HD22	2.01	0.41
23:O:106:LEU:C	23:O:106:LEU:HD12	2.46	0.41
25:Q:82:LEU:HD12	25:Q:112:ALA:HB2	2.02	0.41
1:0:42:ILE:HD12	22:N:99:LYS:O	2.20	0.41
6:5:37:LYS:O	6:5:38:MET:C	2.63	0.41
9:A:179:C:C2	9:A:180:G:C8	3.08	0.41
9:A:959:A:H62	21:M:82:MET:HE1	1.84	0.41
9:A:1674:G:N2	9:A:1677:A:N1	2.69	0.41
9:A:2063:C:N4	9:A:2064:C:N4	2.69	0.41
9:A:2580:U:C5	9:A:2581:G:C6	3.08	0.41
9:A:2618:G:C6	9:A:2619:C:C4	3.09	0.41
13:E:79:ARG:HG2	13:E:80:SER:N	2.35	0.41
14:F:151:LEU:CD1	14:F:153:ILE:HG23	2.51	0.41
17:I:52:LEU:HB3	17:I:53:PRO:HD2	2.03	0.41
17:I:74:PRO:HG2	17:I:77:VAL:HB	2.01	0.41
18:J:4:PHE:HB3	18:J:44:TYR:CE2	2.55	0.41
18:J:29:ALA:O	18:J:30:THR:C	2.63	0.41
18:J:65:THR:HG22	18:J:68:LYS:NZ	2.36	0.41
26:R:61:ALA:HB1	26:R:98:ILE:H	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:S:63:GLY:O	27:S:64:ALA:HB3	2.21	0.41
6:5:64:VAL:C	6:5:66:GLY:N	2.77	0.41
9:A:608:A:C8	9:A:621:A:N6	2.89	0.41
9:A:947:A:HO2'	9:A:984:A:H2	1.68	0.41
9:A:1020:A:C2	9:A:1141:U:C2	3.09	0.41
9:A:1381:G:H1'	9:A:1571:A:N1	2.36	0.41
9:A:1494:A:C6	9:A:1495:A:C5	3.08	0.41
9:A:1587:G:C4	9:A:1588:G:C8	3.09	0.41
9:A:1647:U:P	9:A:1647:U:H3'	2.60	0.41
9:A:1691:C:C4	9:A:1692:U:C4	3.08	0.41
9:A:1722:A:C2	9:A:1739:A:N3	2.89	0.41
9:A:1843:C:H5'	11:C:250:GLN:NE2	2.36	0.41
9:A:2063:C:H41	9:A:2064:C:N4	2.18	0.41
12:D:46:ARG:HB3	12:D:46:ARG:CZ	2.50	0.41
14:F:10:GLU:HG2	14:F:13:LYS:HD3	2.02	0.41
14:F:169:LEU:O	14:F:174:PHE:HB2	2.21	0.41
16:H:39:ALA:HB1	16:H:44:ILE:HG22	2.01	0.41
19:K:15:GLY:O	19:K:46:ALA:HA	2.20	0.41
20:L:29:LYS:HG2	20:L:30:THR:N	2.36	0.41
21:M:63:ILE:HG22	21:M:64:TRP:N	2.36	0.41
24:P:92:ARG:HH11	24:P:92:ARG:HB2	1.85	0.41
27:S:69:LEU:HG	27:S:107:VAL:HG22	2.03	0.41
27:S:88:ARG:HD2	27:S:94:ASP:OD2	2.20	0.41
30:V:6:ALA:HB1	30:V:40:ILE:CG2	2.50	0.41
31:W:19:ARG:HG2	31:W:19:ARG:HH21	1.86	0.41
6:5:108:VAL:HG12	6:5:109:LYS:N	2.35	0.41
9:A:58:G:N2	9:A:70:G:C4	2.89	0.41
9:A:301:G:H2'	9:A:334:C:H2'	2.01	0.41
9:A:996:A:C6	9:A:1160:G:C2	3.08	0.41
9:A:1044:C:O2'	9:A:1111:A:N1	2.42	0.41
9:A:1069:A:C2'	9:A:1070:A:OP2	2.68	0.41
9:A:1301:A:N3	9:A:1301:A:H2'	2.35	0.41
9:A:1392:A:C6	9:A:1393:A:C6	3.09	0.41
9:A:1494:A:C6	9:A:1495:A:C6	3.08	0.41
9:A:1868:C:O2	9:A:1873:G:N2	2.44	0.41
9:A:2298:A:C6	9:A:2321:U:C4	3.09	0.41
9:A:2409:G:H2'	9:A:2410:G:O4'	2.20	0.41
13:E:109:LEU:O	13:E:112:LEU:N	2.54	0.41
13:E:149:ILE:HD12	13:E:188:MET:HE3	2.03	0.41
18:J:35:ARG:HG2	18:J:40:HIS:HD2	1.85	0.41
18:J:88:THR:HG23	18:J:91:GLU:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:N:24:MET:CE	22:N:36:THR:HG21	2.51	0.41
22:N:87:PHE:O	22:N:89:SER:N	2.54	0.41
23:O:49:VAL:HG12	23:O:50:ALA:N	2.35	0.41
34:Z:2:LYS:CB	34:Z:39:ASP:HB3	2.51	0.41
6:5:131:THR:HA	6:5:134:GLU:HG3	2.03	0.41
9:A:535:G:C6	9:A:559:G:C6	3.09	0.41
9:A:1069:A:N3	9:A:1073:A:C6	2.88	0.41
9:A:1403:A:C2	9:A:1404:C:C2	3.09	0.41
9:A:1509:A:H1'	9:A:1510:G:O5'	2.20	0.41
9:A:1714:U:H5'	9:A:1715:G:H5'	2.02	0.41
9:A:2070:A:C2	9:A:2071:A:C4	3.09	0.41
9:A:2180:U:N3	9:A:2181:U:C5	2.89	0.41
9:A:2601:C:C2	9:A:2603:G:N7	2.89	0.41
9:A:2682:A:C8	12:D:11:MET:CG	3.04	0.41
17:I:104:GLN:O	17:I:105:LEU:CB	2.69	0.41
22:N:8:ARG:HB2	22:N:43:GLU:CD	2.46	0.41
22:N:51:LEU:HD21	22:N:70:THR:CG2	2.51	0.41
24:P:50:ARG:CD	24:P:56:SER:HB3	2.51	0.41
26:R:38:VAL:O	26:R:53:PHE:HA	2.20	0.41
27:S:18:ARG:HG3	27:S:76:VAL:CG1	2.50	0.41
31:W:55:ASP:O	31:W:55:ASP:CG	2.63	0.41
33:Y:12:GLU:O	33:Y:15:ASN:HB2	2.21	0.41
1:O:12:ARG:HD2	1:O:16:ARG:NH2	2.36	0.41
3:2:9:VAL:O	3:2:10:LEU:C	2.64	0.41
5:4:32:LYS:HD3	9:A:2478:A:H5'	2.02	0.41
6:5:47:GLU:CG	6:5:95:LEU:HD21	2.51	0.41
6:5:59:LEU:HD23	6:5:62:ARG:HE	1.85	0.41
6:5:127:ALA:C	6:5:129:LEU:N	2.79	0.41
9:A:138:U:H5'	9:A:139:U:C5'	2.51	0.41
9:A:307:G:N2	9:A:310:A:C8	2.89	0.41
9:A:659:G:H4'	13:E:95:LYS:HD3	2.02	0.41
9:A:749:A:C5	9:A:1618:A:C2	3.09	0.41
9:A:1063:G:H2'	9:A:1064:C:O4'	2.20	0.41
9:A:1068:G:H3'	9:A:1069:A:H5''	2.03	0.41
9:A:1078:U:H5''	9:A:1079:C:OP1	2.20	0.41
9:A:1378:A:H4'	9:A:1379:U:OP1	2.20	0.41
9:A:2017:U:H5''	9:A:2018:G:P	2.61	0.41
9:A:2038:G:H2'	9:A:2039:U:O4'	2.21	0.41
9:A:2103:C:N4	9:A:2186:G:H1	2.19	0.41
9:A:2145:C:N3	9:A:2146:C:N3	2.69	0.41
9:A:2674:G:H4'	19:K:30:ARG:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:114:C:H1'	23:O:47:VAL:HG11	2.03	0.41
11:C:143:VAL:HB	11:C:153:LEU:HB2	2.02	0.41
14:F:46:LYS:H	14:F:46:LYS:HD3	1.86	0.41
15:G:68:ARG:HH21	15:G:72:ASN:ND2	2.19	0.41
17:I:52:LEU:HB3	17:I:53:PRO:CD	2.51	0.41
18:J:20:ALA:O	18:J:21:THR:C	2.63	0.41
19:K:71:ARG:O	19:K:72:PRO:O	2.39	0.41
22:N:12:ARG:HB3	22:N:16:HIS:HB3	2.01	0.41
23:O:75:GLY:HA3	23:O:106:LEU:HA	2.03	0.41
24:P:64:SER:O	24:P:65:ASN:C	2.64	0.41
26:R:80:ARG:O	26:R:81:LYS:HD3	2.20	0.41
30:V:2:PHE:HB3	30:V:50:MET:HE3	2.03	0.41
31:W:19:ARG:NH2	31:W:22:VAL:CG2	2.83	0.41
31:W:41:GLY:O	31:W:42:THR:C	2.61	0.41
33:Y:2:LYS:N	33:Y:2:LYS:HD2	2.36	0.41
33:Y:14:LEU:C	33:Y:17:GLU:HB3	2.46	0.41
6:5:88:HIS:HB3	6:5:89:PRO:HD3	2.03	0.41
9:A:301:G:C6	9:A:317:G:C6	3.09	0.41
9:A:629:G:H4'	9:A:650:C:O2	2.21	0.41
9:A:2785:C:O2'	12:D:67:HIS:ND1	2.52	0.41
9:A:2845:U:H5''	24:P:51:ASN:O	2.20	0.41
12:D:104:VAL:HG12	12:D:106:LYS:H	1.86	0.41
14:F:148:VAL:HG23	14:F:149:ARG:N	2.36	0.41
15:G:19:ASN:O	15:G:22:VAL:HG22	2.21	0.41
16:H:24:GLY:O	16:H:28:ASN:HB2	2.21	0.41
17:I:91:LYS:O	17:I:92:PRO:C	2.64	0.41
17:I:116:MET:CB	17:I:124:MET:HE3	2.50	0.41
19:K:19:VAL:HG13	19:K:41:ILE:HG12	2.02	0.41
25:Q:46:TYR:CZ	25:Q:50:ARG:NH2	2.89	0.41
31:W:22:VAL:O	31:W:23:LYS:HG3	2.21	0.41
6:5:23:LEU:HD22	6:5:92:ALA:O	2.21	0.40
6:5:110:ALA:C	6:5:113:PHE:H	2.27	0.40
6:5:111:ALA:C	6:5:113:PHE:N	2.75	0.40
9:A:176:A:N7	9:A:177:G:C6	2.89	0.40
9:A:635:C:P	20:L:126:ARG:HH11	2.44	0.40
9:A:783:A:C8	9:A:784:G:H4'	2.56	0.40
9:A:996:A:C5	9:A:1160:G:N2	2.89	0.40
9:A:1245:G:OP1	20:L:13:LYS:NZ	2.46	0.40
9:A:2868:A:C2	9:A:2869:G:C4	3.09	0.40
11:C:158:GLY:H	11:C:194:VAL:HG22	1.86	0.40
11:C:184:GLU:O	11:C:185:ALA:HB3	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D:46:ARG:HH21	12:D:86:GLU:H	1.69	0.40
17:I:19:PRO:HG2	17:I:24:GLY:H	1.86	0.40
23:O:7:ARG:HA	23:O:10:ARG:NH2	2.36	0.40
24:P:30:TRP:CE3	24:P:39:LEU:HD12	2.56	0.40
25:Q:105:PHE:O	25:Q:106:THR:C	2.64	0.40
31:W:39:GLN:OE1	31:W:43:LYS:HB2	2.21	0.40
31:W:67:LYS:O	31:W:68:PHE:HB2	2.20	0.40
9:A:84:A:P	29:U:5:ARG:HH22	2.42	0.40
9:A:580:U:O3'	25:Q:30:VAL:CG1	2.70	0.40
9:A:1579:A:H2'	9:A:1580:A:C8	2.56	0.40
9:A:1613:G:O6	9:A:1617:C:H2'	2.21	0.40
9:A:1905:C:N4	9:A:1930:G:C2	2.89	0.40
9:A:2392:A:C2	20:L:55:MET:HE3	2.56	0.40
9:A:2646:C:OP2	9:A:2732:G:O2'	2.36	0.40
9:A:2766:A:N3	9:A:2766:A:H2'	2.36	0.40
11:C:172:THR:HG22	11:C:182:LYS:HG2	2.02	0.40
12:D:68:PHE:CE2	12:D:75:ALA:HB1	2.56	0.40
21:M:64:TRP:HZ3	21:M:106:ASP:HB2	1.86	0.40
28:T:35:ALA:C	28:T:36:LYS:HG2	2.46	0.40
32:X:67:LEU:HD22	32:X:77:TYR:CZ	2.57	0.40
3:2:9:VAL:HG13	9:A:1309:G:OP1	2.21	0.40
5:4:38:GLY:OXT	9:A:1124:G:H1'	2.21	0.40
9:A:230:G:N2	9:A:231:A:C4	2.90	0.40
9:A:364:C:H2'	9:A:365:U:H6	1.87	0.40
9:A:544:C:N4	9:A:548:G:OP1	2.45	0.40
9:A:811:U:H2'	20:L:21:ARG:HA	2.04	0.40
9:A:1773:A:N7	9:A:1829:A:C1'	2.85	0.40
9:A:2347:C:H2'	9:A:2348:U:C6	2.56	0.40
10:B:77:U:OP1	30:V:21:ARG:NH1	2.54	0.40
11:C:254:LYS:O	11:C:256:THR:N	2.51	0.40
14:F:148:VAL:HG23	14:F:149:ARG:H	1.87	0.40
17:I:100:ILE:CD1	17:I:137:LEU:HD12	2.51	0.40
20:L:127:VAL:HG11	20:L:142:ILE:HG21	2.03	0.40
29:U:82:VAL:HG13	29:U:93:ARG:HB3	2.03	0.40
1:0:24:VAL:C	1:0:26:SER:H	2.29	0.40
1:0:33:SER:OG	1:0:35:GLU:HG3	2.21	0.40
2:1:35:LEU:HD22	2:1:35:LEU:N	2.37	0.40
4:3:30:HIS:ND1	4:3:31:ILE:HG23	2.37	0.40
9:A:136:G:H1	9:A:143:C:H42	1.69	0.40
9:A:347:A:C2	9:A:348:A:C4	3.09	0.40
9:A:669:G:N3	9:A:669:G:C2'	2.83	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:726:G:O2'	9:A:727:A:OP2	2.37	0.40
9:A:1096:A:N6	9:A:1097:U:C4	2.89	0.40
9:A:1149:G:H2'	9:A:1150:C:C6	2.57	0.40
9:A:1365:A:OP1	32:X:2:ARG:NE	2.48	0.40
9:A:1967:C:H2'	9:A:1968:G:H5'	2.03	0.40
9:A:2318:G:C5	9:A:2319:G:C6	3.10	0.40
9:A:2469:A:C6	9:A:2482:A:C8	3.10	0.40
9:A:2555:U:C5	9:A:2556:C:C2	3.09	0.40
36:A:9000:ERY:H343	36:A:9000:ERY:O13	2.21	0.40
12:D:106:LYS:HB3	12:D:206:ALA:CB	2.52	0.40
14:F:111:ARG:HA	14:F:111:ARG:CZ	2.51	0.40
15:G:137:LYS:HA	15:G:140:ILE:HG22	2.02	0.40
17:I:11:GLN:OE1	17:I:11:GLN:N	2.43	0.40
19:K:39:ILE:HD12	19:K:41:ILE:HD11	2.02	0.40
20:L:57:LEU:C	20:L:59:ARG:H	2.30	0.40
24:P:3:ILE:C	24:P:4:ILE:O	2.60	0.40
6:5:34:THR:O	6:5:38:MET:HG3	2.22	0.40
6:5:132:TYR:HE1	7:6:19:VAL:HG13	1.85	0.40
9:A:45:G:C5'	9:A:46:G:H5'	2.51	0.40
9:A:528:A:H2	9:A:2043:C:C5'	2.34	0.40
9:A:841:G:C2	9:A:938:G:C2	3.10	0.40
9:A:1847:A:H4'	9:A:1848:A:OP2	2.21	0.40
9:A:1864:U:O3'	9:A:2409:G:N2	2.54	0.40
9:A:2134:A:H2'	9:A:2135:A:H8	1.85	0.40
9:A:2514:U:H2'	9:A:2515:C:C6	2.57	0.40
9:A:2537:U:C4	9:A:2538:C:N4	2.89	0.40
9:A:2681:C:C2	9:A:2724:U:O4	2.74	0.40
9:A:2684:U:C4	9:A:2685:G:N7	2.90	0.40
11:C:115:ILE:HG22	11:C:116:GLN:N	2.36	0.40
12:D:88:GLU:O	12:D:89:GLU:HG3	2.21	0.40
13:E:178:VAL:HG23	13:E:179:SER:N	2.36	0.40
14:F:112:ASP:N	14:F:112:ASP:OD1	2.54	0.40
14:F:114:ARG:N	14:F:114:ARG:HD2	2.37	0.40
17:I:14:ALA:HB1	17:I:45:THR:CG2	2.52	0.40
18:J:4:PHE:C	18:J:44:TYR:CE2	3.00	0.40
18:J:26:GLY:HA2	18:J:29:ALA:HB3	2.02	0.40
18:J:132:HIS:O	18:J:133:ALA:C	2.65	0.40
19:K:76:VAL:HG12	19:K:77:ILE:N	2.37	0.40
29:U:12:VAL:HG21	29:U:38:ILE:CD1	2.52	0.40
31:W:19:ARG:HG2	31:W:19:ARG:NH2	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/57 (95%)	43 (80%)	7 (13%)	4 (7%)	1	12
2	1	48/55 (87%)	42 (88%)	3 (6%)	3 (6%)	1	15
3	2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
4	3	62/65 (95%)	53 (86%)	7 (11%)	2 (3%)	3	25
5	4	36/38 (95%)	29 (81%)	4 (11%)	3 (8%)	0	10
6	5	146/165 (88%)	77 (53%)	40 (27%)	29 (20%)	0	1
7	6	28/121 (23%)	20 (71%)	7 (25%)	1 (4%)	2	23
11	C	269/273 (98%)	211 (78%)	43 (16%)	15 (6%)	1	16
12	D	207/209 (99%)	163 (79%)	30 (14%)	14 (7%)	1	14
13	E	199/201 (99%)	162 (81%)	27 (14%)	10 (5%)	1	18
14	F	175/179 (98%)	141 (81%)	30 (17%)	4 (2%)	5	30
15	G	174/177 (98%)	127 (73%)	30 (17%)	17 (10%)	0	8
16	H	48/149 (32%)	29 (60%)	14 (29%)	5 (10%)	0	7
17	I	139/142 (98%)	97 (70%)	33 (24%)	9 (6%)	1	15
18	J	140/142 (99%)	113 (81%)	18 (13%)	9 (6%)	1	15
19	K	120/123 (98%)	95 (79%)	15 (12%)	10 (8%)	0	10
20	L	141/144 (98%)	104 (74%)	32 (23%)	5 (4%)	3	23
21	M	134/136 (98%)	107 (80%)	16 (12%)	11 (8%)	0	11
22	N	118/127 (93%)	101 (86%)	16 (14%)	1 (1%)	16	50
23	O	114/117 (97%)	95 (83%)	18 (16%)	1 (1%)	14	47
24	P	112/115 (97%)	86 (77%)	17 (15%)	9 (8%)	1	11
25	Q	115/118 (98%)	99 (86%)	12 (10%)	4 (4%)	3	23
26	R	101/103 (98%)	83 (82%)	15 (15%)	3 (3%)	3	26
27	S	108/110 (98%)	94 (87%)	9 (8%)	5 (5%)	2	19
28	T	91/100 (91%)	57 (63%)	24 (26%)	10 (11%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	U	100/104 (96%)	74 (74%)	16 (16%)	10 (10%)	0	7
30	V	92/94 (98%)	81 (88%)	11 (12%)	0	100	100
31	W	77/85 (91%)	39 (51%)	22 (29%)	16 (21%)	0	1
32	X	75/78 (96%)	64 (85%)	8 (11%)	3 (4%)	2	21
33	Y	61/63 (97%)	39 (64%)	18 (30%)	4 (7%)	1	14
34	Z	56/59 (95%)	46 (82%)	8 (14%)	2 (4%)	2	23
35	a	1/19 (5%)	1 (100%)	0	0	100	100
All	All	3385/3714 (91%)	2613 (77%)	553 (16%)	219 (6%)	2	15

All (219) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	23	ALA
4	3	22	LYS
5	4	8	LYS
6	5	27	VAL
6	5	48	ALA
6	5	54	VAL
6	5	55	VAL
6	5	58	THR
6	5	69	PHE
6	5	93	ALA
6	5	107	GLU
6	5	108	VAL
6	5	120	ALA
6	5	124	ASP
6	5	130	PRO
11	C	70	LYS
11	C	104	LEU
11	C	121	ALA
11	C	140	VAL
12	D	43	ASP
12	D	73	VAL
12	D	170	VAL
13	E	79	ARG
14	F	111	ARG
15	G	2	ARG
15	G	16	VAL
15	G	28	LYS
15	G	31	GLU

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Mol	Chain	Res	Type
15	G	84	LYS
15	G	164	ALA
15	G	168	VAL
16	H	3	VAL
18	J	13	ARG
18	J	21	THR
18	J	44	TYR
18	J	45	THR
18	J	81	ILE
18	J	125	TYR
20	L	66	PHE
21	M	14	LYS
21	M	77	PRO
22	N	119	SER
24	P	50	ARG
24	P	51	ASN
24	P	93	LYS
27	S	3	THR
27	S	14	ALA
27	S	64	ALA
28	T	27	SER
28	T	29	THR
28	T	40	LYS
29	U	6	ARG
29	U	87	GLU
29	U	92	VAL
29	U	98	ASN
29	U	99	SER
31	W	9	THR
31	W	18	LYS
31	W	29	SER
31	W	36	ILE
31	W	56	HIS
34	Z	9	THR
1	0	35	GLU
2	1	4	ILE
2	1	50	GLU
6	5	3	LEU
6	5	33	VAL
6	5	88	HIS
6	5	92	ALA
6	5	116	GLU

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Mol	Chain	Res	Type
6	5	119	PRO
11	C	37	SER
11	C	77	VAL
11	C	238	ASN
11	C	256	THR
12	D	92	VAL
12	D	99	GLU
12	D	107	VAL
12	D	118	PHE
14	F	135	ILE
14	F	176	PHE
15	G	169	ARG
16	H	9	VAL
16	H	16	GLY
17	I	20	SER
17	I	79	LEU
18	J	111	LYS
19	K	35	VAL
19	K	71	ARG
20	L	111	ILE
21	M	2	LEU
21	M	36	VAL
21	M	56	ALA
26	R	65	ALA
27	S	19	LEU
27	S	96	ILE
28	T	36	LYS
28	T	49	LYS
29	U	51	LEU
31	W	14	ASP
31	W	47	GLY
31	W	50	VAL
31	W	74	LYS
33	Y	37	LEU
2	1	51	ALA
5	4	4	ARG
6	5	5	LEU
6	5	78	GLY
6	5	118	ILE
7	6	14	MET
11	C	110	LYS
12	D	95	SER

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Mol	Chain	Res	Type
12	D	109	VAL
12	D	192	ALA
13	E	7	ASP
13	E	70	SER
13	E	123	LYS
15	G	32	LEU
15	G	117	PRO
15	G	170	THR
16	H	10	ALA
17	I	11	GLN
18	J	74	TYR
19	K	13	ASN
19	K	46	ALA
19	K	93	GLN
21	M	69	PRO
23	O	3	LYS
24	P	113	LEU
26	R	98	ILE
29	U	85	ARG
29	U	101	THR
31	W	34	SER
32	X	17	ARG
32	X	34	SER
34	Z	34	THR
1	0	54	ILE
5	4	16	ILE
6	5	89	PRO
11	C	59	GLN
11	C	197	ALA
12	D	169	ARG
12	D	175	LEU
14	F	132	ARG
15	G	33	THR
15	G	173	ALA
17	I	64	ARG
19	K	119	ALA
20	L	29	LYS
21	M	23	GLY
21	M	134	THR
24	P	4	ILE
24	P	92	ARG
24	P	103	THR

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Mol	Chain	Res	Type
25	Q	87	VAL
25	Q	88	GLU
25	Q	95	ALA
28	T	28	ASN
28	T	51	PHE
28	T	55	VAL
31	W	37	VAL
32	X	76	LYS
33	Y	7	ARG
6	5	36	ASP
6	5	72	LEU
6	5	128	THR
11	C	64	VAL
11	C	120	ASP
11	C	196	ASN
12	D	183	GLU
13	E	46	GLN
13	E	96	VAL
15	G	97	VAL
15	G	163	TYR
15	G	166	GLU
17	I	12	VAL
17	I	71	LYS
18	J	65	THR
19	K	49	ARG
19	K	108	ARG
20	L	5	THR
20	L	41	ARG
21	M	35	ALA
21	M	73	ILE
24	P	34	GLY
25	Q	85	ALA
28	T	86	THR
28	T	89	GLU
29	U	88	ASP
31	W	46	ALA
31	W	76	ARG
33	Y	9	LYS
6	5	59	LEU
6	5	94	ARG
6	5	102	ALA
13	E	83	VAL

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Mol	Chain	Res	Type
13	E	153	LEU
15	G	118	ALA
16	H	14	SER
17	I	93	ASN
19	K	6	THR
19	K	50	GLY
21	M	13	HIS
26	R	40	MET
29	U	16	LYS
31	W	10	ARG
31	W	78	PHE
24	P	63	ILE
31	W	41	GLY
6	5	32	GLY
13	E	148	ILE
33	Y	62	GLY
4	3	6	VAL
11	C	232	GLY
12	D	122	VAL
17	I	22	PRO
17	I	88	GLY
1	0	24	VAL
13	E	71	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/48 (98%)	46 (98%)	1 (2%)	47	65
2	1	45/49 (92%)	42 (93%)	3 (7%)	15	41
3	2	38/38 (100%)	35 (92%)	3 (8%)	11	36
4	3	51/52 (98%)	45 (88%)	6 (12%)	5	21
5	4	34/34 (100%)	29 (85%)	5 (15%)	3	16
6	5	112/123 (91%)	93 (83%)	19 (17%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	6	26/85 (31%)	21 (81%)	5 (19%)	1	9
11	C	216/218 (99%)	199 (92%)	17 (8%)	11	36
12	D	164/164 (100%)	143 (87%)	21 (13%)	4	20
13	E	165/165 (100%)	146 (88%)	19 (12%)	5	22
14	F	148/150 (99%)	135 (91%)	13 (9%)	9	32
15	G	137/138 (99%)	122 (89%)	15 (11%)	6	24
16	H	40/114 (35%)	38 (95%)	2 (5%)	22	47
17	I	109/110 (99%)	106 (97%)	3 (3%)	38	59
18	J	116/116 (100%)	97 (84%)	19 (16%)	2	13
19	K	103/104 (99%)	88 (85%)	15 (15%)	3	16
20	L	102/103 (99%)	89 (87%)	13 (13%)	4	20
21	M	109/109 (100%)	93 (85%)	16 (15%)	3	16
22	N	100/103 (97%)	90 (90%)	10 (10%)	7	27
23	O	86/87 (99%)	78 (91%)	8 (9%)	8	30
24	P	99/100 (99%)	86 (87%)	13 (13%)	4	19
25	Q	89/90 (99%)	80 (90%)	9 (10%)	7	27
26	R	84/84 (100%)	74 (88%)	10 (12%)	5	21
27	S	93/93 (100%)	83 (89%)	10 (11%)	6	24
28	T	80/84 (95%)	75 (94%)	5 (6%)	16	42
29	U	83/85 (98%)	75 (90%)	8 (10%)	8	29
30	V	78/78 (100%)	73 (94%)	5 (6%)	16	42
31	W	59/63 (94%)	50 (85%)	9 (15%)	3	15
32	X	67/68 (98%)	59 (88%)	8 (12%)	5	21
33	Y	55/55 (100%)	51 (93%)	4 (7%)	13	39
34	Z	48/49 (98%)	38 (79%)	10 (21%)	1	7
35	a	4/18 (22%)	4 (100%)	0	100	100
All	All	2787/2977 (94%)	2483 (89%)	304 (11%)	8	24

All (304) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	24	VAL
2	1	8	ILE

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Mol	Chain	Res	Type
2	1	35	LEU
2	1	47	ILE
3	2	9	VAL
3	2	21	ARG
3	2	24	THR
4	3	15	LYS
4	3	29	ARG
4	3	30	HIS
4	3	31	ILE
4	3	49	VAL
4	3	56	LEU
5	4	4	ARG
5	4	15	LYS
5	4	16	ILE
5	4	26	ILE
5	4	27	CYS
6	5	1	MET
6	5	3	LEU
6	5	26	VAL
6	5	42	ARG
6	5	43	LYS
6	5	51	TYR
6	5	54	VAL
6	5	59	LEU
6	5	65	GLU
6	5	69	PHE
6	5	70	GLU
6	5	96	PHE
6	5	106	PHE
6	5	107	GLU
6	5	116	GLU
6	5	121	SER
6	5	125	ARG
6	5	130	PRO
6	5	132	TYR
7	6	17	MET
7	6	18	ASP
7	6	20	VAL
7	6	24	SER
7	6	26	MET
11	C	50	THR
11	C	51	ARG

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Mol	Chain	Res	Type
11	C	70	LYS
11	C	93	VAL
11	C	103	ILE
11	C	109	LEU
11	C	117	SER
11	C	124	LYS
11	C	129	LEU
11	C	142	ASN
11	C	152	GLN
11	C	155	ARG
11	C	166	ARG
11	C	176	ARG
11	C	194	VAL
11	C	251	THR
11	C	270	ARG
12	D	9	VAL
12	D	24	VAL
12	D	33	ARG
12	D	37	VAL
12	D	74	GLU
12	D	86	GLU
12	D	98	VAL
12	D	100	LEU
12	D	103	ASP
12	D	107	VAL
12	D	124	ARG
12	D	129	THR
12	D	159	LYS
12	D	170	VAL
12	D	171	THR
12	D	172	VAL
12	D	177	VAL
12	D	183	GLU
12	D	193	VAL
12	D	201	LEU
12	D	203	VAL
13	E	5	LEU
13	E	12	LEU
13	E	28	VAL
13	E	40	ARG
13	E	44	ARG
13	E	51	GLU

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Mol	Chain	Res	Type
13	E	65	THR
13	E	69	ARG
13	E	88	ARG
13	E	109	LEU
13	E	113	VAL
13	E	118	LEU
13	E	120	VAL
13	E	126	VAL
13	E	131	THR
13	E	147	LEU
13	E	149	ILE
13	E	167	VAL
13	E	171	ASP
14	F	3	LEU
14	F	9	ASP
14	F	16	MET
14	F	34	THR
14	F	35	LEU
14	F	41	GLU
14	F	46	LYS
14	F	56	LEU
14	F	90	LEU
14	F	94	ARG
14	F	114	ARG
14	F	131	VAL
14	F	154	THR
15	G	3	VAL
15	G	16	VAL
15	G	36	LEU
15	G	38	ASP
15	G	84	LYS
15	G	94	ARG
15	G	103	ASN
15	G	110	HIS
15	G	121	THR
15	G	126	THR
15	G	131	VAL
15	G	132	LEU
15	G	151	ARG
15	G	170	THR
15	G	176	LYS
16	H	3	VAL

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Mol	Chain	Res	Type
16	H	6	LEU
17	I	23	VAL
17	I	102	ARG
17	I	137	LEU
18	J	2	LYS
18	J	17	VAL
18	J	24	THR
18	J	25	LEU
18	J	30	THR
18	J	36	LEU
18	J	40	HIS
18	J	54	ILE
18	J	55	ILE
18	J	65	THR
18	J	72	LYS
18	J	73	VAL
18	J	95	ARG
18	J	103	ILE
18	J	105	VAL
18	J	123	LYS
18	J	129	GLU
18	J	131	ASN
18	J	140	LEU
19	K	3	GLN
19	K	8	LEU
19	K	13	ASN
19	K	18	ARG
19	K	19	VAL
19	K	23	LYS
19	K	38	ILE
19	K	41	ILE
19	K	47	ILE
19	K	54	LYS
19	K	61	VAL
19	K	73	ASP
19	K	93	GLN
19	K	105	ARG
19	K	110	GLU
20	L	5	THR
20	L	10	GLU
20	L	19	LEU
20	L	48	ARG

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Mol	Chain	Res	Type
20	L	67	THR
20	L	82	LEU
20	L	91	ASP
20	L	95	LEU
20	L	100	ILE
20	L	101	ILE
20	L	121	THR
20	L	122	VAL
20	L	127	VAL
21	M	12	MET
21	M	13	HIS
21	M	33	LEU
21	M	46	ILE
21	M	53	MET
21	M	72	PRO
21	M	76	LYS
21	M	81	ARG
21	M	88	ASN
21	M	95	LEU
21	M	96	ILE
21	M	100	LYS
21	M	110	GLU
21	M	115	GLU
21	M	126	ILE
21	M	134	THR
22	N	6	SER
22	N	8	ARG
22	N	33	ILE
22	N	51	LEU
22	N	65	LEU
22	N	69	ARG
22	N	70	THR
22	N	71	ARG
22	N	82	GLU
22	N	118	ARG
23	O	18	LEU
23	O	31	THR
23	O	33	ARG
23	O	36	TYR
23	O	38	GLN
23	O	47	VAL
23	O	106	LEU

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Mol	Chain	Res	Type
23	O	115	LEU
24	P	16	VAL
24	P	19	PHE
24	P	20	ARG
24	P	39	LEU
24	P	62	LYS
24	P	69	VAL
24	P	79	VAL
24	P	80	VAL
24	P	83	ILE
24	P	85	VAL
24	P	92	ARG
24	P	95	LYS
24	P	103	THR
25	Q	16	ILE
25	Q	17	LEU
25	Q	50	ARG
25	Q	55	GLN
25	Q	59	LEU
25	Q	63	ARG
25	Q	88	GLU
25	Q	93	ILE
25	Q	97	ILE
26	R	4	VAL
26	R	29	THR
26	R	38	VAL
26	R	40	MET
26	R	46	GLU
26	R	47	VAL
26	R	48	LYS
26	R	49	ILE
26	R	63	VAL
26	R	73	LYS
27	S	3	THR
27	S	4	ILE
27	S	33	LEU
27	S	36	LEU
27	S	45	VAL
27	S	66	ILE
27	S	71	VAL
27	S	76	VAL
27	S	96	ILE

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Mol	Chain	Res	Type
27	S	101	SER
28	T	32	LEU
28	T	34	VAL
28	T	43	ILE
28	T	58	VAL
28	T	67	VAL
29	U	6	ARG
29	U	30	SER
29	U	38	ILE
29	U	43	LYS
29	U	48	VAL
29	U	61	GLU
29	U	86	PHE
29	U	92	VAL
30	V	29	ILE
30	V	61	LEU
30	V	65	VAL
30	V	87	GLN
30	V	92	VAL
31	W	19	ARG
31	W	22	VAL
31	W	23	LYS
31	W	30	VAL
31	W	36	ILE
31	W	49	ASN
31	W	61	LYS
31	W	63	ASP
31	W	76	ARG
32	X	10	ARG
32	X	24	THR
32	X	26	ARG
32	X	29	LEU
32	X	34	SER
32	X	40	GLU
32	X	57	VAL
32	X	77	TYR
33	Y	10	SER
33	Y	16	THR
33	Y	21	LEU
33	Y	57	LEU
34	Z	2	LYS
34	Z	9	THR

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Mol	Chain	Res	Type
34	Z	15	ARG
34	Z	17	PRO
34	Z	23	LEU
34	Z	30	ARG
34	Z	31	ILE
34	Z	37	ARG
34	Z	40	THR
34	Z	56	VAL

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

Mol	Chain	Res	Type
4	3	30	HIS
5	4	13	ASN
5	4	37	GLN
11	C	36	ASN
11	C	52	HIS
11	C	59	GLN
12	D	49	GLN
12	D	173	GLN
14	F	4	HIS
15	G	87	GLN
16	H	18	GLN
16	H	33	GLN
18	J	80	HIS
19	K	5	GLN
19	K	93	GLN
21	M	22	GLN
23	O	116	GLN
24	P	55	HIS
24	P	76	HIS
25	Q	43	GLN
25	Q	80	ASN
26	R	82	HIS
27	S	102	HIS
30	V	24	ASN
30	V	80	HIS
33	Y	41	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	117/118 (99%)	17 (14%)	0
8	7	1/3 (33%)	0	0
9	A	2850/2903 (98%)	468 (16%)	43 (1%)
All	All	2968/3024 (98%)	485 (16%)	43 (1%)

All (485) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	10	A
9	A	12	U
9	A	15	G
9	A	34	U
9	A	35	G
9	A	42	A
9	A	43	G
9	A	45	G
9	A	46	G
9	A	51	G
9	A	61	C
9	A	71	A
9	A	74	A
9	A	75	G
9	A	80	G
9	A	82	U
9	A	84	A
9	A	96	C
9	A	101	A
9	A	118	A
9	A	119	A
9	A	120	U
9	A	131	A
9	A	135	U
9	A	136	G
9	A	137	U
9	A	138	U
9	A	139	U
9	A	140	C
9	A	141	G
9	A	142	A
9	A	144	A
9	A	149	A
9	A	162	U
9	A	163	C

Continued on next page...

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Mol	Chain	Res	Type
9	A	164	C
9	A	181	A
9	A	188	G
9	A	196	A
9	A	199	A
9	A	215	G
9	A	216	A
9	A	222	A
9	A	226	A
9	A	230	G
9	A	248	G
9	A	255	A
9	A	264	C
9	A	265	A
9	A	266	G
9	A	267	C
9	A	272	A
9	A	273	G
9	A	276	U
9	A	277	G
9	A	278	A
9	A	281	C
9	A	285	G
9	A	302	C
9	A	311	A
9	A	329	G
9	A	330	A
9	A	346	A
9	A	347	A
9	A	353	C
9	A	355	U
9	A	361	G
9	A	362	A
9	A	371	A
9	A	372	G
9	A	382	A
9	A	383	C
9	A	386	G
9	A	388	G
9	A	396	G
9	A	404	A
9	A	405	U

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Mol	Chain	Res	Type
9	A	411	G
9	A	412	A
9	A	424	G
9	A	451	U
9	A	455	C
9	A	481	G
9	A	491	G
9	A	503	A
9	A	504	A
9	A	505	A
9	A	509	C
9	A	528	A
9	A	531	C
9	A	532	A
9	A	533	G
9	A	538	A
9	A	543	G
9	A	544	C
9	A	546	U
9	A	547	A
9	A	548	G
9	A	549	G
9	A	563	A
9	A	573	U
9	A	575	A
9	A	586	A
9	A	603	A
9	A	604	G
9	A	613	A
9	A	614	A
9	A	615	U
9	A	627	A
9	A	631	A
9	A	637	A
9	A	645	C
9	A	646	U
9	A	647	G
9	A	648	G
9	A	654	A
9	A	655	A
9	A	656	G
9	A	686	U

Continued on next page...

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Mol	Chain	Res	Type
9	A	714	U
9	A	715	A
9	A	730	A
9	A	738	G
9	A	747	U
9	A	775	G
9	A	776	G
9	A	782	A
9	A	784	G
9	A	785	G
9	A	805	G
9	A	812	C
9	A	819	A
9	A	827	U
9	A	828	U
9	A	845	A
9	A	846	U
9	A	847	U
9	A	859	G
9	A	878	A
9	A	883	G
9	A	884	U
9	A	896	A
9	A	897	C
9	A	910	A
9	A	914	G
9	A	915	C
9	A	932	U
9	A	941	A
9	A	946	C
9	A	961	C
9	A	974	G
9	A	983	A
9	A	985	C
9	A	995	C
9	A	996	A
9	A	1003	G
9	A	1012	U
9	A	1013	C
9	A	1021	A
9	A	1022	G
9	A	1023	U

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Mol	Chain	Res	Type
9	A	1025	G
9	A	1026	G
9	A	1033	U
9	A	1045	C
9	A	1046	A
9	A	1047	G
9	A	1051	G
9	A	1053	C
9	A	1059	G
9	A	1060	U
9	A	1061	U
9	A	1062	G
9	A	1067	A
9	A	1069	A
9	A	1070	A
9	A	1072	C
9	A	1074	G
9	A	1078	U
9	A	1083	U
9	A	1084	A
9	A	1088	A
9	A	1089	A
9	A	1090	A
9	A	1091	G
9	A	1097	U
9	A	1098	A
9	A	1110	G
9	A	1111	A
9	A	1112	G
9	A	1129	A
9	A	1132	U
9	A	1133	A
9	A	1135	C
9	A	1136	G
9	A	1139	G
9	A	1142	A
9	A	1151	A
9	A	1155	A
9	A	1169	A
9	A	1170	C
9	A	1172	C
9	A	1174	U

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Mol	Chain	Res	Type
9	A	1175	A
9	A	1176	U
9	A	1180	U
9	A	1186	G
9	A	1238	G
9	A	1248	G
9	A	1250	G
9	A	1253	A
9	A	1256	G
9	A	1266	G
9	A	1268	A
9	A	1271	G
9	A	1272	A
9	A	1273	U
9	A	1281	G
9	A	1300	G
9	A	1301	A
9	A	1313	U
9	A	1317	G
9	A	1352	U
9	A	1365	A
9	A	1368	G
9	A	1378	A
9	A	1379	U
9	A	1383	A
9	A	1395	A
9	A	1415	U
9	A	1416	G
9	A	1419	A
9	A	1420	A
9	A	1428	C
9	A	1435	G
9	A	1452	G
9	A	1459	G
9	A	1482	G
9	A	1493	C
9	A	1504	A
9	A	1508	A
9	A	1510	G
9	A	1515	A
9	A	1524	G
9	A	1533	C

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Mol	Chain	Res	Type
9	A	1534	U
9	A	1535	A
9	A	1536	C
9	A	1566	A
9	A	1569	A
9	A	1578	U
9	A	1583	A
9	A	1584	U
9	A	1585	C
9	A	1607	C
9	A	1608	A
9	A	1610	A
9	A	1613	G
9	A	1627	G
9	A	1647	U
9	A	1648	U
9	A	1649	G
9	A	1652	A
9	A	1653	G
9	A	1674	G
9	A	1714	U
9	A	1715	G
9	A	1723	G
9	A	1729	U
9	A	1730	C
9	A	1737	G
9	A	1738	G
9	A	1739	A
9	A	1744	A
9	A	1758	U
9	A	1764	C
9	A	1773	A
9	A	1776	G
9	A	1791	A
9	A	1800	C
9	A	1801	A
9	A	1802	A
9	A	1808	A
9	A	1811	G
9	A	1816	C
9	A	1829	A
9	A	1833	C

Continued on next page...

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Mol	Chain	Res	Type
9	A	1847	A
9	A	1848	A
9	A	1858	A
9	A	1869	G
9	A	1870	C
9	A	1871	A
9	A	1872	A
9	A	1873	G
9	A	1884	G
9	A	1906	G
9	A	1913	A
9	A	1914	C
9	A	1927	A
9	A	1929	G
9	A	1930	G
9	A	1937	A
9	A	1938	A
9	A	1939	U
9	A	1940	U
9	A	1955	U
9	A	1960	A
9	A	1966	A
9	A	1967	C
9	A	1970	A
9	A	1971	U
9	A	1972	G
9	A	1991	U
9	A	1993	U
9	A	1997	C
9	A	2017	U
9	A	2020	A
9	A	2022	U
9	A	2023	C
9	A	2031	A
9	A	2033	A
9	A	2043	C
9	A	2055	C
9	A	2056	G
9	A	2060	A
9	A	2061	G
9	A	2063	C
9	A	2064	C

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Mol	Chain	Res	Type
9	A	2069	G
9	A	2072	C
9	A	2093	G
9	A	2104	C
9	A	2106	U
9	A	2107	G
9	A	2108	A
9	A	2109	U
9	A	2110	G
9	A	2134	A
9	A	2135	A
9	A	2137	U
9	A	2138	G
9	A	2139	U
9	A	2140	G
9	A	2142	A
9	A	2143	C
9	A	2144	G
9	A	2145	C
9	A	2146	C
9	A	2147	A
9	A	2148	G
9	A	2149	U
9	A	2150	C
9	A	2151	U
9	A	2153	C
9	A	2154	A
9	A	2155	U
9	A	2156	G
9	A	2157	G
9	A	2180	U
9	A	2183	A
9	A	2185	U
9	A	2194	U
9	A	2198	A
9	A	2199	A
9	A	2204	G
9	A	2211	A
9	A	2212	A
9	A	2214	C
9	A	2225	A
9	A	2226	C

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Mol	Chain	Res	Type
9	A	2238	G
9	A	2239	G
9	A	2250	G
9	A	2268	A
9	A	2278	A
9	A	2283	C
9	A	2284	A
9	A	2286	G
9	A	2287	A
9	A	2305	U
9	A	2308	G
9	A	2311	A
9	A	2322	A
9	A	2325	G
9	A	2327	A
9	A	2333	A
9	A	2336	A
9	A	2347	C
9	A	2354	C
9	A	2361	G
9	A	2383	G
9	A	2385	C
9	A	2402	U
9	A	2403	C
9	A	2406	A
9	A	2423	U
9	A	2424	C
9	A	2425	A
9	A	2429	G
9	A	2430	A
9	A	2435	A
9	A	2441	U
9	A	2448	A
9	A	2470	G
9	A	2476	A
9	A	2491	U
9	A	2502	G
9	A	2503	A
9	A	2504	U
9	A	2505	G
9	A	2506	U
9	A	2508	G

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Mol	Chain	Res	Type
9	A	2518	A
9	A	2529	G
9	A	2554	U
9	A	2556	C
9	A	2566	A
9	A	2567	G
9	A	2572	A
9	A	2573	C
9	A	2575	C
9	A	2576	G
9	A	2577	A
9	A	2583	G
9	A	2585	U
9	A	2586	U
9	A	2587	A
9	A	2601	C
9	A	2602	A
9	A	2608	G
9	A	2609	U
9	A	2610	C
9	A	2611	C
9	A	2613	U
9	A	2629	U
9	A	2663	G
9	A	2671	G
9	A	2681	C
9	A	2682	A
9	A	2689	U
9	A	2690	U
9	A	2714	G
9	A	2716	C
9	A	2726	A
9	A	2733	A
9	A	2744	G
9	A	2748	A
9	A	2757	A
9	A	2760	C
9	A	2765	A
9	A	2778	A
9	A	2791	G
9	A	2798	U
9	A	2800	A

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Mol	Chain	Res	Type
9	A	2801	G
9	A	2818	U
9	A	2820	A
9	A	2821	A
9	A	2861	U
9	A	2867	G
9	A	2873	A
9	A	2874	C
9	A	2883	A
9	A	2884	U
9	A	2885	G
9	A	2891	U
9	A	2903	U
10	B	3	C
10	B	15	A
10	B	16	G
10	B	21	G
10	B	30	C
10	B	35	C
10	B	42	C
10	B	44	G
10	B	45	A
10	B	56	G
10	B	84	G
10	B	87	U
10	B	88	C
10	B	89	U
10	B	90	C
10	B	99	A
10	B	109	A

All (43) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	119	A
9	A	271	G
9	A	277	G
9	A	301	G
9	A	403	U
9	A	404	A
9	A	503	A
9	A	527	C

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Mol	Chain	Res	Type
9	A	613	A
9	A	655	A
9	A	784	G
9	A	827	U
9	A	846	U
9	A	882	G
9	A	931	U
9	A	1020	A
9	A	1025	G
9	A	1069	A
9	A	1088	A
9	A	1110	G
9	A	1247	A
9	A	1378	A
9	A	1458	U
9	A	1509	A
9	A	1535	A
9	A	1626	A
9	A	1738	G
9	A	1757	A
9	A	1847	A
9	A	1870	C
9	A	1939	U
9	A	2108	A
9	A	2142	A
9	A	2211	A
9	A	2286	G
9	A	2326	C
9	A	2423	U
9	A	2503	A
9	A	2576	G
9	A	2601	C
9	A	2756	U
9	A	2873	A
9	A	2902	C

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	ERY	A	9000	-	53,53,53	0.81	1 (1%)	82,82,82	1.69	18 (21%)

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
36	ERY	A	9000	-	-	9/72/107/107	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	A	9000	ERY	C6-C5	2.41	1.59	1.55

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A	9000	ERY	C25-C24-C23	-5.07	102.73	110.02
36	A	9000	ERY	O7-C5-C6	-4.98	100.47	106.40
36	A	9000	ERY	O2-C1-O1	-3.72	117.24	123.95
36	A	9000	ERY	C3-C2-C1	-3.46	102.94	109.93
36	A	9000	ERY	C27-C26-C25	-3.18	108.46	113.27
36	A	9000	ERY	C32-C6-C7	-3.02	106.19	111.09
36	A	9000	ERY	O3-C14-C15	-2.80	104.31	108.99
36	A	9000	ERY	O6-C17-C18	-2.72	104.78	109.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A	9000	ERY	O3-C3-C2	-2.60	106.78	111.16
36	A	9000	ERY	O3-C3-C4	-2.59	105.19	108.23
36	A	9000	ERY	C19-C16-C17	2.55	116.20	111.19
36	A	9000	ERY	O11-C9-C8	-2.42	116.93	121.30
36	A	9000	ERY	C6-C7-C8	-2.42	110.78	115.61
36	A	9000	ERY	C32-C6-C5	2.37	114.17	110.13
36	A	9000	ERY	O2-C13-C12	-2.32	103.62	107.28
36	A	9000	ERY	C16-C17-C18	-2.28	107.80	111.12
36	A	9000	ERY	C8-C9-C10	2.16	122.79	119.13
36	A	9000	ERY	C15-C16-C17	-2.11	104.03	107.64

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	A	9000	ERY	C15-C16-O5-C20
36	A	9000	ERY	C19-C16-O5-C20
36	A	9000	ERY	C10-C11-C12-O13
36	A	9000	ERY	C25-C24-N1-C28
36	A	9000	ERY	C4-C5-C6-C32
36	A	9000	ERY	C17-C16-O5-C20
36	A	9000	ERY	O2-C13-C36-C37
36	A	9000	ERY	O12-C11-C12-O13
36	A	9000	ERY	O12-C11-C12-C13

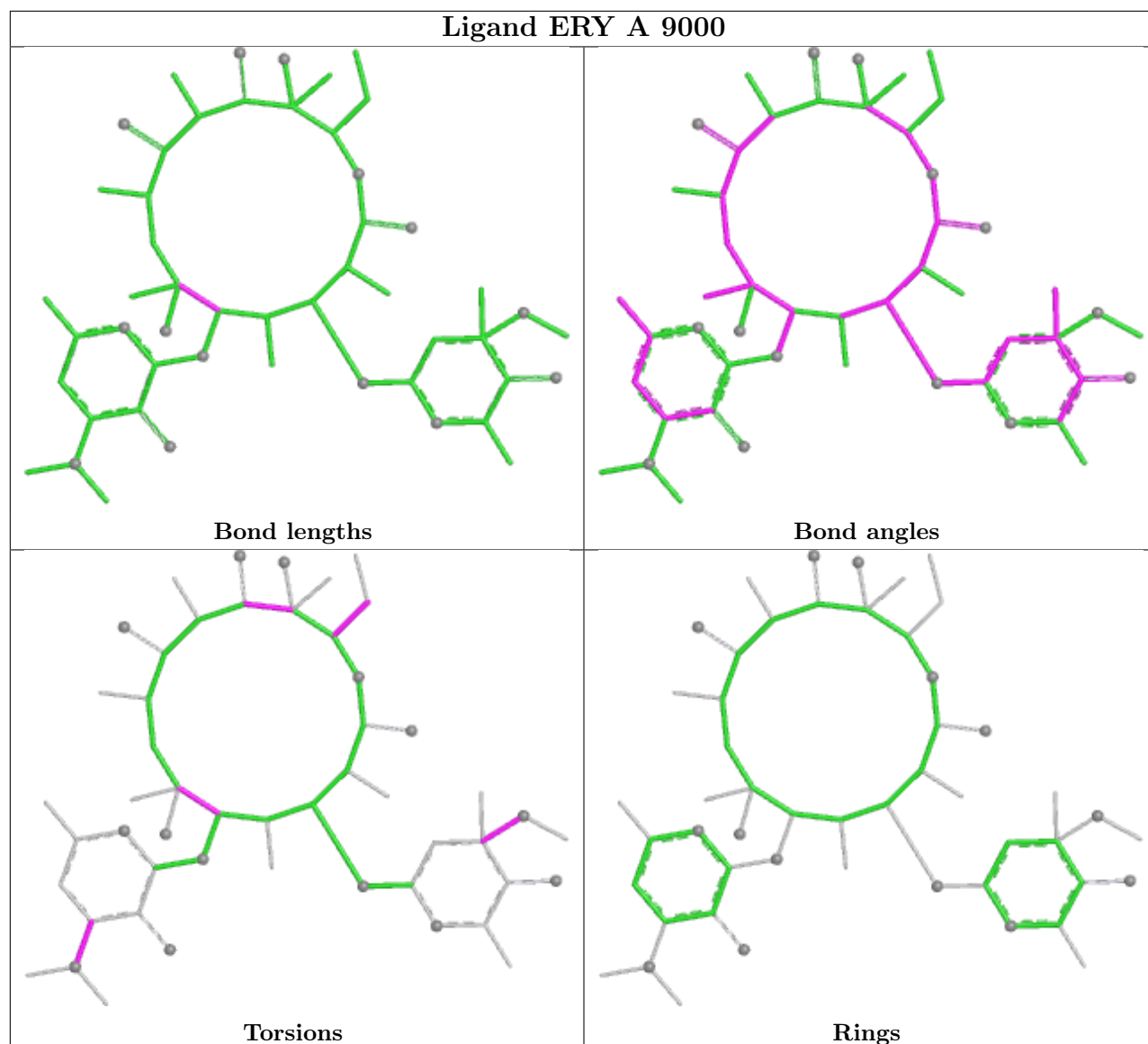
There are no ring outliers.

1 monomer is involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	A	9000	ERY	12	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

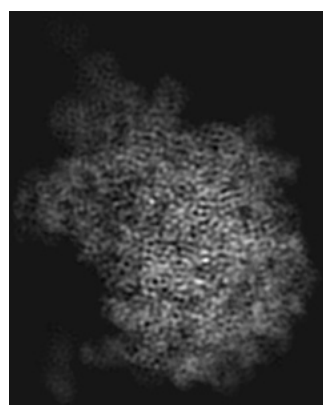
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6057. These allow visual inspection of the internal detail of the map and identification of artifacts.

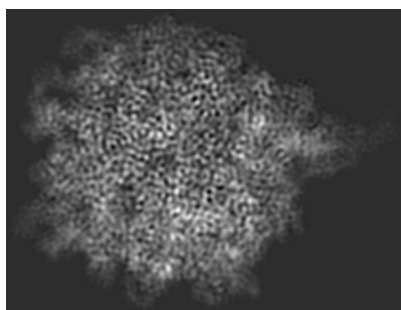
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

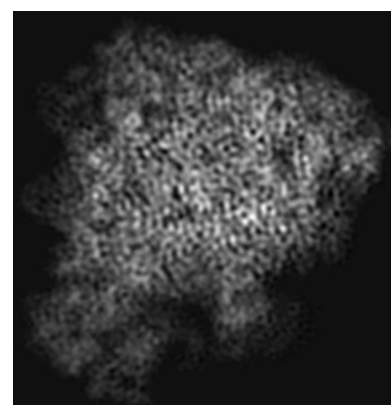
6.1.1 Primary map



X



Y

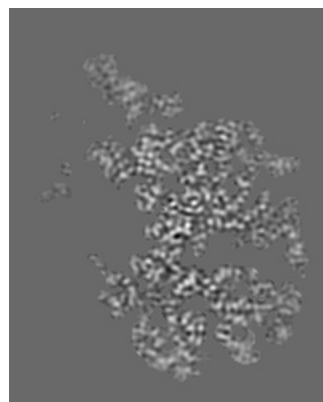


Z

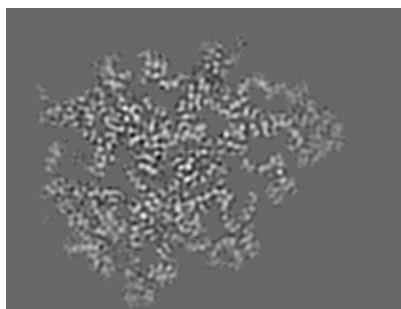
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

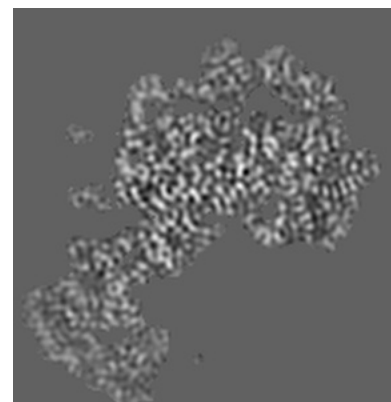
6.2.1 Primary map



X Index: 88



Y Index: 91

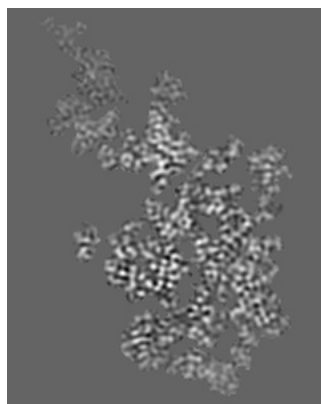


Z Index: 115

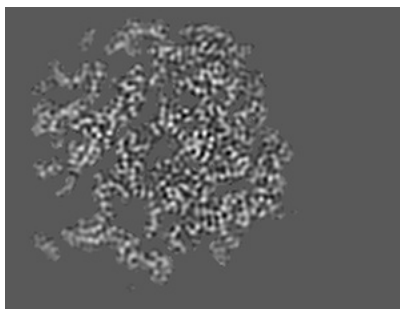
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

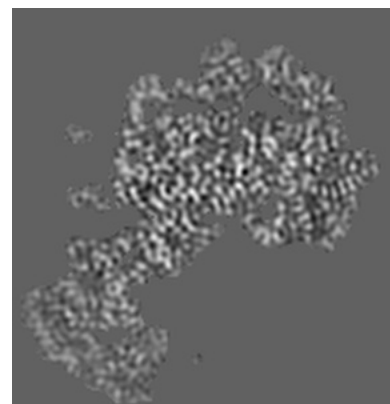
6.3.1 Primary map



X Index: 109



Y Index: 110

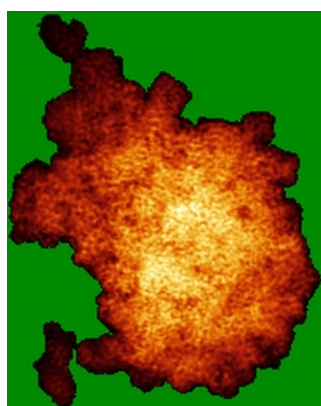


Z Index: 115

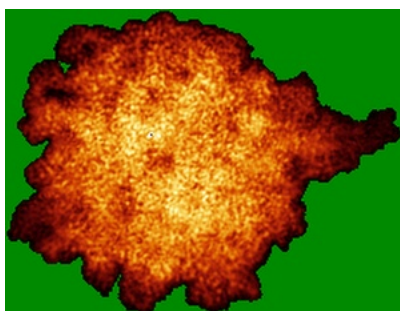
The images above show the largest variance slices of the map in three orthogonal directions.

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

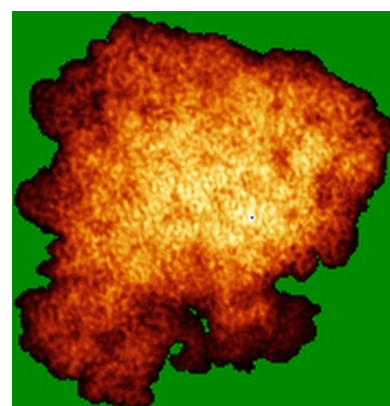
6.4.1 Primary map



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

This section was not generated.

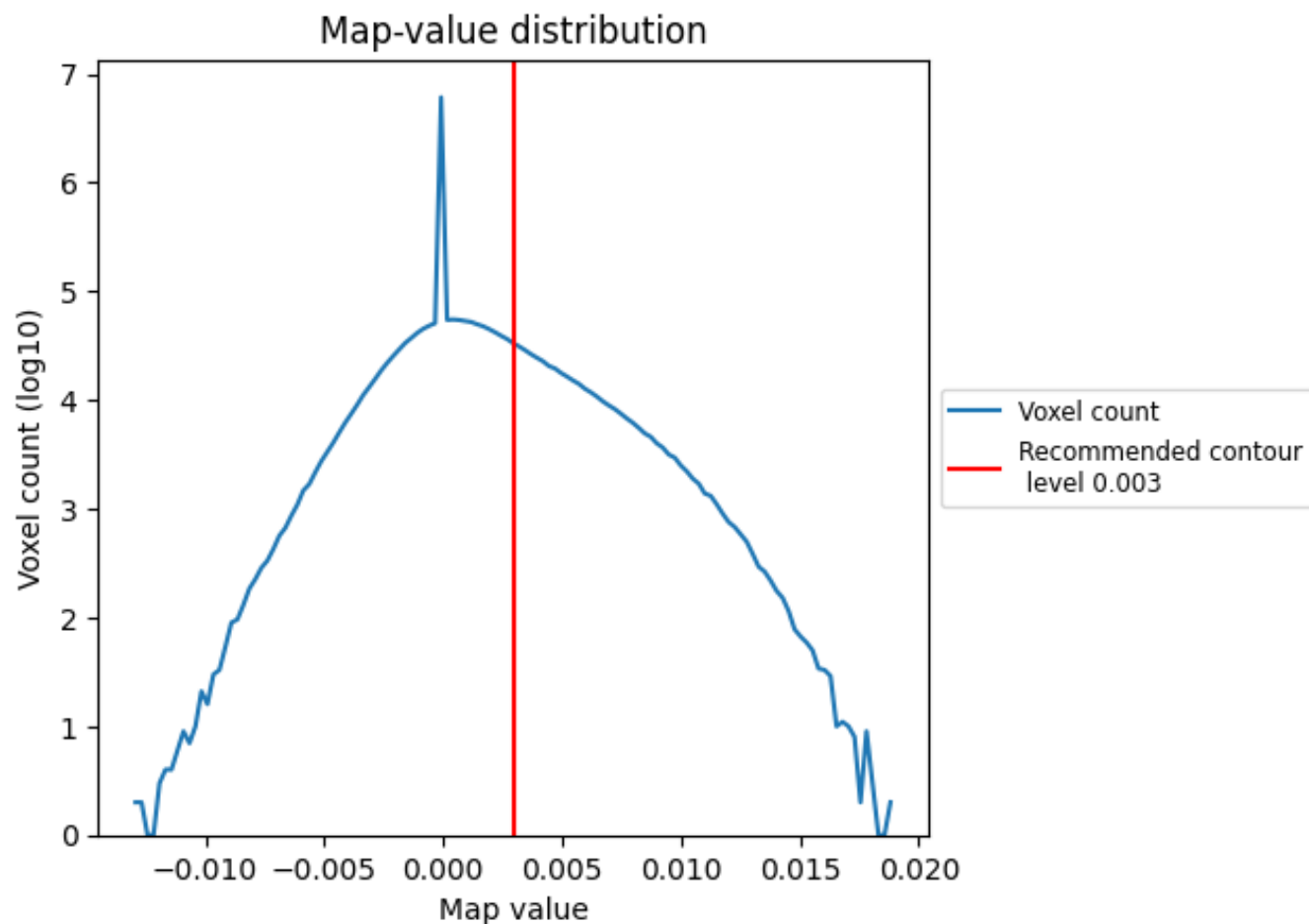
6.6 Mask visualisation

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

7 Map analysis [i](#)

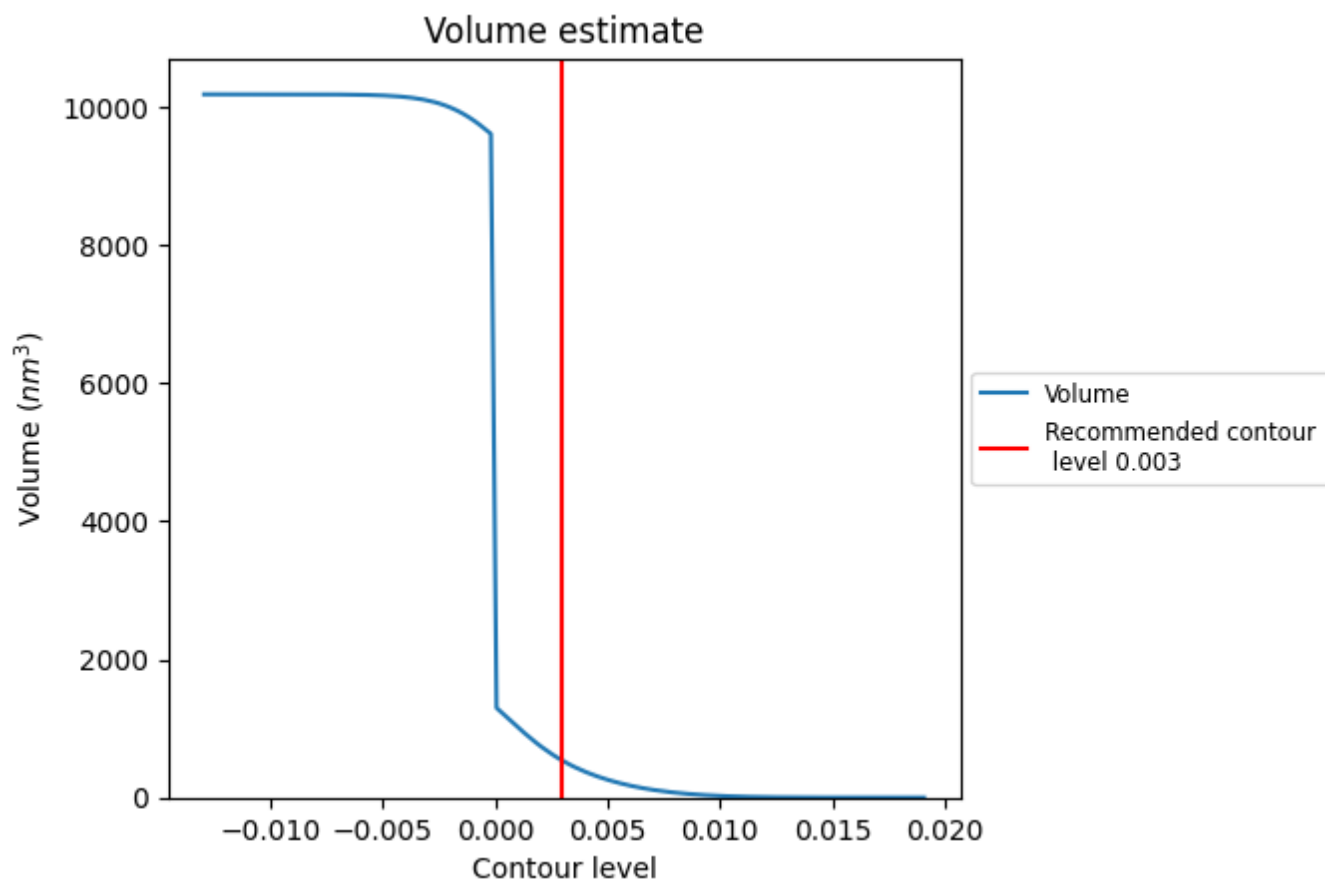
This section contains the results of statistical analysis of the map.

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 534 nm³; this corresponds to an approximate mass of 483 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 [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

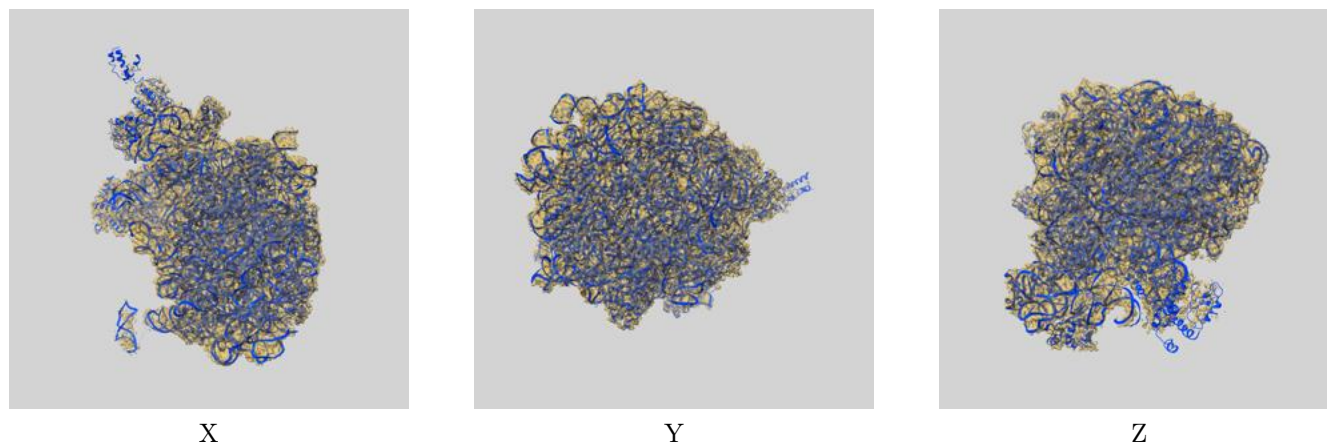
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

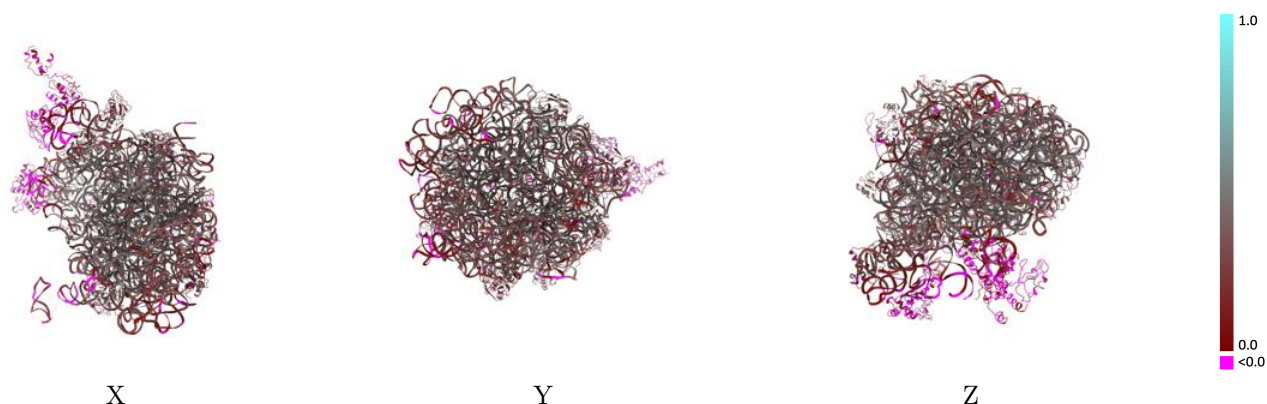
This section contains information regarding the fit between EMDB map EMD-6057 and PDB model 3J7Z. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.003 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](#)

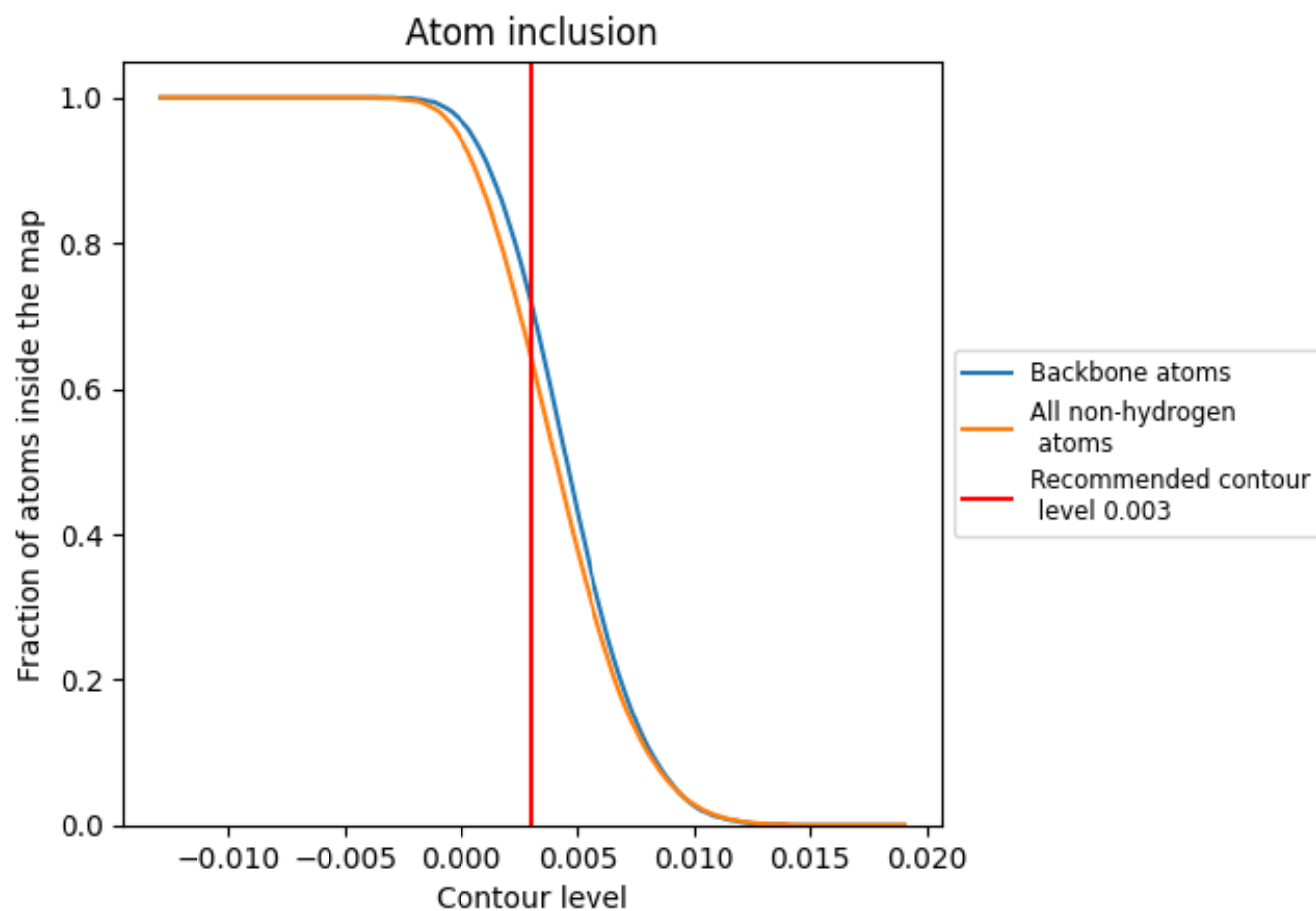


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 64% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6430	 0.3120
0	 0.5960	 0.3310
1	 0.1100	 0.1330
2	 0.6530	 0.3740
3	 0.6660	 0.4030
4	 0.6470	 0.3940
5	 0.0740	 0.0490
6	 0.0090	 0.0340
7	 0.8620	 0.4460
A	 0.7120	 0.3290
B	 0.5930	 0.2290
C	 0.6130	 0.3460
D	 0.5870	 0.3600
E	 0.5030	 0.2980
F	 0.1770	 -0.0030
G	 0.4430	 0.2540
H	 0.2770	 0.2090
I	 0.0550	 -0.0030
J	 0.5940	 0.3350
K	 0.5840	 0.3730
L	 0.5350	 0.3210
M	 0.6050	 0.3730
N	 0.6400	 0.3690
O	 0.4760	 0.2560
P	 0.5730	 0.3430
Q	 0.6390	 0.3450
R	 0.5380	 0.3170
S	 0.5890	 0.3470
T	 0.5220	 0.2860
U	 0.4300	 0.2430
V	 0.5080	 0.3020
W	 0.5790	 0.3410
X	 0.5970	 0.3600
Y	 0.4410	 0.2310
Z	 0.5720	 0.3550
a	 0.6670	 0.4460

